Supporting Information
for

"Bioinspired preparation of monolithic ordered mesoporous silica for enrichment of endogenous peptides"

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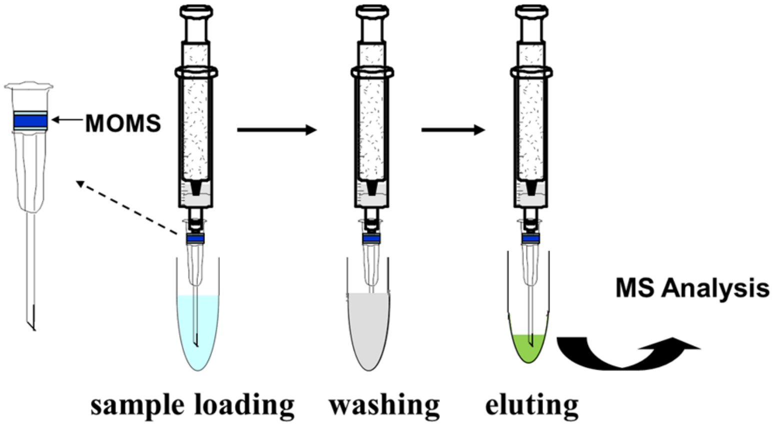
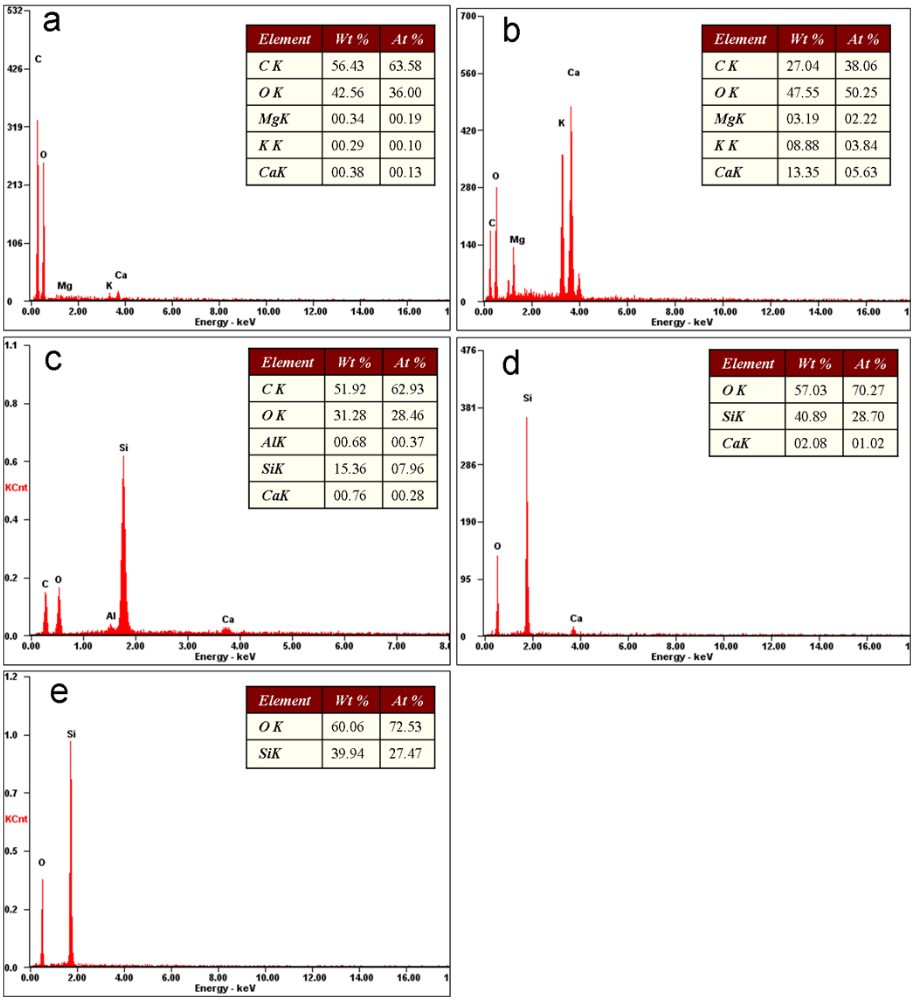


Figure S1. Schematic diagram of the procedure for the enrichment of endogenous peptides with MOMS using the lab-in-syringe system.



a

Element	Wt %	At %
C K	56.43	63.58
O K	42.56	36.00
MgK	00.34	00.19
K K	00.29	00.10
CaK	00.38	00.13

b

Element	Wt %	At %
C K	27.04	38.06
O K	47.55	50.25
MgK	03.19	02.22
K K	08.88	03.84
CaK	13.35	05.63

c

Element	Wt %	At %
C K	51.92	62.93
O K	31.28	28.46
AlK	00.68	00.37
SiK	15.36	07.96
CaK	00.76	00.28

d

Element	Wt %	At %
O K	57.03	70.27
SiK	40.89	28.70
CaK	02.08	01.02

e

Element	Wt %	At %
O K	60.06	72.53
SiK	39.94	27.47

Figure S2. The EDX analysis of pomelo peel (a), the ash of pomelo peel after calcination at 550ºC (b), pomelo peel/CTAB/SiO_2 composite before (c) and after (d) calcination at 550ºC, and pure MOMS after acid treatment (e).

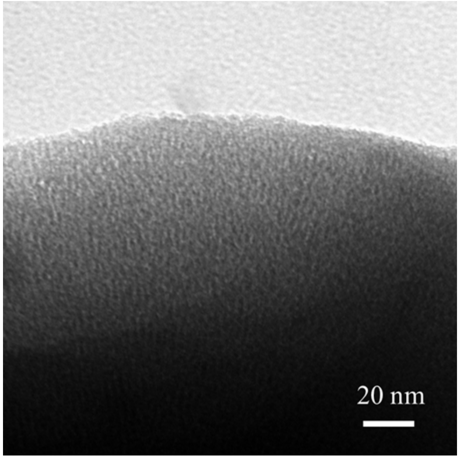


Figure S3. HR-TEM image of MOMS.

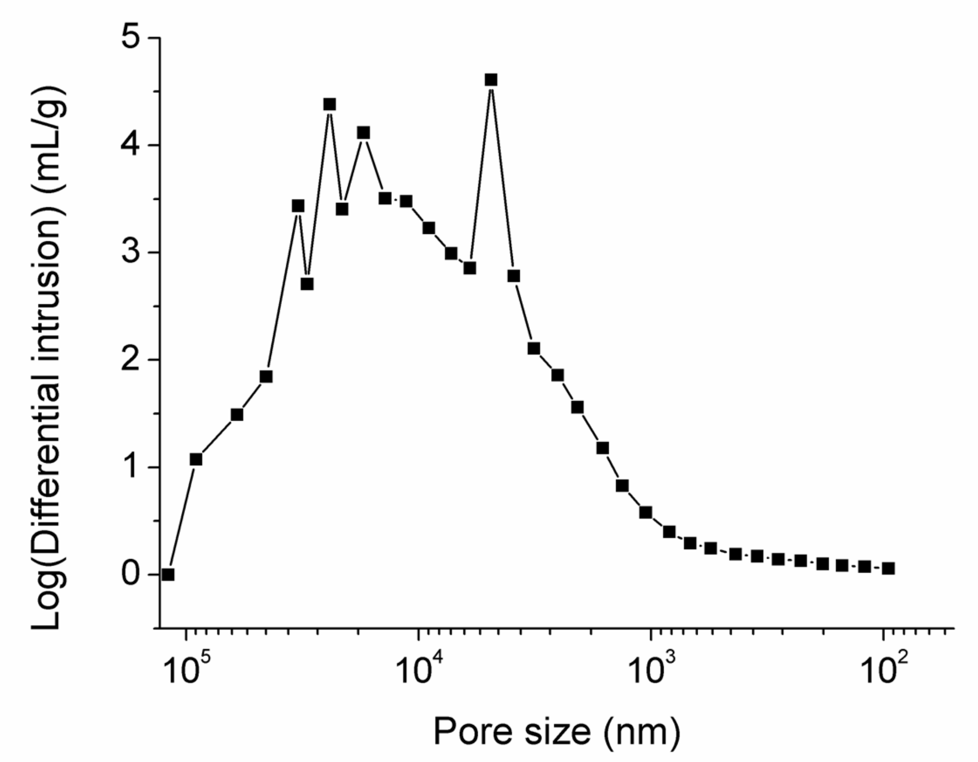


Figure S4. The macropore size distribution curve of MOMS measured by mercury intrusion porosimeter.

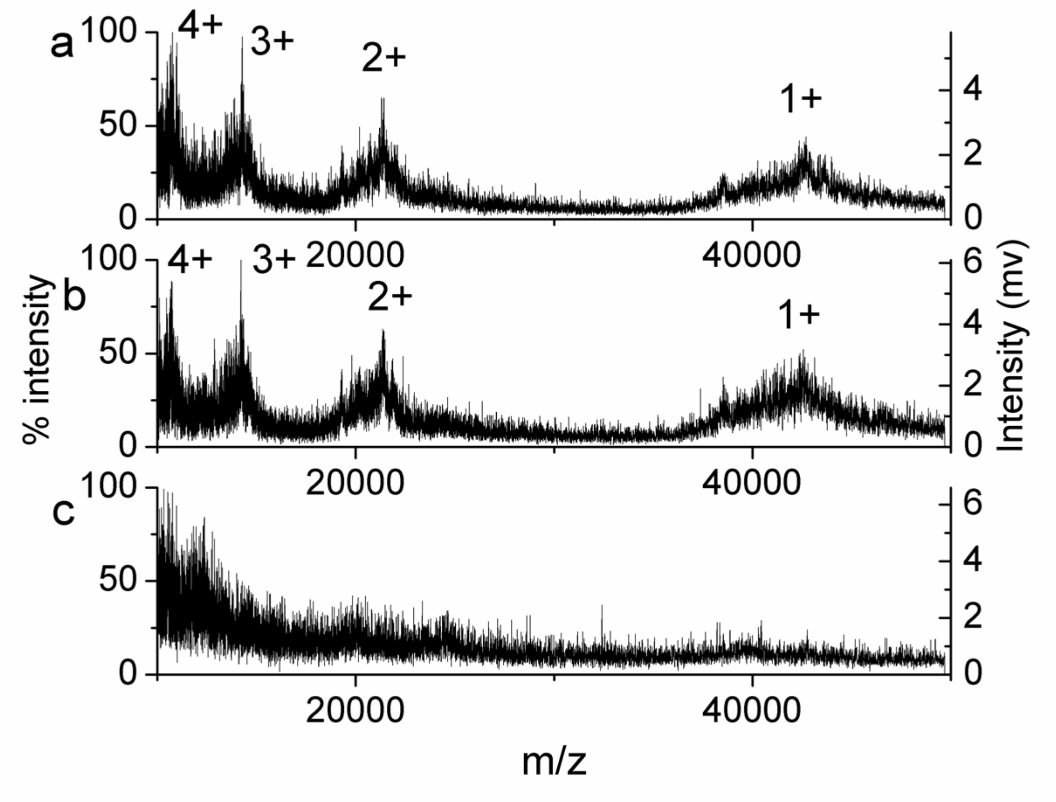


Figure S5. MALDI-TOF mass spectra of 500 nM HRP (MW 44.0 kDa) without any treatment (a), and solution after extraction (c) or eluate (e) after enrichment with MOMS.

Table S1. Detailed information of the observed peptides from BSA digests.

Calculated *m/z*	Database sequence	A	B	C
		Without treatment	OMS particles	MOMS
1163.32	K.LVNELTEFAK.T		√	√
1283.48	R.HPEYAVSVLLR.L		√	√
1305.48	K.HLVDEPQNLIK.Q		√	√
1399.61	K.TVMENFVAFVDK.C		√	√
1414.68	K.TVMENFVAFVDK.C		√	√
1419.60	K.SLHTLFGDELCK.V		√	√
1438.80	R.RHPEYAVSVLLR.L		√	√
1456.85	K.YICDNQDTISSK.L		√	√
1463.55	K.TCVADESHAGCEK.S		√	√
1467.76	R.DTHKSEIAHRFK.D		√	√
1478. 58	R.ETYGDMADCCEK.Q	√	√	√
1493.92	K.QIKKQTALVELLK.H		√	√
1502.62	K.EYEATLEECCAK.D			√
1511.72	K.VPQVSTPTLVEVSR.S		√	
1538.81	R.LCVLHEKTPVSEK.V	√	√	√
1576.76	K.LKPDPNTLCDEFK.A			√
1638.93	R.KVPQVSTPTLVEVSR.S		√	√
1672.76	K.QEPERNECFLSHK.D		√	√
1725.00	R.MPCTEDYLSLILNR.L		√	√
1747.93	R.QRLRCASIQKFGER.A		√	√
1881.11	R.RPCFSALTPDETYVPK.A	√	√	√
1908.14	K.LFTFHADICTLPDTEK.Q		√	√
2492.85	K.GLVLIAFSQYLQQCPFDEHVK.L		√	√
Peptides identified		3	21	22

Mascot from Matrix Science Ltd. (London, U.K.) was used for the peptides search and identification. Search parameters: database, SwissProt; enzyme, trypsin; maximum of missed cleavages, 1; mass tolerance, 1 Da. ‘A’ represents the results of BSA digests (20 nM) without any treatment. ‘B’ represents the results of BSA digests (20 nM) upon enrichment with OMS particles. ‘C’ represents the results of BSA digests (20 nM) upon enrichment with MOMS. ‘√’ represents the peptides identified by MALDI-TOF mass spectra from BSA digests.

Table S2. The identified peptides from human plasma after enrichment with MOMS followed by 1D LC-MS/MS analysis.

Protein information	Sequence	MW
sp|P01024|CO3_HUMAN	HRIHWESASLLR	1503.8020
sp|P01024|CO3_HUMAN	ITHRIHWESASLLR	1717.9307
sp|P01024|CO3_HUMAN	KITHRIHWESAS	1445.7521
sp|P01024|CO3_HUMAN	KITHRIHWESASLL	1689.9302
sp|P01024|CO3_HUMAN	KITHRIHWESASLLR	1846.0317
sp|P01024|CO3_HUMAN	RIHWESASLLR	1366.7424
sp|P01024|CO3_HUMAN	SKITHRIHWE	1305.6948
sp|P01024|CO3_HUMAN	SKITHRIHWESA	1463.7637
sp|P01024|CO3_HUMAN	SKITHRIHWESASLL	1776.9661
sp|P01024|CO3_HUMAN	SKITHRIHWESASLLR	1933.0618
sp|P01024|CO3_HUMAN	SSKITHRIHWE	1392.7255
sp|P01024|CO3_HUMAN	SSKITHRIHWES	1479.7570
sp|P01024|CO3_HUMAN	SSKITHRIHWESA	1550.7958
sp|P01024|CO3_HUMAN	SSKITHRIHWESASL	1732.8934
sp|P01024|CO3_HUMAN	SSKITHRIHWESASLL	1864.0035
sp|P01024|CO3_HUMAN	SSKITHRIHWESASLLR	2036.0981
sp|P01024|CO3_HUMAN	SSKITHRIHWESASLLRSEETKENEGFT	3266.6201
sp|P01024|CO3_HUMAN	THRIHWESASLLR	1604.8491
sp|P01024|CO3_HUMAN	RIHWESASLL	1210.6346
sp|P01024|CO3_HUMAN	THRIHWESASLL	1448.7474
sp|P01024|CO3_HUMAN	SSKITHRIHWESAS	1619.8088
sp|P01024|CO3_HUMAN	ITHRIHWESASLL	1561.8329
sp|P01024|CO3_HUMAN	HRIHWESASLL	1347.6948
sp|P01024|CO3_HUMAN	IHWESASLL	1054.5325
sp|P01024|CO3_HUMAN	KITHRIHWESA	1376.7303
sp|P01024|CO3_HUMAN	KITHRIHWE	1218.6610
sp|P01024|CO3_HUMAN	THRIHWE	977.4773
sp|P01024|CO3_HUMAN	KITHRIHW	1089.6178
sp|P01024|CO3_HUMAN	IHWESASLLR	1210.6353
sp|Q14624|ITIH4_HUMAN	GVLSSRQLGLPGPPDVPDHAAYHPF	2626.3245
sp|Q14624|ITIH4_HUMAN	MNFRPGVLSSRQLGLPGPPDVPDHAAYHPF	3271.6196
sp|Q14624|ITIH4_HUMAN	MNFRPGVLSSRQLGLPGPPDVPDHAAYHPFR	3427.7485
sp|Q14624|ITIH4_HUMAN	NFRPGVLSSRQLGLPGPPDVPDHAAYHPF	3140.5886
sp|Q14624|ITIH4_HUMAN	NVHSGSTFFKYYLQGAKIPKPEA	2581.3313
sp|Q14624|ITIH4_HUMAN	NVHSGSTFFKYYLQGAKIPKPEAS	2668.3638
sp|Q14624|ITIH4_HUMAN	NVHSGSTFFKYYLQGAKIPKPEASFSPR	3155.6118
sp|Q14624|ITIH4_HUMAN	PGVLSSRQLGLPGPPDVPDHAAYHPF	2723.3789
sp|Q14624|ITIH4_HUMAN	QAGAAGSRMNFRPGVLS	1700.8276
sp|Q14624|ITIH4_HUMAN	QAGAAGSRMNFRPGVLSS	1787.8624

sp|Q14624|ITIH4_HUMAN	QAGAAGSRMNFRPGVLSSRQLGLPGPPDVPDHA	3337.6682
sp|Q14624|ITIH4_HUMAN	QAGAAGSRMNFRPGVLSSRQLGLPGPPDVPDHAAYHPF	3952.9607
sp|Q14624|ITIH4_HUMAN	QAGAAGSRMNFRPGVLSSRQLGLPGPPDVPDHAAYHPFR	4126.0879
sp|Q14624|ITIH4_HUMAN	SRQLGLPGPPDVPDHAAYHPF	2270.1140
sp|Q14624|ITIH4_HUMAN	YLQGAKIPKPEASFSPR	1888.0149
sp|Q14624|ITIH4_HUMAN	QAGAAGSRMNFRPGVLSSRQL	2201.1045
sp|Q14624|ITIH4_HUMAN	KIPKPEASFSPR	1355.7507
sp|Q14624|ITIH4_HUMAN	YYLQGAKIPKPEASFSPR	2051.0811
sp|Q14624|ITIH4_HUMAN	QAGAAGSRMNFRPGVLSSRQLGLPGPPDVPDHAAYHP	3821.8965
sp|Q14624|ITIH4_HUMAN	LQGAKIPKPEASFSPR	1724.9520
sp|Q14624|ITIH4_HUMAN	RQLGLPGPPDVPDHAAYHPF	2183.0811
sp|Q14624|ITIH4_HUMAN	RPGVLSSRQL	1111.6378
sp|Q14624|ITIH4_HUMAN	HAAYHPF	841.3859
sp|P02671|FIBA_HUMAN	ADSGEGDFLAEGGGVR	1535.6819
sp|P02671|FIBA_HUMAN	ADSGEGDFLAEGGGVRGPR	1845.8588
sp|P02671|FIBA_HUMAN	DEAGSEADHEGTHSTKRGHAKSRPV	2658.2517
sp|P02671|FIBA_HUMAN	EYHTEKLVTSKGDKELR	2032.0646
sp|P02671|FIBA_HUMAN	GKSSSYSKQFTSSTSYNR	2013.9369
sp|P02671|FIBA_HUMAN	GSTGNRNPGSSGTGGTATWKPGSSGP	2374.0881
sp|P02671|FIBA_HUMAN	MELERPGGNEITRGGSTSYGTGSETESPR	3054.4026
sp|P02671|FIBA_HUMAN	REYHTEKLVTSKGDKELR	2188.1846
sp|P02671|FIBA_HUMAN	SQLQKVPPEWKALTDMPQMR	2382.2148
sp|P02671|FIBA_HUMAN	SSSYSKQFTSSTSYNRGDSTFESKSY	2931.2883
sp|P02671|FIBA_HUMAN	SYKMADEAGSEADHEGTHSTKRGHAKSRPV	3238.5520
sp|P02671|FIBA_HUMAN	GKSSSYSKQFTSSTSYNRG	2070.9692
sp|P02671|FIBA_HUMAN	MADEAGSEADHEGTHSTKRGHAKSRPV	2860.3489
sp|P02671|FIBA_HUMAN	GKSSSYSKQFTSSTSYNRGDST	2374.0759
sp|P02671|FIBA_HUMAN	DSGEGDFLAEGGGVRGPR	1774.8132
sp|P02671|FIBA_HUMAN	SSSYSKQFTSSTSYNRGDSTFESKSYKM	3205.4238
sp|P02671|FIBA_HUMAN	GKSSSYSKQFTSSTSYNRGDSTFESKSYKM	3390.5278
sp|P02671|FIBA_HUMAN	GKSSSYSKQFTSSTSYN	1857.8350
sp|P02671|FIBA_HUMAN	ALTDMPQMR	1077.4893
sp|P02671|FIBA_HUMAN	SSSYSKQFTSSTSYNRGDSTFESKSYKMA	3276.4558
sp|P35527|K1C9_HUMAN	GGGGGGGLGSGGSIR	1144.5581
sp|P35527|K1C9_HUMAN	GGGGGGGLGSGGSIRSS	1318.6152
sp|P35527|K1C9_HUMAN	GGSGGSYGGGGSGGGYGGGSGSR	1790.7086
sp|P35527|K1C9_HUMAN	RSGGGGGGGLGSGGSIR	1387.6887
sp|P35527|K1C9_HUMAN	SGGGGGGGLGSGGSIR	1231.5831
sp|P35527|K1C9_HUMAN	SRSGGGGGGGLGSGGSIR	1474.7197
sp|P35527|K1C9_HUMAN	SRSGGGGGGGLGSGGSIRSS	1648.7817
sp|P35527|K1C9_HUMAN	SRSGGGGGGGLGSGGSIRSSY	1811.8470

sp|P35527|K1C9_HUMAN	GSGGGSGGGY	749.4420
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sp|P0C0L4|CO4A_HUMAN	NGFKSHALQLNNRQIR	1895.0233
sp|P0C0L4|CO4A_HUMAN	NGFKSHALQLNNRQI	1738.9200
sp|Q6FHJ7|SFRP4_HUMAN	KPKGKPPAPKPA	1207.4514
sp|Q6FHJ7|SFRP4_HUMAN	SNPPKPKGKPPAPKPASPK	1922.1113
sp|Q6FHJ7|SFRP4_HUMAN	SNPPKPKGKPPAPKPA	1609.9318
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tr|B7ZKJ8|B7ZKJ8_HUMAN	KIPKPGLDHTEASFSPR	1878.9957
tr|B7ZKJ8|B7ZKJ8_HUMAN	YYLQGAKIPKPGLDHTEASFSPR	2574.3223
tr|B7ZKJ8|B7ZKJ8_HUMAN	GAKIPKPGLDHTEASFSPR	1999.0408
tr|B7ZKJ8|B7ZKJ8_HUMAN	GVLSSRQLGLPGPPDVPDHAAYHPF	2626.3245
tr|B7ZKJ8|B7ZKJ8_HUMAN	HAAYHPF	841.3859
tr|B7ZKJ8|B7ZKJ8_HUMAN	MNFRPGVLSSRQLGLPGPPDVPDHAAYHPF	3271.6196
tr|B7ZKJ8|B7ZKJ8_HUMAN	MNFRPGVLSSRQLGLPGPPDVPDHAAYHPFR	3427.7485
tr|B7ZKJ8|B7ZKJ8_HUMAN	NFRPGVLSSRQLGLPGPPDVPDHAAYHPF	3140.5886
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tr|B7ZKJ8|B7ZKJ8_HUMAN	QAGAAGSRMNFRPGVLSS	1787.8624
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tr|B7ZKJ8|B7ZKJ8_HUMAN	RQLGLPGPPDVPDHAAYHPF	2183.0811
tr|B7ZKJ8|B7ZKJ8_HUMAN	SRQLGLPGPPDVPDHAAYHPF	2270.1140
sp|P10909|CLUS_HUMAN	HFFFPKSRIV	1276.7068
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sp|P02649|APOE_HUMAN	KVEQAVETEPEPELR	1752.8878
sp|P02649|APOE_HUMAN	SWFEPLVEDMQRQWAGLVEKVQAAVGTSAAPVPSDNH	4065.9670
sp|Q15942|ZYX_HUMAN	LANTQPRGPPASSPAPAPKFSPVTPKFTPVAS	3214.7114
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sp|P02675|FIBB_HUMAN	GHRPLDKKREEAPSL	1731.9421
sp|P02675|FIBB_HUMAN	GHRPLDKKREEAPSLRPAPPPISGGGY	2881.5498
sp|P02675|FIBB_HUMAN	QGVNDNEEGFFSARGHRPLDKKREEAPSLRPAPPP	4415.2100

	ISGGGY	
tr|H7C0L5|H7C0L5_HUMAN	NVHSAGAAGSRMNFRPGVLSSRQLGLPGPPDVPDHAAYHPF	4295.1196
tr|H7C0L5|H7C0L5_HUMAN	NVHSAGAAGSRMNFRPGVLSS	2130.0349
tr|H7C0L5|H7C0L5_HUMAN	NVHSAGAAGSRMNFRPGVLS	2043.0007
tr|H7C0L5|H7C0L5_HUMAN	NVHSAGAAGSRMNFRPGVLSSRQLGLPGPPDVPDHAAYHPFR	4451.2485
tr|H7C0L5|H7C0L5_HUMAN	GVLSSRQLGLPGPPDVPDHAAYHPF	2626.3245
tr|H7C0L5|H7C0L5_HUMAN	HAAYHPF	841.3859
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tr|H7C0L5|H7C0L5_HUMAN	MNFRPGVLSSRQLGLPGPPDVPDHAAYHPFR	3427.7485
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tr|H7C0L5|H7C0L5_HUMAN	SRQLGLPGPPDVPDHAAYHPF	2270.1140
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sp|P01042|KNG1_HUMAN	RPPGFSPFR	1059.5535
sp|P01042|KNG1_HUMAN	QVVAGLNFR	1002.5541
sp|P02765|FETUA_HUMAN	AHYDLRHTFMGVVSLGSPSGEVSHPRKT	3064.5386
sp|P02765|FETUA_HUMAN	HTFMGVVSLGSPSGEVSHPRKT	2325.1521
tr|F8WAH6|F8WAH6_HUMAN	AGPAAAAAAAKAAAKAAQFG	1683.8884
tr|F8WAH6|F8WAH6_HUMAN	GVPGVGGLGVSAGAVVPQPGAGV	1901.1252
sp|P02647|APOA1_HUMAN	THLAPYSDELRQR	1584.7987
sp|P06396|GELS_HUMAN	VRAATASRGASQAGAPQGR	1810.9530
tr|Q9BR87|Q9BR87_HUMAN	QQEPLGHLSPSL	1304.7671
sp|P02654|APOC1_HUMAN	FQKVKEKLKIDS	1461.8524
sp|P02654|APOC1_HUMAN	VKEKLKIDS	1058.6277
tr|F8WAE5|F8WAE5_HUMAN	AGPHAALANK	945.5709
sp|P17936|IBP3_HUMAN	IIIIKKGHAKDSQRY	1769.0349
tr|E9PGV9|E9PGV9_HUMAN	VAQSLGLLIGAA	1112.5513
tr|E9PGV9|E9PGV9_HUMAN	EGGPSLLGLRDMV	1342.7067
RRRRRsp|Q92545|TM131_HUMAN	SQDSLSSKEFEPLSSII	1866.0060
sp|P04264|K2C1_HUMAN	YRSGGGFSSGSAG	1188.5111
sp|P13645|K1C10_HUMAN	FNEKSKEL	993.5077
sp|P13645|K1C10_HUMAN	RNVSTGDVNVE	1188.5723
sp|Q567U6|CCD93_HUMAN	RMKMEKKKQENKMR	1863.9886
RRRRRsp|Q6ZR37|PKHG7_HUMAN	LKGEYLLHRS	1214.6227
tr|A6NJ97|A6NJ97_HUMAN; sp|Q86XN7|PRSR1_HUMAN	VSCGSSASLLR	1044.6096
sp|Q9Y5Z0|BACE2_HUMAN	AGSGTNGGSLVLG	1088.6462
sp|P06731|CEAM5_HUMAN	ASGTSPGLSAGATVGIMIGVL	1858.1353

tr|B4DV37|B4DV37_HUMAN; sp|Q8N1L9|BATF2_HUMAN	FASHTGSSLQGSSSKLSAL	1863.9965
sp|Q86XE5|HOGA1_HUMAN	AVGGVCALANV	972.4849
RRRRRtr|B8ZZE3|B8ZZE3_HUMAN; RRRRRtr|B8ZZC8|B8ZZC8_HUMAN; RRRRRsp|Q9NRN9|METL5_HUMAN	AGLMATGISLVG	1088.6423
sp|Q96AG4|LRC59_HUMAN	GLVACRVTEL	1059.6284
RRRRRsp|Q76L83|ASXL2_HUMAN	AACHVPSAGSILAPGTPSP	1731.9421
RRRRRtr|E5RFG9|E5RFG9_HUMAN	ISASGTKFAGGPFWVLVK	1863.9957
RRRRRsp|Q9NPF0|CD320_HUMAN	LPSAAAELGLGLGL	1280.7699
RRRRRsp|Q6P5Q4|LMOD2_HUMAN	EASLSALLED	1046.5964
RRRRRsp|Q969Y0|NXPE3_HUMAN	ELSNTEKIR	1088.6437
sp|Q99570|PI3R4_HUMAN	PRSESSAGICVP	1201.6149
sp|B7Z6K7|ZN814_HUMAN	NHQQIHTGDRL	1317.6483
sp|A1L453|PRS38_HUMAN	PAQPAPALSPALGPTLSVLMA	2001.1475
sp|Q92614|MY18A_HUMAN	ERMSAAELR	1061.4974
sp|Q86WB7|UN93A_HUMAN	QSSGVWGNLI	1059.6279
sp|Q8TBB6|S7A14_HUMAN	FDSLANHT	903.4553
RRRRRsp|C9JR72|KBTBD_HUMAN	ARFGGASLVGL	1046.5011