

Additional File 1. The sequences and masses of identified peptides in the zebra finch by MS.

Prohormone	Peptide	Mass _{obs}	Mass _{theo}	Mass error (ppm)
ADCYAP1	MYTLYYPPEK	1303.57	1303.62	-38
	QMAVKKYLA AVL-amide*	1332.76	1332.78	-15
	VGGASGGLGDDAEPLT	1414.70	1414.67	21
	HIDGIFTDSYSRY	1572.70	1572.72	-13
AVP	CAEEDFLPSPCQAGGQ	1649.65	1649.68	-18
	CYIQNCPRG-amide	1049.51	1049.45	57
CCK	LDGHPVPAELE	1175.53	1175.58	-43
CRF	p-EQKSLDTDDSD	1233.81	1233.50	251
CHGA	WNKMDEL	934.45	934.42	32
	WNKMDELA	1005.53	1005.46	70
	YAFSSPEEDV	1142.53	1142.48	44
	WNKMDELAKQL	1374.71	1374.70	7
	WNKMDELAKQLT	1475.77	1475.74	20
	WNKMDELAKQLTS	1562.77	1562.78	-6
	REENDSEEDPDRSMKKTFRS	2455.10	2455.11	-4
CHGB	SAELPGLY	848.42	848.43	-12
	YDVERQY	971.53	971.43	103
	SEYRGHLPA	1028.59	1028.63	-39
	KKSHSEGMSM	1120.61	1120.50	98
	MDQLAQLLNY	1207.59	1207.59	0
	SAELPGLYSSGEE	1337.67	1337.60	52
	SEYRGHLP AEKE	1414.65	1414.68	-21
	SAELPGLYSSGEEL	1450.67	1450.68	-7
	GKTNR YDVERQY	1527.65	1527.74	-59
	SSDQVEDEEEERF	1597.61	1597.64	-19
	SSDQVEDEEEERFA	1668.11	1668.68	-342
	NPGKTNR YDVERQY	1738.73	1738.84	-63
	SSDQVEDEEEERFAE	1797.65	1797.72	-39
	DPAETEKHPAGSVEKEQ	1850.65	1850.86	-113
	SAGEQLPEGREEGRPALSE	2012.10	2011.97	65
	DSAGEQLPEGREEGRPALSE	2125.77	2125.99	-103
GH	p-QNYGLLSCKF	1154.57	1154.54	26
GNRH1	p-QHWSYGLQPG-amide	1153.57	1153.53	35
GRP	APLQPGGTPALTKIYP	1622.87	1622.90	-18
NPVF	SIKPFSNLPLRF-amide	1416.88	1416.81	49
	SPLVKGFSQSLLNLPQRF-amide	2029.00	2029.13	-64
NPY	SSPDTLISDLLL	1272.71	1272.68	24
NTS	p-QLHVN	592.21	592.30	-152
	p-QLHVNKARRPYIL [†]	1589.73	1589.92	-120
	KNPYI	633.32	633.35	-47
	KNPYIL	746.41	746.43	-27
OXT	ICCGE	523.10	523.18	-153

PENK	YGGF	442.19	442.19	0
	YGGFL	555.24	555.27	-54
	YGGFM	573.20	573.23	-52
	MDELY	669.21	669.27	-90
	YGGFMRF	876.33	876.40	-80
	YGGFMRSI	929.47	929.44	32
	YGGFMKKDSD	1146.50	1146.50	0
	ELEDEAKELQ	1202.63	1202.57	50
	SPELEDEAKEL	1258.75	1258.59	127
	RPEWWLDYQ	1291.68	1291.61	54
	ELDENHLLAKK*	1308.73	1308.71	15
	SPELEDEAKELQ	1386.63	1386.65	-14
	VGRPEWWLDYQ	1447.69	1447.69	0
	MDELYRAEPEDEANGGE	1923.61	1923.78	-88
	MDELYRAEPEDEANGGEM	2054.61	2054.82	-102
	MDELYRAEPEDEANGGEML	2167.73	2167.90	-78
	MDELYRAEPEDEANGGEMLA	2238.71	2238.94	-103
POMC	YGGFMSSE	876.30	876.40	-114
	YGGFMSSERI	1145.41	1145.52	-96
	NAIGKSFAKDGQ	1234.61	1234.63	-16
	PEFPWNSRKE	1288.57	1288.62	-39
	FKNAIGKSFAKDGQ	1509.71	1509.79	-53
	SYSMEHFRWGKPV-amide	1621.79	1621.78	6
	SYSMEHFRWGKPVG	1679.69	1679.79	-60
	EEFSGKNAGIPDFSRLFSEEAKDG	2516.10	2516.15	-20
PRL	GRVHSGDVE	954.49	954.45	42
PTHLH	QNLIE	615.29	615.32	-49
RLN3	AGDLKKLVRQV	1224.80	1224.77	24
SCG2	AMENM	594.16	594.21	-84
	ASFQQHQL	957.45	957.47	-21
	PEVANTNQM	1002.39	1002.44	-50
	ASFQQHQLL	1070.67	1070.55	112
	SGKLSFLEDE	1123.57	1123.54	27
	ASFQQHQLLQ	1198.59	1198.61	-17
	EDMLAKVLEY	1208.60	1208.61	-8
	SGKLSFLEDEI	1236.65	1236.62	24
SCG5	LQHLGPYGNL	1110.67	1110.58	81
	SVPQFSDEDKGP	1304.69	1304.59	77
	SVPQFSDEDKGPK	1432.59	1432.68	-63
	SVNPYLQGQRLDNVVA	1771.87	1771.93	-34
SST	SANSNPALAPRE	1225.63	1225.61	16
TAC1	HKTDSFVGLM-amide	1132.61	1132.57	35
	RPRPQQFFGLM-amide	1374.77	1374.73	29
	SLNSGSSEGSTAQNYE	1629.55	1629.68	-80
	DAGYGQIS	809.28	809.36	-99
UCN3	VRSGDDGSGAGSHPDEASLSLLEGPE	2538.10	2538.15	-20
VIP	YLHSLIRKRVSSQDSPV*	1984.11	1984.09	10
	HSDAVFTDNYSRF	1557.57	1557.68	-71