# REFERENCES

Aronson, L. 1995 HTML3 Manual of Style. United States of America : Macmillan Computer Publishing USA.

Barker, W.C., George, D.G. and Hunt, L.T. 1990. Protein Sequence Database. Methods in Enzymology Vol. 183 : 31-49.

Burks, C., *et al.* 1990. GenBank. Methods in Enzymology Vol. 183 : 3-5.

Elmasri, R., Navathe, S.B. 1994. Fundamentals of Database Systems. California : The Benjamin/Cummings Publishing Company, Inc.

Garrels, J.I. and Franza, B.R. 1989. The REF52 Protein Database. Journal of Biochemical Chemistry Vol. 264, No. 9 : 5283-5298.

Graf, L. and Li, C.H. 1974. Isolation and Properties of Two Biologically Active Fragments from Limited Tryptic Hydrolysis of Bovine and Ovine Pituitary Growth Hormones. Biochemistry Vol. 13, No. 26 : 5408-5415.

Kauzmann, W. 1958. Some factors in the interpretation of protein denaturation, Adv. Protein Chem. Vol. 14 : 1-63.

Kyte, J. and Doolittle, R.F. 1982. A Simple Method for Displaying the Hydropathic Character of a Protein. J. Mol. Biol. Vol. 157 : 105-132.

Orcutt, B.C., George, D.G., Fredrickson, J.A. and Dayhoff, M.O. 1982. Nucleic acid sequence database computer system. Nucleic Acids Research Vol. 10, No. 1 : 157-182.

RFC 821, 1995. The Internet Activity Board : 1-2.

RFC 854, 1995. The Internet Activity Board : 1-2.

Savola, T., Westesbroek, A., Heck, J. 1995. Using HTML. United States of America : Que Corporation.

Schwartz, S.A. 1994. FileMaker Pro 2.0/2.1 Bible. United States of America : IDG Books Worldwide, Inc.

Shobe, M. and Rirchey, T., 1996. JavaScript for Macintosh. United States of America : Hayden Books.

Souza, L.M., *et al.* 1984. Recombinant DNA Technologies to studies on Growth Hormone. The Journal of Experimental Zoology Vol. 232 : 465-473.

Staden, R. 1980. A new computer method for the storage and manipulation of DNA gel reading data. Nucleic Acids Research Vol. 8, No. 16 : 3673-3693.

Stockwell, P.A. 1982. A large database DNA sequence handling program with generalized searching specifications. Nucleic Acids Research Vol. 10, No. 1 : 115-125.

Stryer, L. 1988. Biochemistry. United States of America : W. H. Freeman and company.

Voet, D. and Voet J.G. 1990. Biochemistry. United States of America : John wiley & sons, Inc.

Wiederspan, J. and Shotton, C. 1995. Web Sites on the Macintosh. United States of America : Addison-Wesley Developers Press.

# APPENDIX

# APPENDIX A

## PEPTIDE AND AMINO ACIDS INFORMATION

Appendix A is composed of some properties of standard amino acids and list of all peptide in the database.

**Table A-1** Some properties of standard amino acids

| Standard Amino Acids | MW | $pK_R$ | Charge in Acid Form | Charge in Base Form | Hydropathy |
|---|---|---|---|---|---|
| Ala | 71.0 | | | | 1.8 |
| Arg | 157.2 | 12.48 | 1 | 0 | -4.5 |
| Asn | 114.1 | | | | -3.5 |
| Asp | 114.0 | 3.90 | 0 | -1 | -3.5 |
| Cys | 103.1 | 8.33 | 0 | -1 | 2.5 |
| Gln | 128.1 | | | | -3.5 |
| Glu | 128.1 | 4.07 | 0 | -1 | -3.5 |
| Gly | 57.0 | | | | -0.4 |
| His | 137.1 | 6.04 | 1 | 0 | -3.2 |
| Ile | 113.1 | | | | 4.5 |
| Leu | 113.1 | | | | 3.8 |
| Lys | 129.1 | 10.79 | 1 | 0 | -3.9 |
| Met | 131.1 | | | | 1.9 |
| Phe | 147.1 | | | | 2.8 |
| Pro | 97.1 | | | | -1.6 |
| Ser | 87.0 | | | | -0.8 |
| Thr | 101.1 | | | | -0.7 |
| Trp | 186.2 | | | | -0.9 |
| Tyr | 163.19 | 10.13 | 0 | -1 | -1.3 |
| Val | 9.1 | | | | 4.2 |

**Table A-2** **List of peptides in the CU Peptide Database**

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 1. | ADRENOCORTICOTROPIC HORMONE (ACTH 1-39 ; Corticotropin A) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val-Lys-Val-Tyr-Pro-Asn-Gly-Ala-Glu-Asp-Glu-Ser-Ala-Glu-Ala-Phe-Pro-Leu-Glu-Phe | 39 | Human | | 4540.3 | 9.3455 | -10.3 -9.9 -8.6 -13.3 -11 -7.9 -4.7 -15.9 -10.8 -14.4 -20.1 -12 -10.4 -14.3 -15.2 -12.9 -13.5 -8.4 -2.1 -4 -12.1 -11.3 -16.3 -13.2 -15.1 -9.8 -6.6 -10 -2.7 -2.7 3.6 | A 0423 |
| 2. | ADRENOCORTICOTROPIC HORMONE (ACTH 1-39 ; Corticotropin A) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val-Lys-Val-Tyr-Pro-Asn-Val-Ala-Glu-Asn-Glu-Ser-Ala-Glu-Ala-Phe-Pro-Leu-Glu-Phe | 39 | Rat | | 4582.5 | 9.8846 | -10.3 -9.9 -8.6 -13.3 -11 -7.9 -4.7 -15.9 -10.8 -14.4 -20.1 -12 -10.4 -14.3 -15.2 -12.9 -13.5 -3.8 2.5 .6 -7.5 -6.7 -11.7 -8.6 -10.5 -5.2 -6.6 -10 -2.7 -2.7 3.6 | A 7075 |
| 3. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 1-4) | #1 | Ser-Tyr-Ser-Met | 4 | Human | | 486.2 | 5.7 | | A 2782 |
| 4. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 1-10) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly | 10 | Human | | 1298.9 | 7.602 | -10.3 -9.9 | A 1709 |
| 5. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 1-13) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val | 13 | Human | | 1624.2 | 9.6 | -10.3 -9.9 -8.6 -13.3 -11 | A 5555 |
| 6. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 1-14) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val-Gly | 14 | Human | | 1681.2 | 9.6 | -10.3 -9.9 -8.6 -13.3 -11 -7.9 | A 8804 |
| 7. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 1-16) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys | 16 | Human | | 1939.4 | 10.6464 | -10.3 -9.9 -8.6 -13.3 -11 -7.9 -4.7 -15.9 | A 8929 |
| 8. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 1-17) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys-Arg | 17 | Human | | 2096.6 | 11.1082 | -10.3 -9.9 -8.6 -13.3 -11 -7.9 -4.7 -15.9 -10.8 | A 2407 |
| 9. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 1-24) | #1 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val-Lys-Val-Tyr-Pro | 24 | Human | | 2938.4 | 11.2554 | -10.3 -9.9 -8.6 -13.3 -11 -7.9 -4.7 -15.9 -10.8 -14.4 -20.1 -12 -10.4 -14.3 -15.2 -12.9 | A 0298 |
| 10. | ADRENOCORTICOTROPIC | #1 | Ser-Phe-Ser-Nle-Glu-His-Phe- | 24 | Human | | 2922.5 | | | A 6552 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | HORMONE FRAGMENTS ([Phe2,Nle4]-Fragment 1-24) |  | Arg-Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val-Lys-Val-Tyr-Pro |  |  |  |  |  |  |  |
| 11. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS ([Met(O)4,D-Lys8,Phe9]-Fragment 4-9) | #1 | Met[O]-Glu-His-Phe-D-Lys-Phe | 6 | Human |  | 706.5 |  |  | A 0526 |
| 12. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Tyr-Fragment 4-9) | #1 | Tyr-Met-Glu-His-Phe-Arg-Trp | 7 | Human |  | 1067.9 | 7.557 |  | A 7181 |
| 13. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 4-10) | #1 | Met-Glu-His-Phe-Arg-Trp-Gly | 7 | Human |  | 961.8 | 7.663 |  | A 0401 |
| 14. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Tyr-Fragment 4-10) | #1 | Tyr-Met-Glu-His-Phe-Arg-Trp-Gly | 8 | Human |  | 1124.9 | 7.557 |  | A 9054 |
| 15. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 4-11) | #1 | Met-Glu-His-Phe-Arg-Trp-Gly-Lys | 8 | Human |  | 1090.9 | 10.029 |  | A 7056 |
| 16. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 7-38) | #1 | Phe-Arg-Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val-Lys-Val-Tyr-Pro-Asn-Gly-Ala-Glu-Asp-Glu-Ser-Ala-Glu-Ala-Phe-Pro-Leu-Glu | 32 | Human |  | 3659.8 | 10.0684 | -4.7 -15.9 -10.8 -14.4 -20.1 -12 -10.4 -14.3 -15.2 -12.9 -13.5 -8.4 -2.1 -4 -12.1 -11.3 -16.3 -13.2 -15.1 -9.8 -6.6 -10 -2.7 -2.7 | A 1527 |
| 17. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 11-24) | #1 | Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val-Lys-Val-Tyr-Pro | 14 | Human |  | 1657.5 | 11.8232 | -20.1 -12 -10.4 -14.3 -15.2 -12.9 | A 2532 |
| 18. | ADRENOCORTICOTROPIC HORMONE FRAGMENTS (Fragment 18-39 ; CLIP) | #1 | Arg-Pro-Val-Lys-Val-Tyr-Pro-Asn-Gly-Ala-Glu-Asp-Glu-Ser-Ala-Glu-Ala-Phe-Pro-Leu-Glu-Phe | 22 | Human |  | 2461.7 | 3.86608 | -8.4 -2.1 -4 -12.1 -11.3 -16.3 -13.2 -15.1 -9.8 -6.6 -10 -2.7 -2.7 3.6 | A 0673 |
| 19. | ANGIOTENSIN I (Hypertensin I) | #2 | Asp-Arg-Val-Tyr-Ile-His-Pro-Phe-His-Leu | 10 | Human |  | 1296 | 8.02 | -5.8 1.5 | A 9650 |
| 20. | ANGIOTENSIN I | #2 | Asp-Arg-Val-Tyr-Val-His-Pro-Phe-Asn-Leu | 10 | Bullfrog |  | 1259 | 7.87 | -6.4 .9 | A 3053 |
| 21. | ANGIOTENSIN I | #2 | Asn-Arg-Val-Tyr-Val-His-Pro-Phe-His-Leu | 10 | Goosefish |  | 1282.1 | 9.4845 | -6.1 1.2 | A 3178 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 22. | ANGIOTENSIN I | #2 | Asn-Arg-Val-Tyr-Val-His-Pro-Phe-Asn-Leu | 10 | Salmon | | 1259.1 | 9.484 | -6.4 .9 | A 2928 |
| 23. | ANGIOTENSIN I (des-Asp1-Angiotensin I) | #2 | Arg-Val-Tyr-Ile-His-Pro-Phe-His-Leu | 9 | | | 1182 | 9.5591 | 1.5 | A 5778 |
| 24. | ANGIOTENSIN I ([Val5]-Angiotensin I) | #2 | Asp-Arg-Val-Tyr-Val-His-Pro-Phe-His-Leu | 10 | | | 1282 | 8.02 | -6.1 1.2 | A 9402 |
| 25. | ANGIOTENSIN II | #2 | Asp-Arg-Val-Tyr-Ile-His-Pro-Phe | 8 | Human | | 1045.8 | 7.87 | | A 9525 |
| 26. | ANGIOTENSIN II ((p-Amino-Phe6)-Angiotensin II) | #2 | Asp-Arg-Val-Tyr-Ile-p-Amino-Phe-Pro-Phe | 8 | | | 1070.8 | | | A 1811 |
| 27. | ANGIOTENSIN II ([b-Asp1]-Angiotensin II) | #2 | b-Asp-Arg-Val-Tyr-Ile-His-Pro-Ph | 8 | | | 931.8 | | | A 9410 |
| 28. | ANGIOTENSIN II ([Sar1]-Angiotensin II) | #2 | Sar-Arg-Val-Tyr-Ile-His-Pro-Phe | 8 | | | 1020.9 | | | A 4410 |
| 29. | ANGIOTENSIN II ([Val5]-Angiotensin II) | #2 | Asp-Arg-Val-Tyr-Val-His-Pro-Phe | 8 | | | 1031.8 | 7.87 | | A 2900 |
| 30. | ANGIOTENSIN II ([Asn1,Val5]-Angiotensin II) | #2 | Asn-Arg-Val-Tyr-Val-His-Pro-Phe | 8 | | | 1031.9 | 9.484 | | A 6402 |
| 31. | ANGIOTENSIN II ([Sar1,Ala8]-Angiotensin II) | #2 | Sar-Arg-Val-Tyr-Ile-His-Pro-Ala | 8 | | | 944.8 | | | A 8026 |
| 32. | ANGIOTENSIN II ([Sar1,Gly8]-Angiotensin II) | #2 | Sar-Arg-Val-Tyr-Ile-His-Pro-Gly | 8 | | | 930.8 | | | A 7401 |
| 33. | ANGIOTENSIN II ([Sar1,Ile8]-Angiotensin II) | #2 | Sar-Arg-Val-Tyr-Ile-His-Pro-Ile | 8 | | | 986.9 | | | A 8776 |
| 34. | ANGIOTENSIN II ([Sar1,Leu8]-Angiotensin II) | #2 | Sar-Arg-Val-Tyr-Ile-His-Pro-Leu | 8 | | | 986.9 | | | A 8276 |
| 35. | ANGIOTENSIN II ([Sar1,Thr8]-Angiotensin II) | #2 | Sar-Arg-Val-Tyr-Ile-His-Pro-Thr | 8 | | | 974.9 | | | A 9900 |
| 36. | ANGIOTENSIN II ([Sar1,Val5,Ala8]-Angiotensin II ; Saralasin) | #2 | Sar-Arg-Val-Tyr-Val-His-Pro-Ala | 8 | | | 930.8 | | | A 2275 |
| 37. | ANGIOTENSIN II (Ala-Pro-Gly-[Ile3,Val5]-Angiotensin II) | #2 | Ala-Pro-Gly-Asp-Arg-Ile-Tyr-Val-His-Pro-Phe | 11 | | | 1270.9 | 7.86 | -4 -7.4 -3 | A 0289 |
| 38. | ANGIOTENSIN II FRAGMENT 3-8 | #2 | Val-Tyr-Ile-His-Pro-Phe | 6 | Human | | 774.6 | 7.815 | | A 3950 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | (Angiotensin IV) |  |  |  |  |  |  |  |  |  |
| 39. | ANGIOTENSIN II ANTIPEPTIDE | #2 | Glu-Gly-Val-Tyr-Val-His-Pro-Val | 8 |  |  | 897.7 | 5.059 |  | A 4184 |
| 40. | ANGIOTENSIN III (des-Asp1-Angiotensin II) | #2 | Arg-Val-Tyr-Ile-His-Pro-Phe | 7 |  |  | 931.8 | 9.5588 |  | A 0903 |
| 41. | ANGIOTENSIN III ([Ile7]-Angiotensin III) | #2 | Arg-Val-Tyr-Ile-His-Pro-Ile | 7 |  |  | 897.8 | 9.5588 |  | A 0911 |
| 42. | ANGIOTENSIN III ([Val4]-Angiotensin III) | #2 | Arg-Val-Tyr-Val-His-Pro-Phe | 7 |  |  | 917.8 | 9.5588 |  | A 6277 |
| 43. | ANGIOTENSIN III ([Val4,Ile7]-Angiotensin III) | #2 | Arg-Val-Tyr-Val-His-Pro-Ile | 7 |  |  | 883.8 | 9.5588 |  | A 1036 |
| 44. | ANGIOTENSIN III ANTIPEPTIDE | #2 | Gly-Val-Tyr-Val-His-Pro-Val | 7 |  |  | 769.6 | 7.829 |  | A 4809 |
| 45. | ANGIOTENSIN-CONVERTING ENZYME INHIBITOR | #2 | pGlu-Trp-Pro-Arg-Pro-Gln-Ile-Pro-Pro | 9 |  |  | 1119.1 |  |  | A 0773 |
| 46. | ANGIOTENSINOGEN FRAGMENTS (Fragment 1-13 ; Angiotensinogen 1-13) | #2 | Asp-Arg-Val-Tyr-Ile-His-Pro-Phe-His-Leu-Val-Ile-His | 13 | Human |  | 1645.3 | 8.11 | -5.8 1.5 10.2 10.5 8.6 | A 4057 |
| 47. | ANGIOTENSINOGEN FRAGMENTS (Fragment 11-14) | #2 | Val-Ile-His-Asn | 4 |  |  | 481.4 | 7.89 |  | A 0417 |
| 48. | N-NICOTINOYL-TYR-Ne-(Na-CBZ-ARG)-LYS-HIS-PRO-ILE | #2 | N-Nicotinoyl-Tyr-Ne-(Na-CBZ-Arg)-Lys-His-Pro-Ile | 5 |  |  | 365.3 |  |  | N 5014 |
| 49. | RENIN SUBSTRATE TETRADECAPEPTIDE (Angiotensinogen 1-14) | #2 | Asp-Arg-Val-Tyr-Ile-His-Pro-Phe-His-Leu-Val-Ile-His-Asn | 14 | Human |  | 1759.4 | 8.11 | -5.8 1.5 10.2 10.5 8.6 4.1 | R 5880 |
| 50. | RENIN SUBSTRATE TETRADECAPEPTIDE (Angiotensinogen 1-14) | #2 | Asp-Arg-Val-Tyr-Ile-His-Pro-Phe-His-Leu-Leu-Val-Tyr-Ser | 14 | Porcine |  | 1758.3 | 7.952 | -5.8 1.5 9.8 9.8 9.8 4.5 | R 8380 |
| 51. | N -Acetyl-RENIN SUBSTRATE TETRADECAPEPTIDE | #2 | Acetyl-Asp-Arg-Val-Tyr-Ile-His-Pro-Phe-His-Leu-Val-Ile-His-Asn | 14 | Human |  | 1801.4 |  |  | R 5755 |
| 52. | N -Acetyl-RENIN | #2 | Acetyl-Asp-Arg-Val-Tyr-Ile-His- | 14 | Porcine |  | 1800.3 |  |  | R 5380 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | SUBSTRATE TETRADECAPEPTIDE |  | **Pro**-Phe-His-Leu-Leu-Val-Tyr-Ser |  |  |  |  |  |  |  |
| 53. | ATRIAL NATRIURETIC PEPTIDE | #3 | **Met**-Met-Arg-Asp-Ser-Gly-Cys-**Phe**-Gly-Arg-Arg-Ile-Asp-Arg-Ile-**Gly**-Ser-Leu-Ser-Gly-Met-Gly-**Cys**-Asn-Gly-Ser-Arg-Lys-Asn | 29 | Chicken | 7-23 | 3165.2 | 11.243 | -.5 -2.4 -13.3 -4.3 -.8 -3.5 -3.1 -6 -9.6 -5.4 -1.7 2.4 -.2 2.9 9.9 5.4 1.9 1.9 -1.9 -5.6 -9.1 | A 9052 |
| 54. | ATRIAL NATRIURETIC PEPTIDE (fANP-24) | #3 | **Ser**-Ser-Asp-Cys-Phe-Gly-Ser-**Arg**-Ile-Asp-Arg-Ile-Gly-Ala-Gln-**Ser**-Gly-Met-Gly-Cys-Gly-Arg-Arg **Phe** | 24 | Frog | 4-20 | 2564.6 | 8.9751 | -1 -.2 -6.4 .6 -2.3 -3.3 -6.4 -6.4 -2.3 -4.9 -1.8 5.2 .3 .7 -5.6 -3.8 | A 0929 |
| 55. | ATRIAL NATRIURETIC PEPTIDE (Fragment 4-24 ; fANP-21) | #3 | **Cys**-Phe-Gly-Ser-Arg-Ile-Asp-Arg-**Ile**-Gly-Ala-Gln-Ser-Gly-Met-Gly-**Cys**-Gly-Arg-Arg-Phe | 21 | Frog | 4-20 | 2276.6 | 11.2854 | .6 -2.3 -3.3 -6.4 -6.4 -2.3 -4.9 -1.8 5.2 .3 .7 -5.6 -3.8 | A 0804 |
| 56. | ATRIAL NATRIURETIC PEPTIDE | #3 | **Ser**-Leu-Arg-Arg-Ser-Ser-Cys-**Phe**-Gly-Gly-Arg-Met-Asp-Arg-Ile-**Gly**-Ala-Gln-Ser-Gly-Leu-Gly-Cys-**Asn**-Ser-Phe-Arg-Tyr | 28 | Human | 7-23 | 3085.1 | 10.967 | -2.7 -2.3 -10.6 -4.2 .3 -2.4 -1.6 -4.5 -5.5 -8.6 -9 -4.9 -3 .1 7.1 2.6 -1.3 -.3 3.2 -1.8 | A 1663 |
| 57. | ATRIAL NATRIURETIC PEPTIDE (rANP) | #3 | **Ser**-Leu-Arg-Arg-Ser-Ser-Cys-**Phe**-Gly-Gly-Arg-Ile-Asp-Arg-Ile-**Gly**-Ala-Gln-Ser-Gly-Leu-Gly-Cys-**Asn**-Ser-Phe-Arg-Tyr | 28 | Rat | 7-23 | 3067.1 | 10.967 | -2.7 -2.3 -10.6 -1.6 2.9 .2 1 -1.9 -2.9 -6 -6.4 -2.3 -3 .1 7.1 2.6 -1.3 -.3 3.2 -1.8 | A 2288 |
| 58. | ATRIAL NATRIURETIC PEPTIDE (des-(Gln18,Ser19,Gly20,Leu21,Gly22)-Fragment 4-23 Amide) | #3 | **Arg**-Ser-Ser-Cys-Phe-Gly-Gly-**Arg**-Ile-Asp-Arg-Ile-Gly-Ala-Cys-**NH2** | 15 | Rat | 7-23 | 1615.1 | 12.1795 | -1.6 2.9 .2 1 -1.9 -2.9 0 -4.1 | A 1802 |
| 59. | ISO-ATRIAL NATRIURETIC PEPTIDE (Iso-rANP) | #3 | **Ser**-Gln-Asp-Ser-Ala-Glu-Arg-Ile-**Gln**-Glu-Arg-Leu-Arg-Asn-Ser-**Lys**-Met-Ala-His-Ser-Ser-Ser-Cys-**Phe**-Gly-Gln-Lys-Ile-Asp-Arg-Ile-**Gly**-Ala-Val-Ser-Arg-Leu-Gly-Cys-**Asp**-Gly-Leu-Arg-Gln-Phe | 45 | Rat | 23-39 | 5040.4 | 9.8767 | -13.8 -16.5 -16.5 -10.2 -9.4 -15.7 -16.5 -12 -18.5 -13.2 -12.9 -9.2 -13.8 -10.1 -4.1 -.5 3 -2.4 -4.2 -.4 .4 -2.3 -1.5 -4.4 -5.4 -.8 1.9 5.8 .6 3.7 10.7 6.2 2.7 4.7 .5 -6.7 .6 | A 9179 |
| 60. | [deamino-Cys3,D-Ala5]-ATRIOPEPTIN III FRAGMENT 3-24 AMIDE | #3 | **3-Mercaptopropionyl**-Phe-D-Ala-**Gly**-Arg-Ile-Asp-Arg-Ile-Gly-Ala-**Gln**-Ser-Gly-Leu-Gly-Cys-Asn- | 21 | Rat | 3-19 | 2394.6 |  |  | A 7171 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  | Ser-Phe-Arg-Tyr-NH2 |  |  |  |  |  |  |  |
| 61. | URODILATIN (Thr-Ala-Pro-Arg-Arial Natriuretic Peptide | #3 | Thr-Ala-Pro-Arg-Ser-Leu-Arg-Arg-Ser-Ser-Cys-Phe-Gly-Gly-Arg-Met-Asp-Arg-Ile-Gly-Ala-Gln-Ser-Gly-Leu-Gly-Cys-Asn-Ser-Phe-Arg-Tyr | 32 | Human | 11-27 | 3511.5 | 11.7934 | -11.8 -11.9 -11.2 -6.8 -2.7 -2.3 -10.6 -4.2 .3 -2.4 -1.6 -4.5 -5.5 -8.6 -9 -4.9 -3 .1 7.1 2.6 -1.3 -.3 3.2 -1.8 | U 5754 |
| 62. | BRADYKININ | #4 | Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 9 |  |  | 1061.9 | 12.4802 | -9.4 | B 3259 |
| 63. | Ile-Ser-BRADYKININ (T-Kinin) | #4 | Ile-Ser-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 11 |  |  | 1262 | 12.4816 | -4 -5.7 -9.4 | B 1643 |
| 64. | Lys-BRADYKININ (Kallidin) | #4 | Lys-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 10 |  |  | 1191 | 12.4971 | -8.8 -9.4 | B 4889 |
| 65. | Lys-[Ala3]-BRADYKININ | #4 | Lys-Arg-Pro-Ala-Gly-Phe-Ser-Pro-Phe-Arg | 10 |  |  | 1164.9 | 12.4971 | -5.4 -6 | B 1525 |
| 66. | Met-Lys-BRADYKININ | #4 | Met-Lys-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 11 |  |  | 1322.1 | 12.4972 | -9.7 -8.8 -9.4 | B 5014 |
| 67. | Tyr-BRADYKININ | #4 | Tyr-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 10 |  |  | 1225 | 11.167 | -6.2 -9.4 | B 4764 |
| 68. | [Hyp3]-BRADYKININ | #4 | Arg-Pro-Hyp-Gly-Phe-Ser-Pro-Phe-Arg | 9 |  |  | 1077.9 |  |  | B 7775 |
| 69. | [Lys1]-BRADYKININ | #4 | Lys-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 9 |  |  | 1033.8 | 11.642 | -8.2 | B 0890 |
| 70. | [D-Phe7]-BRADYKININ | #4 | Arg-Pro-Pro-Gly-Phe-Ser-D-Phe-Phe-Arg | 9 |  |  | 1111.9 | 12.4802 | -10.6 -1.6 | B 7894 |
| 71. | [Thr6]-BRADYKININ | #4 | Arg-Pro-Pro-Gly-Phe-Thr-Pro-Phe-Arg | 9 |  |  | 1076 | 12.4802 | -9.3 | B 1400 |
| 72. | [Tyr8]-BRADYKININ | #4 | Arg-Pro-Pro-Gly-Phe-Ser-Pro-Tyr-Arg | 9 |  |  | 1077.9 | 11.162 | -13.5 | B 7885 |
| 73. | [p-Cl-Phe5,8]-BRADYKININ | #4 | Arg-Pro-Pro-Gly-p-Chloro-Phe-Ser-Pro-p-Chloro-Phe-Arg | 9 |  |  | 1130.9 |  |  | B 1776 |
| 74. | D-Arg,[Hyp3,D-Phe7]-BRADYKININ | #4 | D-Arg-Arg-Pro-Hydroxy-Pro-Gly-Phe-Ser-D-Phe-Phe-Arg | 10 |  |  | 1285.1 |  |  | B 1775 |
| 75. | [Thi5,8,D-Phe7]-BRADYKININ | #4 | Arg-Pro-Pro-Gly-b-[2-Thienyl]Ala-Ser-D-Phe-b-[2-Thienyl]Ala-Arg | 9 |  |  | 817.7 |  |  | B 8144 |
| 76. | D-Arg,[Hyp3,Thi5,8,D-Phe7] | #4 | D-Arg-Arg-Pro-Hydroxy-Pro-Gly- | 10 |  |  | 990.9 |  |  | B 1650 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | -BRADYKININ |  | b-[2-Thienyl]Ala-Ser-D-Phe-b-[2-Thienyl]Ala-Arg |  |  |  |  |  |  |  |
| 77. | Na-Adamantaneacetyl-D-Arg-[Hyp3,Thi5,8,D-Phe7]-BRADYKININ | #4 | Na-Adamantaneacetyl-D-Arg-Arg-Pro-Hydroxy-Pro-Gly-b-[2-Thienyl]Ala-Ser-D-Phe-b-[2-Thienyl]Ala-Arg | 10 |  |  | 833.7 |  |  | B 6029 |
| 78. | BRADYKININ FRAGMENTS (Fragment 1-5) | #4 | Arg-Pro-Pro-Gly-Phe | 5 |  |  | 573.5 | 10.736 |  | B 1401 |
| 79. | BRADYKININ FRAGMENTS (Fragment 1-6) | #4 | Arg-Pro-Pro-Gly-Phe-Ser | 6 |  |  | 660.5 | 10.736 |  | B 1526 |
| 80. | BRADYKININ FRAGMENTS (Fragment 1-7) | #4 | Arg-Pro-Pro-Gly-Phe-Ser-Pro | 7 |  |  | 757.6 | 10.736 |  | B 1651 |
| 81. | BRADYKININ FRAGMENTS (Fragment 2-7) | #4 | Pro-Pro-Gly-Phe-Ser-Pro | 6 |  |  | 600.4 | 6.9 |  | B 2151 |
| 82. | des-Arg1-BRADYKININ | #4 | Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 8 |  |  | 904.7 | 11.565 |  | B 1901 |
| 83. | des-Pro2-BRADYKININ | #4 | Arg-Pro-Gly-Phe-Ser-Pro-Phe-Arg | 8 |  |  | 964.8 | 12.4802 |  | B 2026 |
| 84. | des-Arg9-BRADYKININ | #4 | Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe | 8 |  |  | 904.7 | 10.736 |  | B 4397 |
| 85. | des-Arg9,[Leu8]-BRADYKININ | #4 | Arg-Pro-Pro-Gly-Phe-Ser-Pro-Leu | 8 |  |  | 870.7 | 10.736 |  | B 6769 |
| 86. | BRADYKININ POTENTIATOR B | #4 | pGlu-Gly-Leu-Pro-Pro-Arg-Pro-Lys-Ile-Pro-Pro | 11 |  |  | 1201.1 |  |  | B 0507 |
| 87. | BRADYKININ POTENTIATOR C | #4 | pGlu-Gly-Leu-Pro-Pro-Gly-Pro-Pro-Ile-Pro-Pro | 11 |  |  | 1068.9 |  |  | B 0632 |
| 88. | pGLU-LYS-TRP-ALA-PRO | #4 | pGlu-Lys-Trp-Ala-Pro | 5 |  |  | 629.5 |  |  | P 8772 |
| 89. | VAL-GLU-SER-SER-LYS | #4 | Val-Glu-Ser-Ser-Lys | 5 |  |  | 548.3 | 6.9 |  | V 6128 |
| 90. | N-ACETYL-MET-LEU-PHE | #5 | Acetyl-Met-Leu-Phe | 3 |  |  | 278.2 |  |  | A 4536 |
| 91. | ALA-GLY-SER-GLU | #5 | Ala-Gly-Ser-Glu | 4 |  |  | 361.1 | 3.085 |  | A 5902 |
| 92. | N-t-BOC-MET-LEU-PHE | #5 | N-t-BOC-Met-Leu-Phe | 3 |  |  | 278.2 |  |  | B 0511 |
| 93. | N-t-BOC-NLE-LEU-PHE | #5 | N-t-BOC-Nle-Leu-Phe | 3 |  |  | 278.2 |  |  | B 3886 |
| 94. | N-t-BOC-PHE-D-LEU-PHE-D-LEU-PHE | #5 | N-t-BOC-Phe-D-Leu-Phe-D-Leu-Phe | 5 |  |  | 538.4 |  |  | B 2386 |
| 95. | N-t-BOC-PHE-LEU-PHE-LEU-PHE | #5 | N-t-BOC-Phe-Leu-Phe-Leu-Phe | 5 |  |  | 538.4 |  |  | B 5639 |
| 96. | N-FORMYL-ALA-GLY-SER- | #5 | Formyl-Ala-Gly-Ser-Glu | 4 |  |  | 389.1 |  |  | F 8631 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | GLU | | | | | | | | | |
| 97. | N-FORMYL-MET-ALA | #5 | Formyl-Met-Ala | 2 | | | 248.1 | | | F 8502 |
| 98. | N-FORMYL-MET-LEU-p-IODO-PHE | #5 | Formyl-Met-Leu-p-Iodo-Phe | 3 | | | 563.2 | | | F 6882 |
| 99. | N-FORMYL-MET-LEU-PHE (Chemotactic peptide) | #5 | Formyl-Met-Leu-Phe | 3 | | | 437.3 | | | F 3506 |
| 100. | N-FORMYL-MET-LEU-PHE BENZYLAMIDE | #5 | Formyl-Met-Leu-Phe Benzylamide | 3 | | | 290.2 | | | F 9758 |
| 101. | N-FORMYL-MET-LEU-PHE BENZYL ESTER | #5 | Formyl-Met-Leu-Phe Benzyl Ester | 3 | | | 290.2 | | | F 6758 |
| 102. | N-FORMYL-MET-LEU-PHE-o-FLUOROBENZYLAMIDE | #5 | Formyl-Met-Leu-Phe-o-Fluorobenzylamide | 3 | | | 290.2 | | | F 0762 |
| 103. | N-FORMYL-MET-LEU-PHE-m-FLUOROBENZYLAMIDE | #5 | Formyl-Met-Leu-Phe-m-Fluorobenzylamide | 3 | | | 290.2 | | | F 0887 |
| 104. | N-FORMYL-MET-LEU-PHE-p-FLUOROBENZYLAMIDE | #5 | Formyl-Met-Leu-Phe-p-Fluorobenzylamide | 3 | | | 290.2 | | | F 1012 |
| 105. | N-FORMYL-MET-LEU-PHE-LYS | #5 | Formyl-Met-Leu-Phe-Lys | 4 | | | 566.4 | | | F 2385 |
| 106. | N-FORMYL-MET-LEU-PHE METHYL ESTER | #5 | Formyl-Met-Leu-Phe-OMe | 3 | | | 290.2 | | | F 6632 |
| 107. | N-FORMYL-MET-LEU-PHE-PHE | #5 | Formyl-Met-Leu-Phe-Phe | 4 | | | 584.4 | | | F 2009 |
| 108. | N-FORMYL-MET-LEU-TYR | #5 | Formyl-Met-Leu-Tyr | 3 | | | 453.3 | | | F 5256 |
| 109. | N-FORMYL-MET-MET-MET | #5 | Formyl-Met-Met-Met | 3 | | | 439.3 | | | F 2635 |
| 110. | N-FORMYL-MET-PHE (Neutrophil Dysfunction Test Peptide) | #5 | Formyl-Met-Phe | 2 | | | 324.2 | | | F 8506 |
| 111. | N-FORMYL-MET-PHE-MET | #5 | Formyl-Met-Phe-Met | 3 | | | 455.3 | | | F 2510 |
| 112. | N-FORMYL-MET-TRP | #5 | Formyl-Met-Trp | 2 | | | 363.3 | | | F 6128 |
| 113. | N-FORMYL-MET-VAL | #5 | Formyl-Met-Val | 2 | | | 276.2 | | | F 5003 |
| 114. | N-FORMYL-NLE-LEU-PHE | #5 | Formyl-Nle-Leu-Phe | 3 | | | 278.2 | | | F 3631 |
| 115. | N-FORMYL-NLE-LEU-PHE-3,5-DIIODO-TYR | #5 | Formyl-Nle-Leu-Phe-3,5-Diiodo-Tyr | 4 | | | 693.1 | | | F 2259 |
| 116. | N-FORMYL-NLE-LEU-PHE | #5 | Formyl-Nle-Leu-Phe-OMe | 3 | | | 131.1 | | | F 1760 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | METHYL ESTER |  |  |  |  |  |  |  |  |  |
| 117. | N-FORMYL-NLE-LEU-PHE-NLE-TYR-LYS | #5 | **Formyl**-Nle-Leu-Phe-Nle-Tyr-Lys | 6 |  |  | 701.6 |  |  | F 0267 |
| 118. | N-FORMYL-NLE-LEU-PHE-TYR | #5 | **Formyl**-Nle-Leu-Phe-Tyr | 4 |  |  | 441.3 |  |  | F 2134 |
| 119. | ILE-VAL-PRO-PHE-LEU-GLY-PRO-LEU-LEU-GLY-LEU-LEU-THR-AMIDE | #5 | **Ile**-Val-Pro-Phe-Leu-Gly-Pro-Leu-Leu-Gly-Leu-Leu-Thr-NH2 | 13 |  |  | 1368.1 | 14 | 19.3 14.4 14 19.4 15.9 12.1 | I 3516 |
| 120. | MET-LEU-PHE | #5 | **Met**-Leu-Phe | 3 |  |  | 409.3 | 5.7 |  | M 6014 |
| 121. | VAL-GLY-ASP-GLU | #5 | **Val**-Gly-Asp-Glu | 4 |  |  | 416.2 | 2.8707 |  | V 6253 |
| 122. | VAL-GLY-SER-GLU | #5 | **Val**-Gly-Ser-Glu | 4 |  |  | 389.2 | 3.085 |  | V 8878 |
| 123. | VAL-GLY-VAL-ALA-PRO-GLY | #5 | **Val**-Gly-Val-Ala-Pro-Gly | 6 |  |  | 498.3 | 6 |  | V 1008 |
| 124. | DYNORPHIN A | #6 | **Tyr**-Gly-Gly-Phe-Leu-Arg-Arg-Ile-Arg-Pro-Lys-Leu-Lys-Trp-Asp-Asn-Gln | 17 | Porcine |  | 2150.8 | 11.5658 | 0 -4.8 -4.4 -4.1 -6.9 -15.5 -15.5 -10 -21.5 | D 8147 |
| 125. | DYNORPHIN A FRAGMENTS (Fragment 1-7) | #6 | **Tyr**-Gly-Gly-Phe-Leu-Arg-Arg | 7 | Porcine |  | 869.7 | 11.167 |  | D 4524 |
| 126. | DYNORPHIN A FRAGMENTS (Fragment 1-8) | #6 | **Tyr**-Gly-Gly-Phe-Leu-Arg-Arg-Ile | 8 | Porcine |  | 982.8 | 11.167 |  | D 4899 |
| 127. | DYNORPHIN A FRAGMENTS (Fragment 1-9) | #6 | **Tyr**-Gly-Gly-Phe-Leu-Arg-Arg-Ile-Arg | 9 | Porcine |  | 1140 | 12.1852 | 0 | D 4036 |
| 128. | DYNORPHIN A FRAGMENTS (Fragment 1-10) | #6 | **Tyr**-Gly-Gly-Phe-Leu-Arg-Arg-Ile-Arg-Pro | 10 | Porcine |  | 1237.1 | 12.1852 | 0 -4.8 | D 4774 |
| 129. | DYNORPHIN A FRAGMENTS (Fragment 1-13) | #6 | **Tyr**-Gly-Gly-Phe-Leu-Arg-Arg-Ile-Arg-Pro-Lys-Leu-Lys | 13 | Porcine |  | 1608.4 | 12.2294 | 0 -4.8 -4.4 -4.1 -6.9 | D 7017 |
| 130. | DYNORPHIN A FRAGMENTS ([D-Arg6]-Fragment 1-13) | #6 | **Tyr**-Gly-Gly-Phe-Leu-D-Arg-Arg-Ile-Arg-Pro-Lys-Leu-Lys | 13 | Porcine |  | 1608.4 | 11.6658 | 4.5 5.8 6.2 6.6 3.8 | D 9148 |
| 131. | DYNORPHIN A | #6 | **Tyr**-Gly-Gly-Phe-Leu-Arg-Arg-D- | 13 | Porcine |  | 1652.5 | 12.2294 | -4.5 -3.2 -2.8 -2.4 -5.2 -13.5 | D 9783 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | FRAGMENTS ([D-Arg8]-Fragment 1-13) |  | Arg-Arg-Pro-Lys-Leu-Lys |  |  |  |  |  |  |  |
| 132. | DYNORPHIN A FRAGMENTS (Fragment 2-13) | #6 | Gly-Gly-Phe-Leu-Arg-Arg-Ile-Arg-Pro-Lys-Leu-Lys | 12 | Porcine |  | 1445.3 | 12.7945 | -4.8 -4.4 -4.1 -6.9 | D 4399 |
| 133. | DYNORPHIN B (Rimorphin ; Prodynorphin 228-240) | #6 | Tyr-Gly-Gly-Phe-Leu-Arg-Arg-Gln Phe-Lys-Val-Val-Thr | 13 | Porcine |  | 1573.3 | 11.523 | -5.2 -3.9 -3.2 1.4 -2.1 | D 1398 |
| 134. | TYR-GLY-GLY-PHE-LEU-ARG-ARG-ILE-ARG-PRO-ARG-LEU-ARG-GLY 5-AMINOPENTYLAMIDE (Dynorphin A analog k ligand ; DAKLI) | #6 | Tyr-Gly-Gly-Phe-Leu-Arg-Arg-Ile-Arg-Pro-Arg-Leu-Arg-Gly 5-Aminopentylamide | 14 |  |  | 1664.6 |  |  | T 7908 |
| 135. | N-t-BOC-TYR-GLY-GLY-PHE-LEU-ARG-ARG-ILE-ARG-PRO-ARG-LEU-ARG-GLY 5-AMINOPENTYLAMIDE (BOC-DAKLI) | #6 | N-t-BOC-Tyr-Gly-Gly-Phe-Leu-Arg-Arg-Ile-Arg-Pro-Arg-Leu-Arg-Gly 5-Aminopentylamide | 14 |  |  | 1501.5 |  |  | B 5277 |
| 136. | a-ENDORPHIN (b-Lipotropin 61-76) | #7 | Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr | 16 | Human |  | 1745.2 | 6.57 | -2.4 -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 | E 6136 |
| 137. | b-ENDORPHIN (b-Lipotropin 61-91) | #7 | Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-His-Lys-Lys-Gly-Gln | 31 | Bovine, Camel, Ovine |  | 3440.4 | 10.69859 | -2.4 -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 .6 7.3 8.1 7.7 6.7 12.8 13.5 9.3 6.1 .6 -5.4 -5 -1.9 -8 -16 | E 0637 |
| 138. | b-ENDORPHIN (b-Lipotropin 61-91) | #7 | Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-Tyr-Lys-Lys-Gly-Glu | 31 | Human |  | 3466.4 | 10.1913 | -2.4 -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 .6 7.3 8.1 7.7 6.7 12.8 13.5 9.3 6.1 .6 -3.5 -3.1 0 -6.1 -14.1 | E 6261 |
| 139. | b-ENDORPHIN (b-Lipotropin 61-91) | #7 | Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Val-His-Lys-Lys-Gly-Gln | 31 | Rat |  | 3468.5 | 10.69859 | -2.4 -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 .6 7.3 8.1 7.7 6.7 12.8 13.5 9.3 6.1 3 -3 -2.6 .5 -5.6 -13.6 | E 1142 |
| 140. | N-Ac-b-ENDORPHIN | #7 | Acetyl-Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu- | 31 | Human |  | 3303.3 |  |  | A 1660 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-Tyr-Lys-Lys-Gly-Glu | | | | | | | |
| 141. | Arg-b-ENDORPHIN | #7 | Arg-Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-Tyr-Lys-Lys-Gly-Glu | 32 | Human | | 3623.6 | 10.47869 | -6.9 -2.4 -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 .6 7.3 8.1 7.7 6.7 12.8 13.5 9.3 6.1 .6 -3.5 -3.1 0 -6.1 -14.1 | E 7638 |
| 142. | BIOCYTIN-b-ENDORPHIN | #7 | Ne-Biotinyl-Lys-Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-Tyr-Lys-Lys-Gly-Glu | 32 | Human | | 3466.4 | | | E 8139 |
| 143. | [Leu5]-b-ENDORPHIN | #7 | Tyr-Gly-Gly-Phe-Leu-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-Tyr-Lys-Lys-Gly-Glu | 31 | Human | | 3448.4 | 10.1913 | -.5 -3.9 -7 -7.3 -11.7 -11.7 -6.8 -6.7 .6 7.3 8.1 7.7 6.7 12.8 13.5 9.3 6.1 .6 -3.5 -3.1 0 -6.1 -14.1 | E 3130 |
| 144. | N-Ac-b-ENDORPHIN (Fragment 1-27) | #7 | Acetyl-Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-Tyr | 27 | Human | | 2860 | | | E 0762 |
| 145. | b-ENDORPHIN (Fragment 1-27) | #7 | Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu-Phe-Lys-Asn-Ala-Ile-Ile-Lys-Asn-Ala-Tyr | 27 | Human | | 3023.1 | 9.9271 | -2.4 -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 .6 7.3 8.1 7.7 6.7 12.8 13.5 9.3 6.1 .6 -3.5 | E 6636 |
| 146. | g-ENDORPHIN (b-Lipotropin 61-77) | #7 | Tyr-Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu | 17 | | | 1858.3 | 6.57 | -2.4 -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 .6 | E 6386 |
| 147. | des-Tyr1-g-ENDORPHIN (b-Lipotropin 62-77) | #7 | Gly-Gly-Phe-Met-Thr-Ser-Glu-Lys-Ser-Gln-Thr-Pro-Leu-Val-Thr-Leu | 16 | | | 1695.2 | 6.9 | -5.8 -8.9 -9.2 -13.6 -11.7 -6.8 -6.7 .6 | E 3005 |
| 148. | b-LIPOTROPIN FRAGMENTS (Fragment 1-10) | #7 | Glu-Leu-Ala-Gly-Ala-Pro-Pro-Glu-Pro-Ala | 10 | Porcine | | 948.6 | 3.0382 | -4.8 .5 | L 5261 |
| 149. | b-LIPOTROPIN FRAGMENTS (Fragment | #7 | Asn-Ala-Gly-Ala | 4 | Human | | 331.1 | 5.6 | | L 5894 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | 14-17) |  |  |  |  |  |  |  |  |  |
| 150. | b-LIPOTROPIN FRAGMENTS (Fragment 39-45) | #7 | Lys-Lys-Asp-Ser-Gly-Pro-Tyr | 7 |  |  | 794.4 | 9.5335 |  | L 2759 |
| 151. | b-LIPOTROPIN FRAGMENTS (Fragment 88-91) | #7 | Lys-Lys-Gly-Glu | 4 | Human |  | 461.3 | 9.8104 |  | L 0134 |
| 152. | a-NEOENDORPHIN | #7 | Tyr-Gly-Gly-Phe-Leu-Arg-Lys-Tyr-Pro-Lys | 10 |  |  | 1230.9 | 10.47579 | -6.8 -5.5 | N 9633 |
| 153. | b-NEOENDORPHIN | #7 | Tyr-Gly-Gly-Phe-Leu-Arg-Lys-Tyr-Pro | 9 |  |  | 1101.8 | 10.0723 | -6.8 | N 9758 |
| 154. | TYR-GLY-GLY-PHE-LEU-ARG-LYS-ARG ([Arg8]-a-Neoendorphin 1-8) | #7 | Tyr-Gly-Gly-Phe-Leu-Arg-Lys-Arg | 8 |  |  | 998.8 | 11.523 |  | T 5765 |
| 155. | LEUCINE ENKEPHALIN | #8 | Tyr-Gly-Gly-Phe-Leu | 5 |  |  | 555.3 | 5.7 |  | L 9133 |
| 156. | [3,5-DiBr-Tyr1]-LEUCINE ENKEPHALIN | #8 | 3,5-Dibromo-Tyr-Gly-Gly-Phe-Leu | 5 |  |  | 713.1 |  |  | E 8257 |
| 157. | [D-Ala2]-LEUCINE ENKEPHALIN | #8 | Tyr-D-Ala-Gly-Phe-Leu | 5 |  |  | 569.3 | 5.7 |  | E 5008 |
| 158. | [Ala2]-LEUCINE ENKEPHALIN | #8 | Tyr-Ala-Gly-Phe-Leu | 5 |  |  | 569.3 | 5.7 |  | E 1892 |
| 159. | [D-Ala2,D-Leu5]-ENKEPHALIN | #8 | Tyr-D-Ala-Gly-Phe-D-Leu | 5 |  |  | 569.3 | 5.7 |  | E 7131 |
| 160. | [D-Ala2]-LEUCINE ENKEPHALIN-Arg (Dalargin) | #8 | Tyr-D-Ala-Gly-Phe-Leu-Arg | 6 |  |  | 726.5 | 9.6183 |  | E 1766 |
| 161. | des-Tyr1-LEUCINE ENKEPHALIN | #8 | Gly-Gly-Phe-Leu | 4 |  |  | 392.2 | 6 |  | E 7255 |
| 162. | des-Tyr1,[D-Ala2,D-Leu5]-ENKEPHALIN | #8 | D-Ala-Gly-Phe-D-Leu | 4 |  |  | 406.2 | 0 |  | E 5390 |
| 163. | LEUCINE ENKEPHALIN-Arg (Dynorphin A Fragment 1-6) | #8 | Tyr-Gly-Gly-Phe-Leu-Arg | 6 |  |  | 712.5 | 9.6183 |  | E 8757 |
| 164. | LEUCINE ENKEPHALIN-Lys | #8 | Tyr-Gly-Gly-Phe-Leu-Lys | 6 |  |  | 684.4 | 9.554 |  | E 0134 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 165. | [D-Ser2]-LEUCINE ENKEPHALIN-Thr | #8 | Tyr-D-Ser-Gly-Phe-Leu-Thr | 6 | | | 686.4 | 5.6 | | E 7388 |
| 166. | [D-Thr2]-LEUCINE ENKEPHALIN-Thr | #8 | Tyr-D-Thr-Gly-Phe-Leu-Thr | 6 | | | 700.5 | 5.6 | | E 0139 |
| 167. | [3,5-DiI-Tyr1,D-Thr2]-LEUCINE ENKEPHALIN-Th | #8 | 3,5-Diiodo-Tyr-D-Thr-Gly-Phe-Leu-Thr | 6 | | | 952.3 | | | E 8884 |
| 168. | LEUCINE ENKEPHALINAMIDE | #8 | Tyr-Gly-Gly-Phe-Leu-NH2 | 5 | | | 571.3 | 9.62 | | E 3756 |
| 169. | [D-Ala2]-LEUCINE ENKEPHALINAMIDE | #8 | Tyr-D-Ala-Gly-Phe-Leu-NH2 | 5 | | | 585.3 | 9.62 | | E 3381 |
| 170. | [D-Ala2,D-Leu5]-ENKEPHALINAMIDE | #8 | Tyr-D-Ala-Gly-Phe-D-Leu-NH2 | 5 | | | 585.3 | | | E 7756 |
| 171. | des-Tyr1-LEUCINE ENKEPHALINAMIDE | #8 | Gly-Gly-Phe-Leu-NH2 | 4 | | | 408.2 | 14 | | E 3506 |
| 172. | des-Tyr1,[D-Ala2]-LEUCINE ENKEPHALINAMIDE | #8 | D-Ala-Gly-Phe-Leu-NH2 | 4 | | | 422.2 | 1 | | E 5256 |
| 173. | METHIONINE ENKEPHALIN | #8 | Tyr-Gly-Gly-Phe-Met | 5 | | | 573.3 | 5.6 | | M 6638 |
| 174. | [D-Ala2]-METHIONINE ENKEPHALIN | #8 | Tyr-D-Ala-Gly-Phe-Met | 5 | | | 587.3 | 5.6 | | E 2757 |
| 175. | [Ala2]-METHIONINE ENKEPHALIN | #8 | Tyr-Ala-Gly-Phe-Met | 5 | | | 587.3 | 5.6 | | E 3757 |
| 176. | [Met(O)5]-ENKEPHALIN (Methionine-enkephalin sulfoxide) | #8 | Tyr-Gly-Gly-Phe-Met[O] | 5 | | | 442.2 | | | E 7133 |
| 177. | [D-Trp2]-METHIONINE ENKEPHALIN | #8 | Tyr-D-Trp-Gly-Phe-Met | 5 | | | 702.5 | 5.6 | | E 2882 |
| 178. | [D-Ala2,3]-METHIONINE ENKEPHALIN | #8 | Tyr-D-Ala-D-Ala-Phe-Met | 5 | | | 601.3 | 5.6 | | E 5631 |
| 179. | [D-Ala2,D-Met5]-ENKEPHALIN | #8 | Tyr-D-Ala-Gly-Phe-D-Met | 5 | | | 587.3 | 5.6 | | E 3507 |
| 180. | des-Met5-METHIONINE ENKEPHALIN | #8 | Tyr-Gly-Gly-Phe | 4 | | | 442.2 | 5.6 | | E 2628 |
| 181. | des-Tyr1-METHIONINE ENKEPHALIN | #8 | Gly-Gly-Phe-Met | 4 | | | 410.2 | 6 | | E 2256 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 182. | des-Tyr1,[D-Ala2,D-Met5]-ENKEPHALIN | #8 | **D-Ala**-Gly-Phe-D-Met | 4 | | | 424.2 | 0 | | E 3632 |
| 183. | METHIONINE ENKEPHALIN-Arg-Phe | #8 | **Tyr**-Gly-Gly-Phe-Met-Arg-Phe | 7 | | | 877.6 | 9.6183 | | E 5757 |
| 184. | METHIONINE ENKEPHALIN-Arg-Gly-Leu | #8 | **Tyr**-Gly-Gly-Phe-Met-Arg-Gly-Leu | 8 | | | 900.6 | 9.6183 | | E 6515 |
| 185. | METHIONINE ENKEPHALIN-Lys | #8 | **Tyr**-Gly-Gly-Phe-Met-Lys | 6 | | | 702.4 | 9.554 | | E 1760 |
| 186. | METHIONINE ENKEPHALINAMIDE | #8 | **Tyr**-Gly-Gly-Phe-Met-NH2 | 5 | | | 589.3 | 9.62 | | E 5381 |
| 187. | [D-Ala2]-METHIONINE ENKEPHALINAMIDE | #8 | **Tyr**-D-Ala-Gly-Phe-Met-NH2 | 5 | | | 603.3 | 9.62 | | E 2006 |
| 188. | [Ala2]-METHIONINE ENKEPHALINAMIDE | #8 | **Tyr**-Ala-Gly-Phe-Met-NH2 | 5 | | | 603.3 | 9.62 | | E 3382 |
| 189. | [D-Trp2]-METHIONINE ENKEPHALINAMIDE | #8 | **Tyr**-D-Trp-Gly-Phe-Met-NH2 | 5 | | | 718.5 | 9.62 | | E 3007 |
| 190. | [D-Ala2,3]-METHIONINE ENKEPHALINAMIDE | #8 | **Tyr**-D-Ala-D-Ala-Phe-Met-NH2 | 5 | | | 617.3 | 9.62 | | E 9881 |
| 191. | [D-Ala2,D-Met5]-ENKEPHALINAMIDE | #8 | **Tyr**-D-Ala-Gly-Phe-D-Met-NH2 | 5 | | | 603.3 | | | E 3882 |
| 192. | des-Tyr1-METHIONINE ENKEPHALINAMIDE | #8 | **Gly**-Gly-Phe-Met-NH2 | 4 | | | 426.2 | 14 | | E 3631 |
| 193. | des-Tyr1,[D-Ala2]-METHIONINE ENKEPHALINAMIDE | #8 | **D-Ala**-Gly-Phe-Met-NH2 | 4 | | | 440.2 | 1 | | E 5131 |
| 194. | [3,5-DiI-Tyr1,D-Ala2]-METHIONINE ENKEPHALINAMIDE | #8 | **3,5**-Diiodo-Tyr-D-Ala-Gly-Phe-**Met**-NH2 | 5 | | | 855.1 | | | E 9009 |
| 195. | TYR-D-ALA-PHE-MET AMIDE (des-gly3,[D-Ala2]-Methionine Enkephalinamide) | #8 | **Tyr**-D-Ala-Phe-Met-NH2 | 4 | | | 546.3 | 9.62 | | T 0395 |
| 196. | N-CARBOXYMETHYL-PHE-LEU | #8 | **N-Carboxymethyl**-Phe-Leu | 2 | | | 131.1 | | | C 7030 |
| 197. | N-([R,S]-CARBOXY-3- | #8 | **N-**([R,S]-Carboxy-3-Phenyl- | 1 | | | | | | C 8906 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | PHENYL-PROPIONYL)-L-LEUCINE |  | Propionyl)-L-Leu |  |  |  |  |  |  |  |
| 198. | DERMENKEPHALIN | #8 | Tyr-D-Met-Phe-His-Leu-Met-Asp | 7 |  |  | 970.6 | 9.6202 |  | D 2289 |
| 199. | [D-Met2,Pro5]-ENKEPHALINAMIDE | #8 | Tyr-D-Met-Gly-Phe-Pro-NH2 | 5 |  |  | 629.4 | 9.62 |  | E 8380 |
| 200. | [D-Pen2,5]-ENKEPHALIN | #8 | Tyr-D-Pen-Gly-Phe-D-Pen | 5 |  | 2-5 | 385.2 |  |  | E 3888 |
| 201. | [D-Pen2,5,p-Cl-Phe4]-ENKEPHALIN | #8 | Tyr-D-Pen-Gly-p-Chloro-Phe-D-Pen | 5 |  | 2-5 | 419.7 |  |  | E 6264 |
| 202. | [D-Pen2,Pen5]-ENKEPHALIN | #8 | Tyr-D-Pen-Gly-Phe-Pen | 5 |  | 2-5 | 385.2 |  |  | E 2260 |
| 203. | [D-Ala2,N-Me-Phe4,Gly5-ol]-ENKEPHALIN (DAGO) | #8 | Tyr-D-Ala-Gly-N-Methyl-Phe-Gly-ol | 5 |  |  | 309.1 |  |  | E 7384 |
| 204. | [3,5-DiI-Tyr1,D-Ala2,N-Me-Phe4,Gly5-ol]-ENKEPHALIN | #8 | 3,5-Diiodo-Tyr-D-Ala-Gly-N-Methyl-Phe-Gly-ol | 5 |  |  | 560.9 |  |  | E 9134 |
| 205. | [D-Ala2,N-Me-Phe4,Met(O)5-ol]-ENKEPHALIN | #8 | Tyr-D-Ala-Gly-[N-Methyl-Phe]-Met[O]-ol | 4 |  |  | 309.1 |  |  | E 0506 |
| 206. | PREPROENKEPHALIN FRAGMENT 128-140 | #8 | Gly-Gly-Glu-Val-Leu-Gly-Lys-Arg-Tyr-Gly-Gly-Phe-Met | 13 | Ovine,bovine |  | 1370.9 | 9.8578 | -6.4 -6.4 -6.4 -.1 -2.4 | P 7162 |
| 207. | DL-THIORPHAN | #8 | DL-3-Mercapto-2-benzyl | 1 |  |  |  |  |  | T 6031 |
| 208. | TYR-D-ALA-GLY | #8 | Tyr-D-Ala-Gly | 3 |  |  | 309.1 | 5.7 |  | T 2774 |
| 209. | TYR-GLY-GLY | #8 | Tyr-Gly-Gly | 3 |  |  | 295.1 | 5.7 |  | T 9005 |
| 210. | CALPAIN INHIBITOR II | #9 | N-Acetyl-Leu-Leu-Methioninal | 2 | - | - |  |  |  | - |
| 211. | CALPAIN INHIBITOR I | #9 | N-Acetyl-Leu-Leu-Norleucinal | 2 | - | - |  |  |  | - |
| 212. | ACETYL PEPSTATIN | #9 | Acetyl-Val-Val-Sta-Ala-Sta | 5 | - | - |  |  |  | - |
| 213. | AMASTATIN | #9 | [(2S,3R)-3-Amino-2-hydroxy-5-methyhexanoyl]-Val-Val-Asp | 3 | - | - |  |  |  | - |
| 214. | (4-NITROPHENYL) BUTANOYL-L-LEUCINE | #9 | (4-NITROPHENYL) BUTANOYL-L-LEUCINE | 1 | - | - |  |  |  | - |
| 215. | ANTIPAIN | #9 | Phe-CO-Arg-Val-Arg-al | 4 | - | - |  |  |  | - |
| 216. | BASTATIN | #9 | (2S,3R)-3-AMINO-2-HYDROXY-4-phynylbutanoyl]-L-leucine) | 1 | - | - |  |  |  | - |
| 217. | Na-t-BOC-DEACETYLLEUPEPTIN | #9 | Na-t-BOC-Leu-Leu-Arg-al | 3 | - | - |  |  |  | - |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 218. | CHYMOSTATIN | #9 | Phe-CO-Cpd-X-Phe-al | 3 | - | - | | | | - |
| 219. | EGLIN c FRAGMENT 60-63 METHYL ESTER | #9 | Thr-Asn-Val-Val-OMe | 4 | - | - | | | | - |
| 220. | ELASTATINAL | #9 | Leu-CO-Cpd-Gln-Ala-al | 4 | - | - | | | | - |
| 221. | EPIAMASTATIN | #9 | 5-Methylhexanoyl-Val-Val-Asp | 3 | - | - | | | | - |
| 222. | EPIBASTATIN | #9 | 4-Phenylbutanoyl-L-Leucine | 1 | - | - | | | | - |
| 223. | LEUPEPTIN | #9 | Acetyl-Leu-Leu-Arg-al | 3 | - | - | | | | - |
| 224. | PROPIONYL-LEUPEPTIN | #9 | Propionyl-Leu-Leu-Arg-al | 3 | - | - | | | | - |
| 225. | NAZUMAMIDE A | #9 | 2,5 Dihydroxybenzoyl-Arg-Pro-Ile-Abu | 4 | - | - | | | | - |
| 226. | NLE-STA-ALA-STA | #9 | Nle-Sta-Ala-Sta | 4 | - | - | | | | - |
| 227. | PEPSINOSTREPTIN | #9 | Isobutyryl-Val-Val-Sta-Ala-Sta | 4 | - | - | | | | - |
| 228. | PEPSTATIN A | #9 | Isovaleryl-Val-Val-Sta-Ala-Sta | 4 | - | - | | | | - |
| 229. | HYDROXYPHOSPHINYL-LEU-TRP | #9 | Hydroxyphosphinyl-Leu-Trp | 2 | - | - | | | | - |
| 230. | ARG-GLY-ASP | #10 | Arg-Gly-Asp | 3 | | | 346.2 | 6.44 | | A 8052 |
| 231. | ARG-GLY-ASP-SER | #10 | Arg-Gly-Asp-Ser | 4 | | | 433.2 | 6.45 | | A 9041 |
| 232. | ARG-GLY-ASP-SER-PRO | #10 | Arg-Gly-Asp-Ser-Pro | 10 | | | 1001.5 | 9.8843 | -15.1 -11.6 | A 6677 |
| 233. | ARG-GLY-GLU-SER | #10 | Arg-Gly-Glu-Ser | 4 | | | 447.3 | 6.53 | | A 5686 |
| 234. | ARG-PHE-ASP-SER | #10 | Arg-Phe-Asp-Ser | 4 | | | 523.3 | 6.45 | | A 1675 |
| 235. | CYS-GLN-ASP-SER-GLU | #10 | Cys-Gln-Asp-Ser-Glu | 10 | | | 1247.9 | 3.9986 | -11.9 -15.7 | C 8287 |
| 236. | ECHISTATIN | #10 | Glu-Cys-Glu-Ser-Gly-Pro-Cys-Cys-Arg-Asn-Cys-Lys-Phe-Leu-Lys-Glu-Gly-Thr-Ile-Cys-Lys-Arg-Ala-Arg-Gly-Asp-Asp-Met-Asp-Asp-Tyr-Cys-Asn-Gly-Lys-Thr-Cys-Asp-Cys-Pro-Arg-Asn-Pro-His-Lys-Gly-Pro-Ala-Thr | 49 | | | 5424 | 7.4952 | -2.3 -3.3 -6.8 -3.3 -3.6 .6 2.2 -7.7 -10.6 -6.8 1.2 1.2 5.1 -1.6 -8.1 -4.2 -5.6 -5.2 -8 -14.1 -20.5 -20.7 -16.5 -15.8 -11.3 -14.8 -14.8 -12.4 -11.8 -11.8 -5.8 -6.1 -12.1 -9.6 -14.3 -13.6 -12.9 -19.7 -17.8 -18.5 -17.6 | E 2138 |
| 237. | FIBRINOGEN-BINDING INHIBITOR PEPTIDE (Human fibrinogen-g fragment 400-411) | #10 | His-His-Leu-Gly-Gly-Ala-Lys-Gln-Ala-Gly-Asp-Val | 12 | | | 1188.6 | 7.832 | -7.2 -4.4 -1.2 -4.3 | F 9145 |
| 238. | FIBRINOGEN RELATED PEPTIDE | #10 | Gly-Gln-Gln-His-His-Leu-Gly-Gly-Ala-Lys-Gln-Ala-Gly-Asp-Val | 15 | | | 1501.8 | 8.043 | -9 -8.6 -12.5 -7.2 -4.4 -1.2 -4.3 | F 3643 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pl | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | **Glu**-Asp-Thr-Leu-Pro-Lys-Val | | | | | | 4.7 -5.5 -13.2 -5.9 | |
| 240. | FIBRONECTIN TYPE III CONNECTING SEGMENT (Fragment 1-25) | #10 | **Asp**-Glu-Leu-Pro-Gln-Leu-Val-**Thr**-Leu-Pro-His-Pro-Asn-Leu-His **Gly**-Pro-Glu-Ile-Leu-Asp-Val-Pro-**Ser**-Thr | 25 | | | 2727.1 | 3.9829 | 2.8 4.7 5 -.4 1.2 5 -2 -6.6 -7.5 -14.8 -8.7 -1.7 -3.6 4.1 -1.3 1.1 .8 | F 5007 |
| 241. | FIBRONECTIN TYPE III CONNECTING SEGMENT (Fragment 90-109) | #10 | **Gly**-Glu-Glu-Ile-Gln-Ile-Gly-His-**Ile-Pro**-Arg-Glu-Asp-Val-Asp-Tyr-**His**-Leu-Tyr-Pro | 20 | | | 2375.7 | 4.1895 | -1 -2.2 1.3 -3.2 -7.7 -3.5 -8 -12.4 -12.4 -13.1 -12.8 -9.9 | F 6398 |
| 242. | GLY-ARG-ALA-ASP-SER-PRO-LYS | #10 | **Gly**-Arg-Ala-Asp-Ser-Pro-Lys | 7 | | | 730.4 | 10.2775 | | G 4144 |
| 243. | GLY-ARG-GLY-ASP | #10 | **Gly**-Arg-Gly-Asp | 4 | | | 403.2 | 6.83 | | G 9022 |
| 244. | GLY-ARG-GLY-ASP-SER | #10 | **Gly**-Arg-Gly-Asp-Ser | 5 | | | 490.2 | 6.83 | | G 4391 |
| 245. | GLY-ARG-GLY-ASP-SER-PRO-LYS | #10 | **Gly**-Arg-Gly-Asp-Ser-Pro-Lys | 7 | | | 716.4 | 10.2775 | | G 1269 |
| 246. | GLY-ARG-GLY-ASP-THR-PRO | #10 | **Gly**-Arg-Gly-Asp-Thr-Pro | 6 | | | 601.4 | 6.85 | | G 5646 |
| 247. | GLY-ARG-TYR-ASP-SER | #10 | **Gly**-Arg-Tyr-Asp-Ser | 5 | | | 596.3 | 6.75 | | G 2275 |
| 248. | SER-ASP-GLY-ARG-GLY | #10 | **Ser**-Asp-Gly-Arg-Gly | 5 | | | 490.2 | 6.56 | | S 3771 |
| 249. | b-ALA-TRP-MET-ASP-PHE AMIDE (des-BOC-Pentagastrin) | #11 | **b-Ala**-Trp-Met-Asp-Phe-NH2 | 5 | | | 612.4 | | | A 4032 |
| 250. | ALYTESIN ([Gly2,thr6]-Bombesin) | #11 | **pGlu**-Gly-Arg-Leu-Gly-Thr-Gln-**Trp**-Ala-Val-Gly-His-Leu-Met-NH2 | 14 | | | 1570.2 | | | A 2803 |
| 251. | N-t-AMYLOXYCARBONYL-TRP-MET-ASP-PHE AMIDE (Gastrin Related Tetrapeptide) | #11 | **N-t-**Amyloxycarbonyl-Trp-Met-**Asp**-Phe-NH2 | 4 | | | 426.2 | | | A 5771 |
| 252. | BIOCYTIN-NEUROPEPTIDE Y (Biocytin porcine neuropeptide Y) | #11 | **e-**Biotinyl-Lys-Tyr-Pro-Ser-Lys-**Pro**-Asp-Asn-Pro-Gly-Glu-Asp-**Ala**-Pro-Ala-Glu-Asp-Leu-Ala-Arg-**Tyr**-Tyr-Ser-Ala-Leu-Arg-His-Tyr-**Ile**-Asn-Leu-Ile-Thr-Arg-Gln-Arg-**Tyr**-NH2 | 37 | | | 4269 | | | B 8530 |
| 253. | N-t-BOC-b-ALA-TRP-MET-ASP-PHE AMIDE | #11 | **N-t-**BOC-b-Ala-Trp-Met-Asp-Phe-**NH2** | 5 | | | 612.4 | | | B 1636 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | (Pentagastrin) |  |  |  |  |  |  |  |  |  |
| 254. | N-t-BOC-b-ALA-TRP-MET-ASP(Benzyl)-PHE AMIDE (Pentagastrin, blocked) | #11 | N-t-BOC-b-Ala-Trp-Met-Asp(Benzyl)-Phe-NH2 | 5 |  |  | 688.4 |  |  | B 9758 |
| 255. | N-t-BOC-GLY-TRP-MET-ASP-PHE AMIDE (N-t-BOC-CCK Fragment 29-33) | #11 | N-t-BOC-Gly-Trp-Met-Asp-Phe-NH2 | 5 |  |  | 612.4 |  |  | B 1386 |
| 256. | N-t-BOC-GLY-TRP-MET-ASP(Benzyl)-PHE AMIDE (Gastrin Related Pentapeptide, blocked) | #11 | N-t-BOC-Gly-Trp-Met-Asp(Benzyl-Phe-NH2 | 5 |  |  | 688.4 |  |  | B 9883 |
| 257. | N-t-BOC-MET-ASP-PHE AMIDE | #11 | N-t-BOC-Met-Asp-Phe-NH2 | 3 |  |  | 295.1 |  |  | B 3884 |
| 258. | N-t-BOC-TRP-ASP-PHE AMIDE (des-Met2-Gastrin Related Peptide) | #11 | N-t-BOC-Trp-Asp-Phe-NH2 | 3 |  |  | 295.1 |  |  | B 3019 |
| 259. | N-t-BOC-TRP-MET-ASP-PHE AMIDE (Gastrin Related Tetrapeptide) | #11 | N-t-BOC-Trp-Met-Asp-Phe-NH2 | 4 |  |  | 426.2 |  |  | B 4009 |
| 260. | N-t-BOC-TRP-MET-PHE AMIDE (des-Asp3-Gastrin Related peptide) | #11 | N-t-BOC-Trp-Met-Phe-NH2 | 3 |  |  | 312.2 |  |  | B 3144 |
| 261. | BOMBESIN | #11 | pGlu-Gln-Arg-Leu-Gly-Asn-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 14 |  |  | 1654.3 |  |  | B 4272 |
| 262. | [Leu13-y(CH2NH)-Leu14]-BOMBESIN | #11 | pGlu-Gln-Arg-Leu-Gly-Asn-Gln-Trp-Ala-Val-Gly-His-Leu-y-[CH2NH]-Leu | 14 |  |  | 1507.2 |  |  | B 1025 |
| 263. | [Lys3]-BOMBESIN | #11 | pGlu-Gln-Lys-Leu-Gly-Asn-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 14 |  |  | 1626.2 |  |  | B 1647 |
| 264. | [D-Phe12]-BOMBESIN | #11 | pGlu-Gln-Arg-Leu-Gly-Asn-Gln-Trp-Ala-Val-Gly-D-Phe-Leu-Met-NH2 | 14 |  |  | 1664.3 |  |  | B 0775 |
| 265. | [D-Phe12,Leu14]-BOMBESIN | #11 | pGlu-Gln-Arg-Leu-Gly-Asn-Gln-Trp-Ala-Val-Gly-D-Phe-Leu-Leu-NH2 | 14 |  |  | 1646.3 |  |  | B 0990 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 266. | [Tyr4]-BOMBESIN | #11 | pGlu-Gln-Arg-Tyr-Gly-Asn-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 14 | | | 1704.3 | | | B 5397 |
| 267. | [Tyr4,D-Phe12]-BOMBESIN | #11 | pGlu-Gln-Arg-Tyr-Gly-Asn-Gln-Trp-Ala-Val-Gly-D-Phe-Leu-Met-NH2 | 14 | | | 1714.3 | | | B 0650 |
| 268. | [deamino-Phe6,His7,D-Ala11,D-Pro13-y(CH2NH)-Phe14]-BOMBESIN FRAGMENT 6-14 | #11 | Deamino-Phe-His-Trp-Ala-Val-D-Ala-His-D-Pro-y[CH2NH]-Phe-NH2 | 9 | | | 949.7 | | | B 7033 |
| 269. | BOMBESIN FRAGMENT 8-14 | #11 | Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 7 | | | 828.6 | 14 | | B 1150 |
| 270. | CAERULEIN | #11 | pGlu-Gln-Asp-Tyr[SO3H]-Thr-Gly-Trp-Met-Asp-Phe-NH2 | 10 | | | 1140.7 | | | C 9026 |
| 271. | CHOLECYSTOKININ (CCK) FRAGMENTS (Fragment 10-20) | #11 | Ile-Lys-Asn-Leu-Gln-Ser-Leu-Asp-Pro-Ser-His | 11 | | | 1250.8 | 7.883 | -4.7 -10 -9.3 | C 9269 |
| 272. | CHOLECYSTOKININ (CCK) FRAGMENTS (Fragment 1-21) | #11 | Lys-Ala-Pro-Ser-Gly-Arg-Val-Ser-Met-Ile-Lys-Asn-Leu-Gln-Ser-Leu-Asp-Pro-Ser-His-Arg | 21 | | | 2323.6 | 11.6384 | -4.1 4.3 2.5 .2 1.3 -1.8 1.9 1.5 2.3 -4.7 -10 -9.3 -5.8 | C 2296 |
| 273. | CHOLECYSTOKININ (CCK) FRAGMENTS ([Tyr(SO3H) 27]-Fragment 26-29 Amide) | #11 | Asp-Tyr[SO3H]-Met-Gly-NH2 | 4 | | | 336.1 | | | C 5033 |
| 274. | CHOLECYSTOKININ (CCK) FRAGMENTS ([Tyr(SO3H) 27,Thr28,Nle31]-Fragment 25-33 Amide) | #11 | Arg-Asp-Tyr[SO3H]-Thr-Gly-Trp-Nle-Asp-Phe-NH2 | 9 | | | 1041.8 | | | C 2421 |
| 275. | CHOLECYSTOKININ (CCK) FRAGMENTS ([Tyr(SO3H) 27]-Fragment 26-33 Amide ; CCK-8,sulfated) | #11 | Asp-Tyr[SO3H]-Met-Gly-Trp-Met-Asp-Phe-NH2 | 8 | | | 914.5 | | | C 2175 |
| 276. | CHOLECYSTOKININ (CCK) FRAGMENTS (Fragment 26-33 Amide Non-Sulfated) | #11 | Asp-Tyr-Met-Gly-Trp-Met-Asp-Phe-NH2 | 8 | | | 914.5 | | | C 2901 |
| 277. | N-Acetyl-CHOLECYSTOKININ | #11 | Acetyl-Asp-Tyr-Met-Gly-NH2 | 4 | | | 541.2 | | | C 3422 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | FRAGMENTS (Ac-Fragment 26-29 Amide Non-Sulfated) | | | | | | | | | |
| 278. | N-Acetyl-CHOLECYSTOKININ FRAGMENTS (Ac-[Tyr (SO3H)27]-Fragment 26-30 Amide) | #11 | Acetyl-Asp-Tyr[SO3H]-Met-Gly-Trp-NH2 | 5 | | | 564.3 | | | C 4408 |
| 279. | N-Acetyl-CHOLECYSTOKININ FRAGMENTS (Ac-Fragment 26-30 Amide Non-Sulfated) | #11 | Acetyl-Asp-Tyr-Met-Gly-Trp-NH2 | 5 | | | 727.4 | | | C 4533 |
| 280. | N-Acetyl-CHOLECYSTOKININ FRAGMENTS (Ac-[Tyr (SO3H)27]-Fragment 26-31 Amide) | #11 | Acetyl-Asp-Tyr[SO3H]-Met-Gly-Trp-Met-NH2 | 6 | | | 695.4 | | | C 2795 |
| 281. | N-Acetyl-CHOLECYSTOKININ FRAGMENTS (Ac-Fragment 26-31 Amide Non-Sulfated) | #11 | Acetyl-Asp-Tyr-Met-Gly-Trp-Met-NH2 | 6 | | | 858.5 | | | C 2546 |
| 282. | N-Acetyl-CHOLECYSTOKININ FRAGMENTS (Ac-[Tyr (SO3H)27]-Fragment 27-33 Amide) | #11 | Acetyl-Tyr[SO3H]-Met-Gly-Trp-Met-Asp-Phe-NH2 | 7 | | | 800.5 | | | C 9524 |
| 283. | b-ENDOTHELIN (Vasoactive intestinal contractor) | #11 | Cys-Ser-Cys-Asn-Ser-Trp-Leu-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp | 21 | Mouse | [Disulfide Bridges: 1-15; 3-11 | 2574.9 | 4.2587 | -.7 -10.6 -7.3 -5.6 -3.4 .2 3.6 -3.4 3.9 7.8 12.3 14.3 9.2 | E 9512 |
| 284. | GALANIN | #11 | Gly-Trp-Thr-Leu-Asn-Ser-Ala-Gly-Tyr-Leu-Leu-Gly-Pro-His-Ala-Val- | 30 | Human | | 3157 | 9.858 | -2.4 1.8 6.5 6.8 1.4 1.7 4.3 6.7 6.7 8 -2.5 -6.3 -11.2 -6.8 -4.4 - | G 0278 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Gly-Asn-His-Arg-Ser-Phe-Ser-Asp-Lys-Asn-Gly-Leu-Thr-Ser | | | | | | 6.2 -13.9 -20.9 -17.8 -10.8 -7 -7 | |
| 285. | GALANIN | #11 | Gly-Trp-Thr-Leu-Asn-Ser-Ala-Gly-Tyr-Leu-Leu-Gly-Pro-His-Ala-Ile-Asp-Asn-His-Arg-Ser-Phe-His-Asp-Lys-Tyr-Gly-Leu-Ala-NH2 | 29 | Porcine | | 3226 | 9.6554 | -2.4 1.8 6.5 6.8 1.4 1.7 4.3 7 7.4 5.2 -5.3 -9.1 -14 -9.6 -9.6 -11.4 -22.9 -21.1 -18 -11 -4.7 -3.9 | G 5773 |
| 286. | GALANIN | #11 | Gly-Trp-Thr-Leu-Asn-Ser-Ala-Gly-Tyr-Leu-Leu-Gly-Pro-His-Ala-Ile-Asp-Asn-His-Arg-Ser-Phe-Ser-Asp-Lys-His-Gly-Leu-Thr-NH2 | 29 | Rat | | 3180 | 9.8582 | -2.4 1.8 6.5 6.8 1.4 1.7 4.3 7 7.4 5.2 -5.3 -9.1 -14 -9.6 -7.2 -9 -20.5 -20.6 -17.5 -10.5 -6.7 -5.9 | G 8272 |
| 287. | GALANIN MESSAGE ASSOCIATED PEPTIDE FRAGMENTS (Fragment 1-41 Amide ; Preprogalanin 65-105 amide) | #11 | Glu-Leu-Glu-Pro-Glu-Asp-Glu-Ala-Arg-Pro-Gly-Gly-Phe-Asp-Arg-Leu-Gln-Ser-Glu-Asp-Lys-Ala-Ile-Arg-Thr-Ile-Met-Glu-Phe-Leu-Ala-Phe-Leu-His-Leu-Lys-Glu-Ala-Gly-Ala-Leu-NH2 | 41 | Porcine | | 4653.2 | 4.38537 | -13.5 -16.1 -20.3 -17.2 -12.8 -12.8 -9.3 -6.5 -11.8 -8.1 -10 -9.6 -12.7 -17.6 -9.6 -5.1 -14.1 -6.1 -3.4 -3.4 2.9 10.6 10.6 8.9 17.2 14.7 14 12.1 8.2 7.2 3 3 4 .2 | G 4646 |
| 288. | GALANIN MESSAGE ASSOCIATED PEPTIDE FRAGMENTS (Fragment 16-41 Amide ; Preprogalani 80-105 amide) | #11 | Leu-Gln-Ser-Glu-Asp-Lys-Ala-Ile-Arg-Thr-Ile-Met-Glu-Phe-Leu-Ala-Phe-Leu-His-Leu-Lys-Glu-Ala-Gly-Ala-Leu-NH2 | 26 | | | 2959 | 7.863 | -5.1 -14.1 -6.1 -3.4 -3.4 2.9 10.6 10.6 8.9 17.2 14.7 14 12.1 8.2 7.2 3 3 4 .2 | G 4521 |
| 289. | GALANIN MESSAGE ASSOCIATED PEPTIDE FRAGMENTS (Fragment 25-41 Amide ; Preprogalani 89-105 amide) | #11 | Thr-Ile-Met-Glu-Phe-Leu-Ala-Phe-Leu-His-Leu-Lys-Glu-Ala-Gly-Ala-Leu-NH2 | 17 | | | 1918.3 | 7.57 | 17.2 14.7 14 12.1 8.2 7.2 3 3 4 .2 | G 4396 |
| 290. | GALANIN MESSAGE ASSOCIATED PEPTIDE FRAGMENTS (Fragment 44-59 Amide ; Preprogalani 108-123 amide) | #11 | Leu-Pro-Gly-Leu-Pro-Ser-Ala-Ala-Ser-Ser-Glu-Asp-Ala-Gly-Gln-Ser-NH2 | 16 | | | 1499.6 | 3.985 | 6 1.4 -.5 -.1 -5.6 -4.4 -7.1 -9.7 -11.5 | G 4271 |
| 291. | GASTRIC INHIBITORY POLYPEPTIDE (GIP) | #11 | Tyr-Ala-Glu-Gly-Thr-Phe-Ile-Ser-Asp-Tyr-Ser-Ile-Ala-Met-Asp-Lys-Ile-His-Gln-Gln-Asp-Phe-Val-Asn-Trp-Leu-Leu-Ala-Gln-Lys-Gly-Lys- | 42 | Human | | 4981.3 | 7.675 | 2.4 -1.1 -3.7 4.3 6.5 9.1 6.3 -1.7 -.3 0 -2.2 -4.9 -9.4 -11.9 -9.6 -10 -6.6 -7.3 -.3 5 5 8.5 1.4 -6.3 -3.2 -6.2 -13.5 -21.7 -23.5 -27.1 -23.2 | G 2269 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  | Lys-Asn-Asp-Trp-Lys-His-Asn-Ile-Thr-Gln |  |  |  |  |  | -21.8 -18.6 -18.2 |  |
| 292. | GASTRIC INHIBITORY POLYPEPTIDE (GIP) | #11 | Tyr-Ala-Glu-Gly-Thr-Phe-Ile-Ser-Asp-Tyr-Ser-Ile-Ala-Met-Asp-Lys-Ile-Arg-Gln-Gln-Asp-Phe-Val-Asn-Trp-Leu-Leu-Ala-Gln-Lys-Gly-Lys-Lys-Ser-Asp-Trp-Lys-His-Asn-Ile-Thr-Gln | 42 | Porcine |  | 4974.3 | 9.2842 | 2.4 -1.1 -3.7 4.3 6.5 9.1 6.3 -1.7 -.3 3.2 -3.5 -6.2 -10.7 -13.2 -10.9 -11.3 -7.9 -8.6 -.3 5 5 8.5 1.4 -6.3 -3.2 -7 -10.8 -19 -20.8 -24.4 -20.5 -19.1 -15.9 -15.5 | G 5512 |
| 293. | GASTRIC INHIBITORY POLYPEPTIDE FRAGMENT 1-30 AMIDE | #11 | Tyr-Ala-Glu-Gly-Thr-Phe-Ile-Ser-Asp-Tyr-Ser-Ile-Ala-Met-Asp-Lys-Ile-Arg-Gln-Gln-Asp-Phe-Val-Asn-Trp-Leu-Leu-Ala-Gln-Lys-NH2 | 30 | Porcine |  | 3565.3 | 4.4227 | 2.4 -1.1 -3.7 4.3 6.5 9.1 6.3 -1.7 -.3 3.2 -3.5 -6.2 -10.7 -13.2 -10.9 -11.3 -7.9 -8.6 -.3 5 5 8.5 1.8 | G 5404 |
| 294. | GASTRIN (Big Gastrin I ; HG-34 ; Gregory structure) | #11 | pGlu-Leu-Gly-Pro-Gln-Gly-Pro-Pro-His-Leu-Val-Ala-Asp-Pro-Ser-Lys-Lys-Gln-Gly-Pro-Trp-Leu-Glu-Glu-Glu-Glu-Glu-Ala-Tyr-Gly-Trp-Met-Asp-Phe-NH2 | 34 | Human |  | 3876.7 |  |  | G 5024 |
| 295. | GASTRIN (Gastrin I) | #11 | pGlu-Gly-Pro-Trp-Leu-Glu-Glu-Glu-Glu-Glu-Ala-Tyr-Gly-Trp-Met-Asp-Phe-NH2 | 17 | Human |  | 2125.5 |  |  | G 9020 |
| 296. | GASTRIN (Gastrin I) | #11 | pGlu-Arg-Pro-Pro-Met-Glu-Glu-Glu-Glu-Glu-Ala-Tyr-Gly-Trp-Met-Asp-Phe-NH2 | 17 | Rat |  | 2154.6 |  |  | G 1276 |
| 297. | GASTRIN ([Leu15]-Gastrin I) | #11 | pGlu-Gly-Pro-Trp-Leu-Glu-Glu-Glu-Glu-Glu-Ala-Tyr-Gly-Trp-Leu-Asp-Phe-NH2 | 17 | Human |  | 2107.5 |  |  | G 9145 |
| 298. | GASTRIN (Mini Gastrin I ; HG-13) | #11 | Leu-Glu-Glu-Glu-Glu-Glu-Ala-Tyr-Gly-Trp-Met-Asp-Phe-NH2 | 13 | Human |  | 1657.1 | 3.3396 | -13.6 -18.3 -12.9 -9.4 -6.6 -3.1 | G 0267 |
| 299. | GASTRIN I FRAGMENTS (Fragment 1-13) | #11 | pGlu-Gly-Pro-Trp-Leu-Glu-Glu-Glu-Glu-Glu-Ala-Tyr-Gly | 13 | Human |  | 1531.1 |  |  | G 6261 |
| 300. | GASTRIN I FRAGMENTS (Fragment 1-14) | #11 | pGlu-Gly-Pro-Trp-Leu-Glu-Glu-Glu-Glu-Glu-Ala-Tyr-Gly-Trp | 14 | Human |  | 1717.3 |  |  | G 6386 |
| 301. | GASTRIN II | #11 | pGlu-Gly-Pro-Trp-Leu-Glu-Glu-Glu-Glu-Glu-Ala-Tyr[SO3H]-Gly-Trp-Met-Asp-Phe-NH2 | 17 |  |  | 1962.4 |  |  | G 1260 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 302. | GASTRIN RELEASING PEPTIDE (GRP) | #11 | Val-Pro-Leu-Pro-Ala-Gly-Gly-Gly-Thr-Val-Leu-Thr-Lys-Met-Tyr-Pro-Arg-Gly-Asn-His-Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 27 | Human |  | 2877.2 | 11.7071 | 4.7 4.7 10.1 5.6 7.2 3.4 2.5 1.3 1.7 -2.5 -6.7 -17.2 -17.4 -11.7 -9.4 -8.5 -10.1 -1.8 .5 4 | G 8022 |
| 303. | GASTRIN RELEASING PEPTIDE (GRP) | #11 | Ala-Pro-Val-Ser-Val-Gly-Gly-Gly-Thr-Val-Leu-Ala-Lys-Met-Tyr-Pro-Arg-Gly-Asn-His-Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 27 | Porcine |  | 2823 | 11.7133 | 5.9 8.3 13.7 11.3 12.1 5.9 5 3.8 4.2 0 -4.2 -14.7 -17.4 -11.7 -9.4 -8.5 -10.1 -1.8 .5 4 | G 1649 |
| 304. | GLUCAGON | #11 | His-Ser-Gln-Gly-Thr-Phe-Thr-Ser-Asp-Tyr-Ser-Lys-Tyr-Leu-Asp-Ser-Arg-Arg-Ala-Gln-Asp-Phe-Val-Gln-Trp-Leu-Met-Asn-Thr | 29 | Human, Bovine, Porcine |  | 3481.3 | 7.622 | -7.3 -8.9 -8.9 -5.4 -10.2 -5.7 -8.5 -12.1 -14.8 -12.3 -13.7 -16.4 -12.5 -11.9 -11.5 -11.5 -11.6 -3.3 3.1 1.3 .6 | G 1774 |
| 305. | des-His1,[Glu9]-GLUCAGON AMIDE | #11 | Ser-Gln-Gly-Thr-Phe-Thr-Ser-Glu-Tyr-Ser-Lys-Tyr-Leu-Asp-Ser-Arg-Arg-Ala-Gln-Asp-Phe-Val-Gln-Trp Leu-Met-Asn-Thr-NH2 | 28 |  |  | 3374.3 | 9.4298 | -8.9 -8.9 -5.4 -10.2 -5.7 -8.5 -12.1 -11.3 -12.3 -13.7 -16.4 -12.5 -11.9 -11.5 -11.5 -11.6 -3.3 3.1 1.3 .6 4.1 | G 1651 |
| 306. | GLUCAGON 37 (Oxyntomodulin) | #11 | His-Ser-Gln-Gly-Thr-Phe-Thr-Ser-Asp-Tyr-Ser-Lys-Tyr-Leu-Asp-Ser-Arg-Arg-Ala-Gln-Asp-Phe-Val-Gln-Trp-Leu-Met-Asn-Thr-Lys-Arg-Asn-Lys-Asn-Asn-Ile-Ala | 37 |  |  | 4423.1 | 10.3568 | -7.3 -8.9 -8.9 -5.4 -10.2 -5.7 -8.5 -12.1 -14.8 -12.3 -13.7 -16.4 -12.5 -11.9 -11.5 -11.5 -11.6 -3.3 3.1 1.3 .6 4.1 -2.6 -11.3 -11.3 -14.3 -21.6 -22.5 -17.2 | G 4146 |
| 307. | GLUCAGON 37 FRAGMENT 30-37 | #11 | Lys-Arg-Asn-Lys-Asn-Asn-Ile-Ala | 8 |  |  | 959.8 | 11.8107 |  | G 5899 |
| 308. | GLUCAGON-LIKE PEPTIDE I (GLP 1 ; Preproglucagon 72-108) | #11 | His-Asp-Glu-Phe-Glu-Arg-His-Ala-Glu-Gly-Thr-Phe-Thr-Ser-Asp-Val Ser-Ser-Tyr-Leu-Glu-Gly-Gln-Ala-Ala-Lys-Glu-Phe-Ile-Ala-Trp-Leu-Val-Lys-Gly-Arg-Gly | 37 | Human |  | 4164.7 | 4.75768 | -20.3 -17.5 -14.7 -8.4 -11.9 -9.2 -4.7 -.8 -3.4 -.7 -1.6 2.9 -3.4 -3.1 -5.8 -.5 -2.9 -2.1 -8.7 -4.6 -3.9 1.4 .9 8.2 10.6 4.9 8.4 11.9 4.2 | G 3265 |
| 309. | GLUCAGON-LIKE PEPTIDE I FRAGMENTS (Fragment 7-36 Amide ; Preproglucagon 78-107 Amide) | #11 | His-Ala-Glu-Gly-Thr-Phe-Thr-Ser-Asp-Val-Ser-Ser-Tyr-Leu-Glu-Gly-Gln-Ala-Ala-Lys-Glu-Phe-Ile-Ala-Trp-Leu-Val-Lys-Gly-Arg-NH2 | 30 | Human |  | 3312.1 | 5.3695 | -4.7 -.8 -3.4 -.7 -1.6 2.9 -3.4 -3.1 -5.8 -.5 -2.9 -2.1 -8.7 -4.6 -3.9 1.4 .9 8.2 10.6 4.9 8.4 11.9 4.6 | G 8147 |
| 310. | GLY-TRP-THR-LEU-ASN-SER-ALA-GLY-TYR-LEU- | #11 | Gly-Trp-Thr-Leu-Asn-Ser-Ala-Gly-Tyr-Leu-Leu-Gly-Pro-Gln-Gln- | 20 |  |  | 2215.5 | 9.955 | -2.4 1.8 6.5 6.8 1.4 1.4 -1.3 -.3 2.9 3.8 3.8 1.9 2.3 | G 1278 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | LEU-GLY-PRO-GLN-GLN-PHE-PHE-GLY-LEU-MET AMIDE (Galantide) |  | **Phe**-Phe-Gly-Leu-Met-NH2 |  |  |  |  |  |  |  |
| 311. | MOTILIN (Gastric motor stimulatory peptide) | #11 | **Phe**-Val-Pro-Ile-Phe-Thr-His-Ser-**Glu**-Leu-Gln-Lys-Ile-Arg-Glu-Lys-**Glu**-Arg-Asn-Lys-Gly-Gln | 22 | Canine |  | 2686.2 | 10.5047 | 4.5 5.5 -2.2 -.6 -4.5 -7.3 -14.6 -11.4 -18 -14.5 -22.8 -26.7 -23.2 -31.2 | M 3278 |
| 312. | MOTILIN (Gastric motor stimulatory peptide) | #11 | **Phe**-Val-Pro-Ile-Phe-Thr-Tyr-Gly-**Glu**-Leu-Gln-Arg-Met-Gln-Glu-**Lys**-Glu-Arg-Asn-Lys-Gly-Gln | 22 | Porcine |  | 2699.2 | 9.5314 | 6.8 7.8 .1 1.7 -5.4 -11.7 -14.5 -13.2 -20.2 -16.7 -25 -29.5 -24.8 -30.2 | M 4505 |
| 313. | [Leu13]-MOTILIN | #11 | **Phe**-Val-Pro-Ile-Phe-Thr-Tyr-Gly-**Glu**-Leu-Gln-Arg-leu-Gln-Glu-Lys-**Glu**-Arg-Asn-Lys-Gly-Gln | 22 | Porcine |  | 2681.2 | 9.5314 | 6.8 7.8 .1 1.7 -3.5 -9.8 -12.6 -11.3 -18.3 -14.8 -23.1 -27.6 -22.9 -30.2 | M 7530 |
| 314. | NEUROPEPTIDE K (Substance K precursor peptide) | #11 | **Asp**-Ala-Asp-Ser-Ser-Ile-Glu-Lys-**Gln**-Val-Ala-Leu-Leu-Lys-Ala-Leu-**Tyr**-Gly-His-Gly-Gln-Ile-Ser-His-**Lys**-Arg-His-Lys-Thr-Asp-Ser-**Phe**-Val-Gly-Leu-Met-NH2 | 36 | Porcine |  | 3996.4 | 10.1887 | -13.2 -5.5 -5.5 1.8 6.4 7.2 .6 7.9 10.5 13.6 6.2 4 -3.3 -2.6 .5 -4.5 -8.3 -10.9 -18.2 -15 -19.2 -15.7 -24.5 -20.9 -13.5 -10 -1.7 3.4 7.3 | N 7392 |
| 315. | NEUROPEPTIDE Y (NPY) | #11 | **Tyr**-Pro-Ser-Lys-Pro-Asp-Asn-**Pro**-Gly-Glu-Asp-Ala-Pro-Ala-Glu-**Asp**-Met-Ala-Arg-Tyr-Tyr-Ser-Ala-**Leu**-Arg-His-Tyr-Ile-Asn-Leu-Ile-**Thr**-Arg-Gln-Arg-Tyr-NH2 | 36 | Human |  | 4287 | 9.2009 | -18.2 -20.4 -18.8 -19.7 -17.4 -14 -14 -10.5 -10.5 -8.3 -8.3 -7.1 -10.2 -9.4 -9.4 -2.1 1.4 -8.2 -11.3 -2.3 -1 .6 5.9 3.4 -4.9 -3.9 -.7 -5.2 -13.2 | N 5017 |
| 316. | NEUROPEPTIDE Y (NPY) | #11 | **Tyr**-Pro-Ser-Lys-Pro-Asp-Asn-**Pro**-Gly-Glu-Asp-Ala-Pro-Ala-Glu-**Asp**-Leu-Ala-Arg-Tyr-Tyr-Ser-Ala-**Leu**-Arg-His-Tyr-Ile-Asn-Leu-Ile-**Thr**-Arg-Gln-Arg-Tyr-NH2 | 36 | Porcine |  | 4269 | 9.2009 | -18.2 -20.4 -18.8 -19.7 -17.4 -14 -14 -10.5 -8.6 -6.4 -6.4 -5.2 -8.3 -7.5 -7.5 -.2 3.3 -8.2 -11.3 -2.3 -1 .6 5.9 3.4 -4.9 -3.9 -.7 -5.2 -13.2 | N 3266 |
| 317. | NEUROPEPTIDE Y | #11 | **Tyr**-Pro-Ser-Lys-Pro-Asp-Asn-**Pro**-Gly-Asp-Asp-Ala-Pro-Ala-Glu-**Asp**-Leu-Ala-Arg-Tyr-Tyr-Ser-Ala-**Leu**-Arg-His-Tyr-Ile-Asn-Leu-Ile-**Thr**-Arg-Gln-Arg-Tyr-NH2 | 36 | Sheep |  | 4254.9 | 9.2009 | -18.2 -16.9 -18.8 -19.7 -17.4 -14 -14 -10.5 -8.6 -6.4 -6.4 -5.2 -8.3 -7.5 -7.5 -.2 3.3 -8.2 -11.3 -2.3 -1 .6 5.9 3.4 -4.9 -3.9 -.7 -5.2 -13.2 | N 6269 |
| 318. | [O-Methyl-Tyr21]-NEUROPEPTIDE Y | #11 | **Tyr**-Pro-Ser-Lys-Pro-Asp-Asn-**Pro**-Gly-Glu-Asp-Ala-Pro-Ala-Glu-**Asp**-Met-Ala-Arg-Tyr-Tyr[Me]-Ser- | 36 | Human |  | 4107.9 |  |  | N 5771 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Ala-Leu-Arg-His-Tyr-Ile-Asn-Leu-Ile-Thr-Arg-Gln-Arg-Tyr | | | | | | | |
| 319. | [Leu31,Pro34]-NEUROPEPTIDE Y | #11 | Tyr-Pro-Ser-Lys-Pro-Asp-Asn-Pro-Gly-Glu-Asp-Ala-Pro-Ala-Glu-Asp-Met-Ala-Arg-Tyr-Tyr-Ser-Ala-Leu-Arg-His-Tyr-Ile-Asn-Leu-Leu-Thr-Arg-Pro-Arg-Tyr-NH2 | 36 | Human | | 4256 | 9.2009 | -18.2 -20.4 -18.8 -19.7 -17.4 -14 -14 -10.5 -10.5 -8.3 -8.3 -7.1 -10.2 -9.4 -9.4 -2.1 1.4 -8.2 -11.3 -2.3 -1 .6 5.2 2.7 -5.6 -2.7 .5 -4 -12 | N 6146 |
| 320. | [Leu31,Pro34]-NEUROPEPTIDE Y | #11 | Tyr-Pro-Ser-Lys-Pro-Asp-Asn-Pro-Gly-Glu-Asp-Ala-Pro-Ala-Glu-Asp-Leu-Ala-Arg-Tyr-Tyr-Ser-Ala-Leu-Arg-His-Tyr-Ile-Asn-Leu-Leu-Thr-Arg-Pro-Arg-Tyr-NH2 | 36 | Porcine | | 4238 | 9.2009 | -18.2 -20.4 -18.8 -19.7 -17.4 -14 -14 -10.5 -8.6 -6.4 -6.4 -5.2 -8.3 -7.5 -7.5 -.2 3.3 -8.2 -11.3 -2.3 -1 .6 5.2 2.7 -5.6 -2.7 .5 -4 -12 | N 7768 |
| 321. | NEUROPEPTIDE Y FRAGMENTS (Fragment 1-24 Amide) | #11 | Tyr-Pro-Ser-Lys-Pro-Asp-Asn-Pro-Gly-Glu-Asp-Ala-Pro-Ala-Glu-Asp-Met-Ala-Arg-Tyr-Tyr-Ser-Ala-Leu-NH2 | 24 | Human | | 2669.5 | 4.1456 | -18.2 -20.4 -18.8 -19.7 -17.4 -14 -14 -10.5 -10.5 -8.3 -8.3 -7.1 -10.2 -9.4 -9.4 -2.1 1.4 | N 4896 |
| 322. | NEUROPEPTIDE Y FRAGMENTS (Fragment 13-36) | #11 | Pro-Ala-Glu-Asp-Leu-Ala-Arg-Tyr-Tyr-Ser-Ala-Leu-Arg-His-Tyr-Ile-Asn-Leu-Ile-Thr-Arg-Gln-Arg-Tyr-NH2 | 24 | Porcine | | 3000.3 | 10.7227 | -8.3 -7.5 -7.5 -.2 3.3 -8.2 -11.3 -2.3 -1 .6 5.9 3.4 -4.9 -3.9 -.7 -5.2 -13.2 | N 6521 |
| 323. | NEUROPEPTIDE Y FRAGMENTS (Fragment 18-36) | #11 | Ala-Arg-Tyr-Tyr-Ser-Ala-Leu-Arg-His-Tyr-Ile-Asn-Leu-Ile-Thr-Arg-Gln-Arg-Tyr-NH2 | 19 | Human, Porcine | | 2477 | 12.0282 | -8.2 -11.3 -2.3 -1 .6 5.9 3.4 -4.9 -3.9 -.7 -5.2 -13.2 | N 1272 |
| 324. | NEUROPEPTIDE Y FRAGMENTS ((Tyr-OH)36-Fragment 18-36) | #11 | Ala-Arg-Tyr-Thr-Ser-Ala-Leu-Arg-His-Tyr-Ile-Asn-Leu-Ile-Thr-Arg-Gln-Arg-Tyr | 19 | Human, Porcine | | 2399 | 11.2784 | -7.6 -10.7 -1.7 -.4 .6 5.9 3.4 -4.9 -3.9 -.7 -5.2 | N 1147 |
| 325. | PANCREASTATIN | #11 | Gly-Trp-Pro-Gln-Ala-Pro-Ala-Met-Asp-Gly-Ala-Gly-Lys-Thr-Gly-Ala-Glu-Glu-Ala-Gln-Pro-Pro-Glu-Gly-Lys-Gly-Ala-Arg-Glu-His-Ser-Arg-Gln-Glu-Glu-Glu-Glu-Glu-Thr-Ala-Gly-Ala-Pro-Gln-Gly-Leu-Phe-Arg Gly-NH2 | 49 | Porcine | | 5113.4 | 4.41744 | -2.5 -6 -3.3 -2.1 1.4 -5 -3.8 -3.8 -9.2 -9.2 -7 -12.3 -13.5 -11.2 -14 -14 -15.8 -16.6 -11.3 -13.1 -17.6 -19.2 -18.4 -14.9 -22.5 -22.1 -25.2 -30.5 -29.5 -29.5 -27 -24.4 -20.3 -15 -13.1 -13.1 -10 -2.7 3.6 4.3 -2.4 -2 | P 2794 |
| 326. | PANCREASTATIN FRAGMENTS (Fragment | #11 | Gln-Glu-Glu-Glu-Glu-Glu-Thr-Ala-Gly-Ala-Pro-Gln-Gly-Leu-Phe-Arg | 17 | Porcine | | 1859.3 | 3.8939 | -20.3 -15 -13.1 -13.1 -10 -2.7 3.6 4.3 -2.4 -2 | P 2919 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | 33-49) | | Gly-NH2 | | | | | | | |
| 327. | PANCREASTATIN FRAGMENTS (Fragment 37-52 ; Chromograinin A Fragment 286-301) | #11 | Glu-Glu-Glu-Glu-Glu-Met-Ala-Val-Val-Pro-Gln-Gly-Leu-Phe-Arg-Gly NH2 | 16 | Human | | 1831.4 | 3.8939 | -5.4 -3.5 -3.5 -.4 6.9 13.2 11.3 4.6 .4 | P 9809 |
| 328. | PANCREATIC POLYPEPTIDE | #11 | Gly-Pro-Ser-Gln-Pro-Thr-Tyr-Pro-Gly-Asp-Asp-Ala-Pro-Val-Glu-Asp-Leu-Ile-Arg-Phe-Tyr-Asp-Asn-Leu-Gln-Gln-Tyr-Leu-Asn-Val-Val-Thr-Arg-His-Arg-Tyr-NH2 | 36 | Avian | | 4251.1 | 5.3735 | -11.9 -11.5 -13.4 -14.3 -12.4 -6.6 -9.4 -8.1 -6.2 -1.3 -1.3 4 .9 2.5 -5.2 -1.4 -1.4 -8.7 -14.5 -6.2 -9 -7 .7 3.5 -.3 -4.5 -1 -5.5 -12.8 | P 9653 |
| 329. | PANCREATIC POLYPEPTIDE | #11 | Ala-Pro-Leu-Glu-Pro-Glu-Tyr-Pro-Gly-Asp-Asp-Ala-Thr-Pro-Glu-Gln Met-Ala-Gln-Tyr-Ala-Ala-Glu-Leu-Arg-Arg-Tyr-Ile-Asn-Met-Leu-Thr-Arg-Pro-Arg-Tyr-NH2 | 36 | Bovine | | 4240.2 | 4.7172 | -7.9 -9.7 -11.6 -17.1 -14.3 -14.3 -14.3 -16.5 -13 -10.8 -10.8 -8.6 -8.6 -6.1 -8 -.7 2.8 -3.6 -11.2 -3.2 -1.9 -5.3 -3.3 -.5 -8.8 -5.9 -1.4 -5.9 -13.9 | P 9778 |
| 330. | PANCREATIC POLYPEPTIDE | #11 | Ala-Pro-Leu-Glu-Pro-Val-Tyr-Pro-Gly-Asp-Asn-Ala-Thr-Pro-Glu-Gln Met-Ala-Gln-Tyr-Ala-Ala-Asp-Leu-Arg-Arg-Tyr-Ile-Asn-Met-Leu-Thr-Arg-Pro-Arg-Tyr-NH2 | 36 | Human | | 4197.2 | 9.5779 | -.2 -2 -3.9 -9.4 -6.6 -6.6 -14.3 -16.5 -13 -10.8 -10.8 -8.6 -8.6 -6.1 -4.5 -.7 2.8 -3.6 -11.2 -3.2 -1.9 -5.3 -3.3 -.5 -8.8 -5.9 -1.4 -5.9 -13.9 | P 9903 |
| 331. | PANCREATIC POLYPEPTIDE | #11 | Ala-Pro-Leu-Glu-Pro-Met-Tyr-Pro-Gly-Asp-Tyr-Ala-Thr-His-Glu-Gln-Arg-Ala-Gln-Tyr-Glu-Thr-Gln-Leu-Arg-Arg-Tyr-Ile-Asn-Thr-Leu-Thr-Arg-Pro-Arg-Tyr-NH2 | 36 | Rat | | 4415.6 | 9.8954 | -2.5 -4.3 -7.5 -9.5 -6.7 -8.3 -13.7 -15.9 -14.3 -16.6 -16.6 -16.6 -21.9 -21.9 -22.2 -14.9 -15.9 -11.4 -19 -11 -9.7 -10.4 -5.9 -3.1 -11.4 -8.5 -4 -8.5 -16.5 | P 6410 |
| 332. | PEPTIDE YY | #11 | Tyr-Pro-Ile-Lys-Pro-Glu-Ala-Pro-Gly-Glu-Asp-Ala-Ser-Pro-Glu-Glu-Leu-Asn-Arg-Tyr-Tyr-Ala-Ser-Leu-Arg-His-Tyr-Leu-Asn-Leu-Val-Thr-Arg-Gln-Arg-Tyr-NH2 | 36 | Human | | 4325.3 | 9.2009 | -7.6 -9.8 -8.2 -14.4 -11.3 -11.3 -11.3 -16.6 -11.2 -10.8 -14.3 -13.1 -16.2 -13.6 -12.8 -5.5 -2 -13.5 -11.3 -3 -1.7 -.1 2.3 2.4 -5.9 -4.9 -1.7 -6.2 -13.5 | P 1306 |
| 333. | PEPTIDE YY (PYY) | #11 | Tyr-Pro-Ala-Lys-Pro-Glu-Ala-Pro-Gly-Glu-Asp-Ala-Ser-Pro-Glu-Glu-Leu-Ser-Arg-Tyr-Tyr-Ala-Ser-Leu-Arg-His-Tyr-Leu-Asn-Leu-Val-Thr-Arg-Gln-Arg-Tyr-NH2 | 36 | Porcine | | 4256.1 | 9.2009 | -10.3 -12.5 -10.9 -14.4 -11.3 -11.3 -11.3 -16.6 -11.2 -11.6 -11.6 -10.4 -13.5 -10.9 -10.1 -2.8 .7 -10.8 -11.3 -3 -1.7 -.1 2.3 2.4 -5.9 -4.9 -1.7 -6.2 -13.5 | P 5801 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 334. | PHI-27 | #11 | His-Ala-Asp-Gly-Val-Phe-Thr-Ser-Asp-Phe-Ser-Arg-Leu-Leu-Gly-Gln-Leu-Ser-Ala-Lys-Lys-Tyr-Leu-Glu-Ser-Leu-Ile-NH2 | 27 | Porcine | | 3010.8 | 9.5993 | .2 2.7 .1 3.6 3.3 2.9 -.3 -3.1 1.5 4.2 3.2 -.5 4.6 -4.4 -4.4 -7.5 -4.8 -4.8 .5 -5.2 | P 5048 |
| 335. | PHI-27 | #11 | His-Ala-Asp-Gly-Val-Phe-Thr-Ser-Asp-Tyr-Ser-Arg-Leu-Leu-Gly-Gln-Ile-Ser-Ala-Lys-Lys-Tyr-Leu-Glu-Ser-Leu-Ile-NH2 | 27 | Rat | | 3026.8 | 9.4484 | .2 -1.4 -4 -.5 -.8 -1.2 -4.4 -7.2 -1.9 .8 3.9 .2 5.3 -3.7 -3.7 -6.8 -4.1 -4.8 .5 -5.2 | P 4420 |
| 336. | PHM-27 (Human PHI) | #11 | His-Ala-Asp-Gly-Val-Phe-Thr-Ser-Asp-Phe-Ser-Lys-Leu-Leu-Gly-Gln-Leu-Ser-Ala-Lys-Lys-Tyr-Leu-Glu-Ser-Leu-Met-NH2 | 27 | | | 3000.7 | 9.5537 | .2 2.7 .1 3.6 3.9 3.5 .3 -2.5 2.1 4.8 3.8 .7 4.6 -4.4 -4.4 -7.5 -4.8 -4.8 -2.1 -7.8 | P 4295 |
| 337. | SECRETIN | #11 | His-Ser-Asp-Gly-Thr-Phe-Thr-Ser Glu-Leu-Ser-Arg-Leu-Arg-Glu-Gly-Ala-Arg-Leu-Gln-Arg-Leu-Leu-Gln-Gly-Leu-Val-NH2 | 27 | Human | | 3056.3 | 12.0041 | -10.8 -3.8 -3.8 -.3 -.6 .1 -10.7 -10.4 -7.8 -4.3 -8.8 -11.5 -7 -11.5 -3.2 -3.2 -3.2 -1.2 7.5 3.7 | S 7147 |
| 338. | SECRETIN | #11 | His-Ser-Asp-Gly-Thr-Phe-Thr-Ser Glu-Leu-Ser-Arg-Leu-Arg-Asp-Ser-Ala-Arg-Leu-Gln-Arg-Leu-Leu-Gln-Gly-Leu-Val-NH2 | 27 | Porcine | | 3072.2 | 12.0041 | -10.8 -3.8 -3.8 -.3 -.6 .1 -7.2 -10.8 -8.2 -4.7 -9.2 -11.9 -7.4 -11.9 -3.6 -3.6 -3.2 -1.2 7.5 3.7 | S 0137 |
| 339. | deamino-Tyr-b-Ala-SECRETIN | #11 | 3-[4-Hydroxyphenyl]propionyl-b-Ala-His-Ser-Asp-Gly-Thr-Phe-Thr-Ser-Glu-Leu-Ser-Arg-Leu-Arg-Asp-Ser-Ala-Arg-Leu-Gln-Arg-Leu-Leu-Gln-Gly-Leu-Val-NH2 | 28 | | | 3072.2 | | | S 4515 |
| 340. | TRP-MET-ASP-PHE AMIDE | #11 | Trp-Met-Asp-Phe-NH2 | 4 | | | 612.4 | 6.66 | | T 6515 |
| 341. | VALOSIN (Peptide VQY) | #11 | Val-Gln-Tyr-Pro-Val-Glu-His-Pro-Asp-Lys-Phe-Leu-Lys-Phe-Gly-Met-Thr-Pro-Ser-Lys-Gly-Val-Leu-Phe-Tyr | 25 | Porcine | | 2928.1 | 9.5668 | -6.3 -14 -11.6 -6.5 -4.9 -10.2 -7.1 -2 -1.1 .8 3.9 1.1 -7 1.1 2.1 5.3 2.1 | V 6505 |
| 342. | VASOACTIVE INTESTINAL PEPTIDE (VIP) | #11 | His-Ser-Asp-Ala-Val-Phe-Thr-Asp-Asn-Tyr-Thr-Arg-Leu-Arg-Lys-Gln-Met-Ala-Val-Lys-Lys-Tyr-Leu-Asn-Ser-Ile-Leu-Asn-NH2 | 28 | Porcine | | 3344.4 | 10.7332 | -2.9 -4.5 -4.4 -.9 -3.4 -7.6 -14.9 -21.6 -16.2 -10.9 -5.4 -9.2 -4.1 -13.1 -4.8 -.9 -1.7 .9 2.9 -5.2 -4.8 | V 3628 |
| 343. | [D-Phe2]-VASOACTIVE | #11 | His-D-Phe-Asp-Ala-Val-Phe-Thr- | 28 | Porcine | | 3404.5 | 10.7332 | -3.2 | V 8754 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | INTESTINAL PEPTIDE |  | Asp-Asn-Tyr-Thr-Arg-Leu-Arg-Lys-Gln-Met-Ala-Val-Lys-Lys-Tyr-Leu-Asn-Ser-Ile-Leu-Asn-NH2 |  |  |  |  |  |  |  |
| 344. | [D-p-Cl-Phe6,Leu17]-VASOACTIVE INTESTINAL PEPTIDE | #11 | His-Ser-Asp-Ala-Val-D-p-Chloro-Phe-Thr-Asp-Asn-Tyr-Thr-Arg-Leu-Arg-Lys-Gln-Leu-Ala-Val-Lys-Lys-Tyr-Leu-Asn-Ser-Ile-Leu-Asn-NH2 | 28 | Porcine |  | 3360.9 |  |  | V 4380 |
| 345. | [Lys1,Pro2,5,Arg3,4,Tyr6]-VASOACTIVE INTESTINAL PEPTIDE (Vasoactive Intestinal Peptide Antagonist) | #11 | Lys-Pro-Arg-Arg-Pro-Tyr-Thr-Asp-Asn-Tyr-Thr-Arg-Leu-Arg-Lys-Gln Met-Ala-Val-Lys-Lys-Tyr-Leu-Asn-Ser-Ile-Leu-Asn-NH2 | 28 | Porcine |  | 3489.9 | 11.6776 | -25.5 -22.5 -21.6 -21.6 -13.3 -11.7 -14.9 -21.6 -16.2 -10.9 -5.4 -9.2 -4.1 -13.1 -4.8 -.9 -1.7 .9 2.9 -5.2 -4.8 | V 2132 |
| 346. | VASOACTIVE INTESTINAL PEPTIDE (Fragment 1-12) | #11 | His-Ser-Asp-Ala-Val-Phe-Thr-Asp-Asn-Tyr-Thr-Arg | 12 | Human |  | 1423.9 | 5.1343 | -2.9 -4.5 -4.4 -.9 | V 0131 |
| 347. | VASOACTIVE INTESTINAL PEPTIDE (Fragment 10-28 ; VIP 10-28) | #11 | Tyr-Thr-Arg-Leu-Arg-Lys-Gln-Met-Ala-Val-Lys-Lys-Tyr-Leu-Asn-Ser-Ile-Leu-Asn-NH2 | 19 | Porcine |  | 2229.8 |  |  | V 5380 |
| 348. | [pGlu16]-VASOACTIVE INTESTINAL PEPTIDE (Fragment 16-28 ; VIP 16-28) | #11 | pGlu-Met-Ala-Val-Lys-Lys-Tyr-Leu-Asn-Ser-Val-Leu-Thr-NH2 | 13 | Chicken |  | 1512.1 |  |  | V 0879 |
| 349. | GROWTH HORMONE RELEASING FACTOR | #12 | Tyr-Ala-Asp-Ala-Ile-Phe-Thr-Asn-Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Asn-Arg-Gln-Gln-Gly-Glu-Arg-Asn-Gln-Glu-Gln-Gly-Ala-Lys-Val-Arg-Leu-NH2 | 44 | Bovine |  | 5126.8 | 11.0958 | 1.1 1.1 -4.2 -1.7 -3.2 -3.9 -7.1 -9.9 -2.6 -2.6 .5 1.1 4.4 .1 .1 -3 .5 -2.3 .4 -5.9 -4.3 -4.5 -11.8 -16 -16 -12.5 -21.5 -30.4 -30.4 -29.4 -26.3 -21 -20.6 -16.8 -15.8 -9.5 -6 | G 0644 |
| 350. | GROWTH HORMONE RELEASING FACTOR | #12 | Tyr-Ala-Asp-Ala-Ile-Phe-Thr-Asn-Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Ser-Arg-Gln-Gln-Gly-Glu-Ser-Asn-Gln-Glu-Arg-Gly-Ala-Arg-Ala-Arg-Leu-NH2 | 44 | Human |  | 5058.6 | 11.4208 | 1.1 1.1 -4.2 -1.7 -3.2 -3.9 -7.1 -9.9 -2.6 -2.6 .5 1.1 4.4 .1 .1 -3 .5 -2.3 .4 -2.2 -1.6 -1.8 -9.1 -13.3 -13.3 -10.6 -15.1 -24 -26.7 -22.2 -23.6 -18.3 -17.9 -17.1 -19.8 -13.5 -10 | G 8895 |
| 351. | GROWTH HORMONE | #12 | Tyr-Ala-Asp-Ala-Ile-Phe-Thr-Asn- | 44 | Porcine |  | 5127.8 | 11.4208 | 1.1 1.1 -4.2 -1.7 -3.2 -3.9 -7.1 - | G 0769 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | RELEASING FACTOR | | Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Ser-Arg-Gln-Gln-Gly-Glu-Arg-Asn-Gln-Glu-Gln-Gly-Ala-Arg-Val-Arg-Leu-NH2 | | | | | | 9.9 -2.6 -2.6 .5 1.1 4.4 .1 .1 -3 .5 -2.3 .4 -2.2 -1.6 -1.8 -9.1 -13.3 -13.3 -9.8 -18.8 -27.7 -30.4 -29.4 -26.3 -21 -20.6 -17.4 -16.4 -10.1 -6.6 | |
| 352. | GROWTH HORMONE RELEASING FACTOR | #12 | His-Ala-Asp-Ala-Ile-Phe-Thr-Ser-Ser-Tyr-Arg-Arg-Ile-Leu-Gly-Gln-Leu-Tyr-Ala-Arg-Lys-Leu-Leu-His-Glu-Ile-Met-Asn-Arg-Gln-Gln-Gly-Glu-Arg-Asn-Gln-Glu-Gln-Arg-Ser-Arg-Phe-Asn | 43 | Rat | | 5235.1 | 11.263 | 1.9 3.8 -1.5 1 -.8 -1.5 -4.7 -7.5 -2.9 -3.4 -.3 -.3 4.2 -.4 -.4 -3.2 -3.2 -2.5 .7 -5.6 -4 -4.2 -11.5 -15.7 -16 -12.5 -21.5 -30.4 -30.4 -29.4 -25.9 -27.7 -27.3 -25.5 -24.5 | G 6646 |
| 353. | GROWTH HORMONE RELEASING FACTOR FRAGMENTS (Fragment 1-40) | #12 | Tyr-Ala-Asp-Ala-Ile-Phe-Thr-Asn-Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Ser-Arg-Gln-Gln-Gly-Glu-Ser-Asn-Gln-Glu-Arg-Gly-Ala | 40 | Human | | 4544.1 | 9.9847 | 1.1 1.1 -4.2 -1.7 -3.2 -3.9 -7.1 -9.9 -2.6 -2.6 .5 1.1 4.4 .1 .1 -3 .5 -2.3 .4 -2.2 -1.6 -1.8 -9.1 -13.3 -13.3 -10.6 -15.1 -24 -26.7 -22.2 -23.6 -18.3 | G 8770 |
| 354. | GROWTH HORMONE RELEASING FACTOR FRAGMENTS (Fragment 1-29 Amide) | #12 | Tyr-Ala-Asp-Ala-Ile-Phe-Thr-Asn-Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Asn-Arg-NH2 | 29 | Bovine | | 3403.4 | 10.4712 | 1.1 1.1 -4.2 -1.7 -3.2 -3.9 -7.1 -9.9 -2.6 -2.6 .5 1.1 4.4 .1 .1 -3 .5 -2.3 .4 -5.9 -4.3 -1 | G 0394 |
| 355. | GROWTH HORMONE RELEASING FACTOR FRAGMENTS (Fragment 1-29 Amide) | #12 | Tyr-Ala-Asp-Ala-Ile-Phe-Thr-Asn-Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Ser-Arg-NH2 | 29 | Human | | 3376.3 | 10.4712 | 1.1 1.1 -4.2 -1.7 -3.2 -3.9 -7.1 -9.9 -2.6 -2.6 .5 1.1 4.4 .1 .1 -3 .5 -2.3 .4 -2.2 -1.6 1.7 | G 6771 |
| 356. | GROWTH HORMONE RELEASING FACTOR FRAGMENTS ([D-Ala2]-Fragment 1-29 Amide) | #12 | Tyr-D-Ala-Asp-Ala-Ile-Phe-Thr-Asn-Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Ser-Arg-NH2 | 29 | Human | | 3376.3 | 10.4712 | -1.3 | G 3646 |
| 357. | GROWTH HORMONE RELEASING FACTOR FRAGMENTS ([N-Acetyl-Tyr1,D-Arg2]-Fragment 1-29 Amide) | #12 | N-Acetyl-Tyr-D-Arg-Asp-Ala-Ile-Phe-Thr-Asn-Ser-Tyr-Arg-Lys-Val Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Met-Ser-Arg-NH2 | 29 | Human | | 3299.4 | | | G 3644 |
| 358. | GROWTH HORMONE | #12 | Tyr-Ala-Asp-Ala-Ile-Phe-Thr-Asn- | 29 | Human | | 3376.4 | | | G 6521 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | RELEASING FACTOR FRAGMENTS ([Nle27]-Fragment 1-29 Amide) |  | Ser-Tyr-Arg-Lys-Val-Leu-Gly-Gln-Leu-Ser-Ala-Arg-Lys-Leu-Leu-Gln-Asp-Ile-Nle-Ser-Arg-NH2 |  |  |  |  |  |  |  |
| 359. | GROWTH HORMONE RELEASING FACTOR FRAGMENTS (Fragment 1-29 Amide) | #12 | His-Ala-Asp-Ala-Ile-Phe-Thr-Ser-Ser-Tyr-Arg-Arg-Ile-Leu-Gly-Gln-Leu-Tyr-Ala-Arg-Lys-Leu-Leu-His-Glu-Ile-Met-Asn-Arg-NH2 | 29 | Rat |  | 3491.6 | 10.6792 | 1.9 3.8 -1.5 1 -.8 -1.5 -4.7 -7.5 -2.9 -3.4 -.3 -.3 4.2 -.4 -.4 -3.2 -3.2 -2.5 .7 -5.6 -4 -.7 | G 0519 |
| 360. | D-LYS-TYR-D-TRP-D-TRP-PHE AMIDE | #12 | D-Lys-Tyr-D-Trp-D-Trp-Phe-NH2 | 5 |  |  | 845.7 | 0 |  | L 4135 |
| 361. | D-TRP-ALA-TRP-D-PHE AMIDE | #12 | D-Trp-Ala-Trp-D-Phe-NH2 | 4 |  |  | 624.5 |  |  | T 9768 |
| 362. | TYR-GLY-D-TRP-PHE-D-PHE AMIDE | #12 | Tyr-Gly-D-Trp-Phe-D-Phe-NH2 | 5 |  |  | 734.5 |  |  | T 4517 |
| 363. | TYR-D-TRP-ALA-TRP-D-PHE AMIDE | #12 | Tyr-D-Trp-Ala-Trp-D-Phe-NH2 | 5 |  |  | 787.6 |  |  | T 5517 |
| 364. | TYR-D-TRP-ALA-TRP-D-PHE METHYLAMIDE | #12 | Tyr-D-Trp-Ala-Trp-D-Phe-NHMe | 5 |  |  | 801.6 |  |  | T 9142 |
| 365. | LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH2 | 10 | Human |  | 1216.9 |  |  | L 7134 |
| 366. | LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-Gly-Trp-Leu-Pro-Gly-NH2 | 10 | Salmon |  | 1245.9 |  |  | L 4897 |
| 367. | [Gln8]-LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-Gly-Leu-Gln-Pro-Gly-NH2 | 10 | Avian |  | 1187.8 |  |  | L 0637 |
| 368. | [Gly-OH10]-LH-RH (LH-RH free acid) | #13 | pGlu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly | 10 |  |  | 1200.9 |  |  | L 8008 |
| 369. | [D-Ala6]-LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-D-Ala-Leu-Arg-Pro-Gly-NH2 | 10 |  |  | 1230.9 |  |  | L 1898 |
| 370. | [D-Lys6]-LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-D-Lys-Leu-Arg-Pro-Gly-NH2 | 10 |  |  | 1289 |  |  | L 5022 |
| 371. | [D-Trp6]-LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-D-Trp-Leu-Arg-Pro-Gly-NH2 | 10 |  |  | 1346.1 |  |  | L 9761 |
| 372. | [Hyp9]-LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Hyp-Gly-NH2 | 10 |  |  | 1232.9 |  |  | L 7154 |
| 373. | des-pGlu1-LH-RH | #13 | His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH2 | 9 |  |  | 1088.8 | 11.341 | -9.3 -6.1 | L 8762 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 374. | [D-Ala6,N-Me-Leu7]-LH-RH | #13 | pGlu-His-Trp-Ser-Tyr-D-Ala-N-Methyl-Leu-Arg-Pro-Gly-NH2 | 10 | | | 1117.8 | | | L 6884 |
| 375. | [D-Phe2,D-Ala6]-LH-RH | #13 | pGlu-D-Phe-Trp-Ser-Tyr-D-Ala-Leu-Arg-Pro-Gly-NH2 | 10 | | | 1240.9 | | | L 0387 |
| 376. | [D-Phe2,6,Pro3]-LH-RH | #13 | pGlu-D-Phe-Pro-Ser-Tyr-D-Phe-Leu-Arg-Pro-Gly-NH2 | 10 | | | 1227.9 | | | L 4261 |
| 377. | [D-pGlu1,D-Phe2,D-Trp3,6]-LH-RH | #13 | D-pGlu-D-Phe-D-Trp-Ser-Tyr-D-Trp-Leu-Arg-Pro-Gly-NH2 | 10 | | | 1228 | | | L 6524 |
| 378. | [Ac-3,4-dehydro-Pro1,D-p-F Phe2,D-Trp3,6]-LH-RH | #13 | Acetyl-D3-Pro-D-p-Fluoro-Phe-D-Trp-Ser-Tyr-D-Trp-Leu-Arg-Pro-Gly-NH2 | 10 | | | 1246 | | | L 9886 |
| 379. | [Ac-D-p-Cl-Phe1,2,D-Trp3,D-Arg6,D-Ala10]-LH-RH | #13 | Acetyl-D-p-Chloro-Phe-D-p-Chloro-Phe-D-Trp-Ser-Tyr-D-Arg-Leu-Arg-Pro-D-Ala-NH2 | 10 | | | 1247.5 | | | L 9011 |
| 380. | [Ac-D-Trp1,D-p-Cl-Phe2,D-Trp3,D-Arg6,D-Ala10]-LH-RH | #13 | Acetyl-D-Trp-D-p-Chloro-Phe-D-Trp-Ser-Tyr-D-Arg-Leu-Arg-Pro-D-Ala-NH2 | 10 | | | 1475.7 | | | L 0137 |
| 381. | des-Gly10-LH-RH Ethylamide | #13 | pGlu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-NHEt | 9 | | | 1046.8 | | | L 0262 |
| 382. | des-Gly10,[D-Ala6]-LH-RH Ethylamide | #13 | pGlu-His-Trp-Ser-Tyr-D-Ala-Leu-Arg-Pro-NHEt | 9 | | | 1060.8 | | | L 4513 |
| 383. | des-Gly10,[D-Phe6]-LH-RH Ethylamide | #13 | pGlu-His-Trp-Ser-Tyr-D-Phe-Leu-Arg-Pro-NHEt | 9 | | | 1136.9 | | | L 8886 |
| 384. | des-Gly10,[D-Trp6]-LH-RH Ethylamide (Deslorelin) | #13 | pGlu-His-Trp-Ser-Tyr-D-Trp-Leu-Arg-Pro-NHEt | 9 | | | 1176 | | | L 5386 |
| 385. | des-Gly10,[D-His(Bzl)6]-LH-RH Ethylamide | #13 | pGlu-His-Trp-Ser-Tyr-D-His[Bzl]-Leu-Arg-Pro-NHEt | 9 | | | 989.8 | | | L 2761 |
| 386. | LUTEINIZING HORMONE RELEASING HORMONE FRAGMENTS (Fragment 3-10) | #13 | Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH2 | 8 | | | 951.7 | 11.35 | | L 5512 |
| 387. | LUTEINIZING HORMONE RELEASING HORMONE FRAGMENTS (Fragment 4-10) | #13 | Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH2 | 7 | | | 765.5 | 11.333 | | L 5387 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 388. | LUTEINIZING HORMONE RELEASING HORMONE FRAGMENTS (Fragment 7-10) | #13 | Leu-Arg-Pro-Gly-NH2 | 4 | | | 458.4 | 17 | | L 3398 |
| 389. | ANTIDE | #13 | Acetyl-b-[2-Naphthyl]-D-Ala-D-p-Chloro-Phe-b-[3-Pyridyl]-D-Ala-Ser-Ne-[Nicotinoyl]-Lys-Ne-[Nicotinoyl]-D-Lys-Leu-Ne-[Isopropyl]-Lys-Pro-D-Ala-NH2 | 10 | | | 583.8 | | | A 8802 |
| 390. | a-MELANOCYTE STIMULATING HORMONE (a-MSH) | #14 | N-Acetyl-Ser-Tyr-Ser-Met-Glu-His-Phe-Arg-Trp-Gly-Lys-Pro-Val-NH2 | 13 | | | 1683.2 | | | M 4135 |
| 391. | a-MELANOCYTE STIMULATING HORMONE ([Val-OH13]-a-MSH ; a-MSH free acid) | #14 | N-Acetyl-Ser-Tyr-Ser-Met-Glu-His-Phe-Arg-Trp-Gly-Lys-Pro-Val | 13 | | | 1667.2 | | | M 7892 |
| 392. | a-MELANOCYTE STIMULATING HORMONE (des-Ac-a-MSH) | #14 | Ser-Tyr-Ser-Met-Glu-His-Phe-Arg Trp-Gly-Lys-Pro-Val-NH2 | 13 | | | 1640.2 | 10.4986 | -10.3 -9.9 -8.6 -13.3 -11 -7.5 | M 8267 |
| 393. | a-MELANOCYTE STIMULATING HORMONE ([Di-Ac]-a-MSH) | #14 | N-Acetyl-Ser[Ac]-Tyr-Ser-Met-Glu-His-Phe-Arg-Trp-Gly-Lys-Pro-Val-NH2 | 1 | | | 133.1 | 1 | | M7896 |
| 394. | a-MELANOCYTE STIMULATING HORMONE ([Nle4,D-Phe7]-a-MSH) | #14 | N-Acetyl-Ser-Tyr-Ser-Nle-Glu-His-D-Phe-Arg-Trp-Gly-Lys-Pro-Val-NH2 | 13 | | | 1683.3 | | | M 8901 |
| 395. | N-Ac-[Cys4,10,D-Phe7]-a-MELANOCYTE STIMULATING HORMONE FRAGMENT 4-13 | #14 | N-Acetyl-Cys-Glu-His-D-Phe-Arg-Trp-Cys-Lys-Pro-Val-NH2 | 10 | | [Disulfide Bridge; 4-10 | 1249.1 | | | M 7907 |
| 396. | [D-Trp7,Ala8,D-Phe10]-a-MELANOCYTE STIMULATING HORMONE FRAGMENT 6-11 AMIDE | #14 | His-D-Trp-Ala-Trp-D-Phe-Lys-NH2 | 6 | | | 890.7 | 14 | | M 2910 |
| 397. | b-MELANOCYTE STIMULATING HORMONE | #14 | Ala-Glu-Lys-Lys-Asp-Glu-Gly-Pro-Tyr-Arg-Met-Glu-His-Phe-Arg-Trp- | 22 | Human | | 2659.9 | 7.823 | -19.8 -21.6 -20.7 -20.3 -19.6 -13.3 -9.8 -14.8 -13.6 -13.1 -10.2 | M 6513 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Gly-Ser-Pro-Pro-Lys-Asp | | | | | | -13.7 -10.2 -10.9 | |
| 398. | b-MELANOCYTE STIMULATING HORMONE | #14 | Asp-Glu-Gly-Pro-Tyr-Lys-Met-Glu His-Phe-Arg-Trp-Gly-Ser-Pro-Pro-Lys-Asp | 18 | Porcine | | 2174.5 | 5.3486 | -19 -12.7 -9.2 -14.2 -13 -12.5 -10.2 -13.7 -10.2 -10.9 | M 2018 |
| 399. | g-MELANOCYTE STIMULATING HORMONE | #14 | Tyr-Val-Met-Gly-His-Phe-Arg-Trp-Asp-Arg-Phe-Gly | 12 | | | 1571.2 | 9.617 | -1.4 -3.6 -9.5 -11.8 | M 9638 |
| 400. | d-MELANOCYTE STIMULATING HORMONE | #14 | Ser-Met-Glu-Val-Arg-Gly-Trp | 7 | | | 863.7 | 6.64 | | M 4517 |
| 401. | Tyr-[Trp2]-MSH Inhibiting Factor | #14 | Tyr-Pro-Trp-Gly-NH2 | 4 | | | 537.4 | 9.62 | | M 8009 |
| 402. | KINETENSIN | #15 | Ile-Ala-Arg-Arg-His-Pro-Tyr-Phe-Leu | 9 | | | 1174 | 11.2296 | -2.2 | K 1879 |
| 403. | NEUROTENSIN | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-Tyr-Ile-Leu | 13 | | | 1691.5 | | | N 6383 |
| 404. | [3,5-DiBr-Tyr11]-NEUROTENSIN | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-3,5-Dibromo-Tyr-Ile-Leu | 13 | | | 1849.3 | | | N 3010 |
| 405. | [Gln4]-NEUROTENSIN | #15 | pGlu-Leu-Tyr-Gln-Asn-Lys-Pro-Arg-Arg-Pro-Tyr-Ile-Leu | 13 | | | 1691.5 | | | N 9885 |
| 406. | [D-Phe11]-NEUROTENSIN | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-D-Phe-Ile-Leu | 13 | | | 1675.5 | | | N 0136 |
| 407. | [Phe11]-NEUROTENSIN | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-Phe-Ile-Leu | 13 | | | 1675.5 | | | N 0386 |
| 408. | [D-Trp11]-NEUROTENSIN | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-D-Trp-Ile-Leu | 13 | | | 1714.6 | | | N 2760 |
| 409. | [D-Tyr11]-NEUROTENSIN | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-D-Tyr-Ile-Leu | 13 | | | 1691.5 | | | N 0261 |
| 410. | NEUROTENSIN FRAGMENTS (Fragment 1-6) | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys | 6 | | | 793.6 | | | N 9760 |
| 411. | NEUROTENSIN FRAGMENTS (Fragment 1-8) | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg | 8 | | | 1047.9 | | | N 0509 |
| 412. | NEUROTENSIN FRAGMENTS ([Thr3]- | #15 | pGlu-Leu-Thr-Glu-Asn-Lys-Pro-Arg | 8 | | | 985.9 | | | N 6638 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | Fragment 1-8) |  |  |  |  |  |  |  |  |  |
| 413. | NEUROTENSIN FRAGMENTS (Fragment 1-11) | #15 | pGlu-Leu-Tyr-Glu-Asn-Lys-Pro-Arg-Arg-Pro-Tyr | 11 |  |  | 1465.3 |  |  | N 0634 |
| 414. | NEUROTENSIN FRAGMENTS (Fragment 8-13) | #15 | Arg-Arg-Pro-Tyr-Ile-Leu | 6 |  |  | 818.8 | 11.162 |  | N 5266 |
| 415. | NEUROTENSIN FRAGMENTS (Na-Ac-Fragment 8-13) | #15 | Acetyl-Arg-Arg-Pro-Tyr-Ile-Leu | 6 |  |  | 860.8 |  |  | N 0511 |
| 416. | NEUROTENSIN FRAGMENTS (Lys8-y-(CH2NH)-Lys9]-Fragment 8-13) | #15 | Lys-y-[CH2NH]-Lys-Pro-Tyr-Ile-Leu | 6 |  |  | 633.5 |  |  | N 0522 |
| 417. | Na,Ne-di-t-BOC-[Lys9]-Fragment 9-13 Methyl Ester | #15 | [t-BOC]2-Lys-Pro-Tyr-Ile-Leu-OMe | 5 |  |  | 535.4 |  |  | N 9140 |
| 418. | ADRENAL PEPTIDE E (BAM-3200) | #16 | Tyr-Gly-Gly-Phe-Met-Arg-Arg-Val-Gly-Arg-Pro-Glu-Trp-Trp-Met-Asp Tyr-Gln-Lys-Arg-Tyr-Gly-Gly-Phe-Leu | 25 | Bovine |  | 3158.5 | 10.3 | -2.6 -1.3 -7 -10.1 -13.8 -16.6 -10.2 -5.7 -14.7 -17.8 -13.3 -15.6 -17.9 -17.4 -16.9 -16 -8.7 | A 2159 |
| 419. | ALA-GLY-GLU-GLY-LEU-SER-SER-PRO-PHE-TRP-SER-LEU-ALA-ALA-PRO-GLN-ARG-PHE AMIDE | #16 | Ala-Gly-Glu-Gly-Leu-Ser-Ser-Pro-Phe-Trp-Ser-Leu-Ala-Ala-Pro-Gln-Arg-Phe-NH2 | 18 |  |  | 1936.2 | 11.175 | .9 -1.8 -2.2 5.1 7.3 5.3 4.5 1.8 3.4 -1.1 -.2 | A 5296 |
| 420. | BOVINE ADRENAL MEDULLA DOCOSAPEPTIDE (BAM-22P) | #16 | Tyr-Gly-Gly-Phe-Met-Arg-Arg-Val-Gly-Arg-Pro-Glu-Trp-Trp-Met-Asp Tyr-Gln-Lys-Arg-Tyr-Gly | 22 |  |  | 2841.3 | 10.3 | -2.6 -1.3 -7 -10.1 -13.8 -16.6 -10.2 -5.7 -14.7 -17.8 -13.3 -15.6 -17.9 -17.4 | B 4264 |
| 421. | BOVINE ADRENAL MEDULLA DODECAPEPTIDE (BAM-12P) | #16 | Tyr-Gly-Gly-Phe-Met-Arg-Arg-Val-Gly-Arg-Pro-Glu | 12 |  |  | 1426.2 | 11.073 | -2.6 -1.3 -7 -10.1 | B 4139 |
| 422. | a-CASEIN FRAGMENTS (Fragment 90-95) | #16 | Arg-Tyr-Leu-Gly-Tyr-Leu | 6 |  |  | 784.6 | 9.3674 |  | C 1658 |
| 423. | a-CASEIN FRAGMENTS | #16 | Arg-Tyr-Leu-Gly-Tyr-Leu-Glu | 7 |  |  | 912.7 | 6.5 |  | C 1783 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | (Fragment 90-96) |  |  |  |  |  |  |  |  |  |
| 424. | b-CASOMORPHIN | #16 | Tyr-Pro-Phe-Pro-Gly-Pro-Ile | 7 | Bovine |  | 789.6 | 5.7 |  | C 5900 |
| 425. | b-CASOMORPHIN | #16 | Tyr-Pro-Phe-Val-Glu-Pro-Ile | 7 | Human |  | 862.7 | 3.195 |  | C 0783 |
| 426. | b-CASOMORPHIN FRAGMENTS (Fragment 1-3) | #16 | Tyr-Pro-Phe | 3 | Bovine |  | 425.3 | 5.6 |  | C 3146 |
| 427. | b-CASOMORPHIN FRAGMENTS ([D-Ala2,p-Cl-Phe3]-Fragment 1-4 Amide) | #16 | Tyr-D-Ala-p-Chloro-Phe-Pro-NH2 | 4 | Bovine |  | 546.8 |  |  | C 2408 |
| 428. | b-CASOMORPHIN FRAGMENTS (Fragment 1-5) | #16 | Tyr-Pro-Phe-Pro-Gly | 5 | Bovine |  | 579.4 | 5.7 |  | C 5147 |
| 429. | b-CASOMORPHIN FRAGMENTS ([D-Ala2,4,Tyr5]-Fragment 1-5 Amide) | #16 | Tyr-D-Ala-Phe-D-Ala-Tyr-NH2 | 5 |  |  | 649.3 | 9.62 |  | C 2283 |
| 430. | b-CASOMORPHIN FRAGMENTS (des-Tyr1-Fragment) | #16 | Pro-Phe-Pro-Gly-Pro-Ile | 6 | Bovine |  | 626.5 | 6.7 |  | C 3396 |
| 431. | N-CBZ-PRO-D-LEU | #16 | N-CBZ-Pro-D-Leu | 2 |  |  | 131.1 |  |  | C 4644 |
| 432. | CYCLO(LEU-GLY) (Morphine tolerance peptide ; 3-Isobutyl-2,5-piperazinedione) | #16 | Cyclo(Leu-Gly) | 2 |  |  | 188.1 |  |  | C 3526 |
| 433. | DERMORPHIN | #16 | Tyr-D-Ala-Phe-Gly-Tyr-Pro-Ser-NH2 | 7 |  |  | 819.4 | 9.4221 |  | D 6160 |
| 434. | [Ser(Ac)7]-DERMORPHIN | #16 | Tyr-D-Ala-Phe-Gly-Tyr-Pro-Ser [Ac]-NH2 | 7 |  |  | 716.4 |  |  | D 9910 |
| 435. | DERMORPHIN FRAGMENTS ([D-Arg2,Lys4]-Fragment 1-4 Amide) | #16 | Tyr-D-Arg-Phe-Lys-NH2 | 4 |  |  | 630.5 | 9.62 |  | D 9424 |
| 436. | DERMORPHIN FRAGMENTS ([Phe4- | #16 | Tyr-D-Arg-Phe-Phe-NH2 | 4 |  |  | 648.5 | 9.62 |  | D 9549 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | Fragment 1-4 Amide) | | | | | | | | | |
| 437. | KYOTORPHIN | #16 | Tyr-Arg | 2 | | | 338.3 | 9.6183 | | K 2001 |
| 438. | [D-Arg2]-KYOTORPHIN | #16 | Tyr-D-Arg | 2 | | | 338.3 | 5.5 | | K 0252 |
| 439. | MORPHICEPTIN (b-Casomorphin[1-4] amide) | #16 | Tyr-Pro-Phe-Pro-NH2 | 4 | | | 538.4 | 9.62 | | M 4264 |
| 440. | PHE-LEU-PHE-GLN-PRO-GLN-ARG-PHE AMIDE | #16 | Phe-Leu-Phe-Gln-Pro-Gln-Arg-Phe-NH2 | 8 | | | 1098.9 | 17 | | P 3293 |
| 441. | TYR-D-ALA-PHE-ASP-VAL-VAL-GLY AMIDE ([D-Ala2]-Deltorphin I) | #16 | Tyr-D-Ala-Phe-Asp-Val-Val-Gly-NH2 | 7 | | | 784.4 | 6.48 | | T 0533 |
| 442. | TYR-D-ALA-PHE-GLU-VAL-VAL-GLY AMIDE ([D-Ala2]-Deltorphin II) | #16 | Tyr-D-Ala-Phe-Glu-Val-Val-Gly-NH2 | 7 | | | 798.5 | 6.57 | | T 0675 |
| 443. | TYR-GLY-GLY-PHE-MET-ARG-ARG-VAL (Metorphamide, free acid ; Adrenorphin, free acid) | #16 | Tyr-Gly-Gly-Phe-Met-Arg-Arg-Val | 8 | | | 986.8 | 11.167 | | T 8156 |
| 444. | TYR-GLY-GLY-PHE-MET-ARG-ARG-VAL AMIDE (Metorphamide ; Adrenorphin) | #16 | Tyr-Gly-Gly-Phe-Met-Arg-Arg-Val-NH2 | 8 | | | 1002.8 | 12.4842 | | T 8281 |
| 445. | TYR-PRO-VAL-PRO AMIDE ([Val3]-Morphiceptin) | #16 | Tyr-Pro-Val-Pro-NH2 | 4 | | | 490.4 | 9.62 | | T 3024 |
| 446. | ISOTOCIN | #17 | Cys-Tyr-Ile-Ser-Asn-Cys-Pro-Ile-Gly-NH2 | 9 | | 1-6 | 984.7 | 8.314 | 6.4 3.9 | I 6131 |
| 447. | OXYTOCIN (a-Hypophamine) | #17 | Cys-Tyr-Ile-Gln-Asn-Cys-Pro-Leu-Gly-NH2 | 9 | | 1-6 | 1025.8 | 8.314 | 3 .5 | O 6379 |
| 448. | [Asu1,6]-OXYTOCIN | #17 | Tyr-Ile-Gln-Asn-Asu-Pro-Leu-Gly-NH2 | 8 | | | 819.6 | | | O 1627 |
| 449. | [Thr4,Gly7]-OXYTOCIN | #17 | Cys-Tyr-Ile-Thr-Asn-Cys-Gly-Leu-Gly-NH2 | 9 | | 1-6 | 958.7 | 8.314 | 7 4.5 | O 6380 |
| 450. | TYR-PRO-LEU-GLY AMIDE ([Tyr6]-Oxytocin Fragment 6-9) | #17 | Tyr-Pro-Leu-Gly-NH2 | 4 | | | 464.3 | 9.62 | | T 2899 |
| 451. | TOCINOIC ACID ([Ile3]- | #17 | Cys-Tyr-Ile-Gln-Asn-Cys | 6 | | 1-6 | 742.6 | 4.95 | | T 3149 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | Pressinoic acid) | | | | | | | | | |
| 452. | [Arg8]-VASOPRESSIN (Antidiuretic hormone ; b-Hypophamine ; Arginine vasopressin) | #17 | Cys-Tyr-Phe-Gln-Asn-Cys-Pro-Arg-Gly-NH2 | 9 | | 1-6 | 1103.9 | 9.3437 | -7 -9.5 | V 9879 |
| 453. | [Lys8]-VASOPRESSIN (Lysine vasopressin ; Lyspressin) | #17 | Cys-Tyr-Phe-Gln-Asn-Cys-Pro-Lys-Gly-NH2 | 9 | | 1-6 | 1075.8 | 9.3016 | -6.4 -8.9 | V 6879 |
| 454. | [Arg8,Gly-OH9]-VASOPRESSIN | #17 | Cys-Tyr-Phe-Gln-Asn-Cys-Pro-Arg-Gly | 9 | | 1-6 | 1087.9 | 8.3139 | -7 | V 2380 |
| 455. | [Asu1,6,Arg8]-VASOPRESSIN | #17 | Tyr-Phe-Gln-Asn-Asu-Pro-Arg-Gly-NH2 | 8 | | | 897.7 | | | V 6254 |
| 456. | [deamino-Cys1,D-Arg8]-VASOPRESSIN (Desmopressin) | #17 | 3-Mercaptopropionyl-Tyr-Phe-Gln-Asn-Cys-Pro-D-Arg-Gly-NH2 | 8 | | 1-6 | 1089.9 | | | V 1005 |
| 457. | [deamino-Cys1,D-3-(Pyridyl)-Ala2,Arg8]-VASOPRESSIN | #17 | 3-Mercaptopropionyl-D-3-[Pyridyl]-Ala-Phe-Gln-Asn-Cys-Pro-Arg-Gly-NH2 | 8 | | 1-6 | 1074.8 | | | V 2257 |
| 458. | [deamino-Pen1,Val4,D-Arg8]-VASOPRESSIN | #17 | 3-Mercapto-3-methylbutyryl-Tyr-Phe-Val-Asn-Cys-Pro-D-Arg-Gly-NH2 | 8 | | 1-6 | 1088.9 | | | V 2005 |
| 459. | [deamino-Pen1,O-Me-Tyr2,Arg8]-VASOPRESSIN | #17 | 3-Mercapto-3-methylbutyryl-Tyr [O-Methyl]-Phe-Gln-Asn-Cys-Pro-Arg-Gly-NH2 | 8 | | 1-6 | 1131.9 | | | V 1880 |
| 460. | [b-Mercapto-b,b-cyclopentamethylenepropionyl1,O-Et-Tyr2,Val4,Arg8]-VASOPRESSIN | #17 | [1-Mercaptocyclohexyl]acetyl-Tyr [O-Ethyl]-Phe-Val-Asn-Cys-Pro-Arg-Gly-NH2 | 8 | | 1-6 | 808.7 | | | V 4253 |
| 461. | [b-Mercapto-b,b-cyclopentamethylenepropionyl1,O-Me-Tyr2,Arg8]-VASOPRESSIN (Manning Compound) | #17 | [1-Mercaptocyclohexyl]acetyl-Tyr [O-Methyl]-Phe-Gln-Asn-Cys-Pro-Arg-Gly-NH2 | 8 | | 1-6 | 837.7 | | | V 2255 |
| 462. | des-Gly-NH29,[Arg8]-VASOPRESSIN | #17 | Cys-Tyr-Phe-Gln-Asn-Cys-Pro-Arg | 8 | | 1-6 | 1030.9 | 8.3139 | | V 0380 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 463. | Ala-Gly-[Arg8]-VASOPRESSIN | #17 | Ala-Gly-Cys-Tyr-Phe-Gln-Asn-Cys-Pro-Arg-Gly-NH2 | 11 |  | 1-6 | 1231.9 | 9.1573 | -.7 -2.5 -7 -9.5 | V 5378 |
| 464. | Val-Asp-[Arg8]-VASOPRESSIN | #17 | Val-Asp-Cys-Tyr-Phe-Gln-Asn-Cys-Pro-Arg-Gly-NH2 | 11 |  | 1-6 | 1317 | 8.288 | -1.4 -9.1 -7 -9.5 | V 5253 |
| 465. | [pGlu4,Cyt6,Arg8]-VASOPRESSIN (Fragment 4-9) | #17 | pGlu-Asn-Cys[Cys]-Pro-Arg-Gly-NH2 | 6 |  |  | 791.7 |  |  | V 0255 |
| 466. | des-Gly9-[b-Mercapto-b,b-cyclopentamethylenepropionyl1,O-Et-Tyr2,Val4,Arg8]-VASOPRESSIN | #17 | [1-Mercaptocyclohexyl]acetyl-Tyr[O-Ethyl]-Phe-Val-Asn-Cys-Pro-Arg-NH2 | 7 |  | 1-6 | 751.7 |  |  | V 4503 |
| 467. | [Adamantaneacetyl1,O-Et-D-Tyr2,Val4, Aminobutyryl6,Arg8,9]-VASOPRESSIN | #17 | 1-Adamantaneacetyl-D-Tyr[O-Ethyl]-Phe-Val-Asn-Abu-Pro-Arg-Arg-NH2 | 8 |  |  | 1257.9 |  |  | V 2381 |
| 468. | VASOTOCIN ([Arg8]-Vasotocin) | #17 | Cys-Tyr-Ile-Gln-Asn-Cys-Pro-Arg-Gly-NH2 | 9 |  | 1-6 | 1069.9 | 9.3437 | -5.3 -7.8 | V 0130 |
| 469. | VASOTOCIN ([Arg8,Gly10]-Vasotocin ; Hydrin 2) | #17 | Cys-Tyr-Ile-Gln-Asn-Cys-Pro-Arg-Gly-Gly | 10 |  | 1-6 | 1110.9 | 8.3139 | -5.3 -8.2 | V 1133 |
| 470. | VASOTOCIN ([Lys8,Gly-OH9]-Vasotocin) | #17 | Cys-Tyr-Ile-Gln-Asn-Cys-Pro-Lys-Gly | 9 |  | 1-6 | 1025.8 | 8.3112 | -4.7 | V 2880 |
| 471. | VASOTOCIN ([Asu1,6,Arg8]-Vasotocin) | #17 | Tyr-Ile-Gln-Asn-Asu-Pro-Arg-Gly-NH2 | 8 |  |  | 863.7 |  |  | V 6877 |
| 472. | VASOTOCIN ([Arg8,Gly10,Lys11,Arg12]-Vasotocin ; Hydrin I) | #17 | Cys-Tyr-Ile-Gln-Asn-Cys-Pro-Arg-Gly-Gly-Lys-Arg | 12 |  | 1-6 | 1397.2 | 10.2442 | -5.3 -8.2 -6.9 -15.3 | V 1258 |
| 473. | HYPERCALCEMIA OF MALIGNANCY FACTOR-40 (PTH-Like Adenylate Cyclase Stimulating Protein ; PTH-Related Peptide [1-40]) | #18 | Ala-Val-Ser-Glu-His-Gln-Leu-Leu-His-Asp-Lys-Gly-Lys-Ser-Ile-Gln-Asp-Leu-Arg-Arg-Arg-Phe-Phe-Leu-His-His-Leu-Ile-Ala-Glu-Ile-His-Thr-Ala-Glu-Ile-Arg-Ala-Thr-Ser | 40 | Human |  | 4674.4 | 10.1124 | -.6 -2.4 -10.1 -13.6 -10.1 -11.6 -3.6 -10.9 -14.7 -11.2 -11.6 -8.3 -16.3 -10.2 -6.6 -7.3 -7 -6.7 -6.7 2.3 8.6 9.6 11.3 5.3 .8 5.8 5.5 6.2 1.7 -2.8 0 -5.3 | H 4644 |
| 474. | HYPERCALCEMIA OF MALIGNANCY FACTOR FRAGMENT 1-16 (PTH- | #18 | Ala-Val-Ser-Glu-His-Gln-Leu-Leu-His-Asp-Lys-Gly-Lys-Ser-Ile-Gln | 16 | Human |  | 1789.1 | 8.062 | -.6 -2.4 -10.1 -13.6 -10.1 -11.6 -3.6 -10.9 | H 3270 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | Related Peptide [1-16]) |  |  |  |  |  |  |  |  |  |
| 475. | HYPERCALCEMIA OF MALIGNANCY FACTOR FRAGMENT 1-34 AMIDE (PTH-Related Peptide [1-34] Amide) | #18 | Ala-Val-Ser-Glu-His-Gln-Leu-Leu-His-Asp-Lys-Gly-Lys-Ser-Ile-Gln-Asp-Leu-Arg-Arg-Arg-Phe-Phe-Leu-His-His-Leu-Ile-Ala-Glu-Ile-His-Thr-Ala-NH2 | 34 | Human |  | 4032.9 | 10.8215 | -.6 -2.4 -10.1 -13.6 -10.1 -11.6 -3.6 -10.9 -14.7 -11.2 -11.6 -8.3 -16.3 -10.2 -6.6 -7.3 -7 -6.7 -6.7 2.3 8.6 9.6 11.3 5.3 .8 5.8 9 | H 9148 |
| 476. | HYPERCALCEMIA OF MALIGNANCY FACTOR FRAGMENT 7-34 AMIDE (PTH-Related Peptide [7-34] Amide) | #18 | Leu-Leu-His-Asp-Lys-Gly-Lys-Ser-Ile-Gln-Asp-Leu-Arg-Arg-Arg-Phe-Phe-Leu-His-His-Leu-Ile-Ala-Glu-Ile-His-Thr-Ala-NH2 | 28 | Human |  | 3382.5 | 11.5468 | -3.6 -10.9 -14.7 -11.2 -11.6 -8.3 -16.3 -10.2 -6.6 -7.3 -7 -6.7 -6.7 2.3 8.6 9.6 11.3 5.3 .8 5.8 9 | H 4022 |
| 477. | HYPERCALCEMIA OF MALIGNANCY FACTOR FRAGMENT 107-111 | #18 | Thr-Arg-Ser-Ala-Trp | 5 |  |  | 620.5 | 10.79 |  | H 2649 |
| 478. | HYPERCALCEMIA OF MALIGNANCY FACTOR FRAGMENT 107-139 | #18 | Thr-Arg-Ser-Ala-Trp-Leu-Asp-Ser-Gly-Val-Thr-Gly-Ser-Gly-leu-Glu-Gly-Asp-His-Leu-Ser-Asp-Thr-Ser-Thr-Thr-Ser-Leu-Glu-Leu-Asp-Ser-Arg | 33 |  |  | 3446 | 3.95626 | -6 -1.1 2.7 3.1 .5 1 1 1 1.4 1.8 -9.1 -4.6 -5 -4.2 -8 -12.6 -9.8 -10.1 -7.4 -.4 -7.7 -3.1 .4 -3.2 -2.4 | H 2774 |
| 479. | PARATHYROID HORMONE FRAGMENTS (Fragment 1-34) | #18 | Ala-Val-Ser-Glu-Ile-Gln-Phe-Met-His-Asn-Leu-Gly-Lys-His-Leu-Ser-Ser-Met-Glu-Arg-Val-Glu-Trp-Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Phe | 34 | Bovine |  | 4108.1 | 10.0006 | 4.2 2.4 -1.5 -1.1 2.4 -9.2 -1.9 -5.5 -8.2 -3.1 -3.1 -6.9 -6.8 -6.4 -4.1 -4.1 -3.3 -7 -12.8 -9.4 -8.4 -12.6 -8.4 -10.7 -19 -10.7 | P 3671 |
| 480. | PARATHYROID HORMONE FRAGMENTS (Fragment 1-34) | #18 | Ser-Val-Ser-Glu-Ile-Gln-Leu-Met-His-Asn-Leu-Gly-Lys-His-Leu-Asn-Ser-Met-Glu-Arg-Val-Glu-Trp Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Phe | 34 | Human |  | 4117.2 | 9.7177 | 2.6 3.4 -.5 -.1 3.4 -8.2 -.9 -4.7 -10.9 -5.8 -5.8 -9.6 -9.5 -9.1 -6.8 -6.8 -3.3 -7 -12.8 -9.4 -8.4 -12.6 -8.4 -10.7 -19 -10.7 | P 3796 |
| 481. | PARATHYROID HORMONE FRAGMENTS (Fragment 1-34) | #18 | Ala-Val-Ser-Glu-Ile-Gln-Leu-Met-His-Asn-Leu-Gly-Lys-His-Leu-Ala-Ser-Val-Glu-Arg-Met-Gln-Trp-Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Phe | 34 | Rat |  | 4058.1 | 10.5771 | 5.2 3.4 -.5 -.1 3.4 -8.2 -.9 -2.9 -5.6 1.8 1.8 -2 -4.2 -3.8 -1.5 -1.5 -3.3 -7 -15.1 -11.7 -10.7 -12.6 -8.4 -10.7 -19 -10.7 | P 3921 |
| 482. | PARATHYROID HORMONE | #18 | Ala-Val-Ser-Glu-Ile-Gln-Phe-Nle- | 34 |  |  | 4140.3 |  |  | P 2905 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | FRAGMENTS ([Nle8,18,Tyr34]-Bovine Fragment 1-34 Amide) |  | His-Asn-Leu-Gly-Lys-His-Leu-Ser-Ser-Nle-Glu-Arg-Val-Glu-Trp-Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Tyr-NH2 |  |  |  |  |  |  |  |
| 483. | PARATHYROID HORMONE FRAGMENTS ([Nle8,21,Tyr34]-Rat Fragment 1-34 Amide) | #18 | Ala-Val-Ser-Glu-Ile-Gln-Leu-Nle-His-Asn-Leu-Gly-Lys-His-Leu-Ala-Ser-Val-Glu-Arg-Nle-Gln-Trp-Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Tyr-NH2 | 34 |  |  | 4090.3 |  |  | P 1803 |
| 484. | PARATHYROID HORMONE FRAGMENTS (Fragment 1-38) | #18 | Ser-Val-Ser-Glu-Ile-Gln-Leu-Met-His-Asn-Leu-Gly-Lys-His-Leu-Asn-Ser-Met-Glu-Arg-Val-Glu-Trp Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Phe-Val-Ala-Leu-Gly | 38 | Human |  | 4457.4 | 9.7177 | 2.6 3.4 -.5 -.1 3.4 -8.2 -.9 -4.7 -10.9 -5.8 -5.8 -9.6 -9.5 -9.1 -6.8 -6.8 -3.3 -7 -12.8 -9.4 -8.4 -12.6 -8.4 -10.7 -19 -10.7 -2.6 3.1 3.1 6.2 | P 9034 |
| 485. | PARATHYROID HORMONE FRAGMENTS (Fragment 1-44) | #18 | Ser-Val-Ser-Glu-Ile-Gln-Leu-Met-His-Asn-Leu-Gly-Lys-His-Leu-Asn-Ser-Met-Glu-Arg-Val-Glu-Trp Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Phe-Val-Ala-Leu-Gly-Ala-Pro-Leu-Ala-Pro-Arg | 44 | Human |  | 5063.9 | 10.5005 | 2.6 3.4 -.5 -.1 3.4 -8.2 -.9 -4.7 -10.9 -5.8 -5.8 -9.6 -9.5 -9.1 -6.8 -6.8 -3.3 -7 -12.8 -9.4 -8.4 -12.6 -8.4 -10.7 -19 -10.7 -2.6 3.1 3.1 6.2 11.5 5.7 12.7 18 13.6 9.4 | P 0279 |
| 486. | PARATHYROID HORMONE FRAGMENTS ([Nle8,18,Tyr34]-Bovine Fragment 3-34 Amide) | #18 | Ser-Glu-Ile-Gln-Phe-Nle-His-Asn-Leu-Gly-Lys-His-Leu-Ser-Ser-Nle-Glu-Arg-Val-Glu-Trp-Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Tyr-NH2 | 32 |  |  | 3970.2 |  |  | P 3030 |
| 487. | PARATHYROID HORMONE FRAGMENTS (Fragment 13-34) | #18 | Lys-His-Leu-Asn-Ser-Met-Glu-Arg-Val-Glu-Trp-Leu-Arg-Lys-Lys-Leu-Gln-Asp-Val-His-Asn-Phe | 22 | Human |  | 2809.3 | 10.5047 | -9.5 -9.1 -6.8 -6.8 -3.3 -7 -12.8 -9.4 -8.4 -12.6 -8.4 -10.7 -19 -10.7 | P 2780 |
| 488. | PARATHYROID HORMONE FRAGMENTS ([Tyr27]-Human ; Fragment 27-48) | #18 | Tyr-Leu-Gln-Asp-Val-His-Asn-Phe-Val-Ala-Leu-Gly-Ala-Pro-Leu-Ala-Pro-Arg-Asp-Ala-Gly-Ser | 22 |  |  | 2309.4 | 5.1356 | 0 3.1 3.1 6.2 11.5 5.7 12.7 18 13.6 9.4 3.1 -2.4 -2.4 -5 | P 2405 |
| 489. | PARATHYROID HORMONE FRAGMENTS (Fragment 28-48) | #18 | Leu-Gln-Asp-Val-His-Asn-Phe-Val-Ala-Leu-Gly-Ala-Pro-Leu-Ala-Pro-Arg-Asp-Ala-Gly-Ser | 21 | Human |  | 2146.3 | 5.136 | 3.1 3.1 6.2 11.5 5.7 12.7 18 13.6 9.4 3.1 -2.4 -2.4 -5 | P 5519 |
| 490. | PARATHYROID HORMONE | #18 | Ala-Pro-Leu-Ala-Pro-Arg-Asp-Ala- | 30 | Human |  | 3285.3 | 9.9981 | -2.4 -5 -6.9 -10.7 -18.6 -21.5 - | P 4403 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | FRAGMENTS (Fragment 39-68) |  | Gly-Ser-Gln-Arg-Pro-Arg-Lys-Lys-Glu-Asp-Asn-Val-Leu-Val-Glu-Ser-His-Glu-Lys-Ser-Leu-Gly |  |  |  |  |  | 20.5 -17.4 -26.6 -26.2 -28.9 -24.7 -16.4 -10.6 -9.6 -6.5 -5.8 -5.8 -5.8 -3.5 -3.9 -8.1 |  |
| 491. | PARATHYROID HORMONE FRAGMENTS ([Asn76]-Human : Fragment 39-84) | #18 | Ala-Pro-Leu-Ala-Pro-Arg-Asp-Ala-Gly-Ser-Gln-Arg-Pro-Arg-Lys-Lys-Glu-Asp-Asn-Val-Leu-Val-Glu-Ser-His-Glu-Lys-Ser-Leu-Gly-Glu-Ala-Asp-Lys-Ala-Asp-Val-Asn-Val-Leu-Thr-Lys-Ala-Lys-Ser-Gln | 46 |  |  | 4983.3 | 9.7868 | -2.4 -5 -6.9 -10.7 -18.6 -21.5 -20.5 -17.4 -26.6 -26.2 -28.9 -24.7 -16.4 -10.6 -9.6 -6.5 -5.8 -5.8 -5.8 -3.5 -3.9 -8.1 -15.8 -10.5 -9.7 -10 -8.6 -4.7 -3.2 -7 -5.9 1.4 -1.1 -1.5 4.2 -1.1 1.2 -6.5 | P 7046 |
| 492. | PARATHYROID HORMONE FRAGMENTS ([Tyr43]-Human : Fragment 43-68) | #18 | Tyr-Arg-Asp-Ala-Gly-Ser-Gln-Arg-Pro-Arg-Lys-Lys-Glu-Asp-Asn-Val-Leu-Val-Glu-Ser-His-Glu-Lys-Ser-Leu-Gly | 26 |  |  | 2999.1 | 9.4565 | -18.3 -21.5 -20.5 -17.4 -26.6 -26.2 -28.9 -24.7 -16.4 -10.6 -9.6 -6.5 -5.8 -5.8 -5.8 -3.5 -3.9 -8.1 | P 2530 |
| 493. | PARATHYROID HORMONE FRAGMENTS (Fragment 44-68) | #18 | Arg-Asp-Ala-Gly-Ser-Gln-Arg-Pro-Arg-Lys-Lys-Glu-Asp-Asn-Val-Leu-Val-Glu-Ser-His-Glu-Lys-Ser-Leu-Gly | 25 | Human |  | 2836 | 9.615 | -21.5 -20.5 -17.4 -26.6 -26.2 -28.9 -24.7 -16.4 -10.6 -9.6 -6.5 -5.8 -5.8 -5.8 -3.5 -3.9 -8.1 | P 3155 |
| 494. | PARATHYROID HORMONE FRAGMENTS ([Tyr52,Asn76]-Human : Fragment 52-84) | #18 | Tyr-Lys-Lys-Glu-Asp-Asn-Val-Leu-Val-Glu-Ser-His-Glu-Lys-Ser-Leu-Gly-Glu-Ala-Asp-Lys-Ala-Asp-Val-Asn-Val-Leu-Thr-Lys-Ala-Lys-Ser-Gln | 33 |  |  | 3671.3 | 5.4922 | -7.4 -9.6 -6.5 -5.8 -5.8 -5.8 -3.5 -3.9 -8.1 -15.8 -10.5 -9.7 -10 -8.6 -4.7 -3.2 -7 -5.9 1.4 -1.1 -1.5 4.2 -1.1 1.2 -6.5 | P 5046 |
| 495. | PARATHYROID HORMONE FRAGMENTS ([Tyr52,Asp76]-Human : Fragment 52-84) | #18 | Tyr-Lys-Lys-Glu-Asp-Asn-Val-Leu-Val-Glu-Ser-His-Glu-Lys-Ser-Leu-Gly-Glu-Ala-Asp-Lys-Ala-Asp-Val-Asp-Val-Leu-Thr-Lys-Ala-Lys-Ser-Gln | 33 |  |  | 3671.2 | 4.8103 | -7.4 -9.6 -6.5 -5.8 -5.8 -5.8 -3.5 -3.9 -8.1 -15.8 -10.5 -9.7 -10 -8.6 -4.7 -3.2 -7 -5.9 1.4 -1.1 -1.5 4.2 -1.1 1.2 -6.5 | P 2655 |
| 496. | PARATHYROID HORMONE FRAGMENTS ([Asn76]-Human : Fragment 53-84) | #18 | Lys-Lys-Glu-Asp-Asn-Val-Leu-Val-Glu-Ser-His-Glu-Lys-Ser-Leu-Gly-Glu-Ala-Asp-Lys-Ala-Asp-Val-Asn-Val-Leu-Thr-Lys-Ala-Lys-Ser-Gln | 32 |  |  | 3508.2 | 5.4923 | -9.6 -6.5 -5.8 -5.8 -5.8 -3.5 -3.9 -8.1 -15.8 -10.5 -9.7 -10 -8.6 -4.7 -3.2 -7 -5.9 1.4 -1.1 -1.5 4.2 -1.1 1.2 -6.5 | P 1921 |
| 497. | PARATHYROID HORMONE FRAGMENTS ([Asp76]-Human : Fragment 64-84) | #18 | Glu-Lys-Ser-Leu-Gly-Glu-Ala-Asp Lys-Ala-Asp-Val-Asp-Val-Leu-Thr-Lys-Ala-Lys-Ser-Gln | 21 |  |  | 2230.2 | 4.577 | -10 -8.6 -4.7 -3.2 -7 -5.9 1.4 -1.1 -1.5 4.2 -1.1 1.2 -6.5 | P 6157 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 498. | PARATHYROID HORMONE FRAGMENTS ([Asp76]-Human : Fragment 73-84) | #18 | **Ala**-Asp-Val-Asp-Val-Leu-Thr-Lys-**Ala**-Lys-Ser-Gln | 12 | | | 1273.7 | 7 | 4.2 -1.1 1.2 -6.5 | P 1905 |
| 499. | ALA-ASP-ALA-GLN-HIS-ALA-THR-PRO-PRO-LYS-LYS-LYS-ARG-LYS-VAL-GLU-ASP-PRO-LYS-ASP-PHE (CSH 103) | #19 | **Ala**-Asp-Ala-Gln-His-Ala-Thr-Pro-**Pro**-Lys-Lys-Lys-Arg-Lys-Val-Glu-**Asp**-Pro-Lys-Asp-Phe | 21 | | | 2407.6 | 10.3161 | -8.7 -14 -10.9 -16.6 -17 -18.3 -19.8 -22.6 -21 -24.5 -24.5 -24.5 -17.4 | A 5688 |
| 500. | ALA-GLY-ASN-LYS-VAL-ILE-SER-PRO-SER-GLU-ASP-ARG-ARG-GLN-CYS (Cys327-Protein Kinase C Isozyme Fragment 313-326) | #19 | **Ala**-Gly-Asn-Lys-Val-Ile-Ser-Pro-**Ser**-Glu-Asp-Arg-Arg-Gln-Cys | 15 | | | 1660.2 | 9.0661 | -.5 -5.8 -8.9 -9.3 -6 -18.2 -20.2 | A 5314 |
| 501. | ARG-ARG-LEU-ILE-GLU-ASP-ALA-GLU-TYR-ALA-ALA-ARG-GLY | #19 | **Arg**-Arg-Leu-Ile-Glu-Asp-Ala-Glu-**Tyr**-Ala-Ala-Arg-Gly | 13 | | | 1519.1 | 6.73 | -10.7 -4.4 1.9 -1.9 -11.3 | A 7433 |
| 502. | ARG-ARG-LEU-ILE-GLU-ASP-ASN-GLU-TYR-THR-ALA-ARG-GLY | #19 | **Arg**-Arg-Leu-Ile-Glu-Asp-Asn-Glu-**Tyr**-Thr-Ala-Arg-Gly | 13 | | | 1592.3 | 6.73 | -16 -12.2 -5.9 -9.7 -19.1 | A 7907 |
| 503. | ARG-ARG-LYS-ALA-SER-GLY-PRO | #19 | **Arg**-Arg-Lys-Ala-Ser-Gly-Pro | 7 | | | 773.6 | 12.497 | | A 3651 |
| 504. | ARG-LYS-ARG-ALA-ARG-LYS-GLU | #19 | **Arg**-Lys-Arg-Ala-Arg-Lys-Glu | 7 | | | 946.9 | 12.2247 | | A 8186 |
| 505. | ARG-THR-LYS-ARG-SER-GLY-SER-VAL-TYR-GLU-PRO-LEU-LYS-ILE (Malantide) | #19 | **Arg**-Thr-Lys-Arg-Ser-Gly-Ser-Val-**Tyr**-Glu-Pro-Leu-Lys-Ile | 14 | | | 1636.3 | 10.8873 | -12.7 -11.7 -12.6 -4.9 -.4 1 | A 3317 |
| 506. | CALMODULIN-DEPENDENT PROTEIN KINASE II FRAGMENT 290-309 | #19 | **Leu**-Lys-Lys-Phe-Asn-Ala-Arg-**Arg**-Lys-Leu-Lys-Gly-Ala-Ile-Leu-**Thr**-Thr-Met-Leu-Ala | 20 | | | 2278.8 | 12.5419 | -11.9 -15.8 -15.8 -12.3 -13.3 -5.3 -3.3 .5 4.3 10.1 10.1 15.8 | C 4926 |
| 507. | GLN-LYS-ARG-PRO-SER-GLN-ARG-SER-LYS-TYR-LEU (Bovine myelin basic protein fragment 4-14) | #19 | **Gln**-Lys-Arg-Pro-Ser-Gln-Arg-Ser-**Lys**-Tyr-Leu | 11 | | | 1394.1 | 11.666 | -23.1 -24.8 -17.1 | G 5777 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 508. | GLY-ARG-GLY-LEU-SER-LEU-SER-ARG | #19 | **Gly**-Arg-Gly-Leu-Ser-Leu-Ser-Arg | 8 | | | 846.6 | 12.4817 | | G 1391 |
| 509. | [Val6,Ala7]-KEMPTIDE | #19 | **Leu**-Arg-Arg-Ala-Ser-Val-Ala | 7 | | | 773.6 | 12.4815 | | K 2877 |
| 510. | KEMPTIDE (Phosphate acceptor peptide) | #19 | **Leu**-Arg-Arg-Ala-Ser-Leu-Gly | 7 | | | 773.6 | 12.4815 | | K 1127 |
| 511. | LEU-ARG-ARG-ALA-HSE-LEU-GLY | #19 | **Leu**-Arg-Arg-Ala-Hse-Leu-Gly | 7 | | | 686.6 | | | L 8022 |
| 512. | LEU-ARG-ARG-TRP-SER-LEU-GLY | #19 | **Leu**-Arg-Arg-Trp-Ser-Leu-Gly | 7 | | | 888.8 | 12.4815 | | L 3523 |
| 513. | LYS-ARG-THR-LEU-ARG-ARG | #19 | **Lys**-Arg-Thr-Leu-Arg-Arg | 6 | | | 832.9 | 12.7877 | | L 7897 |
| 514. | pGLU-LYS-ARG-PRO-SER-GLN-ARG-SER-LYS-TYR-LEU ([pGlu4]-Myelin Basic Protein 4-14) | #19 | **pGlu**-Lys-Arg-Pro-Ser-Gln-Arg-**Ser**-Lys-Tyr-Leu | 11 | | | 1394.1 | | | P 2186 |
| 515. | PRO-LEU-SER-ARG-THR-LEU-SER-VAL-ALA-ALA-LYS-LYS | #19 | **Pro**-Leu-Ser-Arg-Thr-Leu-Ser-Val-**Ala**-Ala-Lys-Lys | 12 | | | 1272.9 | 11.8863 | 5.2 8.6 4.8 -2.8 | P 5307 |
| 516. | PROTEIN KINASE A INHIBITOR FRAGMENT 6-22 AMIDE | #19 | **Thr**-Tyr-Ala-Asp-Phe-Ile-Ala-Ser-**Gly**-Arg-Thr-Gly-Arg-Arg-Asn-Ala-**Ile**-NH2 | 17 | | | 1886.3 | 12.1852 | 4.2 4.9 1 -1.2 2.3 -5 -14 -17.5 -12.2 -16.3 | P 6062 |
| 517. | PROTEIN KINASE C FRAGMENT 530-558 | #19 | **Leu**-Leu-Tyr-Glu-Met-Leu-Ala-**Gly**-Gln-Ala-Pro-Phe-Glu-Gly-Glu-**Asp**-Glu-Asp-Glu-Leu-Phe-Gln-**Ser**-Ile-Met-Glu-His-Asn-Val-NH2 | 29 | | | 3362.2 | 3.5464 | 6.4 4.4 -1 3.1 3.1 .8 -6.5 -8.3 -14.9 -11.4 -20.2 -14.8 -14.8 -14.8 -15.2 -7.2 -1.8 -1.8 -1.5 2 -1.1 -3.9 | P 2303 |
| 518. | PROTEIN KINASE INHIBITOR (Rabbit Sequence) | #19 | **Thr**-Thr-Tyr-Ala-Asn-Phe-Ile-Ala-**Ser**-Gly-Arg-Thr-Gly-Arg-Arg-Asn-**Ala**-Ile-His-Asp | 20 | | | 2222.6 | 11.0724 | 3.9 4.2 4.9 1 -1.2 2.3 -5 -14 -17.5 -12.2 -15 -10.5 | P 0300 |
| 519. | SYNTIDE 2 | #19 | **Pro**-Leu-Ala-Arg-Thr-Leu-Ser-Val-**Ala**-Gly-Leu-Pro-Gly-Lys-Lys | 15 | | | 1510.1 | 11.8863 | 7.8 9 9 5.6 9.7 10.4 2.7 | S 2525 |
| 520. | VAL-ARG-LYS-ARG-THR-LEU-ARG-ARG-LEU (Protein kinase C substrate) | #19 | **Val**-Arg-Lys-Arg-Thr-Leu-Arg-Arg-**Leu** | 9 | | | 1202.3 | 12.9613 | -10.8 | V 2131 |
| 521. | SOMATOSTATIN (SRIF ; Growth hormone release | #20 | **Ala**-Gly-Cys-Lys-Asn-Phe-Phe-**Trp**-Lys-Thr-Phe-Thr-Ser-Cys | 14 | | 3-14 | 1641.2 | 9.2123 | 1.2 -5.2 -2 -5.2 -2.1 3.9 | S 9129 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | inhibiting factor) | | | | | | | | | |
| 522. | SOMATOSTATIN (Tyr-Somatostatin) | #20 | Tyr-Ala-Gly-Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cy | 15 | | 3-14 | 1804.3 | 9.5979 | -.1 1.2 -5.2 -2 -5.2 -2.1 3.9 1.1 | S 8133 |
| 523. | SOMATOSTATIN ([D-Trp8] Somatostatin) | #20 | Ala-Gly-Cys-Lys-Asn-Phe-Phe-D-Trp-Lys-Thr-Phr-Thr-Ser-Cys | 14 | | 3-14 | 1494.1 | | | S 2511 |
| 524. | SOMATOSTATIN ([Tyr1]-Somatostatin) | #20 | Tyr-Gly-Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cys | 14 | | 3-14 | 1733.3 | 8.8744 | -1.9 -5.2 -2 -5.2 -2.1 3.9 | S 4633 |
| 525. | SOMATOSTATIN ([Tyr11]-Somatostatin) | #20 | Ala-Gly-Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Tyr-Thr-Ser-Cys | 14 | | 3-14 | 1657.2 | 9.1175 | 1.2 -5.2 -6.1 -9.3 -6.2 -.2 | S 8508 |
| 526. | SOMATOSTATIN ([D-Trp8,D-Cys14]-Somatostatin) | #20 | Ala-Gly-Cys-Lys-Asn-Phe-Phe-D-Trp-Lys-Thr-Phe-Thr-Ser-D-Cys | 14 | | 3-14 | 1641.2 | 10.139 | 2.1 .3 .7 -5.7 -1.4 5.6 5.3 | S 4508 |
| 527. | SOMATOSTATIN (des-Ala1,Gly2,[His4,5,D-Trp8]-Somatostatin) | #20 | Cys-His-His-Phe-Phe-D-Trp-Lys-Thr-Phe-Thr-Ser-Cys | 12 | | 3-14 | 1544.2 | 8.3327 | 1.7 -.8 2.4 5.6 2.8 | S 2261 |
| 528. | SOMATOSTATIN 25 | #20 | Ser-Asn-Pro-Ala-Met-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Gly-Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cys | 25 | | 14-25 | 2881.2 | 10.5141 | -10 -12.7 -10.2 -10.7 -12.9 -12.3 -14.1 -20.9 -12.6 -6.3 -2.7 1.2 -5.2 -2 -5.2 -2.1 3.9 | S 1007 |
| 529. | SOMATOSTATIN 28 (Prosomatostatin) | #20 | Ser-Ala-Asn-Ser-Asn-Pro-Ala-Met-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Gly-Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cys | 28 | | 17-28 | 3153.3 | 11.0558 | -2.9 -3.7 -9 -10 -12.7 -10.2 -10.7 -12.9 -12.3 -14.1 -20.9 -12.6 -6.3 -2.7 1.2 -5.2 -2 -5.2 -2.1 3.9 1.1 | S 6135 |
| 530. | Tyr-SOMATOSTATIN 28 | #20 | Tyr-Ser-Ala-Asn-Ser-Asn-Pro-Ala-Met-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Gly-Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cys | 29 | | 17-28 | 3316.4 | 10.1676 | -6 -2.9 -3.7 -9 -10 -12.7 -10.2 -10.7 -12.9 -12.3 -14.1 -20.9 -12.6 -6.3 -2.7 1.2 -5.2 -2 -5.2 -2.1 3.9 | S 6260 |
| 531. | [Leu8,D-Trp22,Tyr25]-SOMATOSTATIN 28 | #20 | Ser-Ala-Asn-Ser-Asn-Pro-Ala-Leu-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Gly-Cys-Lys-Asn-Phe-Phe-D-Trp-Lys-Thr-Tyr-Thr-Ser-Cys | 28 | | 17-28 | 3151.3 | 10.1773 | -1 -1.8 -7.1 -8.1 -10.8 -8.3 -8.8 -11 -12.3 -14.1 -20.9 -12.6 -6.3 -5.7 2.1 .3 .7 -5.7 -1.4 5.6 2.8 | S 2636 |
| 532. | SOMATOSTATIN 28 (Fragment 1-14) | #20 | Ser-Ala-Asn-Ser-Asn-Pro-Ala-Met-Ala-Pro-Arg-Glu-Arg-Lys | 14 | | | 1530.1 | 11.4702 | -2.9 -3.7 -9 -10 -12.7 -10.2 | S 2386 |
| 533. | CYCLO(7-AMINOHEPTANOYL-PHE- | #20 | Cyclo(7-Aminoheptanoyl-Phe-D-Trp-Lys-Thr[BZL]) | 4 | | | 607.4 | | | C 4801 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | D-TRP-LYS-THR[BZL]) | | | | | | | | | |
| 534. | CYCLO(D-TRP-LYS-THR-PHE-PRO-PHE) | #20 | Cyclo(D-Trp-Lys-Thr-Phe-Pro-Phe) | 6 | | | 825.7 | | | C 6273 |
| 535. | CYCLO(D-TRP-LYS-THR-PHE-PRO-TYR) | #20 | Cyclo(D-Trp-Lys-Thr-Phe-Pro-Tyr | 6 | | | 678.6 | | | C 6398 |
| 536. | b-(2-NAPHTHYL)-D-ALA-CYS-TYR-D-TRP-LYS-VAL-CYS-THR AMIDE | #20 | b-(2-Naphthyl)-D-Ala-Cys-Tyr-D-Trp-Lys-Val-Cys-Thr-NH2 | 8 | | 2-7 | 918.8 | | | N 9642 |
| 537. | SUBSTANCE P (Substance P) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 11 | | | 1366.1 | 17 | -13.4 -5.1 -1.6 2.3 | S 6883 |
| 538. | SUBSTANCE P ([Met-OH11]-Substance P ; Substance P free acid) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu-Met | 11 | | | 1350.1 | 11.6393 | -13.4 -5.1 -1.6 | S 2136 |
| 539. | SUBSTANCE P ([Met-OMe11]-Substance P ; Substance P methyl ester) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu-Met-OMe | 11 | | | 1381.1 | | | S 2011 |
| 540. | SUBSTANCE P ([Nle11]-Substance P) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu-Nle-NH2 | 11 | | | 1219 | | | S 1136 |
| 541. | SUBSTANCE P ([Pro9]-Substance P) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Pro-Leu-Met-NH2 | 11 | | | 1406.2 | 17 | -14.6 -6.3 -2.8 1.1 | S 7029 |
| 542. | SUBSTANCE P ([Sar9]-Substance P) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Sar-Leu-Met-NH2 | 11 | | | 1398.2 | | | S 6636 |
| 543. | SUBSTANCE P ([Tyr8]-Substance P) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Tyr Gly-Leu-Met-NH2 | 11 | | | 1382.1 | 11.692 | -17.5 -9.2 -5.7 -1.8 | S 6008 |
| 544. | SUBSTANCE P ([p-Cl-Phe7,8]-Substance P) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-p-Chloro-Phe-p-Choloro-Phe-Gly-Leu-Met-NH2 | 11 | | | 1435.1 | | | S 5382 |
| 545. | SUBSTANCE P ([Dehydro-Pro2,4]-Substance P) | #21 | Arg-DPro-Lys-DPro-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 11 | | | 1171.9 | | | S 3258 |
| 546. | SUBSTANCE P ([Dehydro-Pro2,4,Pro9]-Substance P) | #21 | Arg-DPro-Lys-DPro-Gln-Gln-Phe-Phe-Pro-Leu-Met-NH2 | 11 | | | 1212 | | | S 7154 |
| 547. | SUBSTANCE P ([Sar9,Met (O2)11]-Substance P) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Sar-Leu-Met[O2] | 11 | | | 1251.1 | | | S 2150 |
| 548. | SUBSTANCE P ([D-Pro2,D-Trp7,9]-Substance P) | #21 | Arg-D-Pro-Lys-Pro-Gln-Gln-D-Trp-Phe-D-Trp-Leu-Met-NH2 | 11 | | | 1534.4 | 17 | -2.6 1.9 1.9 1.9 1.9 1.9 | S 0145 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 549. | SUBSTANCE P ([D-Pro2,D-Phe7,D-Trp9]-Substance P) | #21 | Arg-D-Pro-Lys-Pro-Gln-Gln-D-Phe-Phe-D-Trp-Leu-Met-NH2 | 11 | | | 1495.3 | 17 | 1.1 5.6 5.6 5.6 5.6 5.6 | S 5635 |
| 550. | SUBSTANCE P ([D-Trp2,7,9]-Substance P) | #21 | Arg-D-Trp-Lys-Pro-Gln-Gln-D-Trp Phe-D-Trp-Leu-Met-NH2 | 11 | | | 1623.5 | 17 | -2.6 1.9 1.9 1.9 1.9 1.9 | S 1636 |
| 551. | SUBSTANCE P ([D-Arg1,D-Pro2,D-Phe7,D-His9]-Substance P) | #21 | D-Arg-D-Pro-Lys-Pro-Gln-Gln-D-Phe-Phe-D-His-Leu-Met-NH2 | 11 | | | 1446.2 | 15 | -14.1 -14.1 -17.3 -11.9 -6.1 -4.5 | S 3639 |
| 552. | SUBSTANCE P ([D-Arg1,D-Trp7,9,Leu11]-Substance P ; Spantide) | #21 | D-Arg-Pro-Lys-Pro-Gln-Gln-D-Trp-Phe-D-Trp-Leu-Leu-NH2 | 11 | | | 1516.4 | 15 | 1.9 1.9 1.9 1.9 1.9 1.9 | S 0274 |
| 553. | SUBSTANCE P ([D-Arg1,D-Pro2,D-Trp7,9,Leu11]-Substance P) | #21 | D-Arg-D-Pro-Lys-Pro-Gln-Gln-D-Trp-Phe-D-Trp-Leu-Leu-NH2 | 11 | | | 1516.4 | 15 | -14.1 -14.1 -15 -9.6 -1.9 -.3 | S 4152 |
| 554. | SUBSTANCE P ([D-Arg1,D-Phe5,D-Trp7,9,Leu11]-Substance P) | #21 | D-Arg-Pro-Lys-Pro-D-Phe-Gln-D-Trp-Phe-D-Trp-Leu-Leu-NH2 | 11 | | | 1535.4 | 15 | -.7 -.7 -1.6 2.2 6 6 | S 3144 |
| 555. | SUBSTANCE P FRAGMENTS (Fragment 1-4) | #21 | Arg-Pro-Lys-Pro | 4 | | | 498.5 | 11.6393 | | S 7646 |
| 556. | SUBSTANCE P FRAGMENTS (Fragment 1-7) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe | 7 | | | 901.8 | 11.6393 | | S 6272 |
| 557. | SUBSTANCE P FRAGMENTS (Fragment 1-9) | #21 | Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Gly | 9 | | | 1105.9 | 11.6393 | -13.4 | S 1761 |
| 558. | SUBSTANCE P FRAGMENTS (Fragment 2-11) | #21 | Pro-Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 10 | | | 1061.8 | | | S 0272 |
| 559. | SUBSTANCE P FRAGMENTS (Fragment 3-11) | #21 | Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 9 | | | 1111.8 | 15 | -1.6 2.3 | S 7511 |
| 560. | SUBSTANCE P FRAGMENTS (Arg4,Gly5,D-Trp7,Asp(di-t-butyl)10]-Fragment 4-10) | #21 | Arg-Gly-Gln-D-Trp-Phe-Gly-Asp [O-tBu]2 | 7 | | | 976.6 | | | S 6642 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 561. | SUBSTANCE P FRAGMENTS (Fragment 4-11) | #21 | Pro-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 8 | | | 982.7 | 15 | | S 0397 |
| 562. | SUBSTANCE P FRAGMENTS ([D-Ala4]-Fragment 4-11) | #21 | D-Ala-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 8 | | | 956.6 | 1 | | S 3383 |
| 563. | SUBSTANCE P FRAGMENTS ([D-Pro4,D-Trp7,9,Nle11]-Fragment 4-11) | #21 | D-Pro-Gln-Gln-D-Trp-Phe-D-Trp-Leu-Nle-NH2 | 8 | | | 1003.9 | | | S 6647 |
| 564. | SUBSTANCE P FRAGMENTS ([D-Pro4,D-Trp7,9,10]-Fragment 4-11) | #21 | D-Pro-Gln-Gln-D-Trp-Phe-D-Trp-D-Trp-Met-NH2 | 8 | | | 1224.1 | 1 | | S 6397 |
| 565. | SUBSTANCE P FRAGMENTS ([D-Pro4,D-Trp7,9,10,Phe11]-Fragment 4-11) | #21 | D-Pro-Gln-Gln-D-Trp-Phe-D-Trp-D-Trp-Phe-NH2 | 8 | | | 1240.1 | 1 | | S 6522 |
| 566. | SUBSTANCE P FRAGMENTS (Fragment 5-11) | #21 | Gln-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 7 | | | 885.6 | 14 | | S 1261 |
| 567. | SUBSTANCE P FRAGMENTS ([pGlu5]-Fragment 5-11) | #21 | pGlu-Gln-Phe-Phe-Gly-Leu-Met-NH2 | 7 | | | 885.6 | | | S 2886 |
| 568. | SUBSTANCE P FRAGMENTS ([pGlu5,N-Me-Phe8,Sar9]-Fragment 5-11) | #21 | pGlu-Gln-Phe-N-Methyl-Phe-Sar-Leu-Met-NH2 | 7 | | | 770.6 | | | S 4391 |
| 569. | SUBSTANCE P FRAGMENTS (Fragment 6-11) | #21 | Gln-Phe-Phe-Gly-Leu-Met-NH2 | 6 | | | 757.5 | 14 | | S 0772 |
| 570. | SUBSTANCE P FRAGMENTS ([pGlu6]-Fragment 6-11) | #21 | pGlu-Phe-Phe-Gly-Leu-Met-NH2 | 6 | | | 757.5 | | | S 3136 |
| 571. | SUBSTANCE P FRAGMENTS ([pGlu6,Pro9 | #21 | pGlu-Phe-Phe-Pro-Leu-Met-NH2 | 6 | | | 797.6 | | | S 6764 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 572. | SUBSTANCE P FRAGMENTS ([Arg6,D-Trp7,9,N-Me-Phe8]-Fragment 6-11) | #21 | Arg-D-Trp-N-Methyl-Phe-D-Trp-Leu-Met-NH2 | 6 | | | 807.8 | | | S 6392 |
| 573. | SUBSTANCE P FRAGMENTS (Acetyl-[Arg6,Sar9,Met(O2)11]-Substance P Fragment 6-11) | #21 | Acetyl-Arg-Phe-Phe-Sar-Leu-Met [O2] | 6 | | | 713.6 | | | S 2275 |
| 574. | SUBSTANCE P FRAGMENTS (Succinyl-[Asp6,N-Me-Phe8]-Fragment 6-11 ; Senktide) | #21 | Succinyl-Asp-Phe-N-Methyl-Phe-Gly-Leu-Met-NH2 | 6 | | | 482.3 | | | S 6772 |
| 575. | SUBSTANCE P FRAGMENTS (Fragment 7-11) | #21 | Phe-Phe-Gly-Leu-Met-NH2 | 5 | | | 629.4 | 14 | | S 2394 |
| 576. | SUBSTANCE P FRAGMENTS (Fragment 8-11) | #21 | Phe-Gly-Leu-Met-NH2 | 4 | | | 482.3 | 14 | | S 0897 |
| 577. | SUBSTANCE P FRAGMENTS (Fragment 9-11) | #21 | Gly-Leu-Met-NH2 | 3 | | | 335.2 | 14 | | S 1022 |
| 578. | 4-(2-ACETAMIDO-2-DEOXY-b-D-GLUCOPYRANOSYL)-N-ACETYLMURAMYL-L-ALA-D-GLU AMIDE (N-Acetyl-D-glucosaminyl-b-[1-4]-N-acetylmuramyl-L-ala-D-isoglutamine) | #22 | N-Acetyl-D-Glucosaminyl-b-[1-4]-N-Acetylmuramyl-L-Ala-D-Isoglutamine | 2 | | | 146.1 | | | A 4310 |
| 579. | N-ACETYL-ASP-GLU | #22 | Acetyl-Asp-Glu | 2 | | | 302.1 | | | A 5930 |
| 580. | N-ACETYL-MET-ASP-ARG-VAL-LEU-SER-ARG-TYR | #22 | Acetyl-Met-Asp-Arg-Val-Leu-Ser-Arg-Tyr | 8 | | | 908.7 | | | A 9924 |
| 581. | N-ACETYLMURAMYL-D-ALANYL-D-ISOGLUTAMINE | #22 | N-Acetylmuramyl-D-Alanyl-D-Isoglutamine | 1 | | | | | | A 0640 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 582. | N-ACETYLMURAMYL-L-ALANYL-L-ISOGLUTAMINE | #22 | N-Acetylmuramyl-L-Alanyl-L-Isoglutamine | 1 | | | | | | A 4773 |
| 583. | N-ACETYLMURAMYL-ALA-D-ISOGLUTAMINYL-N-e-STEAROYL-LYS | #22 | N-Acetylmuramyl-Ala-D-Isoglutaminyl-N-e-Stearoyl-Lys | 2 | | | | | | A 0936 |
| 584. | N-ACETYLMURAMYL-6-O-STEAROYL-L-ALANYL-D-ISOGLUTAMINE | #22 | N-Acetylmuramyl-6-O-Stearoyl-L-Alanyl-D-Isoglutamine | 1 | | | | | | A 0300 |
| 585. | N-ACETYL-PHE-NLE-ARG-PHE AMIDE | #22 | Acetyl-Phe-Nle-Arg-Phe-NH2 | 4 | | | 469.5 | | | A 2163 |
| 586. | ACETYL-SER-ASP-LYS-PRO | #22 | Acetyl-Ser-Asp-Lys-Pro | 4 | | | 358.2 | | | A 6433 |
| 587. | ACETYL-SER-GLN-ASP-TYR | #22 | Acetyl-Ser-Gln-Asp-Tyr | 4 | | | 423.2 | | | A 0931 |
| 588. | ACETYL-SER-GLN-ASP-TYR-PRO-VAL-VAL AMIDE | #22 | Acetyl-Ser-Gln-Asp-Tyr-Pro-Val-Val-NH2 | 7 | | | 734.5 | | | A 0806 |
| 589. | N-ACETYL-THR-ILE-NLE-y-[CH2NH]-NLE-GLN-ARG AMIDE | #22 | Acetyl-Thr-Ile-Nle-y-[CH2NH]-Nle-Gln-Arg-NH2 | 6 | | | 563.6 | | | A 8305 |
| 590. | ACYL CARRIER PROTEIN FRAGMENT 65-74 | #22 | Val-Gln-Ala-Ala-Ile-Asp-Tyr-Ile-Asn-Gly | 10 | | | 1061.6 | 3.125 | 8.5 .4 | A 6700 |
| 591. | ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-27 (PACAP-27) | #22 | His-Ser-Asp-Gly-Ile-Phe-Thr-Asp-Ser-Tyr-Ser-Arg-Tyr-Arg-Lys-Gln-Met-Ala-Val-Lys-Lys-Tyr-Leu-Ala-Ala-Val-Leu-NH2 | 27 | Ovine | | 3166 | 10.4757 | -5.6 -3.7 -3.7 -.2 -5.6 -10.1 -17.4 -24.1 -18.7 -16.1 -10.6 -14.3 -9.2 -13.1 -4.8 .9 6.2 8.5 10.5 2.4 | A 9808 |
| 592. | ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE FRAGMENT 6-27 AMIDE | #22 | Phe-Thr-Asp-Ser-Tyr-Ser-Arg-Tyr Arg-Lys-Gln-Met-Ala-Val-Lys-Lys-Tyr-Leu-Ala-Ala-Val-Leu-NH2 | 22 | | | 2657.8 | 10.7978 | -10.1 -17.4 -24.1 -18.7 -16.1 -10.6 -14.3 -9.2 -13.1 -4.8 .9 6.2 8.5 10.5 2.4 | A 6938 |
| 593. | ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-38 (PACAP-38) | #22 | His-Ser-Asp-Gly-Ile-Phe-Thr-Asp-Ser-Tyr-Ser-Arg-Tyr-Arg-Lys-Gln-Met-Ala-Val-Lys-Lys-Tyr-Leu-Ala-Ala-Val-Leu-Gly-Lys-Arg-Tyr-Lys-Gln-Arg-Val-Lys-Asn-Lys-NH2 | 38 | | | 4558.2 | 11.152 | -5.6 -3.7 -3.7 -.2 -5.6 -10.1 -17.4 -24.1 -18.7 -16.1 -10.6 -14.3 -9.2 -13.1 -4.8 .9 6.2 8.5 10.5 5.9 5.9 9.8 5.3 1.5 -7.7 -9.5 -14 -17.8 -25.2 -25.4 -20.3 | A 1439 |
| 594. | ADIPOKINETIC HORMONE | #22 | pGlu-Leu-Asn-Phe-Ser-Ala-Gly- | 8 | Locusta | | 937.6 | | | A 8421 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | II |  | Trp-NH2 |  | migratoria |  |  |  |  |  |
| 595. | ADIPOKINETIC HORMONE II | #22 | pGlu-Leu-Asn-Phe-Ser-Thr-Gly-Trp-NH2 | 8 | Schistocrca gregaria |  | 967.7 |  |  | A 3797 |
| 596. | ADJUVANT PEPTIDE | #22 | N-Acetylmuramyl-L-Alanyl-D-Isoglutamine | 1 |  |  |  |  |  | A 9519 |
| 597. | ALA-ARG-PRO-GLY-TYR-LEU-ALA-PHE-PRO-ARG-MET AMIDE (Small Cardioactive Peptide A ; SCPa) | #22 | Ala-Arg-Pro-Gly-Tyr-Leu-Ala-Phe-Pro-Arg-Met-NH2 | 11 |  |  | 1296 | 12.4859 | .8 -5.5 .9 2.5 | A 7052 |
| 598. | b-ALA-ARG-SER-ALA-PRO-THR-PRO-MET-SER-PRO-TYR | #22 | b-Ala-Arg-Ser-Ala-Pro-Thr-Pro-Met-Ser-Pro-Tyr | 11 |  |  | 1106.8 |  |  | A 2666 |
| 599. | ALA-D-g-GLU-LYS-D-ALA-D-ALA | #22 | Ala-D-g-Glu-Lys-D-Ala-D-Ala | 5 |  |  | 360.1 |  |  | A 0910 |
| 600. | ALA-D-ISOGLUTAMINYL-LYS-D-ALA-D-ALA | #22 | Ala-D-Isoglutaminyl-Lys-D-Ala-D-Ala | 4 |  |  | 231 |  |  | A 1035 |
| 601. | ALA-LEU-ALA-LEU | #22 | Ala-Leu-Ala-Leu | 4 |  |  | 386.2 | 6 |  | A 3546 |
| 602. | ALA-LEU-ILE-LEU-THR-LEU-VAL-SER | #22 | Ala-Leu-Ile-Leu-Thr-Leu-Val-Ser | 8 |  |  | 828.6 | 6 |  | A 1061 |
| 603. | ALA-LYS-PRO-SER-TYR-HYP-HYP-THR-TYR-LYS | #22 | Ala-Lys-Pro-Ser-Tyr-Hyp-Hyp-Thr-Tyr-Lys | 10 |  |  | 1184.8 |  |  | A 7060 |
| 604. | ALA-PRO-ARG-LEU-ARG-PHE-TYR (a-Bag Cell Peptide 1-7) | #22 | Ala-Pro-Arg-Leu-Arg-Phe-Tyr | 7 |  |  | 923.8 | 11.2484 |  | A 5058 |
| 605. | ALA-PRO-ARG-LEU-ARG-PHE-TYR-SER (a-Bag Cell Peptide 1-8) | #22 | Ala-Pro-Arg-Leu-Arg-Phe-Tyr-Ser | 8 |  |  | 1010.8 | 11.2484 |  | A 5183 |
| 606. | ALA-PRO-ARG-LEU-ARG-PHE-TYR-SER-LEU (a-Bag Cell Peptide 1-9) | #22 | Ala-Pro-Arg-Leu-Arg-Phe-Tyr-Ser Leu | 9 |  |  | 1123.9 | 11.2484 | -.5 | A 5308 |
| 607. | ALA-PRO-GLY-PRO-ARG | #22 | Ala-Pro-Gly-Pro-Arg | 5 |  |  | 497.4 | 11.175 |  | A 6931 |
| 608. | ALA-PRO-GLY-TRP-NH2 | #22 | Ala-Pro-Gly-Trp-NH2 | 4 |  |  | 445.3 | 14 |  | A 0813 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 609. | ALA-SER-HIS-LEU-GLY-LEU-ALA-ARG (Anaphylatoxin C3a Fragment 70-77) | #22 | Ala-Ser-His-Leu-Gly-Leu-Ala-Arg | 8 | | | 824.5 | 11.175 | | A 8651 |
| 610. | b-ALA-SER-HIS-LEU-GLY-LEU-ALA-ARG ([b-Ala1]-Anaphylatoxin C3a Fragment 70-77) | #22 | b-Ala-Ser-His-Leu-Gly-Leu-Ala-Arg | 8 | | | 753.5 | | | A 2916 |
| 611. | ALA-SER-THR-THR-THR-ASN-3,5-DIIODO-TYR-THR ([3,5-Diiodo-Tyr7]-Peptide T | #22 | Ala-Ser-Thr-Thr-Thr-Asn-3,5-Diiodo-Tyr-Thr | 8 | | | 1109.4 | | | A 0800 |
| 612. | ALA-SER-THR-THR-THR-ASN-TYR-THR (Peptide T) | #22 | Ala-Ser-Thr-Thr-Thr-Asn-Tyr-Thr | 8 | | | 857.6 | 6 | | A 2297 |
| 613. | D-ALA-SER-THR-THR-THR-ASN-TYR-THR AMIDE ([D-Ala1]-Peptide T amide) | #22 | D-Ala-Ser-Thr-Thr-Thr-Asn-Tyr-Thr-NH2 | 8 | | | 873.6 | 0 | | A 2422 |
| 614. | ALA-LYS(TFA)-PRO-SER-TYR-HYP-HYP-THR-TYR-LYS | #22 | Ala-Lys(TFA)-Pro-Ser-Tyr-Hyp-Hyp-Thr-Tyr-Lys | 10 | | | 1055.7 | | | A 7185 |
| 615. | ALDOSTERONE SECRETION INHIBITING FACTOR (1-35 ; ASIF) | #22 | Ala-Leu-Arg-Gly-Pro-Lys-Met-Met-Arg-Asp-Ser-Gly-Cys-Phe-Gly-Arg-Arg-Leu-Asp-Arg-Ile-Gly-Ser-Leu-Ser-Gly-Leu-Gly-Cys-Asn-Val-Leu-Arg-Arg-Tyr | 35 | Bovine | 13-29 | 3917 | 11.7652 | -1 -7.3 -15.4 -11.3 -8.4 -4 -.5 -2.4 -13.3 -5 -1.5 -4.2 -3.8 -6.7 -10.3 -6.1 -2.4 1.7 1.7 4.8 11.8 7.3 8.4 13 9.2 5.5 .1 | A 7555 |
| 616. | ALLATOSTATIN I | #22 | Ala-Pro-Ser-Gly-Ala-Gln-Arg-Leu-Tyr-Gly-Phe-Gly-Leu-NH2 | 13 | | | 1352.8 | 11.4082 | -4.7 -6.9 -2.5 -2.1 2.1 .3 | A 9929 |
| 617. | ALLATOSTATIN II | #22 | Gly-Asp-Gly-Arg-Leu-Tyr-Ala-Phe-Gly-Leu-NH2 | 10 | | | 1083.6 | 9.9523 | -2.1 2.1 5.6 | A 9804 |
| 618. | ALLATOSTATIN III | #22 | Gly-Gly-Ser-Leu-Tyr-Ser-Phe-Gly-Leu-NH2 | 9 | | | 915.4 | 9.955 | 6.3 6.7 | A 9679 |
| 619. | ALLATOSTATIN IV | #22 | Asp-Arg-Leu-Tyr-Ser-Phe-Gly-Leu-NH2 | 8 | | | 985.6 | 10.012 | | A 9554 |
| 620. | ALLATOSTATIN B2 (Cockroach) | #22 | Ala-Tyr-Ser-Tyr-Val-Ser-Glu-Tyr-Lys-Arg-Leu-Pro-Val-Tyr-Asn-Phe-Gly-Leu-NH2 | 18 | | | 2185.5 | 9.8602 | -3 -8.7 -8.1 -8.9 -3.4 -8.9 -8.1 -5.3 -4.4 3.3 7.8 | A 6575 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 629. | AMYLOID b-PROTEIN FRAGMENTS (Fragment 10-20) | #22 | Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe | 11 | | | 1446.1 | 7.706 | -6.4 -2.3 4 | A 6825 |
| 630. | AMYLOID b-PROTEIN FRAGMENTS (Fragment 12-28) | #22 | Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys | 17 | | | 1954.3 | 8.009 | 4 1.6 1.3 4.5 8.7 12.2 7.6 3.4 -2.9 | A 3180 |
| 631. | AMYLOID b-PROTEIN FRAGMENTS (Fragment 25-35) | #22 | Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met | 11 | | | 1060.6 | 10.285 | 1.4 5.6 8.3 | A 4559 |
| 632. | AMYLOID b-PROTEIN FRAGMENTS (Fragment 31-35) | #22 | Ile-Ile-Gly-Leu-Met | 5 | | | 545.4 | 6 | | A 5075 |
| 633. | AMYLOID b-PROTEIN FRAGMENTS (Fragment 32-35) | #22 | Ile-Gly-Leu-Met | 4 | | | 432.3 | 6 | | A 4950 |
| 634. | AMYLOID b-PROTEIN FRAGMENTS (Fragment 40-1) | #22 | Val-Val-Gly-Gly-Val-Met-Leu-Gly-Ile-Ile-Ala-Gly-Lys-Asn-Ser-Gly-Val-Asp-Glu-Ala-Phe-Phe-Val-Leu-Lys-Gln-His-His-Val-Glu-Tyr-Gly-Ser-Asp-His-Arg-Phe-Glu-Ala Asp | 40 | | | 4324.7 | 5.1816 | 21.6 21.9 19.5 19.5 19.9 11.8 5.6 1.4 6 1.5 -10 -10 -6.8 -.1 7.6 12.2 12.6 1 1.3 1.6 4 -2.3 -6.4 -11 -15.6 -11.7 -14.9 -11.7 -10.2 -17.9 -12.6 -11.3 | A 2326 |
| 635. | ANANTIN | #22 | Cyclo[Gly-Phe-Ile-Gly-Trp-Gly-Asn-b-Asp]-Ile-Phe-Gly-His-Tyr-Ser-Gly-Asp-Phe | 17 | | | 1772 | | | A 4316 |
| 636. | ANEMONIA SULCATA TOXIN II,ILE-ISOTOXIN | #22 | Gly-Ile-Pro-Cys-Leu-Cys-Asp-Ser-Asp-Gly-Pro-Ser-Val-Arg-Gly-Asn Thr-Leu-Ser-Gly-Ile-Ile-Trp-Leu-Ala-Gly-Cys-Pro-Ser-Gly-Trp-His-Asn-Cys-Lys-Lys-His-Gly-Pro-Thr-Ile-Gly-Trp-Cys-Cys-Lys-Gln | 47 | | [Disulfide Bridges: 4-44; 6-34; 27-45 | 4954.6 | 8.0283 | 7 3.5 -2.6 -1.8 -.1 -3.9 -11.3 -7.8 -11.2 -3.9 -4.3 -3.1 2.2 2.5 6.1 10.3 15.6 15.9 14.6 13.8 13.4 8.5 3.1 .8 -3 -5.8 -5.4 -11.8 -17.3 -16.9 -18.1 -17.9 -10.2 -7.1 -10.5 -4.1 2.3 5.5 -1.5 | A 6061 |
| 637. | ANGIOGENIN FRAGMENTS (Fragment 108-122) | #22 | Glu-Asn-Gly-Leu-Pro-Val-His-Leu Asp-Gln-Ser-Ile-Phe-Arg-Arg | 15 | | | 1780.4 | 7.759 | -.4 -3.9 -1.2 3.7 2.7 4.3 -4.4 | A 9429 |
| 638. | ANGIOGENIN FRAGMENTS (Fragment | #22 | Glu-Asn-Gly-Leu-Pro-Val-His-Leu Asp-Gln-Ser-Ile-Phe-Arg-Arg-Pro | 16 | | | 1877.5 | 7.759 | -.4 -3.9 -1.2 3.7 2.7 4.3 -4.4 -7.3 | A 9304 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | 108-123) | | | | | | | | | |
| 639. | APAMIN | #22 | Cys-Asn-Cys-Lys-Ala-Pro-Glu-Thr-Ala-Leu-Cys-Ala-Arg-Arg-Cys-Gln-Gln-His-NH2 | 18 | | [Disulfide Bridges: 1-11; 3-15 | 2049.7 | 8.7952 | -4.6 -3.3 2.7 2 5.9 -.4 -.8 -.8 -3.6 -8.6 -12.4 | A 1289 |
| 640. | APOLIPOPROTEIN B FRAGMENT 3358-3372 AMIDE | #22 | Thr-Arg-Leu-Thr-Arg-Lys-Arg-Gly-Leu-Lys-Leu-Ala-Thr-Ala-Leu-NH2 | 15 | | | 1718.5 | 17 | -11.6 -15.4 -6.5 -8.5 -8.5 -2.2 5.5 10 | A 4183 |
| 641. | ARG-GLY-PRO-PHE-PRO-ILE | #22 | Arg-Gly-Pro-Phe-Pro-Ile | 6 | | | 686.6 | 10.736 | | A 2152 |
| 642. | ARG-HIS-PHE | #22 | Arg-His-Phe | 3 | | | 459.4 | 10.736 | | A 2541 |
| 643. | ARG-LYS-ASP-VAL-TYR (Thymopoietin II Fragment 32-36 ; TP-5) | #22 | Arg-Lys-Asp-Val-Tyr | 5 | | | 680.5 | 9.4958 | | A 4777 |
| 644. | ARG-LYS-GLU-VAL-TYR (Splenin Fragment 32-36 ; Splenopentin ; SP-5) | #22 | Arg-Lys-Glu-Val-Tyr | 5 | | | 694.6 | 9.4958 | | A 2042 |
| 645. | ARG-SER-ARG-HIS-PHE | #22 | Arg-Ser-Arg-His-Phe | 5 | | | 703.6 | 12.4802 | | A 2791 |
| 646. | ARG-TYR-VAL-VAL-LEU-PRO-ARG-PRO-VAL-CYS-PHE-GLU-LYS-GLY-MET-ASN-TYR-THR-VAL-ARG (Laminin B1 Chain 641-660) | #22 | Arg-Tyr-Val-Val-Leu-Pro-Arg-Pro-Val-Cys-Phe-Glu-Lys-Gly-Met-Asn-Tyr-Thr-Val-Arg | 20 | | | 2430.2 | 10.0652 | 2.9 9.9 14 6.3 2.1 -6 -2.5 2 -1.2 6.1 -4.4 -7.2 | A 8430 |
| 647. | ASN-GLU-ALA-TYR-VAL-HIS-ASP-ALA-PRO-VAL-ARG-SER-LEU-ASN | #22 | Asn-Glu-Ala-Tyr-Val-His-Asp-Ala-Pro-Val-Arg-Ser-Leu-Asn | 14 | | | 1583.1 | 5.1822 | -8.8 -1.1 2.4 -4.7 .4 -3.8 | A 4940 |
| 648. | ASP-ALA-GLU-ASN-LEU-ILE-ASP-SER-PHE-GLN-GLU-ILE-VAL | #22 | Asp-Ala-Glu-Asn-Leu-Ile-Asp-Ser-Phe-Gln-Glu-Ile-Val | 13 | | | 1487.9 | 2.7862 | -1.9 -1.9 -7.2 .8 8.5 | A 5667 |
| 649. | ASP-LEU-TRP-GLN-LYS (U5-Peptide) | #22 | Asp-Leu-Trp-Gln-Lys | 5 | | | 688.5 | 6.86 | | A 4182 |
| 650. | ASP-SER-ASP-PRO-ARG (IgE peptide III ; Hamburger pentapeptide) | #22 | Asp-Ser-Asp-Pro-Arg | 5 | | | 587.3 | 3.907 | | A 3526 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 651. | BEAUVERICIN | #22 | Cyclo-[D-a-Hydroxyisovaleryl-L-N Methylphenylalanyl]3 | 3 | | | | | | B 7510 |
| 652. | N-t-BOC-GLU-GLU-ILE METHYL ESTER | #22 | N-t-BOC-Glu-Glu-Ile-OMe | 3 | | | 146.1 | | | B 2137 |
| 653. | N-t-BOC-GLU-GLU-LEU METHYL ESTER | #22 | N-t-BOC-Glu-Glu-Leu-OMe | 3 | | | 290.2 | | | B 1011 |
| 654. | N-t-BOC-GLU-GLU-VAL METHYL ESTER | #22 | N-t-BOC-Glu-Glu-Val-OMe | 3 | | | 146.1 | | | B 9886 |
| 655. | BRAIN NATRIURETIC PEPTIDE-32 (BNP-32) | #22 | Ser-Pro-Lys-Met-Val-Gln-Gly-Ser-Gly-Cys-Phe-Gly-Arg-Lys-Met-Asp-Arg-Ile-Ser-Ser-Ser-Ser-Gly-Leu-Gly-Cys-Lys-Val-Leu-Arg-Arg-His | 32 | Human | 10-26 | 3470.4 | 11.5668 | -5.3 -2 2.4 5.9 4 -4.7 -3.2 -2.8 -5.5 -5.1 -8.4 -12 -12.4 -8.7 -5.2 -3.3 -.2 6.8 2.3 3.4 8 8.8 5.1 -2.2 | B 5900 |
| 656. | BRAIN NATRIURETIC PEPTIDE-32 (BNP-32) | #22 | Ser-Pro-Lys-Thr-Met-Arg-Asp-Ser-Gly-Cys-Phe-Gly-Arg-Arg-Leu-Asp-Arg-Ile-Gly-Ser-Leu-Ser-Gly-Leu-Gly-Cys-Asn-Val-Leu-Arg-Arg-Tyr | 32 | Porcine | 10-26 | 3575.7 | 11.2543 | -14.3 -11 -6.6 -3.1 -2.4 -13.3 -5 -1.5 -4.2 -3.8 -6.7 -10.3 -6.1 -2.4 1.7 1.7 4.8 11.8 7.3 8.4 13 9.2 5.5 .1 | B 6651 |
| 657. | BRAIN NATRIURETIC PEPTIDE-32 (BNP-32) | #22 | Asn-Ser-Lys-Met-Ala-His-Ser-Ser-Ser-Cys-Phe-Gly-Gln-Lys-Ile-Asp-Arg-Ile-Gly-Ala-Val-Ser-Arg-Leu-Gly-Cys-Asp-Gly-Leu-Arg-Leu-Phe | 32 | Rat | 10-26 | 3456.2 | 9.7636 | -10.1 -4.1 -.5 3 -2.4 -4.2 -.4 .4 -2.3 -1.5 -4.4 -5.4 -.8 1.9 5.8 .6 3.7 10.7 6.2 2.7 4.7 .5 .6 7.9 | B 9901 |
| 658. | BRAIN NATRIURETIC PEPTIDE-45 (BNP-45) | #22 | Ser-Gln-Asp-Ser-Ala-Phe-Arg-Ile-Gln-Glu-Arg-Leu-Arg-Asn-Ser-Lys-Met-Ala-His-Ser-Ser-Ser-Cys-Phe-Gly-Gln-Lys-Ile-Asp-Arg-Ile-Gly-Ala-Val-Ser-Arg-Leu-Gly-Cys-Asp-Gly-Leu-Arg-Leu-Phe | 45 | Rat | 23-39 | 5044.4 | 10.731 | -7.5 -10.2 -10.2 -3.9 -3.1 -9.4 -16.5 -12 -18.5 -13.2 -12.9 -9.2 -13.8 -10.1 -4.1 -.5 3 -2.4 -4.2 -.4 .4 -2.3 -1.5 -4.4 -5.4 -.8 1.9 5.8 .6 3.7 10.7 6.2 2.7 4.7 .5 .6 7.9 | B 6154 |
| 659. | BUCCALIN | #22 | Gly-Met-Asp-Ser-Leu-Ala-Phe-Ser-Gly-Gly-Leu-NH2 | 11 | | | 1068.4 | 6.83 | 4.4 4.4 6.3 9.8 | B 4528 |
| 660. | BURSIN | #22 | Lys-His-Gly-NH2 | 3 | | | 357.2 | 15 | | B 5644 |
| 661. | CALCITONIN GENE RELATED PEPTIDE | #22 | Ala-Cys-Asp-Thr-Ala-Thr-Cys-Val-Thr-His-Arg-Leu-Ala-Gly-Leu-Leu-Ser-Arg-Ser-Gly-Gly-Val-Val-Lys- | 37 | Human | 2-7 | 3809.7 | 10.8404 | 7.2 2.2 -3.8 2.5 5 2.8 7.3 8.6 3.6 4.3 2.2 6.3 2.1 4.5 9.1 5.3 -2.4 -9.6 -1.3 3.7 2.5 2.2 -2 -5.5 -2 .7 | C 0167 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Asn-Asn-Phe-Val-Pro-Thr-Asn-Val-Gly-Ser-Lys-Ala-Phe-NH2 | | | | | | 4.2 -.7 -2.1 -.5 | |
| 662. | CALCITONIN GENE RELATED PEPTIDE | #22 | Ser-Cys-Asn-Thr-Ala-Thr-Cys-Val-Thr-His-Arg-Leu-Ala-Gly-Leu-Leu-Ser-Arg-Ser-Gly-Gly-Val-Val-Lys-Asp-Asn-Phe-Val-Pro-Thr-Asn-Val-Gly-Ser-Glu-Ala-Phe-NH2 | 37 | Rat | 2-7 | 3824.7 | 8.9646 | 4.6 2.2 -3.8 2.5 5 2.8 7.3 8.6 3.6 4.3 2.2 6.3 2.1 4.5 9.1 5.3 -2.4 -9.6 -1.3 3.7 2.5 2.2 -2 -5.5 -2 .7 .7 -.3 -1.7 -.1 | C 0292 |
| 663. | CALCITONIN GENE RELATED PEPTIDE FRAGMENT 8-37 | #22 | Val-Thr-His-Arg-Leu-Ala-Gly-Leu-Leu-Ser-Arg-Ser-Gly-Gly-Val-Val-Lys-Asn-Asn-Phe-Val-Pro-Thr-Asn-Val-Gly-Ser-Lys-Ala-Phe-NH2 | 30 | Human | | 3145.3 | 17 | 8.6 3.6 4.3 2.2 6.3 2.1 4.5 9.1 5.3 -2.4 -9.6 -1.3 3.7 2.5 2.2 -2 -5.5 -2 .7 4.2 -.7 -2.1 -.5 | C 2806 |
| 664. | b-CALCITONIN GENE RELATED PEPTIDE (CGRP-II) | #22 | Ala-Cys-Asn-Thr-Ala-Thr-Cys-Val-Thr-His-Arg-Leu-Ala-Gly-Leu-Leu-Ser-Arg-Ser-Gly-Gly-Met-Val-Lys-Ser-Asn-Phe-Val-Pro-Thr-Asn-Val-Gly-Ser-Lys-Ala-Phe-NH2 | 37 | Human | 2-7 | 3814.7 | 11.652 | 7.2 2.2 -3.8 2.5 5 2.8 7.3 8.6 3.6 4.3 2.2 6.3 2.1 2.2 6.8 3 -5.5 -9.2 -.9 4.1 2.9 2.6 .7 -2.8 .7 .7 4.2 -.7 -2.1 -.5 | C 1044 |
| 665. | CALPAIN INHIBITOR PEPTIDE | #22 | Asp-Pro-Met-Ser-Ser-Thr-Tyr-Ile-Glu-Glu-Leu-Gly-Lys-Arg-Glu-Val-Thr-Ile-Pro-Pro-Lys-Tyr-Arg-Glu-Leu-Leu-Ala | 27 | | | 3134.4 | 4.644 | -5.8 -5.8 -.4 -2.7 -1.9 -5 -12.3 -6.8 -12 -4 -2.1 -7.5 -11 -8.4 -3.9 -8.4 -8.8 -4.3 -7 | C 9181 |
| 666. | CARASSIN | #22 | Ser-Pro-Ala-Asn-Ala-Gln-Ile-Thr-Arg-Lys-Arg-His-Lys-Ile-Asn-Ser-Phe-Val-Gly-Leu-Met-NH2 | 21 | | | 2387.8 | 17 | -2 -5.7 -8 -17.5 -14 -15.2 -11.7 -20.5 -17 -8.3 -4.8 3.5 8.6 12.5 | C 2055 |
| 667. | CARBOMETHOXYCARBONYL-D-PRO-D-PHE BENZYL ESTER | #22 | Carbomethoxycarbonyl-D-Pro-D-Phe Benzyl Ester | 2 | | | | | | C 4924 |
| 668. | Na-CBZ-ARG-ARG-PRO-PHE-HIS-STA-ILE-HIS-Ne-BOC-LYS METHYL ESTER | #22 | Na-CBZ-Arg-Arg-Pro-Phe-His-Sta-Ile-His-Ne-BOC-Lys-OMe | 9 | | | 806.7 | | | C 9415 |
| 669. | CBZ-LEU-VAL-GLY DIAZOMETHYL KETONE | #22 | CBZ-Leu-Val-Gly Diazomethyl Ketone | 3 | | | 117.1 | | | C 9546 |
| 670. | N-CBZ-D-PHE-PHE-GLY | #22 | N-CBZ-D-Phe-Phe-Gly | 3 | | | 222.1 | | | C 9405 |
| 671. | N-CBZ-PRO-LEU-GLY | #22 | N-CBZ-Pro-Leu-Gly Hydroxamate | 3 | | | 131.1 | | | C 8537 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | HYDROXAMATE | | | | | | | | | |
| 672. | CD4 FRAGMENTS (Fragment 25-58) | #22 | Ser-Ile-Gln-Phe-His-Trp-Lys-Asn-Ser-Asn-Gln-Ile-Lys-Ile-Leu-Gly-Asn-Gln-Gly-Ser-Phe-Leu-Thr-Lys-Gly-Pro-Ser-Lys-Leu-Asn-Asp-Arg-Ala-Asp | 34 | | | 3844.6 | 10.79238 | -9.3 -8.5 -20 -12 -14.8 -11 -6.3 -2.8 .7 -5.5 -2.4 .3 -1.4 6.3 1.1 -2.7 -6.6 -4.7 -2 -1.6 -.9 -3.7 -11 -17.7 -12.6 -12.2 | C 5292 |
| 673. | CD4 FRAGMENTS (Fragment 37-53) | #22 | Lys-Ile-Leu-Gly-Asn-Gln-Gly-Ser-Phe-Leu-Thr-Lys-Gly-Pro-Ser-Lys-Leu | 17 | | | 1790.2 | 11.0988 | -1.4 6.3 1.1 -2.7 -6.6 -4.7 -2 -1.6 -.9 | C 5167 |
| 674. | CD4 FRAGMENTS ([Cys (Bzl)]84-Fragment 81-92) | #22 | Thr-Tyr-Ile-Cys[Bzl]-Glu-Val-Glu-Asp-Gln-Lys-Glu-Glu | 12 | | | 1378 | | | C 2796 |
| 675. | CECROPINS (Cecropin A) | #22 | Lys-Trp-Lys-Leu-Phe-Lys-Lys-Ile-Glu-Lys-Val-Gly-Gln-Asn-Ile-Arg-Asp-Gly-Ile-Ile-Lys-Ala-Gly-Pro-Ala-Val-Ala-Val-Val-Gly-Gln-Ala-Thr-Gln-Ile-Ala-Lys-NH2 | 37 | | | 4024.9 | 11.4487 | -8.9 -5 -3.8 -.3 -7.6 -14.3 -5.5 -1.6 -10.6 -11 -2.6 -2.3 -1.9 -.5 2.6 -3.5 2.8 10.5 12.7 12.4 12.1 15.6 10.3 12.5 13.4 8.1 8.4 8.4 4.2 -3.9 | C 9421 |
| 676. | CECROPINS (Cecropin B) | #22 | Lys-Trp-Lys-Val-Phe-Lys-Lys-Ile-Glu-Lys-Met-Gly-Arg-Asn-Ile-Arg-Asn-Gly-Ile-Val-Lys-Ala-Gly-Pro-Ala-Ile-Ala-Val-Leu-Gly-Glu-Ala-Lys-Ala-Leu-NH2 | 35 | | | 3856.9 | 11.9494 | -8.5 -4.6 -5.7 -2.2 -6.4 -17.6 -8.8 -4.9 -13.9 -14.3 -5.9 -3.6 -7.7 -.8 2.3 -3.8 2.5 10.5 12.7 12.4 12 15.5 10.2 12.4 14 10.1 9.4 7.6 | C 1796 |
| 677. | CECROPINS (Cecropin P1) | #22 | Ser-Trp-Leu-Ser-Lys-Thr-Ala-Lys-Lys-Leu-Glu-Asn-Ser-Ala-Lys-Lys-Arg-Ile-Ser-Glu-Gly-Ile-Ala-Ile-Ala-Ile-Gln-Gly-Gly-Pro-Arg | 31 | Porcine | | 3342.3 | 11.3276 | -5.4 -4.7 -7.3 -11.1 -14.6 -8.9 -8.2 -17.8 -17.8 -10 -14.6 -14.6 -11.5 -6.2 -6.2 2.2 7.9 16.9 8.9 9.3 12.4 11.2 6.7 | C 7927 |
| 678. | CEREBELLIN | #22 | Ser-Gly-Ser-Ala-Lys-Val-Ala-Phe-Ser-Ala-Ile-Arg-Ser-Thr-Asn-His | 16 | | | 1633.9 | 11.6422 | 3.9 6.5 11.4 12.2 5.1 8.3 4.1 -4.4 | C 8412 |
| 679. | CHARYBDOTOXIN | #22 | Glu-Phe-Thr-Asn-Val-Ser-Cys-Thr-Thr-Ser-Lys-Glu-Cys-Trp-Ser-Val-Cys-Gln-Arg-Leu-His-Asn-Thr-Ser-Arg-Gly-Lys-Cys-Met-Asn-Lys-Lys-Cys-Arg-Cys-Tyr-Ser | 37 | | [Disulfide Bridges: 7-28; 13-33; 17-35 | 4323.5 | 8.8846 | -.4 2.3 -.5 -7.2 -1.2 -6.3 -6.3 -4.6 -1.4 -4.2 -7.3 -.2 .1 -2.4 -5.7 -5.7 -9.9 -17.3 -18.3 -10.7 -12.6 -12.9 -9.4 -12.6 -13.2 -8.7 -10.3 -7.7 -11 | C 7802 |
| 680. | CHORIONIC GONADOTROPIN (b-Chain | #22 | Thr-Cys-Asp-Asp-Pro-Arg-Phe-Gln-Asp-Ser-Ser-Ser-Ser-Lys-Ala- | 37 | Human | | 3873.5 | 4.3806 | -12 -15.6 -18.9 -16.2 -13.5 -16.4 -9.5 -13.9 -12 -10.1 -10.1 -5.5 - | C 9288 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | Fragment 109-145) |  | Pro-Pro-Pro-Ser-Leu-Pro-Ser-Pro Ser-Arg-Leu-Pro-Gly-Pro-Ser-Asp-Thr-Pro-Ile-Leu-Pro-Gln |  |  |  |  |  | 6.3 -6.3 -4 -6.6 -5 -4.1 -4.1 -3.7 -9.1 -8.3 -7.5 -10.1 -10.9 -1.9 -1.9 -1.9 -5 |  |
| 681. | CHROMOGRANIN A FRAGMENT 324-337 | #22 | Trp-Ser-Lys-Met-Asp-Gln-Leu-Ala-Lys-Glu-Leu-Thr-Ala-Glu | 14 | Human |  | 1648.1 | 4.3208 | -5.1 -11.6 -7 -3.8 -3.9 -3.9 | C 6446 |
| 682. | CHROMOSTATIN-20 | #22 | Ser-Asp-Glu-Asp-Ser-Asp-Gly-Asp-Arg-Pro-Gln-Ala-Ser-Pro-Gly-Leu-Gly-Pro-Gly-Pro | 20 |  |  | 1948.9 | 3.4497 | -19.5 -24.8 -24.8 -19.5 -16.8 -17.6 -14.5 -10.3 -7.2 -4.3 -3.1 -1.2 | C 1680 |
| 683. | ASN-PRO-ASN-ALA-ASN-PRO-ASN-ALA-ASN-PRO-ASN-ALA | #22 | Asn-Pro-Asn-Ala-Asn-Pro-Asn-Ala-Asn-Pro-Asn-Ala | 12 |  |  | 1206.9 | 5.6 | -17.1 -15.2 -17.1 -11.8 | A 6546 |
| 684. | CONANTOKIN G | #22 | Gly-Glu-g-CarboxyGlu-g-CarboxyGlu-Leu-Gln-g-CarboxyGlu-Asn-Gln-g-CarboxyGlu-Leu-Ile-Arg-g-CarboxyGlu-Lys-Ser-Asn-NH2 | 17 |  |  | 1416.1 |  |  | C 4311 |
| 685. | [Asn-OH17]-CONANTOKIN-G (Conantokin-G Free Acid | #22 | Gly-Glu-g-CarboxyGlu-g-CarboxyGlu-Leu-Gln-g-CarboxyGlu-Asn-Gln-g-CarboxyGlu-Leu-Ile-Arg-g-CarboxyGlu-Lys-Ser-Asn | 17 |  |  | 1400.1 |  |  | C 2051 |
| 686. | [Ala-OH21]-CONANTOKIN-T (Conantokin-T Free Acid) | #22 | Gly-Glu-g-CarboxyGlu-g-CarboxyGlu-Tyr-Gln-Lys-Met-Leu-g-CarboxyGlu-Asn-Leu-Arg-g-CarboxyGlu-Ala-Glu-Val-Lys-Lys-Asn-Ala | 21 |  |  | 1993.5 |  |  | C 2176 |
| 687. | CONOTOXIN GI | #22 | Glu-Cys-Cys-Asn-Pro-Ala-Cys-Gly-Arg-His-Tyr-Ser-Cys-NH2 | 13 |  | [Disulfide Bridges: 2-7; 3-13 | 1458.1 | 8.0091 | .3 -3.9 -7.7 -11 -5 -3.4 | C 8653 |
| 688. | m-CONOTOXIN GIIIA | #22 | Arg-Asp-Cys-Cys-Thr-Hyp-Hyp-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Hyp-Gln-Arg-Cys-Cys-Ala-NH2 | 22 |  | [Disulfide Bridges: Undefin | 2636.2 |  |  | C 7420 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Gly-Trp-Thr-Asn-NH2 | | | | | | | |
| 696. | CORTICOSTATIN (CS-I) | #22 | Gly-Ile-Cys-Ala-Cys-Arg-Arg-Arg-Phe-Cys-Pro-Asn-Ser-Glu-Arg-Phe-Ser-Gly-Tyr-Cys-Arg-Val-Asn-Gly-Ala-Arg-Tyr-Val-Arg-Cys-Cys-Ser-Arg-Arg | 34 | Rabbit | | 4010.5 | 10.3242 | .2 3.1 -3 -5.5 -11.6 -17.6 -17.6 -10.3 -6.6 -9.8 -13.6 -9.5 -6 -5.5 -6.5 -1.4 -2.4 -1.6 -7 -1.5 -8.5 -1.5 -3.2 -.5 -.1 -10.9 | C 1921 |
| 697. | CORTICOTROPIN RELEASING FACTOR (CRF ; CRH) | #22 | Ser-Gln-Glu-Pro-Pro-Ile-Ser-Leu-Asp-Leu-Thr-Phe-His-Leu-Leu-Arg-Glu-Val-Leu-Glu-Met-Thr-Lys-Ala-Asp-Gln-Leu-Ala-Gln-Gln-Ala-His-Asn-Asn-Arg-Lys-Leu-Leu-Asp-Ile-Ala-NH2 | 41 | Bovine | | 4710.4 | 6.0815 | -3.5 -2.4 .4 6.7 5.1 10.5 9.8 10.6 -1.2 6.5 6.5 3.7 2.8 5.3 1.5 -4.4 .1 -3.4 -3.8 -5.8 -5.8 -11.2 -8.7 -8 -13.3 -9.8 -9.8 -18.1 -20 -12.7 -9.2 -10 -5 -5 | C 2671 |
| 698. | CORTICOTROPIN RELEASING FACTOR (CRF ; CRH) | #22 | Ser-Glu-Glu-Pro-Pro-Ile-Ser-Leu-Asp-Leu-Thr-Phe-His-Leu-Leu-Arg-Glu-Val-Leu-Glu-Met-Ala-Arg-Ala-Glu-Gln-Leu-Ala-Gln-Gln-Ala-His-Ser-Asn-Arg-Lys-Leu-Met-Glu-Ile-Ile-NH2 | 41 | Human, Rat | | 4769.6 | 5.3458 | -3.5 -2.4 .4 6.7 5.1 10.5 9.8 10.6 -1.2 6.5 6.5 3.7 2.8 7.8 4 -2.5 -1.5 -1.5 -1.9 -3.9 -3.9 -9.3 -9.3 -8 -10.6 -7.1 -7.1 -15.4 -17.3 -11.9 -11.9 -9.2 -1.5 -4.2 | C 3042 |
| 699. | CORTICOTROPIN RELEASING FACTOR (CRF ; CRH) | #22 | Ser-Gln-Glu-Pro-Pro-Ile-Ser-Leu-Asp-Leu-Thr-Phe-His-Leu-Leu-Arg-Glu-Val-Leu-Glu-Met-Thr-Lys-Ala-Asp-Gln-Leu-Ala-Gln-Gln-Ala-His-Ser-Asn-Arg-Lys-Leu-Leu-Asp-Ile-Ala-NH2 | 41 | Sheep | | 4683.3 | 6.0815 | -3.5 -2.4 .4 6.7 5.1 10.5 9.8 10.6 -1.2 6.5 6.5 3.7 2.8 5.3 1.5 -4.4 .1 -3.4 -3.8 -5.8 -5.8 -11.2 -8.7 -8 -10.6 -7.1 -7.1 -15.4 -17.3 -10 -6.5 -7.3 -2.3 -5 | C 3167 |
| 700. | Tyr-CORTICOTROPIN RELEASING FACTOR | #22 | Tyr-Ser-Glu-Glu-Pro-Pro-Ile-Ser-Leu-Asp-Leu-Thr-Phe-His-Leu-Leu-Arg-Glu-Val-Leu-Glu-Met-Ala Arg-Ala-Glu-Gln-Leu-Ala-Gln-Gln-Ala-His-Ser-Asn-Arg-Lys-Leu-Met-Glu-Ile-Ile-NH2 | 42 | Human, Rat | | 4932.7 | 5.3457 | -4.8 -3.5 -2.4 .4 6.7 5.1 10.5 9.8 10.6 -1.2 6.5 6.5 3.7 2.8 7.8 4 -2.5 -1.5 -1.5 -1.9 -3.9 -3.9 -9.3 -9.3 -8 -10.6 -7.1 -7.1 -15.4 -17.3 -11.9 -11.9 -9.2 -1.5 -4.2 | C 6426 |
| 701. | Tyr-CORTICOTROPIN RELEASING FACTOR | #22 | Tyr-Ser-Gln-Glu-Pro-Pro-Ile-Ser-Leu-Asp-Leu-Thr-Phe-His-Leu-Leu-Arg-Glu-Val-Leu-Glu-Met-Thr-Lys-Ala-Asp-Gln-Leu-Ala-Gln-Gln-Ala-His-Ser-Asn-Arg-Lys-Leu- | 42 | Ovine | | 4846.4 | 6.0813 | -4.8 -3.5 -2.4 .4 6.7 5.1 10.5 9.8 10.6 -1.2 6.5 6.5 3.7 2.8 5.3 1.5 -4.4 .1 -3.4 -3.8 -5.8 -5.8 -11.2 -8.7 -8 -10.6 -7.1 -7.1 -15.4 -17.3 -10 -6.5 -7.3 -2.3 -5 | C 0922 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Leu-Asp-Ile-Ala-NH2 | | | | | | | |
| 702. | CORTICOTROPIN RELEASING FACTOR ANTAGONIST (a-Helical CRF [9-41]) | #22 | Asp-Leu-Thr-Phe-His-Leu-Leu-Arg-Glu-Met-Leu-Glu-Met-Ala-Lys-Ala-Glu-Gln-Glu-Ala-Glu-Gln-Ala-Ala-Leu-Asn-Arg-Leu-Leu-Leu-Glu-Glu-Ala-NH2 | 33 | | | 3836.8 | 4.2678 | -1.2 4.2 4.2 1.4 .5 5.5 1.7 -4.2 -3.2 -3.2 -8.6 -10.6 -10.6 -16 -16 -10.3 -8.3 -4.8 -4.8 -2 0 7.3 7.3 2 2 -5.3 | C 2917 |
| 703. | C-PEPTIDE (Insulin Chain C) | #22 | Arg-Arg-Glu-Ala-Glu-Asp-Leu-Gln-Val-Gly-Gln-Val-Glu-Leu-Gly-Gly-Gly-Pro-Gly-Ala-Gly-Ser-Leu-Gln-Pro-Leu-Ala-Leu-Glu-Gly-Ser-Leu-Gln-Lys-Arg | 35 | Human | | 3614.5 | 4.642 | -13.2 -9.1 -8.1 -.4 -5.7 1.6 4.7 .5 3.6 -2.2 -2.2 3.1 -1.5 1.2 1.2 -1.9 -3.1 1.1 4.5 8.7 3.4 3.4 3.4 3.4 3.4 5 -2.7 | C 5051 |
| 704. | Tyr-C-PEPTIDE (Tyr-Insulin Chain C) | #22 | Tyr-Arg-Arg-Glu-Ala-Glu-Asp-Leu-Gln-Val-Gly-Gln-Val-Glu-Leu-Gly-Gly-Gly-Pro-Gly-Ala-Gly-Ser-Leu-Gln-Pro-Leu-Ala-Leu-Glu-Gly-Ser-Leu-Gln-Lys-Arg | 36 | Human | | 3777.6 | 4.642 | -18.7 -13.2 -9.1 -8.1 -.4 -5.7 1.6 4.7 .5 3.6 -2.2 -2.2 3.1 -1.5 1.2 1.2 -1.9 -3.1 1.1 4.5 8.7 3.4 3.4 3.4 3.4 3.4 5 -2.7 | C 9781 |
| 705. | C-PEPTIDE Fragment 3-33 | #22 | Glu-Ala-Glu-Asp-Leu-Gln-Val-Gly-Gln-Val-Glu-Leu-Gly-Gly-Gly- Pro Gly-Ala-Gly-Ser-Leu-Gln-Pro-Leu-Ala-Leu-Glu-Gly-Ser-Leu-Gln | 31 | Human | | 2916.7 | | | C 8662 |
| 706. | CLCLO(D-ASP-PRO-D-VAL-LEU-D-TRP) | #22 | Cyclo(D-Asp-Pro-D-Val-Leu-D-Trp) | 5 | | | 627.5 | | | C 1306 |
| 707. | CYCLO(D-GLU-ALA-D-allo-ILE-LEU-D-TRP) | #22 | Cyclo(D-Glu-Ala-D-allo-Ile-Leu-D-Trp) | 5 | | | 629.5 | | | C 1307 |
| 708. | CYCLOHEXYLACETYL-PHE-ARG-SER-VAL-GLN AMIDE | #22 | Cyclohexylacetyl-Phe-Arg-Ser-Val-Gln-NH2 | 5 | | | 505.4 | | | C 6922 |
| 709. | CYCLO(HIS-PHE) | #22 | Cyclo(His-Phe) | 2 | | | 302.2 | | | C 2651 |
| 710. | CYCLO(HIS-PRO) | #22 | Cyclo(His-Pro) | 2 | | | 155.1 | | | C 3772 |
| 711. | CYCLO(PHE-SER) | #22 | Cyclo(Phe-Ser) | 2 | | | 252.1 | | | C 2524 |
| 712. | CYCLO(PRO-GLY)3 | #22 | Cyclo(Pro-Gly)3 | 6 | | | 383.2 | | | C 7297 |
| 713. | CYS-ASP-PRO-GLY-TYR-ILE-GLY-SER-ARG (Laminin Fragment 925-933) | #22 | Cys-Asp-Pro-Gly-Tyr-Ile-Gly-Ser-Arg | 9 | | | 966.6 | 6.11 | -1 | C 0668 |
| 714. | CYS-ASP-PRO-GLY-TYR- | #22 | Cys-Asp-Pro-Gly-Tyr-Ile-Gly-Ser- | 9 | | | 982.6 | 6.11 | -1 -11.5 | C 1668 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ILE-GLY-SER-ARG Amide (Laminin Fragment 925-933 Amide) |  | Arg-NH2 |  |  |  |  |  |  |  |
| 715. | CYS-GLY-TYR-GLY-PRO-LYS-LYS-LYS-ARG-LYS-VAL-GLY-GLY | #22 | Cys-Gly-Tyr-Gly-Pro-Lys-Lys-Lys-Arg-Lys-Val-Gly-Gly | 13 |  |  | 1382 | 10.9969 | -12.9 -19.9 -19.2 -18.3 -18.3 | C 4547 |
| 716. | CYS-SER-ARG-ALA-ARG-LYS-GLN-ALA-ALA-SER-ILE-LYS-VAL-ALA-VAL-SER-ALA-ASP-ARG (Laminin A chain 2091-2108) | #22 | Cys-Ser-Arg-Ala-Arg-Lys-Gln-Ala-Ala-Ser-Ile-Lys-Val-Ala-Val-Ser-Ala-Asp-Arg | 19 |  |  | 2020.3 | 11.6337 | -9.3 -12.6 -7.3 -2.8 -4.3 2 10.1 12.8 12.8 11 8.3 | C 6171 |
| 717. | DEFENSIN HNP-1 (Human Neutrophil Peptide-1) | #22 | Ala-Cys-Tyr-Cys-Arg-Ile-Pro-Ala-Cys-Ile-Ala-Gly-Glu-Arg-Arg-Tyr-Gly-Thr-Cys-Ile-Tyr-Gln-Gly-Arg-Leu-Trp-Ala-Phe-Cys-Cys | 30 | Human | [Disulfide Bridges: 2-30; 4-19; 9-29 | 3449.8 | 8.30928 | 8.2 10.9 10.2 11.1 5.1 9.6 .6 -3.6 -5.8 -9 -11 -8.3 -9.2 -9.2 -5.1 -.6 0 -.5 2 2.3 .3 4.1 | D 2043 |
| 718. | DEFENSIN HNP-2 (Human Neutrophil Peptide-2) | #22 | Cys-Tyr-Cys-Arg-Ile-Pro-Ala-Cys-Ile-Ala-Gly-Glu-Arg-Arg-Tyr-Gly-Thr-Cys-Ile-Tyr-Gln-Gly-Arg-Leu-Trp-Ala-Phe-Cys-Cys | 29 | Human | [Disulfide Bridges: 1-29; 3-18; 8-28 | 3378.8 | 8.3158 | 10.9 10.2 11.1 5.1 9.6 .6 -3.6 -5.8 -9 -11 -8.3 -9.2 -9.2 -5.1 -.6 0 -.5 2 2.3 .3 4.1 | D 6790 |
| 719. | DERMASEPTIN | #22 | Ala-Leu-Trp-Lys-Thr-Met-Leu-Lys-Lys-Leu-Gly-Thr-Met-Ala-Leu-His-Ala-Gly-Lys-Ala-Ala-Leu-Gly-Ala-Ala-Ala-Asp-Thr-Ile-Ser-Gln-Gly-Thr-Gln | 34 |  |  | 3456.1 | 10.8327 | 1.9 0 -4.2 -4 1.8 4.3 6.2 -.8 4.9 8.4 4.6 2.9 5.4 7.3 5.1 3.1 8.1 8.1 4.6 8.2 10.9 8.3 1 1 -1.5 -6.8 | D 4671 |
| 720. | DIABETES ASSOCIATED PEPTIDE AMIDE (Amylin ; DAP ; Insulinoma or Islet Amyloid Polypeptide ; IAPP) | #22 | Lys-Cys-Asn-Thr-Ala-Thr-Cys-Ala-Thr-Gln-Arg-Leu-Ala-Asn-Phe-Leu-Val-His-Ser-Ser-Asn-Asn-Phe-Gly-Ala-Ile-Leu-Ser-Ser-Thr-Asn-Val-Gly-Ser-Asn-Thr-Tyr-NH2 | 37 | Human | 2-7 | 3922.7 | 10.048 | -.9 -.5 -6.5 -.2 2.3 .5 .5 1.8 4.2 1.7 4.4 8.1 4.3 -4.5 1.8 -1.4 -3.4 3.1 3.9 3.9 3.9 6.7 10.2 8.1 8.1 5.5 1 -7 -7.5 -6.7 | D 2162 |
| 721. | DIABETES ASSOCIATED PEPTIDE AMIDE | #22 | Ala-Thr-Gln-Arg-Leu-Ala-Asn-Phe-Leu-Val-Arg-Ser-Ser-Asn- | 30 | Rat |  | 3218.5 | 17 | 1.8 4.2 4.9 3.1 6.8 3 -5.8 1.5 -1.7 -7.1 -7.1 1.2 .4 -.4 2.4 5.9 2.8 | D 6170 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | (Fragment 8-37 ; Amylin 8-37) |  | Asn-Leu-Gly-Pro-Val-Leu-Pro-Pro-Thr-Asn-Val-Gly-Ser-Asn-Thr-Tyr-NH2 |  |  |  |  |  | 2.8 3.6 -.6 -8.6 -8.3 -6.7 |  |
| 722. | ELEDOISIN | #22 | pGlu-Pro-Ser-Lys-Asp-Ala-Phe-Ile-Gly-Leu-Met-NH2 | 11 |  |  | 1221.7 |  |  | E 7880 |
| 723. | ELEDOISIN-RELATED PEPTIDE | #22 | Lys-Phe-Ile-Gly-Leu-Met-NH2 | 6 |  |  | 724.5 | 15 |  | E 3253 |
| 724. | ENDOTHELINS (Big Endothelin 2) | #22 | Cys-Ser-Cys-Ser-Ser-Trp-Leu-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp-Val-Asn-Thr-Pro-Glu-Gln-Thr-Ala-Pro-Tyr-Gly-Leu-Gly-Asn-Pro-Pro | 37 | Human | [Disulfide Bridges: 1-15; 3-11 | 4183.1 | 4.0155 | 2 -7.9 -4.6 -2.9 -3.4 .2 3.6 -3.4 3.9 7.8 12.3 14.3 9.2 14.7 11.9 5.2 6.8 -.5 -.5 -5.7 -8.4 -9.1 -14.6 -11.5 -7 -5.8 -2.3 -3.9 -4.8 | E 6139 |
| 725. | ENDOTHELINS (Big Endothelin 38) | #22 | Cys-Ser-Cys-Ser-Ser-Leu-Met-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp-Val-Asn-Thr-Pro-Glu-His-Val-Val-Pro-Tyr-Gly-Leu-Gly-Ser-Pro-Arg-Ser | 38 | Human | [Disulfide Bridges: 1-15; 3-11 | 4283.1 | 5.1793 | 4.8 -5.1 -1.8 -.1 -.6 3 1.7 -3.4 3.9 7.8 12.3 14.3 9.2 14.7 11.9 5.2 6.8 -.5 -.2 -.5 -.8 -1.5 -7 -3.9 .6 1.8 4.5 6.1 1.9 -7.6 | E 9387 |
| 726. | ENDOTHELINS (Big Endothelin 39) | #22 | Cys-Ser-Cys-Ser-Ser-Leu-Met-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp-Val-Asn-Thr-Pro-Glu-His-Val-Val-Pro-Tyr-Gly-Leu-Gly-Ser-Pro-Ser-Arg-Ser | 39 | Bovine | [Disulfide Bridges: 1-15; 3-11 | 4370.1 | 5.1793 | 4.8 -5.1 -1.8 -.1 -.6 3 1.7 -3.4 3.9 7.8 12.3 14.3 9.2 14.7 11.9 5.2 6.8 -.5 -.2 -.5 -.8 -1.5 -7 -3.9 .6 1.8 4.5 6.1 1.1 -3.1 -6.8 | E 6389 |
| 727. | ENDOTHELINS (Big Endothelin 39) | #22 | Cys-Ser-Cys-Ser-Ser-Leu-Met-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp-Val-Asn-Thr-Pro-Glu-His-Ile-Val-Pro-Tyr-Gly-Leu-Gly-Ser-Pro-Ser-Arg-Ser | 39 | Porcine | [Disulfide Bridges: 1-15; 3-11 | 4384.1 | 5.1793 | 4.8 -5.1 -1.8 -.1 -.6 3 1.7 -3.4 3.9 7.8 12.3 14.3 9.2 14.7 11.9 5.2 6.8 -.5 -.2 -.2 -.5 -1.2 -6.7 -3.6 .9 2.1 4.8 6.4 1.1 -3.1 -6.8 | E 8887 |
| 728. | ENDOTHELINS (Big Endothelin 39) | #22 | Cys-Ser-Cys-Ser-Ser-Leu-Met-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp-Val-Asn-Thr-Pro-Glu-Arg-Val-Val-Pro-Tyr-Gly-Leu-Gly-Ser-Pro-Ser-Arg-Ser | 39 | Rat | [Disulfide Bridges: 1-15; 3-11 | 4390.2 | 5.3431 | 4.8 -5.1 -1.8 -.1 -.6 3 1.7 -3.4 3.9 7.8 12.3 14.3 9.2 14.7 11.9 5.2 6.8 -.5 3 -1.8 -2.1 -2.8 -8.3 -5.2 -.7 .5 3.2 6.1 1.1 -3.1 -6.8 | E 7265 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 729. | ENDOTHELINS (Big Endothelin Fragment 22-39) | #22 | Val-Asn-Thr-Pro-Glu-His-Val-Val-Pro-Tyr-Gly-Leu-Gly-Ser-Pro-Ser-Arg-Ser | 18 | Bovine |  | 1895.4 | 7.817 | -1.5 -7 -3.9 .6 1.8 4.5 6.1 1.1 -3.1 -6.8 | E 6014 |
| 730. | ENDOTHELINS (Endothelin 1) | #22 | Cys-Ser-Cys-Ser-Ser-Leu-Met-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp | 21 | Human, Porcine | [Disulfide Bridges: 1-15; 3-11 | 2492.7 | 4.2587 | 4.8 -5.1 -1.8 -.1 -.6 3 1.7 -3.4 3.9 7.8 12.3 14.3 9.2 | E 7764 |
| 731. | ENDOTHELINS (Endothelin 2) | #22 | Cys-Ser-Cys-Ser-Ser-Trp-Leu-Asp-Lys-Glu-Cys-Val-Tyr-Phe-Cys-His-Leu-Asp-Ile-Ile-Trp | 21 | Human | [Disulfide Bridges: 1-15; 3-11 | 2547.8 | 4.2587 | 2 -7.9 -4.6 -2.9 -3.4 .2 3.6 -3.4 3.9 7.8 12.3 14.3 9.2 | E 9012 |
| 732. | ENDOTHELINS (Endothelin 3) | #22 | Cys-Thr-Cys-Phe-Thr-Tyr-Lys-Asp-Lys-Glu-Cys-Val-Tyr-Tyr-Cys-His-Leu-Asp-Ile-Ile-Trp | 21 | Human, Rat | [Disulfide Bridges: 1-15; 3-11 | 2645 | 5.26 | -2.3 -12.2 -9 -7.3 -11.4 -12 -8.2 -7.5 -.2 3.7 8.2 10.2 5.1 | E 9137 |
| 733. | ENDOTHELINS (N-Succinyl-[Glu9,Ala11,15]-Endothelin 1 Fragment 8-21 | #22 | N-Suc-Asp-Glu-Glu-Ala-Val-Tyr-Phe-Ala-His-Leu-Asp-Ile-Ile-Trp | 14 |  |  | 1602.1 |  |  | E 4518 |
| 734. | [Cys(Acm)20,31]-EPIDERMAL GROWTH FACTOR FRAGMENT 20-31 | #22 | Cys[S-Acetamidomethyl]-Met-His-Ile-Glu-Ser-Leu-Asp-Ser-Tyr-Thr-Cys[Acm] | 12 |  |  | 1366.8 |  |  | E 9384 |
| 735. | EPIDERMAL GROWTH FACTOR RECEPTOR (Fragment 1005-1016) | #22 | Asp-Val-Val-Asp-Ala-Asp-Glu-Tyr-Leu-Ile-Pro-Gln | 12 | Human |  | 1371.8 | 2.71 | -1.3 6.7 .9 -6.8 | E 1886 |
| 736. | EPIDERMAL MITOSIS INHIBITING PENTAPEPTIDE | #22 | pGlu-Glu-Asp-Ser-Gly | 5 |  |  | 532.2 |  |  | E 1638 |
| 737. | ERYTHROPOIETIN (Fragment 1-26) | #22 | Ala-Pro-Pro-Arg-Leu-Ile-Cys-Asp-Ser-Arg-Val-Leu-Glu-Arg-Tyr-Leu-Leu-Glu-Ala-Lys-Glu-Ala-Glu-Asn-Ile-Thr | 26 | Human |  | 2998.4 | 4.6426 | .6 -1.2 .1 5.5 6.5 2.7 -7.6 -6.3 1 1.7 4.6 .4 -10.8 -5.5 -4.5 -3.2 -6 -10.5 | E 8013 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 738. | [Asn7,Lys24]-ERYTHROPOIETIN (Fragment 1-26) | #22 | Ala-Pro-Pro-Arg-Leu-Ile-Asn-Asp-Ser-Arg-Val-Leu-Glu-Arg-Tyr-Leu-Leu-Glu-Ala-Lys-Glu-Ala-Glu-Lys-Ile-Thr | 26 | Human | | 3024.4 | 7.18 | -5.4 -7.2 -5.9 -.5 .5 -3.3 -13.6 -6.3 1 -1.7 4.6 .4 -10.8 -5.5 -4.5 -3.2 -6.4 -10.9 | E 8138 |
| 739. | FIBRINOPEPTIDE A | #22 | Ala-Asp-Ser-Gly-Glu-Gly-Asp-Phe-Leu-Ala-Glu-Gly-Gly-Gly-Val-Arg | 16 | Human | | 1532.7 | 3.5152 | -3.7 -3.7 -3.7 -3.3 -3.3 -.2 4.4 7.9 | F 5765 |
| 740. | Tyr-FIBRINOPEPTIDE A | #22 | Tyr-Ala-Asp-Ser-Gly-Glu-Gly-Asp-Phe-Leu-Ala-Glu-Gly-Gly-Gly-Val-Arg | 17 | Human | | 1695.8 | 3.5152 | -8.8 -3.7 -3.7 -3.7 -3.3 -3.3 -.2 4.4 7.9 | F 5260 |
| 741. | FIBRINOPEPTIDE B | #22 | pGlu-Gly-Val-Asn-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg | 14 | Human | | 1567 | | | F 3379 |
| 742. | [Glu1]-FIBRINOPEPTIDE B | #22 | Glu-Gly-Val-Asn-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg | 14 | Human | | 1567 | 3.5577 | -17.6 -11.3 -8.1 -13.1 -7.8 -7.8 | F 3261 |
| 743. | FIBRINOPEPTIDE B-Tyr | #22 | pGlu-Gly-Val-Asn-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg-Tyr | 15 | | | 1730.1 | | | F 7767 |
| 744. | FIBROBLAST GROWTH FACTER, ACIDIC (Fragment 1-11) | #22 | Phe-Asn-Leu-Pro-Leu-Gly-Asn-Tyr-Lys-Lys-Pro | 11 | Bovine | | 1292 | 10.2903 | .099999999999998 -10.1 -8.6 | F 3635 |
| 745. | FIBROBLAST GROWTH FACTER, BASIC (Fragment 1-24) | #22 | Pro-Ala-Leu-Pro-Glu-Asp-Gly-Gly-Ser-Gly-Ala-Phe-Pro-Pro-Gly-His-Phe-Lys-Asp-Pro-Lys-Arg-Leu-Tyr | 24 | Bovine | | 2552.6 | 7.97 | -6.2 -5 -5 -6 -6 -4.1 -1 -3.8 -.6 .2 -3.3 -10.2 -13 -15.3 -14.4 -15.3 | F 5895 |
| 746. | FIBROBLAST GROWTH FACTER, BASIC (Fragment 106-120) | #22 | Tyr-Arg-Ser-Arg-Lys-Tyr-Ser-Ser-Trp-Tyr-Val-Ala-Leu-Lys-Arg | 15 | | | 1967.5 | 11.0176 | -18.8 -18.8 -10.1 -7.5 .8 4.7 2.1 | F 3768 |
| 747. | FOLLICULAR GONADOTROPIN-RELEASING PEPTIDE | #22 | Thr-Asp-Thr-Ser-His-His-Asp-Gln-Asp-His-Pro-Thr-Phe-Asn | 14 | Human | | 1648 | 4.9712 | -19.1 -25.1 -23.2 -23.2 -19.6 -16.4 | F 7892 |
| 748. | GLN-ALA-THR-VAL-GLY-ASP-ILE-ASN-THR-GLU-ARG-PRO-GLY-MET-LEU-ASP-PHE-THR-GLY-LYS (Diazepam Binding Inhibitor [DBI] Fragment 51-70) | #22 | Gln-Ala-Thr-Val-Gly-Asp-Ile-Asn-Thr-Glu-Arg-Pro-Gly-Met-Leu-Asp-Phe-Thr-Gly-Lys | 20 | Human | | 2148.5 | 4.2652 | -1.8 -1.8 -3.6 -9 -13.6 -11.3 -4 -12 -5.7 -5.7 -2.6 1.9 | G 9898 |
| 749. | GLN-ALA-THR-VAL-GLY- | #22 | Gln-Ala-Thr-Val-Gly-Asp-Val-Asn- | 18 | | | 1910.3 | 4.2068 | -2.1 1.4 -3.9 -9.3 -13.9 -9.7 -2.4 | G 3642 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ASP-VAL-ASN-THR-ASP-ARG-PRO-GLY-LEU-LEU-ASP-LEU-LYS (Octadecaneuropeptide ; ODN) |  | Thr-Asp-Arg-Pro-Gly-Leu-Leu-Asp-Leu-Lys |  |  |  |  |  | -10.1 -2.8 -5.6 |  |
| 750. | GLN-ARG-ARG-GLN-ARG-LYS-SER-ARG-ARG-THR-ILE | #22 | Gln-Arg-Arg-Gln-Arg-Lys-Ser-Arg-Arg-Thr-Ile | 11 |  |  | 1490.5 | 13.0849 | -29.7 -31.4 -22.4 | G 9016 |
| 751. | GLU-ALA-GLU (Thymosin a1 Fragment 25-27) | #22 | Glu-Ala-Glu | 3 |  |  | 345.2 | 2.9185 |  | G 2637 |
| 752. | GLU-ALA-GLU-ASN (Thymosin a1 Fragment 25-28) | #22 | Glu-Ala-Glu-Asn | 4 |  |  | 459.3 | 2.9185 |  | G 5775 |
| 753. | g-D-GLU-GLY | #22 | g-D-Glu-Gly | 2 |  |  | 75 |  |  | G 3765 |
| 754. | GLU-SER-PRO-LEU-ILE-ALA-LYS-VAL-LEU-THR-THR-GLU-PRO-PRO-ILE-ILE-THR-PRO-VAL-ARG-ARG (Phospholipase A2 activating peptide) | #22 | Glu-Ser-Pro-Leu-Ile-Ala-Lys-Val-Leu-Thr-Thr-Glu-Pro-Pro-Ile-Ile-Thr-Pro-Val-Arg-Arg | 21 |  |  | 2331.1 | 10.1172 | 8.3 11.1 11.2 9.3 3.9 -2.2 .5 8.9 4 -1.4 3.5 4.2 3.2 | G 1153 |
| 755. | GLY-ARG-GLY-ASP-ASN-PRO | #22 | Gly-Arg-Gly-Asp-Asn-Pro | 6 |  |  | 614.4 | 6.85 |  | G 2529 |
| 756. | GLY-GLN | #22 | Gly-Gln | 2 |  |  | 203.1 | 6 |  | G 5149 |
| 757. | GLY-GLU-GLN-ARG-LYS-ASP-VAL-TYR-VAL-GLN-LEU-TYR-LEU (Thymopoietin II Fragment 29-41) | #22 | Gly-Glu-Gln-Arg-Lys-Asp-Val-Tyr-Val-Gln-Leu-Tyr-Leu | 13 |  |  | 1610.2 | 6.89 | -12.2 -15.3 -8 -5.8 2.5 | G 3774 |
| 758. | GLY-GLY-ARG | #22 | Gly-Gly-Arg | 3 |  |  | 289.2 | 11.13 |  | G 6887 |
| 759. | GLY-GLY-HIS (Copper binding peptide) | #22 | Gly-Gly-His | 3 |  |  | 269.1 | 7.91 |  | G 5772 |
| 760. | GLY-GLY-TYR-ARG | #22 | Gly-Gly-Tyr-Arg | 4 |  |  | 452.3 | 9.9523 |  | G 5386 |
| 761. | GLY-HIS-ARG-PRO (Human fibrin b-chain fragment 1-4) | #22 | Gly-His-Arg-Pro | 4 |  |  | 466.4 | 11.13 |  | G 8636 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 762. | GLY-HIS-LYS (Liver cell growth factor) | #22 | Gly-His-Lys | 3 | | | 341.2 | 10.285 | | G 1887 |
| 763. | GLY-PEN-GLY-ARG-GLY-ASP-SER-PRO-CYS-ALA (Pen2,Cys9 cyclic) | #22 | Gly-Pen-Gly-Arg-Gly-Asp-Ser-Pro-Cys-Ala | 10 | | | 818.4 | | | G 5275 |
| 764. | GLY-PHE-ASP-LEU-ASN-GLY-GLY-GLY-VAL-GLY (Speract) | #22 | Gly-Phe-Asp-Leu-Asn-Gly-Gly-Gly-Val-Gly | 10 | | | 890.4 | 3.125 | 2.2 2.2 | G 9773 |
| 765. | GLY-PRO-ARG-PRO | #22 | Gly-Pro-Arg-Pro | 4 | | | 426.4 | 11.13 | | G 1895 |
| 766. | GLY-PRO-ARG-PRO AMIDE | #22 | Gly-Pro-Arg-Pro-NH2 | 4 | | | 442.4 | 17 | | G 5779 |
| 767. | GLY-PRO-GLY-GLY | #22 | Gly-Pro-Gly-Gly | 4 | | | 286.1 | 6 | | G 6011 |
| 768. | GLY-VAL-LEU-SER-ASN-VAL-ILE-GLY-TYR-LEU-LYS-LYS-LEU-GLY-THR-GLY-ALA-LEU-ASN-ALA-VAL-LEU-LYS-GLN (PDQ) | #22 | Gly-Val-Leu-Ser-Asn-Val-Ile-Gly-Tyr-Leu-Lys-Lys-Leu-Gly-Thr-Gly-Ala-Leu-Asn-Ala-Val-Leu-Lys-Gln | 24 | | | 2458.7 | 10.6889 | 10.3 14.5 10.3 2.6 3.3 6.4 1.5 -3.4 -1.2 3.9 -3.8 2.3 10.4 10.4 10.8 4.1 | G 9031 |
| 769. | GRANULIBERIN R | #22 | Phe-Gly-Phe-Leu-Pro-Ile-Tyr-Arg-Arg-Pro-Ala-Ser-NH2 | 12 | | | 1441.1 | 12.4842 | 6.1 -2.8 -.6 -4.2 -8 | G 7897 |
| 770. | HEAT SHOCK PROTEIN, 65 kD, Mycobacterium bovis BCG, FRAGMENT 180-188 | #22 | Thr-Phe-Gly-Leu-Gln-Leu-Glu-Leu-Thr | 9 | | | 1019.8 | 3.08 | 5.4 | H 1899 |
| 771. | [Ser442,447]-HEAT SHOCK PROTEIN, 65 kD FRAGMENT 437-460 | #22 | Val-Leu-Gly-Gly-Gly-Ser-Ala-Leu-Leu-Arg-Ser-Ile-Pro-Ala-Leu-Asp-Ser-Leu-Thr-Pro-Ala-Asn-Glu-Asp | 24 | Human | | 2363.4 | 3.6665 | 15.4 11.2 2.1 7 5.8 8 12.6 10.8 2.7 2.7 6.5 5.7 3 4.6 -4.2 -11.5 | H 2148 |
| 772. | HEPATITIS B VIRUS PRE-REGION (120-145) | #22 | Met-Gln-Trp-Asn-Ser-Thr-Thr-Phe-His-Gln-Thr-Leu-Gln-Asp-Pro-Arg-Val-Arg-Gly-Leu-Tyr-Phe-Pro-Ala-Gly-Gly | 26 | | | 3008.3 | 9.7015 | -8.6 -14 -11.2 -6.5 -6.5 -5.7 -10.1 -9.4 -12.5 -9.3 -10.7 -6.2 -11.3 -5 -3.1 .3 4.4 -.2 | H 7395 |
| 773. | HIRUDIN FRAGMENTS ([Tyr(SO3H)63]-Fragment 54-65) | #22 | Gly-Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr[SO3H]-Leu-Gln | 12 | | | 1299.9 | | | H 6894 |
| 774. | HIRUDIN FRAGMENTS (Fragment 54-65 Non-Sulfated) | #22 | Gly-Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr-Leu-Gln | 12 | | | 1463 | 2.7054 | -12.2 -13.1 -5.8 -12.1 | H 6769 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 775. | HIRUDIN FRAGMENTS ([Tyr(SO3H)63]-Fragment 55-65) | #22 | Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr[SO3H]-Leu-Gln | 11 | | | 1242.9 | | | H 8894 |
| 776. | HIRUDIN FRAGMENTS (Fragment 55-65 Non-Sulfated) | #22 | Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr-Leu-Gln | 11 | | | 1406 | 2.7054 | -13.1 -5.8 -12.1 | H 7019 |
| 777. | N-Acetyl-HIRUDIN FRAGMENTS (Ac-[Tyr (SO3H)63]-Fragment 54-65) | #22 | Acetyl-Gly-Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr[SO3H]-Leu-Gln | 12 | | | 1242.9 | | | H 7144 |
| 778. | N-Acetyl-HIRUDIN FRAGMENTS (Ac-[Tyr (SO3H)63]-Fragment 55-65) | #22 | Acetyl-Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr[SO3H]-Leu-Gln | 11 | | | 1284.9 | | | H 9144 |
| 779. | N-Acetyl-HIRUDIN FRAGMENTS (Ac-Fragment 54-65 Non-Sulfated) | #22 | Acetyl-Gly-Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr-Leu-Gln | 12 | | | 1406 | | | H 7269 |
| 780. | N-Acetyl-HIRUDIN FRAGMENTS (Ac-Fragment 55-65 Non-Sulfated) | #22 | Acetyl-Asp-Phe-Glu-Glu-Ile-Pro-Glu-Glu-Tyr-Leu-Gln | 11 | | | 1448 | | | H 9019 |
| 781. | HIS-ASP-MET-ASN-LYS-VAL-LEU-ASP-LEU (Anti-Inflammatory Peptide 2) | #22 | His-Asp-Met-Asn-Lys-Val-Leu-Asp-Leu | 9 | | | 1082.7 | 5.1366 | -3.9 | H 3021 |
| 782. | HIS-LEU-GLY-LEU-ALA-ARG (Anaphylatoxin peptide C3a, human: 72-77) | #22 | His-Leu-Gly-Leu-Ala-Arg | 6 | | | 666.5 | 10.905 | | H 0765 |
| 783. | HIS-LYS-ALA-ARG-VAL-LEU-p-NITRO-PHE-GLU-ALA-NLE-SER AMIDE (HIV Protease Substrate) | #22 | His-Lys-Ala-Arg-Val-Leu-p-Nitro-Phe-Glu-Ala-Nle-Ser-NH2 | 11 | | | 1157.9 | | | H 5397 |
| 784. | HIS-PRO-PHE-HIS-LEU-D-LEU-VAL-TYR | #22 | His-Pro-Phe-His-Leu-D-Leu-Val-Tyr | 8 | | | 1024.8 | 7.806 | | H 5396 |
| 785. | D-HIS-PRO-PHE-HIS-LEU-y-[CH2NH]-LEU-VAL-TYR | #22 | D-His-Pro-Phe-His-Leu-y-[CH2NH]-Leu-Val-Tyr | 8 | | | 911.7 | | | H 6137 |
| 786. | HISTONE H2A FRAGMENT | #22 | Ala-Ile-Arg-Asn-Asp-Glu-Glu-Leu- | 35 | | | 3755.9 | 10.4264 | -8.4 -13.7 -18.3 -10 -6.9 -3.4 .4 | H 8647 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | 86-120 (MB-35) |  | Asn-Lys-Leu-Leu-Gly-Lys-Val-Thr-Ile-Ala-Gln-Gly-Gly-Val-Leu-Pro-Asn-Ile-Gln-Ala-Val-Leu-Leu-Pro-Lys-Lys-Thr |  |  |  |  | 8 | 3.2 3.9 9.2 9.6 5.4 1.2 5.8 13.5 7.7 8.4 4.9 -.4 4.9 9.5 13.7 13.3 7.9 6 9.1 0 |  |
| 787. | HIV ENVELOPE PROTEIN (gp41) FRAGMENT 579-601 | #22 | Arg-Ile-Leu-Ala-Val-Glu-Arg-Tyr-Leu-Lys-Asp-Gln-Gln-Leu-Leu-Gly-Ile-Trp-Gly-Cys-Ser-Gly-Lys | 23 |  |  | 2648 | 9.5087 | 4.3 8.8 .4 -10.4 -15.7 -16.1 -8.8 -4.7 1.1 -3.6 -.1 5.9 8.6 11.7 7.9 | H 4521 |
| 788. | HIV ENVELOPE PROTEIN (gp120) FRAGMENTS (Fragment 254-274) | #22 | Cys-Thr-His-Gly-Ile-Arg-Pro-Val-Val-Ser-Thr-Gln-Leu-Leu-Leu-Asn-Gly-Ser-Leu-Ala-Glu | 21 |  |  | 2207.7 | 7.187 | 5 1.7 1.7 1.4 5.6 4.9 13.2 14.8 6.7 1.7 6.3 8.8 8.8 | H 7769 |
| 789. | HIV ENVELOPE PROTEIN (gp120) FRAGMENTS (Fragment 307-330) | #22 | Asn-Asn-Thr-Arg-Lys-Ser-Ile-Arg-Ile-Gln-Arg-Gly-Pro-Gly-Arg-Ala-Phe-Val-Thr-Ile-Gly-Lys-Ile-Gly | 24 |  |  | 2645.2 | 12.9649 | -12.4 -12.4 -8.9 -13.1 -10.2 -6.7 -5.9 -13.1 -5.8 -6.1 -3.3 5.7 5.7 7.3 8.3 12.4 | H 7894 |
| 790. | HYDRA PEPTIDE | #22 | pGlu-Pro-Pro-Gly-Gly-Ser-Lys-Val-Ile-Leu-Phe | 11 |  |  | 1142.8 |  |  | H 4770 |
| 791. | HYDRA PEPTIDE FRAGMENT 7-11 | #22 | Lys-Val-Ile-Leu-Phe | 5 |  |  | 619.5 | 9.985 |  | H 6263 |
| 792. | IBERIOTOXIN | #22 | pGlu-Phe-Thr-Asp-Val-Asp-Cys-Ser-Val-Ser-Lys-Glu-Cys-Trp-Ser-Val-Cys-Lys-Asp-Leu-Phe-Gly-Val-Asp-Arg-Gly-Lys-Cys-Met-Gly-Lys-Lys-Cys-Arg-Cys-Tyr-Gln | 37 | Scorpion Buthus tamulus | [Disulfide Bridges: 7-28; 13-35; 17-33 | 4254 |  |  | I 2141 |
| 793. | ILE-PRO-ILE (Diprotin A) | #22 | Ile-Pro-Ile | 3 |  |  | 341.3 | 6 |  | I 9759 |
| 794. | INDOLICIDIN | #22 | Ile-Leu-Pro-Trp-Lys-Trp-Pro-Trp-Trp-Pro-Trp-Arg-Arg-NH2 | 13 |  |  | 1926 | 17 | -2.4 -8.5 -13.2 -11.6 -19.1 -15.8 | I 0144 |
| 795. | INHIBIN-LIKE PEPTIDE | #22 | His-Asn-Lys-Gln-Glu-Gly-Arg-Asp-His-Asp-Lys-Ser-Lys-Gly-His-Phe-His-Arg-Val-Val-Ile-His-His-Lys-Gly-Gly-Lys-Ala-His-Arg-Gly | 31 | Human |  | 3594.5 | 11.302 | -29.2 -29.5 -29.9 -26.8 -23.3 -24.1 -26.9 -19.6 -19.3 -19.6 -12.9 -4.8 .5 1.2 -1.6 1.6 -5.5 -2.7 1.8 -4.5 -11.9 -16.4 -18.1 | I 9638 |
| 796. | INHIBIN, a-Subunit, FRAGMENT 1-32 | #22 | Ser-Thr-Pro-Leu-Met-Ser-Trp-Pro Trp-Ser-Pro-Ser-Ala-Leu-Arg-Leu-Leu-Gln-Arg-Pro-Pro-Glu-Glu-Pro Ala-Ala-His-Ala-Asn-Cys-His-Arg | 32 | Human |  | 3636.9 | 8.7734 | -1.6 -1.6 -2.5 -1.7 -3.7 -1.8 -1 -.8 4.6 2 2.8 -1.7 -2.5 -7.8 -15.1 -12.2 -14.2 -16.2 -15.9 -9.6 -8 -7.4 -7.1 -3.6 | I 8516 |
| 797. | INHIBIN, a-Subunit, | #22 | Ser-Thr-Ala-Pro-Leu-Pro-Trp-Pro- | 32 | Porcine |  | 3598.9 | 7.319 | -2.5 -2.5 -3.4 -3.4 0 0 1.6 1.8 7. | I 8641 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | FRAGMENT 1-32 |  | Trp-Ser-Pro-Ala-Ala-Leu-Arg-Leu-Leu-Gln-Arg-Pro-Pro-Glu-Glu-Pro Ala-Val-His-Ala-Asp-Cys-His-Arg |  |  |  |  |  | 4.6 5.4 .9 -2.5 -7.8 -15.1 -12.2 -14.2 -13.8 -13.5 -7.2 -5.6 -5 -4.7 -1.2 |  |
| 798. | INSULIN (Chain A, Oxidized From Bovine Insulin) | #22 | Gly-Ile-Val-Glu-Gln-Cys[SO3H]-Cys[SO3H]-Ala-Ser-Val-Cys[SO3H]-Ser-Leu-Tyr-Gln-Leu-Glu-Asn-Tyr-Cys[SO3H]-Asn | 21 |  |  | 2657.1 |  |  | I 1633 |
| 799. | INSULIN (Chain B, Oxidized From Bovine Insulin) | #22 | Phe-Val-Asn-Gln-His-Leu-Cys[SO3H]-Gly-Ser-His-Leu-Val-Glu-Ala-Leu-Tyr-Leu-Val-Cys[SO3H]-Gly-Glu-Arg-Gly-Phe-Phe-Tyr-Thr-Pro-Lys-Ala | 30 |  |  | 3558.7 |  |  | I 6383 |
| 800. | INSULIN CHAIN B FRAGMENT 22-30 | #22 | Arg-Gly-Phe-Phe-Tyr-Thr-Pro-Lys-Ala | 9 |  |  | 1087.8 | 10.4813 | -5 | I 5508 |
| 801. | INSULIN-LIKE GROWTH FACTOR II FRAGMENT 33-40 | #22 | Ser-Arg-Val-Ser-Arg-Arg-Ser-Arg | 8 |  |  | 1006.9 | 12.9572 |  | I 3263 |
| 802. | INTERLEUKIN-1b FRAGMENT 163-171 | #22 | Val-Gln-Gly-Glu-Glu-Ser-Asn-Asp-Lys | 9 | Human |  | 1002.6 | 3.7271 | -14.5 | I 4638 |
| 803. | KALIOTOXIN | #22 | Gly-Val-Glu-Ile-Asn-Val-Lys-Cys-Ser-Gly-Ser-Pro-Gln-Cys-Leu-Lys-Pro-Cys-Lys-Asp-Ala-Gly-Met-Arg-Phe-Gly-Lys-Cys-Met-Asn-Arg-Lys-Cys-His-Cys-Thr-Pro | 37 |  | [Disulfide Bridges: 8-28; 14-33; 18-35 | 4031.1 | 8.9351 | 3.3 3.3 -1.7 .2 -7.8 -1.8 -2.2 1.7 -6.3 -3 -2.6 -5.7 -5.8 -2.7 -3.3 -11 -4.9 -3.7 -10.1 -3.7 1.7 -.1 -3.2 -14.1 -6.5 -12.5 -9.6 -6.4 -10.5 | K 3630 |
| 804. | KASSININ | #22 | Asp-Val-Pro-Lys-Ser-Asp-Gln-Phe-Val-Gly-Leu-Met-NH2 | 12 |  |  | 1349.8 | 7.01 | -5.6 -2.5 -2.9 .6 4.5 | K 0876 |
| 805. | KATACALCIN (Human calcitonin precursor peptide ; PDN-21) | #22 | Asp-Met-Ser-Ser-Asp-Leu-Glu-Arg-Asp-His-Arg-Pro-His-Val-Ser-Met-Pro-Gln-Asn-Ala-Asn | 21 |  |  | 2433.6 | 5.1593 | -14.4 -14.1 -16 -21.3 -23.7 -16 -20.6 -15.2 -12.3 -12.3 -13.6 -6.3 -4.7 | K 2627 |
| 806. | KENTSIN (Contraceptive tetrapeptide) | #22 | Thr-Pro-Arg-Lys | 4 |  |  | 502.5 | 11.6406 |  | K 0751 |
| 807. | LEUCOKININ I | #22 | Asp-Pro-Ala-Phe-Asn-Ser-Trp-Gly-NH2 | 8 |  |  | 907.5 | 6.9 |  | L 2896 |
| 808. | LEUCOKININ II | #22 | Asp-Pro-Gly-Phe-Ser-Ser-Trp- | 8 |  |  | 866.4 | 6.9 |  | L 3021 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Gly-NH2 | | | | | | | |
| 809. | LEUCOPYROKININ | #22 | pGlu-Thr-Ser-Phe-Thr-Pro-Arg-Leu-NH2 | 8 | | | 965.8 | | | L 6268 |
| 810. | LEUCOPYROKININ FRAGMENT 4-8 | #22 | Phe-Thr-Pro-Arg-Leu-NH2 | 5 | | | 649.6 | 17 | | L 5018 |
| 811. | LEU-LEU METHYL ESTER | #22 | Leu-Leu-OMe | 2 | | | 275.2 | | | L 7393 |
| 812. | LEU-MET-TYR-PRO-THR-TYR-LEU-LYS (VIP-Receptor binding inhibitor) | #22 | Leu-Met-Tyr-Pro-Thr-Tyr-Leu-Lys | 8 | | | 1028.8 | 9.6414 | | L 0146 |
| 813. | LEU-PRO-PRO-SER-ARG | #22 | Leu-Pro-Pro-Ser-Arg | 5 | | | 569.5 | 11.11 | | L 3146 |
| 814. | LEU-SER-p-Nitro-PHE-NLE-ALA-LEU METHYL ESTER | #22 | Leu-Ser-p-Nitro-Phe-Nle-Ala-Leu-OMe | 6 | | | 564.4 | | | L 8138 |
| 815. | LEVITIDE | #22 | pGlu-Gly-Met-Ile-Gly-Thr-Leu-Thr-Ser-Lys-Arg-Ile-Lys-Gln-NH2 | 14 | | | 1579.2 | | | L 5522 |
| 816. | LITORIN | #22 | pGlu-Gln-Trp-Ala-Val-Gly-His-Phe-Met-NH2 | 9 | | | 1118.8 | | | L 2258 |
| 817. | LOCUSTAPYROKININ | #22 | pGlu-Asp-Ser-Gly-Asp-Glu-Trp-Pro-Gln-Gln-Pro-Phe-Val-Pro-Arg Leu-NH2 | 16 | Locusta migratoria | | 1912.4 | | | L 1658 |
| 818. | [Gly6]-LOCUSTAPYROKININ | #22 | pGlu-Asp-Ser-Gly-Asp-Gly-Trp-Pro-Gln-Gln-Pro-Phe-Val-Pro-Arg Leu-NH2 | 16 | | | 1841.3 | | | L 7279 |
| 819. | LYS-ALA-ARG-VAL-NLE-p-Nitro-PHE-GLU-ALA-NLE AMIDE (HIV Protease Substrate) | #22 | Lys-Ala-Arg-Val-Nle-p-Nitro-Phe-Glu-Ala-Nle-NH2 | 9 | | | 804.7 | | | L 6525 |
| 820. | LYS-ARG-GLN-HIS-PRO-GLY (TRH precursor peptide fragment 1-6) | #22 | Lys-Arg-Gln-His-Pro-Gly | 6 | | | 723.6 | 11.642 | | L 4647 |
| 821. | LYS-ARG-GLN-HIS-PRO-GLY-LYS-ARG | #22 | Lys-Arg-Gln-His-Pro-Gly-Lys-Arg | 8 | | | 1009.9 | 12.5127 | | L 4772 |
| 822. | LYS-CYS-THR-CYS-CYS-ALA | #22 | Lys-Cys-Thr-Cys-Cys-Ala | 6 | | | 628.5 | 7.988 | | L 4512 |
| 823. | LYS-GLN-ALA-GLY-ASP-VAL | #22 | Lys-Gln-Ala-Gly-Asp-Val | 6 | | | 616.3 | 6.54 | | L 2776 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 824. | LYS-GLU-GLU-ALA-GLU ([Lys23]-Thymosin a1 Fragment 23-27) | #22 | Lys-Glu-Glu-Ala-Glu | 5 | | | 602.4 | 3.7822 | | L 3760 |
| 825. | LYS-LYS-ARG-ALA-ALA-ARG-ALA-THR-SER AMIDE (Myosin kinase inhibitor) | #22 | Lys-Lys-Arg-Ala-Ala-Arg-Ala-Thr-Ser-NH2 | 9 | | | 1007.7 | 17 | -12.9 -12.9 | L 2275 |
| 826. | LYS-PHE-HIS-GLU-LYS-HIS-HIS-SER-HIS-ARG-GLY-TYR (Histatin 8) | #22 | Lys-Phe-His-Glu-Lys-His-His-Ser-His-Arg-Gly-Tyr | 12 | | | 1564.1 | 10.2863 | -22.1 -18.2 -25.9 -24 | L 7404 |
| 827. | LYS-PRO-PRO-THR-PRO-PRO-PRO-GLU-PRO-GLU-THR | #22 | Lys-Pro-Pro-Thr-Pro-Pro-Pro-Glu-Pro-Glu-Thr | 11 | | | 1188.1 | 4.0788 | -17.7 -17.3 -16.4 | L 0765 |
| 828. | LYS-THR-LYS-CYS-LYS-PHE-LEU-LYS-LYS-CYS | #22 | Lys-Thr-Lys-Cys-Lys-Phe-Leu-Lys-Lys-Cys | 10 | | 4-10 | 1231 | 10.6299 | -11.1 -4.7 | L 8027 |
| 829. | LYS-TRP-LYS | #22 | Lys-Trp-Lys | 3 | | | 462.4 | 10.8099 | | L 5384 |
| 830. | LYS-TYR-LYS | #22 | Lys-Tyr-Lys | 3 | | | 439.3 | 10.2903 | | L 3271 |
| 831. | MAGAININ I | #22 | Gly-Ile-Gly-Lys-Phe-Leu-His-Ser-Ala-Gly-Lys-Phe-Gly-Lys-Ala-Phe-Val-Gly-Glu-Ile-Met-Lys-Ser | 23 | | | 2411.4 | 10.8259 | 4.2 4.2 -.3 -1 2.5 -.3 -6.2 -.2 4.8 2.6 -.5 7.9 7 3.5 6.6 | M 7152 |
| 832. | MAGAININ II | #22 | Gly-Ile-Gly-Lys-Phe-Leu-His-Ser-Ala-Lys-Lys-Phe-Gly-Lys-Ala-Phe-Val-Gly-Glu-Ile-Met-Asn-Ser | 23 | | | 2468.5 | 10.8259 | 4.2 4.6 -3.8 -4.5 -1 -3.8 -9.7 -3.7 1.3 -.9 -.5 7.9 7 3.5 7 | M 7402 |
| 833. | [Ala8,13,18]-MAGAININ II AMIDE | #22 | Gly-Ile-Gly-Lys-Phe-Leu-His-Ala-Ala-Lys-Lys-Phe-Ala-Lys-Ala-Phe-Val-Ala-Glu-Ile-Met-Asn-Ser-NH2 | 23 | | | 2496.5 | 11.2849 | 6.8 7.2 -1.2 -1.9 3.8 1 -4.9 1.1 3.5 3.5 3.9 12.3 11.4 5.7 9.2 7.4 | M 8155 |
| 834. | MAST CELL DEGRANULATING PEPTIDE (MCD Peptide) | #22 | Ile-Lys-Cys-Asn-Cys-Lys-Arg-His-Val-Ile-Lys-Pro-His-Ile-Cys-Arg-Lys-Ile-Cys-Gly-Lys-Asn-NH2 | 22 | | [Disulfide Bridges: 3-15; 5-19 | 2614.3 | 10.96888 | -5.3 -5.3 -1.4 -9.4 -9.1 -7.1 -.7 3.8 2.5 -1.1 -3.1 .4 2 1.3 -6.7 | M 8036 |
| 835. | MAST CELL DEGRANULATING PEPTIDE HR1 | #22 | Ile-Asn-Leu-Lys-Ala-Ile-Ala-Ala-Leu-Val-Lys-Lys-Val-Leu-NH2 | 14 | | | 1512.1 | 16 | 14.6 14.3 17.8 6.2 14.3 16.3 11.8 | M 8655 |
| 836. | MAST CELL | #22 | Phe-Leu-Pro-Leu-Ile-Leu-Gly-Lys- | 14 | | | 1541.2 | 16 | 16.6 18 14.2 11.5 11.5 10.8 7 | M 8780 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | DEGRANULATING PEPTIDE HR2 |  | Leu-Val-Lys-Gly-Leu-Leu-NH2 |  |  |  |  |  |  |  |
| 837. | MASTOPARAN | #22 | Val-Asp-Trp-Lys-Lys-Ile-Gly-Gln-His-Ile-Leu-Ser-Val-Leu-NH2 | 14 | Polistes jadwagae |  | 1652.2 | 10.8523 | -10.6 -10.3 -3 -2.9 5.2 12.9 8.4 | M 8528 |
| 838. | MASTOPARAN | #22 | Ile-Asn-Leu-Lys-Ala-Leu-Ala-Ala-Leu-Ala-Lys-Lys-Ile-Leu-NH2 | 14 | Vespula lewisii |  | 1498 | 16 | 13.9 11.2 14.7 3.1 11.5 13.5 9.7 | M 5280 |
| 839. | MELANIN CONCENTRATING HORMONE | #22 | Asp-Phe-Asp-Met-Leu-Arg-Cys-Met-Leu-Gly-Arg-Val-Tyr-Arg-Pro-Cys-Trp-Gln-Val | 19 | Rat | 7-16 | 2389 | 8.2962 | 5.2 8.3 2 8.7 5.5 -2.8 .1 .1 -2.7 -10 -5.4 | M 4542 |
| 840. | MET-ASN-TYR-LEU-ALA-PHE-PRO-ARG-MET AMIDE (Small cardioactive peptide B) | #22 | Met-Asn-Tyr-Leu-Ala-Phe-Pro-Arg-Met-NH2 | 9 |  |  | 1158.9 | 11.337 | 1.3 -4.1 | M 6779 |
| 841. | MET-GLN-MET-LYS-LYS-VAL-LEU-ASP-SER (Anti-Inflammatory Peptide 1) | #22 | Met-Gln-Met-Lys-Lys-Val-Leu-Asp-Ser | 9 |  |  | 1079.7 | 9.8574 | -3.8 | M 7782 |
| 842. | MYELIN BASIC PROTEIN FRAGMENT 4-14 | #22 | Gln-Lys-Arg-Pro-Ser-Gln-Arg-Ser-Lys-Tyr-Leu | 11 |  |  | 1394.1 | 11.666 | -23.1 -24.8 -17.1 | M 6913 |
| 843. | des-Gly77,des-His78-MYELIN BASIC PROTEIN FRAGMENT 68-84 | #22 | Tyr-Gly-Ser-Leu-Pro-Gln-Lys-Ala-Gln-Arg-Pro-Gln-Asp-Glu-Asn | 15 | Bovine |  | 1730.2 | 6.68 | -9.4 -8.1 -13.8 -16.5 -20.3 -25.7 -26.1 | M 3630 |
| 844. | MYELIN BASIC PROTEIN FRAGMENT 68-82 (des [Gly77,His78]-Ser75,80-Myelin Basic Protein Bovine Fragment 68-84) | #22 | Tyr-Gly-Ser-Leu-Pro-Gln-Lys-Ser-Gln-Arg-Ser-Gln-Asp-Glu-Asn | 15 | Guinea Pig |  | 1736.1 | 6.68 | -12 -10.7 -15.6 -18.3 -22.1 -27.5 -27.9 | M 5167 |
| 845. | C-TYPE NATRIURETIC PEPTIDE (CNP) | #22 | Gly-Leu-Ser-Lys-Gly-Cys-Phe-Gly-Leu-Lys-Leu-Asp-Arg-Ile-Gly-Ser-Met-Ser-Gly-Leu-Gly-Cys | 22 |  | 6-22 | 2200.3 | 9.1783 | 7 7.4 3.5 .4 4.7 5.1 2.2 -1.4 .9 -3.7 -.2 -.2 2.9 9.9 | N 8768 |
| 846. | C-TYPE NATRIURETIC PEPTIDE-53 | #22 | Asp-Leu-Arg-Val-Asp-Thr-Lys-Ser-Arg-Ala-Ala-Trp-Ala-Arg-Leu-Leu-Gln-Glu-His-Pro-Asn-Ala-Arg-Lys-Tyr-Lys-Gly-Ala-Asn-Lys-Lys-Gly-Leu-Ser-Lys-Gly-Cys-Phe-Gly-Leu-Lys-Leu-Asp-Arg-Ile-Gly- | 53 | Human | 37-53 | 5809 | 10.93659 | -12.4 -8.1 -10.1 -6.5 -8.9 -5.4 -5.4 2.3 -.4 .6 -4.4 -7.8 -6.9 -10.4 -5.9 -14.2 -23.2 -19.7 -20.5 -15.5 -17.4 -13.9 -24.1 -19.4 -11.7 -11.2 -7.3 -11.2 -10.5 -4.2 -.7 7 7.4 3.5 .4 4.7 5.1 2.2 -1.4 .9 -3.7 | N 1021 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Ser-Met-Ser-Gly-Leu-Gly-Cys | | | | | | -.2 -.2 2.9 9.9 | |
| 847. | a-NEUROKININ (Substanc K ; Neurokinin A ; Neuromedin L) | #22 | His-Lys-Thr-Asp-Ser-Phe-Val-Gly-Leu-Met-NH2 | 10 | | | 1149.7 | 10.06 | -1.7 3.4 7.3 | N 4267 |
| 848. | a-NEUROKININ FRAGMENT 4-10 | #22 | Asp-Ser-Phe-Val-Gly-Leu-Met-NH2 | 7 | | | 782.4 | 6.9 | | N 5141 |
| 849. | [Ala5,b-Ala8]-a-NEUROKININ FRAGMENT 4-10 | #22 | Asp-Ala-Phe-Val-b-Ala-Leu-Met-NH2 | 7 | | | 709.4 | | | N 6144 |
| 850. | [Tyr5,D-Trp6,8,9,Lys10]-a-NEUROKININ FRAGMENT 4-10 | #22 | Asp-Tyr-D-Trp-Val-D-Trp-D-Trp-Lys-NH2 | 7 | | | 1097.9 | 6.8 | | N 2272 |
| 851. | NEUROMEDIN B | #22 | Gly-Asn-Leu-Trp-Ala-Thr-Gly-His-Phe-Met-NH2 | 10 | Porcine | | 1148.8 | 14 | -.7 1.6 5.1 | N 3762 |
| 852. | NEUROMEDIN C (GRP [18-27]) | #22 | Gly-Asn-His-Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 10 | | | 1136.8 | 14 | -1.8 .5 4 | N 6388 |
| 853. | [Ser2]-NEUROMEDIN C | #22 | Gly-Ser-His-Trp-Ala-Val-Gly-His-Leu-Met-NH2 | 10 | | | 1109.7 | 14 | .9 3.2 4 | N 1773 |
| 854. | NEUROMEDIN K (b-Neurokinin) | #22 | Asp-Met-His-Asp-Phe-Phe-Val-Gly-Leu-Met-NH2 | 10 | | | 1224.7 | 5.1334 | 4.9 10.3 8.4 | N 4143 |
| 855. | NEUROMEDIN N | #22 | Lys-Ile-Pro-Tyr-Ile-Leu | 6 | Porcine | | 746.6 | 9.5868 | | N 6513 |
| 856. | NEUROMEDIN U-8 | #22 | Tyr-Phe-Leu-Phe-Arg-Pro-Arg-Asn-NH2 | 8 | | | 1130 | 12.4842 | | N 4263 |
| 857. | NEUROMEDIN U-25 | #22 | Phe-Lys-Val-Asp-Glu-Glu-Phe-Gln-Gly-Pro-Ile-Val-Ser-Gln-Asn-Arg-Arg-Tyr-Phe-Leu-Phe-Arg-Pro-Arg-Asn-NH2 | 25 | | | 3160.6 | 11.353 | -8.5 -12.9 -4.5 -4.5 -1.8 -1.8 1.7 -4.6 -5.6 -11 -6.6 -7.3 -8.7 -7.9 -10.5 -11.5 -11.5 -6 | N 8138 |
| 858. | NLE-ARG-PHE AMIDE | #22 | Nle-Arg-Phe-NH2 | 3 | | | 469.5 | | | N 3637 |
| 859. | OSTEOCALCIN FRAGMENTS (Fragment 7-19) | #22 | Gly-Ala-Pro-Val-Pro-Tyr-Pro-Asp-Pro-Leu-Glu-Pro-Arg | 13 | Human | | 1406.1 | 3.9908 | -5.6 -1.4 -6.7 -6.7 -10.9 | O 3632 |
| 860. | OSTEOCALCIN FRAGMENTS (Fragment 37-49) | #22 | Gly-Phe-Gln-Glu-Ala-Tyr-Arg-Arg-Phe-Tyr-Gly-Pro-Val | 13 | Human | | 1590.2 | 9.7005 | -10.3 -11.2 -14.4 -12.5 -4.8 | O 4507 |
| 861. | OSTEOCALCIN | #22 | Phe-Tyr-Gly-Pro-Val | 5 | Human | | 581.4 | 5.7 | | O 4382 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | FRAGMENTS (Fragment 45-49) |  |  |  |  |  |  |  |  |  |
| 862. | [Tyr38,Phe42,46]-OSTEOCALCIN FRAGMENT 38-49 | #22 | **Tyr**-Gln-Glu-Ala-Phe-Arg-Arg-**Phe**-Phe-Gly-Pro-Val | 12 | Human |  | 1517.2 | 9.6166 | -7.1 -6.2 -4.3 3.4 | O 4632 |
| 863. | PARDAXIN ([Gly31]-Pardaxin P1) | #22 | **Gly**-Phe-Phe-Ala-Leu-Ile-Pro-Lys-**Ile**-Ile-Ser-Ser-Pro-Leu-Phe-Lys-**Thr**-Leu-Leu-Ser-Ala-Val-Gly-Ser-**Ala**-Leu-Ser-Ser-Ser-Gly-Gly-Gln-**Glu** | 33 | Moses sole |  | 3322.9 | 10.0865 | 14.3 19.2 15.6 12 8.6 8.6 6.9 4.6 7.8 7.1 6.4 6.4 9 14.8 10.6 7 12.7 17.2 12.6 8 8 5.8 1.2 -1.9 -4.6 | P 0435 |
| 864. | PEPTIDE I OF T. wagleri VENOM | #22 | **Gly**-Gly-Lys-Pro-Asp-Leu-Arg-**Pro**-Cys-His-Pro-Pro-Cys-His-Tyr-**Ile**-Pro-Arg-Pro-Lys-Pro-Arg | 22 |  | 9-13 | 2525.2 | 10.3772 | -9.6 -12.4 -13.6 -11.3 -7.2 -6.9 -12 -3 -3 -5.5 -8.4 -6.8 -10.7 -13.2 | P 2312 |
| 865. | PEPTIDE II OF T. wagleri VENOM | #22 | **Gly**-Gly-Lys-Pro-Asp-Leu-Arg-**Pro**-Cys-Tyr-Pro-Pro-Cys-His-Tyr-**Ile**-Pro-Arg-Pro-Lys-Pro-Arg | 22 |  | 9-13 | 2551.2 | 10.11668 | -9.6 -10.5 -11.7 -9.4 -5.3 -5 -10.1 -1.1 -1.1 -3.6 -8.4 -6.8 -10.7 -13.2 | P 2437 |
| 866. | pGLU-ALA-GLU | #22 | **pGlu**-Ala-Glu | 3 |  |  | 345.2 |  |  | P 3037 |
| 867. | pGLU-ASN-GLY | #22 | **pGlu**-Asn-Gly | 3 |  |  | 317.2 |  |  | P 5148 |
| 868. | pGLU-ASP-PRO-PHE-LEU-ARG-PHE AMIDE | #22 | **pGlu**-Asp-Pro-Phe-Leu-Arg-Phe-**NH2** | 7 |  |  | 937.7 |  |  | P 3807 |
| 869. | pGLU-GLU-PRO AMIDE | #22 | **pGlu**-Glu-Pro-NH2 | 3 |  |  | 387.3 |  |  | P 2053 |
| 870. | pGLU-GLY-ARG-PHE AMIDE | #22 | **pGlu**-Gly-Arg-Phe-NH2 | 4 |  |  | 523.4 |  |  | P 9799 |
| 871. | pGLU-HIS-GLY | #22 | **pGlu**-His-Gly | 3 |  |  | 340.2 |  |  | P 4147 |
| 872. | pGLU-HIS-GLY AMIDE | #22 | **pGlu**-His-Gly-NH2 | 3 |  |  | 356.2 |  |  | P 4022 |
| 873. | pGLU-HIS-PRO (TRH free acid) | #22 | **pGlu**-His-Pro | 3 |  |  | 380.3 |  |  | P 3905 |
| 874. | pGLU-HIS-PRO AMIDE (TRH ; Thyrotropin releasing hormone) | #22 | **pGlu**-His-Pro-NH2 | 3 |  |  | 396.3 |  |  | P 1319 |
| 875. | pGLU-HIS-PRO-GLY (TRH-Gly) | #22 | **pGlu**-His-Pro-Gly | 4 |  |  | 437.3 |  |  | P 2687 |
| 876. | pGLU-3-METHYL-HIS-PRO AMIDE ([3-Methyl-His2]-Thyrotropin Releasing | #22 | **pGlu**-3-Methyl-His-Pro-NH2 | 3 |  |  | 410.3 |  |  | P 5173 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| | Hormone) | | | | | | | | | |
| 877. | pGLU-SER-LEU-ARG-TRP AMIDE | #22 | pGlu-Ser-Leu-Arg-Trp-NH2 | 5 | | | 705.6 | | | P 9924 |
| 878. | pGLU-VAL-ASN-PHE-SER-PRO-GLY-TRP-GLY-THR AMIDE | #22 | pGlu-Val-Asn-Phe-Ser-Pro-Gly-Trp-Gly-Thr-NH2 | 10 | | | 1107.8 | | | P 0175 |
| 879. | PHE-GLY-GLY-PHE | #22 | Phe-Gly-Gly-Phe | 4 | | | 426.2 | 5.7 | | P 3626 |
| 880. | PHE-GLY-PHE-GLY | #22 | Phe-Gly-Phe-Gly | 4 | | | 426.2 | 5.8 | | P 3751 |
| 881. | PHE-LEU-ARG-PHE AMIDE | #22 | Phe-Leu-Arg-Phe-NH2 | 4 | | | 598.5 | 17 | | P 5652 |
| 882. | PHE LEU-GLU-GLU-ILE (Rat prothrombin precursor sequence 5-9) | #22 | Phe-Leu-Glu-Glu-Ile | 5 | | | 647.5 | 3.024 | | P 9396 |
| 883. | PHE-LEU-GLU-GLU-LEU | #22 | Phe-Leu-Glu-Glu-Leu | 5 | | | 647.5 | 3.0287 | | P 5523 |
| 884. | PHE-LEU-GLU-GLU-VAL | #22 | Phe-Leu-Glu-Glu-Val | 5 | | | 633.5 | 3.0096 | | P 5398 |
| 885. | PHE-LYS-ALA-b-CYCLOHEXYL-ALA-b-CYCLOHEXYL-ALA-LEU-D-ALA-ARG (C5a Inhibitory Sequence) | #22 | Phe-Lys-Ala-b-Cyclohexyl-Ala-b-Cyclohexyl-Ala-Leu-D-Ala-Arg | 8 | | | 706.5 | | | P 9067 |
| 886. | PHE-MET-ARG-PHE AMID | #22 | Phe-Met-Arg-Phe-NH2 | 4 | | | 616.5 | 17 | | P 5325 |
| 887. | PHE-MET-ARG-D-PHE AMIDE | #22 | Phe-Met-Arg-D-Phe-NH2 | 4 | | | 616.5 | | | P 6785 |
| 888. | PHE-MET-D-ARG-PHE AMIDE | #22 | Phe-Met-D-Arg-Phe-NH2 | 4 | | | 616.5 | 14 | | P 6910 |
| 889. | PHE-D-MET-ARG-PHE AMIDE | #22 | Phe-D-Met-Arg-Phe-NH2 | 4 | | | 616.5 | 17 | | P 6660 |
| 890. | D-PHE-MET-ARG-PHE AMIDE | #22 | D-Phe-Met-Arg-Phe-NH2 | 4 | | | 616.5 | 17 | | P 6535 |
| 891. | PHEROMONOTROPIN | #22 | Lys-Leu-Ser-Tyr-Asp-Asp-Lys-Val-Phe-Glu-Asn-Val-Glu-Phe-Thr-Pro-Arg-Leu-NH2 | 18 | | | 2214.6 | 6.859 | -6.1 -5.7 -9.5 -8 -10.2 -3.9 -1.1 1.2 -3 -6.5 -6.5 | P 0701 |
| 892. | PHE-SER-TRP-GLY-ALA-GLU-GLY-GLN-ARG (Experimental allergic encephalogenic peptide) | #22 | Phe-Ser-Trp-Gly-Ala-Glu-Gly-Gln-Arg | 9 | | | 1036.7 | 6.62 | -4.9 | P 6272 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 893. | PHYSALAEMIN | #22 | pGlu-Ala-Asp-Pro-Asn-Lys-Phe-Tyr-Gly-Leu-Met-NH2 | 11 | | | 1298.8 | | | P 2149 |
| 894. | PLATELET MEMBRANE GLYCOPROTEIN IIB PEPTIDE FRAGMENT 296-306 | #22 | Thr-Asp-Val-Asn-Gly-Asp-Gly-Arg-His-Asp-Leu | 11 | | | 1195.7 | 4.2004 | -15.5 -18.3 -11 | P 9684 |
| 895. | PNEUMADIN | #22 | Ala-Gly-Glu-Pro-Lys-Leu-Asp-Ala-Gly-Val-NH2 | 10 | Human | | 970.5 | 7.05 | -5.9 -3.5 -3.1 | P 9317 |
| 896. | PNEUMADIN | #22 | Tyr-Gly-Glu-Pro-Lys-Leu-Asp-Ala-Gly-Val-NH2 | 10 | Rat | | 1062.6 | 6.68 | -9 -3.5 -3.1 | P 9192 |
| 897. | PRO-ASP-VAL-ASP-HIS-VAL-PHE-LEU-ARG-PHE AMIDE | #22 | Pro-Asp-Val-Asp-His-Val-Phe-Leu-Arg-Phe-NH2 | 10 | | | 1258.9 | 8.349 | 3.2 3.1 6.6 | P 2178 |
| 898. | N-proCALCITONIN 1-57 (N proCT) | #22 | Ala-Pro-Phe-Arg-Ser-Ala-Leu-Glu Ser-Ser-Pro-Ala-Asp-Pro-Ala-Thr-Leu-Ser-Glu-Asp-Glu-Ala-Arg-Leu-Leu-Leu-Ala-Ala-Leu-Val-Gln-Asp-Tyr-Val-Gln-Met-Lys-Ala-Ser-Glu-Leu-Glu-Gln-Glu-Gln-Glu Arg-Glu-Gly-Ser-Ser-Leu-Asp-Ser-Pro-Arg-Ser | 57 | Human | | 6210.9 | 3.8692 | -1 -3.6 -3.6 -4.6 -.1 -4.4 -4.4 -8.9 -1.6 -1.6 -4.3 -2.7 -11.5 -6.2 -4.6 -7.1 -2.6 -2.6 0 5.3 12.6 20.3 15 19.5 10.9 11.3 4 4.1 2.3 -3.6 -8.6 -8.6 -1.3 -3.5 -11.2 -11.2 -16.6 -16.2 -18 -25.2 -22.1 -26.7 -24 -16.7 -13.2 -14 -12.1 -7.6 -9.4 | P 8424 |
| 899. | PROCTOLIN | #22 | Arg-Tyr-Leu-Pro-Thr | 5 | | | 649.6 | 9.5584 | | P 4280 |
| 900. | PRO-HIS-PRO-PHE-HIS-PHE-PHE-VAL-TYR-LYS (Renin Inhibitor ; Pro-[Phe5,6]-Octapeptidyl Lysine) | #22 | Pro-His-Pro-Phe-His-Phe-Phe-Val-Tyr-Lys | 10 | | | 1319 | 10.1953 | 1.7 3.3 | P 2402 |
| 901. | PRO-LEU-GLY AMIDE | #22 | Pro-Leu-Gly-NH2 | 3 | | | 301.2 | 15 | | P 9887 |
| 902. | PRO-LYS-LYS-LYS-ARG-LYS-VAL-GLU-ASP-PRO-TYR-CYS | #22 | Pro-Lys-Lys-Lys-Arg-Lys-Val-Glu-Asp-Pro-Tyr-Cys | 12 | | | 1493.2 | 10.34267 | -21 -24.5 -21.9 -15.5 | P 6296 |
| 903. | PRO-PHE-GLY-LYS | #22 | Pro-Phe-Gly-Lys | 4 | | | 448.3 | 10.72 | | P 6691 |
| 904. | PROTEIN C,ACTIVATED,FRAGMENT 390-404 | #22 | Tyr-Gly-Val-Tyr-Thr-Lys-Val-Ser-Arg-Tyr-Leu-Asp-Trp-Ile-His | 15 | | | 1900.4 | 9.2815 | 0 -4.5 -.3 -4.5 -7.6 -2.4 -1.7 | P 5818 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 905. | PRO-THR-PRO-SER AMIDE | #22 | Pro-Thr-Pro-Ser-NH2 | 4 | | | 416.3 | 15 | | P 8179 |
| 906. | RANAKININ | #22 | Lys-Pro-Asn-Pro-Glu-Arg-Phe-Tyr-Gly-Leu-Met-NH2 | 11 | | | 1368.1 | 10.4958 | -17.5 -9.8 -6.3 -2.8 | R 4892 |
| 907. | RANATENSIN | #22 | pGlu-Val-Pro-Gln-Trp-Ala-Val-Gly His-Phe-Met-NH2 | 11 | | | 1315 | | | R 9002 |
| 908. | SARAFOTOXIN S6a1 | #22 | Cys-Ser-Cys-Lys-Asp-Met-Thr-Asp-Lys-Glu-Cys-Leu-Asn-Phe-Cys-His-Gln-Asp-Val-Ile-Trp | 21 | | [Disulfide Bridges: 1-15; 3-11 | 2515.8 | 4.4149 | -5.5 -15.4 -12.1 -10.8 -10.4 -4.1 -3.5 -6 -6 -2.1 2.1 4.1 -.6 | S 1522 |
| 909. | SARAFOTOXIN S6b | #22 | Cys-Ser-Cys-Lys-Asp-Met-Thr-Asp-Lys-Glu-Cys-Leu-Tyr-Phe-Cys-His-Gln-Asp-Val-Ile-Trp | 21 | | [Disulfide Bridges: 1-15; 3-11 | 2564.8 | 4.4149 | -5.5 -15.4 -12.1 -10.8 -8.2 -1.9 -1.3 -3.8 -3.8 .1 4.3 6.3 1.6 | S 4146 |
| 910. | SARAFOTOXIN S6c | #22 | Cys-Thr-Cys-Asn-Asp-Met-Thr-Asp-Glu-Glu-Cys-Leu-Asn-Phe-Cys-His-Gln-Asp-Val-Ile-Trp | 21 | | [Disulfide Bridges: 1-15; 3-11 | 2513.9 | 3.41 | -8.5 -14.5 -11.3 -10 -10 -3.7 -3.1 -5.6 -5.6 -2.1 2.1 4.1 -.6 | S 5023 |
| 911. | [Lys4]-SARAFOTOXIN S6c | #22 | Cys-Thr-Cys-Lys-Asp-Met-Thr-Asp-Glu-Glu-Cys-Leu-Asn-Phe-Cys-His-Gln-Asp-Val-Ile-Trp | 21 | | [Disulfide Bridges: 1-15; 3-11 | 2528.9 | 3.8029 | -8.9 -14.9 -11.7 -10.4 -10 -3.7 -3.1 -5.6 -5.6 -2.1 2.1 4.1 -.6 | S 1397 |
| 912. | SAR-ARG-GLY-ASP-SER-PRO | #22 | Sar-Arg-Gly-Asp-Ser-Pro | 6 | | | 619.4 | | | S 8649 |
| 913. | SAUVAGINE | #22 | pGlu-Gly-Pro-Pro-Ile-Ser-Ile-Asp-Leu-Ser-Leu-Glu-Leu-Leu-Arg-Lys-Met-Ile-Glu-Ile-Glu-Lys-Gln-Glu-Lys-Glu-Lys-Gln-Gln-Ala-Ala-Asn-Asn-Arg-Leu-Leu-Leu-Asp-Thr-Ile-NH2 | 40 | | | 4630.5 | | | S 3884 |
| 914. | SCYLLATOXIN (Leiurotoxin | #22 | Ala-Phe-Cys-Asn-Leu-Arg-Met- | 31 | | | 3447.6 | 8.6079 | 3.8 5.8 2.2 2.2 5.7 -3.4 4.9 2.6 | S 3277 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | l) |  | Cys-Gln-Leu-Ser-Cys-Arg-Ser-Leu-Gly-Leu-Leu-Gly-Lys-Cys-Ile-Gly-Asp-Lys-Cys-Glu-Cys-Val-Lys-His-NH2 |  |  |  |  |  | 3.9 11.2 7 7.8 3.9 12.9 13.3 9.5 6.4 1.2 -6.1 -3.2 4.9 2.4 -9.2 -12.3 |  |
| 915. | SER-ALA-LYS-LEU-CYS-PRO-GLY-GLY-ASN-CYS-VAL (Sperm Activating Peptide) | #22 | Ser-Ala-Lys-Leu-Cys-Pro-Gly-Gly-Asn-Cys-Val | 11 | Sea Urchin | 5-10 | 1048.7 | 8.2427 | 1 .8 3.2 | S 8665 |
| 916. | SER-GLN-ASN-PHE-y (CH2N)-PRO-ILE-VAL-GLN | #22 | Ser-Gln-Asn-Phe-y(CH2N)-Pro-Ile-Val-Gln | 8 |  |  | 834.6 |  |  | S 1398 |
| 917. | SER-GLN-ASP-TYR-PRO-ILE-VAL (HIV gag fragment 129-135) | #22 | Ser-Gln-Asp-Tyr-Pro-Ile-Val | 7 |  |  | 819.5 | 3.095 |  | S 5151 |
| 918. | SER-GLY-GLN-SER-TRP-ARG-PRO-GLN-GLY-ARG-PHE AMIDE | #22 | Ser-Gly-Gln-Ser-Trp-Arg-Pro-Gln-Gly-Arg-Phe-NH2 | 11 |  |  | 1323 | 17 | -16.4 -15.6 -16.9 -13.4 | S 8540 |
| 919. | SER-ILE-GLY-SER-LEU-ALA-LYS | #22 | Ser-Ile-Gly-Ser-Leu-Ala-Lys | 7 |  |  | 675.3 | 10 |  | S 3019 |
| 920. | SER-PHE-LEU-LEU-ARG-ASN-PRO-ASN-ASP-LYS-TYR-GLU-PRO-PHE (Thrombin Receptor Activator) | #22 | Ser-Phe-Leu-Leu-Arg-Asn-Pro-Asn-Asp-Lys-Tyr-Glu-Pro-Phe | 14 |  |  | 1739.3 | 6.72 | -3.5 -6.2 -14.2 -21.5 -26.9 -19.6 | S 7152 |
| 921. | SERUM THYMIC FACTOR (FTS) | #22 | pGlu-Ala-Lys-Ser-Gln-Gly-Gly-Ser-Asn | 9 |  |  | 876.4 |  |  | S 8256 |
| 922. | Lys-SERUM THYMIC FACTOR | #22 | Lys-Glu-Ala-Lys-Ser-Gln-Gly-Gly-Ser-Asn | 10 |  |  | 1005.5 | 9.8104 | -15.4 -11.5 | S 7019 |
| 923. | N-SUCCINYL-LYS-ASP-SER-SER-LEU-TYR-PRO-ALA-LEU-THR-PHE-ASP-LYS | #22 | N-Succinyl-Lys-Asp-Ser-Ser-Leu-Tyr-Pro-Ala-Leu-Thr-Phe-Asp-Lys | 13 |  |  | 1354.7 |  |  | S 4021 |
| 924. | THR-CYS-VAL-GLU-TRP-LEU-ARG-ARG-TYR-LEU-LYS-ASN (MHC antigen H-2Kb fragment 163-174) | #22 | Thr-Cys-Val-Glu-Trp-Leu-Arg-Arg-Tyr-Leu-Lys-Asn | 12 |  |  | 1582.5 | 9.6 | -4.9 -.4 -2.9 -11 | T 8033 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 925. | THR-PHE-GLN-ALA-TYR-PRO-LEU-ARG-GLU-ALA | #22 | Thr-Phe-Gln-Ala-Tyr-Pro-Leu-Arg-Glu-Ala | 10 | | | 1194.9 | 6.57 | -6.7 -4.2 | T 8786 |
| 926. | THR-SER-LYS (Antireproductive tripeptide) | #22 | Thr-Ser-Lys | 3 | | | 335.2 | 9.945 | | T 8765 |
| 927. | THR-TYR-SER | #22 | Thr-Tyr-Ser | 3 | | | 369.2 | 5.6 | | T 0148 |
| 928. | THR-VAL-LEU | #22 | Thr-Val-Leu | 3 | | | 331.3 | 5.7 | | T 3391 |
| 929. | THYMOSIN a1 | #22 | Acetyl-Ser-Asp-Ala-Ala-Val-Asp-Thr-Ser-Ser-Glu-Ile-Thr-Thr-Lys-Asp-Leu-Lys-Glu-Lys-Lys-Glu-Val-Val-Glu-Glu-Ala-Glu-Asn | 28 | Bovine | | 2972.9 | | | T 3410 |
| 930. | THYROCALCITONIN (Calcitonin) | #22 | Cys-Ala-Ser-Leu-Ser-Thr-Cys-Val-Leu-Gly-Lys-Leu-Ser-Gln-Glu-Leu-His-Lys-Leu-Gln-Thr-Tyr-Pro-Arg-Thr-Asp-Val-Gly-Ala-Gly-Thr-Pro-NH2 | 32 | Chicken | 1-7 | 3390.4 | 9.2654 | 16.3 13.4 11.6 12.3 7.7 5 2.2 3.5 -3.9 -7.7 -7.4 -7 -11.5 -12 -10.1 -6.6 -15.6 -16.3 -7.8 -12 -6.7 -6.4 -5.8 -5.8 -1.3 | T 9907 |
| 931. | THYROCALCITONIN (Calcitonin) | #22 | Cys-Ser-Asn-Leu-Ser-Thr-Cys-Val-Leu-Gly-Lys-Leu-Ser-Gln-Glu-Leu-His-Lys-Leu-Gln-Thr-Tyr-Pro-Arg-Thr-Asp-Val-Gly-Ala-Gly-Thr-Pro-NH2 | 32 | Eel | 1-7 | 3433.5 | 9.2654 | 11 8.1 5.4 12.3 7.7 5 2.2 3.5 -3.9 -7.7 -7.4 -7 -11.5 -12 -10.1 -6.6 -15.6 -16.3 -7.8 -12 -6.7 -6.4 -5.8 -5.8 -1.3 | T 1284 |
| 932. | THYROCALCITONIN (Calcitonin) | #22 | Cys-Gly-Asn-Leu-Ser-Thr-Cys-Met-Leu-Gly-Thr-Tyr-Thr-Gln-Asp Phe-Asn-Lys-Phe-His-Thr-Phe-Pro-Gln-Thr-Ala-Ile-Gly-Val-Gly-Ala-Pro-NH2 | 32 | Human | 1-7 | 3435.4 | 8.3156 | 9.1 6.2 5.9 8.1 3.6 .9 1.6 -1.6 -3.5 -10.8 -11.5 -14 -13.4 -9.9 -8 -8 -11.5 -6.2 2.2 -1 6.4 6.7 5.7 5.7 9.2 | T 3535 |
| 933. | THYROCALCITONIN (Calcitonin) | #22 | Cys-Ser-Asn-Leu-Ser-Thr-Cys-Val-Leu-Ser-Ala-Tyr-Trp-Arg-Asn-Leu-Asn-Asn-Phe-His-Arg-Phe-Ser-Gly-Met-Gly-Phe-Gly-Pro-Glu-Thr-Pro-NH2 | 32 | Porcine | 1-7 | 3622.7 | 9.3434 | 11 7.7 10.3 12.5 7.8 8.6 4.8 2.6 -1.6 -8.9 -8.8 -13.8 -12.5 -13.3 -9.6 -6.5 -8.4 -5.3 1 -2.2 -.6 .4 -3.1 -3.9 -3.5 | T 0158 |
| 934. | THYROCALCITONIN (Calcitonin) | #22 | Cys-Gly-Asn-Leu-Ser-Thr-Cys-Met-Leu-Gly-Thr-Tyr-Thr-Gln-Asp Leu-Asn-Lys-Phe-His-Thr-Phe-Pro-Gln-Thr-Ser-Ile-Gly-Val-Gly-Ala-Pro-NH2 | 32 | Rat | 1-7 | 3417.4 | 8.3156 | 9.1 6.2 5.9 8.1 3.6 .9 1.6 -.6 -2.5 -9.8 -10.5 -13 -12.4 -8.9 -7 -7 -11.5 -8.8 -.4 -3.6 3.8 4.1 3.1 3.1 6.6 | T 0283 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
| 935. | THYROCALCITONIN (Calcitonin) | #22 | Cys-Ser-Asn-Leu-Ser-Thr-Cys-Val-Leu-Gly-Lys-Leu-Ser-Gln-Glu-Leu-His-Lys-Leu-Gln-Thr-Tyr-Pro-Arg-Thr-Asn-Thr-Gly-Ser-Gly-Thr-Pro-NH2 | 32 | Salmon | 1-7 | 3451.6 | 10.121 | 11 8.1 5.4 12.3 7.7 5 2.2 3.5 -3.9 -7.7 -7.4 -7 -11.5 -12 -10.1 -6.6 -15.6 -16.3 -12.7 -16.9 -14.2 -13.9 -13.3 -13.3 -8.8 | T 3660 |
| 936. | TRANSFORMING GROWTH FACTOR-a (TGF-a) | #22 | Val-Val-Ser-His-Phe-Asn-Asp-Cys-Pro-Asp-Ser-His-Thr-Gln-Phe-Cys-Phe-His-Gly-Thr-Cys-Arg-Phe-Leu-Val-Gln-Glu-Asp-Lys-Pro-Ala-Cys-Val-Cys-His-Ser-Gly-Tyr-Val-Gly-Ala-Arg-Cys-Glu-His-Ala-Asp-Leu-Leu-Ala | 50 | Human | [Disulfide Bridges: 8-21; 16-32; 34-43 | 5546.8 | 5.8821 | 1.1 -3.1 -11.6 -14 -11.5 -17.8 -11.5 -5.5 -5.2 -6.8 -3.7 -3.6 2.1 2.8 4.6 5.6 7.3 1 .7 1.1 -1.7 -9.7 -3.4 -3.7 -3.3 -5 -4.7 -2 1.1 3.7 9.5 7.3 6.6 2.4 -2.1 -2.4 -4.8 -2.6 -1.3 -5.2 -1 -1 | T 5403 |
| 937. | TRANSFORMING GROWTH FACTOR-a (TGF-a) | #22 | Val-Val-Ser-His-Phe-Asn-Lys-Cys-Pro-Asp-Ser-His-Thr-Gln-Tyr-Cys-Phe-His-Gly-Thr-Cys-Arg-Phe-Leu-Val-Gln-Glu-Glu-Lys-Pro-Ala-Cys-Val-Cys-His-Ser-Gly-Tyr-Val-Gly-Val-Arg-Cys-Glu-His-Ala-Asp-Leu-Leu-Ala | 50 | Rat | [Disulfide Bridges: 8-21; 16-32; 34-43 | 5620.1 | 6.5917 | .7 -3.5 -12 -14.4 -11.9 -18.2 -16 -9.6 -9.3 -10.9 -7.8 -7.7 -2 -1.3 .5 5.6 7.3 1 .7 -2.4 -1.7 -9.7 -3.4 -3.7 -3.3 -5 -4.7 -2 1.1 3.7 9.5 7.3 9 4.8 .3 0 -2.4 -.2 1.1 -2.8 1.4 -1 | T 5278 |
| 938. | TRANSFORMING GROWTH FACTOR-a FRAGMENT 34-43 | #22 | Cys-His-Ser-Gly-Tyr-Val-Gly-Val-Arg-Cys | 10 | Rat | 34-43 | 1080.8 | 8.3183 | 4.8 .3 | T 8661 |
| 939. | N-Acetyl-TRANSFORMING GROWTH FACTOR-a FRAGMENT 34-43 ETHYLAMIDE | #22 | Acetyl-Cys-His-Ser-Gly-Tyr-Val-Gly-Ala-Arg-Cys-NHEt | 10 | Human | 34-43 | 991.6 | | | A 2553 |
| 940. | N-Acetyl-TRANSFORMING GROWTH FACTOR-a FRAGMENT 34-43 METHY ESTER | #22 | Acetyl-Cys-His-Ser-Gly-Tyr-Val-Gly-Ala-Arg-Cys-OMe | 10 | Human | 34-43 | 991.6 | | | A 2678 |
| 941. | TRP-ALA-GLY-GLY-ASP-ALA-SER-GLY-GLU (Sleep inducing peptide) | #22 | Trp-Ala-Gly-Gly-Asp-Ala-Ser-Gly-Glu | 9 | | | 846.3 | 2.8707 | -6.3 | T 1762 |
| 942. | TRP-GLY | #22 | Trp-Gly | 2 | | | 261.2 | 5.9 | | T 1754 |
| 943. | TRP-HIS-TRP-LEU-GLN- | #22 | Trp-His-Trp-Leu-Gln-Leu | 6 | | | 881.8 | 7.74 | | T 2903 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  | LEU (a1-Mating factor Fragment 1-6) |  |  |  |  |  |  |  |  |  |
| 944. | TRP-HIS-TRP-LEU-GLN-LEU-LYS-PRO-GLY-GLN-PRO-MET-TYR (a1-Mating Factor) | #22 | Trp-His-Trp-Leu-Gln-Leu-Lys-Pro-Gly-Gln-Pro-Met-Tyr | 13 |  |  | 1684.4 | 9.7077 | -6.8 -9.4 -7.8 -5 -10.1 | T 6901 |
| 945. | TRP-HIS-TRP-LEU-SER-PHE-SER-LYS-GLY-GLU-PRO-MET-TYR | #22 | Trp-His-Trp-Leu-Ser-Phe-Ser-Lys Gly-Glu-Pro-Met-Tyr | 13 |  |  | 1667.2 | 7.693 | -4.3 -6.9 -5.3 -2.5 -7.6 | T 0779 |
| 946. | TRP-NLE-ARG-PHE AMIDE | #22 | Trp-Nle-Arg-Phe-NH2 | 4 |  |  | 655.7 |  |  | T 9897 |
| 947. | TUFTSIN | #22 | Thr-Lys-Pro-Arg | 4 |  |  | 502.5 | 11.6406 |  | T 5897 |
| 948. | p-Aminophenylacetyl-TUFTSIN | #22 | p-Aminophenylacetyl-Thr-Lys-Pro-Arg | 4 |  |  | 401.4 |  |  | T 6153 |
| 949. | TUFTSIN FRAGMENT 1-3 | #22 | Thr-Lys-Pro | 3 |  |  | 345.3 | 9.945 |  | T 4157 |
| 950. | TUMOR NECROSIS FACTER-a (Fragment 10-36) | #22 | Asp-Lys-Pro-Val-Ala-His-Val-Val-Ala-Asn-Pro-Gln-Ala-Glu-Gly-Gln-Leu-Gln-Trp-Leu-Asn-Arg-Arg-Ala-Asn-Ala-Leu | 27 | Human |  | 2996.3 | 10.3293 | 4 3.6 6.3 4.4 2 -3.3 -.5 -8.2 -8.6 -13.9 -11.3 -5.9 -2.4 -7.7 -8.7 -11 -7.5 -13 -5.7 | T 1042 |
| 951. | TUMOR NECROSIS FACTER-a (Fragment 31-45) | #22 | Arg-Arg-Ala-Asn-Ala-Leu-Leu-Ala-Asn-Gly-Val-Glu-Leu-Arg-Asp | 15 | Human |  | 1668.3 | 10.492 | -4 1.1 9.8 4.5 11.8 10 1.7 | T 1167 |
| 952. | TUMOR NECROSIS FACTER-a (Fragment 46-65) | #22 | Asn-Gln-Leu-Val-Val-Pro-Ser-Glu-Gly-Leu-Tyr-Leu-Ile-Tyr-Ser-Gln-Val-Leu-Phe-Lys | 20 | Human |  | 2309.7 | 6.43 | -1.1 6.2 8.4 8.4 8.7 3.2 4 1.3 9 13.2 12.2 13.5 | T 1292 |
| 953. | TYR-ALA-GLY-ALA-VAL-VAL-ASN-ASP-LEU | #22 | Tyr-Ala-Gly-Ala-Val-Val-Asn-Asp-Leu | 9 |  |  | 919.5 | 3.115 | 7.1 | T 5028 |
| 954. | TYR-GLY-ALA-VAL-VAL-ASN-ASP-LEU | #22 | Tyr-Gly-Ala-Val-Val-Asn-Asp-Leu | 8 |  |  | 848.5 | 3.115 |  | T 5153 |
| 955. | TYR-ILE-GLY-SER-ARG (Laminin Fragment 929-933) | #22 | Tyr-Ile-Gly-Ser-Arg | 5 |  |  | 595.4 | 9.6183 |  | T 7154 |
| 956. | TYR-PHE-MET-ARG-PHE AMIDE | #22 | Tyr-Phe-Met-Arg-Phe-NH2 | 5 |  |  | 779.6 | 11.327 |  | T 3274 |
| 957. | UROTENSIN I | #22 | Asn-Asp-Asp-Pro-Pro-Ile-Ser-Ile-Asp-Leu-Thr-Phe-His-Leu-Leu-Arg-Asn-Met-Ile-Glu-Met-Ala-Arg- | 41 | Teleost Fish |  | 4880.7 | 4.5346 | -9 -1.7 1.1 7.4 5.8 11.2 10.5 11.3 -1.2 4.2 4.9 2.1 1.2 6.2 2.4 -1.4 -.4 3.1 -5.8 -10.3 -14.8 -20.2 | U 7253 |

| No. | Peptide Name | Category | Sequemce | Total Residue | Source | Disulfid Bridge | MW | pI | Hydropathic index | Product Code |
|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  | Ile-Glu-Asn-Glu-Arg-Glu-Gln-Ala-Gly-Leu-Asn-Arg-Lys-Tyr-Leu-Asp-Glu-Val-NH2 |  |  |  |  |  | -20.2 -16.1 -16.8 -16.8 -13.3 -18.8 -15 -7.7 -4.2 -13 -8.4 -15.7 |  |
| 958. | UROTENSIN II | #22 | Ala-Gly-Thr-Ala-Asp-Cys-Phe-Trp-Lys-Tyr-Cys-Val | 12 |  | 6-11 | 1362.9 | 5.966 | 3.4 -3.6 -.7 4.2 | U 4753 |
| 959. | VAL-ALA-ALA-PHE | #22 | Val-Ala-Ala-Phe | 4 |  |  | 406.2 | 6 |  | V 8251 |
| 960. | VAL-ALA-ILE-THR-VAL-LEU-VAL-LYS (Calcium-Like Peptide) | #22 | Val-Ala-Ile-Thr-Val-Leu-Val-Lys | 8 |  |  | 842.7 | 10.265 |  | V 2757 |
| 961. | VAL-GLU-GLU-ALA-GLU (Thymosin a1 Fragment 23-27) | #22 | Val-Glu-Glu-Ala-Glu | 5 |  |  | 572.4 | 2.8204 |  | V 3004 |
| 962. | VAL-GLU-PRO-ILE-PRO-TYR | #22 | Val-Glu-Pro-Ile-Pro-Tyr | 6 |  |  | 715.6 | 3.135 |  | V 2256 |
| 963. | VAL-GLY-GLY-TYR-GLY-TYR-GLY-ALA-LYS | #22 | Val-Gly-Gly-Tyr-Gly-Tyr-Gly-Ala-Lys | 9 |  |  | 871.4 | 9.6414 | 1.8 | V 0757 |
| 964. | VAL-HIS-LEU-THR-PRO | #22 | Val-His-Leu-Thr-Pro | 5 |  |  | 565.5 | 7.89 |  | V 3505 |
| 965. | VAL-HIS-LEU-THR-PRO-VAL-GLU-LYS | #22 | Val-His-Leu-Thr-Pro-Val-Glu-Lys | 8 |  |  | 921.8 | 7.874 |  | V 5130 |
| 966. | VAL-PRO-ASP-PRO-ARG | #22 | Val-Pro-Asp-Pro-Arg | 5 |  |  | 582.5 | 6.81 |  | V 0256 |
| 967. | VAL-PRO-LEU (Diprotin B) | #22 | Val-Pro-Leu | 3 |  |  | 327.3 | 6 |  | V 3255 |
| 968. | VAL-THR-CYS-GLY | #22 | Val-Thr-Cys-Gly | 4 |  |  | 378.3 | 5.32 |  | V 2632 |
| 969. | VAL-THR-LYS-GLY | #22 | Val-Thr-Lys-Gly | 4 |  |  | 404.3 | 10.265 |  | V 9006 |
| 970. | XENOPSIN | #22 | pGlu-Gly-Lys-Arg-Pro-Trp-Ile-Leu | 8 |  |  | 998.9 |  |  | X 6375 |
| 971. | XENOPSIN-25 | #22 | Met-Leu-Thr-Lys-Phe-Glu-Thr-Lys-Ser-Ala-Arg-Val-Lys-Gly-Leu-Ser-Phe-His-Pro-Lys-Arg-Pro-Trp-Ile-Leu | 25 | Human |  | 2975.4 | 11.8095 |  | X 2127 |

Category

#1 Adrenocorticotropic Hormone and Fragments
#2 Angiotensin and related peptides
#3 Atrial Natriuretic Peptides
#4 Bradykinin and Related Peptides

#5 Chemotactic Peptides
#6 Dynorphin and Related Peptides
#7 Endorphins and β-Lipotropin Fragments
#8 Enkephalin and Related Peptides
#9 Enzyme Inhibitors
#10 Fibronectin Fragments and Related Peptides
#11 Gastrointestinal Peptides
#12 Growth Hormone Releasing Peptides
#13 Luteinizing Hormone Releasing Hormone and Related Peptides
#14 Melanocyte Stimulating Hormone and Related Peptides
#15 Neurotensin and Related Peptides
#16 Opioid Peptides
#17 Oxytocin, Vasopressin,Vasotocin and Related Peptides
#18 Parathyroid Hormone and Fragments
#19 Protein Kinase Related Peptides
#20 Somatostatin and Related Peptides
#21 Substance P and Related Peptides
#22 Miscellaneous Peptides

# APPENDIX B

## FILEMAKER PRO SCRIPTS FOR CALCULATING PEPTIDE PROPERTIES

### Script for Calculating Molecular Weight

```
Case(ThreeLetterCode = "Ala",71.0,
ThreeLetterCode = "D-Ala",71.0 ,
ThreeLetterCode = "Ala-NH2",71.0+NH2MW ,
ThreeLetterCode = "Arg",157.2 ,
ThreeLetterCode = "D-Arg",157.2 ,
ThreeLetterCode = "Arg-NH2",157.2+NH2MW ,
ThreeLetterCode = "Asn",114.1 ,
ThreeLetterCode = "D-Asn",114.1 ,
ThreeLetterCode = "Asn-NH2",114.1+NH2MW ,
ThreeLetterCode = "Asp",114.0 ,
ThreeLetterCode = "D-Asp",114.0 ,
ThreeLetterCode = "Asp-NH2",114.0+NH2MW ,
ThreeLetterCode = "Cys",103.1 ,
ThreeLetterCode = "D-Cys",103.1 ,
ThreeLetterCode = "Cys-NH2",103.1+NH2MW ,
ThreeLetterCode = "Glu",128.1 ,
ThreeLetterCode = "D-Glu",128.1 ,
ThreeLetterCode = "Glu-NH2",128.1+NH2MW ,
ThreeLetterCode = "Gln",128.1 ,
ThreeLetterCode = "D-Gln",128.1 ,
ThreeLetterCode = "Gln-NH2",128.1+NH2MW ,
ThreeLetterCode = "Gly",57.0 ,
ThreeLetterCode = "D-Gly",57.0 ,
ThreeLetterCode = "Gly-NH2",57.0+NH2MW ,
ThreeLetterCode = "His",137.1 ,
ThreeLetterCode = "D-His",137.1 ,
```

```
ThreeLetterCode = "His-NH2",137.1+NH2MW ,
ThreeLetterCode = "Ile",113.1 ,
ThreeLetterCode = "D-Ile",113.1 ,
ThreeLetterCode = "Ile-NH2",113.1+NH2MW ,
ThreeLetterCode = "Leu",113.1 ,
ThreeLetterCode = "D-Leu",113.1 ,
ThreeLetterCode = "Leu-NH2",113.1+NH2MW ,
ThreeLetterCode = "Lys",129.1 ,
ThreeLetterCode = "D-Lys",129.1 ,
ThreeLetterCode = "Lys-NH2",129.1+NH2MW ,
ThreeLetterCode = "Met",131.1 ,
ThreeLetterCode = "D-Met",131.1 ,
ThreeLetterCode = "Met-NH2",131.1+NH2MW ,
ThreeLetterCode = "Phe",147.1 ,
ThreeLetterCode = "D-Phe",147.1 ,
ThreeLetterCode = "Phe-NH2",147.1+NH2MW ,
ThreeLetterCode = "Pro",97.1 ,
ThreeLetterCode = "D-Pro",97.1 ,
ThreeLetterCode = "Pro-NH2",97.1+NH2MW ,
ThreeLetterCode = "Ser",87.0 ,
ThreeLetterCode = "D-Ser",87.0 ,
ThreeLetterCode = "Ser-NH2",87.0+NH2MW ,
ThreeLetterCode = "Thr",101.1 ,
ThreeLetterCode = "D-Thr",101.1 ,
ThreeLetterCode = "Thr-NH2",101.1+NH2MW ,
ThreeLetterCode = "Trp",186.2 ,
ThreeLetterCode = "D-Trp",186.2 ,
ThreeLetterCode = "Trp-NH2",186.2+NH2MW ,
ThreeLetterCode = "Tyr",163.1 ,
ThreeLetterCode = "D-Tyr",163.1 ,
ThreeLetterCode = "Tyr-NH2",163.1+NH2MW ,
ThreeLetterCode = "Val",99.1 ,
ThreeLetterCode = "D-Val",99.1 ,
ThreeLetterCode = "Val-NH2",99.1+NH2MW ,
ThreeLetterCode = "Hyp",113.1 ,
ThreeLetterCode = "1-Adamantaneacetyl-D-Tyr[O-ETHYL]",367.1 ,
```

```
ThreeLetterCode = "3-Mercapto-3-Methylbutyryl-Tyr",280.2 ,
ThreeLetterCode = "3-Mercapto-3-Methylbutyryl-Tyr[O-Methyl]",294.2 ,
ThreeLetterCode = "3-Mercaptopropionyl-D-3-[Pyridyl]-Ala",237.1 ,
ThreeLetterCode = "3-Mercaptopropionyl-Phe",236.2 ,
ThreeLetterCode = "3-Mercaptopropionyl-Tyr",252.2 ,
ThreeLetterCode = "3-Methyl-His",151.1 ,
ThreeLetterCode = "7-Aminoheptanoyl-Phe~",274.1 ,
ThreeLetterCode = "3,5-Dibromo-Tyr",320.9 ,
ThreeLetterCode = "3,5-Diiodo-Tyr",414.9 ,
ThreeLetterCode = "[1-Mercaptocyclohexyl]acetyl-Tyr[O-Ethyl]",348.2 ,
ThreeLetterCode = "[1-Mercaptocyclohexyl]acetyl-Tyr[O-Methyl]",334.2 ,
ThreeLetterCode = "Abu",85.0 ,
ThreeLetterCode = "Acetyl-Arg",199.2 ,
ThreeLetterCode = "Acetyl-Asp",156.0 ,
ThreeLetterCode = "Acetyl-Cys",145.1 ,
ThreeLetterCode = "Acetyl-D-Trp",228.2 ,
ThreeLetterCode = "Asp(Benzyl)",190.0 ,
ThreeLetterCode = "Asp[O-tBu]2",226.0 ,
ThreeLetterCode = "[3-Pyridyl]-D-Ala",148.0 ,
ThreeLetterCode = "Cys[Cys]",204.2 ,
ThreeLetterCode = "Cys[S-Acetamidomethyl]",174.1 ,
ThreeLetterCode = "Cys[SO3H]",183.2 ,
ThreeLetterCode = "D-Ala-NH2",87 ,
ThreeLetterCode = "D-allo-Ile",113.1 ,
ThreeLetterCode = "D-Asp~",114.0 ,
ThreeLetterCode = "D-Glu~",128.1 ,
ThreeLetterCode = "D-Isoglutamine",128.1 ,
ThreeLetterCode = "D-Leu-NH2",129.1 ,
ThreeLetterCode = "D-Met-NH2",147.1 ,
ThreeLetterCode = "D-p-Chloro-Phe",181.6 ,
ThreeLetterCode = "D-p-Fluoro-Phe",165.1 ,
ThreeLetterCode = "D-Phe-NH2",163.1 ,
ThreeLetterCode = "D-Phe-NHMe",177.1 ,
ThreeLetterCode = "D-Trp~",186.2 ,
ThreeLetterCode = "Deamino-Phe",133.1 ,
ThreeLetterCode = "Formyl-Ala",99.0 ,
```

```
ThreeLetterCode = "Formyl-Met",159.1 ,
ThreeLetterCode = "Gly~",57.0 ,
ThreeLetterCode = "His~",137.1 ,
ThreeLetterCode = "Leu~",113.1 ,
ThreeLetterCode = "Leu-OMe",144.1 ,
ThreeLetterCode = "Met-NH2",147.1 ,
ThreeLetterCode = "Met-OMe",162.1 ,
ThreeLetterCode = "N-Acetyl-Cys",146.1 ,
ThreeLetterCode = "N-Acetyl-Ser",130.0 ,
ThreeLetterCode = "p-Amino-Phe",162.1 ,
ThreeLetterCode = "p-Chloro-Phe",181.6 ,
ThreeLetterCode = "p-Iodo-Phe",273.0 ,
ThreeLetterCode = "Phe~",147.1 ,
ThreeLetterCode = "Phe-NH2",163.1 ,
ThreeLetterCode = "Ser~",87.0 ,
ThreeLetterCode = "Pro",97.1 ,
ThreeLetterCode = "Tyr",163.1 ,
ThreeLetterCode = "Val-NH2",115.1,
ThreeLetterCode = "pGlu",128.1 ,
ThreeLetterCode = "Nle",131.2 ,
ThreeLetterCode = "Sar",89.1)

Sum(CUPeptideDatabaseChild::ResidueWeight)
```

## Script for Calculating Net Charge

### Define pK1

```
Case(ThreeLetterCode = "Ala",2.35,
ThreeLetterCode = "D-Ala",2.35 ,
ThreeLetterCode = "Ala-NH2",2.35 ,
ThreeLetterCode = "Arg",1.82 ,
ThreeLetterCode = "D-Arg",1.82 ,
ThreeLetterCode = "Arg-NH2",1.82 ,
ThreeLetterCode = "Asn",2.1 ,
ThreeLetterCode = "D-Asn",2.1 ,
```

```
ThreeLetterCode = "Asn-NH2",2.1 ,
ThreeLetterCode = "Asp",1.99 ,
ThreeLetterCode = "D-Asp",1.99 ,
ThreeLetterCode = "Asp-NH2",1.99 ,
ThreeLetterCode = "Cys",1.92 ,
ThreeLetterCode = "D-Cys",1.92 ,
ThreeLetterCode = "Cys-NH2",1.92 ,
ThreeLetterCode = "Glu",2.10 ,
ThreeLetterCode = "D-Glu",2.10 ,
ThreeLetterCode = "Glu-NH2",2.10 ,
ThreeLetterCode = "Gln",2.17 ,
ThreeLetterCode = "D-Gln",2.17 ,
ThreeLetterCode = "Gln-NH2",2.17 ,
ThreeLetterCode = "Gly",2.35 ,
ThreeLetterCode = "D-Gly",2.35 ,
ThreeLetterCode = "Gly-NH2",2.35 ,
ThreeLetterCode = "His",1.80 ,
ThreeLetterCode = "D-His",1.80 ,
ThreeLetterCode = "His-NH2",1.80 ,
ThreeLetterCode = "Ile",2.32 ,
ThreeLetterCode = "D-Ile",2.32 ,
ThreeLetterCode = "Ile-NH2",2.32 ,
ThreeLetterCode = "Leu",2.33 ,
ThreeLetterCode = "D-Leu",2.33 ,
ThreeLetterCode = "Leu-NH2",2.33 ,
ThreeLetterCode = "Lys",2.16 ,
ThreeLetterCode = "D-Lys",2.16 ,
ThreeLetterCode = "Lys-NH2",2.16 ,
ThreeLetterCode = "Met",2.13 ,
ThreeLetterCode = "D-Met",2.13 ,
ThreeLetterCode = "Met-NH2",2.13 ,
ThreeLetterCode = "Phe",2.16 ,
ThreeLetterCode = "D-Phe",2.16 ,
ThreeLetterCode = "Phe-NH2",2.16 ,
ThreeLetterCode = "Pro",2.95 ,
ThreeLetterCode = "D-Pro",2.95 ,
```

```
ThreeLetterCode = "Pro-NH2",2.95 ,
ThreeLetterCode = "Ser",2.19 ,
ThreeLetterCode = "D-Ser",2.19 ,
ThreeLetterCode = "Ser-NH2",2.19 ,
ThreeLetterCode = "Thr",2.09 ,
ThreeLetterCode = "D-Thr",2.09 ,
ThreeLetterCode = "Thr-NH2",2.09 ,
ThreeLetterCode = "Trp",2.43 ,
ThreeLetterCode = "D-Trp",2.43 ,
ThreeLetterCode = "Trp-NH2",2.43 ,
ThreeLetterCode = "Tyr",2.20 ,
ThreeLetterCode = "D-Tyr",2.20 ,
ThreeLetterCode = "Tyr-NH2",2.20 ,
ThreeLetterCode = "Val",2.29 ,
ThreeLetterCode = "D-Val",2.29 ,
ThreeLetterCode = "Val-NH2",2.29)
```

Define pK2

```
Case(ThreeLetterCode = "Ala",9.87,
ThreeLetterCode = "D-Ala",9.87 ,
ThreeLetterCode = "Ala-NH2",9.87 ,
ThreeLetterCode = "Arg",8.99 ,
ThreeLetterCode = "D-Arg",8.99 ,
ThreeLetterCode = "Arg-NH2",8.99 ,
ThreeLetterCode = "Asn",8.84 ,
ThreeLetterCode = "D-Asn",8.84 ,
ThreeLetterCode = "Asn-NH2",8.84 ,
ThreeLetterCode = "Asp",9.90 ,
ThreeLetterCode = "D-Asp",9.90 ,
ThreeLetterCode = "Asp-NH2",9.90 ,
ThreeLetterCode = "Cys",10.78 ,
ThreeLetterCode = "D-Cys",10.78 ,
ThreeLetterCode = "Cys-NH2",10.78 ,
ThreeLetterCode = "Glu",9.47 ,
ThreeLetterCode = "D-Glu",9.47 ,
```

```
ThreeLetterCode = "Glu-NH2",9.47 ,
ThreeLetterCode = "Gln",9.13 ,
ThreeLetterCode = "D-Gln",9.13 ,
ThreeLetterCode = "Gln-NH2",9.13 ,
ThreeLetterCode = "Gly",9.78 ,
ThreeLetterCode = "D-Gly",9.78 ,
ThreeLetterCode = "Gly-NH2",9.78 ,
ThreeLetterCode = "His",9.33 ,
ThreeLetterCode = "D-His",9.33 ,
ThreeLetterCode = "His-NH2",9.33 ,
ThreeLetterCode = "Ile",9.76 ,
ThreeLetterCode = "D-Ile",9.76 ,
ThreeLetterCode = "Ile-NH2",9.76 ,
ThreeLetterCode = "Leu",9.74 ,
ThreeLetterCode = "D-Leu",9.74 ,
ThreeLetterCode = "Leu-NH2",9.74 ,
ThreeLetterCode = "Lys",9.18 ,
ThreeLetterCode = "D-Lys",9.18 ,
ThreeLetterCode = "Lys-NH2",9.18 ,
ThreeLetterCode = "Met",9.28 ,
ThreeLetterCode = "D-Met",9.28 ,
ThreeLetterCode = "Met-NH2",9.28 ,
ThreeLetterCode = "Phe",9.18 ,
ThreeLetterCode = "D-Phe",9.18 ,
ThreeLetterCode = "Phe-NH2",9.18 ,
ThreeLetterCode = "Pro",10.65 ,
ThreeLetterCode = "D-Pro",10.65 ,
ThreeLetterCode = "Pro-NH2",10.65 ,
ThreeLetterCode = "Ser",9.21 ,
ThreeLetterCode = "D-Ser",9.21 ,
ThreeLetterCode = "Ser-NH2",9.21 ,
ThreeLetterCode = "Thr",9.10 ,
ThreeLetterCode = "D-Thr",9.10 ,
ThreeLetterCode = "Thr-NH2",9.10 ,
ThreeLetterCode = "Trp",9.44 ,
ThreeLetterCode = "D-Trp",9.44 ,
```

```
ThreeLetterCode = "Trp-NH2",9.44 ,
ThreeLetterCode = "Tyr",9.11 ,
ThreeLetterCode = "D-Tyr",9.11 ,
ThreeLetterCode = "Tyr-NH2",9.11 ,
ThreeLetterCode = "Val",9.74 ,
ThreeLetterCode = "D-Val",9.74 ,
ThreeLetterCode = "Val-NH2",9.74)
```

<u>Define pKR</u>

```
Case(ThreeLetterCode = "Arg",12.48 ,
ThreeLetterCode = "D-Arg",12.48 ,
ThreeLetterCode = "Arg-NH2",12.48 ,
ThreeLetterCode = "Asp",3.90 ,
ThreeLetterCode = "D-Asp",3.90 ,
ThreeLetterCode = "Asp-NH2",3.90 ,
ThreeLetterCode = "Cys",8.33 ,
ThreeLetterCode = "D-Cys",8.33 ,
ThreeLetterCode = "Cys-NH2",8.33 ,
ThreeLetterCode = "Glu",4.07 ,
ThreeLetterCode = "D-Glu",4.07 ,
ThreeLetterCode = "Glu-NH2",4.07 ,
ThreeLetterCode = "His",6.04 ,
ThreeLetterCode = "D-His",6.04 ,
ThreeLetterCode = "His-NH2",6.04 ,
ThreeLetterCode = "Lys",10.79 ,
ThreeLetterCode = "D-Lys",10.79 ,
ThreeLetterCode = "Lys-NH2",10.79 ,
ThreeLetterCode = "Tyr",10.13 ,
ThreeLetterCode = "D-Tyr",10.13 ,
ThreeLetterCode = "Tyr-NH2",10.13)
```

Define Residue pI

```
If(IsEmpty(pK1), "", If(ThreeLetterCode = "Asp", (pK1 + pKR) / 2, If(ThreeLetterCode = "Glu",
            (pK1 + pKR) / 2, If(ThreeLetterCode = "Cys", (pK1 + pKR) / 2, If(ThreeLetterCode
            = "Arg", (pKR + pK2) / 2, If(ThreeLetterCode = "His", (pKR + pK2) / 2, If
            (ThreeLetterCode = "Lys", (pKR + pK2) / 2, (pK1 + pK2) / 2)))))))
```

Define Side Chain Acid Charge

```
If(ThreeLetterCode = "Asp", 0, If(ThreeLetterCode = "Glu", 0, If(ThreeLetterCode = "Arg", 1, If
            (ThreeLetterCode = "His", 1, If(ThreeLetterCode = "Lys", 1,If(ThreeLetterCode = "
            Tyr", 0, If(ThreeLetterCode = "Cys", 0, "")))))))
```

Define Side Chain Salt Charge

```
If(ThreeLetterCode = "Asp", -1, If(ThreeLetterCode = "Glu", -1, If(ThreeLetterCode = "Arg", 0,
            If(ThreeLetterCode = "His", 0, If(ThreeLetterCode = "Lys", 0,If(ThreeLetterCode =
            "Tyr", -1, If(ThreeLetterCode = "Cys", -1, "")))))))
```

Define Residue Net Charge

```
If(IsEmpty(pK1), "", 10 ^ (pKR - AtpH) / (10 ^ (pKR - AtpH) + 1) * AcidCharge + 1 / (10 ^ (pKR -
            AtpH) + 1) * SaltCharge)
```

Define Total Net Charge

```
Sum(CUPeptideDatabaseChild::ResidueNetCharge)
```

## Script for Calculating Hydropathic Index

```
If(TotalResidue > 8,(Case(Middle(Sequence2, 1, 3) = "Ile", 4.5,
Middle(Sequence2, 1, 3) = "Val", 4.2,
Middle(Sequence2, 1, 3) = "Leu", 3.8,
Middle(Sequence2, 1, 3) = "Phe", 2.8,
Middle(Sequence2, 1, 3) = "Cys", 2.5,
```

```
Middle(Sequence2, 1, 3) = "Met", 1.9,
Middle(Sequence2, 1, 3) = "Ala", 1.8,
Middle(Sequence2, 1, 3) = "Gly", -0.4,
Middle(Sequence2, 1, 3) = "Thr", -0.7,
Middle(Sequence2, 1, 3) = "Ser", -0.8,
Middle(Sequence2, 1, 3) = "Trp", -0.9,
Middle(Sequence2, 1, 3) = "Tyr", -1.3,
Middle(Sequence2, 1, 3) = "Pro", -1.6,
Middle(Sequence2, 1, 3) = "His", -3.2,
Middle(Sequence2, 1, 3) = "Glu", -3.5,
Middle(Sequence2, 1, 3) = "Gln", -3.5,
Middle(Sequence2, 1, 3) = "Asp", -3.5,
Middle(Sequence2, 1, 3) = "Asn", -3.5,
Middle(Sequence2, 1, 3) = "Lys", -3.9,
Middle(Sequence2, 1, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 5, 3) = "Ile", 4.5,
Middle(Sequence2, 5, 3) = "Val", 4.2,
Middle(Sequence2, 5, 3) = "Leu", 3.8,
Middle(Sequence2, 5, 3) = "Phe", 2.8,
Middle(Sequence2, 5, 3) = "Cys", 2.5,
Middle(Sequence2, 5, 3) = "Met", 1.9,
Middle(Sequence2, 5, 3) = "Ala", 1.8,
Middle(Sequence2, 5, 3) = "Gly", -0.4,
Middle(Sequence2, 5, 3) = "Thr", -0.7,
Middle(Sequence2, 5, 3) = "Ser", -0.8,
Middle(Sequence2, 5, 3) = "Trp", -0.9,
Middle(Sequence2, 5, 3) = "Tyr", -1.3,
Middle(Sequence2, 5, 3) = "Pro", -1.6,
Middle(Sequence2, 5, 3) = "His", -3.2,
Middle(Sequence2, 5, 3) = "Glu", -3.5,
Middle(Sequence2, 5, 3) = "Gln", -3.5,
Middle(Sequence2, 5, 3) = "Asp", -3.5,
Middle(Sequence2, 5, 3) = "Asn", -3.5,
Middle(Sequence2, 5, 3) = "Lys", -3.9,
Middle(Sequence2, 5, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 9, 3) = "Ile", 4.5,
```

```
Middle(Sequence2, 9, 3) = "Val", 4.2,
Middle(Sequence2, 9, 3) = "Leu", 3.8,
Middle(Sequence2, 9, 3) = "Phe", 2.8,
Middle(Sequence2, 9, 3) = "Cys", 2.5,
Middle(Sequence2, 9, 3) = "Met", 1.9,
Middle(Sequence2, 9, 3) = "Ala", 1.8,
Middle(Sequence2, 9, 3) = "Gly", -0.4,
Middle(Sequence2, 9, 3) = "Thr", -0.7,
Middle(Sequence2, 9, 3) = "Ser", -0.8,
Middle(Sequence2, 9, 3) = "Trp", -0.9,
Middle(Sequence2, 9, 3) = "Tyr", -1.3,
Middle(Sequence2, 9, 3) = "Pro", -1.6,
Middle(Sequence2, 9, 3) = "His", -3.2,
Middle(Sequence2, 9, 3) = "Glu", -3.5,
Middle(Sequence2, 9, 3) = "Gln", -3.5,
Middle(Sequence2, 9, 3) = "Asp", -3.5,
Middle(Sequence2, 9, 3) = "Asn", -3.5,
Middle(Sequence2, 9, 3) = "Lys", -3.9,
Middle(Sequence2, 9, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 13, 3) = "Ile", 4.5,
Middle(Sequence2, 13, 3) = "Val", 4.2,
Middle(Sequence2, 13, 3) = "Leu", 3.8,
Middle(Sequence2, 13, 3) = "Phe", 2.8,
Middle(Sequence2, 13, 3) = "Cys", 2.5,
Middle(Sequence2, 13, 3) = "Met", 1.9,
Middle(Sequence2, 13, 3) = "Ala", 1.8,
Middle(Sequence2, 13, 3) = "Gly", -0.4,
Middle(Sequence2, 13, 3) = "Thr", -0.7,
Middle(Sequence2, 13, 3) = "Ser", -0.8,
Middle(Sequence2, 13, 3) = "Trp", -0.9,
Middle(Sequence2, 13, 3) = "Tyr", -1.3,
Middle(Sequence2, 13, 3) = "Pro", -1.6,
Middle(Sequence2, 13, 3) = "His", -3.2,
Middle(Sequence2, 13, 3) = "Glu", -3.5,
Middle(Sequence2, 13, 3) = "Gln", -3.5,
Middle(Sequence2, 13, 3) = "Asp", -3.5,
```

```
Middle(Sequence2, 13, 3) = "Asn", -3.5,
Middle(Sequence2, 13, 3) = "Lys", -3.9,
Middle(Sequence2, 13, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 17, 3) = "Ile", 4.5,
Middle(Sequence2, 17, 3) = "Val", 4.2,
Middle(Sequence2, 17, 3) = "Leu", 3.8,
Middle(Sequence2, 17, 3) = "Phe", 2.8,
Middle(Sequence2, 17, 3) = "Cys", 2.5,
Middle(Sequence2, 17, 3) = "Met", 1.9,
Middle(Sequence2, 17, 3) = "Ala", 1.8,
Middle(Sequence2, 17, 3) = "Gly", -0.4,
Middle(Sequence2, 17, 3) = "Thr", -0.7,
Middle(Sequence2, 17, 3) = "Ser", -0.8,
Middle(Sequence2, 17, 3) = "Trp", -0.9,
Middle(Sequence2, 17, 3) = "Tyr", -1.3,
Middle(Sequence2, 17, 3) = "Pro", -1.6,
Middle(Sequence2, 17, 3) = "His", -3.2,
Middle(Sequence2, 17, 3) = "Glu", -3.5,
Middle(Sequence2, 17, 3) = "Gln", -3.5,
Middle(Sequence2, 17, 3) = "Asp", -3.5,
Middle(Sequence2, 17, 3) = "Asn", -3.5,
Middle(Sequence2, 17, 3) = "Lys", -3.9,
Middle(Sequence2, 17, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 21, 3) = "Ile", 4.5,
Middle(Sequence2, 21, 3) = "Val", 4.2,
Middle(Sequence2, 21, 3) = "Leu", 3.8,
Middle(Sequence2, 21, 3) = "Phe", 2.8,
Middle(Sequence2, 21, 3) = "Cys", 2.5,
Middle(Sequence2, 21, 3) = "Met", 1.9,
Middle(Sequence2, 21, 3) = "Ala", 1.8,
Middle(Sequence2, 21, 3) = "Gly", -0.4,
Middle(Sequence2, 21, 3) = "Thr", -0.7,
Middle(Sequence2, 21, 3) = "Ser", -0.8,
Middle(Sequence2, 21, 3) = "Trp", -0.9,
Middle(Sequence2, 21, 3) = "Tyr", -1.3,
Middle(Sequence2, 21, 3) = "Pro", -1.6,
```

```
Middle(Sequence2, 21, 3) = "His", -3.2,
Middle(Sequence2, 21, 3) = "Glu", -3.5,
Middle(Sequence2, 21, 3) = "Gln", -3.5,
Middle(Sequence2, 21, 3) = "Asp", -3.5,
Middle(Sequence2, 21, 3) = "Asn", -3.5,
Middle(Sequence2, 21, 3) = "Lys", -3.9,
Middle(Sequence2, 21, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 25, 3) = "Ile", 4.5,
Middle(Sequence2, 25, 3) = "Val", 4.2,
Middle(Sequence2, 25, 3) = "Leu", 3.8,
Middle(Sequence2, 25, 3) = "Phe", 2.8,
Middle(Sequence2, 25, 3) = "Cys", 2.5,
Middle(Sequence2, 25, 3) = "Met", 1.9,
Middle(Sequence2, 25, 3) = "Ala", 1.8,
Middle(Sequence2, 25, 3) = "Gly", -0.4,
Middle(Sequence2, 25, 3) = "Thr", -0.7,
Middle(Sequence2, 25, 3) = "Ser", -0.8,
Middle(Sequence2, 25, 3) = "Trp", -0.9,
Middle(Sequence2, 25, 3) = "Tyr", -1.3,
Middle(Sequence2, 25, 3) = "Pro", -1.6,
Middle(Sequence2, 25, 3) = "His", -3.2,
Middle(Sequence2, 25, 3) = "Glu", -3.5,
Middle(Sequence2, 25, 3) = "Gln", -3.5,
Middle(Sequence2, 25, 3) = "Asp", -3.5,
Middle(Sequence2, 25, 3) = "Asn", -3.5,
Middle(Sequence2, 25, 3) = "Lys", -3.9,
Middle(Sequence2, 25, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 29, 3) = "Ile", 4.5,
Middle(Sequence2, 29, 3) = "Val", 4.2,
Middle(Sequence2, 29, 3) = "Leu", 3.8,
Middle(Sequence2, 29, 3) = "Phe", 2.8,
Middle(Sequence2, 29, 3) = "Cys", 2.5,
Middle(Sequence2, 29, 3) = "Met", 1.9,
Middle(Sequence2, 29, 3) = "Ala", 1.8,
Middle(Sequence2, 29, 3) = "Gly", -0.4,
Middle(Sequence2, 29, 3) = "Thr", -0.7,
```

```
Middle(Sequence2, 29, 3) = "Ser", -0.8,
Middle(Sequence2, 29, 3) = "Trp", -0.9,
Middle(Sequence2, 29, 3) = "Tyr", -1.3,
Middle(Sequence2, 29, 3) = "Pro", -1.6,
Middle(Sequence2, 29, 3) = "His", -3.2,
Middle(Sequence2, 29, 3) = "Glu", -3.5,
Middle(Sequence2, 29, 3) = "Gln", -3.5,
Middle(Sequence2, 29, 3) = "Asp", -3.5,
Middle(Sequence2, 29, 3) = "Asn", -3.5,
Middle(Sequence2, 29, 3) = "Lys", -3.9,
Middle(Sequence2, 29, 3) = "Arg", -4.5)
+Case(Middle(Sequence2, 33, 3) = "Ile", 4.5,
Middle(Sequence2, 33, 3) = "Val", 4.2,
Middle(Sequence2, 33, 3) = "Leu", 3.8,
Middle(Sequence2, 33, 3) = "Phe", 2.8,
Middle(Sequence2, 33, 3) = "Cys", 2.5,
Middle(Sequence2, 33, 3) = "Met", 1.9,
Middle(Sequence2, 33, 3) = "Ala", 1.8,
Middle(Sequence2, 33, 3) = "Gly", -0.4,
Middle(Sequence2, 33, 3) = "Thr", -0.7,
Middle(Sequence2, 33, 3) = "Ser", -0.8,
Middle(Sequence2, 33, 3) = "Trp", -0.9,
Middle(Sequence2, 33, 3) = "Tyr", -1.3,
Middle(Sequence2, 33, 3) = "Pro", -1.6,
Middle(Sequence2, 33, 3) = "His", -3.2,
Middle(Sequence2, 33, 3) = "Glu", -3.5,
Middle(Sequence2, 33, 3) = "Gln", -3.5,
Middle(Sequence2, 1, 3) = "Asp", -3.5,
Middle(Sequence2, 1, 3) = "Asn", -3.5,
Middle(Sequence2, 1, 3) = "Lys", -3.9,
Middle(Sequence2, 1, 3) = "Arg", -4.5)),"")
```

# APPENDIX C

# WEB PAGE SCRIPT

**Table C-1** **Introductory Page script**

| Script | Comments |
|---|---|
| <HTML> | Signify the begining line of HyperText Markup Language (HTML). A command, called *HTML tag*, that tells interpreter how document should be, is presented in angle bracket <> and is all capital. |
| <HEAD><TITLE>CU Peptide Database Home Page</TITLE> | Define heading of web page and define title of the document. When users access web page, they can only see texts between HTML tags, the tags are hidden. |
| </HEAD> | End of heading tag |
| <BODY BACKGROUND="file:///Macintosh%20 HD/Desktop%20Folder/KlaewklaNew/graphics/CUPDBbg.jpg" BGCOLOR="#000000"> | Define body of the document and also specify backgroung graphic and color. |
| <CENTER> | Start aligning text or graphic in the center of document |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20 | <IMG> tag specify which |

| Script | Comments |
|---|---|
| Folder/KlaewklaNew/graphics/cpdlogo.jpg"><BR> | graphic will be presented and <BR> tag terminate the line. |
| </CENTER> | end of <CENTER> tag. |
| <FONT SIZE=+3 COLOR=#000000><B><CENTER>Welcome! </CENTER></B></FONT> | Authors can specify size of text by using <FONT> tag. |
| <HR width=100> | |
| <BLOCKQUOTE><FONT SIZE=+5 COLOR=#00AAAA><B>C</B></FONT><FONT SIZE=+1 COLOR=#000000><B>U Peptide Database</B> is designed to help you search the property information of peptide of your interest. Those properties are, for example, Molecular weight, Net charge at any pH, Isoelectric point (pI), and Hydrophobicity. A 1000 of peptides in my database are ready for your search. Only enter in my <A HREF="http://10.0.2.15/CUPdbHtmlDocs/SearchForm.html"> search form</A>, you will receive the information about it.</FONT></BLOCKQUOTE><BR> | |
| <CENTER><IMG SRC="file:///C\|/BEE/THESIS/graphics/divide11.gif'<BR></CENTER><br><PRE> | |
| <B><U><FONT SIZE=+1>Links to other biochemical database</FONT></U></B> | |
| <A HREF="http://expasy.hcuge.ch/sprot/sprot-top.html">SWISS-PROT</A><br><A HREF="http://pdb.pdb.bnl.gov/">The Protein Data Bank (PDB)</A><br><A HREF="http://www.ncbi.nlm.nih.gov/">GenBank</A><br><A HREF="http://www.embl-heidelberg.de/">EMBL Nucleotide Sequence Data Library</A><br></PRE> | Anchor tag (<A>) specify link to other web page |
| <CENTER> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/divide11.gif'<BR> | |
| </CENTER> | |
| <I>Klaewkla Kaewthai<BR> | |

| Script | Comments |
|---|---|

```
Department of Biochemistry<BR>
Faculty of science<BR>
Chulalongkorn University<BR>
tel. 2185429<BR>
E. Mail : klaewkla@loxinfo.co.th</I>
<CENTER>
<IMG SRC="file:///Macintosh%20HD/Desktop%20
Folder/KlaewklaNew/graphics/divide11.gif"><BR>
</CENTER>
</BODY>
</HTML>
```

**<u>Table C-2</u> Search Form Page script**

| Script | Comments |
|---|---|
| <HTML> | |
| <HEAD><TITLE>CU Peptide Database Home Page</TITLE> | |
| <SCRIPT LANGUAGE="JavaScript"> | This line is the opening of JavaScript tag inserted into HTML document. In this research, JavaScript is used to make an interactive event for users in filling the form. For example, users can fill the operator into the field with out typing into it. |
| <!-- | This line hides the script from browsers which has no interpreter for JavaScript |
| var operator0 = ""<br>var operator1 = "="<br>var operator2 = "<"<br>var operator3 = "<="<br>var operator4 = ">"<br>var operator5 = ">="<br>var operator6 = "..."<br>var operator7 = "@"<br>var operator8 = "*"<br>var fieldToInsertOperator = "" | This line declare variable of fuction |
| function clearField1() {<br>document.SearchForm.PeptideName.value ="" | This is the starting line of function |

| Script | Comments |
|---|---|
| } | This is the ending line of function |

```
function clearField2() {
  document.SearchForm.Sequence.value =""
}
function clearField3() {
  document.SearchForm.Source.value =""
}
function clearField4() {
  document.SearchForm.TotalResidue.value =""
}
function clearField5() {
  document.SearchForm.MW.value =""
}
function clearField6() {
  document.SearchForm.IsoElectricPoint.value =""
}
function clickField1() {
  fieldToInsertOperator = "PeptideName"
}
function clickField2() {
  fieldToInsertOperator = "Sequence"
}
function clickField3() {
  fieldToInsertOperator = "Source"
}
```

| Script | Comments |
|---|---|

```
function clickField4() {
  fieldToInsertOperator = "TotalResidue"
}
function clickField5() {
  fieldToInsertOperator = "MW"
}
function clickField6() {
  fieldToInsertOperator = "IsoElectricPoint"
}
function insertOperator() {
  if(fieldToInsertOperator=="PeptideName") {
    if(document.SearchForm.select1.options[0].selected == true)
      document.SearchForm.PeptideName.value += operator0
    if(document.SearchForm.select1.options[1].selected == true)
      document.SearchForm.PeptideName.value += operator1
    if(document.SearchForm.select1.options[2].selected == true)
      document.SearchForm.PeptideName.value += operator2
    if(document.SearchForm.select1.options[3].selected == true)
      document.SearchForm.PeptideName.value += operator3
    if(document.SearchForm.select1.options[4].selected == true)
      document.SearchForm.PeptideName.value += operator4
    if(document.SearchForm.select1.options[5].selected == true)
      document.SearchForm.PeptideName.value += operator5
    if(document.SearchForm.select1.options[6].selected == true)
      document.SearchForm.PeptideName.value += operator6
    if(document.SearchForm.select1.options[7].selected == true)
```

| Script | Comments |
|---|---|

```
        document.SearchForm.PeptideName.value += operator7
    if(document.SearchForm.select1.options[8].selected == true)
        document.SearchForm.PeptideName.value += operator8
}
else if(fieldToInsertOperator=="Sequence") {
    if(document.SearchForm.select1.options[0].selected == true)
        document.SearchForm.Sequence.value += operator0
    if(document.SearchForm.select1.options[1].selected == true)
        document.SearchForm.Sequence.value += operator1
    if(document.SearchForm.select1.options[2].selected == true)
        document.SearchForm.Sequence.value += operator2
    if(document.SearchForm.select1.options[3].selected == true)
        document.SearchForm.Sequence.value += operator3
    if(document.SearchForm.select1.options[4].selected == true)
        document.SearchForm.Sequence.value += operator4
    if(document.SearchForm.select1.options[5].selected == true)
        document.SearchForm.Sequence.value += operator5
    if(document.SearchForm.select1.options[6].selected == true)
        document.SearchForm.Sequence.value += operator6
    if(document.SearchForm.select1.options[7].selected == true)
        document.SearchForm.Sequence.value += operator7
    if(document.SearchForm.select1.options[8].selected == true)
        document.SearchForm.Sequence.value += operator8
}
else if(fieldToInsertOperator=="Source") {
    if(document.SearchForm.select1.options[0].selected == true)
```

| Script | Comments |
|---|---|

```
    document.SearchForm.Source.value += operator0
  if(document.SearchForm.select1.options[1].selected == true)
    document.SearchForm.Source.value += operator1
  if(document.SearchForm.select1.options[2].selected == true)
    document.SearchForm.Source.value += operator2
  if(document.SearchForm.select1.options[3].selected == true)
    document.SearchForm.Source.value += operator3
  if(document.SearchForm.select1.options[4].selected == true)
    document.SearchForm.Source.value += operator4
  if(document.SearchForm.select1.options[5].selected == true)
    document.SearchForm.Source.value += operator5
  if(document.SearchForm.select1.options[6].selected == true)
    document.SearchForm.Source.value += operator6
  if(document.SearchForm.select1.options[7].selected == true)
    document.SearchForm.Source.value += operator7
  if(document.SearchForm.select1.options[8].selected == true)
    document.SearchForm.Source.value += operator8
}
else if(fieldToInsertOperator=="TotalResidue") {
  if(document.SearchForm.select1.options[0].selected == true)
    document.SearchForm.TotalResidue.value += operator0
  if(document.SearchForm.select1.options[1].selected == true)
    document.SearchForm.TotalResidue.value += operator1
  if(document.SearchForm.select1.options[2].selected == true)
    document.SearchForm.TotalResidue.value += operator2
  if(document.SearchForm.select1.options[3].selected == true)
```

| Script | Comments |
|---|---|

```
    document.SearchForm.TotalResidue.value += operator3
  if(document.SearchForm.select1.options[4].selected == true)
    document.SearchForm.TotalResidue.value += operator4
  if(document.SearchForm.select1.options[5].selected == true)
    document.SearchForm.TotalResidue.value += operator5
  if(document.SearchForm.select1.options[6].selected == true)
    document.SearchForm.TotalResidue.value += operator6
  if(document.SearchForm.select1.options[7].selected == true)
    document.SearchForm.TotalResidue.value += operator7
  if(document.SearchForm.select1.options[8].selected == true)
    document.SearchForm.TotalResidue.value += operator8
}
else if(fieldToInsertOperator=="MW") {
  if(document.SearchForm.select1.options[0].selected == true)
    document.SearchForm.MW.value += operator0
  if(document.SearchForm.select1.options[1].selected == true)
    document.SearchForm.MW.value += operator1
  if(document.SearchForm.select1.options[2].selected == true)
    document.SearchForm.MW.value += operator2
  if(document.SearchForm.select1.options[3].selected == true)
    document.SearchForm.MW.value += operator3
  if(document.SearchForm.select1.options[4].selected == true)
    document.SearchForm.MW.value += operator4
  if(document.SearchForm.select1.options[5].selected == true)
    document.SearchForm.MW.value += operator5
  if(document.SearchForm.select1.options[6].selected == true)
```

| Script | Comments |
|---|---|

```
    document.SearchForm.MW.value += operator6
  if(document.SearchForm.select1.options[7].selected == true)
    document.SearchForm.MW.value += operator7
  if(document.SearchForm.select1.options[8].selected == true)
    document.SearchForm.MW.value += operator8
}
else if(fieldToInsertOperator=="IsoElectricPoint") {
  if(document.SearchForm.select1.options[0].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator0
  if(document.SearchForm.select1.options[1].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator1
  if(document.SearchForm.select1.options[2].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator2
  if(document.SearchForm.select1.options[3].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator3
  if(document.SearchForm.select1.options[4].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator4
  if(document.SearchForm.select1.options[5].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator5
  if(document.SearchForm.select1.options[6].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator6
  if(document.SearchForm.select1.options[7].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator7
  if(document.SearchForm.select1.options[8].selected == true)
    document.SearchForm.IsoElectricPoint.value += operator8
}
```

| Script | Comments |
|---|---|
| } | |
| //--> | This line is an ending line for hiding the script from browsers which has no interpreter for JavaScript |
| </SCRIPT> | This is an terminate line of JavaScript |
| </HEAD> | |
| <BODY BACKGROUND="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/CUPDBbg.jpg" BGCOLOR="#FFFFFF"> | |
| <CENTER> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/search11.gif"><BR> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/divide11.gif"> | |
| </CENTER> | |
| <FORM METHOD="POST" NAME="SearchForm" ACTION="CUPeptideDatabase.fm$FIND"> | This is the starting line of FORM, one of the capability of HTML, allowing server to receive user's information. |
| <INPUT TYPE="hidden" NAME="html"  VALUE="html1"> | |
| <INPUT TYPE="hidden" NAME="header" VALUE="header1"> | |
| <INPUT TYPE="hidden" NAME="footer" VALUE="footer1"> | |
| <INPUT TYPE="hidden" NAME="error" VALUE="error1"> | |
| <PRE> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif"><FONT  SIZE=+1 COLOR=#00FFAA90>Category  </FONT><SELECT NAME="Category"> | |
| <OPTION SELECTED VALUE=""> None | |
| <OPTION VALUE="Adrenocorticotropic Hormone and | |

| Script | Comments |
|---|---|
| Fragments"> Adrenocorticotropic Hormone and Fragments<br><OPTION VALUE="Angiotensin and Related Peptides"> Angiotensin and Related Peptides<br><OPTION VALUE="Atrial Natriuretic Peptides"> Atrial Natriuretic Peptides<br><OPTION VALUE="Bradykinin and Related Peptides"> Bradykinin and Related Peptides<br><OPTION VALUE="Chemotactic Peptides"> Chemotactic Peptides<br><OPTION VALUE="Dynorphin and Related Peptides"> Dynorphin and Related Peptides<br><OPTION VALUE="Endorphins and b-Lipotropin Fragments"> Endorphins and b-Lipotropin Fragments<br><OPTION VALUE="Enkephalin and Related Peptides"> Enkephalin and Related Peptides<br><OPTION VALUE="Enzyme Inhibitors"> Enzyme Inhibitors<br><OPTION VALUE="Fibronectin Fragments and Related Peptides"> Fibronectin Fragments and Related Peptides<br><OPTION VALUE="Gastrointestinal Peptides"> Gastrointestinal Peptides<br><OPTION VALUE="Growth Hormone Releasing Peptides"> Growth Hormone Releasing Peptides<br><OPTION VALUE="Luteinizing Hormone Releasing Hormone and Related Peptides"> Luteinizing Hormone Releasing Hormone and Related Peptides<br><OPTION VALUE="Melanocyte Stimulating Hormone and Related Peptides"> Melanocyte Stimulating Hormone and Related Peptides<br><OPTION VALUE="Neurotensin and Related Peptides"> Neurotensin and Related Peptides<br><OPTION VALUE="Opioid Peptides"> Opioid Peptides | |

| Script | Comments |
|---|---|
| <OPTION VALUE="Oxytocin, Vasopressin,Vasotocin and Related Peptides"> Oxytocin, Vasopressin,Vasotocin and Related Peptides | |
| <OPTION VALUE="Parathyroid Hormone and Fragments"> Parathyroid Hormone and Fragments | |
| <OPTION VALUE="Protein Kinase Related Peptides"> Protein Kinase Related Peptides | |
| <OPTION VALUE="Somatostatin and Related Peptides"> Somatostatin and Related Peptides | |
| <OPTION VALUE="Substance P and Related Peptides"> Substance P and Related Peptides | |
| <OPTION VALUE="Miscellaneous Bioactive Peptides"> Miscellaneous Bioactive Peptides | |
| </SELECT> | |
| <SELECT NAME = "select1" onChange="insertOperator()"> | |
| <OPTION SELECTED VALUE=""> select operator | |
| <OPTION VALUE=""> = (equals) | |
| <OPTION VALUE=""> < (less than) | |
| <OPTION VALUE=""> <= (less than or equal) | |
| <OPTION VALUE=""> > (greater than) | |
| <OPTION VALUE=""> >= (greater than or equal) | |
| <OPTION VALUE=""> ... (range) | |
| <OPTION VALUE=""> @ (one character) | |
| <OPTION VALUE=""> * (zero or more character) | |
| </SELECT> <INPUT TYPE="RESET" VALUE="clear all"> | |
| <P><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90> Peptide Name </FONT><INPUT NAME="PeptideName" SIZE=36 VALUE="" onFocus="clickField1()"> <INPUT | |

| Script | Comments |
|---|---|

```
TYPE="button" VALUE="clear" onClick="clearField1()">

<P><IMG
SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/
graphics/bullet1.gif"><FONT  SIZE=+1 COLOR=#00FFAA90>
Sequence</FONT><INPUT NAME="Sequence" SIZE=36
VALUE="" onFocus="clickField2()">  <INPUT TYPE="button"
VALUE="clear" onClick="clearField2()">

<P><IMG
SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/
graphics/bullet1.gif"><FONT  SIZE=+1 COLOR=#00FFAA90>
Source  </FONT><INPUT NAME="Source" SIZE=36 VALUE=""
onFocus="clickField3()">  <INPUT TYPE="button"
VALUE="clear" onClick="clearField3()">   <INPUT
TYPE="SUBMIT" NAME="submit" VALUE="SEARCH NOW!">

<P><IMG
SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/
graphics/bullet1.gif"><FONT  SIZE=+1 COLOR=#00FFAA90>
Total Residue </FONT><INPUT NAME="TotalResidue" SIZE=36
VALUE="" onFocus="clickField4()">  <INPUT TYPE="button"
VALUE="clear" onClick="clearField4()">

<P><IMG
SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/
graphics/bullet1.gif"><FONT  SIZE=+1 COLOR=#00FFAA90>
MW</FONT><INPUT NAME="MW" SIZE=36 VALUE=""
onFocus="clickField5()">  <INPUT TYPE="button"
VALUE="clear" onClick="clearField5()">

<P><IMG
SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/
graphics/bullet1.gif"><FONT  SIZE=+1 COLOR=#00FFAA90>pI
   </FONT><INPUT NAME="IsoElectricPoint" SIZE=36
VALUE="" onFocus="clickField6()">  <INPUT TYPE="button"
VALUE="clear" onClick="clearField6()">

</PRE>

</FORM>

<P>
```

| Script | Comments |
|---|---|
| <CENTER><br><!--IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/advanc12.gif"--><PRE>  </PRE><br><IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/divide11.gif"><BR><br></CENTER><br></BODY><br></HTML> | |

## **<u>Table C-3</u> Results Page script**

| Script | Comments |
|---|---|
| `<HTML>`<br>`<HEAD>`<br>`<TITLE>Search Result</TITLE>`<br>`</HEAD>`<br>`<BODY BACKGROUND="file:///Macintosh%20 HD/Desktop%20Folder/KlaewklaNew/graphics/CUPDBbg.jpg" BGCOLOR="#FFFFFF">`<br>`<CENTER>`<br>`<IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/search12.gif">`<br>`</CENTER>`<br>`<P>`<br>`<FONT  SIZE=+3 COLOR=#00EE00FF><B><CENTER> <BLINK>4 total records found!</BLINK></CENTER></B></FONT>`<br>`<P>`<br>`<IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/divide11.gif"><BR><TD><IMG ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A href="CUPeptideDatabase.fm$RETRIEVE?value=798&field=Serial&html=detail1"><B>INSULIN:</B></A>(Chain A, Oxidized From Bovine Insulin)<P><TD><IMG  ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A href="CUPeptideDatabase.fm$RETRIEVE?value=799&field=Serial&html=detail1"><B>INSULIN:</B></A>(Chain B, Oxidized From Bovine Insulin)<P><TD><IMG  ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A` | |

| Script | Comments |
|---|---|
| href="CUPeptideDatabase.fm$RETRIEVE?value=800&field=Serial&html=detail1"><B>INSULIN CHAIN B FRAGMENT 22-30:</B></A><P><TD><IMG  ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A href="CUPeptideDatabase.fm$RETRIEVE?value=801&field=Serial&html=detail1"><B>INSULIN-LIKE GROWTH FACTOR II FRAGMENT 33-40:</B></A><P><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/divide11.gif"> | |

## Details Page Script

This Page is divided into two types. If all residue of the peptide are standard amino acid, the details page consist of table of information of that peptide plus Calculation Area, else the details page have no calculation part.

**Table C- 4 Details Page (with calculation part) script**

| Script | Comments |
|---|---|
| <HTML> | |
| <HEAD> | |
| <TITLE>ADRENOCORTICOTROPIC HORMONE</TITLE> | |
| </HEAD> | |
| <BODY BACKGROUND="file:///Macintosh%20 HD/Desktop%20Folder/KlaewklaNew/graphics/CUPDBbg.jpg" BGCOLOR=#FFFFFF> | |
| <CENTER><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/Detail11.gif"></CENTER> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/divide11.gif"><P> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+2 COLOR=#00EEAA90><U><B>ADRENOCORTICOTROPIC HORMONE (ACTH 1-39 ; Corticotropin A)</B></U></FONT> | |
| <CENTER><P> | |
| <TABLE BORDER=2 WIDTH=550 HEIGHT=1 CELLPADDING=5 CELLSPACING=1> | |
| <TR><TD COLSPAN=70><IMG SRC="file:/// Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bul | |

| Script | Comments |
|---|---|
| let1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>Category</FONT></TD><TD><FONT SIZE=+1 COLOR=#000000> Adrenocorticotropic Hormone and Fragments</FONT></TD></TR><br><TR><TD COLSPAN=70><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>Sequence</FONT></TD><TD><FONT SIZE=+1 COLOR=#000000>Ser-Tyr-Ser-Met-Glu-His-Phe-Arg-Trp-Gly- Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val- Lys-Val-Tyr-Pro-Asn-Gly-Ala-Glu-Asp-Glu- Ser-Ala-Glu-Ala-Phe-Pro-Leu-Glu-Phe</FONT></TD></TR><br><TR><TD COLSPAN=70><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>Total Residue </FONT></TD><TD><FONT SIZE=+1 SIZE=+1 COLOR=#000000>39</FONT></TD></TR><br><TR><TD COLSPAN=70><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>Source</FONT></TD><TD><FONT SIZE=+1 SIZE=+1 COLOR=#000000>Human</FONT></TD></TR><br><TR><TD COLSPAN=70><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>Disulfide Bridge</FONT></TD><TD><FONT SIZE=+1 SIZE=+1 COLOR=#000000>-</FONT></TD></TR><br><TR><TD COLSPAN=70><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>Cross Reference</FONT></TD><TD><FONT SIZE=+1 SIZE=+1 COLOR=#000000><A href="http://expasy.hcuge.ch/cgi-bin/get-sprot-entry?P12718">http://expasy.hcuge.ch/cgi-bin/get-sprot-entry?P12718</A><br><BR>see <A href="http://expasy.hcuge.ch/cgi-bin/get-pdb-entry?1atn">http://expasy.hcuge.ch/cgi-bin/get-pdb-entry?1atn</A></FONT></TD></TR> |  |

| Script | Comments |
|---|---|

```
</TABLE></CENTER><P>
<SCRIPT LANGUAGE="Javascript">
<!--
function fillAla() {
  document.Form6.Sequence.value += "Ala-"
}
function fillArg() {
  document.Form6.Sequence.value += "Arg-"
}
function fillAsn() {
  document.Form6.Sequence.value += "Asn-"
}
function fillAsp() {
  document.Form6.Sequence.value += "Asp-"
}
function fillCys() {
  document.Form6.Sequence.value += "Cys-"
}
function fillGlu() {
  document.Form6.Sequence.value += "Glu-"
}
function fillGln() {
  document.Form6.Sequence.value += "Gln-"
}
function fillGly() {
  document.Form6.Sequence.value += "Gly-"
```

| Script | Comments |
|---|---|

```
}
function fillHis() {
   document.Form6.Sequence.value += "His-"
}
function fillIle() {
   document.Form6.Sequence.value += "Ile-"
}
function fillLeu() {
   document.Form6.Sequence.value += "Leu-"
}
function fillLys() {
   document.Form6.Sequence.value += "Lys-"
}
function fillMet() {
   document.Form6.Sequence.value += "Met-"
}
function fillPhe() {
   document.Form6.Sequence.value += "Phe-"
}
function fillPro() {
   document.Form6.Sequence.value += "Pro-"
}
function fillSer() {
   document.Form6.Sequence.value += "Ser-"
}
function fillThr() {
```

| Script | Comments |
|---|---|

```
    document.Form6.Sequence.value += "Thr-"
  }
  function fillTrp() {
    document.Form6.Sequence.value += "Trp-"
  }
  function fillTyr() {
    document.Form6.Sequence.value += "Tyr-"
  }
  function fillVal() {
    document.Form6.Sequence.value += "Val-"
  }
  function clearSequenceField() {
    document.Form6.Sequence.value = ""
  }
  function calculateMW1() {
    var position1 = 0
    var position2 = 1
    var MW1 = 0
    var sequenceLength =
document.Form6.Sequence.value.length
    while (position2*4-1 <= sequenceLength) {
      if (document.Form6.Sequence.value.substring((position1)*4,
(position2)*4-1) == "Ala")
        MW1 += 71.0
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Arg")
        MW1 += 157.2
```

| Script | Comments |
|---|---|

```
    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Asn")

       MW1 += 114.1

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Asp")

       MW1 += 114.0

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Cys")

       MW1 += 103.1

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Glu")

       MW1 += 128.1

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Gln")

       MW1 += 128.1

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Gly")

       MW1 += 57.0

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "His")

       MW1 += 137.1

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Ile")

       MW1 += 113.1

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Leu")

       MW1 += 113.1

    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Lys")
```

| Script | Comments |
|---|---|

```
        MW1 += 129.1
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Met")
        MW1 += 131.1
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Phe")
        MW1 += 147.1
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Pro")
        MW1 += 97.1
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Ser")
        MW1 += 87.0
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Thr")
        MW1 += 101.1
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Trp")
        MW1 += 186.2
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Tyr")
        MW1 += 163.1
      else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Val")
        MW1 += 99.1
    position1++
    position2++
  }
```

| Script | Comments |
|---|---|

```
  document.Form6.MW.value = MW1
}
var NetCharge = 0
function definepHForNetCharge1() {
  if(document.Form6.AtpH.options[0].selected == true)
      pH = 0
  if(document.Form6.AtpH.options[1].selected == true)
      pH = 1
  if(document.Form6.AtpH.options[2].selected == true)
      pH = 2
  if(document.Form6.AtpH.options[3].selected == true)
      pH = 3
  if(document.Form6.AtpH.options[4].selected == true)
      pH = 4
  if(document.Form6.AtpH.options[5].selected == true)
      pH = 5
  if(document.Form6.AtpH.options[6].selected == true)
      pH = 6
  if(document.Form6.AtpH.options[7].selected == true)
      pH = 7
  if(document.Form6.AtpH.options[8].selected == true)
      pH = 8
  if(document.Form6.AtpH.options[9].selected == true)
      pH = 9
  if(document.Form6.AtpH.options[10].selected == true)
      pH = 10
```

| Script | Comments |
|---|---|
| | |

```
   if(document.Form6.AtpH.options[11].selected == true)
        pH = 11
   if(document.Form6.AtpH.options[12].selected == true)
        pH = 12
   if(document.Form6.AtpH.options[13].selected == true)
        pH = 13
   if(document.Form6.AtpH.options[14].selected == true)
        pH = 14
   calculateNetCharge1()
}
function calculateNetCharge1() {
   var position1 = 0
   var position2 = 1
   var pKR = 0
   var acidCharge = 0
   var saltCharge = 0
   var netCharge0 = 0
   var sequenceLength =
document.Form6.Sequence.value.length
   if (document.Form6.Sequence.value=="") {
   NTerminusCharge = 0
   CTerminusCharge = 0
   }
else {
   while (position2*4-1 <= sequenceLength) {
      if (document.Form6.Sequence.value.substring((position1)*4,
```

| Script | Comments |
|---|---|

```
(position2)*4-1) == "Arg") {
        pKR = 12.48
        acidCharge = 1
        saltCharge = 0
    }
    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Asp") {
        pKR = 3.90
        acidCharge = 0
        saltCharge = -1
    }
    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Cys") {
        pKR = 8.33
        acidCharge = 0
        saltCharge = -1
    }
    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Glu") {
        pKR = 4.07
        acidCharge = 0
        saltCharge = -1
    }
    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "His") {
        pKR = 6.04
        acidCharge = 1
```

| Script | Comments |
|---|---|

```
      saltCharge = 0
    }
    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Lys") {
      pKR = 10.79
      acidCharge = 1
      saltCharge = 0
    }
    else if (document.Form6.Sequence.value.substring
((position1)*4,(position2)*4-1) == "Tyr") {
      pKR = 10.13
      acidCharge = 0
      saltCharge = -1
    }
    else {
      acidCharge = 0
      saltCharge = 0
    }
    with(Math) {
      netCharge0 += pow(10,pKR-pH)/(pow(10,pKR-pH)+1)*
acidCharge + 1/(pow(10,pKR-pH)+1)*saltCharge
    }
  position1++
  position2++
  }
  var pK1 = 0
  var pK2 = 0
```

| Script | Comments |
|---|---|

```
   var NTerminusCharge = 0
   var CTerminusCharge = 0
     if (document.Form6.Sequence.value.substring(0,3) == "Ala")
       pK2 = 9.87
     else if (document.Form6.Sequence.value.substring(0,3) == "
Arg")
       pK2 = 8.99
     else if (document.Form6.Sequence.value.substring(0,3) == "
Asn")
       pK2 = 8.84
     else if (document.Form6.Sequence.value.substring(0,3) == "
Asp")
       pK2 = 9.90
     else if (document.Form6.Sequence.value.substring(0,3) == "
Cys")
       pK2 = 10.78
     else if (document.Form6.Sequence.value.substring(0,3) == "
Glu")
       pK2 = 9.47
     else if (document.Form6.Sequence.value.substring(0,3) == "
Gln")
       pK2 = 9.13
     else if (document.Form6.Sequence.value.substring(0,3) == "
Gly")
       pK2 = 9.78
     else if (document.Form6.Sequence.value.substring(0,3) == "
His")
       pK2 = 9.33
     else if (document.Form6.Sequence.value.substring(0,3) == "
```

| Script | Comments |
|---|---|

```
Ile")
        pK2 = 9.76
      else if (document.Form6.Sequence.value.substring(0,3) == "
Leu")
        pK2 = 9.74
      else if (document.Form6.Sequence.value.substring(0,3) == "
Lys")
        pK2 = 9.18
      else if (document.Form6.Sequence.value.substring(0,3) == "
Met")
        pK2 = 9.28
      else if (document.Form6.Sequence.value.substring(0,3) == "
Phe")
        pK2 = 9.18
      else if (document.Form6.Sequence.value.substring(0,3) == "
Pro")
        pK2 = 10.65
      else if (document.Form6.Sequence.value.substring(0,3) == "
Ser")
        pK2 = 9.21
      else if (document.Form6.Sequence.value.substring(0,3) == "
Thr")
        pK2 = 9.10
      else if (document.Form6.Sequence.value.substring(0,3) == "
Trp")
        pK2 = 9.44
      else if (document.Form6.Sequence.value.substring(0,3) == "
Tyr")
        pK2 = 9.11
```

| Script | Comments |
|---|---|

```
    else if (document.Form6.Sequence.value.substring(0,3) == "
Val")
      pK2 = 9.74
    if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength) == "-") {
      if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Ala")
        pK1 = 2.35
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Arg")
        pK1 = 1.82
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Asn")
        pK1 = 2.10
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Asp")
        pK1 = 1.99
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Cys")
        pK1 = 1.92
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Glu")
        pK1 = 2.10
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Gln")
        pK1 = 2.17
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Gly")
        pK1 = 2.35
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "His")
        pK1 = 1.80
```

| Script | Comments |
|---|---|

```
(sequenceLength-1,sequenceLength-4) == "His")
        pK1 = 1.80
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Ile")
        pK1 = 2.32
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Leu")
        pK1 = 2.33
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Lys")
        pK1 = 2.16
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Met")
        pK1 = 2.13
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Phe")
        pK1 = 2.16
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Pro")
        pK1 = 2.95
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Ser")
        pK1 = 2.19
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Thr")
        pK1 = 2.09
      else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Trp")
        pK1 = 2.43
```

| Script | Comments |
|---|---|

```
        else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Tyr")
            pK1 = 2.20
        else if (document.Form6.Sequence.value.substring
(sequenceLength-1,sequenceLength-4) == "Val")
            pK1 = 2.29
    }
    else {
        if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Ala")
            pK1 = 2.35
        else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Arg")
            pK1 = 1.82
        else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Asn")
            pK1 = 2.10
        else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Asp")
            pK1 = 1.99
        else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Cys")
            pK1 = 1.92
        else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Glu")
            pK1 = 2.10
        else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Gln")
            pK1 = 2.17
```

| Script | Comments |
|---|---|

```
      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Gly")

        pK1 = 2.35

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "His")

        pK1 = 1.80

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Ile")

        pK1 = 2.32

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Leu")

        pK1 = 2.33

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Lys")

        pK1 = 2.16

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Met")

        pK1 = 2.13

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Phe")

        pK1 = 2.16

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Pro")

        pK1 = 2.95

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Ser")

        pK1 = 2.19

      else if (document.Form6.Sequence.value.substring
(sequenceLength,sequenceLength-3) == "Thr")
```

| Script | Comments |
|---|---|

```
            pK1 = 2.09
         else if (document.Form6.Sequence.value.substring
 (sequenceLength,sequenceLength-3) == "Trp")
            pK1 = 2.43
         else if (document.Form6.Sequence.value.substring
 (sequenceLength,sequenceLength-3) == "Tyr")
            pK1 = 2.20
         else if (document.Form6.Sequence.value.substring
 (sequenceLength,sequenceLength-3) == "Val")
            pK1 = 2.29
      }
      with(Math) {
         NTerminusCharge += pow(10,pK2-pH)/(pow(10,pK2-pH)
+1)
      }
      with(Math) {
         CTerminusCharge += (-1)/(pow(10,pK1-pH)+1)
      }
 }
   netCharge = netCharge0 + NTerminusCharge +
CTerminusCharge
}
function fillNetCharge() {
   definepHForNetCharge1()
   document.Form6.NetCharge.value = netCharge
}
function calculatepI1() {
```

| Script | Comments |
|---|---|

```
var pI = 0
pH = 0
calculateNetCharge1()
if (netCharge > -0.0001 && netCharge < 0.0001) {
  pI = pH
}
else {
  while (netCharge < -0.0001 || netCharge > 0.0001) {
    pH += 1
    calculateNetCharge1()
    if (netCharge > -0.0001 && netCharge < 0.0001) {
      pI = pH
    }
    else if (netCharge < 0) {
      while (netCharge < -0.0001 || netCharge > 0.0001) {
        pH -= 0.1
        calculateNetCharge1()
        if (netCharge > -0.0001 && netCharge < 0.0001) {
          pI = pH
        }
        else if (netCharge > 0) {
          while (netCharge < -0.0001 || netCharge > 0.0001) {
            pH += 0.01
            calculateNetCharge1()
            if (netCharge > -0.0001 && netCharge < 0.0001) {
              pI = pH
```

| Script | Comments |
|---|---|

```
                  }
                  else if (netCharge < 0) {
                     while (netCharge < -0.0001 || netCharge >
0.0001) {
                       pH -= 0.001
                       calculateNetCharge1()
                       if (netCharge > -0.0001 && netCharge <
0.0001) {
                         pI = pH
                       }
                       else if (netCharge > 0) {
                         while (netCharge < -0.0001 || netCharge >
0.0001) {
                           pH += 0.0001
                           calculateNetCharge1()
                           if (netCharge > -0.0001 && netCharge <
0.0001) {
                              pI = pH
                           }
                           else if (netCharge < 0) {
                              while (netCharge < -0.0001 || netCharge
> 0.0001) {
                                pH -= 0.00001
                                calculateNetCharge1()
                                if (netCharge > -0.0001 && netCharge
< 0.0001) {
                                  pI = pH
                                }
```

| Script | Comments |
|---|---|

```
            }
           }
          }
         }
        }
       }
      }
     }
    }
   }
  }
 }
 document.Form6.pI.value = pI
}
//-->
</SCRIPT>
<PRE>  </PRE><CENTER><IMG SRC="file:///
Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cal
area.gif"></CENTER><BR>
<FORM METHOD="POST" NAME="Form6"
ACTION="CUPeptideDatabase.fm$ADD">
<PRE>
    <INPUT Type="button" NAME="Ala" VALUE="Ala"
onClick="fillAla()"><INPUT Type="button" NAME="Arg"
VALUE="Arg" onClick="fillArg()"><INPUT Type="button"
NAME="Asn" VALUE="Asn" onClick="fillAsn()"><INPUT
Type="button" NAME="Asp" VALUE="Asp" onClick="fillAsp()">
<INPUT Type="button" NAME="Cys" VALUE="Cys"
onClick="fillCys()"><INPUT Type="button" NAME="Glu"
VALUE="Glu" onClick="fillGlu()"><INPUT Type="button"
```

| Script | Comments |
|---|---|
| NAME="Gln" VALUE="Gln" onClick="fillGln()"><INPUT Type="button" NAME="Gly" VALUE="Gly" onClick="fillGly()"> <INPUT Type="button" NAME="His" VALUE="His" onClick="fillHis()"><INPUT Type="button" NAME="Ile" VALUE="Ile" onClick="fillIle()"> | |
| <INPUT Type="button" NAME="Leu" VALUE="Leu" onClick="fillLeu()"><INPUT Type="button" NAME="Lys" VALUE="Lys" onClick="fillLys()"><INPUT Type="button" NAME="Met" VALUE="Met" onClick="fillMet()"><INPUT Type="button" NAME="Phe" VALUE="Phe" onClick="fillPhe()"> <INPUT Type="button" NAME="Pro" VALUE="Pro" onClick="fillPro()"><INPUT Type="button" NAME="Ser" VALUE="Ser" onClick="fillSer()"><INPUT Type="button" NAME="Thr" VALUE="Thr" onClick="fillThr()"><INPUT Type="button" NAME="Trp" VALUE="Trp" onClick="fillTrp()"> <INPUT Type="button" NAME="Tyr" VALUE="Tyr" onClick="fillTyr()"><INPUT Type="button" NAME="Val" VALUE="Val" onClick="fillVal()"> | |
| </PRE> | |
| <PRE> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>Sequence</FONT><INPUT NAME="Sequence" SIZE=50 VALUE=Ser-Tyr-Ser-Met-Glu-His-Phe-Arg-Trp-Gly-Lys-Pro-Val-Gly-Lys-Lys-Arg-Arg-Pro-Val-Lys-Val-Tyr-Pro-Asn-Gly-Ala-Glu-Asp-Glu-Ser-Ala-Glu-Ala-Phe-Pro-Leu-Glu-Phe> <INPUT Type="button" VALUE="clear" onClick="clearSequenceField()"> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 COLOR=#00FFAA90>MW </FONT><INPUT NAME="MW" SIZE=50 VALUE=""> <INPUT TYPE="button" NAME="calculateMW" VALUE="calculate MW" onClick="calculateMW1()"> | |
| <IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/bullet1.gif"><FONT SIZE=+1 | |

| Script | Comments |
|---|---|

```html
COLOR=#00FFAA90>At pH </FONT><Select NAME="AtpH"
onChange="fillNetCharge()">

<OPTION>0

<OPTION>1

<OPTION>2

<OPTION>3

<OPTION>4

<OPTION>5

<OPTION>6

<OPTION SELECTED>7

<OPTION>8

<OPTION>9

<OPTION>10

<OPTION>11

<OPTION>12

<OPTION>13

<OPTION>14

</SELECT> <IMG SRC="file:///Macintosh%20
HD/Desktop%20Folder/KlaewklaNew/graphics/bullet1.gif">
<FONT  SIZE=+1 COLOR=#00FFAA90>Net Charge = </FONT>
<INPUT NAME="NetCharge" SIZE=20 VALUE=""> <INPUT
TYPE="button" NAME="calculateNetCharge" VALUE="Calculate
Net Charge" onClick="fillNetCharge()">

<IMG SRC="file:///Macintosh%20HD/Desktop%20
Folder/KlaewklaNew/graphics/bullet1.gif"><FONT  SIZE=+1
COLOR=#00FFAA90>pI    </FONT><INPUT NAME="pI"
SIZE=50 VALUE=""> <INPUT TYPE="button"
NAME="calculatepI" VALUE="calculate pI" onClick="calculatepI1
()"><P>

</PRE>
```

| Script | Comments |
|---|---|
| </FORM><br></BODY><br></HTML> | |

**<u>Table C-5</u> Details Page (without calculation part) Script**

| Script | Comments |
|---|---|
| <HTML><br><HEAD><br><TITLE>Search Result</TITLE><br></HEAD><br><BODY BACKGROUND="file:///Macintosh%20 HD/Desktop%20Folder/KlaewklaNew/graphics/CUPDBbg.jpg" BGCOLOR="#FFFFFF"><br><CENTER><br><IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/search12.gif"><br></CENTER><br><P><br><FONT  SIZE=+3 COLOR=#00EE00FF><B><CENTER> <BLINK>4 total records found!</BLINK></CENTER></B></ FONT><br><P><br><IMG SRC="file:///Macintosh%20HD/Desktop%20 Folder/KlaewklaNew/graphics/divide11.gif"><BR><TD><IMG | |

| Script | Comments |
|---|---|
| ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A href="CUPeptideDatabase.fm$RETRIEVE?value=798&field=Serial&html=detail1"><B>INSULIN:</B></A>(Chain A, Oxidized From Bovine Insulin)<P><TD><IMG ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A href="CUPeptideDatabase.fm$RETRIEVE?value=799&field=Serial&html=detail1"><B>INSULIN:</B></A>(Chain B, Oxidized From Bovine Insulin)<P><TD><IMG ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A href="CUPeptideDatabase.fm$RETRIEVE?value=800&field=Serial&html=detail1"><B>INSULIN CHAIN B FRAGMENT 22-30:</B></A><P><TD><IMG ALIGN=MIDDLE SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/cupdbbtn.gif"><A href="CUPeptideDatabase.fm$RETRIEVE?value=801&field=Serial&html=detail1"><B>INSULIN-LIKE GROWTH FACTOR II FRAGMENT 33-40:</B></A><P><IMG SRC="file:///Macintosh%20HD/Desktop%20Folder/KlaewklaNew/graphics/divide11.gif"> |  |

# BIOGRAPHY

Klaewkla Kaewthai was born on April 7, 1971. He graduated with A Bachelor degree in the Department of Biochemistry from the Faculty of Science, Chulalongkorn University in 1992 and continued his study in the Master Degree in the Program of Biochemistry at the same University.