

**Sexual selection and proteinaceous diversity in the femoral gland secretions  
of lacertid lizards**

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Sacchi

SUPPLEMENTARY MATERIAL

## Methods M1. Protocol details for mass spectrometry (MS) analysis

For the mass spectrometry analysis, we used a total of six samples of femoral gland secretions coming from six different males from the two species (*Acanthodactylus scutellatus*, *Gallotia stehlini*) showing the highest protein expression in the five molecular regions associated with male-biased SSD. Samples were chosen among those still available from the original collection used in previous works by two of the co-authors (SB and JM) and correctly preserved in freezer (-20 °C) till the time of current analysis. Details about sample size, localities, and collection year are synthesized below.

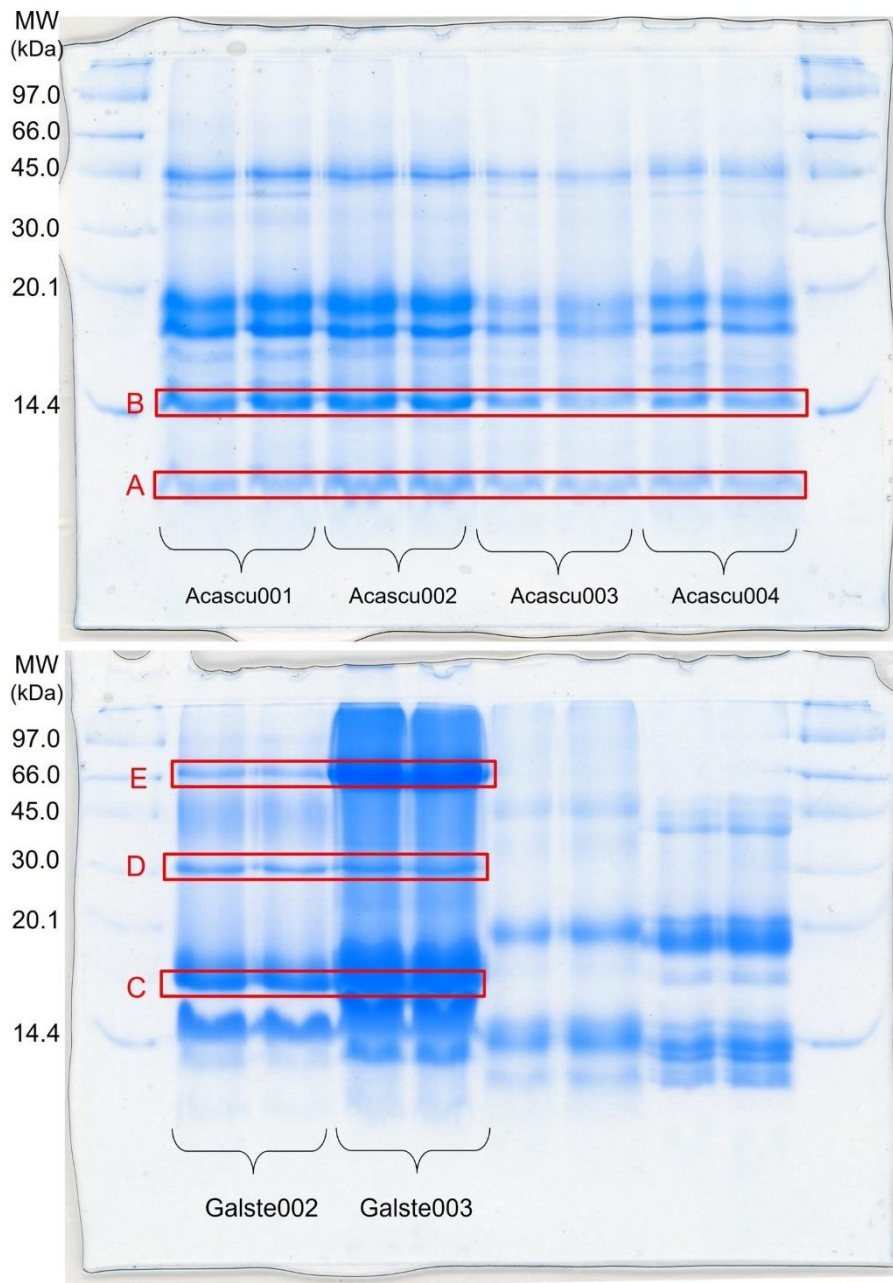
Species	Samples size	Labels	Year	Locality
<i>Acanthodactylus scutellatus</i>	4	Acascu001	2014	Israel 32°N; 34.79°E
		Acascu002		
		Acascu003		
		Acascu004		
<i>Gallotia stehlini</i>	2	Galste002	2013	Gran Canaria (Canary Islands) 27.74°N; 15.6°W
		Galste003		

From the fresh gels, we excised the bands of the regions of interest (Fig. S1), and individually prepared them for mass spectrometry analysis following [1]. Briefly, we completely de-stained the gel pieces by washing twice with 200 µL of 100 mM ammonium bicarbonate buffer pH 7.8, 50 % acetonitrile (ACN) and keeping under stirring overnight; we dehydrated the samples with 100 µL ACN; we performed reduction of the samples by adding 100 µL of 10 mM Dithiothreitol (DTT) solution (30 min at 37°C), replaced with 100 µL of 55 mM iodoacetamide for 45 min at 60°C; we washed the gel pieces twice with 200 µL of 100 mM ammonium bicarbonate for 10 min; we dehydrated by addition of 100 µL of ACN; we removed ACN and dried samples under vacuum; we performed protein digestion overnight at 37 °C by adding 100 µL of 100 mM ammonium bicarbonate buffer pH 7.8, containing 20 ng/µL sequencing grade trypsin (Promega, Madison, WI, USA); we extracted the obtained peptides by adding twice 100 µL of 50 % ACN in water, 5 % formic acid (FA), and pooling the supernatant from each step after stirring and centrifuging; we dried each pool and stored at -20°C until mass spectrometry analysis. Before mass spectrometry, peptide mixtures were solubilized in 100µL of 0.1% FA. Before mass spectrometry, peptide mixtures were solubilized in 100µL of 0.1% FA.

Mass spectrometry (MS) analyses were carried out with a LC unit (ExionLCTM AD) equipped with a column oven thermostated at 40°C, an autosampler cooled at 10 °C and a

binary gradient pump system. MS instrument consists of a high resolution QTOF mass spectrometer (AB Sciex X500B) equipped with a Turbo V Ion source and a Twin Sprayer ESI (electrospray ionization) probe, controlled by SCIEX OS 2.1 software. Peptides were separated by reverse phase (RP) HPLC on a Hypersil Gold (Thermo Fisher Scientific, USA) C18 column ( $150 \times 2.1$  mm, 3  $\mu$ m particle size, 175 Å pore size) using a linear gradient (2-50 % solvent B in 15 min) in which solvent A consisted of 0.1 % aqueous FA and solvent B of ACN containing 0.1% FA. Flow rate was 0.2 mL/min. Mass spectra were generated in positive polarity under constant instrumental conditions: ion spray voltage 4500 V, declustering potential 100 V, curtain gas 30 psi, ion source gas 1 40 psi, ion source gas 2 45 psi, temperature 350 °C, collision energy 10 V. Spectra were acquired with SCIEX OS 2.1 software.

**Fig. S1.** SDS-PAGE of the samples used to excise the bands associated with the SSD increase and analyzed by mass spectrometry (MS). *Top panel:* gel of the four samples of *Acanthodactylus scutellatus* (each run twice to ensure having enough protein concentration for MS) used for bands A and B highlighted in Fig. 3); *bottom panel:* gel of the two samples of *Gallotia stehlini* (each run twice) used for bands C, D, and E.



**Table S1.** Morphometrics measures used for the computation of the sexual dimorphism indexes: sexual size dimorphism (SSD) based on snout-to-vent length (SVL); sexual head dimorphism (SHD) based on the ratio between head length (HL) and SVL. See methods for computational details. Literature source of the data are reported in the last column.

Species	SVL <sub>♂</sub>	HL <sub>♂</sub>	N <sub>♂</sub>	SVL <sub>♀</sub>	HL <sub>♀</sub>	N <sub>♀</sub>	SSD	SHD	Location	Reference
<i>Acanthodactylus opheodurus</i>	53.33	12.97	12	50.48	11.98	10	1.056	1.033	Jordania, Saudi Arabia	[2]
<i>Acanthodactylus boskianus</i>	65.36	16.86	61	61.26	15.31	37	1.067	1.043	Tunisia	[3]
<i>Acanthodactylus schreiberi</i>	73.00	19.12	25	65.03	16.60	36	1.123	1.035	Cyprus	[4]
<i>Acanthodactylus scutellatus</i>	58.32	14.66	13	54.47	13.49	11	1.071	1.020	Egypt	[2]
<i>Acanthodactylus beershebensis</i>	66.26	16.25	130	63.80	14.59	137	1.039	1.096	Israel	[5]
<i>Mesalina olivieri</i>	42.07	10.05	18	41.46	9.46	17	1.015	1.062	Algeria, Egypt, Mauretania	[2]
<i>Mesalina guttulata</i>	43.70	10.53	10	44.60	10.12	5	0.979	1.075	Egypt	[6]
<i>Holaspis guentheri</i>	45.93	11.75	6	46.46	12.22	6	0.988	0.962	Tanzania	[2]
<i>Podarcis gaigeae</i>	59.06	14.88	251	53.71	12.20	227	1.100	1.146	Skyros	[7]
<i>Podarcis milensis</i>	56.11	13.36	137	49.78	10.83	239	1.127	1.124	Greece	[8]
<i>Podarcis melisellensis</i>	60.90	14.90	25	51.30	11.50	13	1.187	1.121	Croatia	[9]
<i>Podarcis erhardii</i>	58.97	14.63	36	56.81	12.62	30	1.038	1.155	mainland Greece	[10]
<i>Podarcis peloponnesiacus</i>	70.60	17.32	12	71.50	15.05	11	0.987	1.180	Greece	[10]
<i>Podarcis muralis</i>	57.23	20.52	39	57.10	17.69	42	1.002	1.245	Spain	[11]
<i>Podarcis liolepis</i>	47.75	19.81	47	46.42	16.61	48	1.029	1.272	Spain	[12]
<i>Podarcis vaucheri</i>	44.57	18.93	330	44.39	16.23	310	1.004	1.281	Morocco, Spain	[12]
<i>Podarcis bocagei</i>	55.30	20.25	41	53.51	17.08	47	1.033	1.232	Spain	[11]
<i>Podarcis gadarramae</i>	51.29	17.38	33	50.12	14.79	30	1.023	1.224	Spain	[13]
<i>Podarcis carbonelli</i>	42.10	17.94	180	41.29	15.31	147	1.020	1.260	Portugal	[12]
<i>Zootoca vivipara</i>	47.91	15.75	18	53.64	15.10	34	0.880	1.120	Spain	[11]
<i>Algyroides moreoticus</i>	50.70	12.71	6	46.24	10.34	7	1.096	1.161	Greece	[2]
<i>Algyroides nigropunctatus</i>	63.24	16.64	12	56.16	13.54	9	1.126	1.124	Croatia, Greece, Italy	[2]
<i>Dalmatolacerta oxycephala</i>	58.40	15.10	34	52.90	13.20	13	1.103	1.049	Croatia	[9]
<i>Phoenicolacerta kulzeri</i>	55.44	13.43	12	54.69	12.23	13	1.014	1.110	Syria	[2]
<i>Iberolacerta galani</i>	60.78	14.92	24	64.19	13.52	26	0.944	1.180	Spain	[14]
<i>Iberolacerta monticola</i>	63.12	15.46	14	63.19	13.41	18	0.999	1.170	Spain	[2]
<i>Iberolacerta cyreni</i>	63.48	15.04	49	65.29	13.58	79	0.971	1.154	Spain	[15]
<i>Iberolacerta bonnali</i>	52.01	11.96	67	54.61	11.69	80	0.950	1.088	Spain	[16]
<i>Lacerta media</i>	107.72	23.69	17	95.61	20.36	14	1.127	1.042	Armenia, Turkey	[2]

<i>Lacerta bilineata</i>	104.75	25.24	15	100.63	21.94	21	1.041	1.139	France, Italy, Spain	[2]
<i>Lacerta viridis</i>	107.15	37.55	14	108.54	33.10	13	0.987	1.187	Spain	[11]
<i>Lacerta schreiberi</i>	102.31	36.66	15	101.90	32.33	24	1.004	1.202	Spain	[11]
<i>Psammodromus algirus</i>	63.38	14.75	32	61.15	13.33	30	1.036	1.088	Spain	[17]
<i>Gallotia stehlini</i>	189.10	48.20	16	156.80	35.60	25	1.206	1.165	Canary Islands	[18]
<i>Gallotia galloti</i>	109.65	28.18	56	93.33	22.13	83	1.175	1.113	Canary Islands	[19]
<i>Gallotia simonyi</i>	236.50	56.80	11	196.10	42.60	14	1.206	1.139	Canary Islands	[18]

## References

1. Mangiacotti, M.; Fumagalli, M.; Cagnone, M.; Viglio, S.; Bardoni, A.M.; Scali, S.; Sacchi, R. Morph-Specific Protein Patterns in the Femoral Gland Secretions of a Colour Polymorphic Lizard. *Scientific Reports* **2019**, *9*, 8412, doi:10.1038/s41598-019-44889-7.
2. Baeckens, S.; Martín, J.; García-Roa, R.; Van Damme, R. Sexual Selection and the Chemical Signal Design of Lacertid Lizards. *Zoological Journal of the Linnean Society* **2018**, *183*, 445–457, doi:10.1093/zoolinnean/zlx075.
3. Nasri, I.; Hammouda, A.; Hamza, F.; Selmi, S. Sexual Size Dimorphism in a Tunisian Population of Bosk's Fringe-Toed Lizards *Acanthodactylus Boskianus Asper*. *African Journal of Herpetology* **2015**, *64*, 103–115, doi:10.1080/21564574.2015.1103786.
4. Yalçinkaya, D.; Göçmen, B. A New Subspecies from Anatolia, *Acanthodactylus Schreiberi* Boulenger, 1879 *Ataturi* n. Ssp. (Squamata: Lacertidae). *Biharean Biologist* **2012**, *6*, 19–31.
5. Moravec, J.; El Din, S.B.; Seligmann, H.; Sivan, N.; Werner, Y.L. Systematics and Distribution of the *Acanthodactylus Pardalis* Group (Lacertidae) in Egypt and Israel. *Zoology in the Middle East* **1999**, *17*, 21–50, doi:10.1080/09397140.1999.10637767.
6. Werner, Y.L.; Ashkenazi, S. Notes on Some Egyptian Lacertidae, Including a New Subspecies of *Mesalina*, Involving the Seligmann Effect. *Turkish Journal of Zoology* **2010**, *34*, 123–133, doi:10.3906/zoo-0905-8.
7. Runemark, A.; Sagonas, K.; Svensson, E.I. Ecological Explanations to Island Gigantism: Dietary Niche Divergence, Predation, and Size in an Endemic Lizard. *Ecology* **2015**, *96*, 2077–2092, doi:10.1890/14-1996.1.
8. Adamopoulou, C. Structure and Function of Epigeic Animal Communities with Emphasis in the Lizard *Podarcis Milensis* (Sauria: Lacertidae), in Insular Ecosystems of the Aegean. unpublished PhD dissertation, University of Athens, 1999.
9. Verwajen, D.; Van Damme, R.; Herrel, A. Relationships between Head Size, Bite Force, Prey Handling Efficiency and Diet in Two Sympatric Lacertid Lizards. *Functional Ecology* **2002**, *16*, 842–850, doi:10.1046/j.1365-2435.2002.00696.x.

10. Lymberakis, P.; Poulakakis, N.; Kaliontzopoulou, A.; Valakos, E.; Mylonas, M. Two New Species of *Podarcis* (Squamata: Lacertidae) from Greece. *Systematics and Biodiversity* **2008**, *6*, 307–318, doi:10.1017/S1477200008002727.
11. Braña, F. Sexual Dimorphism in Lacertid Lizards: Male Head Increase vs Female Abdomen Increase? *Oikos* **1996**, *75*, 511, doi:10.2307/3545893.
12. Kaliontzopoulou, A.; Carretero, M.A.; Llorente, G.A. Morphology of the *Podarcis* Wall Lizards (Squamata: Lacertidae) from the Iberian Peninsula and North Africa: Patterns of Variation in a Putative Cryptic Species Complex. *Zoological Journal of the Linnean Society* **2012**, *164*, 173–193, doi:10.1111/j.1096-3642.2011.00760.x.
13. Kaliontzopoulou, A.; Adams, D.C.; van der Meijden, A.; Perera, A.; Carretero, M.A. Relationships between Head Morphology, Bite Performance and Ecology in Two Species of *Podarcis* Wall Lizards. *Evolutionary Ecology* **2012**, *26*, 825–845, doi:10.1007/s10682-011-9538-y.
14. Arribas, O.; Carranza, S.; Odierna, G. Description Of A New Endemic Species Of Mountain Lizard From Northwestern Spain: *Iberolacerta Galani* Sp. Nov. (Squamata: Lacertidae). *Zootaxa* **2006**, *1240*, 1–55, doi:10.5281/zenodo.172862.
15. Arribas, O.; Carranza, S. Morphological and Genetic Evidence of the Full Species Status of *Iberolacerta Cyreni Martinezricai* (Arribas, 1996). *Zootaxa* **2004**, *634*, 1, doi:10.11646/zootaxa.634.1.1.
16. Arribas, Ó. Una Nueva Especie de Lagartija de Los Pirineos Orientales: *Lacerta (Archaeolacerta) Aurelioi* Sp. Nov. (Reptilia: Lacertidae). *Bollettino Museo Regionale di Scienze Naturali Torino* **1994**, *12*, 327–351.
17. Carretero, M.A.; Llorente, G.A. Morfometria de *Psammodromus Algirus* i *Acanthodactylus Erythrurus* al Delta De L'Ebre. *Buttl. Parc Natural de l'Ebre* **1994**, *8*, 19–26.
18. Lopez-Darias, M.; Vanhooydonck, B.; Cornette, R.; Herrel, A. Sex-Specific Differences in Ecomorphological Relationships in Lizards of the Genus *Gallotia*. *Functional Ecology* **2015**, *29*, 506–514, doi:10.1111/1365-2435.12353.
19. Herrel, A.; Spithoven, L.; Van Damme, R.; De Vree, F. Sexual Dimorphism of Head Size in *Gallotia Galloti*: Testing the Niche Divergence Hypothesis by Functional Analyses. *Functional Ecology* **1999**, *13*, 289–297, doi:10.1046/j.1365-2435.1999.00305.x.

**Table S2.** Complete list of the identified peptides from tandem MS. Band = gel region originating the sample (Figg. 3 and S1); ID = spectrum ID; score = MSGF+ spectrum E-value (-log10 transformed); error= difference between measured and calculated parental ion mass (Da); UniProtID = unique uniprotKB identifier; description = uniprotKB description; coverage = percent protein sequence covered by the identified peptide; MW = predicted molecular weight (kDa) of the corresponding protein. Peptides in bold refer to those showing FDR below 0.01.

band	ID	Peptide	score	error	UniProt ID	description	Coverage (%)	MW
A	3336	VAQLVSPR	6.814	1.020	A0A670JJE1	MAM domain containing 2	0.95%	92.6
	3009	VDDGKLK	6.119	0.001	A0A670ISX8	Protein phosphatase 1 regulatory subunit 37	1.03%	75.2
	<b>3544</b>	<b>SCIDTELCVGYGSASITSSMYIQSK</b>	<b>9.374</b>	<b>0.036</b>	<b>A0A670IP55</b>	<b>UPAR/Ly6 domain-containing protein</b>	<b>17.81%</b>	<b>15.8</b>
	<b>2948</b>	<b>AHDGIR</b>	<b>8.026</b>	<b>-0.009</b>	<b>A0A670JC88</b>	<b>Zinc finger protein 436-like</b>	<b>1.16%</b>	<b>58.8</b>
	<b>2948</b>	<b>AHDGLR</b>	<b>8.026</b>	<b>-0.009</b>	<b>A0A670JYQ1</b>	<b>SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1</b>	<b>0.61%</b>	<b>109.1</b>
	3270	RPVLSPR	7.576	-0.009	A0A670KH22	RBPJ-interacting and tubulin-associated protein 1	2.56%	30.2
	4154	TWTCWGRILGSSTAAERWKPRRSTS	7.538	0.945	A0A670JY26	Reverse transcriptase	1.99%	143.3
	3881	LPLLWRSK	7.453	0.012	A0A670HRL2	Myosin IIIB	0.94%	110.3
	2780	PEPERR	7.364	0.000	A0A670HYR8	Aprataxin and PNKP like factor	1.17%	57.6
B	3284	VATAKKPR	6.899	-0.010	A0A670JHJ6	Homologous recombination factor with OB-fold	1.17%	74.5
	3898	LPKHVANQLK	6.533	0.016	A0A670IV37	Guanylate cyclase	1.54%	74.2
	2774	RASPMHR	6.408	0.007	A0A670KB76	Vasopressin V2 receptor	2.00%	39.0
	2959	DEYEAHQDR	5.979	-0.013	A0A670HR35	RING-type E3 ubiquitin transferase	1.81%	53.8
	2959	EDSGFYECR	5.979	0.016	A0A670J0D7	Interleukin 1 receptor type 1	1.63%	62.8
	3771	CLETPSHPEEPSDLEE	5.762	-0.020	A0A670IMN3	POU domain protein	2.32%	72.5
	3771	SSRPSSSQSTEGIDAGGDM	5.762	-0.027	A0A670K987	Polycystin 2, transient receptor potential cation channel	2.01%	107.1
	2871	EDQADSGDGER	5.599	0.002	A0A670KJZ2	KN motif and ankyrin repeat domains 2	1.16%	101.2
	<b>3168</b>	<b>QMIKINFK</b>	<b>8.341</b>	<b>-0.005</b>	<b>A0A670KI84</b>	<b>COP9 signalosome complex subunit 2</b>	<b>1.78%</b>	<b>52.4</b>
	3362	LQDMLDGFIIK	7.876	0.985	A0A670HKG3	Eukaryotic translation initiation factor 5	2.55%	49.2
C	3209	VLSVLSR	7.749	0.001	A0A670KIJ4	Plexin A3	0.44%	201.1
	3176	GASGNNGGGGGGGAEGGGGGGGG GGGGGGGTGESEGAIDASKNEEDEGK	7.461	-0.049	A0A670KFL5	Heterogeneous nuclear ribonucleoprotein D	15.11%	35.6
	3100	YLSQFPKAK	7.453	-0.014	A0A670JJJ1	Filamin C	0.36%	268.4



	2741	QSINKPK	7.449	0.003	A0A670IZ61	SCY1 like pseudokinase 2	0.76%	102.6
	3116	AEGSSSHVHFDEK	7.350	-0.002	A0A670IUZ2	Chromosome 9 C20orf27 homolog	7.30%	19.7
	3040	EAETHRNREMR	7.283	0.995	A0A670HN26	Kinesin family member 20B	0.62%	202.9
	3016	DDVTYNIVCKK	7.220	1.016	A0A670JGC4	Receptor protein-tyrosine kinase	1.09%	112.5
	3095	VIEFLNEASRR	7.162	-0.022	A0A670IWZ0	Mesoderm induction early response protein 1	2.19%	57.1
	3036	VLCRARK	7.102	0.017	A0A670I7F0	Hermansky-Pudlak syndrome 5 protein homolog	0.61%	130.7
	3089	YLQLFYEK	7.069	-0.006	A0A670HV88	Stonin-2	0.97%	93.4
	3071	EENRGIVASLDCDESEIENK	6.996	-0.041	A0A670HM85	Zinc finger protein 420-like	2.93%	77.3
	3130	VNTTKDQQFR	6.984	1.012	A0A670K299	Lipoprotein lipase	2.39%	51.9
	3481	FHNPSAHNLSSAFDGMAR	6.966	-0.025	A0A670IKS2	Cell cycle control protein	5.20%	39.3
	3614	IGEISYAEKVA	6.963	-0.004	A0A670J318	Transferrin receptor 2	1.54%	78.6
	2972	TETVYLAVNYLDR	6.949	0.985	A0A670IEP1	Cyclin A1	3.14%	46.9
	3110	VLNLMK	6.932	-0.001	A0A670J6W9	T-complex protein 11 homolog	1.32%	51.4
	3989	PFKMECGKGFSRCSH	6.927	0.023	A0A670HNT9	Gastrula zinc finger protein XICGF57.1-like	2.85%	64.0
	3208	RLDFQLMLK	6.892	0.983	A0A670KFA7	Semaphorin 6D	0.87%	115.4
C	3104	HNIQQILK	6.858	0.003	A0A670KGH4	Protein kinase cAMP-dependent type I regulatory subunit beta	1.68%	53.9
	3104	HNIQQLLK	6.858	0.003	A0A670I253	Protein kinase cAMP-dependent type I regulatory subunit alpha	2.10%	43.3
	3733	TCGEGYQFRIVRCWK	6.837	0.968	A0A670KEZ0	ADAMTS like 2	1.64%	103.0
	3172	LTVTAYDCGKKR	6.812	-0.004	A0A670J4B0	Calsyntenin 1	1.35%	99.6
	3139	EKEKEKEEEK	6.807	1.010	A0A670JZR2	THO complex subunit 2	0.68%	168.9
	3022	KMGGIK	6.693	0.000	A0A670IP53	Signal recognition particle 54 kDa protein	1.07%	62.9
	3294	EASNYSRPGMGQVNGDCK	6.692	0.992	A0A670K9R3	SAM domain-containing protein	3.67%	52.8
	3913	FAFVEVIAMIK	6.652	-0.015	A0A670IH88	Cytoplasmic FMR1-interacting protein	0.84%	152.1
	4113	LRTRHRVSAGK	6.547	-0.001	A0A670KDL9	Myosin-16	0.57%	221.0
	3224	WYRSYK	6.465	-0.007	A0A670IFP9	ShKT domain-containing protein	2.67%	24.9
	2973	TTVTFDLMLGILCK	6.425	1.008	A0A670J1D2	Fem-1 homolog C	2.27%	68.8
	3044	SIETPNVRADP	6.390	-0.012	A0A670IH45	Delta-sarcoglycan	5.73%	20.8
	3143	KDEESGSGSNPFQHLEK	6.364	0.967	A0A670JEW1	Coatomer subunit gamma	1.95%	97.7
	2948	VKLSNVDDD	6.329	0.993	A0A670JU92	Protein-tyrosine-phosphatase	0.40%	250.2
	3195	LYKCSSCSKSFCDQSR	6.328	0.984	A0A670HPN8	Zinc finger and SCAN domain-containing protein 29	2.06%	89.0

C	3085	NTLRPEEK	6.295	-0.009	A0A670IIF5	Zinc finger BED-type containing 1	1.04%	87.5
	2944	FVCALGR	6.273	-0.008	A0A670J9B3	Integrin subunit alpha 3	0.66%	117.9
	3931	CCFQGKRCCFQGK	6.270	0.024	A0A670K425	Pentapeptide repeat-containing protein	9.49%	15.6
	3078	ASAGFGASSDSHMLDSTLKC	6.239	-0.021	A0A670JF65	Ectopic P-granules autophagy protein 5 homolog	0.85%	278.6
	3128	HMFYRQPSHTFSYYGK	6.145	0.993	A0A670IA93	Solute carrier family 45 member 4	2.03%	87.4
	3020	AEQEEYVQEGIK	6.107	0.978	A0A670K627	Myosin IF	1.09%	126.2
	2877	KESSSDSTDEVK	6.087	-0.005	A0A670HVV3	Protein-histidine N-methyltransferase	2.02%	67.3
	2877	SNCSSSRLEDR	6.087	1.010	A0A670HZK7	ATP-dependent DNA helicase	1.11%	109.9
	3717	LSHAVELCDAGFQAYDF	6.045	-0.031	A0A670HTF6	Valine--tRNA ligase	1.40%	136.8
	4197	PYECSDCGKSFIQK	6.044	-0.024	A0A670HLY8	Zinc finger protein 2 homolog	2.79%	57.8
	3141	GPTRDDGTGMCERDVSK	6.043	-0.031	A0A670JQL6	TPR_REGION domain-containing protein	0.64%	314.6
	3206	TCEGEGRIEWCCSVSR	6.013	1.015	A0A670IWD4	S-adenosylmethionine sensor upstream of mTORC1	3.98%	46.1
	3112	FNNSPCEEYFPK	5.823	0.987	M1GNS9	V(D)J recombination-activating protein 1 (Fragment)	3.56%	38.2
	3165	MAATGEEDDSQNSTEPSVK	5.786	-0.030	A0A670KHF2	Zinc finger protein 239-like	4.81%	45.2
	3190	SHCLSEGITHPKMSHSNSMHGR	5.728	0.986	A0A670I1K2	TIAM Rac1 associated GEF 1	1.38%	179.1
	4194	PFKCMECGKSFSNNG	5.691	-0.023	A0A670JCI2	Zinc finger protein 845-like	2.61%	65.6
	3203	SDLEDMEDEPDAAEGGSQAK	5.670	1.000	A0A670JS10	SMG5 nonsense mediated mRNA decay factor	1.51%	138.9
	3101	QTDSSDEQDDREKNFIHN	5.597	0.971	A0A670J7A8	Zinc finger BED-type containing 4	1.54%	131.2
	3161	VLEMYSK	5.388	-0.016	A0A670ISU3	Exocyst complex component	0.93%	87.8
	3355	VEINLEFICECECHK	5.195	0.971	A0A670J1K3	Integrin beta	2.00%	82.7
D	<b>3157</b>	<b>YSMELHIVHTK</b>	<b>14.85</b>	<b>0.005</b>	<b>A0A670JE51</b>	<b>Carbonic anhydrase</b>	<b>4.25%</b>	<b>28.4</b>
	3661	FHGAKAISDAEPYSR	7.537	0.002	A0A670KHB8	Rab-GAP TBC domain-containing protein	3.40%	50.8
	3207	VLSVLSPR	7.230	0.004	A0A670KIJ4	Plexin A3	0.44%	201.1
	3820	EYQLEGVNWLLFNWYNR	6.989	-0.036	A0A670JDQ2	Chromodomain-helicase-DNA-binding protein 8	0.68%	276.8
	3030	HNIQQILK	6.909	0.002	A0A670KGH4	Protein kinase cAMP-dependent type I regulatory subunit beta	1.68%	53.9
	3030	HNIQQLLK	6.909	0.002	A0A670I253	Protein kinase cAMP-dependent type I regulatory subunit alpha	2.10%	43.3
	3254	LFLWWHK	6.899	0.014	A0A670JF65	Ectopic P-granules autophagy protein 5 homolog	0.28%	278.6
	3713	HQRIHTEEK	6.813	1.006	A0A670HMX4	Zinc finger protein 501-like	2.00%	51.6
	2909	VIEMLLK	6.791	0.013	A0A670JEZ4	Sodium channel protein	0.35%	227.7

D	2909	VLEMLLK	6.791	0.013	A0A670J0E0	Sodium channel protein	0.40%	200.7
	3816	MADPAAAAATAGAPSGSEEGEPVR	6.731	1.029	A0A670KGA4	Protein kinase C	3.68%	77.1
	3084	VLQMVK	6.534	0.002	A0A670IQN7	UDP-glucose 4-epimerase	1.73%	38.3
	3184	RLFLCDLAGSERCTR	6.364	1.003	A0A670HPG8	Kinesin family member 20B	0.84%	203.4
E	3381	QMIKINFK	9.012	-0.012	A0A670KI84	COP9 signalosome complex subunit 2	1.78%	52.4
	3515	DLVVIDDR	8.391	0.018	A0A670HZU9	FIG4 phosphoinositide 5-phosphatase	0.88%	103.4
	3394	LTEAYKCLSKAK	8.365	-0.028	A0A670JJV1	Intraflagellar transport 140	0.83%	164.0
	3519	AHGAGGGGGSGRCCMGKSGK	8.162	0.005	A0A670IRY6	Mothers against decapentaplegic homolog	4.60%	50.7
	2945	HDCISR	7.949	-0.005	A0A670JVT7	Otogelin like	0.27%	249.2
	3204	VTTEEFMNTK	7.654	0.016	A0A670J1G8	Chloride channel protein	1.44%	77.3
	2794	KCPRSNR	7.413	0.010	A0A670I187	Transmembrane protein with EGF like and two follistatin like domains 2	1.86%	41.4
	3291	AEGSSSHVHFDEK	7.400	-0.007	A0A670IUZ2	Chromosome 9 C20orf27 homolog	7.30%	19.7
	2912	QDSQESMR	7.163	1.020	A0A670HNM6	Elongator complex protein 4	1.93%	45.5
	3401	VATAKKPR	7.121	-0.010	A0A670JHJ6	Homologous recombination factor with OB-fold	1.17%	74.5
	3401	VLSVLSPR	7.121	0.001	A0A670KIJ4	Plexin A3	0.44%	201.1
	3658	PMVVRVID	7.081	-0.000	A0A670J6W6	Methylcytosine dioxygenase TET	0.55%	159.8
	3076	ESDSSERR	6.987	-0.002	A0A670KMM8	Chromosome 11 open reading frame 57	2.68%	34.8
	3115	FGDMTNEEFR	6.971	-0.024	A0A670JKL2	CATL1 protein	2.96%	38.4
	3282	VLNLMK	6.944	-0.002	A0A670J6W9	T-complex protein 11 homolog	1.32%	51.4
	3251	HNIQQILK	6.803	-0.002	A0A670KGH4	Protein kinase cAMP-dependent type I regulatory subunit beta	1.68%	53.9
	3251	HNIQQLLK	6.803	-0.002	A0A670I253	Protein kinase cAMP-dependent type I regulatory subunit alpha	2.10%	43.3
	2940	QSSQKCSDNNGSGESDG	6.768	-0.018	A0A670IVS8	Spalt like transcription factor 4	1.54%	111.9
	3463	WYRSYK	6.752	-0.007	A0A670IFP9	ShKT domain-containing protein	2.67%	24.9
	4194	KAFAATCSCGRAAPCCR	6.608	0.023	A0A670HVG1	Gastrin/cholecystokinin type B receptor	4.16%	45.1
	2952	KESSSDSTDEVK	6.535	-0.009	A0A670HVV3	Protein-histidine N-methyltransferase	2.02%	67.3
	3271	CESSIEQMCFVAA	6.458	1.004	A0A670JGT0	Oxysterol-binding protein	1.72%	85.5
	2973	YQMCPK	6.427	1.013	A0A670IBU2	Mucin 6, oligomeric mucus/gel-forming	0.18%	353.6
	3254	WHENIYCGTPSSPK	6.291	1.021	A0A670J793	Oxysterol-binding protein	1.58%	101.5
	3439	SPSAINESDQNSTK	6.090	0.984	A0A670I767	Spermatogenesis associated serine rich 2 like	2.51%	62.1

E	3589	WTEDIQMAIDLAENCNG	5.812	0.981	A0A670KCN5	FERM, ARH/RhoGEF and pleckstrin domain protein 1	1.64%	118.0
E	3529	ESLGDSTSEEEGGVTESEK	5.796	1.006	A0A670K8M4	Phosphatidate phosphatase	2.10%	100.0
E	3383	SSSADFSDDDDFSQKSGSL	5.479	0.996	A0A670IAF5	Dystonin	0.30%	713.7