

**Additional File 1**

**The *Cepaea nemoralis* shell proteome - accepted identifications.**

<b>Contig</b>	<b>Similar to (best match)</b>	<b>FASTA E-value</b>	<b>Iden- tity</b>	<b>Protein</b>	<b>Shell color &amp; Fraction</b>	<b>Unique + razor peptides</b>	<b>% of total (iBAQ)</b>
<b>10054</b>				Uncharacterized; 16% Q, 10% S	<b>-H</b> <b>Y,O;</b> S<I	2	0.0003
					<b>+H</b> <b>Y,O;</b> S,I	3	0.0014
<b>100974</b>				Uncharacterized; 10% R, 10% N, 13% Q; signal peptide	<b>-H</b> <b>Y,O,B;</b> S<I	2	0.0088
					<b>+H</b> <b>Y,O,B;</b> S<I	2	0.0287
<b>10133</b>	GRP78_APLCA (aa86-544)	8.2e-160	90.8%	78kDa glucose-regulated protein; domains: HSP70; shares peptide with contig_695; Lotgi1 216416 (0e0)	<b>-H</b> <b>Y,O,B;</b> S<I	7	0.0102
					<b>+H</b> <b>Y,O,B;</b> S<I	11	0.0184
<b>10182</b>	A6N8F4_HALAI (aa1-474)	1.2e-101	85.7%	HSP90A; domains: HSP90A Lotgi1 161608 (0e0)	<b>-H</b> <b>Y,O,B;</b> S<I	9	0.0098
					<b>+H</b> <b>Y,O,B;</b> S<I	12	0.0134
<b>101824</b>	K1QJK2_CRAGI (aa1063-1449)	2.1e-22	29.4%	Uncharacterized; domains: CBM_14/ CHIT_BIND_II; shares peptide with contig_14003 Lotgi1 231869 (2.3e-70); see also contig_84589!	<b>-H</b> <b>Y,O,B;</b> S<I	19	0.0573
					<b>+H</b> <b>Y,O,B;</b> S<I	29	0.3066
<b>1021</b>				Uncharacterized; signal peptide	<b>-H</b> <b>Y,O,B;</b> S>I	2	0.0082
					<b>+H</b> -	-	-
<b>102484</b>	K1RCY7_CRAGI	5.7e-104	63.9%	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B; Lotgi1 180287 (0e0)	<b>-H</b> -	-	-
					<b>+H</b> <b>Y;</b> I	2	0.0001
<b>102677</b>	Q9NL16_BRABE (aa147-453)	3.3e-22	29,1%	Similar to AmPTP10 protein (Fragment); domain: protein_tyrosine_phosphatase; Lotgi1 181300 (7.6e-26)	<b>-H</b> -	-	-
					<b>+H</b> <b>Y,O;</b> I	2	0.0008

	G3FPE5_HELLU			Hemocyanin $\beta$ -subunit					
<b>11358</b>	(aa1-431)	1.0e-186	92.1%		<b>-H</b>	<b>Y,O,B; I</b>	7	0.0137	
<b>1031</b>	(aa611-1371)	0e0	93.3%			<b>Y,O,B; S&lt;I</b>	17	0.0159	
<b>2283</b>	(aa1365-2093)	0e0	94.9%			<b>Y,O,B; S&lt;I</b>	10	0.0105	
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	11	0.0167	
						<b>Y,O,B; I</b>	16	0.0133	
						<b>Y,O,B; I</b>	10	0.0054	
<b>104312</b>	R7TB34_9ANNE (aa221-273)	2.4e-5	45.5%	Similar to $\alpha$ -carbonic anhydrase; domain: $\alpha$ -CA_2	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	3	0.0379	
					<b>+H</b>	<b>Y,O,B; S,I</b>	4	0.1382	
<b>10507</b>	K1R401_CRAGI (aa785-1076)	2.6e-88	86.2%	Spectrin $\alpha$ -chain; Lotgi1 202396 (1.1e-167)	<b>-H</b>	-	-	-	
<b>112929</b>	(aa171-720)	4.2e-136	74.4%		<b>+H</b>	<b>Y,B; I</b>	2	0.0004	
						<b>Y,O; I</b>	4	0.0007	
<b>105370</b>	J7HZQ3_POMCA (aa83-275)	2.7e-39	60.6%	Apoptosis-inducing factor 3-like protein; Lotgi1 214061 (1.7e-63)	<b>-H</b>	-	-	-	
					<b>+H</b>	<b>Y,O; I</b>	6	0.0125	
<b>10584</b>				Uncharacterized protein; 16% D, 10% E	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	12	0.4573	
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	14	1.3578	
<b>10656</b>	R7TYY9_9ANNE (aa1-1757)	0e0	64.7%	Uncharacterized/similar to NADPH-dependent glutamate synthase; Lotgi1 133427 (0e0)	<b>-H</b>	-	-	-	
					<b>+H</b>	<b>Y; I</b>	2	<0.0001	
<b>10722</b>	A6YM37_9EUPU (aa194-388)	5.7e-34	48.7%	Similar to matrilin-like 40kDa; domains: VWA; Lotgi1 234764 (3.8e-16);	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	7	0.0709	
<b>2338</b>	(aa17-147)	1.5e-13	31.3%	EGF, signal peptide; Lotgi1 133178 (1.9e-8)		<b>Y,O,B; I</b>	3	0.0278	
<b>619</b>	(aa201-348)	1.6e-17	40.5%	Lotgi1 122049 (1.4e-18), several proteins?		<b>Y,O,B; I</b>	5	0.0130	
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	6	0.0829	
						<b>Y,O,B; S&lt;I</b>	3	0.0302	
						<b>Y,O; I</b>	4	0.0051	
<b>107621</b>				Uncharacterized; 11% P, 18% S, 19% T; Lotgi1 163383 (1.2e-25)	<b>-H</b>	<b>Y,O,B; S</b>	2	0.0027	
					<b>+H</b>	<b>B; S</b>	2	0.0005	

<b>108124</b>	G7YE09_CLOSI (aa157-271)	0.0019	27.6%	aa157-272 similar to fasciclin-1; domains: FAS1, signal pept; Lotgi1 237218 (1.4e-21)	-H	Y,O,B; S<I	2	0.0092
					+H	Y,B; S<I	5	0.0278
<b>1089</b>	R7VGL7_9ANNE Q2HZD8_PINFU	2.0e-155	81.7%	ATP synthase subunit $\beta$ ; Lotgi1 201878 (0e0)	-H	Y,O,B; S<I	19	0.0459
		2.1e-153	81.1%		+H	Y,O,B; S<I	20	0.0679
<b>109239</b>	KCY_BOVIN	3.2e-45	63.6%	UMP-CMP kinase; Lotgi1 149165 (1.3e-83)	-H	-	-	-
					+H	Y,O; I	3	0.0028
<b>222793</b>	GNAI_LYMST	1.5e-146	97.7%	Guanine nucleotide-binding protein G(i) subunit $\alpha$	-H	Y,O; I	1	0.0003
<b>109421</b>	GNAO_LYMST	1.5e-146	89.5%	Guanine nucleotide-binding protein G(o) su $\alpha$	+H	Y,O; I	3	0.0018
<b>110180</b>	GNAS_LYMST	5.5e-156	94.1%	Guanine nucleotide-binding protein G(s) subunit $\alpha$ ; Lotgi1 226384 (0e0)				
<b>10986</b>	K1PPK3_CRAGI (aa339-543)	4.9e-24	37.6%	Fibropellin-1; domains: CHIT_BIND_II; Lotgi1 234405 (1.3e-31)	-H	Y,B; S<I	5	0.0143
					+H	Y,B; S,I	2	0.0031
<b>110158</b>				Uncharacterized; 20% P, 18% S	-H	Y,O,B; S>I	3	0.0128
					+H	Y,O,B; S	2	0.0107
<b>110175</b>	K1QLH8_CRAGI (aa600-767)	2.5e-28	43.8%	Peroxidasin; Lotgi1 163527 (1.2e-34)	-H	O,B; I	2	0.0015
					+H	-	-	-
<b>110398</b>	E0W375_PEDHC	6.5e-55	30.4%	Uncharacterized/similar to cadherin-23; domains: cadherin, signal pept; Lotgi1 229248 (4.1e-116)	-H	Y,O,B; I	3	0.0012
					+H	Y,O,B; I	7	0.0047
<b>1108</b>	K1QX01_CRAGI	0.005	29.5%	Uncharacterized; domain: EFh; 13% D; Lotgi1 238177 (1.7e-10)	-H	B; I	4	0.0099
					+H	B; I	2	0.0024
<b>11108</b>	Q45RT7_BIOGL (aa209-455)	1.6e-61	79.8%	Intermediate filament protein; domain: IF; Lotgi1 204921 (7.5e-71)	-H	Y,O,B; I	2	0.0024
					+H	Y,O,B; I	4	0.0679
<b>11180</b>	B7Q2Q7_IXOSC (aa5-764)	1.4e-110	39.7%	Receptor tyrosine phosphatase type r2a, putative; domains: IG, FN3; Lotgi1 128794 (0e0)	-H	-	-	-
					+H	Y,O,B; I	7	0.0039
<b>111860</b>	YCF2E_CAEEL (aa139-381)	1.1e-55	51.0%	Uncharacterized peptidase C1-like protein F26E4.3/similar to cathepsin B; domain: Peptidase_C1A; Lotgi1 118077 (3.0e-102)	-H	-	-	-
					+H	Y,O; I	2	0.0012

<b>112077</b>	Q9NL47_CIOIN (aa216-388)	1.4e-10	38.2%	Cadherin; domains: cadherin; Lotgi1 229248 (2.5e-13)	-H	Y,O,B; I	1	0.0009
					+H	Y,O,B; S<I	1	0.0022
<b>11304</b>	G3PTN0_GASAC (aa132-412)	2.8e-82	63.2%	$\beta$ -hexosaminidase; shares 2 peptides with contig_35849; Lotgi1 120422 (3.3e-127)	-H	Y,O,B; I	1	0.0011
					+H	Y,O;I	6	0.0080
<b>11338</b>	Q3V653_9EUPU (aa872-1245)	1.2e-120	73.8%	Thioester-containing protein; domains: terpenoid cyclase/protein prenyltransferase, A2M/A2M_N_2; AeM_N, signal peptide	-H	Y,O; I	5	0.0060
						Y,O,B; I	9	0.0116
<b>21999</b>	(aa264-567)	1.5e-45	66.5%			Y,O,B; I	3	0.0045
<b>92485</b>	(aa4-270)	1.2e-61	60.7%	Lotgi1 209261 (3.3e-87)/162872 (1.2e-27)/233231 89.8e- 31)	+H	Y,O; I	12	0.0298
						Y,O,B; S<I	10	0.0277
						Y,O,B; I	6	0.0209
<b>1152</b>				Uncharacterized; signal peptide; 16% G, 15% M, 10% S	-H	Y,O,B; S>I	3	18.0689
					+H	Y,O,B; S>I	3	15.5491
<b>116159</b>	Q5MGE8_LONON (aa172-333)	5.9e-44	61.6%	Cysteine peptidase 2 cathepsin-B-like; domain: peptidase_C1A; Lotgi1 197490 (1.0e-58)	-H	Y,O,B; S<I	1	0.0064
					+H	Y,O,B; S<I	2	0.0252
<b>116171</b>	HBB_HUMAN	2.6e-65	100%	Hemoglobin $\beta$ -subunit; shares 1 of 9 peptides with CON	-H	Y,O,B; S<I	9	0.0491
					+H	-	-	-
<b>116744</b>	K1QB61_CRAGI (aa4522-4789)	1.2e-29	38.1%	Protocadherin Fat 4; domains: cadherin; Lotgi1 154324 (3.3e-37/0e0)	-H	Y,O,B; I	2	0.0061
						Y,O,B; I	22	0.0046
<b>25750</b>	(aa2270-4179)	1.7e-143	33.4%		+H	Y,O,B; S<I	3	0.0252
						Y,O,B; S<I	29	0.0001
<b>11813</b>	G2XK75_9BIVA	1.8e-33	56.3%	Glutathione-S transferase 1; domains: GST_N_3, GST_C; Lotgi1 191561 (4.4e-43)	-H	Y, I	1	0.0005
					+H	Y; I	1	0.0007

<b>1188</b> <b>4282</b>	K1P9P0_CRAGI (aa131-296)	1.2e-27	47.0%	Mesenchyme-specific cell surface glycoprotein; domain:WD40/YVTN repeat-like; Lotgi1 190352 (1.3e-38)/162322 (1.6e-26)	-H	Y,O,B; S<I	8	0.2618
	(aa442-548)	4.4e-21	50.9%		+H	Y,O,B; S<I	6	0.3013
<b>11883</b>	K1QSU9_CRAGI	1.6e-75	36.3%	Eosinophil peroxidase; domains: haem peroxidase, signal pept; Lotgi1 233510 (7.4e-85)	-H	B; I	5	0.0004
					+H	-	-	-
<b>11910</b>	G0WX16_TEGGR (aa217-366)	2.3e-47	77.3%	Glutamine synthetase; Lotgi1 230064 (8.0e-76)	-H	-	-	-
					+H	B,Y; I	2	0.0028
<b>11930</b>	B9M8J1_GEOSF	6.4e-13	31.5%	Uncharacterized; signal peptide; 11% G; Lotgi1 234762 (2.6e-22)	-H	Y,O,B; S,I	2	0.0318
					+H	Y,B; S,I	1	0.0060
<b>12039</b>	K1RW67_CRAGI (aa1978-2657)	1.7e-106	44.4%	Uncharacterized; domains: GPS, GPCR family, transmembrane; Lotgi1 164559 (1.6e-176)	-H	Y,O; I	6	0.0007
					+H	Y,O; S<I	9	0.0046
<b>120497</b>	I1G5E0_AMPQE	6.9e-27	51.5%	Uncharacterized; domains: EFh; 15% A, 12% G; Lotgi1 199248 (6.1e-70)	-H	Y,O,B; I	1	0.0179
					+H	Y; I	1	0.0021
<b>1208</b>	B2YHX3_9BILA	9.2e-54	87.7%	Similar to ribosomal protein S16; Lotgi1 98402 (2.7e-69)	-H	Y,B; I	2	0.0009
					+H	Y,B; I	2	0.0007
<b>1219</b>	B6RB63_HALDI	6.0e-117	62.0%	Protein disulfide isomerase; Lotgi1 184255 (3.1e-97)	-H	Y,B,O; I	12	0.0062
					+H	Y,O,B; S<I	17	0.0475
<b>12284</b>	B7Q505_IXOSC	8.3e-67	60.7%	Elongation factor Tu; Lotgi1 178160 (0e0)	-H	-	-	-
					+H	Y; I	2	0.0003
<b>12292</b>	A8UF56_ARENA	4.7e-40	66.7%	Ribosomal protein L14; Lotgi1 229862 (3.9e-45)	-H	Y,O,B; S<I	1	0.0023
					+H	Y,O,B; I	2	0.0021
<b>123</b>				Uncharacterized; 12% G, 18% P	-H	Y,O,B; S>I	13	41.2668
					+H	Y,O,B; S>I	15	26.2241

123124	K1R7R4_CRAGI	1.2e-57	38.8%	Multiple inositol polyphosphate phosphatase 1; signal peptide; Lotgi1 230275 (2.1e-128)	-H	Y,O; I	2	0.0008
					+H	Y,O; S<I	8	0.0062
1237	K1QI28_CRAGI	1.9e-191	89.8%	V-type proton ATPase subunit B; Lotgi1 178589 (0e0)	-H	Y,O,B; S<I	12	0.0167
					+H	Y,O,B; S<I	18	0.1087
124132	K1Q3Y3_CRAGI (aa35-318)	1.6e-32	34.9%	Blastula protease 10; domains: peptidase M12A/astacin, signal peptide; shares peptide with contig_7075; Lotgi1 109273 (2.2e-34)	-H	Y,O,B; S<I	3	0.0037
					+H	Y,O; S,I	4	0.0152
12587	Q9GQB4_NUCLP (aa105-292)	9.9e-58	80.3%	Malate dehydrogenase; Lotgi1 225558 (8.1e-84)	-H	Y,O,B; I	2	0.0062
					+H	Y,O,B; I	2	0.0025
1265				Uncharacterized; 12% G	-H	Y,O,B; S>I	12	3.8779
					+H	Y,O,B; S>I	9	4.3957
126964	K1P8K1_CRAGI	7.9e-34	33.2%	Meteorin-like protein; domain: meteorin_like, signal peptide; Lotgi1 156516 (5.2e-44); see also 159000	-H	Y,O; I	3	0.0008
					+H	Y,O; S<I	5	0.0039
127437				Uncharacterized; signal peptide	-H	Y,O; I	1	0.0004
					+H	O; S<I	3	0.0007
1281				Uncharacterized; signal peptide	-H	-	-	-
					+H	O,B; I	4	0.0021
12872 80303	K1QSW2_CRAGI (aa219-389) (aa2-209)	3.7e-55 1.1e-46	63.2% 49.5%	Protein-glutamine gamma-glutamyltransferase K; domain: transglutaminase; Lotgi1 122446 (2.8e-85)/233545 (3.3e-76)	-H	-	-	-
					+H	Y; I Y,O; I	1 8	0.0016 0.0046
12941				Uncharacterized; 18% D, 14% L	-H	Y,O,B; S<I	9	0.4282
					+H	Y,O,B; S<I	12	1.3727

<b>130482</b>	K1Q4S5_CRAGI (aa1242-1494)	3.3e-27	38.5%	Similar to cadherin-87A; domains: cadherin Lotgi1 229249 (1.3e-43/3.1e-59)	<b>-H</b>	<b>Y,O; I</b>	1	0.0005
<b>70072</b>	(aa276-693)	7.3e-47	41.4%			<b>Y,O,B; I</b>	3	0.0024
					<b>+H</b>	<b>Y,O; I</b>	1	0.0011
						<b>Y,O,B; I</b>	3	0.0053
<b>130771</b>	Q8I9P8_9BIVA (aa7-550)	2.2e-153	51.6%	$\alpha$ -amylase; domain: $\alpha$ -amylase, signal peptide; Lotgi1 82332 (1.2e-71)	<b>-H</b>	<b>Y,O; I</b>	4	0.0022
<b>363559</b>	(aa432-698)	1.3e-55	52.9%			<b>Y,O; I</b>	2	0.0013
					<b>+H</b>	<b>Y,O; S&lt;I</b>	10	0.0117
						<b>Y,O; S&lt;I</b>	4	0.0027
<b>131464</b>				Uncharacterized; signal peptide	<b>-H</b>	<b>Y,B; I</b>	2	0.0011
					<b>+H</b>	<b>Y,O,B; I</b>	3	0.0021
<b>132</b>				Uncharacterized; 12% Q	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	22	0.3538
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	21	0.2887
<b>1323</b>	A7T0W4_NEMVE (aa119-414)	1.3e-26	40.5%	Uncharacterized; domain: polysaccharide deacetylase/chitinase; Lotgi1 153749 (3.5e-39)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	4	0.1272
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	7	0.3197
<b>13233</b>	L1JQJ7_GUIH	1.1e-31	57.3%	Uncharacterized; domain: thioredoxin_like_fold	<b>-H</b>	<b>Y,B; S&lt;I</b>	1	0.0031
					<b>+H</b>	<b>Y,B; S,I</b>	1	0.0011
<b>13347</b>	R7UUB1_9ANNE (aa45-687)	5.5e-190	83.5%	Uncharacterized; domains: DnaK/HSP70; Lotgi1 200867 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O,B; I</b>	2	0.0003
<b>133605</b>	R7UA33_9ANNE (aa16-268)	2.4e-21	30.3%	Uncharacterized; domains: transmembrane, peptidase_M13; Lotgi1 193572 (9.5e-26/3.1e-124)	<b>-H</b>	-	-	-
<b>46072</b>	(aa352-766)	2.2e-76	40.6%		<b>+H</b>	<b>Y; I</b>	1	0.0008
						<b>Y; I</b>	3	0.0018
<b>134534</b>	K1P339_CRAGI (aa1-665)	1.1e-173	73.1%	Vinculin; Lotgi1 102378 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; I</b>	6	0.0003

13504	K1RXH3_CRAGI	4.7e-20	41.2%	Similar to Universal stress protein A-like protein; domain: UspA; Lotgi1 149221 (1.5e-31)	-H	Y,O,B; I	5	0.0150
					+H	Y,O,B; S<I	5	0.0399
13525	C1K7M3_ICTPU	5.8e-15	51.3%	Annexin (A4); domains: annexin; Lotgi1 219490 (7.9e-112)	-H	Y,O,B; I	6	0.0047
					+H	Y,O,B; S<I	8	0.0112
1365	C3Y8Z2-BRAFL (aa20-292)	5.9e-48	51.8%	Similar to periostin; domains: FAS1, signal peptide; Lotgi1 200505 (2.8e-68)	-H	Y,O; S<I	5	0.0043
					+H	Y,O,B; S<I	10	0.0251
136589 29551	K1S4H5_CRAGI (aa35-307) (aa265-404)	1.4e-106 1.5e-56	89.7% 92.8%	Adenosylhomocysteinase; Lotgi1 105848 (9.9e-89)	-H	Y,O,B; I	3	0.0044
						Y,O,B; I	2	0.0010
					+H	Y,O; S<I	3	0.0091
						Y,O; I	3	0.0063
13700	E7D158_LATHE	2.0e-5	28.1%	Profilin fragment; domain: profilin	-H	Y,B; I	2	0.0014
					+H	Y,O; I	2	0.0021
13725	K1QEA6_CRAGI	0e0	74.6%	Phosphoenolpyruvate carboxykinase [GTP]; Lotgi1 203707 (0e0)	-H	Y,O; I	3	0.0008
					+H	Y,O; S<I	13	0.0049
137918				Uncharacterized; domain: chromophore_lyase_CpcT/CPeT	-H	Y,O,B; S<I	4	0.0391
					+H	Y,O,B; S<I	4	0.0535
138139				Uncharacterized; transmembrane; 15% Q, 10% L, 10% S	-H	Y,O,B; S<I	5	0.0078
					+H	Y,O; S<I	5	0.0065
1387	Q86D82_APLCA (aa1-246)	6.7e-109	98.8%	$\beta$ -tubulin; Lotgi1 223043 (8.4e-153)	-H	Y,O,B; S<I	4	0.0419
					+H	Y,O,B; S<I	5	0.0442
139966	K1PPK3_CRAGI (aa279-484)	2.8e-17	33.0%	Similar to fibropellin-1; domains: signal peptide, CBM_14/CHIT_BIND_II; Lotgi1 152043 (3.2e-20)	-H	Y,O; I	1	0.0020
					+H	Y,O; S,I	4	0.0077
13999	R7U801_9ANNE (aa569-977)	2.4e-135	74.6%	Uncharacterized/filamin; domains: filamin/ABP280_repeat; shares 2 peptides with contig_1628; Lotgi1 178063 (0e0)	-H	-	-	-
					+H	Y,O; I	7	0.0026



<b>14003</b>	K1PRD3_CRAGI (aa985-1278)	3.6e-22	30.1%	Similar to IgGFc-binding protein; domains: CBM_14/CHIT_BIND_II; Shares peptide with 101824; Lotgil 231869 (2.6e-51)	-H	Y,O,B; S<I	14	0.0788
					+H	Y,O,B; S,I	18	0.3782
<b>140752</b>	J9JZU3_ACPI	7.5e-69	62.5%	Uncharacterized; domains: EFh; Lotgil 134987 (1.7e-144)	-H	-	-	-
					+H	Y,O; I	3	0.0009
<b>140914</b> <b>54526</b>	Q25017_HELAS (aa1-497) (aa506-646)	5.1e-115 1.5e-58	97.8% 99.3%	Neurofilament protein NF70; shares many peptides with 87417 Lotgil 125719 (0e0)/Lotgil 204366 (3.2e-4372.5e-50)	-H	Y,O;B; S<I	7	0.0213
						Y,O; S<I	4	0.0400
					+H	Y,O,B; I	4	0.0020
						Y,O; I	1	0.0025
<b>17464</b> <b>87417</b>	Q25017_HELAS (aa496-646) (aa1-497)	1.9e-45 1.2e-94	71.5% 81.5%	Similar to NF70; Lotgil 165340 (0e0)	-H	Y,O,B; S<I	8	0.0918
						Y,O,B; S<I	21	0.1645
					+H	Y,O,B; I	3	0.0037
						Y,O,B; I	9	0.0095
<b>141518</b>	K1QRU9_CRAGI	2.4e-73	78.4%	Epidermal growth factor receptor kinase substrate 8-like protein 1; domains: SH3, tensin_phosphotyrosin-binding; Lotgil 115450 (7.4e-147)	-H	Y,O,B; I	2	0.0005
					+H	Y,O,B; S<I	6	0.0011
<b>14188</b>	K1PF62_CRAGI (aa87-287)	4.6e-36	55.2%	Uncharacterized; domain: aldo/keto_reductase; Lotgil 137310 (1.7e-63)	-H	-	-	-
					+H	Y; I	3	0.0005
<b>143358</b>	R7VES2_9ANNE (aa94-477)	8.6e-54	38.5%	Uncharacterized; domains: DUF23/glycol_transf_92, transmembrane; Lotgil 155701 (5.3e-79)	-H	-	-	-
					+H	Y,O; I	2	0.0005
<b>142698</b>	K1R3E8_CRAGI (aa790-1236)	7.9e-20	26.8%	Similar to collagen $\alpha$ 5(VI); domains: VWA, signal peptide; 11% T; Lotgil 232362 (2.1e-25)	-H	Y,O,B; I	5	0.0042
					+H	-	-	-
<b>14344</b>				Uncharacterized; 17% Q, 10% L, 17% P	-H	Y,O,B; S,I	9	1.6592
					+H	Y,O,B; S<I	11	2.9614
<b>143763</b>	K1S2V5_CRAGI (aa8-474)	4.8e-120	58.0%	N-acetylglucosamine-6-sulfatase; Lotgil 152768 (0e0)	-H	-	-	-
					+H	Y,O; S<I	3	0.0020

<b>144901</b>	K1PP66_CRAGI (aa159-317)	6.6e-5	24.8%	Uncharacterized	-H	Y,O,B; I	2	0.0020
					+H	Y,O; S,I	3	0.0039
<b>145325</b>	ENO_DORPE	1.3e-139	78.7%	Enolase; Lotgil 177346 (0e0)	-H	Y,O,B; I	4	0.0013
					+H	Y,O,B; S<I	7	0.0043
<b>14554</b>	D6X2U0_TRICA (aa610-771)	1.5e-40	54.9%	Uncharacterized; domain: peptidase_M13; Lotgil 165736 (2.4e-56)	-H	Y,B; I	3	0.0084
					+H	-	-	-
<b>14570</b> <b>36869</b> <b>6241</b>	G3FPE6_HELLU (aa775-997) (aa2774-2945) (aa1534-1867)	3.0e-75 5.8e-95 4.9e-146	91.9% 94.2% 94.9%	Hemocyanin αD; shares 1 peptide with 1031 (β-chain)	-H	B; I	1	0.0002
						Y,B; I	1	0.0025
						Y,B; I	1	0.0015
					+H	-	-	-
						Y,O,B; I	1	>0.0001
					-	-	-	
<b>14584</b>	M7AZ14_CHEMY	3.4e-6	33.3%	Similar to WAP four-disulfide core domain protein 3; domains: EGF, WAP, signal peptide; 12% C, 10% P, 10% T	-H	Y,O,B; S<I	3	0.0800
					+H	Y,O,B; S>I	3	0.0650
<b>1459</b>	R4WPX3_9HEMI	8.0e-53	71.7%	Ribosomal protein L9; Lotgil 217766 (8.7e-74)	-H	-	-	-
					+H	Y,B; I	2	0.0016
<b>146226</b>	R7VJR9_9ANNE (aa40-310)	2.3e-30	39.2%	Uncharacterized; domains: DUF4139, DUF4140; 11% E, 10%K; Lotgil 230318 (7.4e-65)	-H	Y,O,B; I	3	0.0005
					+H	Y,O,B; I	7	0.0039
<b>14755</b>	C3ZH75_BRAFL (aa166-401)	1.8e-24	34.3%	Uncharacterized/similar to protein yellow; domain: major_royal_jelly_related/TolB_like	-H	O,B; I	3	0.0027
					+H	-	-	-
<b>14802</b>	L7M880_9ACAR	9.4e-142	72.9%	Putative rab geranylgeranyltransferase component a rab escort protein; domains: RAB_GDI; Lotgil 179044 (0e0)	-H	-	-	-
					+H	Y,O; I	4	0.0005
<b>14834</b>	K1RE19_CRAGI (aa56-424)	1.5e-35	33.2%	Similar to V-type proton ATPase subunit S1; domains: transmembrane, ATP_synth_S1; Lotgil 175264 (1.8e-51)	-H	-	-	-
					+H	Y,O; S<I	4	0.0024

<b>149478</b>	L7MKZ3_9ACAR (aa353-529)	3.8e-39	57.8%	Putative phospholipase d3 protein; domain: PLDc, transmembrane; Lotgi1 119020 (3.2e-56)	<b>-H</b>	<b>Y,O; I</b>	1	0.0003
<b>152245</b>	(aa66-359)	7.6e-53	44.5%		<b>+H</b>	<b>Y,O; S&lt;I</b> <b>Y,O; I</b>	3	0.0048
<b>14978</b>	G1KP65_ANOCA (aa455-596)	3.0e-34	67.1%	Uncharacterized/Vacuolar proton ATPase; domains: transmembrane, V-ATPase_I; Lotgi1 108161 (1.7e-62)	<b>-H</b>	-	-	-
<b>14997</b>	K1S6V7_CRAGI (aa1-587)	1.7e-209	83.3%		<b>+H</b>	<b>Y,O; I</b>	2	0.0261
<b>150060</b>	R7TKT4_9ANNE	2.4e-155	75.7%	Uncharacterized/ribosomal protein S6 kinase; Lotgi1 236015 (0e0)	<b>-H</b>	-	-	-
<b>150198</b>	A7RQD5_NEMVE (aa251-495)	1.9e-22	30.7%		<b>+H</b>	<b>Y; I</b>	3	0.0004
<b>150378</b>	H2M677_ORYLA	3.3e-40	33.4%	Uncharacterized; shares peptides with 7323 Uncharacterized; domains: Armadillo_like, ataxin-10; Lotgi1 167953 (1.1e-53)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	7	0.0260
<b>1504</b>					<b>+H</b>	<b>Y,O; S&lt;I</b>	8	0.0007
<b>15054</b>	R7UXV8_9ANNE	0e0	72.9%	Uncharacterized/ATP-citrate synthase	<b>-H</b>	-	-	-
<b>15065</b>	F6U982_XENTR (aa7-360)	1.7e-95	66.9%		<b>+H</b>	<b>Y; S&lt;I</b>	5	0.0011
<b>15106</b>	R7UIL6_9ANNE	2.5e-91	66.7%	Uncharacterized, fragment; signal peptide; without signal peptide 16% G, 12% L, 21% M, 10% S in 58aa; only 1 peptide possible!	<b>-H</b>	<b>Y,O,B; S&gt;I</b>	1	1.2760
<b>1524</b>	F8V2T7_BATAR (aa2-313)	5.2e-105	82.4%		<b>+H</b>	<b>Y,O,B; S&gt;I</b>	1	1.1542
<b>15054</b>	R7UXV8_9ANNE	0e0	72.9%	Uncharacterized/ATP-citrate synthase	<b>-H</b>	-	-	-
<b>15065</b>	F6U982_XENTR (aa7-360)	1.7e-95	66.9%		<b>+H</b>	<b>Y,O; I</b>	3	0.0001
<b>15065</b>	F6U982_XENTR (aa7-360)	1.7e-95	66.9%	Similar to Peptidase (mitochondrial processing) beta; domain: peptidase_M16; Lotgi1 105568 (9.7e-124)	<b>-H</b>	<b>Y,O,B; I</b>	4	0.0021
<b>15106</b>	R7UIL6_9ANNE	2.5e-91	66.7%		<b>+H</b>	<b>Y,O; I</b>	6	0.0044
<b>15106</b>	R7UIL6_9ANNE	2.5e-91	66.7%	Uncharacterized/similar to sorbitol dehydrogenase; Lotgi1 208637 (2.1e-172)	<b>-H</b>	-	-	-
<b>1524</b>	F8V2T7_BATAR (aa2-313)	5.2e-105	82.4%		<b>+H</b>	<b>Y; I</b>	2	0.0002
<b>1524</b>	F8V2T7_BATAR (aa2-313)	5.2e-105	82.4%	Putative Na <sup>+</sup> /K <sup>+</sup> -ATPase alpha subunit; domains: transmembrane, P_type_ATPase; Lotgi1 169373 (1.3e-155)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y; I</b>	2	0.0009

15247	R7VC37_9ANNE	0e0	65.4%	6-phosphofructokinase; Lotgi1 235800 (0e0)	-H	-	-	-
					+H	Y,O; I	10	0.0030
15338	K1P6B3_CRAGI	3.9e-92	60.6%	Endoplasmic reticulum resident protein ERp44; domains: thioredoxin, signal peptide; Lotgi1 131935 (3.0e-161)	-H	Y; I	3	0.0007
					+H	Y,O; S<I	6	0.0046
15360	N6UCC9_9CUCU (aa4-266)	1.3e-22	30.3%	Uncharacterized/serine protease inhibitor; domains: serpin, signal peptide; Lotgi1 129913 (2.2e-29)	-H	Y,O,B; I	2	0.0058
					+H	Y,O; I	4	0.0118
154	G3FPE7_HELLU (aa2266-2871)	0e0	90.9%	Hemocyanin $\alpha$ N; Lotgi1 234481 (2.8e-9)/163934 (4.0e-8)	-H	Y,O,B; I	12	0.0103
157	(aa2056-2226)	4.3e-74	94.2%		Y,O,B; I	3	0.0111	
3460	(aa791-1054)	2.4e-119	93.6%		Y,O,B; I	8	0.0224	
3785	(aa1669-1887)	8.2e-107	99.1%		Y,O,B; I	4	0.0080	
571	(aa1129-1606)	0e0	94.4%		Y,B; I	5		
					+H	Y,O,B; I	14	0.0091
					Y,O,B; S<I	3	0.0071	
					Y,O,B; I	6	0.0192	
					Y,O,B; I	2	0.0060	
					Y,O,B; I	4	0.0027	
15424	K1RH58_CRAGI	5.8e-216	80.7%	Sarcomeric $\alpha$ -actinin; domains: CH, EFh, actinin Lotgi1 189716 (0e0)	-H	Y,O,B; S<I	13	0.0025
					+H	Y,O,B; S<I	26	0.0189
15432	K1QWZ3_CRAGI (aa37-252)	1.8e-46	51.6%	Uncharacterized; 11% G, 13% S; ; shares peptides with 15433 Lotgi1 234011 (1.9e-41)	-H	Y,O,B; I	4	0.0087
					+H	Y,O,B; S<I	5	0.0141
15433	K1QWZ3_CRAGI (aa35-252)	8.0e-49	53.9%	Uncharacterized; domains: SH3_like, bacterial type; 10% A, 11% G, 12% S; shares peptides with 15432; Lotgi1 163736 (1.8e-40)	-H	Y,O,B; I	6	0.0366
					+H	Y,O,B; S<I	3	0.0061
15472	K1QFS4_CRAGI	1.9e-145	85.6%	Actin-related protein 2; Lotgi1 178898 (0e0)	-H	-	-	-
					+H	Y,B; I	2	0.0008
15506				Uncharacterized; signal peptide; 16% L	-H	Y,O,B; S>I	1	0.0686
					+H	Y,O,B; S,I	1	0.0659

<b>157680</b>				Uncharacterized, similarity to very Q-rich proteins; 13% R, 30% Q mainly concentrated in C-term	-H	Y,O,B; I	1	0.0003
					+H	Y,O,B; I	2	0.0004
<b>158</b>	Q9NJ19_ARGIR	5.7e-126	67.7%	Catchin; domain: myosin_tail_1; shares peptides with 1617; Lotgi1 170428 (0e0)	-H	Y,O; I	17	0.0019
					+H	-	-	-
<b>159000</b>	K1P8K1_CRAGI	4.5e-35	32.5%	Meteorin-like protein; see also 126964; Lotgi1156516 (6.8e-48)	-H	Y,O,B; I	2	0.0025
					+H	Y,O; S<I	10	0.0153
<b>1594</b>	Q1EL60_9EUPU	1.6e-6	32.3%	aa173-258 similar to CHAII-like protein; domain: H-lectin; shares peptides with 1595; also similar to Q5F4K1_9EUPU (CHAII protein)	-H	Y,O,B; I	2	0.0050
					+H	O,B; I	3	0.0040
<b>1595</b>	Q1EL60_9EUPU	1.2e-4	29.7%	aa173-258 similar to CHAII-like protein; domain: H-lectin; shares peptides with 1594; also similar to Q5F4K1_9EUPU (CHAII protein)	-H	Y,O,B; I	4	0.0051
					+H	Y,O,B; S<I	5	0.0218
<b>15953</b>				Uncharacterized; 11% G, 11% L	-H	Y,O,B; S<I	3	0.0196
					+H	Y,O,B; S<I	5	0.0489
<b>15995</b>	C3ZEP8_BRAFL (aa1-252)	5.5e-43	44.7%	Uncharacterized/epithelial chloride channel protein; domains: CLCA_N, signal peptide: Lotgi1 238844 (8.7e-110)	-H	Y,O; I	3	0.0006
					+H	Y,O; S<I	6	0.0070
<b>1604</b>				Uncharacterized; 31% Q, 23% P	-H	Y,O,B; S>I	2	0.2137
					+H	Y,O,B; S>I	2	0.4750
<b>1611</b>				Uncharacterized; signal peptide	-H	Y,O,B; S<I	4	0.0795
					+H	O,B; I	3	0.0042
<b>1617</b>	G4V4Y8_DORPE (aa250-1938)	0e0	77.0%	Myosin heavy chain isoform C; shares peptides with 158; Lotgi1198366 (0e0)	-H	Y; I	2	0.0002
					+H	-	-	-
<b>161838</b>	R7TWN6_9ANNE	2.7e-33	37.5%	Uncharacterized; 11% L, 12% S; Lotgi1 152551 (7.0e-64)	-H	Y,O,B; S	2	0.0017
					+H	-	-	-
<b>1628</b>	G7Y5W0_CLOSI (aa1664-2333)	9.0e-192	65.1%	Filamin; Lotgi158607 (0e0)	-H	Y,O,B; I	3	0.0005
					+H	Y,B; I	2	0.0008

<b>1647</b>				Uncharacterized; 12% P, 11% S, 11% T; domain:Sushi/SCR/CCP Lotgi1 159256 (5.2e-10)	-H	Y,O,B; S>I	9	0.3743
					+H	Y,O,B; S>I	9	0.3790
<b>165344</b>				Uncharacterized; 11% T, 11% V; Lotgi169600 (4.6e-7)	-H	Y,O,B; I	4	0.0109
					+H	Y,O,B; S<I	7	0.0467
<b>16679</b>	K3WH68_PYTUL	0e0	62.3%	Urease; Lotgi 105464 (0e0)	-H	-	-	-
					+H	Y; I	5	0.0004
<b>16710</b>	K1QZ49_CRAGI (aa59-407)	2.3e-45	35.0%	Similar to adipocyte plasma membrane-associated protein; domains: signal peptide, TolB_like/ strictosidine synthase; Lotgi1 115637 (3.0e-47); see also contig_221/contig_58150/contig_8812	-H	Y,O; I	4	0.0014
					+H	Y,O; S<I	9	0.0181
<b>16729</b>	Q9BLF6_OCTVU	1.7e-80	56.0%	D-lactate dehydrogenase; Lotgi 125448 (1.3e-134)	-H	-	-	-
					+H	Y,O; I	3	0.0011
<b>168604</b>	A7S7T9_NEMVE (aa1-241)	2.4e-53	56.0%	Uncharacterized; domains:transmembrane, HSP70; Lotgi1 159745 (1.5e-103)	-H	-	-	-
					+H	Y,O; S<I	4	0.0106
<b>16878</b>				Uncharacterized; 29% Q, 16% P;	-H	Y,O,B; S>I	3	0.9451
					+H	Y,O,B; S>I	3	1.0824
<b>1696</b>	Q4H45_CRAGI	2.1e-55	85.8%	Ribosomal protein S18	-H	Y,O,B; I	4	0.0052
					+H	Y,B; I	2	0.0044
<b>1697</b>	K1PTY5_CRAGI (aa2393-4946)	3.1e-49	30.4%	Similar to Protocadherin Fat 4; domains:cadherin Lotgi1 154324 (0e0)/229125 (2.0e-163); 2 proteins?	-H	Y,O,B; I	18	0.0061
					<b>22033</b>	(aa7445-8584)	2.0e-144	37.3%
<b>246989</b>	(aa1090-1277)	3.3e-21	37.8%			Y,O; I	3	0.0058
<b>291505</b>	(aa2381-2937)	1.3e-59	35.1%			Y,O,B; I	4	0.0110
<b>3849</b>	(aa9466-10119)	4.5e-41	34.8%			Y,O,B; I	4	0.0030
					+H	Y,O,B; S<I	25	0.0127
						Y,O,B; S<I	19	0.0082
						Y,O; I	3	0.0143
						Y,O,B; S<I	6	0.0250
						Y,O,B; S<I	6	0.0080

<b>169764</b>	R7VB66_9ANNE (aa53-195)	3.0e-31	54.5%	Uncharacterized; signal peptide	-H	Y,O; S<I	5	0.0302
					+H	Y,O; S<I	6	0.1591
<b>170169</b>	F6MFF0_BRABE (aa29-608)	2.9e-31	26.2%	Similar to $\alpha$ 2-macroglobulin; domains: A2M_N, A2M_N_2; Lotgi1 229818 (4.4e-26)	-H	-	-	-
					+H	Y,O; I	3	0.0005
<b>1703</b>				Uncharacterized; 10% R, 11% Q, 10% G, 14% T	-H	Y,O; I	2	0.0004
					+H	Y,O; S<I	7	0.0020
<b>172966</b>	B4L6S0_DROMO (aa149-455)	7.4e-89	61.6%	Uncharacterized; domain: phosphoesterase; Lotgi1 150028 (3.2e-112)	-H	Y,O; I	2	0.0006
					+H	Y,O; S<I	4	0.0073
<b>1744</b>	Q6H3X5_PINFU	1.1e-84	87.6%	QM protein (ribosomal protein); Lotgi1 229535 (3.4e-127)	-H	-	-	-
					+H	Y,B; I	2	0.0010
<b>1757</b> <b>2598</b>	ESRSV6_HALDI (aa589-860) (aa34-562)	4.2e-45 1.1e-73	75.1% 72.6%	Paramyosin; Lotgi1 205639 (1.1e-103)/104779 (0e0)	-H	Y,O; S<I	14	0.0323
						Y,O; S<I	22	0.0167
					+H	O, I	1	0.0003
						O,B; I	3	0.0004
<b>1758</b>	K1R0Y9_CRAGI	1.1e-109	82.0%	ADP,ATP carrier protein; Lotgi1 232343 (1.0e-161)	-H	Y,O,B; S<I	4	0.0065
					+H	Y,O,B; S<I	4	0.0117
<b>1764</b>	TPM_HELAS	1.6e-22	52.3%	Tropomyosin; shares peptide with 6620; Lotgi1 162586 (2.0e-54)	-H	Y,O,B; I	3	0.0033
					+H	Y,O,B; I	7	0.0105
<b>1768</b>	E9H8M4_DAPPU	4.5e-84	81.1%	Uncharacterized; shares peptides with 19017, 27726,4405, 7641, 8216; domain: 14-3-3; Lotgi1 107549 (1.9e-116)	-H	Y,O,B; I	4	0.0103
					+H	Y,O,B; S<I	6	0.0291
<b>17713</b>				Uncharacterized; signal peptide	-H	Y,O,B; I	5	0.0060
					+H	B; I	2	0.0011
<b>18035</b>	R7U8H5_9ANNE	1.8e-38	40.9%	Uncharacterized/similar to D-beta-hydroxybutyrate dehydrogenase (K1Q2H3_CRAGI); Lotgi1 168913 (2.2e-78)	-H	Y,O; I	2	0.0010
					+H	-	-	-

<b>180559</b>	F7HD86_CALJA (aa80-245)	5.2e-12	34.5%	Uncharacterized; domain: peptidase_S1; Lotgi1 225501 (1.3e-8)	-H	Y,O,B; I	5	0.0262
					+H	Y,O; S<I	6	0.0553
<b>18225</b>	I3J590_ORENI (aa3-304)	4.1e-85	62.9%	Uncharacterized/actin-related protein 2/3 complex subunit 1A; Lotgi1 167800 (2.8e-155)	-H	-	-	-
					+H	Y; I	2	0.0009
<b>18268</b>	A7RQD5_NEMVE	8.0e-38	28.4%	Uncharacterized; signal peptide; Lotgi1 160009 (9.7e-7)	-H	Y,O,B; I	10	0.0117
					+H	Y,O,B; S<I	12	0.0301
<b>18276</b>	B8Y4I8_BIOGL	1.9e-188	91.6%	HSP60; Lotgi1 237408 (0e0)	-H	Y,O,B; I	3	0.0007
					+H	Y,O,B; S<I	8	0.0014
<b>1837</b>				Uncharacterized; 12% I, 15% S in 73aa	-H	Y,O,B; S<I	2	0.3739
					+H	Y,O,B;I	2	0.0434
<b>1850</b>				Uncharacterized; 22% P; transmembrane (or signal peptide if correct sequence starts at the first Met)	-H	Y,O,B; S>I	15	1.5474
					+H	Y,O,B; S>I	15	1.3134
<b>1869</b>	I1SKJ0_APLCA	2.5e-50	100%	Histone H2A; Lotgi1 156628 (1.3e-61)	-H	Y,O,B; S,I	4	0.1482
					+H	Y,O,B; S,I	2	0.0923
<b>188205</b>	H2T7Q9_TAKRU (aa1037-1211)	7.1e-6	31.7%	Uncharacterized; domain: cadherin Lotgi1 154324 (5.6e-10)	-H	O,B; I	1	0.0034
					+H	Y,O; I	1	0.0108
<b>18938</b>	E2C4M7_HARSA	4.0e-46	39.0%	Lamin Dm0; domain: Lamin_tail/IF; Lotgi1 179001 (5.3e-104)	-H	Y,O,B; I	4	0.0009
					+H	Y,O,B; I	4	0.0011
<b>19017</b>	I4331_CAEEL	2.2e-54	62.1%	aa49-287 similar to 14-3-3-like protein 1; shares peptide with 19017, 27726,4405, 7641, 8216; Lotgi1 222442 (7.4e-86)	-H	Y,O,B; S<I	3	0.0038
					+H	Y,O,B; S<I	3	0.0069
<b>190546</b>	A7RPT6_NEMVE (aa41-341)	4.8e-33	37.1%	Uncharacterized/similar to 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase; domains: Phospholipase_C_X, PH, EFh; Lotgi1 62286 (6.2e-65)	-H	-	-	-
					+H	Y; I	2	0.0005
<b>191</b>	K1QW36_CRAGI	1.9e-65	71.2%	60S ribosomal protein L6; Lotgi1 207552 (4.9e-84)	-H	Y,O,B; I	1	0.0005
					+H	Y,O,B; I	1	0.0004



<b>193976</b> <b>36933</b>	K1QSS1_CRAGI (aa1-173)	4.3e-59	74.6%	Uncharacterized; domain: Ndr; Lotgi1 150144 (1.5e-100/4.2e-61)	<b>-H</b>	<b>Y,O,B; I</b>	3	0.0049
	(aa175-356)	1.1e-35	56.6%		<b>Y,O,B; I</b>	3	0.0065	
					<b>+H</b>	<b>Y,O; S&lt;I</b> <b>Y,O,B; I</b>	4 7	0.0194 0.0217
<b>194050</b>	A4L7H3_BIOGL	9.8e-100	53.8%	Gram-negative bacteria binding protein; domains: Glyco_hydro_16/conA_like_lectin, transmembrane; Lotgi1 233531 (3.4e-102)	<b>-H</b>	<b>Y; I</b>	2	0.0012
					<b>+H</b>	-	-	-
<b>195796</b>	K1QBI9_CRAGI (aa169-536)	4.1e-86	54.1%	Cytosolic purine 5'-nucleotidase; domain: HAD_like; Lotgi1 190218 (4.0e-129)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; I</b>	3	0.0007
<b>19597</b>	R7TY81_9ANNE	1.2e-149	57.8%	Uncharacterized/similar to plastin; domains:actinin/CH, EFh; Lotgi1 152582 (0e0)	<b>-H</b>	<b>Y,O; I</b>	3	0.0003
					<b>+H</b>	<b>Y,O; I</b>	11	0.0041
<b>196388</b>				Uncharacterized; 12% A, 11% G, 11% P, 14% S; only 1 peptide possible!	<b>-H</b>	<b>Y,O,B; S,I</b>	1	0.1994
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	1	0.1422
<b>196754</b>				Uncharacterized; 14% P, 12% S; P-rich C-term	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; S</b>	3	0.0001
<b>19784</b>	K1PWM6_CRAGI	1.0e-35	43.8%	Neural/ectodermal development factor IMP-L2; domains: signal peptide, IG; Lotgi1 155640 (1.9e-64)	<b>-H</b>	<b>Y,O; I</b>	2	0.0025
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	2	0.0052
<b>198</b>	A6YM37_9EUPU (aa143-314)	1.2e-29	45.9%	Similar to matrilin_like 40kDa; domains: EGF_like, VWA; Lotgi1 74980 (2.6e-14)	<b>-H</b>	<b>Y,O,B; I</b>	2	0.0051
					<b>+H</b>	<b>Y,O,B; I</b>	4	0.0072
<b>1986</b>	RS3A_APLCA	9.6e-102	92.9%	40S ribosomal protein S3a; Lotgi1 202499 (2.7e-98)	<b>-H</b>	<b>Y,O,B; I</b>	1	0.0013
					<b>+H</b>	<b>Y,O,B; I</b>	3	0.0020
<b>19980</b>	Q56UG2_LYMST	6.4e-34	37.3 %	aa1-215 similar to Lipopolysaccharide binding protein-like protein/Bactericidal permeability increasing protein; Lotgi1 231708 (1.7e-48)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	8	0.0223
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	10	0.0722

20097	Q596I0_CRAGI	0e0	75.5%	Phosphorylase; Lotgi1 201834 (0e0)	-H	-	-	-
					+H	Y,O; I	4	0.0005
201				Uncharacterized; signal peptide; 11% N, 10% Q	-H	Y,O,B; S<I	10	0.5010
					+H	Y,O,B; S<I	11	1.2000
20308	Q2LZN0_DROPS (aa81-527)	1.6e-9	27.0%	aa49-467 similar to Dpse/GA10422/alkaline phosphatase; domains: signal peptide, alk_phos; Lotgi1 236474 (1.3e-13)	-H	Y,O,B; S<I	12	0.0475
					+H	Y,O,B; S<I	14	0.1142
20352	K1QVK3_CRAGI	2.4e-192	45.5%	Glutamyl aminopeptidase; domains: transmembrane, peptidase_M1, ERAP1_C; Lotgi1 130453 (0e0)	-H	-	-	-
					+H	Y,O; I	4	0.0005
20360	H9K6W1_APIME (aa687-1009)	3.9e-37	37.5%	Similar to cadherin; domains: cadherin; Lotgi1 167053 (1.5e-35); see also contig_75801!	-H	Y,O,B; S<I	7	0.0313
					+H	Y,O,B; S<I	8	0.1083
20638	C3Y2H6_BRAFL	1.2e-36	53.1%	Uncharacterized/similar to V-type proton ATPase subunit E (K1PIH2_CRAGI); Lotgi1 209321 (4.5e-60)	-H	Y,O,B; S<I	8	0.0155
					+H	Y,O,B; S<I	14	0.0987
2065				Uncharacterized; signal peptide	-H	Y,O,B; S>I	2	0.0171
					+H	Y,O,B; S	2	0.0107
207220				Uncharacterized; signal peptide; 13%S, 11% T; Lotgi1 169040 (2.6e-9)	-H	Y,O,B; S>I	2	0.0234
					+H	Y,O,B; S,I	2	0.0088
208250				Uncharacterized; 13% Q, 10% G	-H	Y,O,B; S>I	2	0.0074
					+H	Y,O; S	1	0.0036
21046	B7PIZ1_IXOSC	3.4e-142	71.9%	GDI-1 GDP dissociation inhibitor, putative (Fragment); shares peptide with 14802; domains: Rab_GDI; Lotgi1 218952 (0e0)	-H	Y,O,B; S<I	3	0.0007
					+H	Y,O; I	7	0.0031
21066	R7T7N1_9ANNE	5.1e-20	42.1%	Uncharacterized; domains: signal peptide, EFh; Lotgi1 234943 (8.5e-56)	-H	-	-	-
					+H	O; S	3	0.0014
2108				Uncharacterized; 10% A, 10% Q	-H	Y,O,B; S<I	8	0.5032
					+H	Y,O,B; S<I	8	1.3212

21112				Uncharacterized; 18% P, 10% N	-H	Y,O,B; S>I	8	3.5681
					+H	Y,O,B; S>I	8	3.4095
211922				Uncharacterized; transmembrane	-H	Y,O,B; S,I	1	0.0127
					+H	Y,O,B; S,I	1	0.0116
2120	A7RQU4_NEMVE	6.3e-48	65.9%	Uncharacterized/V-type proton ATPase 21 kDa proteolipid subunit; domains: transmembrane, V-ATPase_proteolipid_subunit; Lotgi1 223715 (5.8e-97)	-H	-	-	-
					+H	Y,O; I	3	0.0290
213707				Uncharacterized	-H	Y,O,B; I	2	0.0012
					+H	Y,O,B; S<I	4	0.0027
21551	C3YEW8_BRAFL	1.1e-31	40.4%	Uncharacterized/similar to cysteine proteinase 3 (K1QEW8_CRAGI); domains:signal peptide, peptidase_C1A; Lotgi1 172091 (2.2e-45)	-H	Y; S<I	2	0.0027
					+H	Y,O,B; S,I	6	0.0204
216988				Uncharacterized; domains: FN3	-H	Y,O,B; I	7	0.0054
					+H	Y,O; S<I	14	0.0735
2171	K1RB91_CRAGI	0e0	61.3%	Neutral $\alpha$ -glucosidase AB; domains: signal peptide, glycoside_hydrolase_31; Lotgi1 217135 (0e0)	-H	-	-	-
					+H	Y,O; I	8	0.0007
2177	H3C8Z4_TETNG	3.4e-17	31.1%	Uncharacterized; similarity to BMSP (G1UCX0_MYTGA) and Deleted in malignant brain tumors 1 protein(K1QA70_CRAGI); domains: EGF, VWA; Lotgi1 233176 (2.8e-22)	-H	Y,B; I	5	0.0027
					+H	Y,O,B; I	8	0.0098
22065	D2CLZ7_9PERC	2.0e-6	31.2%	Muscle fatty acid binding protein; domain: calycin	-H	Y,B; I	2	0.0013
					+H	-	-	-
221	K1QZ49_CRAGI (aa62-398)	2.3e-16	34.3%	Adipocyte plasma membrane-associated protein; Shares peptide with 8812; domains: signal peptide, TolB_like/strictosidine_synthase_related; See also contig_16710 and 6697; Lotgi1 115667 (2.4e-46)	-H	Y,O,B; S<I	13	0.0042
					+H	Y,O,B; S<I	24	0.0091
22210	G8DF88_DANPL	1.5e-159	76.5%	Citrate synthase; Lotgi1 170380 (0e0)	-H	-	-	-
					+H	Y; I	2	0.0005

22472	B5X305_SALSA	6.8e-87	44.0%	aa138-595 similar to cathepsin F and aa275-595 similar to aa378-714 of cathepsin F (K1QYP7_CRAGI); domains: signal peptide, peptidase inhibitor I25 (cystatin) and C1A (papain); Lotgil 207656 (6.3e-127)	-H	Y,O,B; I	8	0.0023
					+H	Y,O,B; S<I	10	0.0138
22541	K1PQI4_CRAGI	1.5e-51	58.8%	Enolase-phosphatase E1; 14% E; Lotgil 168703 (8.7e-104)	-H	Y,O,B; S<I	8	0.0104
					+H	Y,O,B; I	4	0.0026
22679	B8K1X2_FENCH	4.4e-38	73.5%	Triosephosphate isomerase	-H	Y,O,B; S,I	1	0.0045
					+H	Y,O,B; S,I	3	0.0161
226862	R7VE82_9ANNE (aa204-838)	3.8e-127	45.2%	Uncharacterized/chitobiase/ $\beta$ -hexosaminidase; domain: glycoside_hydrolase_20; Lotgil 168843 (0e0)	-H	-	-	-
					+H	Y,O; I	3	0.0009
227	D3BGG3_POLPA (aa471-830)	8.1e-5	23.9%	Similar to Zipper-like domain-containing protein; Lotgil 160957 (2.2e-13)	-H	Y,O,B; S<I	16	0.3286
					+H	Y,O,B; S<I	14	0.1975
228379	A9UTT4_MONBE	2.6e-169	92.1%	$\beta$ -tubulin; Lotgil 178823 (0e0)	-H	Y,O,B; S<I	3	0.0061
					+H	Y,O,B; S<I	4	0.0078
23	K1QFW9_CRAGI	0e0	81.5%	Uncharacterized/similar to elongation factor 2; Lotgil 180085	-H	Y,O,B; I	7	0.0017
					+H	Y,O; I	12	0.0063
23080	Q6TU32_APLCA	4.7e-116	74.3%	PKA type II regulatory subunit; Lotgil 51570 (9.8e-146)	-H	-	-	-
					+H	Y; I	2	0.0007
2339	K1QQK6_CRAGI (aa35-165)	6.3e-10	37.1%	Calcium-dependent protein kinase isoform 2; domains: EFh; 11% D, 10% E, 13% K; Lotgil 84721 (1.8e-19)	-H	Y,O,B; I	6	0.0116
					+H	Y,O,B; S<I	6	0.0307
2357				Uncharacterized protein; domains: signal peptide, LDL_recept_a; 15% T; Lotgil 159329 (5.4e-9)	-H	Y,O,B; S<I	13	0.0890
					+H	Y,O,B; S,I	12	0.1907
23598				Uncharacterized; 26% Q, 12% S, 11% T; Lotgil 172698 (1.3e-6)	-H	Y,O,B; S>I	1	0.0054
					+H	Y,O,B; S	1	0.0029

<b>2380</b>	K1QL55_CRAGI (aa413-735)	1.0e-114	77.8%	Protein phosphatase 1B; domain: protein_ phosphatase_2C; Lotgi1 194163 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y; I</b>	2	0.0004
<b>23899</b>	R7TVD2_9ANNE	0e0	57.9%	Uncharacterized/IQGAP protein; domains: IQ, RasGAP, CH; Lotgi1 162747 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y; I</b>	16	0.0011
<b>2429</b>	L7M4W5_9ACAR	2.0e-59	71.7%	Ribosomal protein L13; Lotgi1 197609 (2.6e-68)	<b>-H</b>	<b>Y,O,B; I</b>	2	0.0047
					<b>+H</b>	<b>Y,O,B; I</b>	2	0.0029
<b>24305</b>	K1QNT7_CRAGI	1.6e-152	70.5%	Aldehyde dehydrogenase, mitochondrial; Lotgi1 177987 (0e0)	<b>-H</b>	<b>Y,O,B; I</b>	2	0.0005
					<b>+H</b>	<b>Y,O; I</b>	1	0.0003
<b>24452</b>	N6T3L3_9CUCU	5-1e-117	56.9%	Uncharacterized/purple acid phosphatase; domains: phosphoesterase, signal peptide; Lotgi1 1500028 (1.2e-137)	<b>-H</b>	<b>Y,O; I</b>	1	0.0004
					<b>+H</b>	<b>Y,O; I</b>	4	0.0021
<b>24529</b>				Uncharacterized; signal peptide; 11% Q; Lotgi1 159706 (1.0e-16)	<b>-H</b>	<b>Y,O,B; S,I</b>	11	0.0142
					<b>+H</b>	<b>Y,O,B; S,I</b>	11	0.0128
<b>2456</b>	B3TK66_HALDV	4.4e-68	81.6%	Ribosomal protein S8; Lotgi1 239290 (1.5e-78)	<b>-H</b>	<b>Y,O,B; I</b>	3	0.0059
					<b>+H</b>	<b>Y,B; I</b>	3	0.0060
<b>2468</b>	D7RP02_HALDV	1.1e-90	71.6%	Voltage-dependent anion channel 2-like protein; domains: porin; Lotgi1 168464 (9.4e-1409)	<b>-H</b>	<b>Y,O,B; I</b>	6	0.0102
					<b>+H</b>	<b>Y,O,B; I</b>	6	0.0111
<b>247174</b>	GNAQ_LYMST	1.0e-140	93.2%	Guanine nucleotide-binding protein G(q) subunit alpha; Lotgi1 194019 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; I</b>	4	0.0010
<b>248122</b>	C3Z1I6_BRAFL (aa338-498)	6.1e-15	38.8%	Uncharacterized/similar to chitinase; domains: glyco_hydro_18/chitinase; Lotgi1 195782 82.1e-31)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	3	0.0481
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	4	0.1318
<b>24851</b>	MTAP_DANRE	1.7e-79	64.7%	S-methyl-5'-thioadenosine phosphorylase; Lotgi1 216998 (6.3e-131)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y; I</b>	2	0.0005
<b>2503</b>	H2SK47_TAKRU	4.1e-40	83.9%	Uncharacterized/similar to V-ATPase proteolipid subunit; domains: VACATPASE, transmembrane; Lotgi1 224185 (1.3e-42)	<b>-H</b>	<b>O; I</b>	1	0.0096
					<b>+H</b>	<b>Y,O; S&lt;I</b>	1	0.0570

<b>250568</b> <b>42886</b>	K1QZN3_CRAGI (aa1-424)	1.1e-108	69.3%	Myosin-Id; Lotgi1 143556 (0e0)	<b>-H</b>	-	-	-
	(aa636-1023)	1.6e-101	59.2%		<b>+H</b>	Y; I	6	0.0019
						Y; I	2	0.0005
<b>2521</b>	A5Z1D6_9EUPU (aa1-156)	5.8e-12	34.4%	Epiphragmin; domain: transmembrane	<b>-H</b>	Y,O,B; I	6	0.0738
					<b>+H</b>	Y,O,B; S<I	6	0.0585
<b>25443</b>	K1QAP9_CRAGI (aa94-284)	2.8e-19	38.0%	Similar to collagen $\alpha$ 1(XII) chain non-triple helical domain; domains: VWA; Lotgi1 123318 (2.7e-23)	<b>-H</b>	Y,O,B; I	5	0.0125
					<b>+H</b>	O; S<I	5	0.0063
<b>25444</b>	Q568E7_DANRE	5.6e-35	45.4%	Similar to Zgc:110339; domains: transmembrane, short_chain_dehydrogenase; Lotgi1 131045 (5.6e-35)	<b>-H</b>	Y,O,B; I	3	0.0023
					<b>+H</b>	Y,B; I	3	0.0006
<b>25522</b>	K1RCB4_CRAGI (aa28-746)	1.8e-24	26.0%	Similar to von Willebrand factor D and EGF domain-containing protein; domains: VWD, EGF; Lotgi1 158683 (5.6e-76)	<b>-H</b>	Y,O,B; S<I	16	0.0155
					<b>+H</b>	Y,O,B; S<I	19	0.0218
<b>256482</b>				Uncharacterized; domains: FN3/IG	<b>-H</b>	Y,O; S<I	1	0.0053
					<b>+H</b>	Y,O; S<I	4	0.0710
<b>25670</b>	Q32NX0_XENLA	1.7e-52	46.0%	Uncharacterized; domains: Peptidase_C26/ $\gamma$ -glutamyl hydrolase, transmembrane; Lotgi1 108329 (8.0e-76)	<b>-H</b>	Y,O; I	2	0.0092
					<b>+H</b>	Y,O; S<I	3	0.0364
<b>25804</b> <b>36369</b>	Q9BKQ1_APLCA (aa348-735) (aa27-354)	1.2e-59 1.5e-58	44.6% 45.1%	NCAM-related adhesion molecule; domains: IG, signal peptide; Lotgi1 230852 (4.7e-44)/ Lotgi1 51189 (2.1e-19)	<b>-H</b>	-	-	-
						Y,O,B; S<I	5	0.0173
					<b>+H</b>	Y; I	2	0.0006
						Y,O,B; S<I	6	0.0321
<b>25826</b>	Q45RT8_BIOGL	1.4e-75	81.4%	Fructose-bisphosphate aldolase; Lotgi1 217342 (2.0e-97)	<b>-H</b>	Y,O; I	2	0.0019
					<b>+H</b>	-	-	-
<b>258525</b>	Q5DL74_BIOGL	6.4e-5	31.3%	Similar to Calcium binding protein 1; domains: signal peptide, EFh; Lotgi1 236429 (6.8e-7)	<b>-H</b>	Y,O,B; S,I	3	0.0368
					<b>+H</b>	-	-	-

25891	J7QJT8_PATVU	6.3e-25	34.7%	Carbonic anhydrase; domains: signal peptide, αCA; Lotgi1 144122 (2.4e-65)	-H	Y,O,B; S<I	36	0.2168
					+H	Y,O,B; S<I	42	0.5870
25994	044341_HALRU (aa788-865)	0.0086	38.6%	Similar to lustrin A; signal peptide; 12% C, 10% L, 10% T	-H	Y,O; I	1	0.0092
					+H	Y,O,B; S<I	2	0.0105
261700				Uncharacterized; domain: transmembrane; 12% S	-H	Y,B; S,I	1	0.0009
					+H	Y,B; S	2	0.0013
263				Uncharacterized, many gaps in sequence! only 1 peptide possible!	-H	Y,O,B; S,I	1	0.0467
					+H	Y,O,B; S<I	1	0.2115
263455				Uncharacterized; 20% Q, very Q-rich N-term	-H	Y,O; S>I	1	0.0004
					+H	Y; S,I	2	0.0001
2636	P3476-2 (aa378-714)	4.6e-6	27.2%	Similar to Transmembrane cell adhesion receptor mua-3 (MUA_CAEEL); domain: VWA; Lotgi1 234764 (1.7e-10)	-H	-	-	-
					+H	O; I	3	0.0007
26404	B4N170_DROWI (aa1001-2481)	1.6e-89	29.8%	Similar to GK24802; domains: Sushi/SCR(CCP, EGF, Hyalin, GCC2_GCC3; Lotgi1 230171 (0e0)	-H	-	-	-
					+H	Y; I	2	0.0003
26435				Uncharacterized; 10% A, 13% S, 16% T	-H	Y,O,B; S>I	5	0.0356
					+H	Y,O,B; S>I	4	0.0650
264452	K1Q2S1-CRAGI (aa184-400)	2.6e-5	24.3%	Similar to cartilage matrix protein; domain: CBM_14/CHIT_BIND_II (~aa1-70)	-H	Y,O; S	2	0.0041
					+H	Y,O,B; S>I	3	0.0053
26574	R7TH93_9ANNE (aa1-675)	4.4e-145	51.9%	Uncharacterized/vacuolar-type H(+)-ATPase; domain: V_ATPase_I; Lotgi1 108161 (0e0)	-H	Y,O,B; I	7	0.0030
					+H	Y,O,B; S<I	14	0.0328
2666	A7RH56_NEMVE (aa212-367)			Uncharacterized; domain: peptidase_A1/cathepsin D; Lotgi1 173095 (1.4e-63)	-H	Y; I	2	0.0006
					+H	Y,O; I	4	0.0017
26661	E6Y6Q1_APLCA	2.3e-103	72.8%	Gelsolin; Lotgi1 214936 (5.0e-139)	-H	Y,O,B; I	5	0.0025
					+H	Y,O,B; S<I	10	0.0216

<b>2668</b>				Uncharacterized; domains: Sushi/SCR/CCP, signal peptide; 10% A, 13% G, 10% S; Lotgi1 197362 (4.5e-11)	<b>-H</b>	<b>Y,O,B;</b> S>I	12	3.8981
					<b>+H</b>	<b>Y,O,B;</b> S>I	13	3.8723
<b>2678</b>	R4WRF7_9HEMI	1.2e-37	79.5%	V-type proton ATPase subunit F; Lotgi1 205831 (2.9e-54)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y;</b> I	3	0.0107
<b>269</b>				Uncharacterized; 18% G	<b>-H</b>	<b>Y,O,B;</b> S<I	8	0.6532
					<b>+H</b>	<b>Y,O,B;</b> S<I	8	0.4419
<b>2692</b>	M4VQH6_APLCA	2.0e-107	79.2%	GAPDH; almost the same	<b>-H</b>	<b>Y,O,B;</b> I	8	0.0123
<b>2985</b>		1.6e-110	81.9%	Lotgi1 222542 (1.8e-108)	<b>+H</b>	<b>Y,O,B;</b> S<I	12	0.0177
<b>27174</b>	CCAP_CONVL (aa28-100)	1.1e-10	54.7%	aa80-164 similar to conoaCAP; domains: CCAP, signal peptide; Lotgi1 163724 (4.7e-6)	<b>-H</b>	<b>Y,O;</b> S,I	2	0.0015
					<b>+H</b>	<b>O,B;</b> S>I	2	0.0025
<b>272613</b>				Uncharacterized; domain: transmembrane	<b>-H</b>	<b>O,B;</b> S>I	1	0.0316
					<b>+H</b>	<b>Y,O,B;</b> S>I	2	0.0147
<b>273</b>	M4AKV7_XIPMA	9.5e-35	47.0%	Uncharacterized/similar to sialic acid-binding lectin; domain: fibrinogen_C; Lotgi1 228333 (2.0e-30)	<b>-H</b>	<b>Y,O,B;</b> I	2	0.0065
					<b>+H</b>	<b>O,B;</b> I	6	0.0475
<b>27370</b>	F1NCJ8_CHICK	4.6e-35	35.8%	Uncharacterized; domain: methyltransferase; Lotgi1 167413 (4.7e-96)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y;</b> S<I	4	0.0025
<b>2744</b>				Uncharacterized; 10% K, 10% S	<b>-H</b>	<b>Y,O,B;</b> S<I	10	0.6080
					<b>+H</b>	<b>Y,O,B;</b> S<I	14	0.9048
<b>27726</b>	E7EX29_HUMAN	6.0e-61	66.7%	14-3-3 ζ/δ ; shares peptides with other 14-3-3 proteins; Lotgi1 205379 (8.7e-83)	<b>-H</b>	<b>Y,O,B;</b> I	2	0.0017
					<b>+H</b>	<b>Y,O,B;</b> I	5	0.0054
<b>277362</b>	K1RN67_CRAGI (aa971-1220)	7.3e-37	42.6%	Similar to Receptor-type tyrosine-protein phosphatase T; Lotgi1 102205 (5.3e-53)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O;</b> I	2	0.0020
<b>27801</b>	K1PZK2_CRAGI	3.3e-53	74.9%	Putative myosin regulatory light chain; domains: EFh; Lotgi1 190618 (6.8e-89)	<b>-H</b>	<b>Y,O,B;</b> I	1	0.0017
					<b>+H</b>	<b>Y,B;</b> I	1	0.0019



<b>27819</b>	G1LA32_AILME	9.2e-56	44.4%	Uncharacterized; domain: serpin; Lotgi1 195172 (1.7e-48)	-H	Y,B; I	2	0.0006
					+H	Y,O; I	4	0.0016
<b>27977</b>	H9KHU2_APIME	5.0e-35	34.3%	Uncharacterized/similar to membrane metallo-endopeptidase-like; domain: peptidase M13; Lotgi1 165736 (7.2e-53)	-H	Y,O,B; I	3	0.0034
					+H	-	-	-
<b>28132</b>	C3XVU1_BRAFL (aa512-857)	9.8e-18	28.5%	Uncharacterized/similar to fibrillin; domains: EGF; 11% C, 11% G, 10% S; Lotgi1 230443 (1.4e-29)	-H	Y,O,B; I	3	0.0024
					+H	-	-	-
<b>2836</b>	K1QWX2_CRAGI	1.3e-91	78.6%	60S acidic ribosomal protein P0; Lotgi1 237709 (2.0e-144)	-H	Y,O,B; S<I	4	0.0034
					+H	Y, O; I	5	0.0048
<b>28471</b>	K1PQF1_CRAGI	1.5e-60	33.0%	Similar to neural cell adhesion molecule L1; domains: signal peptide, IG, transmembrane segment; Lotgi1 239531 (7.3e-61)	-H	Y,B; I	2	0.0010
					+H	Y,B; I	1	0.0004
<b>2855</b>	A4LAB0_DORPE	7.6e-52	43.2%	Na <sup>+</sup> /K <sup>+</sup> ATPase beta subunit; Lotgi1 213719 (3.8e-81)	-H	Y,O,B; S<I	2	0.0096
					+H	Y,O; S,I	5	0.0182
<b>2858</b>	H2ZUY5_LATCH (aa165-414)	5.5e-41	44.6%	Uncharacterized/similar to adipocyte plasma membrane-associated protein; domains: TolB_like/strictosidine:synthase_related; Lotgi1 231719 (3.8e-81)	-H	Y,O,B; S<I	8	0.0388
					+H	Y,O,B; S<I	11	0.1403
<b>28685</b>	H1AFK3_APLKU	0e0	58.5%	Beta-D-mannosidase; domains: transmembrane, glycoside_hydrolase_fam_2; Lotgi1 212346 (0e0)	-H	-	-	-
					+H	Y,O; I	3	0.0002
<b>28902</b>	B6DYD6_PROCL	2.7e-50	100%	Calmodulin; Lotgi1 216228 (1.1e-94)	-H	Y,O,B; S<I	5	0.0337
					+H	Y,O,B; S<I	3	0.0285
<b>28994</b>	K1QPM9_CRAGI	1.5e-22	45.6%	Similar to fatty acid-binding protein, brain; Lotgi1 158663 (2.9e-26)	-H	Y,O,B; S,I	5	0.1948
					+H	Y,O,B; S,I	7	0.2396
<b>29148</b>	K1S5N3_CRAGI	1.3e-103	53.4%	Hexokinase type 2; Lotgi1 233221 (0e0)	-H	-	-	-
					+H	Y; I	3	0.0005
<b>29171</b>	G0YL88_MYTGA	8.8e-123	47.0%	MACPF domain-containing protein; domains: MACPF_1/perforin, signal peptide	-H	Y,O,B; I	7	0.0148
					+H	Y,O,B; S<I	9	0.0229

<b>29173</b> <b>59951</b>	G0YL88_MYTGA (aa359-557)	7.3e-49	52.3%	MACPF domain-containing protein; fragment;	<b>-H</b>	<b>Y,O,B; I</b>	3	0.0128
	(aa24-171)	8.9e-22	39.7%	signal peptide		<b>Y,O,B; I</b>	3	0.0020
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	5	0.0293
						<b>Y,O,B; S&lt;I</b>	3	0.0096
<b>29423</b>	Q8MY76_9BIVA	1.3e-140	37.9%	aa209-1416 similar to Se-cadherin, fragment; Lotgi1 167053 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; I</b>	4	0.0005
<b>29324</b>	E1B2D0_9BIVA (aa12-401)	2.5e-135	71.7%	Catalase; Lotgi1 13141 (0e0)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	13	0.0149
					<b>+H</b>	-	-	-
<b>29426</b>	K1QGP8_CRAGI (aa188-2080)	7.9e-65	29.7%	aa304-2129 similar to atrial natriuretic peptide- converting enzyme; domains: MAM, trypsin, LDLRA, frizzled; Lotgi1 167919 (0e0)	<b>-H</b>	<b>Y,O; I</b>	1	<0.0001
					<b>+H</b>	<b>Y,O; I</b>	5	0.0004
<b>29558</b>	F6XNT9_XENTR	4.9e-139	50.3%	$\beta$ -galactosidase; transmembrane/signal peptide; Lotgi1 236200 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; I</b>	3	0.0005
<b>2957</b>	K1PVC1_CRAGI	1.1e-38	37.9%	aa121-395 similar to Carbohydrate sulfotransferase 11; domains; transmembrane/signal sequence, sulfotransf_2; Lotgi1 166777 (2.6e-88)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; S&lt;I</b>	3	0.0013
<b>297</b>	G3FPE5_HELLU (aa2924-3142)	1.0e-70	77.3%	Similar to $\beta$ -hemocyanin (probably not identical!), shares peptide with contig_67	<b>-H</b>	<b>Y,O,B; I</b>	3	0.0068
					<b>+H</b>	<b>Y,O,B; I</b>	3	0.0082
<b>2977</b>	Q8I8Y1_MANSE (aa260-744)	7.2e-103	45.5%	; domains: cupredoxin; Lotgi1 231844 (7.0e-152)	<b>-H</b>	<b>B; I</b>	2	0.0007
					<b>+H</b>	-	-	-
<b>3002</b> <b>39893</b>	Q000T7_PINFU (aa1-302) (aa1-146)	8.4e-114	84.8%	ATP synthase subunit $\alpha$ ; same protein with microheterogeneities? Lotgi1 206617 (0e0)/178690 (2.1e-64)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	9	0.0285
		4.5e-37	75.5%		<b>+H</b>	<b>Y,O,B; S&lt;I</b> <b>Y; I</b>	11 2	0.0384 0.0022
<b>3007</b>	K1QZJ5_CRAGI (aa20-534)	8.8e-80	42.8%	Similar to glucose dehydrogenase [acceptor]; Lotgi1 169492 82.0e-70)	<b>-H</b>	<b>Y,O; I</b>	2	0.0003
					<b>+H</b>	<b>Y,O; I</b>	3	0.0004
<b>30629</b>	R7TIU6_9ANNE	1.5e-95	60.9%	Uncharacterized/Vesicle amine transport protein; domains: ADH, GroES_like; Lotgi1 219806 (8.6e-115)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y; I</b>	2	0.0003

3069	K1QXS6_CRAGI (aa1-303)	5.7e-35	53.9%	Similar to heterogeneous nuclear ribonucleoprotein A2-like protein 1; Lotgi1 166794 (8.5e-68)	-H	Y,O; I	2	0.0003
					+H	Y; I	2	0.0002
3077	B0WIN7_CULQU (aa151-335)	7.4e-22	35.2%	Similar to peritrophic membrane chitin binding protein; domains:chitin deacetylase; Lotgi1 153749 (2.8e-30)	-H	Y,O,B; S<I	6	0.0495
					+H	Y,O,B; S<I	7	0.0548
30790	K1PNR3_CRAGI	0e0	88.3%	Clathrin heavy chain 1; Lotgi1 233411 (0e0)	-H	O,B; S>I	5	0.0002
					+H	Y,O,B; I	6	0.0001
31026	A7SDH9_NEMVE (aa254-665)	1.7e-76	48.3%	Uncharacterized; domains: phospholipase_C, CH; Lotgi1 201534 (7.4e-161)	-H	-	-	-
					+H	Y; I	3	0.0008
3107				Uncharacterized; signal peptide; 12% R, 11% S, 11% T, 10% V	-H	Y,O,B; I	5	0.0116
					+H	Y,O,B; S<I	5	0.0324
31170	K7S1Q8_NASVI (aa431-797)	3.2e-37	35.0%	Uncharacterized; domains: CMB_14/CHIT_BIND_II, signal peptide; Lotgi1 153749 (7.4e-45)	-H	Y,O,B; S<I	13	0.0769
					+H	Y,O,B; S<I	17	0.1140
31301	G3VTN2_SARHA	7.2e-30	29.9%	Uncharacterized/similar to renin receptor; domains: renin_receptor, transmembrane; Lotgi1 211795 (1.1e-71)	-H	Y,O,B; S<I	5	0.0030
					+H	Y,O; S<I	7	0.0173
313922				Uncharacterized; signal peptide	-H	Y,O,B; S<I	3	0.0306
					+H	-	-	-
31433	I1VYY1_MYTTR	3.2e-158	77.7%	Isocitrate dehydrogenase; Lotgi1 220933 (0e0)	-H	Y,O; I	2	0.0006
					+H	Y,O,B; I	4	<0.0001
32001	K1PQI4_CRAGI	1.1e-31	55.2%	Enolase-phosphatase E1; Lotgi1 168703 (4.5e-57)	-H	Y,O,B; I	2	0.0037
					+H	Y,O,B; I	3	0.0025
320130	K1QC92_CRAGI (aa320-509)	4.7e-41	45.8%	Similar to Sulfhydryl oxidase 1; domain: ERV_ALR; Lotgi1 237352 (1.5e-65)	-H	-	-	-
					+H	Y,O; S<I	2	0.0036
32297				Uncharacterized; signal peptide; 14% G, 10% P	-H	Y,O,B; S>I	2	0.2826
					+H	Y,O,B; S>I	2	0.2291

<b>3243</b>				Uncharacterized; domains: signal peptide, H-type_lectin	<b>-H</b>	<b>Y,O,B; I</b>	2	0.0044
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	3	0.0098
<b>324404</b>	K1PUB4_CRAGI	7.8e-13	37.3%	Similar to ADAM family mig-17; domain: peptidase M12B; Lotgi1 228200 (8.0e-29)	<b>-H</b>	<b>Y,O,B; I</b>	2	0.0088
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	2	0.0348
<b>32583</b>	A1L3T3_MOUSE	7.8e-127	54.6%	Similar to N-sulfoglucosamine sulfohydrolase/heparin N-sulfatase; domains: sulfatase, signal peptide; Lotgi1 175173 (0e0)	<b>-H</b>	<b>Y,O,B; I</b>	6	0.0030
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	8	0.0137
<b>32596</b>	Q86DI0_APLCA	1.3e-68	97.7%	Rac; domain: Ras/Rho; Lotgi1 230301 (1.2e-115)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; I</b>	2	0.0014
<b>32713</b>				Uncharacterized; domains: EFh	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	3	0.0093
					<b>+H</b>	<b>Y,O; S&lt;I</b>	4	0.0081
<b>32845</b>				Uncharacterized; domain: ShK	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	4	0.0010
					<b>+H</b>	<b>Y,O,B; S&gt;I</b>	8	0.0030
<b>32858</b>	K1PXG8_CRAGI	1.1e-157	99.1%	Serine/threonine-protein phosphatase; shares peptide with contig_39278	<b>-H</b>	<b>Y,O; S,I</b>	2	0.0005
					<b>+H</b>	<b>Y,O; I</b>	2	0.0009
<b>33806</b>	A7SFM8_NEMVE	7.6e-107	52.3%	Aldehyde dehydrogenase; Lotgi1 229102 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O; I</b>	4	0.0011
<b>34386</b>	K1PD20_CRAGI	7.6e-70	46.3%	Similar to Di-N-acetylchitobiase; domains: chitinase_II, signal peptide; Lotgi1 209107 (7.1e-99)	<b>-H</b>	<b>Y,O; I</b>	3	0.0006
					<b>+H</b>	<b>Y,O; S&lt;I</b>	16	0.0076
<b>34455</b>	H9LSX1_CRAGI	1.6e-90	60.6%	Cathepsin B; Lotgi1 197490 (6.4e-137)	<b>-H</b>	<b>Y,O; I</b>	2	0.0009
					<b>+H</b>	<b>Y,O; S&lt;I</b>	5	0.0122
<b>3453</b>	L7NCQ8_9CAEN	3.1e-51	56.6%	Mu-class glutathione S-transferase; domains: GST_N, GST_C; Lotgi1 233779 (1.5e-68)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y; I</b>	2	0.0002
<b>34537</b>	C3YKY0_CRAGI	7.1e-15	36.6%	Uncharacterized; Lotgi1236424 (1.2e-20)	<b>-H</b>	<b>Y,O,B; S,I</b>	2	0.0054
					<b>+H</b>	-	-	-

34569	S4R9R4_PETMA	6.2e-82	77.1%	Uncharacterized/V-type proton ATPase subunit d 1; Lotgi1 108853 (1.8e-137)	-H	Y,O; I	2	0.0015
					+H	Y,O; S<I	6	0.0143
34894	B3RQ10_TRIAD (aa417-1735)	2.6e-26	24.2%	Uncharacterized; domains: EGF, VWD, extracellular (IPR003886), transmembrane; Lotgi1 166811 (1.9e-66)	-H	-	-	-
					+H	Y; I	5	0.0012
34916	B7PSF8_IXOSC (aa504-655)	3.6e-12	31.2%	Similar to hemocyte protein-glutamine $\gamma$ -glutamyltransferase; domain: transglutam_C; IG; Lotgi1 231723 (4.2e-33)	-H	Y,O,B; I	2	0.0020
					+H	Y,O,B; S<I	5	0.0089
35033	B0JZP5_DANRE	8.1e-55	41.3%	DNAse 2; Lotgi1 125778 (8.9e-64)	-H	Y,O,B; I	2	0.0013
					+H	Y,O; S>I	2	0.0047
35115	B6RB39_HALDI	4.7e-12	26.2%	Similar to X-box binding protein; domain: ependymin, signal peptide; Lotgi1 233583 (1.1e-15)	-H	Y,B; I	1	0.0063
					+H	Y,B; S,I	1	0.0021
351458				Uncharacterized; domains: PDZ; 13% S	-H	Y,O,B; S<I	1	0.0107
					+H	Y,O,B; I	1	0.0041
353	C3YD43_BRAFL	1.7e-30	69.3%	Ribosomal protein L23; Lotgi1 179313 (5.3e-55)	-H	Y,B; I	1	0.0024
					+H	Y,B; I	1	0.0024
353551	Q32R30_EPTBU (aa64-160)	6.9e-6	38.8%	aa4-105 similar to Variable lymphocyte receptor A; domains: Leu-rich repeats; Lotgi1 171753 (1.0e-11)	-H	-	-	-
					+H	Y,O; I	2	0.0007
358462	K1QPM9_CRAGI	8.1e-4	27.9%	Similar to fatty acid binding protein; domain: calycin_like; 15% T, 12% V	-H	Y,O,B; I	4	0.0078
					+H	-	-	-
35849	R7VAX7_9ANNE (aa9-485)	5.1e-117	54.4%	$\beta$ -hexosaminidase; shares 2 peptides with contig_11304; domains: signal sequence, glycol_hydro_20; Lotgi1 120422 (5.5e-177)	-H	-	-	-
					+H	Y,O; S<I	3	0.0011
35852				Uncharacterized; 11% A, 11% P	-H	Y,O,B; S,I	13	0.7909
					+H	Y,O,B; S>I	14	1.4581
359	IFEA_HELAS (aa444-551)	9.4e-51	93.1%	Non-neuronal cytoplasmic intermediate filament protein; Lotgi1 156050 (6.6e-11)	-H	Y,O,B; I	4	0.0702
					+H	Y,O,B; S<I	4	0.0935

36266	R7TC05_9ANNE	4.3e-167	56.0%	Uncharacterized/ $\beta$ -glucuronidase; domains: glycoside_hydrolase_family_2, signal peptide; Lotgi1 165508 (0e0)	-H	Y,O,B; I	1	0.0004
					+H	Y; I	1	0.0004
3631	R7UU94_9ANNE (aa185-275)	1.2e-11	42.9%	Uncharacterized/ $\alpha$ -carbonic anhydrase; domain: $\alpha$ -CA; Lotgi1 163324 (6.0e-13)	-H	Y,O,B; I	3	0.0374
					+H	Y,O,B; S<I	2	0.0702
36446	K1QA50_CRAGI (aa22-427)	8.4e-115	65.3%	V-type proton ATPase subunit H; Lotgi1 207139 (0e0)	-H	Y,O; I	7	0.0016
					+H	Y,O; S<I	14	0.0220
36714				Uncharacterized; domains: FN3	-H	-	-	-
					+H	Y,O; S<I	2	0.0230
37078	K1PXB8_CRAGI (aa25-554)	1.6e-28	25.4%	aa52-552 similar to disintegrin and metalloproteinase with thrombospondin motifs 1; domains: signal peptide, peptidase_M12B; Lotgi1 171445 (1.4e-50)	-H	-	-	-
					+H	Y,O; S,I	2	0.0003
3720	K1PVW0_CRAGI (aa197-410)	8.8e-76	85.0%	S-adenosylmethionine synthetase; Lotgi1 141813 (5.8e-115)	-H	Y,O,B; S<I	1	0.0027
					+H	Y,O,B; I	1	0.0024
37240				Uncharacterized; signal peptide	-H	Y,B; S,I	2	0.0042
					+H	Y,B; S	2	0.0032
37423	B4LLG4_DROVI	4.4e-44	62.2%	GJ22316/FKBP-type peptidyl-prolyl cis-trans isomerase; domans: signal peptide, PPI_FKBP_type; Lotgi1 238515 (1.3e-54)	-H	Y,O; I	1	0.0010
					+H	Y,O; S	1	0.0018
3748	Q0KHB6_CRAGI	2.2e-172	69.2%	Pyruvate kinase; Lotgi1 199626 (0e0)	-H	-	-	-
					+H	Y,O,B; I	19	0.0106
3773	Q45RT8_BIOGL (aa1-175)	8.2e-58	79.4%	Fructose-bisphosphate aldolase; Lotgi1 217342 (5.2e-81)	-H	Y,O,B; I	4	0.0048
					+H	Y,O; I	7	0.0221
3799	K1PJE5_CRAGI (aa119-347)	2.4e-43	49.1%	Pancreatic triacylglycerol lipase (Fragment); Lotgi1 216931 (3.0e-71)	-H	Y,O; I	1	0.0003
					+H	Y,O; S<I	5	0.0010

38327	K1PTI6_CRAGI	3.2e-181	72.1%	Glucose-6-phosphate isomerase; Lotgi1 217535 (0e0)	-H	-	-	-
					+H	Y,B; I	2	0.0007
38376	K1RWX7_CRAGI	3.4e-112	28.3%	Similar to metabotropic glutamate receptor 3; domains: signal peptide, transmembrane, GPCR_3, ANF_receptor, periplasmic_binding_like_1; Lotgi1 152964 (0e0)	-H	-	-	-
					+H	Y,O; I	6	0.0002
38447	K1QHL0_CRAGI (aa10-220)	3.3e-31	42.9%	Allene oxide synthase-lipoxygenase protein; Lotgi1 171809 (9.8e-63)	-H	B; I	1	<0.0001
					+H	Y,O; I	3	0.0035
38612	G3NQT9_GASAC (aa280-662)	6.2e-131	77.9%	Uncharacterized/succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial; Lotgi1221335 (0e0)	-H	Y,O,B; I	3	0.0012
					+H	Y,O,B; I	3	0.0022
3868	D7QYI1_BIOGL (aa378-661)	8.7e-51	48.6%	Thioester-containing protein 1.5; domain: A2M_N_2; Lotgi1 162872 (8.0e-38); see also contig_11338 and 21999	-H	Y,O,B; S<I	8	0.0522
					+H	Y,O,B; S<I	7	0.0172
38710	K1P9R1_CRAGI	2.3e-83	50.6%	Anhydro-N-acetylmuramic acid kinase; Lotgi1 122845 (1.9e-147)	-H	-	-	-
					+H	Y; I	3	0.0012
3883	K1Q9V3_CRAGI	5.9e-190	86.2%	V-type proton ATPase catalytic subunit A; Lotgi1 185986 (0e0)	-H	Y,O,B; S<I	19	0.0247
					+H	Y,O,B; S<I	27	0.1671
38980 39106	K1R401_CRAGI (aa1545-2108) (aa1-381)	2.1e-151 5.4e-53	79.3% 59.5%	Spectrin $\alpha$ -chain; Lotgi1 202396 (0e0)	-H	-	-	-
					+H	Y,B; I Y,O; I	5 3	0.0006 0.0002
39018				Uncharacterized; signal peptide	-H	Y,O,B; I	2	0.0076
					+H	Y,O,B; S<I	3	0.0130
3938				Uncharacterized; signal peptide	-H	Y,O,B; S>I	2	0.5678
					+H	Y,O,B; S>I	2	0.5817
3942	K1QHY1_CRAGI (aa112-696)	2.7e-77	36.2%	Similar to eosinophil peroxidase; domains: Haem_peroxidase, signal peptide; Lotgi1 233510 (7.3e-75); see also contig_11883	-H	Y,O,B; I	5	0.0004
					+H	-	-	-

<b>394728</b>				Uncharacterized	<b>-H</b>	<b>Y,O,B;</b> S<I	4	0.0089
					<b>+H</b>	-	-	-
<b>401</b>	F7A172_CIOIN	2.2e-91	75.0%	Ribosomal protein L5 ; Lotgi1 171614 (8.4e-113)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,B;</b> I	2	0.0021
<b>4048</b>	K1QX26_Cragi (aa608-1082)	7.5e-122	74.0%	Endoplasmin; Lotgi1 197084 (0e0)	<b>-H</b>	<b>Y,O,B;</b> S<I	3	0.0016
					<b>+H</b>	<b>Y,O,B;</b> I	4	0.0014
<b>40858</b>	B1N694_HALDI	1.5e-69	89.6%	Thioredoxin peroxidase 2; Lotgi1 150310 (2.8e-105)	<b>-H</b>	<b>Y,O,B;</b> S<I	2	0.0242
					<b>+H</b>	<b>Y,O,B;</b> S<I	2	0.0290
<b>4111</b>	K1RG91_CRAGI	1.6e-25	50.6%	Transgelin-2; Lotgi1 152623 (8.2e-56); very similar entries but different peptides at the same place! Share 1 peptide.	<b>-H</b>	<b>Y,B;</b> I	2	0.0012
<b>416</b>		2.1e-29	51.5%		<b>+H</b>	<b>Y,B,O;</b> I	3	0.0065
						-	-	-
<b>41145</b>	L5KXM7_PTEAL (aa54-256)	5.1e-79	83.7%	$\alpha$ 3-tubulin; Lotgi1 201713 (3.8e-111)	<b>-H</b>	<b>Y,B;</b> I	1	0.0009
					<b>+H</b>	<b>Y;</b> I	1	0.0008
<b>41290</b>	R7TDC7_9ANNE (aa2-214)	1.4e-33	52.5%	Uncharacterized/similar to hsc70-interacting protein; domain: TPR_2; Lotgi1 64759 (1.6e-68)	<b>-H</b>	<b>Y,B;</b> I	1	0.0004
					<b>+H</b>	<b>Y;</b> I	2	0.0018
<b>4262</b>	R7TCA8_9ANNE (aa70-395)	2.0e-44	51.0%	Uncharacterized/similar to Heterogeneous nuclear ribonucleoprotein K (K1Q324_CRAGI); Lotgi1 121010 (8.3e-69)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,B;</b> I	2	0.0002
<b>41623</b>	K1R2C6_CRAGI	2.0e-107	52.7%	aa43-555 similar to Alkaline phosphatase, tissue- nonspecific isozyme; Lotgi1 236474 (1.9e-118)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O;</b> I	8	0.0019
<b>4164</b>				Uncharacterized; limited similarity to UP2_HALAI (e-value 0.19; 28.1% identity)	<b>-H</b>	<b>Y,O,B;</b> S>I	2	1.4832
					<b>+H</b>	<b>Y,O,B;</b> S>I	3	2.0730
<b>41818</b>				Uncharacterized; signal peptide; 13% A, 10% D, 10% V	<b>-H</b>	<b>Y,O,B;</b> S,I	1	0.0129
					<b>+H</b>	<b>Y,O,B;</b> S<I	1	0.0128
<b>418581</b>	K1PII9_CRAGI (aa173-371)	2.3e-23	36.3%	Reelin; Lotgi1 228850 (5.2e-39)	<b>-H</b>	<b>Y,O;</b> I	1	0.0007
					<b>+H</b>	<b>Y,O;</b> I	1	0.0018



<b>4189</b>				Uncharacterized; fragment?	<b>-H</b>	<b>Y,O,B;</b> S,I	1	0.0745
					<b>+H</b>	<b>O,B;</b> I	1	0.0084
<b>41918</b>	K1S6N9_CRAGI (aa250-484)	6.6e-31	39.7%	Similar to lachesin; domain: IG; Lotgi1 162469 (7.3e-61)	<b>-H</b>	<b>Y,O;</b> I	1	0.0004
					<b>+H</b>	<b>Y,O;</b> S<I	1	0.0023
<b>42513</b>	G6D8P2_DANPL	1.8e-77	38.3%	Uncharacterized/similar to disintegrin and metalloproteinase domain containing protein; domains: peptidase_M12B, disintegrin, ADAM10, signal peptide; Lotgi1 199969 (0e0)	<b>-H</b>	<b>Y,O,B;</b> S>I	2	0.0016
					<b>+H</b>	<b>Y,O,B;</b> S>I	4	0.0040
<b>4265</b>	K1QTT1_CRAGI (aa2-147)	3.4e-28	51.0%	aa42-185 similar to uncharacterized; signal peptide; Lotgi1 232745 (6.7e-34)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O;</b> I	2	0.0036
<b>4275</b>	C5IIM1_HALDV	1.3e-60	48.5%	Cathepsin L-like cysteine proteinase;domains: signal peptide, peptidase_C1A; see also contig_10485; Lotgi1 221163 (4.1e-79)	<b>-H</b>	<b>Y;</b> I	2	0.0005
					<b>+H</b>	<b>Y,O;</b> S<I	4	0.0041
<b>42852</b>	K1QK91_CRAGI	2.3e-152	51.6%	Prestin; domain: sulfate_anion_transporter; Lotgi1 53031 (0e0)	<b>-H</b>	<b>Y,O;</b> I	2	<0.0001
					<b>+H</b>	<b>Y;</b> I	5	0.0008
<b>43333</b>	K1QKM4_CRAGI (aa1-459)	1.7e-157	72.8%	Xylose isomerase; Lotgi1 202268 (0e0)	<b>-H</b>	<b>Y,O;</b> I	4	0.0005
					<b>+H</b>	<b>Y,O;</b> I	8	0.0038
<b>4367</b>	R7V5G0_9ANNE	1.7e-65	88.8%	Uncharacterized/Rab 7; Lotgi1 223383 (3.0e-126)	<b>-H</b>	<b>O;</b> S,I	2	0.0002
					<b>+H</b>	<b>Y,B;</b> I	3	0.0011
<b>4368</b>	K1PVA1_CRAGI (aa7-370)	1.9e-115	94.5%	Transitional endoplasmic reticulum ATPase; Lotgi1 216777 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,B;</b> I	6	0.0020
<b>43829</b>	Q8I819_APLCA (aa26-153)	2.1e-13	37.4%	Uncharacterized/similar to ectonucleoside triphosphate diphosphohydrolase; domains: signal peptide, nucleoside phosphatase GDA1/CD39; Lotgi1 238045 (6.8e-11)	<b>-H</b>	<b>Y,O;</b> I	1	0.0012
					<b>+H</b>	<b>Y,O;</b> S<I	2	0.0040
<b>4386</b>	F2TX66_SALS5 (aa490-698)	4.5e-10	31.6%	Uncharacterized; domain: VWA; Lotgi1 123318 (2.8e-13)	<b>-H</b>	<b>Y,O,B;</b> S<I	3	0.0313
					<b>+H</b>	<b>O,B;</b> I	2	0.0008

4405	I3K648_ORENI	2.7e-61	66.4%	Uncharacterized/14-3-3 ; Lotgi1 207549 (6.1e-87); shares peptides with other 14-3-3 proteins	-H	Y,O,B; I	1	0.0020
					+H	Y,O; S<I	4	0.0064
4409	K1QXR1_CRAGI (aa277-772)	2.9e-51	37.2%	Putative tyrosinase-like protein tyr-3; Lotgi1 166196 (2-1e-92); see also contig_8371!	-H	Y,O,B; S<I	12	0.0684
					+H	Y,O,B; I	3	0.0075
44723	K1R BX7_CRAGI	2.9e-75	37.7%	Uncharacterized; signal peptide	-H	Y,O,B; I	8	0.0019
					+H	Y,O,B; S>I	16	0.0156
44780	R4G5H1_RH0PR	1.9e-101	76.8%	Arp2/3; Lotgi1 220774 (9.7e-168)	-H	-	-	-
					+H	Y; I	2	0.0002
450	68CYM6_PHYAT	9.9e-67	74.2%	G-type lysozyme;signal peptide; Lotgi1 110722 (6.9e-55)	-H	Y,O,B; S<I	5	0.2134
					+H	Y,O,B; S<I	5	0.3560
45203	E9GD19_DAPPU (aa1-482)	1.0e-107	58.2%	Coronin; Lotgi1 114901 (0e0)	-H	Y,O,B; I	2	0.0004
					+H	Y,O; I	4	0.0021
45530	B8YJJ3_LYMST	1.6e-109	83.8%	Retinal dehydrogenase; Lotgi1 192810 (1.1e-133)	-H	Y; I	1	0.0003
					+H	Y; I	8	0.0057
4572	GELS2_LUMTE (aa180-366)	5.0e-26	46.0%	Gelsolin-like protein 2; Lotgi1 192582 (2.4e-34)	-H	Y,O,B; S<I	4	0.0272
					+H	Y,O,B; I	5	0.0009
45754	K1R7T2_CRAGI	1.6e-152	82.2%	Isocitrate dehydrogenase [NADP]; Lotgi1 208961 (0e0)	-H	-	-	-
					+H	Y,O,B; I	2	0.0003
459				Uncharacterized; signal peptide; 14% Q, 11% M, 10% P	-H	Y,O,B; S<I	10	0.0135
					+H	Y,O,B; S<I	8	0.0076
45900	L7LZH1_9ACAR (aa6-375)	1.2e-46	41.6%	Uncharacterized; domains: PDZ; Lotgi1 237252 (5.5e-99)	-H	Y,O,B; I	3	0.0011
					+H	Y; I	7	0.0034
4597	T1DMA1_CROHD (aa344-715)	1.6e-88	57.1%	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial-like protein; Lotgi1 206956 (5.6e-129)	-H	-	-	-
					+H	Y; I	2	0.0003

46005	K1Q014_CRAGI	3.3e-57	33.6%	Similar to Solute carrier family 22 member 21; Lotgi1 168961 (6.2e-74)	-H	-	-	-
					+H	Y; I	2	0.0014
461	K1QRL6_CRAGI	2.1e-55	46.7%	Similar to Methenyltetrahydrofolate synthetase domain-containing protein; Lotgi1 224471 (9.7e-87)	-H	-	-	-
					+H	Y,B; I	2	0.0003
46246	Q8IU44_LOLBL (aa41-279)	8.2e-27	64.2%	Myosinase-III; Lotgi1 209446 (7.1e-37)	-H	Y,O; S	1	0.0011
					+H	Y,O; S	1	0.0009
46337	O44343_BIOGL (aa5-232/389-521)	2.2e-78	65.0%	HSP70; Lotgi1 177837 (0e0); shares peptide with contig_695	-H	Y,O,B; S<I	3	0.0130
					+H	Y,O,B; S<I	4	0.0146
4702	G9K384_HALDV (aa96-403)	6.9e-53	44.5%	Similar to putative procollagen type VI $\alpha$ 4, domain: VWA; Lotgi1 233111 (4.4e-46)	-H	Y,B; I	3	0.0005
					+H	B; I	3	0.0005
47032	K1Q531_CRAGI	1.5e-35	61.6%	Neural proliferation differentiation and control protein 1; domains: NPDC1, transmembrane; Lotgi1 232872 (8.4e-49)	-H	Y,B; S	2	0.0007
					+H	Y,O; S	1	0.0003
47053	R7VGB5_9ANNE (aa1-466)	1.1e-115	54.3%	Uncharacterized; domains: transglutaminase/ $\gamma$ -glutamyltransferase; Lotgi1 231723 (0e0)	-H	Y,O,B; I	2	0.0010
					+H	Y,O; I	9	0.0084
47191	K1PX68_CRAGI (aa211-671)	1.7e-22	29.8%	Similar to tyrosine-protein phosphatase non-receptor type 6; domains: signal peptide, PBP; Lotgi1 173822 (3.0e-27)	-H	Y,O,B; I	1	0.0007
					+H	Y,O; S<I	2	0.0027
47261	K1R091_CRAGI (aa89-695)	6.5e-111	47.5%	Similar to plectin-1; domain: SH3; Lotgi1 232953 (1.2e-176)	-H	-	-	-
					+H	Y,O; I	3	0.0002
47483	K1R973_CRAGI	4.7e-43	77.4%	Chloride intracellular channel exc-4; domain: GST_C; Lotgi1 189089 (5.2e-89)	-H	Y,O; I	4	0.0018
					+H	Y,O; S<I	8	0.0189
4755				Uncharacterized, domains: EGF_like, WAP; Lotgi1 153970 (4.8e-20)	-H	Y,O,B; S<I	14	0.0403
					+H	Y,O,B; S<I	16	0.0778
47828				Uncharacterized	-H	Y,O,B; I	4	0.0079
					+H	Y,O,B; S<I	4	0.0226

47888	B3MFN3_DROAN	1.5e-92	58.2%	Uncharacterized/V-type proton ATPase subunit C; Lotgi1 206255 (9.5e-141)	-H	Y,O; I	4	0.0007
					+H	Y,O,B; S<I	12	0.0140
48400	E9G2W4_DAPPU (aa1-848)	0.e0	59.7%	Uncharacterized/filamin; domains: filamin, CH; Lotgi1 158607 (0e0)	-H	Y,O,B; I	4	0.0008
					+H	Y,O; I	11	0.0023
4865	K1R1B6_CRAGI	1.7e-128	47.8%	D-glucuronyl C5-epimerase; Lotgi1 178848 (0e0)	-H	-	-	-
					+H	Y,O; I	2	0.0004
4900	C3ZEP6_BRAFL (aa335-985)	1.8e-57	30.5%	Uncharacterized/similar to calcium-activated chloride channel regulator 2; domains: VWA, DUF1973; Lotgi1 238844 (2.9e-135)	-H	Y,O; I	3	0.0020
					+H	Y,O,B; S<I	5	0.0067
4963				Uncharacterized; domains: EGF_like, signal peptide	-H	Y,O; I	7	0.0021
					+H	Y,O; S<I	14	0.0136
49657	K1R8I8_CRAGI (aa365-484)	8.5e-40	75.8%	Uncharacterized; domain: Chloramphenicol acetyltransferase-like; Lotgi1 137484 (2.7e-59)	-H	Y,O,B; I	1	0.0005
					+H	Y,B; I	2	0.0015
49666				Uncharacterized; 26% T; Lotgi1 169040 (1.1e-12)	-H	Y,O,B; S	4	0.0095
					+H	Y,O; S<I	2	0.0053
49914	R7V680_CRAGI	5.0e-60	30.6%	Uncharacterized; domains: TSP_1, ADAM, spacer1, PLAC, signal peptide; Lotgi1 237754 (5.2e-163)	-H	Y; I	1	0.0005
					+H	Y,O; S<I	9	0.0046
50	J9JIV2_ACYPI (aa8-210)	9.7e-28	37.9%	Uncharacterized; domains: Chit_bind_3, signal peptide; Lotgi1 96362 (2.0e-29)	-H	Y,O,B; S<I	5	0.0141
					+H	Y,O,B; S,I	6	0.0537
50027	Q8ITH0_BIOGL (aa1-164)	1.8e-71	99.4%	$\alpha$ -actinin; Lotgi1 189716 (3.0e-89)	-H	Y,O,B; I	2	0.0018
					+H	Y,O,B; S<I	6	0.0124
50065				Uncharacterized; domains: signal peptide, RNASE_T2_1; Lotgi1 76871 (1.5e-289)	-H	Y; I	1	0.0004
					+H	Y,O; S>I	1	0.0017
5087				Uncharacterized; transmembrane; Lotgi1 79004 (2.5e-8)	-H	Y,O,B; S<I	33	0.5426
					+H	Y,O,B; S<I	39	1.5962

<b>5102</b>	C3YGQ2_BRAFL (aa322-501)	2.5e-14	32.3%	Uncharacterized; domain: ZP_2	-H	Y,B; I	3	0.0172
					+H	Y,O,B; I	5	0.0221
<b>5116</b> <b>45664</b>	I7EDT1_ANTYA R7U3Y2_9ANNE	8.7e-66 1.4e-51	93.8% 87.1%	ADP-ribosylation factor; Lotgi1 236204 (2.8e-108/2.9e-85); very similar	-H	O; S	2	0.0007
					+H	B,Y; I	3	0.0020
<b>5153</b>	K1QEW1_CRAGI	2.9e-30	51.7%	Glutathione peroxidase; Lotgi1 86188 (5.0e-45)	-H	Y,O; I	2	0.0013
					+H	Y,O; S<I	2	0.0036
<b>51587</b>	K1R005_CRAGI (aa34-401)	7.0e-92	55.7%	Filamin-C fragment; Lotgi1 231195 (4.0e-169)	-H	-	-	-
					+H	Y,O,B; I	2	0.0001
<b>51657</b>				Uncharacterized; signal peptide	-H	Y,O,B; I	1	0.0468
					+H	Y,O,B; I	1	0.0152
<b>5168</b>	E9GA59_DAPPU	1.9e-123	80.6%	Uncharacterized/eukaryotic initiation factor 4A; domains: (signal peptide,) DNA/RNA helicase; Lotgi1 207101 (0e0)	-H	Y,O,B; S<I	4	0.0017
					+H	Y,O,B; I	6	0.0039
<b>51882</b>	Q3S3F8_MYTED (aa647-784)	8.8e-20	39.2%	Similar to phospholipase A2; Lotgi1 222658 (4.3e-35)	-H	Y,O,B; S	1	0.0081
					+H	Y,O,B; S	1	0.0162
<b>5201</b> <b>5202</b>	K1PWR0_CRAGI	5.1e-59	78.2%	SET nuclear oncogene; domain: NAP; Lotgi1 143784 86.3e-110)	-H	Y,O,B; I	3	0.0116
					+H	Y,O,B; I	1	0.0030
<b>52099</b> <b>95524</b>	K1Q1S3_CRAGI (aa301-952) (aa1-299)	4.9e-147 3.4e-104	71.9% 80.9%	Myosin-VI; Lotgi1 133465 (0e0/9.1e-178)	-H	-	-	-
					+H	Y; I Y,O; I	7 2	0.0016 0.0015
<b>521</b>	B2Y143_9BILA	1.7e-35	74.2%	Ribosomal protein L24; Lotgi1 106244 81.0e-45)	-H	O,B; I	1	0.0012
					+H	Y,O,B; I	1	0.0017
<b>5270</b>	K1QVU9_CRAGI (aa58-202)	2.7e-7	37.0%	Uncharacterized; signal peptide	-H	Y,O,B; S,I	6	0.0319
					+H	Y,O,B; S,I	6	0.0457
<b>5306</b>	RL26_LITLI	1.5e-46	84.6%	60S ribosomal protein L26; Lotgi1 189002 (5.4e-57)	-H	B,Y; S,I	1	0.0019
					+H	B; S,I	1	0.0005

53616	K1PUR2_CRAGI	8.1e-52	50.6%	Nucleobindin-2; domains: signal peptide, EFh; Lotgi1 233369 (9.5e-98); also see contig_7760!	-H	Y,O; I	2	0.0007
					+H	Y,O; S<I	6	0.0015
5379	K1PJE5_CRAGI (aa1-261)	8.8e-49	47.7%	Pancreatic triacylglycerol lipase (Fragment); domains: signal peptide, lipase; Lotgi1 216931 (4.5e-80)	-H	Y; I	3	0.0026
					+H	Y,O; I	5	0.0093
5380	K1PJE5_CRAGI (aa1-272)	4.2e-49	48.6%	Pancreatic triacylglycerol lipase (Fragment); domains: signal peptide, lipase; Lotgi1 216931 (3.6e-78)	-H	Y,O; I	3	0.0022
					+H	Y,O; S<I	5	0.0088
5381	F0V4D4_MYTGA	5.0e-20	30.3%	Similar to C1q domain containing protein MgC1q97; domains: complement_C1q/TNF_like; Lotgi1 138166 (4.8e-14)	-H	Y,O,B; I	3	0.0007
					+H	O,B; I	3	0.0048
53924	D2A034_TRICA	6.8e-99	45.7%	Uncharacterized; domains: signal peptide, sulfatase/alkaline_phosphatase; Lotgi1 124040 (0e0)	-H	-	-	-
					+H	Y,O; I	2	<0.0001
5404	B8XY08_OCHTA	1.1e-13	57.6%	ATP synthase-coupling factor 6, mitochondrial; Lotgi1 236637 (7.5e-20)	-H	Y,O,B; I	3	0.0031
					+H	-	-	-
5474	Q6WMS9_BRABE	1.3e-59	53.9%	Interferon gamma-inducible protein 30; domains: signal peptide, saposin_A, GILT; Lotgi1 235566 (1.0e-91)	-H	Y,O; S	1	0.0021
					+H	Y,O,B; S	2	0.0024
54938	R7U8T0_9ANNE (aa1585-2150)	2.2e-38	26.4%	Uncharacterized/similar to cadherin-23 (K1PXB6_CRAGI; aa1252-1831); Lotgi1 229248 81.8e-34)	-H	Y,O; I	1	0.0003
					+H	Y,O; I	6	0.0038
551				Uncharacterized; fragment of 67aa containing 18% G, 22% M, 12% P	-H	Y,O,B; S>I	3	1.0562
					+H	Y,O,B; S>I	3	0.8513
55282	K1RCC7_CRAGI (aa22-234)	4.9e-21	33.5%	Similar to delta-like protein; domains: signal peptide, EGF, DSL; Lotgi1 169085 (2.0e-19)	-H	Y,B; I	2	0.0005
					+H	Y,O; S,I	3	0.0056
553	A5GZU9_APLCA (aa54-172)	5.0e-40	83.2%	Ferritin; Lotgi1 183389 (2.8e-57)	-H	Y,O; I	3	0.0014
					+H	Y,O; S,I	3	0.0026
55330				Uncharacterized; 11% R	-H	Y,O,B; S>I	1	0.0064
					+H	Y,O,B; S>I	2	0.0118

<b>5682</b>				Uncharacterized	<b>-H</b>	<b>Y,O,B;</b> S<I	3	0.0256
					<b>+H</b>	<b>Y,O;</b> I	1	0.0026
<b>57</b>	TPM_HELLAS	1.1e-55	95.1%	Tropomyosin; shares peptides with contig_6620; Lotgi1 162585 (8.7e-106)	<b>-H</b>	<b>Y,O,B;</b> I	8	0.0055
					<b>+H</b>	<b>Y;</b> I	1	0.0018
<b>5701</b>	H9GFP3_ANOCA (aa244-360)	3.9e-37	71.8%	Uncharacterized/V-type proton ATPase subunit d 1; Lotgi1 108853 (3.7e-61)	<b>-H</b>	<b>Y,O;</b> I	5	0.0100
					<b>+H</b>	<b>Y,O;</b> S<I	8	0.0638
<b>57047</b>	G4TBF6_PIRID	4.5e-71	49.6%	Similar to actin; Lotgi1 232973 (2.7e-99)	<b>-H</b>	<b>Y,O,B;</b> I	2	0.0016
					<b>+H</b>	<b>Y,O,B;</b> S<I	13	0.0129
<b>57198</b>	C3ZGK4_BRAFL (aa8-442)	1.1e-116	63.8%	Uncharacterized; domain: ALDH_like; Lotgi1 207312 80e0)	<b>-H</b>	<b>Y,O,B;</b> I	5	0.0021
					<b>+H</b>	<b>Y,O;</b> S<I	12	0.0158
<b>572</b>	IFEA_HELAS	1.7e-118	96.9%	Non-neuronal cytoplasmic intermediate filament protein; Lotgi1 109284 86.9e-119)	<b>-H</b>	<b>Y,O,B;</b> S>I	27	0.1623
					<b>+H</b>	<b>Y,O,B;</b> S<I	32	0.1862
<b>57844</b>	E9GB01_DAPPU	5.3e-65	55.4%	aa97-572 similar to adenylyl cyclase-associated protein; Lotgi1 92365 (1.2e-130)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y;</b> I	2	0.0003
<b>58150</b>	K1QZ49_CRAGI (aa85-348)	1.2e-40	35.1%	Similar to adipocyte plasma membrane-associated protein; domains: signal peptide, TolB_like/strictosidine synthase; Lotgi1 115637 (5.6e-40); see also contig_221 and contig_16710	<b>-H</b>	<b>Y,O,B;</b> S>I	15	0.7376
					<b>+H</b>	<b>Y,O,B;</b> S<I	16	1.9756
<b>5882</b>	K1RAL0_CRAGI	4.6e-105	58.0%	Aspartate aminotransferase, cytoplasmic; Lotgi1 231665 (5.4e-171)	<b>-H</b>	<b>Y,O;</b> I	2	0.0007
					<b>+H</b>	<b>Y,O;</b> S<I	11	0.0056
<b>5888</b>	C3Z7R8_BRAFL	2.6e-55	36.8%	Uncharacterized; domain: peptidase_M16; Lotgi1 156673 (1.4e-49)	<b>-H</b>	<b>Y,O,B;</b> I	7	0.0035
					<b>+H</b>	<b>Y,O,B;</b> I	9	0.0053
<b>59326</b>	F4WIU3_ACREC	2.4e-50	67.3%	Peptidyl-prolyl cis-trans isomerase; Lotgi1 212754 (3.2e-74)	<b>-H</b>	<b>Y,O,B;</b> I	2	0.0049
					<b>+H</b>	<b>Y,O,B;</b> S<I	4	0.0155
<b>5939</b>	ASSY_DANRE	1.0e-113	69.0%	Argininosuccinate synthase; Lotgi1 231283 (0e0)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y;</b> I	2	0.0005

5979	K1RZJ5_CRAGI (aa234-712)	3.3e-28	24.8%	Similar to Alba (D-arabinono-1,4-lactone oxidase)-like protein C9orf23-like protein; domains: signal peptide, FAD_binding, ALO; Lotgil 159383 (0e0)	-H	Y,O,B; I	9	0.0045
					+H	Y,O,B; I	3	0.0018
5989	K1PPZL2_CRAGI (aa923-1649)	1.2e-204	57.0%	Maltase-glucoamylase, intestinal; domains: glycoside_hydrolase_31, transmembrane; Lotgil 102400 (0e0)	-H	Y,O; S<I	5	0.0011
					+H	Y,O,B; S<I	5	0.0032
60305	B7Q2C4_IXOSC	6.8e-14	37.5%	Similar to alpha-B-crystallin; see also contig_6923; Lotgil 104895 (1.6e-19)	-H	Y,O,B; I	1	0.0008
					+H	Y,B; I	2	0.0019
60675				Uncharacterized; domain: CLECT; Lotgil 164559 (2.9e-60)	-H	Y,O; I	2	0.0007
					+H	Y,O; S,I	3	0.0031
60916	R7VDB2_9ANNE (aa53-252)	3.6e-12	32.2%	Uncharacterized; domains: CMB_14/CHIT_BIND_II; Lotgil 157323 (6.0e-38)	-H	Y,O; S,I	2	0.0067
					+H	Y,O; S,I	4	0.0116
6176				Uncharacterized; 11% A, 11% G, 12% M	-H	Y,O,B; S>I	6	0.4285
					+H	Y,O,B; S>I	7	0.4872
61949	D2JPI4_HALDH	7.4-162	66.5%	Selenium-binding protein; Lotgil 203681 (0e0)	-H	Y,O; I	1	0.0001
					+H	Y,O; I	7	0.0040
6246	K1R2H1_CRAGI (aa341-659)	1.1e-21	37.8%	Putative tyrosinase-like protein tyr-3; Lotgil 166196 (1.2e-71)	-H	Y,B; I	1	0.0078
					+H	Y,O,B; S<I	3	0.0106
62484	L7M2C1_9ACAR	1.4e-79	77.0%	Similar to prohibitin; Lotgil 237446 (7.5e-122)	-H	-	-	-
					+H	O; I	2	0.0009
6275	D7R6D6_BIOGL (aa728-1100)	6.2e-71	49.7%	Thioester-containing protein 1.4; domains: A2M; Lotgil 162872 (6.4e-87/1.3e-45)	-H	Y,O,B; S<I	7	0.0357
					+H	Y,O,B; S<I	9	0.0181
660	(aa1191-1445)	3.5e-59	51.2%		-H	Y,O,B; S<I	6	0.0172
					+H	Y,O; S<I	5	0.0063
6295				Uncharacterized	-H	Y,O,B; I	4	0.0072
					+H	B; I	1	0.0010



<b>63304</b>	K1Q365_CRAGI (aa22-658)	9.6e-55	29.8%	aa127-818 similar to lactadherin; domains: CBM_14/CHIT_BIND_II; Lotgi1 231869 (2.7e-110)	-H	Y,O,B; S<I	17	0.0373
					+H	Y,O,B; S<I	26	0.2100
<b>63401</b>	K1QNZ0_CRAGI (aa2-167)	7.2e-19	34.9%	Uncharacterized; signal peptide; Lotgi1 160424 (4.4e-31)	-H	-	-	-
					+H	Y,O; S<I	4	0.0042
<b>63801</b>	D6X1V1_TRICA (aa43-1636)	0e0	60.6%	Uncharacterized/similar to chromodomain-helicase- DNA-binding protein Mi-2-like protein; Lotgi1 165279 (0e0)	-H	Y,O; S,I	2	<0.0001
					+H	-	-	
<b>64075</b>	H3IE31_STRPU (aa101-280)	1.6e-29	42.0%	Deoxyribonuclease; Lotgi1 168246 (1.0e-36)	-H	Y,O; I	3	0.0049
					+H	Y,O; S<I	5	0.0247
<b>6453</b>	A5HJT4_BIOGL (aa142-289)	1.2e-22	45.8%	Tandem-repeat galectin; Lotgi1 129554 (4.6e-22)	-H	Y,O,B; S<I	3	0.0089
					+H	Y,O,B; S<I	4	0.0125
<b>6457</b>	PGAM_DICDI (aa91-249)	3.7e-47	68.6%	Phosphoglycerate mutase; Lotgi1 187919 (1.5e-69)	-H	-	-	-
					+H	Y,O; I	3	0.0054
<b>64786</b>	A7RQD5_NEMVE (aa109-331)	9.0e-17	30.1%	Uncharacterized	-H	O,B; I	1	0.0014
					+H	Y,O; I	3	0.0046
<b>6530</b>	K1QYG7_CRAGI	1.9e-193	68.8%	Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] 1; Lotgi1 235105 (0e0)	-H	Y,O; I	2	0.0002
					+H	Y,O; I	12	0.0034
<b>6553</b>	C1BEZ2_ONCMY	1.1e-52	100%	Histone H3; Lotgi1 150994 (2.0e-86)	-H	Y,O,B; S<I	2	0.0318
					+H	Y,O,B; I	1	0.0206
<b>65969</b>	L8IY93_BOSMU (aa64-1518)	4.9e-49	25.5%	Similar to SCO-spondin; domains: signal peptide, EGF, VWD, LDLR, Trypsin_inhibitor_like; Lotgi1 174711 (1.2e-78)	-H	Y,O,B; S<I	16	0.0083
					+H	-	-	-
<b>6609</b>				Uncharacterized	-H	-	-	-
					+H	Y; I	3	0.0023
<b>6620</b>	TPM1_BIOGL	3.6e-47	78.4%	Tropomyosin-1; Lotgi1 233095 (4.6e-100); shares peptides with contig_57	-H	Y,O; I	4	0.0034
					+H	Y,O,B; I	3	0.0013

<b>66355</b>	B6DVV3_APLCA	2.4e-98	75.2%	Src tyrosine kinase 1; Lotgi1 224844 (0e0)	-H	-	-	-
					+H	Y; I	3	0.0005
<b>6654</b>	C7FPZ1_9TELE	1.6e-52	51.7%	Carbonic anhydrase; domain: $\alpha$ -CA; Lotgi1 205401 81.9e-93)	-H	Y,B; I	2	0.0008
					+H	Y,O; I	4	0.0058
<b>6677</b> <b>14914</b>	Q75R52_LYMST (aa428-539) (aa117-421)	1.0e-12 2.2e-18	40.2% 31.9%	Similar to DEC-1; domain: VWA; Lotgi1 234764 (7.9e11)	-H	Y,B; I	3	0.0021
					+H	Y,O,B; I O; I	4 1	0.0068 0.0019
<b>66822</b>				Uncharacterized; 13% P, 25% T	-H	Y,O,B; S<I	3	0.0117
					+H	Y,O,B; S,I	3	0.0210
<b>6695</b>	M4A0J3_XIPMA	8.5e-153	85.3%	Uncharacterized/Arp3; Lotgi1 193923 (0e0)	-H	-	-	-
					+H	Y,O; I	4	0.0011
<b>6697</b>	K1QZ49_CRAGI (aa176-409)	1.3e-29	37.9%	Similar to adipocyte plasma membrane-associated protein; shares peptide with 8812; domains: signal peptide, TolB_like/strictosidine_synthase_related; See also contig_16710 and 221; Lotgi1 115667 (1.3e-37)	-H	Y,O; I	4	0.0028
					+H	Y,O,B; S<I	8	0.0303
<b>67</b>	G3FPE5_HELLU (aa2976-3299)	1.0e-100	66.7%	Hemocyanin ( $\beta$ ?); shares peptide with contig_297; Lotgi1 234481 (7.1e-7)	-H	Y,O,B; S<I	5	0.0252
					+H	Y,O,B; I	7	0.0164
<b>671</b>	E0D8P7_GRYBI (aa1-214)	5.5e-49	88.4%	Elongation factor 1-alpha; Lotgi1 239271 (4.6e-121)	-H	Y,O,B; S<I	5	0.0433
					+H	Y,O,B; S<I	4	0.0627
<b>67057</b>	L7M2D5_9ACAR	9.2e-12	45.2%	Similar to Vacuolar ATP synthase subunit G; Lotgi1 220690 (1.6e-27)	-H	-	-	-
					+H	Y; S<I	2	0.0010
<b>67514</b> <b>33100</b>	K1QE94-CRAGI (aa272-397) (aa4-209)	4.3e-20 6.5e-64	46.8% 66.2%	$\alpha$ -N-acetylgalactosaminidase; Lotgi1 178842 (9.0e-25)/209340 (7.2e-100)	-H	Y,O; I	2	0.0052
					+H	Y,O; S<I Y,O; I	2 3	0.0205 0.0007

<b>6756</b>	R7V680_9ANNE (166-607)	9.4e-51	38.8%	Aa1041-1494 similar to uncharacterized; domains: signal peptide, TSP_2, ADAM_spacer1, PLAC, peptidase_M12B; Lotgi1 51613 (2.2e-146)	-H	-	-	-
					+H	O; S,I	2	0.0004
<b>6809</b>	Q8ITA1_ARGIR	7.4e-52	76.4%	Ribosomal protein L12; Lotgi1 217320 (1.6e-86)	-H	-	-	-
					+H	Y,B; I	2	0.0021
<b>6813</b>				Uncharacterized; 16% S, 17% T	-H	Y,O,B; S>I	7	0.0292
					+H	Y,O,B; S>I	6	0.0141
<b>6854</b>	E3WTS1_ANODA	3.0e-94	68.5%	Malate dehydrogenase; Lotgi1 188534 (7.4e-132)	-H	Y,O; I	3	0.0014
					+H	Y,O; I	4	0.0129
<b>68877</b>	K1R4D4_CRAGI	1.3e-84	70.5%	40S ribosomal protein SA; Lotgi1 203487 (7.0e-111)	-H	Y,O,B; S<I	3	0.0053
					+H	Y,O,B; I	2	0.0045
<b>68904</b>	R4ZGP6_9ACAR (aa282-601)	3.9e-29	28.4%	Similar to acetylcholinesterase; Lotgi1 113809 (1.3e-26)	-H	Y,O,B; I	6	0.0101
					+H	-	-	-
<b>69084</b>	D2A249_TRICA	9.3e-132	53.8%	Uncharacterized; domains: ricin_B_lectin, glyco_tranf_2, glycol_transf_7C; Lotgi1 194702 (0e0)	-H	Y; I	2	<0.0001
					+H	Y,O; I	8	0.0019
<b>691</b>	A5Z1D6_9EUPU	1.4e-89	43.3%	Similar to epiphragmin; domains: signal peptide, Fibr_C; Lotgi1 83908 (1.7e-27)	-H	Y,O,B; S<I	32	0.3074
					+H	Y,O,B; S<I	31	0.2048
<b>69179</b>	K1R1Q8_CRAGI	1.4e-64	88.3%	Ras-related protein Rab-5C; Lotgi1 222012 (4.9e-119)	-H	-	-	-
					+H	Y,B; I	4	0.0016
<b>6923</b>	B7Q2C4_IXOSC	1.8e-14	41.3%	Similar to $\alpha$ -B-crystallin; see also contig_60305; Lotgi1 104895 (8.9e-21)	-H	Y; I	2	0.0011
					+H	Y; I	2	0.0020
<b>695</b>	C1KC83_HALDV	0e0	89.7%	Heat shock cognate protein 70; Lotgi1 177837 (0e0)	-H	Y,O,B; S<I	17	0.0213
					+H	Y,O,B; S<I	21	0.0463
<b>6969</b>	K1RW85_CRAGI	5.8e-159	83.0%	Adenosylhomocysteinase; Lotgi1 184532 (0e0)	-H	Y,O,B; S<I	1	0.0016
					+H	Y,O,B; I	2	0.0041

<b>70388</b>	Q45R39_APLCA (aa387-586)	1.1e-35	71.0%	Ezrin/radixin/moesin; Lotgi1 59617 (9.3e-109)/106937 (0e0)	<b>-H</b>	<b>Y,O; I</b>	2	0.0006
<b>873</b>	(aa1-586)	4.2e-108	78.7%	Very similar sequences sharing many peptides!		<b>Y,O,B; I</b>	23	0.0146
<b>16517</b>	(aa1-393)	6.2e-113	92.6%			-	-	-
					<b>+H</b>	<b>Y,O; I</b>	3	0.0050
						<b>Y,O,B; S&lt;I</b>	32	0.0645
						<b>Y,O,B; I</b>	7	0.0047
<b>7072</b>	Q2VU37_PINFU (aa23-375)	5.1e-32	32.1%	Similar to astacin-like protein; domains: signal peptide, peptidase_M12A; Lotgi1 109273 (2.9e-37)	<b>-H</b>	<b>Y,O; I</b>	4	0.0010
					<b>+H</b>	<b>Y,O; S&lt;I</b>	10	0.0051
<b>7075</b>	R7V800_9ANNE	9.9e-42	37.7%	Uncharacterized/similar to lachesin; domains: transmembrane, IG; Lotgi1 234163 (5.5e-88)	<b>-H</b>	<b>Y,O; I</b>	2	0.0006
					<b>+H</b>	<b>Y,O; S&lt;I</b>	5	0.0037
<b>71</b>	C3ZKR4_BRAFL (aa193-354)	5.8e-15	38.3%	aa6-167 similar to adipocyte plasma membrane-associated protein (K1QZ49_CRAGI); domain: TolB_like/strictosidine_synthase_related; Lotgi1 115667 (3.1e-26)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	8	0.0310
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	9	0.0494
<b>7158</b>	Q45R40_APLCA (aa181-1225)	0e0	84.3%	Nonmuscle myosin II (Fragment); domains: IQ_motif, myosin_head, myosin_tail_1; Lotgi1 205893 (0e0)	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	27	0.0029
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	48	0.0121
<b>71616</b>	R7UUZ8_9ANNE	0e0	61.9%	aa121-979 similar to Uncharacterized/puromycin-sensitive aminopeptidase; domain: peptidase_M1; Lotgi1 204438 (0e0)	<b>-H</b>	<b>Y,O; I</b>	4	0.0001
					<b>+H</b>	<b>Y,O; I</b>	13	0.0016
<b>72045</b>	K1QDH9_CRAGI (aa1-216)	1.2e-77	83.9%	Myosin-11; Lotgi1 177615 (8.6e-122)	<b>-H</b>	<b>O; S,I</b>	3	0.0006
					<b>+H</b>	<b>Y,O,B; I</b>	6	0.0060
<b>72620</b>	F8RP10_CRAGI (aa12-419)	5.5e-39	30.0%	Similar to Bactericidal permeability increasing protein; domains: BPI, signal peptide; Lotgi231708 (8.7e-52)	<b>-H</b>	<b>Y,O,B; I</b>	1	0.0021
					<b>+H</b>	<b>Y,O; S&lt;I</b>	2	0.0043
<b>7323</b>	A7RQD5_NEMVE	6.2e-41	32.2%	Uncharacterized; signal peptide	<b>-H</b>	<b>Y,O,B; S&lt;I</b>	16	0.0768
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	25	0.1902
<b>7335</b>	F6VEH7_XENTR (aa475-4265)	0e0	46.0%	Uncharacterized/similar to Low-density lipoprotein receptor-related protein; domains: LDLR, EGF, TolB_like; Lotgi1 170222 (0e0)	<b>-H</b>	<b>Y,O,B; I</b>	41	0.0044
					<b>+H</b>	<b>Y,O,B; S&lt;I</b>	88	0.0246

<b>7341</b>				Uncharacterized; very G-rich N-terminus (aa1-80 61% G)	-H	Y,O,B; S<I	4	0.0269
					+H	Y,O,B; S<I	4	0.0240
<b>7386</b>	K1Q7T5_CRAGI	3.5e-115	58.2%	Protein disulfide-isomerase A3; signal peptide; Lotgi1 190816 (3.1e-170)	-H	Y,O,B; I	6	0.0022
					+H	Y,O,B; I	8	0.0026
<b>74050</b>	E9HK57_DAPPU	4.1e-67	58.4%	Uncharacterized/calumenin-B; domains: signal peptide, EFh; Lotgi1 103470 (2.3e-125)	-H	-	-	-
					+H	Y; I	2	0.0005
<b>74063</b>				Uncharacterized; signal peptide; 10% G, 13% L, 20% P; only 1 peptide possible!	-H	Y,O,B; S>I	1	0.2061
					+H	Y,O,B; S,I	1	0.2185
<b>7416</b>	B0L0Y3_PINFU (aa13-540)	5.5e-116	66.4%	RNA-binding protein; Lotgi1 93013 (0e0)	-H	-	-	-
					+H	Y; I	2	0.0002
<b>74191</b>	K1PLV6_CRAGI	5.2e-91	71.0%	F-actin-capping protein subunit alpha; Lotgi1 196809 (7.2e-149)	-H	-	-	-
					+H	Y; I	6	0.0031
<b>7508</b>				Uncharacterized; signal peptide; Lotgi1 234386 (1.4e-31)	-H	Y,O,B; S<I	13	2.7736
					+H	Y,O,B; S<I	15	6.4446
<b>7563</b>				Uncharacterized	-H	Y,O,B; S<I	6	0.1193
					+H	Y,O,B; S,I	6	0.5070
<b>75801</b>	H9K6W2_APIME (aa1146-1454)	7.9e-21	34.9%	Uncharacterized; domains: cadherin; Lotgi1 167053 (1.44e-21); also see contig_20360	-H	Y,O,B; I	6	0.0222
					+H	Y,O,B; S,I	7	0.0732
<b>7594</b>	D8V7I9_BIOGL (aa233-352)	6.6e-46	91.7%	Arginine kinase; Lotgi1 183052 (9.4e-65)	-H	Y,B; I	4	0.0066
					+H	-	-	-
<b>76025</b>	K1QMK1_CRAGI	1.2e-39	48.6%	Uncharacterized; domain: aerolysin_like_toxin; Lotgi1 152519 (3.1e-51)	-H	Y,O,B; I	1	0.0005
					+H	Y,O,B; I	1	0.0010
<b>763</b>	Q95PK2_BIOGL (aa467-667)	3.6e-35	43.7%	BgMFREP7 (Fragment)/fibrinogen-related protein 7; domain: fibrinogen_C; Lotgi1 83908 (1.7e-37)	-H	O,B; I	3	0.0007
					+H	O,B; S<I	7	0.0501

76308	K1Q329_CRAGI	7.6e-117	76.8%	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Lotgi1 226825 (3.8e-180)	-H	-	-	-
					+H	Y; I	3	0.0005
7641	E9BZF3_CAPO3	1.3e-54	61.9%	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; domain: 14-3-3; Lotgi1 222442 (6.2e-84)	-H	-	-	-
					+H	Y,O,B; S<I	5	0.0020
76888	J7HZQ3_POMCA (aa323-528)	4.6e-55	65.0%	Apoptosis-inducing factor 3-like protein; Lotgi1 214061 (5.1e-87)	-H	-	-	-
					+H	Y; I	2	0.0021
77520	K1QWM6_CRAGI (aa106-326)	5.0e-12	29.5%	Similar to Neural-cadherin; domains: cadherin; Lotgi1 167053 (1.9e-16)	-H	Y,O; S<I	2	0.0142
					+H	Y,O,B; S<I	5	0.0867
7760	K1PUR2_CRAGI (aa6-387)	1.3e-39	48.2%	Nucleobindin-2; domains: transmembrane, EFh; Lotgi1 163284 (2.9e-81); see also contig_53616!	-H	Y,O; I	2	0.0006
					+H	Y,O; S<I	9	0.0050
77827	A7RKK8_NEMVE (aa31-190)	2.2e-16	37.6%	Uncharacterized/similar to chitinase; domain: polysaccharide deacetylase/chitinase; Lotgi1 153749 (1.9e-19)	-H	Y,O,B; I	4	0.0060
					+H	Y,O,B; S<I	4	0.0091
7807				Uncharacterized; domains: signal peptide, WAP; 12% A, 11% Q; Lotgi1 201804 (2.2e-11)	-H	Y,O,B; S<I	12	0.0471
					+H	Y,O,B; S<I	15	0.1202
7809				Uncharacterized; 21% D, 16% L	-H	Y,O,B; S<I	16	0.3191
					+H	Y,O,B; S<I	17	0.8317
784				Uncharacterized; signal peptide	-H	Y,O,B; S>I	1	0.0534
					+H	Y,O,B; S>I	1	0.0832
7857	K1RNX0_CRAGI	5.4e-34	89.0%	Small nuclear ribonucleoprotein E; Lotgi1 207212 (3.8e-51)	-H	Y,O,B; I	2	0.0028
					+H	-	-	-
78579	A7RQD5_NEMVE	4.0e-44	31.3%	Uncharacterized	-H	Y,O,B; I	8	0.0033
					+H	Y,O,B; I	15	0.0085
7877				Uncharacterized; 17% P, 22% S	-H	Y,O,B; I	3	0.0043
					+H	-	-	-

<b>79063</b>	L7M8Q4_9ACAR (aa215-442)	2.4e-52	54.5%	Putative carbon-nitrogen hydrolase; domains: HIT, CN_hydrolase; Lotgi1 116186 (1.0e-44)	<b>-H</b> <b>+H</b>	- <b>Y; I</b>	- 3	- 0.0010
<b>79562</b>	H2ZK53_CIOSA (aa250-455)	3.8e-5	28.3%	Uncharacterized; domains: CUB; Lotgi1 173347 (2.3e-7)	<b>-H</b> <b>+H</b>	<b>Y,O,B; S&lt;I</b> <b>Y,O,B; S&lt;I</b>	3 3	0.0321 0.0157
<b>79695</b>	K1QSK4_CRAGI (730-1035)	6.9e-100	78.8%	Calcium-binding mitochondrial carrier protein; Lotgi1 232539 (1.8e-145)	<b>-H</b> <b>+H</b>	- <b>Y; I</b>	- 3	- 0.0003
<b>7977</b>	G2QTA6_THITE	2.6e-44	69.4%	Nucleoside diphosphate kinase; Lotgi1 205662 (3.2e-64)	<b>-H</b> <b>+H</b>	<b>Y,O,B; I</b> <b>Y,O,B; S&lt;I</b>	4 7	0.0110 0.0504
<b>80634</b>	L7N2K8_XENTR	6.0e-110	53.2%	Uncharacterized/prolylcarboxypeptidase (Angiotensinase C); domains: signal peptide, peptidase_S28; Lotgi1 207842 (2.4e-165)	<b>-H</b> <b>+H</b>	- <b>Y,O; I</b>	- 3	- 0.0022
<b>80985</b>	L7M2D2_9ACAR	2.6e-43	54.7%	Rho GDP dissociation inhibitor; Lotgi1 183614 (5.8e-60)	<b>-H</b> <b>+H</b>	- <b>Y,B; I</b>	- 2	- 0.0010
<b>81046</b>	T1DEH2_9DIPT	4.7e-103	73.5%	Uncharacterized; domains: armadillo/Mo25_like; Lotgi1 238430 (2.0e-162)	<b>-H</b> <b>+H</b>	- <b>Y,O; I</b>	- 2	- 0.0007
<b>81408</b>	K1RGK4_CRAGI	0e0	61.1%	Villin-1; Lotgi1 221805 (0e0)	<b>-H</b> <b>+H</b>	- <b>Y,O; I</b>	- 8	- 0.0039
<b>81515</b>	E9GBJ8_DAPPU	1.9e-119	77.6%	Uncharacterized/alcohol dehydrogenase; domains:ADH_ZINC, gelsolin; Lotgi1 228995 (1.0e-121)	<b>-H</b> <b>+H</b>	- <b>Y; I</b>	- 2	- 0.0009
<b>821</b>	J7Q5J6_PATVU (aa213-366)	8.7e-11	29.9%	Similar to BSMP; domain: CBM_14/ CHIT_BIND_II; Lotgi1 236718 (9.6e-15)	<b>-H</b> <b>+H</b>	<b>Y,O,B; S&lt;I</b> <b>Y,O,B; S&lt;I</b>	11 15	1.1640 2.4533
<b>8216</b>	E9H8M4_DAPPU	9.9e-86	80.4%	Uncharacterized; domain: 14-3-3; shares peptides with several other 13-3-3 proteins; Lotgi1 207549 (1.9e-115)	<b>-H</b> <b>+H</b>	<b>Y,O,B; S&lt;I</b> <b>Y,O,B; S&lt;I</b>	11 15	0.0377 0.0896
<b>824</b>	Q5M8U4_XENTR (aa104-281)	9.9e-51	65.7%	Uncharacterized/S-formylglutathione hydrolase; Lotgi1 120210 (3.6e-84)	<b>-H</b> <b>+H</b>	- <b>Y; I</b>	- 2	- 0.0005

<b>8282</b>	K1PHW4_CRAGI	2.7e-19	31.1%	Ganglioside GM2 activator; signal peptide; Lotgi1 154381 (1.4e-19)	-H	Y,O,B; S<I	3	0.0100
					+H	Y,O,B; S<I	3	0.0179
<b>83512</b>	Q4RR82_TETNG	3.0e-16	52.8%	SH3 domain-binding glutamic acid-rich-like protein; 11% D in 92aa; Lotgi1 236598 (4.6e-11)	-H	Y,O,B; S<I	3	0.0274
					+H	Y,O,B; S<I	2	0.0336
<b>8371</b>	K1QXR1_CRAGI (aa223-422)	7.2e-29	40.9%	Putative tyrosinase-like protein tyr-3; Lotgi1 166196 (7.7e-44); see also contig_4409!	-H	Y,B; S<I	1	0.0184
					+H	Y,O,B; S,I	1	0.0216
<b>84589</b>	K1QIK2_CRAGI (aa1112-1793)	5.4e-41	29.2%	Uncharacterized; domains: CBM_14/CHIT_BIND_II; Lotgi1 231869 (1.1e-106); also see contig_101824!	-H	Y,O,B; S<I	19	0.0627
					+H	Y,O,B; S<I	29	0.3022
<b>85080</b>	S4SBL5_CRAGI (aa1-286)	8.3e-71	55.7%	Acid ceramidase; domains: signal peptide, choloylglycine_hydrolase; Lotgi1 142206 (8.8e-112)	-H	-	-	-
					+H	Y,O; I	4	0.0017
<b>85288</b>	D2WPC5_HELAM (aa220-344)	6.1e-13	32.3%	Similar to Chitin deacetylase 5a; Lotgi1 116769 (5.0e-10)	-H	Y,O,B; S<I	3	0.0082
					+H	Y,O,B; I	2	0.0080
<b>85737</b>				Uncharacterized; 19% R, 21% E	-H	-	-	-
					+H	Y,O; I	2	0.0022
<b>86340</b>				Uncharacterized; signal peptide; 13% R, 18% Q	-H	Y,O,B; S<I	8	0.0931
					+H	Y,O,B; S<I	9	0.0784
<b>86405</b>	K1RAG0_CRAGI	2.7e-63	51.2%	Glyoxylate reductase/hydroxypyruvate reductase; Lotgi1234402 (7.1e-114)	-H	-	-	-
					+H	Y; I	2	0.0004
<b>8812</b>	K1QZ49_CRAGI (aa67-398)	7.3e-22	34.3%	Similar to adipocyte plasma membrane-associated protein; domains: signal peptide, TolB_like/strictosidine synthase; Lotgi1 115637 (1.5e-52); see also contig_221/contig_58150/contig_16710!	-H	Y,O,B; S<I	24	0.0188
					+H	Y,O,B; S<I	33	0.0508
<b>8897</b>	K1QN14_CRAGI (aa164-315)	5.7e-10	27.4%	Uncharacterized; Lotgi1 228701 (2.0e-23)	-H	Y,O,B; S<I	6	1.3649
					+H	Y,O,B; S>I	6	0.0415



<b>9053</b>	K1QMD1_CRAGI (aa657-810)	4.7e-16	34.0%	Similar to Putative tyrosinase-like protein tyr-3; domain: CBM_14; Lotgi1 234880 (1.2e-13)	-H	Y,O,B; S<I	1	0.0106
					+H	Y,O,B; I	1	0.0021
<b>9056</b>	K1QMD1_CRAGI (aa657-818)	9.2e-16	33.7%	Similar to Putative tyrosinase-like protein tyr-3; domain: CBM_14; Lotgi1 234880 (2.1e-19)	-H	-	-	-
					+H	O; I	2	0.0046
<b>91173</b>	K1QT97_CRAGI	9.6e-47	40.7%	Similar to N(G),N(G)-dimethylarginine dimethylaminohydrolase 1; domain: amidinotransferase; Lotgi1 170725 (3.7e-85)	-H	Y,O,B; I	2	0.0009
					+H	Y,O,B; I	3	0.0012
<b>91443</b>	K1Q8Q1_CRAGI (aa100-716)	1.1e-133	47.8%	Similar to Laccase-2; domains: signal peptide, cupredoxin; Lotgi1 218365 (7.6e-170)	-H	-	-	-
					+H	Y,O; I	2	0.0004
<b>9158</b>				Uncharacterized; 14% A, 16% E, 17% G, 17% P; only 1 peptide originating from K/P cleavage; a second one (not found) would be possible with two K/P cleavages (less likely). Almost identical to 9159!	-H	Y,O,B; S>I	1	0.1360
					+H	Y,O,B; S<I	1	0.0311
<b>9159</b>				Uncharacterized; 13% A, 15% E, 17% G, 16% P, 10% S; only 1 peptide originating from K/P cleavage; a second one (not found) would be possible with two K/P cleavages (less likely). Almost identical to 9158!	-H	Y,O; S	1	0.0368
					+H	Y,O; S,I	1	0.0401
<b>92424</b>	H3DSC4_PRIPA (aa16-562)	2.0e-19	25.3%	Uncharacterized/similar to zonadhesin; domains: EGF, VWD, TIL, CLECT, mucin2_WxxW; Lotgi1 189815 (4.4e-18)	-H	Y,O,B; I	16	0.0029
					+H	O; I	6	0.0004
<b>9283</b>	Q38RA2_APLKU	1.7e-20	44.2%	Cofilin	-H	-	-	-
					+H	Y,O; S<I	4	0.0071
<b>93705</b>	K1QRH0_CRAGI (aa306-545)	4.8e-72	63.1%	Lactadherin; Lotgi1 152889 (1.3e-119)	-H	-	-	-
					+H	Y,O; I	3	0.0024
<b>93725</b>	K1RJA2_CRAGI	1.1e-32	35.0%	Uncharacterized; domains: transmembrane, tetraspanin; Lotgi1 157852 (2.6e-23)	-H	-	-	-
					+H	Y,O; I	3	0.0028
<b>9415</b>	K1QQS0_CRAGI (aa152-382)	8.5e-13	26.9%	Uncharacterized protein; shares peptide with 7323	-H	Y,O; S	4	0.0020
					+H	Y,O; S<I	7	0.0241

<b>943</b>	G0ZGZ8_9ANNE (aa98-189)	5.2e-38	97.8%	Actin; shares peptides with CON; only Lottia-specific peptides were considered; Lotgi1 227913 (1.2e-56)	-H	Y,O,B; S<I	3	0.0621
					+H	Y,O,B; S<I	3	0.1637
<b>94717</b>	K1P7W2_CRAGI (aa256-648)	4.7e-25	33.3%	Similar to Protocadherin-like wing polarity protein stan; domains: cadherin; Lotgi1 154324 (4.0e-41); aa2-237 similar to cadherin-89D/protocadherin Fat 4	-H	Y,O,B; I	3	0.0017
					+H	Y,O,B; I	3	0.0030
<b>9513</b>	E7EZG1_DANRE (aa1219-2186)	6.6e-28	24.5%	Aa285-1251 similar to Uncharacterized; domains: signal peptide, CLECT (aa49-133); rest T- and S-rich; Lotgi1 148957 (6.2e-24)	-H	Y,O,B; S>I	2	0.0015
					+H	Y,O,B; S>I	3	0.0011
<b>96261</b>	A7S6G6_NEMVE	2.1e-111	57.8%	Uncharacterized/plasma glutamate carboxypeptidase; domains: signal peptide, peptidase_M28; Lotgi1 227502 (1.9e-170)	-H	-	-	-
					+H	O; I	6	0.0012
<b>96767</b>	S4RPI9_PETMA	5.0e-64	69.9%	Uncharacterized/V-type proton ATPase subunit D; Lotgi1 233963 (4.5e-91)	-H	Y,O; I	3	0.0019
					+H	Y,O; S<I	7	0.0238
<b>97036</b>	R7U2H6_9ANNE (aa162-519)	2.1e-93	59.2%	Uncharacterized/similar to galactocerebrosidase; domains: Glyco_hydro_59; Lotgi1 218637 (2.0e-149)	-H	-	-	-
					+H	Y,O; I	2	0.0029
<b>98</b>	K1PV35_CRAGI (aa1-689)	2.9e-178	64.3%	Kyphoscoliosis peptidase; domains: transglutaminase_like/nebulin/Cys_proteinases; Lotgi1 218011 (0e0)	-H	-	-	-
					+H	Y; I	5	0.0003
<b>9860</b>	G7YU18_CLOSI (aa97-716)	2.6e-80	36.6%	Similar to calpain-B; domains: peptidase_C2, EFh; Lotgi1 184301 (7.0e-77)	-H	-	-	-
					+H	Y; I	4	0.0011
<b>9876</b>	E3WUN5_ANODA	3.5e-38	65.3%	Uncharacterized/mitochondrial cytochrome c oxidase subunit Va; Lotgi1 157909 (5.3e-25)	-H	Y,O; I	1	0.0011
					+H	Y; I	1	0.0009
<b>9926</b>	R7VB66_9ANNE (57-324)	1.2e-57	49.6%	Uncharacterized; domain: metridin_like_Shk_toxin; Lotgi1 235549 (1.1e-6); also see contig_65431	-H	-	-	-
					+H	Y,O; S<I	2	0.0015
<b>99566</b>	K1RA95_CRAGI (aa320-837)	8.2e-144	63.5%	aa136-667 similar to filamin-A; domains: filamin/IG; Lotgi1 231196 (0e0)	-H	-	-	-
					+H	Y; I	3	0.0005
<b>99847</b>	HSP74_MOUSE (aa1-670)	4.6e-123	56.5%	Similar to Heat shock 70 kDa protein 4; domains: HSP70; Lotgi1 111562 (0e0)	-H	-	-	-
					+H	Y; I	11	0.0017

<b>99885</b>	Q28X57_DROPS (aa131-396)	4.0e-45	41.9%	aa20-287similar to $\beta$ 1,4-N-acetylglucosaminyltransferase; Lotgi1 229370 (4.6e-50)	<b>-H</b>	-	-	-
					<b>+H</b>	<b>Y,O</b> ; S,I	2	0.0012

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**Y**, yellow shells; **O**, orange shells; **B**, brown (on yellow ground). **S**, acid-soluble matrix; **I**, acid-insoluble matrix. **H**, hypochlorite treatment. The table contains identifications with  $\geq 2$  sequence-unique peptides identified at least three times in total and identifications with only one sequence-unique peptide occurring in at least 3 different replicates and in +H and -H samples. All identified proteins including the ones not accepted are given in Additional files nn.