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Dairy pastoralism sustained eastern Eurasian steppe populations for 5,000 years

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Supplementary Information

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Supplementary Table 1. References and archaeological site information for archaeological sites presented in Table 1.

Archaeological site	Reference/Information Source
Shatar Chuluu	Novgorodova, E.A. 1989 Drevniaia Mongoliia. Nekotorye problemy khronologii i etnokul'turnoi istorii. Moscow
Khundii Gobi	Excavated by Kovalev and Erdenebaatar, International Central Asian Archaeological Expedition ²²
Yagshiin Huduu	Excavated by Kovalev and Erdenebaatar, International Central Asian Archaeological Expedition ²²
Ulaanzuukh	Excavated by Tumen, Khatanbaatar, and Erdene ³
Uliastai River, Central Terrace	Excavated by D. Erdenebaatar, 2005, Mongolian Archaeological Expedition of Central Asian Mongolia. National University of Mongolia samples records
Berkh Uul	Excavated by Munkhbayar in 2012, north of Berkh Mountain. National University of Mongolia sample records
Shunkhlai Uul	Excavated by Tumen, Navaan, and Volkov in 1979
Khoit Tsenkher	Excavated by D. Navaan, and Lhagvasuren in 1987. Khovd Mankhan. National University of Mongolia sample records
Chandman Uul	Excavated by D. Navaan, National University of Mongolia sample records
Dartsagt	Excavated by M. Erdene, and D. Navaan in 2008, as part of the AA-I expedition in Ulaanbaatar, Khan-Uul District, Songino Khaikhan Mountain
Tamiryn Ulaan Khoshuu	Khatanbaatar, D. (2007). Tamiryn Ulaan Khoshuun dakh' khunnugiin ued kholbogdoh buleg orshuulga. Mongolian Journal of Anthropology, Archaeology, and Ethnology, 3, 156–168
Duulaga Uul	Excavated by D. Navaan in 2004. National University of Mongolia sample records
Uliastain dood denj	Excavate by D. Erdenbaatar, Mongolian Archaeological Expedition of Central Asian Mongolia
Sharga Uul	Excavated in 2006 by Z. Batsaikhan. National University of Mongolia sample records;
Del Khad	Excavated by D. Navaan, M. Erdene, and C. Vanchigdash in 2008. National University of Mongolia sample records
Zaraa Tolgoi	Excavated by D. Navaan in 1980. National University of Mongolia sample records
Banzart Khaikhan	Excavated in 2010 during Umengobi Expedition. National University of Mongolia sample records
Tahiltyn Khotgot	Excavated by the NUM School of Anthropology and Archaeology Summer Practice. National University of Mongolia sample records
Burgaldain Khundii	Excavated by Z. Batsaikhan, and S. Ulzibayar AA course II, 2005. National University of Mongolia sample records;
Ganzagad	Excavated 2010, Umungobi, South Gobi. National University of Mongolia sample records;

Uguumur Tsuvaraa Uul	Excavated by NUM Anthrpology and Archaeology II and III Summer Practice. National University of Mongolia sample records
Khoit Tsenkher, Tarvagatain Am	Excavated by D. Navaan, and Lhagvasuren in 1987. Khovd Mankhan. National University of Mongolia sample records
Kharkhorin	Excavated in 1979, at Kharkhorin, by Ser-Odjab, Bayar, and Tumen. National University of Mongolia sample records
Mori Baridag	Excavated by S. Ulziibayar in 2009 on the Northern Mongolian Expedition.

Supplementary Table 2. Deamidation results for dairy peptides, showing the sample identification, time period of individual, number of overall milk protein peptides, and the percentage milk peptides with deamidated asparagine (N) and glutamine (Q) residues.

Individual	Time Period	Peptide Count	% N Deamidation	%Q Deamidation
AT-628	Early Bronze	18	50.3	24.3
AT-590b	Early Bronze	13	40.8	23.4
AT-26	Early Bronze	2	66.8	No Qs
AT-233	Late Bronze	126	32.9	13.5
AT-835	Mongol	28	48.3	3.3

MS-MARGE

MPI-SHH MAscot Report GEnerator

Version 0.6

General Information

CSV generated from:
20170810_03_57741_sw5_z265.mgf

Input file:AT-56_Z265_F001906.csv

E-value cutoff: 0.01

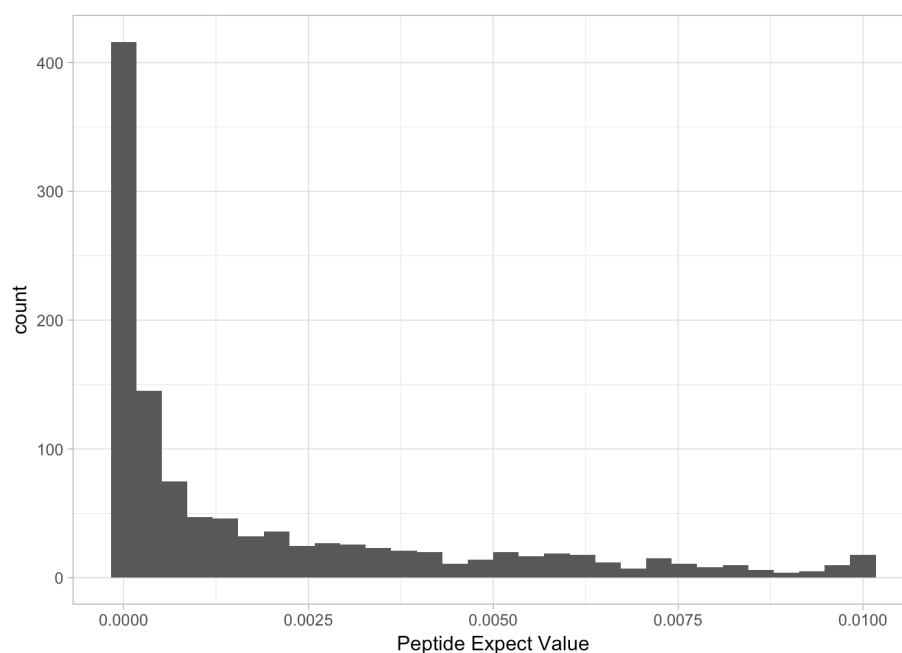
Minimum peptide support: 2

Report generated: 2018-05-04 11:31:50

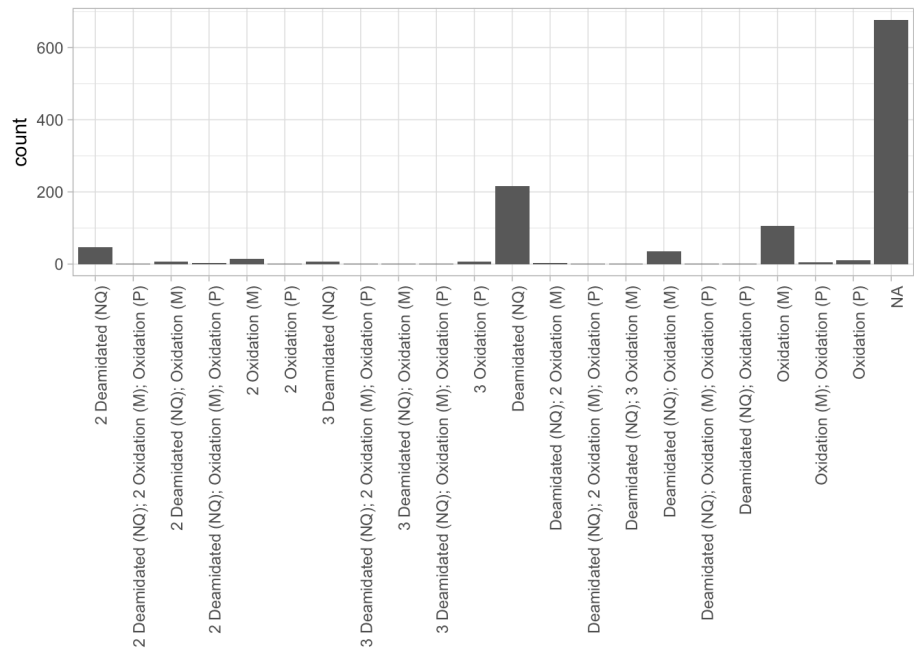
Filtering Summary

	Raw Data	After Unique Query Filter	After E- Value Filter	After Minimum Peptide Support
Peptide	13870	2393	1506	1144
Protein	5972	974	528	166

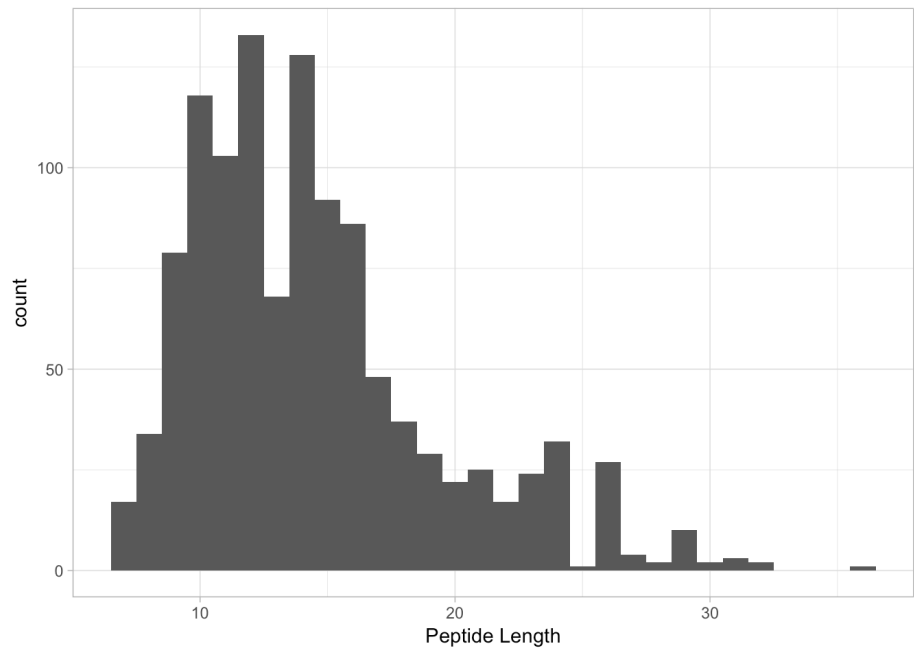
E-value Distribution Below 0.01



Variable Modification Frequency



Peptide Length Distribution



Peptide FDR

Your data contain 6 decoy hits out of 1144 identified peptides, resulting in a peptide FDR of 0.53 percent at an E-value cutoff of 0.01.

Protein FDR

Your data contain 3 decoy protein hits out of 166 identified proteins, resulting in a protein FDR of 1.84 percent at an E-value cutoff of 0.01.

Top Proteins

All unique proteins with at least 2 supporting peptides below E-value of 0.01

Accession	Protein Description	Number of Peptides
2::dd P02754-2 3 Beta-lactoglobulin C OS=Bos taurus	Beta-lactoglobulin C OS=Bos taurus	82
1::sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	61
1::sp P01009 A1AT_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	59
1::sp Q5R5A3 ANT3_PONAB	Antithrombin-III OS=Pongo abelii GN=SERPINC1 PE=2 SV=1	46
1::sp P05164 PERM_HUMAN	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	36
1::sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	25
1::sp Q59906 G3P_STREQ	Glyceraldehyde-3- phosphate dehydrogenase OS=Streptococcus dysgalactiae subsp. equisimilis GN=gap PE=1 SV=2	24
2::dd E7ER44 2 Lactotransferrin OS=Homo sapiens	Lactotransferrin OS=Homo sapiens	24
1::sp A5A6M5 K1H1_PANTR	Keratin, type I cuticular Ha1 OS=Pan troglodytes	23

	GN=KRT31 PE=2 SV=1	
1::sp O43790 KRT86_HUMAN	Keratin, type II cuticular Hb6 OS=Homo sapiens GN=KRT86 PE=1 SV=1	23
1::sp P01011 AACT_HUMAN	Alpha-1- antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2	23
1::sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	21
1::sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	21
1::sp P01024 CO3_HUMAN	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	19
1::sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	17
1::sp B1IBR3 ENO_STRPI	Enolase OS=Streptococcus pneumoniae (strain Hungary19A-6) GN=eno PE=3 SV=1	15
1::sp Q9N655 G3P_MASBA	Glyceraldehyde-3- phosphate dehydrogenase OS=Mastigamoeba balamuthi GN=GAPD PE=2 SV=1	15
2::dd P02756 3 Beta- lactoglobulin OS=Capra hircus	Beta-lactoglobulin OS=Capra hircus	15
1::sp P20160 CAP7_HUMAN	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3	14
1::sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	13

1::sp B0RH60 ENO_CLAMS	Enolase OS=Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) GN=eno PE=3 SV=1	12
1::sp P01834 IGKC_HUMAN	Immunoglobulin kappa constant OS=Homo sapiens GN=IGKC PE=1 SV=2	12
1::sp P30740 ILEU_HUMAN	Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	12
1::sp P67975 LACB_OVIMU	Beta-lactoglobulin OS=Ovis aries musimon GN=LGB PE=1 SV=1	12
1::sp Q6P5S2 LEG1H_HUMAN	Protein LEG1 homolog OS=Homo sapiens GN=LEG1 PE=1 SV=2	12
1::sp P12273 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	11
1::sp A4QHB7 CH602_CORGB	60 kDa chaperonin 2 OS=Corynebacterium glutamicum (strain R) GN=groL2 PE=3 SV=1	10
1::sp P01876 IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 OS=Homo sapiens GN=IGHA1 PE=1 SV=2	10
1::sp P08311 CATG_HUMAN	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	10
1::sp P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	10
1::sp P72197 KGP66_PORGN	Lys-gingipain HG66 OS=Porphyromonas gingivalis GN=kgp PE=1	10

SV=1

1::sp P78386 KRT85_HUMAN	Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	10
1::sp O75594 PGRP1_HUMAN	Peptidoglycan recognition protein 1 OS=Homo sapiens GN=PGLYRP1 PE=1 SV=1	9
1::sp P02452 CO1A1_HUMAN	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	9
2::dd P02758 3 Beta- Lactoglobulin I OS=Equus caballus	Beta-Lactoglobulin I OS=Equus caballus	9
1::sp A5N2N5 ENO_CLOK5	Enolase OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=eno PE=3 SV=1	8
1::sp P0A4S1 ALF_STRPN	Fructose-bisphosphate aldolase OS=Streptococcus pneumoniae serotype 4 (strain ATCC BAA-334 / TIGR4) GN=fba PE=3 SV=1	8
1::sp Q9Z4I3 MSPA_TREMA	Major outer membrane protein MspA OS=Treponema maltophilum GN=mspA PE=1 SV=1	8
1::sp P08123 CO1A2_HUMAN	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	7
1::sp P0C0G6 G3P_STRPY	Glyceraldehyde-3- phosphate dehydrogenase OS=Streptococcus pyogenes GN=gap PE=1 SV=2	7
1::sp P0DOX5 IGG1_HUMAN	Immunoglobulin gamma- 1 heavy chain OS=Homo	7

	sapiens PE=1 SV=1	
1::sp P61626 LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	7
1::sp A2SLF9 EFTU_METPP	Elongation factor Tu OS=Methylibium petroleiphilum (strain ATCC BAA-1232 / LMG 22953 / PM1) GN=tuf1 PE=3 SV=1	6
1::sp B8D851 EFTU_BUCAT	Elongation factor Tu OS=Buchnera aphidicola subsp. Acyrthosiphon pisum (strain Tuc7) GN=tuf PE=3 SV=1	6
1::sp P00450 CERU_HUMAN	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	6
1::sp Q8CJV9 CLPB_STRCO	Chaperone protein ClpB OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) GN=clpB PE=3 SV=1	6
1::sp A8AXG8 RL7_STRGC	50S ribosomal protein L7/L12 OS=Streptococcus gordonii (strain Challis / ATCC 35105 / BCRC 15272 / CH1 / DL1 / V288) GN=rpIL PE=3 SV=1	5
1::sp A9BDH2 ENO_PROM4	Enolase OS=Prochlorococcus marinus (strain MIT 9211) GN=eno PE=3 SV=1	5
1::sp O76011 KRT34_HUMAN	Keratin, type I cuticular Ha4 OS=Homo sapiens GN=KRT34 PE=1 SV=2	5
1::sp P04745 AMY1_HUMAN	Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2	5
1::sp P05155 IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo	5

	sapiens GN=SERPING1 PE=1 SV=2	
1::sp P08246 ELNE_HUMAN	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	5
1::sp P0C940 FIMA1_PORGN	Major fimbrium subunit FimA type-1 OS=Porphyromonas gingivalis GN=fimA PE=1 SV=2	5
1::sp Q9NP70 AMBN_HUMAN	Ameloblastin OS=Homo sapiens GN=AMBN PE=1 SV=1	5
1::sp A0QS66 RPOC_MYCS2	DNA-directed RNA polymerase subunit beta~ OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=rpoC PE=1 SV=1	4
1::sp A9FA52 ENO_SORC5	Enolase OS=Sorangium cellulosum (strain So ce56) GN=eno PE=3 SV=1	4
1::sp B0R755 VATA_HALS3	V-type ATP synthase alpha chain OS=Halobacterium salinarum (strain ATCC 29341 / DSM 671 / R1) GN=atpA PE=3 SV=1	4
1::sp B4U3U1 EFTU_STREM	Elongation factor Tu OS=Streptococcus equi subsp. zooepidemicus (strain MGCS10565) GN=tuf PE=3 SV=1	4
1::sp C0MBK6 OTC_STRE4	Ornithine carbamoyltransferase OS=Streptococcus equi subsp. equi (strain 4047) GN=arcB PE=3 SV=1	4
1::sp P01023 A2MG_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	4

1::sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	4
1::sp P02743 SAMP_HUMAN	Serum amyloid P- component OS=Homo sapiens GN=APCS PE=1 SV=2	4
1::sp P04083 ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	4
1::sp P0DOA1 MFA1_PORGN	Minor fimbrium subunit Mfa1 OS=Porphyromonas gingivalis GN=mfa1 PE=1 SV=1	4
1::sp P29508 SPB3_HUMAN	Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	4
1::sp P31025 LCN1_HUMAN	Lipocalin-1 OS=Homo sapiens GN=LCN1 PE=1 SV=1	4
1::sp P32320 CDD_HUMAN	Cytidine deaminase OS=Homo sapiens GN=CDA PE=1 SV=2	4
1::sp Q00752 MSMK_STRMU	Multiple sugar-binding transport ATP-binding protein MsmK OS=Streptococcus mutans serotype c (strain ATCC 700610 / UA159) GN=msmK PE=3 SV=1	4
1::sp Q14525 KT33B_HUMAN	Keratin, type I cuticular Ha3-II OS=Homo sapiens GN=KRT33B PE=1 SV=3	4
1::sp Q4JU51 ENO_CORJK	Enolase OS=Corynebacterium jeikeium (strain K411) GN=eno PE=3 SV=1	4
1::sp Q5G863 DEF1_PANTR	Neutrophil defensin 1 OS=Pan troglodytes GN=DEFA1 PE=3 SV=1	4

1::sp Q5R1W6 TKT_PANTR	Transketolase OS=Pan troglodytes GN=TKT PE=2 SV=1	4
1::sp Q6NI61 ENO_CORDI	Enolase OS=Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis) GN=eno PE=3 SV=1	4
1::sp Q83NN0 CH60_TROW8	60 kDa chaperonin OS=Tropheryma whipplei (strain TW08/27) GN=groL PE=3 SV=1	4
1::sp Q96DA0 ZG16B_HUMAN	Zymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3	4
1::sp Q9KWX0 FLAB2_TREMA	Flagellar filament 31.3 kDa core protein OS=Treponema maltophilum GN=flaB2 PE=1 SV=1	4
2::dd A0A0P0EVY5 2 Alpha S1 casein (Fragment) OS=Capra hircus	Alpha S1 casein (Fragment) OS=Capra hircus	4
1::sp A0QYY6 RS1_MYCS2	30S ribosomal protein S1 OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=rpsA PE=1 SV=1	3
1::sp A1A3P5 DNAK_BIFAA	Chaperone protein DnaK OS=Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) GN=dnaK PE=3 SV=1	3
1::sp A3CLW6 ARCA_STRSV	Arginine deiminase OS=Streptococcus sanguinis (strain SK36) GN=arcA PE=3 SV=1	3
1::sp A3CPH0 LACG_STRSV	6-phospho-beta- galactosidase	3

	OS=Streptococcus sanguinis (strain SK36) GN=lacG PE=3 SV=1	
1::sp A6LE88 EFTU_PARD8	Elongation factor Tu OS=Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / CIP 104284 / JCM 5825 / NCTC 11152) GN=tuf PE=3 SV=1	3
1::sp B0RB25 RPOB_CLAMS	DNA-directed RNA polymerase subunit beta OS=Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) GN=rpoB PE=3 SV=1	3
1::sp B2RM93 CPG1_PORG3	Gingipain R1 OS=Porphyromonas gingivalis (strain ATCC 33277 / DSM 20709 / CIP 103683 / JCM 12257 / NCTC 11834 / 2561) GN=rgpA PE=3 SV=1	3
1::sp C5BV35 PGK_BEUC1	Phosphoglycerate kinase OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432) GN=pgk PE=3 SV=1	3
1::sp C5CC72 RL7_MICLC	50S ribosomal protein L7/L12 OS=Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) GN=rplL PE=3 SV=1	3
1::sp P02763 A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	3
1::sp P02766 TTHY_HUMAN	Transthyretin OS=Homo	3

	sapiens GN=TTR PE=1 SV=1	
1::sp P04259 K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	3
1::sp P06870 KLK1_HUMAN	Kallikrein-1 OS=Homo sapiens GN=KLK1 PE=1 SV=2	3
1::sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	3
1::sp P0DJG0 APOA1_PANTR	Apolipoprotein A-I OS=Pan troglodytes GN=APOA1 PE=1 SV=1	3
1::sp P12724 ECP_HUMAN	Eosinophil cationic protein OS=Homo sapiens GN=RNASE3 PE=1 SV=2	3
1::sp P17213 BPI_HUMAN	Bactericidal permeability-increasing protein OS=Homo sapiens GN=BPI PE=1 SV=4	3
1::sp P59915 HAGA1_PORGI	Hemagglutinin A OS=Porphyromonas gingivalis (strain ATCC BAA-308 / W83) GN=hagA PE=1 SV=1	3
1::sp P80311 PPIB_BOVIN	Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	3
1::sp Q4JSW4 GPMA_CORJK	2,3- bisphosphoglycerate- dependent phosphoglycerate mutase OS=Corynebacterium jeikeium (strain K411) GN=gpmA PE=3 SV=1	3
1::sp Q5RAB4 G3P_PONAB	Glyceraldehyde-3-	3

	phosphate dehydrogenase OS=Pongo abelii GN=GAPDH PE=2 SV=3	
1::sp Q9UGM3 DMBT1_HUMAN	Deleted in malignant brain tumors 1 protein OS=Homo sapiens GN=DMBT1 PE=1 SV=2	3
2::dd A5JSS8 2 Alpha- lactalbumin OS=Capra hircus	Alpha-lactalbumin OS=Capra hircus	3
2::dd P07380 3 Beta- Lactoglobulin II OS=Equus caballus	Beta-Lactoglobulin II OS=Equus caballus	3
1::rr REV_P21249 ANT1_ONCVO	Major antigen OS=Onchocerca volvulus GN=OVT1 PE=2 SV=2	2
1::rr REV_Q4WZ65 EASM_ASPFU	Cytochrome P450 monooxygenase easM OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=easM PE=1 SV=1	2
1::rr REV_Q5N2S8 RSMA_SYNP6	Ribosomal RNA small subunit methyltransferase A OS=Synechococcus sp. (strain ATCC 27144 / PCC 6301 / SAUG 1402/1) GN=rsmA PE=3 SV=1	2
1::sp A0JX91 RS4_ARTS2	30S ribosomal protein S4 OS=Arthrobacter sp. (strain FB24) GN=rpsD PE=3 SV=1	2
1::sp A0JZ53 IF1_ARTS2	Translation initiation factor IF-1 OS=Arthrobacter sp. (strain FB24) GN=infA PE=3 SV=1	2
1::sp A0LVY3 GLGC_ACIC1	Glucose-1-phosphate adenylyltransferase	2

	OS=Acidothermus cellulolyticus (strain ATCC 43068 / 11B) GN=glgC PE=3 SV=1	
1::sp A0PUI6 GLGB_MYCUA	1,4-alpha-glucan branching enzyme GlgB OS=Mycobacterium ulcerans (strain Agy99) GN=glgB PE=3 SV=1	2
1::sp A0R8J9 RL15_BACAH	50S ribosomal protein L15 OS=Bacillus thuringiensis (strain Al Hakam) GN=rplO PE=3 SV=1	2
1::sp A0RJP7 RS4_BACAH	30S ribosomal protein S4 OS=Bacillus thuringiensis (strain Al Hakam) GN=rpsD PE=3 SV=1	2
1::sp A1A095 RPOA_BIFAA	DNA-directed RNA polymerase subunit alpha OS=Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) GN=rpoA PE=3 SV=2	2
1::sp A1SMD1 NDK_NOCSJ	Nucleoside diphosphate kinase OS=Nocardioides sp. (strain ATCC BAA- 499 / JS614) GN=ndk PE=3 SV=1	2
1::sp A1V4V8 G6PI_BURMS	Glucose-6-phosphate isomerase OS=Burkholderia mallei (strain SAVP1) GN=pgi PE=3 SV=1	2
1::sp A3CKQ4 PGK_STRSV	Phosphoglycerate kinase OS=Streptococcus sanguinis (strain SK36) GN=pgk PE=3 SV=1	2
1::sp A3CMA7 ENO_STRSV	Enolase OS=Streptococcus	2

	sanguinis (strain SK36) GN=eno PE=3 SV=1	
1::sp A5JUY8 PERL_BUBBU	Lactoperoxidase OS=Bubalus bubalis GN=LPO PE=1 SV=1	2
1::sp A6W815 PNP_KINRD	Polyribonucleotide nucleotidyltransferase OS=Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216) GN=pnp PE=3 SV=1	2
1::sp A9AVV4 ATPB_HERA2	ATP synthase subunit beta OS=Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785) GN=atpD PE=3 SV=1	2
1::sp B0K6X6 ENO_THEPX	Enolase OS=Thermoanaerobacter sp. (strain X514) GN=eno PE=3 SV=1	2
1::sp B0V6R7 MDH_ACIBY	Malate dehydrogenase OS=Acinetobacter baumannii (strain AYE) GN=mdh PE=3 SV=1	2
1::sp B1I9A0 ACKA_STRPI	Acetate kinase OS=Streptococcus pneumoniae (strain Hungary19A-6) GN=ackA PE=3 SV=1	2
1::sp B1IBQ8 GLGC_STRPI	Glucose-1-phosphate adenylyltransferase OS=Streptococcus pneumoniae (strain Hungary19A-6) GN=glgC PE=3 SV=1	2
1::sp B1ID02 CODY_STRPI	GTP-sensing transcriptional pleiotropic repressor CodY OS=Streptococcus pneumoniae (strain Hungary19A-6) GN=codY PE=3 SV=1	2

1::sp B2RL46 RL7_PORG3	50S ribosomal protein L7/L12 OS=Porphyromonas gingivalis (strain ATCC 33277 / DSM 20709 / CIP 103683 / JCM 12257 / NCTC 11834 / 2561) GN=rpIL PE=3 SV=1	2
1::sp B3WCW7 ENO_LACCB	Enolase OS=Lactobacillus casei (strain BL23) GN=eno PE=3 SV=1	2
1::sp C0M8Q6 LACA_STRE4	Galactose-6-phosphate isomerase subunit LacA OS=Streptococcus equi subsp. equi (strain 4047) GN=lacA PE=3 SV=1	2
1::sp C0M937 EFG_STRE4	Elongation factor G OS=Streptococcus equi subsp. equi (strain 4047) GN=fusA PE=3 SV=1	2
1::sp C5BZX2 CH10_BEUC1	10 kDa chaperonin OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432) GN=groS PE=3 SV=1	2
1::sp C5C093 ENO_BEUC1	Enolase OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432) GN=eno PE=3 SV=1	2
1::sp E1QWZ1 LEU1_OLSUV	2-isopropylmalate synthase OS=Olsenella uli (strain ATCC 49627 / DSM 7084 / CIP 109912 / JCM 12494 / NCIMB 702895 / VPI D76D-27C) GN=leuA PE=3 SV=1	2
1::sp P00362 G3P_GEOSE	Glyceraldehyde-3- phosphate dehydrogenase OS=Geobacillus stearothermophilus	2

	GN=gap PE=1 SV=5	
1::sp P01591 IGJ_HUMAN	Immunoglobulin J chain OS=Homo sapiens GN=JCHAIN PE=1 SV=4	2
1::sp P09373 PFLB_ECOLI	Formate acetyltransferase 1 OS=Escherichia coli (strain K12) GN=pflB PE=1 SV=2	2
1::sp P0C0L4 CO4A_HUMAN	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	2
1::sp P0DMV8 HS71A_HUMAN	Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1	2
1::sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	2
1::sp P14639 ALBU_SHEEP	Serum albumin OS=Ovis aries GN=ALB PE=1 SV=1	2
1::sp P23528 COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	2
1::sp P24158 PRTN3_HUMAN	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3	2
1::sp P30692 OMP_B_NEISI	Major outer membrane protein P.IB OS=Neisseria sicca GN=por PE=3 SV=1	2
1::sp P55464 RMLA_SINFN	Probable glucose-1- phosphate thymidyltransferase OS=Sinorhizobium fredii (strain NBRC 101917 / NGR234) GN=rmlA PE=3 SV=1	2
1::sp P78385 KRT83_HUMAN	Keratin, type II cuticular Hb3 OS=Homo sapiens	2

1::sp P80188 NGAL_HUMAN	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2	2
1::sp P9WFP6 Y1461_MYCTO	UPF0051 protein MT1508 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=MT1508 PE=3 SV=1	2
1::sp Q07936 ANXA2_RAT	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1 SV=2	2
1::sp Q0PGG4 ACTB_BOSMU	Actin, cytoplasmic 1 OS=Bos mutus grunniens GN=ACTB PE=2 SV=1	2
1::sp Q0RRT2 RL7_FRAAA	50S ribosomal protein L7/L12 OS=Frankia alni (strain ACN14a) GN=rpIL PE=3 SV=1	2
1::sp Q0VCX2 GRP78_BOVIN	78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	2
1::sp Q18CE4 EFTU_PEPD6	Elongation factor Tu OS=Peptoclostridium difficile (strain 630) GN=tuf1 PE=3 SV=1	2
1::sp Q1D2S1 CH602_MYXXD	60 kDa chaperonin 2 OS=Myxococcus xanthus (strain DK 1622) GN=groL2 PE=3 SV=1	2
1::sp Q2RIS7 HPPA1_MOOTA	Putative K(+)-stimulated pyrophosphate-energized sodium pump OS=Moorella thermoacetica (strain ATCC 39073 / JCM 9320) GN=hppA1 PE=1 SV=1	2
1::sp Q56336 CFPA_TREPA	Cytoplasmic filament	2

	protein A OS= <i>Treponema pallidum</i> (strain Nichols) GN=cfpA PE=1 SV=3	
1::sp Q5E946 PARK7_BOVIN	Protein/nucleic acid deglycase DJ-1 OS= <i>Bos taurus</i> GN=PARK7 PE=2 SV=1	2
1::sp Q6A5X5 G6PI_PROAC	Glucose-6-phosphate isomerase OS= <i>Propionibacterium acnes</i> (strain KPA171202 / DSM 16379) GN=pgi PE=3 SV=1	2
1::sp Q6NJD5 EFTU_CORDI	Elongation factor Tu OS= <i>Corynebacterium diphtheriae</i> (strain ATCC 700971 / NCTC 13129 / Biotype gravis) GN=tuf PE=3 SV=1	2
1::sp Q8CWR9 RS1_STRR6	30S Ribosomal protein S1 OS= <i>Streptococcus pneumoniae</i> (strain ATCC BAA-255 / R6) GN=rpsA PE=1 SV=1	2
1::sp Q8E4R6 LACB1_STRA3	Galactose-6-phosphate isomerase subunit LacB 1 OS= <i>Streptococcus agalactiae</i> serotype III (strain NEM316) GN=lacB1 PE=3 SV=1	2
1::sp Q8E4R8 LACD2_STRA3	Tagatose 1,6- diphosphate aldolase 2 OS= <i>Streptococcus agalactiae</i> serotype III (strain NEM316) GN=lacD2 PE=3 SV=1	2
1::sp Q8IUC1 KR111_HUMAN	Keratin-associated protein 11-1 OS= <i>Homo sapiens</i> GN=KRTAP11-1 PE=1 SV=1	2
1::sp Q8R603 EFTU_FUSNN	Elongation factor Tu OS= <i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> (strain ATCC	2

25586 / CIP 101130 /
JCM 8532 / LMG 13131)
GN=tuf PE=3 SV=1

1::sp Q96BY7 ATG2B_HUMAN	Autophagy-related protein 2 homolog B OS=Homo sapiens GN=ATG2B PE=1 SV=5	2
1::sp Q9CE36 ACKA2_LACLA	Acetate kinase 2 OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=ackA2 PE=3 SV=1	2
1::sp Q9DBR4 APBB2_MOUSE	Amyloid-beta A4 precursor protein- binding family B member 2 OS=Mus musculus GN=Apbb2 PE=1 SV=2	2
1::sp Q9HD89 RETN_HUMAN	Resistin OS=Homo sapiens GN=RETN PE=1 SV=1	2
1::sp Q9R4G7 GRDE_PEPAC	Glycine reductase complex component B subunits alpha and beta OS=Peptoclostridium acidaminophilum GN=grdE PE=1 SV=2	2
1::sp Q9SF15 PUB24_ARATH	E3 ubiquitin-protein ligase PUB24 OS=Arabidopsis thaliana GN=PUB24 PE=1 SV=1	2