Figure S1:

ZASP  Q75112|1-84 rank 39 score 10.28
MSYSVTLTGPGPWGRQSGKDFNMLTISRITPGSKAASQSQGDLVVAIDGVNTDTHLEAQNKIKSASYNLSLTQLQSK

ENH  Q96HC4|2-85 rank 19 score 11.17
SNYSVSLVPGAPWGFLQGGKDFNMLTISRLGTKAAQQAGAVGTVLSIDGIAQQGTMTHLEAQNKIKGCTGSLNMTLQRAS

ENIGMA  Q9NR12|1-85 rank 27 score 10.63
MDSFKVVLGAPWGFLQGGKDFNMLTISRITPGSKAASQSQGDLVVAIDGVNTDTHLEAQNKIKSASYNLSLTQLQSK

PDLIM1  000151|3-85 rank 69 score 10.27
TQQIDLQGPGPWGRQSGKDFNMLTISRLGTKAAQQAGAVGTVLSIDGIAQQGTMTHLEAQNKIKGCTGSLNMTLQRAS

PDLIM4  P50479|1-84 rank 69 score 10.27
MPHSVTLRGPSPWGFRLVGGADYDYPLTVVKVTEGSIADEAGLRVEDIIVRINDTAATPLTHDEAHRLIMSUNVSLQMLIK

ALP  Q53GG5|1-84 rank 56 score 10.43
MQTVILGPAPGWFRQGGKDFNMLTISRLGTKAAQQAGAVGTVLSIDGIAQQGTMTHLEAQNKIKGCTGSLNMTLQRAS

PDLIM2  Q96KY6|1-84 rank 77 score 9.87
MALTVVAGPAPGWFRQGGKDFNMLTISRLGTKAAQQAGAVGTVLSIDGIAQQGTMTHLEAQNKIKGCTGSLNMTLQRAS

Myopodin  Q9UMS6|6-88 rank 175 score 7.66
FICISMTGGAPGWFRQGGKDFNMLTISRLGTKAAQQAGAVGTVLSIDGIAQQGTMTHLEAQNKIKGCTGSLNMTLQRAS

CHAP  Q9H987|6-88 rank 71 score 11.27
EVLVTLSSGAPGWFRQGGKDFNMLTISRLGTKAAQQAGAVGTVLSIDGIAQQGTMTHLEAQNKIKGCTGSLNMTLQRAS

Zasp52  A1ZA47|8-90 rank 13 score 8.14
QIKLSRFDAQPWGFRQGGTDFQPLLQVKONASQAGLQPGDAVKNIDVVMHRLHDKARQDIVVRSGNRFVTQRGG

Zasp67  QV6T49|2-83 rank 22 score 9.33
VLDIHKMCDFNVPWGFRQGGGADYDYPLTVVKTEASDEALRDVITRIQNRATPLTHDEAHRLIMGSVVFYFGVY

Zasp66  Q7KUBS|8-88 rank 37 score 6.91
FAVLLLKDQATPFWIGVRVDNLMKTVGQVPSGAPHELRLRQDGIGEGYDARGYDASHADAQQLFRAGNIEURLVH

LMQ7  Q8WWII|1042-1128 rank 953 score 5.38
RISINQTPKGSLDFGFTKWDIPGIVASVAGSPAEPQLQVDDEIAINNTKSYNSKWEEMAKAQETGHLVMDVRRYKAG