

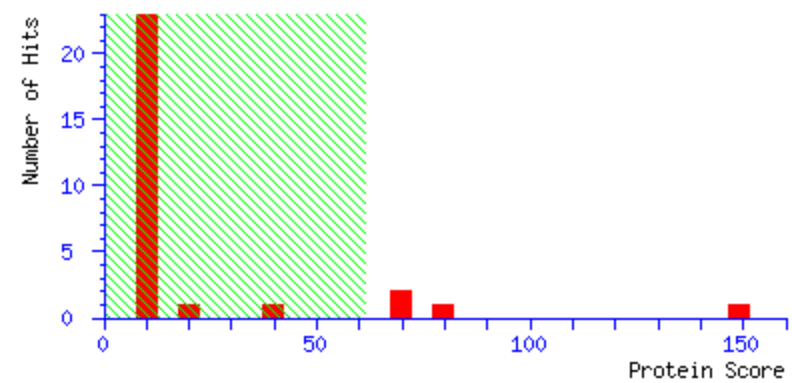
MATRIX SCIENCE Mascot Search Results

User : q
 Email :
 Search title : Bugajev_101118_0_D23_000002.d
 MS data file : D23.mgf
 Database : Uniprot 20210818 (565254 sequences; 203850821 residues)
 Taxonomy : Mammalia (mammals) (67385 sequences)
 Timestamp : 18 Aug 2021 at 14:39:43 GMT
 Top Score : 149 for **Mixture 1**, LOX5_MOUSE + K1C10_HUMAN + K2C1_HUMAN

	Uniprot	Decoy
Protein hits above identity threshold	4	0
Highest scoring protein hit	81	26

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant ($p < 0.05$).



Concise Protein Summary Report

Significance threshold $p <$
 Max. number of hits

1. **Mixture 1** Total score: **149** Expect: $8.5e-011$ Matches: 56
 Components (only one family member shown for each component):

[LOX5_MOUSE](#) Mass: 78602 Score: **81** Expect: 0.00049 Matches: 21
Polyunsaturated fatty acid 5-lipoxygenase OS=Mus musculus OX=10090 GN=Alox5 PE=1 SV=3
[K1C10_HUMAN](#) Mass: 59020 Score: **70** Expect: 0.0061 Matches: 18
Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
[K2C1_HUMAN](#) Mass: 66170 Score: **69** Expect: 0.0089 Matches: 18
Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6

2. [LOX5_MOUSE](#) Mass: 78602 Score: **81** Expect: 0.00049 Matches: 21
Polyunsaturated fatty acid 5-lipoxygenase OS=Mus musculus OX=10090 GN=Alox5 PE=1 SV=3
[LOX5_MESAU](#) Mass: 78565 Score: 44 Expect: 3 Matches: 15
Polyunsaturated fatty acid 5-lipoxygenase OS=Mesocricetus auratus OX=10036 GN=ALOX5 PE=2 SV=2
[LOX5_RAT](#) Mass: 78779 Score: 37 Expect: 12 Matches: 15
Polyunsaturated fatty acid 5-lipoxygenase OS=Rattus norvegicus OX=10116 GN=Alox5 PE=1 SV=3
[LOX5_HUMAN](#) Mass: 78675 Score: 10 Expect: 6.4e+003 Matches: 9
Polyunsaturated fatty acid 5-lipoxygenase OS=Homo sapiens OX=9606 GN=ALOX5 PE=1 SV=2
[LYSC_FELCA](#) Mass: 2369 Score: 9 Expect: 8.2e+003 Matches: 1
Lysozyme C (Fragment) OS=Felis catus OX=9685 GN=LYZ PE=1 SV=1
[PA55H_SHEEP](#) Mass: 2348 Score: 9 Expect: 8.2e+003 Matches: 1
Pregnancy-associated glycoprotein 55h (Fragment) OS=Ovis aries OX=9940 PE=1 SV=1

3. [K1C10_HUMAN](#) Mass: 59020 Score: **70** Expect: 0.0061 Matches: 18
Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
[K1C10_CANLF](#) Mass: 57847 Score: 22 Expect: 4.5e+002 Matches: 11
Keratin, type I cytoskeletal 10 OS=Canis lupus familiaris OX=9615 GN=KRT10 PE=2 SV=1
[THIO_MOUSE](#) Mass: 12010 Score: 10 Expect: 7.1e+003 Matches: 2
Thioredoxin OS=Mus musculus OX=10090 GN=Txn PE=1 SV=3
[THIO_RAT](#) Mass: 12008 Score: 10 Expect: 7.1e+003 Matches: 2
Thioredoxin OS=Rattus norvegicus OX=10116 GN=Txn PE=1 SV=2

4. [K2C1_HUMAN](#) Mass: 66170 Score: **69** Expect: 0.0089 Matches: 18
Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
[K2C1_PANTR](#) Mass: 65621 Score: **62** Expect: 0.04 Matches: 16
Keratin, type II cytoskeletal 1 OS=Pan troglodytes OX=9598 GN=KRT1 PE=2 SV=1
[RL36_RAT](#) Mass: 12317 Score: 10 Expect: 7.1e+003 Matches: 2
60S ribosomal protein L36 OS=Rattus norvegicus OX=10116 GN=Rpl36 PE=1 SV=2
[RL36_HUMAN](#) Mass: 12303 Score: 10 Expect: 7.1e+003 Matches: 2
60S ribosomal protein L36 OS=Homo sapiens OX=9606 GN=RPL36 PE=1 SV=3
[RL36_PONAB](#) Mass: 12303 Score: 10 Expect: 7.1e+003 Matches: 2
60S ribosomal protein L36 OS=Pongo abelii OX=9601 GN=RPL36 PE=3 SV=3
[RL36_BOVIN](#) Mass: 12273 Score: 10 Expect: 7.1e+003 Matches: 2
60S ribosomal protein L36 OS=Bos taurus OX=9913 GN=RPL36 PE=3 SV=3
[COLI_CAMDR](#) Mass: 3436 Score: 9 Expect: 7.6e+003 Matches: 1
Beta-endorphin OS=Camelus dromedarius OX=9838 GN=POMC PE=1 SV=1
[PRR33_MOUSE](#) Mass: 28673 Score: 9 Expect: 8.3e+003 Matches: 3

5. [K1C9_HUMAN](#) Mass: 62255 Score: 36 Expect: 15 Matches: 11
Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3
[PRCD_MOUSE](#) Mass: 5984 Score: 10 Expect: 6.9e+003 Matches: 1
Photoreceptor disk component PRCD OS=Mus musculus OX=10090 GN=Prcd PE=1 SV=1
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Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin/P
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 5 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 2
Number of queries : 117
Selected for scoring : 84

Mascot: <http://www.matrixscience.com/>