| Supplemental Table Fractional Solubility Analysis from Gir | o S4 - Slobal LC-MS/MS Data | Normal Panc Swk Cellular Fraction | Normal Panc (Swk) | Normal Panc Swk aECM Fractio | Normal Panc (Sak) | Normal Panc Sak IDCM Fraction | Normal Panc (Swk) | Normal Pans 20wk Cellular Fracti | Normal Panc (20wk) | Normal Panc 20wk sECM Fraction | Normal Panc (20wk) | Normal Panc 20wk ECM Fraction | Normal Panc (20wk) | KTC PDAC Sek Cellular Fractic | MECM Fractions KTC PDAC (5wk) | KTC PDJ Swk sECM Frac | AC KTC PDAC (Swk) | KTC PD/ Swk ECM Frac | C RTC PDAC (Swk) | KTC PDAC 20wk Cellular Fraction | KTC POAC (20wk) | KTC PDAC 20wk sECM Fraction | KTC PDAC (20wk) | KTC PDAC KTC 20wk PDAI ECM Fraction (20w) | Cethole | | | aECM Comparie | | ECM Comparisons |
|--|---|---|---|---|--|--|---|---|---|---|--|---|---|---|---|--|---|--|--|---|--|--|---|---|--|---|---|--|--|--|
| # Identified Gene Proteins Gene | e Accession Molecular Number Weight | 1 2 3 | (n = 3) Cellular Average | Normal Panc Swk sECM Fractio | a secon Average | Normal Panc Suk IECM Fraction |) ECM Average | 1 2 | 3 Collular Average | Normal Panc 20wk aDCM Fraction | (n = 3) sECM Average | Normal Panc 20wk ECM Fraction | (n = 3) ECM Average | 1 2 | 2 Cellular Avarage | 1 2 | AC KTC PDAC (Swk) (n = 3) | 1 2 | E RTC PDAC (5wk) (n = 3) | 1 2 | PDAC (29wk) (n = 3) Collular Average 1 | 2 3 | sECM , | ECM Praction (n = 1) | p value (Normal p value 20wk/ (KTC 20w Normal KTC Swi | p value pv (KTC Switz (KTC Normal Nor | ratue p varue 20wk/ (Norma crmal Norma | p value p v (KTC 20wk/ Nor | due p value P Saki (KTC 20wid P mai Normal ki 20wki N | value |
| Collagen alpha-1(I) chain Colfat Collagen alpha-1(II) chain Colfat Collagen alpha-1(II) chain Colfat Colfagen alpha-2(I) chain Colfat Percusit alpha-sensions Amount | COSAL MOUSE 138 KDs COSAL MOUSE 139 KDs COSAL MOUSE 130 KDs AMYD MOUSE 57 KDs | 0% 1% 1% 1% 1% 1% 1% 1% 1% 1% 1% 1% 1% 1% | 0% 0.4% 0% 0.3% 0% 0.3% | 37% 38% 22% 20% 41% 20% | 42% 39.2% 24% 21.8% 42% 40.9% | 53% 51% 78% 79% 59% 60% | 58% 60.4% 76% 77.8% 58% 58.8% | 0% 1% 0% 0% 0% 2% | 0% 0.4% 9% 0.4% 0% 0.2% | 24% 19% 19% 10% 22% 24% | 27% 23.2% 24% 16.3% 31% 29.6% | 76% 80% 85% 90% 67% 75% | 73% 75.4% 75% 83.4% 69% 70.2% | 2% 2% 2% 2% 4% 2% | 2% 2.0% 2% 2.0% 3% 3.2% | 28% 315 20% 205 29% 300 | 5 31% 30.0% 5 34% 21.6% 6 31% 29.6% 6 12% 10.4% | 70% 67% 78% 78% 67% 67% | 67% 68.0% 74% 76.5% 66% 66.9% | 4% 4% 3% 3% 5% 4% | 8% 4.7% 3 4% 3.3% 2 5% 4.9% | 5% 33% 3 8% 36% 2 6% 36% 3 | 5% 34.1% 615 P% 24.9% 735 6% 35.6% 591 | 6 63% 60% 611 6 73% 60% 713 N 61% 58% 59.5 | % 0.9466 0.02 % 0.9304 0.11 % 0.9227 0.02 | Hg 0.0318 14 0.0022 96 0.0025 27 0.2400 | 0.0105 0.00 0.0261 0.3 0.0028 0.0 0.1370 0.00 | 963 0.0171 170 0.1431 165 0.0004 970 0.1256 | 0125 0.0028 1.8942 0.1990 10006 0.1994 | |
| 5 Plactin Plac 6 Actin, cytoplasmic 2 Actig1 7 Serum albumin Alb 9 Minosin-9 Mints | PLEC MOUSE 534 KDs ACTG MOUSE 42 KDs ALBU MOUSE 59 KDs MY19 MOUSE 225 KDs | 0% 0% 64% 72% 6 87% 94% 9 48% 58% 4 | 0% 0.0% 66% 68.0% 86% 92.2% 62% 49.5% | 32% 20% 25% 18% 10% 5% 29% 18% | 64% 32.2% 26% 23.2% 5% 6.6% 42% 29.7% | 68% 80% 11% 9% 2% 1% 23% 24% | 56% 67.8% 7% 8.8% 9% 1.2% 15% 20.7% | ON ON 67% 66% 90% 92% 56% 49% | 0% 0.0% 72% 68.1% 92% 91.9% 63% 55.9% | 17% 17% 20% 22% 9% 5% 12% 21% | 12% 15.8% 15% 19.3% 6% 6.5% 8% 13.9% | 82% 82% 12% 12% 1% 2% 2% 20% | 87% 84.2% 12% 12.6% 1% 1.6% 2% 30.2% | 0% 0% 77% 71% 92% 92% 42% 29% | 0% 0.1% 74% 74.0% 89% 90.5% 36% 39.5% | 22% 129 14% 159 7% 69 24% 259 | 6 22% 19.3% 6 56% 15.1% 6 8% 5.9% 6 31% 25.8% | 78% 879 9% 149 2% 39 23% 259 | 77% 80.6% 10% 11.0% 2% 2.6% 23% 33.7% | 2% 1% 82% 70% 88% 88% 65% 57% | 6% 3.4% 82% 81.5% 92% 89.2% 64% 91.6% | 11% 18% 1 8% 11% 8% 8% 10% 18% 1 | 4% 54.2% 861 7% 8.5% 91 6% 7.5% 41 2% 13.2% 251 | N 81% 80% 82.3 N 10% 11% 10.0 N 4% 28 32 N 26% 24% 25.1 | % 0.9653 0.05 % 0.9175 0.34 % 0.3466 0.00 | 99 0.4228 31 0.1563 24 0.5430 30 0.1306 | 0.1730 0.15 0.0063 0.3 0.1554 0.9 0.3132 0.15 | 194 0.0140 1 196 0.4373 1 142 0.0115 | (.0125 0.0228 (.8542 0.1930 (.8505 0.1934 (.1927 0.3437 (.1950 0.5530 (.8505 0.6682 (.8798 0.5035 (.7154 0.8672 | 0.3522 0.0846 0.4532 0.0946 0.4532 0.0946 0.0456 0.0456 0.0456 0.0456 0.0456 0.0456 0.0456 0.0566 0. |
| 10. Virtuelin. Virtuelin. 11. 78 kilo disconnected del recibile 11. 78 kilo disconnected del recibile 11. Rettli. 12. Keralin, type i cytoskeletal 15. Kritti. 13. Hemoglobin subunit alpha. Has | VIME_MOUSE 54 KDs GREYR_MOUSE 72 KDs K1C16_MOUSE 46 KDs HBA_MOUSE 15 KDs | 0% 1% 62% 67% 6 2% 2% 90% 88% 8 | 0% 0.8% 60% 04.4% 2% 2.0% 85% 87.9% | 82N 82N 20N 25N 82N 28N 6N 8N | 85% 82.8% 26% 27.7% 81% 80.1% 9% 7.8% | 17% 18% 9% 8% 17% 21% 4% 4% | 14% 15.4% 2% 7.9% 12% 18.0% 5% 4.2% | ON ON ON GRN GRN GRN GRN GRN GRN GRN GRN GRN GR | 0% 0.0% 60% 67.7% 4% 3.3% 87% 85.8% | 88% 84% 27% 25% 82% 72% 12% 6% | 84% 85.2% 26% 25.0% 28% 77.5% 78 8.5% | 12% 16% 6% 8% 15% 24% 6% 5% | 16% 14.7% 5% 6.3% 18% 19.2% 6% 5.7% | 4% 4% 66% 61% 1% 1% 89% 91% | 2% 3.8% 62% 63.0% 6% 0.7% 93% 91.0% | 77% 769 29% 329 86% 869 7% 59 | 6 28% 75.7% 6 31% 30.8% 6 85% 85.1% 6 4% 5.6% | 19% 209 6% 79 12% 149 4% 29 | 19% 19.5% 6% 6.2% 15% 14.2% 2% 3.4% | 6% 4% 62% 50% 4% 2% 92% 92% | 9% 5.4% 64% 52.2% 6% 3.9% 96% 90.7% | 72% 28% 7 12% 28% 2 72% 86% 7 5% 7% | 25 74.2% 211 25 33.9% 61 95 79.9% 191 45 5.2% 21 | N 18% 18% 19.3 N 2% 2% 40 N 14% 15% 16.2 N 1% 2% 1.7 | % 0.1357 0.20 % 0.1752 0.70 % 0.0890 0.10 % 0.4964 0.20 | 117 0.0023 108 0.5633 175 0.0052 141 0.1727 | 0.1730 0.12 0.0083 0.3 0.1554 0.9 0.3132 0.11 0.0439 0.2 0.0652 0.3 0.6477 0.4 0.0726 0.72 | 000 0.2460 194 0.0140 196 0.4373 196 0.4373 196 0.2075 197 | 0.000 0.0075 1.1820 0.0559 1.0452 0.4955 1.1316 0.2013 | 0.3546 0.8712 0.1058 0.0474 0.2355 0.1167 0.00372 0.1427 0.0993 0.2476 0.0909 0.3683 0.0147 0.1016 0.2025 0.0066 |
| 14 Chymolypainogen B Clib1 15 Steement membrane-specific he Hagg2 16 Fibrillo-1 Fin1 17 Elongation factor 1-alpha 1 Eeftat | CTRB1 MOUSE 28 KDs PGEM MOUSE 398 KDs FEN1 MOUSE 312 KDs EF1A1 MOUSE 50 KDs | 98% 95% 9 9% 9% 9% 9% 72% 72% 7 | 95 94.6% 95 9.0% 95 9.0% 96 73.0% | 5N 5N 62N 57N 0N 0N 24N 21N | 4% 4.4% 57% 58.4% 0% 0.0% 20% 21.4% | 1% 1% 20% 42% 200% 100% 6% 7% | 2% 1.0% 42% 41.0% 200% 100.0% 4% 5.7% | 95% 94% 0% 0% 0% 0% 70% 78% | 97% 95.4% 9% 9.1% 9% 9.9% 76% 74.5% | 4% 4% 60% 47% 0% 0% 24% 16% | 2% 3.2% 65% 57.5% 42% 13.7% 17% 19.0% | 1% 1% 39% 53% 100% 100% 6% 6% | 1% 1.2% 35% 42.4% 59% 85.3% 8% 6.5% | 97% 96% 9% 9% 2% 6% 2% 76% | 96% 96.3% 9% 0.1% 2% 3.2% 78% 76.1% | 2% 29 52% 629 4% 29 17% 189 | 6 3% 2.7% 6 50% 49.8% 6 22% 9.7% 6 21% 18.5% | 9% 19 47% 539 94% 913 4% 69 | 1% 1.0% 50% 50.1% 76% 87.2% 5% 5.4% | 100% 100% 1 1% 0% 2% 0% 75% 82% | 20 100.0% 25 0.0% 26 1.0% | 0% 0% MN 56% 4 15% 6% 2 12% 12% 1 | 0% 0.0% 01 0% 45.5% 561 2% 14.2% 831 2% 15.6% 81 | N 0% 0% 0.0 N 42% 59% 52.8 N 94% 75% 84.0 N 1% 4% 4.5 | % 0.5749 0.00 % 0.4226 0.00 % 0.6305 0.30 | | | 944 0.0107 F13 0.5979 F26 0.5935 F90 0.2323 | 1,028 0,0440 1,0170 0,2037 1,2638 0,9756 1,2136 0,3275 | 0.3749 0.1005 0.3023 0.0032 0.5829 0.5430 0.0144 0.2175 0.4226 0.0394 0.1475 0.8887 0.4909 0.7378 0.8089 0.4381 |
| 3 Cologo et de 20 (ches cologo et de 20 (che | PDIA1 MOUSE 57 KDs COSA2 MOUSE 145 KDs REEPT MOUSE 173 KDs | 81% 89% 8 9% 9% 37% 66% 6 | 995 85.4% 95 9.9% 415 49.6% | 16% 20% 60% 62% 63% 32% | 10% 11.9% 53% 60.0% 64% 41.6% | 2% 2% 60% 22% 20% 19% | 25 1.75 475 40.05 155 17.95 | 87% 90% 0% 0% 45% 37% | 90% 88.8% 0% 0.0% 47% 43.0% | 12% 8% 42% 40% 42% 41% | 9% 9.6% 29% 40.5% 28% 39.8% | 1% 2% 58% 60% 15% 21% | 1% 1.0% 51% 59.5% 15% 17.2% | 89% 88% 9% 9% 44% 46% | 96% 87.9% 6% 0.0% 46% 45.8% | 10% 109 41% 499 44% 329 | 5 11% 10.3% 5 12% 45.1% 6 42% 45.1% 6 39% 40.1% | 18 29 598 519 128 179 | 28 1.8% 53% 53.9% 14% 54.2% | 98% 91% 0% 0% 32% 29% | 95% 91.4% 95% 91.4% 95% 9.0% 42% 34.2% | 11N 9N 5N 50N 5 | 55 8.25 11 65 52.55 45 25 45.45 25 | N ON ON 03 N SON 46N 47.4 N 17N 15N 19.1 | S 0.4496 0.17 | 03 0.1917 179 0.2484 103 0.5309 115 0.1285 150 0.1109 | 0.2918 0.4 0.00 0.1628 0.52 0.0036 0.00 | 122 0.3192 1 199 0.0954 1 139 0.2378 1 | 1.5516 0.5328 1.0488 0.0050 1.6690 0.2184 | 0.0225 0.0397 0.0032 0.0314 0.0239 0.0254 0.0468 0.0050 0.0138 0.2565 0.1460 0.6403 0.0131 0.2006 0.0573 0.5705 |
| 23 Hemoglobin subunit bels-2 Hbb-92 24 Protein dauffide-isomerase A2 Pdis2 25 Februin-A Plas 26 Protein-AC Luma | PDIA2 MOUSE 16 KDs PDIA2 MOUSE 58 KDs FLNA MOUSE 201 KDs LANA MOUSE 74 KDs | 84% 86% 8 77% 81% 7 19% 32% 2 2% 2% | 86% 84.8% 77% 77.9% 21% 24.1% 4% 2.6% | 10% 9% 17% 12% 42% 24% 86% 80% | 11% 10.2% 18% 15.7% 29% 32.0% 86% 84.1% | 6% 5% 7% 7% 28% 62% 12% 18% | 5% 5.0% 6% 6.4% 50% 43.8% 10% 13.4% | 62% 75% 81% 82% 14% 17% 2% 1% | 26% 71.3% 87% 83.8% 12% 14.3% 6% 3.3% | 26% 17% 20% 11% 22% 26% 86% 86% | 15% 18.7% 6% 9.0% 15% 23.6% 86% 85.2% | 12% 8% 9% 6% 54% 59% 12% 12% | 9% 93.0% 6% 7.2% 74% 62.0% 8% 11.5% | 84% 92% 95% 96% 36% 29% 6% 6% | 90% 88.2% 96% 95.6% 25% 33.4% 5% 5.8% | 11% 69 2% 19 25% 189 82% 829 | 6 9% 7.0% 6 3% 2.2% 6 25% 22.9% 6 86% 83.2% | 5% 49 2% 39 39% 529 11% 119 | 2% 4.2% 1% 2.2% 40% 43.7% 10% 10.9% | 89% 86% 100% 100% 5 50% 40% 11% 10% | 92% 89.7% 100% 100.0% 46% 45.4% 14% 11.8% | 6N 20N 0N 0N 11N 24N 1 14N 79N 7 | 2% 6.2% 61 0% 0.0% 01 2% 15.9% 291 6% 76.5% 141 | N 5% 4% 4.7 N 6% 6% 0.0 N 26% 42% 38.8 N 11% 20% 11.8 | % 0.0763 0.75 % 0.0734 0.00 % 0.1344 0.00 % 0.6504 0.00 | 0.0048 01 0.0048 115 0.1478 | 0.0297 0.00 0.0134 0.00 0.0020 0.30 0.0075 0.00 | 134 0.5844 139 0.0300 151 0.2214 153 0.0151 | 1,2253 0,0240 1,0083 0,0267 1,2475 0,2999 1,7422 0,0093 | 0.0512 0.4990 0.2181 0.0450 0.4907 0.0387 0.0004 0.0123 0.0713 0.3756 0.9033 0.0468 0.5554 0.5900 0.4176 0.9051 |
| 27 Fibronectin Frd | GOOGA MASSES. 198 GO. PATE MAS | 0% 0% 0% 0% 1% 4% 81% 87% 8 | 0% 0.0% 0% 0.0% 2% 2.1% 85% 84.4% | 76% 75% 70% 61% 56% 57% 12% 9% | 75% 75.1% 60% 63.4% 54% 55.6% 11% 10.9% | 24% 25% 20% 29% 42% 29% 7% 4% | 25% 24.9% 40% 36.6% 45% 42.3% 4% 4.8% | ON ON ON ON ON ON ON ON ON | 0% 0.0% 0% 0.0% 1% 0.4% 92% 89.9% | 88% 82% 42% 21% 55% 55% 9% 8% | 89% 85.2% 48% 40.6% 36% 48.3% 4% 5.6% | 12% 18% 57% 69% 45% 45% 5% 2% | 11% 13.8% 52% 59.4% 62% 51.3% 2% 3.6% | 7% 7% 6% 0% 8% 8% 95% 96% | 6% 6.6% 6% 0.0% 9% 8.5% 92% 94.5% | 65% 609 52% 559 48% 479 4% 39 | 6 63% 62.7% 6 53% 53.2% 6 68% 47.5% 6 6% 4.3% | 28% 229 48% 459 44% 459 1% 19 | 21% 30.7% 47% 46.8% 42% 44.0% 2% 1.2% | 5% 5% 0% 1% 8% 6% 96% 98% | 7% 5.0% 1 2% 0.4% 1 12% 7.9% 1 | 54% 72% 6 57% 50% 5 11% 47% 3 1% 2% | 9% 68.4% 211 5% 54.1% 421 4% 42.6% 511 0% 0.8% 21 | N 22% 24% 26% N 49% 44% 45.5 N 48% 55% 51.4 N 1% 1% 1% 1.5 | % 0.2153 0.75 % 0.2153 0.77 % 0.1223 0.16 | 10 0.0047 50 52 0.0155 51 0.0194 | 0.0220 0.00 0.1850 0.00 0.0000 0.3 0.0418 0.00 | 02 0.1209 807 0.7073 756 0.1986 028 0.0542 | 1,0719 0,1024 1,0719 0,1024 1,0005 0,3654 1,0143 0,0514 | 0.0322 0.1914 0.0423 0.0195 0.0207 0.5542 0.0719 0.0079 0.2706 0.0000 0.4026 0.0050 0.4150 0.7009 0.0070 0.1464 |
| 31 Consign sprise () (VV) chain Contain 32 005 ribosoms prosise (4 Rp4 33 Tubuln sighs-6A chain Tubels 34 Hemoplobin subunit bets-1 Hbb-b1 | RLA_MOUSE 47 KDs TRAHA_MOUSE 50 KDs HEB1_MOUSE 16 KDs | 24% 21% 2 22% 29% 2 87% 88% 8 | 28% 27.9% 28% 32.8% 88% 87.8% | 60% 59% 65% 40% 85% 95% | 61% 59.9% 69% 44.7% 8% 8.3% | 29% 23% 16% 10% 23% 21% 5% 2% | 11% 12.2% 24% 22.6% 4% 4.0% | 22% 29% 28% 42% 82% 89% | 20% 30.4% 44% 40.9% 92% 87.9% | 57% 56% 27% 34% 12% 6% | 20% 55.5% 20% 33.9% 20% 7.4% | 10% 15% 25% 25% 6% 5% | 255 25.3% 25 4.8% | 25% 25% 25% 25% 42% 27% 89% 92% | 22% 22.0% 22% 30.7% 92% 91.1% | 62% 669 22% 289 27% 49 | 6 65% 64.7% 6 65% 54.7% 8 37% 32.3% 6 5% 5.4% | 12% 159 26% 259 48 29 | 12% 13.3% 12% 29.0% 26% 29.0% | 20% 18% 18% 18% 50% 47% 91% 92% | 26% 19.9% 26% 19.9% 52% 50.0% 94% 92.8% | 710 276 2 710 720 6 120 260 1 50 50 | 25 22.0% 601 6% 70.1% 111 9% 22.4% 281 25 4.2% 51 | N 9% 20% 10.0 N 26% 29% 27.5 N 2% 2% 3% 30 | % 0.3897 0.46 % 0.1103 0.06 % 0.9792 0.30 | 50 0.1026 55 0.1988 118 0.0871 | 0.0155 0.00 0.0207 0.00 0.2765 0.77 | 155 0.0973 1602 0.0418 1800 0.3584 | 0.000 1.000 1.000 1.000 1.001 1.001 1.001 1.001 1.001 1.001 | 0.5220 0.0325 0.0325 0.1504 0.0550 0.0322 0.1553 0.0550 0.4117 0.5325 0.3151 0.1903 0.9000 0.4331 0.0095 0.1502 |
| 35 Collegen ajsha-2(V), chain College 37 Deleted in malionant brain tumor: Drobb! 38 Collegen ajsha-2(V), chain CoHs2 29 Chymotrosui-ibe alsatase family Celaba. | CORAZ MOUSE 110 KDs DMBTI MOUSE 227 KDs CORAZ MOUSE 167 KDs CELZA MOUSE 29 KDs | 0% 1% 42% 44% 5 0% 0% 78% 85% 8 | 0% 0.5% 61% 45.8% 0% 0.0% 84% 82.5% | 57% 60% 60% 40% 16% 9% 16% 11% | 61% 59.2% 60% 40.1% 11% 11.7% 12% 13.0% | 42% 29% 18% 16% 84% 91% 6% 4% | 20% 40.2% 9% 14.7% 89% 80.2% 2% 4.2% | 0% 2% 48% 45% 2% 2% 87% 86% | 0% 0.5% 60% 45.2% 0% 0.4% 87% 85.5% | 57% 53% 45% 39% 34% 6% 9% 8% | 27% 49.1% 29% 40.8% 24% 14.9% 9% 8.5% | 42% 46% 7% 16% 84% 94% 4% 6% | 62% 50.4% 15% 12.9% 26% 54.7% 5% 4.9% | 6% 9% 48% 54% 0% 0% 60% 81% | 6% 7.2% 51% 50.9% 6% 0.0% | 205 425 245 225 275 255 255 99 | 56% 512% 6 35% 322% 6 36% 25.1% 6 36% 20.2% | 41% 449 18% 199 22% 259 15% 99 | 40% 41.6% 14% 16.9% 74% 73.9% 9% 11.0% | 9% 6% 48% 42% 9% 9% 100% 100% | 76 7.0% 1 485 46.4% 06 0.0% | 07% 52% 4 65% 42% 3 11% 21% 1 | 2% 45.9% 441 0% 35.0% 161 5% 19.0% 291 0% 0.0% 0 | N 41N 52N 455 N 15N 22N 17.6 N 79N 85N 81.0 N 0N 11N 37 | % 0.9475 0.77 % 0.8841 0.13 % 0.4226 % 0.1796 0.00 | 0.0079 H8 0.1882 | 0.0008 0.2 0.9006 0.7 0.4226 0.6 0.1184 0.0 | 011 0.3251 131 0.4145 145 0.0706 | 1.0467 0.7622 1.0788 0.2992 1.0788 0.5174 1.3130 0.0002 | 0.2909 0.2997 0.4922 0.5556 0.7943 0.8000 0.4204 0.2722 0.5024 0.0706 0.0138 0.5065 0.6443 0.1775 0.0547 0.7727 |
| 40 Vigilin Hilliop 41 Califori heavy chain 1 Clic 42 Filamin-8 Fish 43 Pancrealic triacylglycerol lipane Philip | VIGLN MOUSE 142 KDs CLH1 MOUSE 152 KDs FUND MOUSE 276 KDs UPP_MOUSE 51 KDs | 49% S6% 4 54% 65% 4 15% 21% 2 81% 84% 8 | 69% 51.2% 66% 54.9% 15% 16.8% 82% 82.1% | 62N 26N 6N 2N 55N 22N 14N 12N | 40% 29.6% 16% 8.2% 48% 45.1% 12% 12.7% | 8% 8% 40% 21% 21% 47% 5% 4% | 11% 9.2% 29% 38.8% 27% 38.1% 6% 5.2% | 50% 58% 58% 59% 17% 28% 82% 82% | 54% 53.8% 63% 50.0% 30% 24.9% 83% 82.3% | 42% 25% 4% 25% 49% 41% 12% 12% | 26% 37.5% 28 3.2% 24% 41.2% 22% 11.7% | 9% 8% 38% 38% 34% 31% 5% 6% | 10% 8.7% 35% 35.8% 37% 33.8% 7% 5.0% | 59% 57% 58% 64% 34% 41% 92% 92% | 62% 65.1% 58% 60.0% 36% 37.0% 84% 88.0% | 28% 289 4% 29 28% 169 9% 69 | 6 36% 29.7% 6 5% 3.9% 6 22% 22.2% 6 12% 8.9% | 28 59 288 249 288 449 28 49 | 4% 4.1% 26% 36.1% 40% 40.8% 4% 3.0% | 70% 71% 70% 75% 51% 50% 100% 1 | 63% 68.0% 76% 73.8% 56% 52.2% | 0% 23% 3 2% 2% 16% 22% 1 | 0% 27.6% 01 4% 2.6% 281 6% 17.9% 221 0% 01 | K 6% 2% 4.4 K 22% 20% 23.5 K 28% 28% 29.8 K 0% | % 0.4714 0.55 % 0.4992 0.00 % 0.1562 0.00 0.0236 0.00 | 03 0.0000 65 0.4651 62 0.0020 69 0.0074 | 0.0127 0.5 0.0046 0.3 0.0061 0.6 0.0005 0.4 | 192 0.5602 341 0.3027 1 375 0.3551 1 381 0.0445 | 1.0094 0.0418 1.3578 0.5081 1.0548 0.0197 1.1809 0.0059 | 0.6776 0.2207 0.0154 0.1761 0.9581 0.0174 0.0256 0.0142 0.4626 0.0100 0.0254 0.1073 0.4881 0.0626 0.0073 0.0139 |
| 44 Frest stock coorses / 1 kJa one; regard 45 405 ribosoms protein 52 Rps2 46 405 ribosoms protein 53 Rps3 47 005 ribosoms protein 17 Rps7 48 ATT professors stock tight only defaul | RS2 NOUSE 31 KGs RS2 NOUSE 27 KGs RS7 NOUSE 27 KGs RS7 NOUSE 31 KGs ATSA MOUSE 50 KGs | 22% 26% 2 40% 41% 4 22% 21% 2 | 90% 47.5% 27% 25.4% 41% 40.8% 36% 30.0% | 59% 52% 44% 44% 41% 42% | 58% 56.5% 66% 44.7% 52% 46.7% | 18% 21% 16% 15% 27% 21% | 15% 18.7% 12% 14.5% 12% 23.7% | 21% 22% 42% 28% 22% 20% | 32% 25.9% 46% 41.9% 34% 32.3% | 46% 48% 42% 48% 45% 46% | 28% 43.9% 28% 40.1% 27% 41.7% | 265 295 165 185 225 265 275 66 | 295 27.2% 295 18.0% 295 25.1% | 22% 18% 42% 42% 24% 20% 24% 20% | 19% 19.9% 19% 40.3% 21% 20.5% | 55% 669 48% 459 60% 569 | 6 57% 59.2% 6 48% 46.9% 6 59% 58.4% | 23% 169 12% 129 15% 149 | 26% 20.9% 16% 12.8% 10% 13.1% | 22% 14% 45% 46% 31% 26% | 20% 18.9% 55% 48.7% 32% 31.4% | 200 | 25 42.25 0 95 59.45 25 45 39.85 15 05 55.55 16 45 28.85 10 | 8 198 208 21.7 8 98 118 11.5 8 118 128 13.1 | S 0.3778 0.74 S 0.6700 0.11 S 0.3550 0.46 | 32 0.0303 76 0.7385 89 0.6024 05 0.6704 | 0.0672 0.00 0.1792 0.20 0.8076 0.21 0.6981 0.50 | 182 0.9730 1 549 0.1471 571 0.5500 | 1.5392 0.0449 1.1997 0.9442 1.0487 0.0504 1.9805 0.0112 | 0.4505 0.9900 0.0356 0.1079 0.4281 0.9057 0.0077 0.0077 0.2417 0.8554 0.3251 0.080 0.0070 0.9565 0.4267 0.1045 0.0070 0.5007 0.200 0.3504 0.9973 0.0728 0.045 0.7534 0.000 0.000 0.505 |
| 49 Soechin albha chain, non-ervinn Splant 50 005 ribosomal protein L6 Rp6 51 Collegen alpha-1(IV) chain CoHat 52 Hadone IH Harth-Ka | SPTN1 MOUSE 285 KDa RL6 MOUSE 33 KDa COMA1 MOUSE 161 KDa HH MOUSE 11 KDa | 17% 20% 2 26% 27% 2 0% 2% 42% 49% 4 | 30% 22.3% 36% 26.2% 0% 0.5% 42% 44.9% | 76% 59% 54% 55% 20% 17% 42% 40% | 71% 68.5% 56% 55.0% 12% 56.4% 47% 43.0% | 8% 11% 20% 18% 80% 82% 15% 11% | 9% 9.2% 19% 18.8% 88% 83.1% 11% 12.2% | 21% 30% 22% 25% 0% 0% 40% 42% | 29% 27.0% 22% 23.5% 0% 0.0% 40% 40.4% | 69% 52% 59% 58% 15% 0% 46% 29% | 59% 63.5% 58% 58.5% 32% 15.6% 47% 43.9% | 10% 7% 19% 17% 85% 100% 14% 19% | 12% 9.5% 18% 18.0% 68% 84.4% 14% 15.7% | 29% 28% 25% 21% 2% 0% 47% 45% | 22% 36.3% 22% 22.6% 0% 0.4% 54% 48.7% | 47% 479 58% 589 32% 299 29% 299 | 6 58% 49.3% 6 61% 59.1% 6 41% 34.1% 6 25% 37.9% | 14% 169 17% 229 67% 719 14% 169 | 12% 54.4% 16% 10.3% 59% 65.6% 10% 13.3% | 59% 42% 23% 20% 0% 0% 55% 52% | 58% 53.0% 22% 21.0% 0 0% 0.0% 53.3% | ISN 48% 3 ISN 67% 6 ISN 30% 2 ISN 35% 3 | 2% 38.3% 61 4% 63.6% 171 9% 28.3% 641 5% 34.3% 121 | N 9% 10% 8.6 N 12% 14% 14.8 N 80% 71% 71.7 N 12% 12% 12.4 | \$ 0.3500 0.44 \$ 0.6500 0.77 \$ 0.4086 0.01 \$ 0.4086 0.51 \$ 0.4426 0.54 \$ 0.422 0.64 \$ 0.426 0.22 \$ 0.3329 0.21 \$ 0.3365 0.33 \$ 0.7967 0.64 | 36 0.0004 39 0.0779 26 0.8748 64 0.3280 | 0.0223 0.44 0.2224 0.00 0.0004 0.77 | 942 0.1545 1 942 0.1545 1 997 0.3743 174 0.0938 | 1,0441 0,0198 1,0004 0,1336 1,0168 0,3020 1,1201 0,0441 | 0.3104 0.08073 0.00722 0.0500 0.5150 0.08073 0.0500 0.5150 0.08080 0.0073 0.00740 0.07740 0.0774 0.0974 0.0974 0.0974 0.0908 0.3500 0.3500 0.0975 0.3500 0.3500 0.3500 0.3500 0.0980 0.3500 0.3500 0.0980 0.0 |
| 53 005 hibosomal protein L7s Rp7s 54 Stachviscoccal rucksass domain Snd1 55 Carbosyspidase A1 Cps1 55 Myosin-11 Myh11 Myh11 | RL7A_MOUSE 30 kDs SND1_MOUSE 102 kDs CBPA1_MOUSE 47 kDs MYN11_MOUSE 227 kDs | 25% 18% 2 72% 76% 8 87% 92% 8 28% 72% | 21% 20.9% 81% 76.5% 89% 89.4% 0% 33.7% | 60% 70% 22% 29% 7% 6% 27% 0% | 66% 65.1% 15% 18.5% 8% 6.9% 72% 36.9% | 15% 12% 7% 5% 5% 2% 34% 27% | 14% 14.0% 2% 5.0% 2% 3.7% 2% 29.4% | 21% 27% 72% 89% 88% 92% 20% 9% | 25% 24.0% 27% 83.1% 91% 90.0% 0% 9.5% | 65% 56% 20% 9% 6% 5% 20% 32% | 60% 80.5% 9% 12.4% 4% 5.0% 22% 24.7% | 16% 17% 7% 2% 6% 4% 61% 59% | 15% 15.5% 4% 4.4% 5% 5.0% 78% 65.8% | 18% 15% 97% 99% 100% 100% 21% 28% | 20% 17.7% 98% 97.9% 98% 99.4% 31% 26.7% | 68% 759 2% 19 0% 09 31% 279 | 6 71% 71.0% 6 1% 1.0% 6 2% 0.0% 6 31% 29.0% | 14% 109 0% 09 0% 09 48% 459 | 9% 10.7% 1% 0.3% 0% 0.0% 28% 43.6% | 14% 17% 97% 100% 1 100% 100% 1 21% 61% | 15% 15.3% 100% 99.0% 100% 100.0% 22% 34.0% | 75% 80% 8 3% 0% 0% 0% 14% 54% 2 | 0% 78.4% 111 0% 1.0% 01 0% 0.0% 01 2% 15.4% 661 | N 4N 5N 6.3 N 0N 0N 0N 0.0 N 0N 0N 0N 0.0 N 25N 56N 42.0 | % 0.3329 0.21 % 0.3285 0.38 % 0.7567 0.40 % 0.3723 0.61 | 26 0.0126 26 0.0126 26 0.0086 46 0.7721 | 0.0004 0.7 0.0004 0.7 0.0008 0.3 0.0009 0.2 0.0008 0.0 0.1009 0.0 | 00 0.5390 60 0.425 57 0.024 | 1.1442 0.0080 10082 0.0039 10022 0.0110 1.7698 0.1561 | 0.2517 0.1912 0.1556 0.0005 0.7653 0.4226 0.0005 0.0007 0.2536 0.0017 0.0014 0.0149 0.7056 0.0009 0.3007 |
| 20 See August 1 S | 100 A 100 | 42% 40% 4 77% 86% 8 | 61% 41.5% 86% 83.0% 0% 1.6% | 20% 26% 20% 26% 20% 77% CVS CVS | 225 19.15 125 15.25 876 83.85 | 28% 64% 2% 0% 12% 19% | 2% 39.4% 2% 1.8% 12% 14.8% | 62% 42% 85% 88% 0% 0% | 47% 43.2% 91% 88.0% 0% 0.0% | 25% 26% 24% 20% 91% 89% | 12N 14.9N 2N 10.4% 96N 91.6N | 42% 42% 1% 2% 9% 11% | 90% 41.9% 2% 1.0% 4% 0.4% | 28% 62% 92% 92% 8% 7% | 60% 39.3% 91% 90.6% 4% 6.3% | 7% 49 9% 89 80% 813 | 6 9% 5.5% 6 8% 5.4% 6 80% 51.8% | 55% 569 1% 29 11% 139 | 52% 56.2% 1% 1.0% 12% 11.9% | 22% 36% 94% 88% 11% 7% | 275 31.7% 95% 92.0% 12% 10.0% | 6N 2N 5N 11N 2N 82N 7 | 8% 5.0% 721 2% 5.2% 11 6% 75.8% 161 | N 60% 54% 52.3 N 1% 2% 1.7 N 11% 11% 12.8 | % 0.4336 0.26 % 0.2628 0.51 % 0.2989 0.10 | 48 0.7721 117 0.2343 190 0.0972 772 0.1382 136 0.0423 | 0.1398 0.1 0.2257 0.2 0.0262 0.1 | 185 0.8348 131 0.5040 115 0.1788 | 1.0054 0.0105 1.1152 0.2000 1.6236 0.0116 | 0.3780 0.2017 0.0077 0.0574 0.8413 0.4410 0.4219 0.8003 0.1203 0.6725 0.3702 0.1776 0.0096 0.0208 0.0761 0.0011 |
| 62 Section beta chain, non-enritro. Spitini 63 Cylostamic dynein I heavy chai Dync Itil. 64 Sile sati-achetel (pase 65 Halore Ho.2 Haliffs). | 5PTB2_MOUSE 274 KDa 1 DYNC1_MOUSE 532 KDa CEL_MOUSE 65 KDa 5 HG2_MOUSE 15 KDa | 24% 32% 1 24% 70% 6 82% 84% 8 29% 31% 2 | 12% 23.3% 62% 68.8% 88% 84.9% 29% 32.9% | 16% 7% 9% 1% 12% 12% 64% 51% | 42% 22.2% 2% 1.2% 10% 11.6% 51% 48.6% | 60% 60% 26% 20% 4% 4% 17% 19% | 42% 54.5% 35% 30.0% 26 3.5% 20% 18.6% | 21% 29% 69% 67% 82% 89% 21% 38% | 25% 25.2% 26% 71.2% 86% 85.6% 22% 27.2% | 22% 9% 2% 0% 12% 8% 60% 16% | 2% 8.5% 6% 0.0% 11% 10.8% 62% 45.9% | 69% 62% 21% 22% 5% 2% 19% 47% | 58% 63.3% 22% 28.8% 2% 3.6% 15% 27.0% | 56% 54% 84% 84% 92% 92% 52% 47% | 69% 52.8% 62% 83.5% 60% 91.2% 64% 54.4% | 7% 50 0% 00 6% 60 28% 440 | 6 9% 6.7% 6 9% 0.0% 6 9% 7.1% 6 29% 37.1% | 37% 419 16% 169 1% 39 10% 99 | 42% 40.5% 18% 95.5% 18 1.7% 6% 0.5% | 92% 92% 100% 100% 58% 56% | 59% 54.4% 94% 50.7% 95% 50.7% 52% 50.0% | 6N 11% 1N 0N 0N 0N 6N 28N 4 | 6% 7.5% 30 0% 0.2% 60 5% 1.5% 00 3% 38.9% 60 | N 20% 25% 28.0 N 7% 6% 6.7 N 0% 0% 0.0 N 6% 4% 5.4 | % 0.5169 0.00 % 0.6439 0.00 % 0.7802 0.00 % 0.4946 0.81 | 06 0.0460 119 0.0234 90 0.0313 | 0.0027 0.33 0.0212 0.25 0.0058 0.63 0.0254 0.63 | 150 0.6866 189 0.4225 165 0.0461 163 0.7288 | 1.2905 0.6067 1.2889 0.4226 1.0358 0.0108 1.0329 0.6897 | 0.2576 0.0061 0.1178 0.0022 0.7543 0.0006 0.0093 0.0097 0.8960 0.1024 0.1400 0.0190 0.4907 0.0800 0.0023 0.1608 0.4907 0.0800 0.0022 0.5151 |
| 65 Fibrinogen beta chain Figb 67 AOPIATP translocase 2 Sb25a5 63 Serobanderin TT 69 Fibrinogen alpha chain Figa | FIRE MOUSE 55 KDs ADT2_MOUSE 33 KDs TREE_MOUSE 77 KDs FIRA_MOUSE 87 KDs | 6% 10% 1 49% 59% 5 98% 99% 9 6% 11% 1 | 14% 9.9% 51% 52.9% 99% 98.7% 12% 10.0% | 92% 22% 29% 27% 2% 1% 61% 61% | 82% 78.6% 26% 30.1% 1% 1.3% 81% 67.7% | 12% 18% 22% 14% 0% 0% 32% 27% | 9% 11.5% 15% 17.1% 9% 0.0% 9% 22.3% | 5N 15N 67N 60N 99N 100N 8N 4N | 75 9.15 605 54.25 995 99.25 75 6.25 | 89% 85% 16% 17% 1% 0% 81% 81% | 72% 81.9% 10% 13.5% 1% 0.8% 60% 74.0% | 5% 0% 19% 22% 0% 0% 11% 15% | 22% 9.0% 24% 22.2% 0% 0.0% 32% 19.8% | 21% 19% 44% 49% 92% 95% 21% 21% | 15% 18.0% 48% 47.0% 92% 96.5% 16% 19.2% | \$7% \$39 17% 109 2% 49 \$5% \$19 | 6 56% 54.8% 6 20% 15.6% 6 26 3.1% 6 52% 52.8% | 22% 289 29% 419 0% 19 24% 289 | 21% 27.1% 21% 37.4% 0% 0.4% 21% 28.0% | 28% 20% 47% 52% 97% 95% 27% 23% | 276 31.7% 465 48.7% 985 96.2% 216 27.7% | 28 588 5 98 128 1 28 58 28 578 5 | 1% 53.7% 91 5% 12.5% 641 2% 3.3% 91 7% 55.9% 201 | N 12% 22% 14.5 N 25% 28% 39.4 N 1% 5% 0.2 N 9% 22% 17.0 | % 0.8330 0.00 % 0.0005 0.00 % 0.3541 0.00 % 0.2176 0.10 | 27 0.0454 82 0.1747 86 0.0416 85 0.0275 | 0.0076 0.00 0.0052 0.00 0.0050 0.30 0.0050 0.5 | 222 0.6743 553 0.4408 541 0.8551 558 0.1745 | 10228 0.7255 10228 0.7255 10373 0.0054 1.1495 0.1176 | 0.7657 0.0642 0.0032 0.5151 0.1791 0.5386 0.00175 0.0002 0.6380 0.2282 0.4226 0.2244 0.0802 0.5558 0.7469 |
| Suz noseona promi Li Jai Ingnia Suzali, Ingnia I Cytoskeleia Z NY Z. ATP-decendent RNA helicase DC DdxDx Z. Heleroceneous nuclear ribonucle Horack Jai Lestric surveyar commo. | NATION MOUSE 23 NOS NATIONAL MOUSE 51 NOS DOXON MOUSE 51 NOS HARPIN MOUSE 51 NOS | 0% 0% 11% 12% 1 16% 14% 2 | 25 0.9% 25 0.9% 12% 12.4% 20% 16.8% | 61% 62% 64% 52% 69% 72% | 87% 88.4% 67% 65.8% 66% 69.2% | 12% 9% 25% 20% 15% 12% | 20% 10.7% 20% 21.8% 21% 21.8% 14% 13.9% | 0% 0% 12% 12% 12% 18% | 0% 0.0% 16% 14.1% 17% 15.9% | 925 895 925 625 775 725 715 245 | 90% 90.0% 54% 50.2% 74% 74.7% | 9% 11% 9% 11% 27% 25% 10% 9% | 10% 10.0% 10% 10.0% 30% 27.5% 9% 9.4% | 28 28 118 118 28 278 | 0% 0.0% 12% 11.6% 29% 27.4% | 86% 823 71% 623 62% 643 | 6 995 87.4% 6 71% 58.3% 6 60% 53.0% | 14% 129 18% 269 11% 99 | 11% 12.6% 17% 20.1% 8% 9.1% | 2% 0% 2% 0% 20% 16% 27% 26% | 25 1.85 215 19.25 225 20.25 | 60 | 25 57.4% 197 25 58.3% 121 45 58.8% 201 65 61.8% 91 | N 8% 12% 25% N 21% 25% 22.1 N 8% 12% 25% 32.1 | 5 0.4226 0.15 5 0.2003 0.65 5 0.7140 0.65 | 05 0.0275 177 0.0835 110 0.4225 177 0.3052 102 0.0177 106 0.1836 | 0.1510 0.25 0.0454 0.05 0.0065 0.15 0.4225 0.9 | 060 0.6666 1 162 0.0611 1 060 0.6069 1 | 14795 0.4662 14696 0.9096 1.1130 0.0031 | 0.5573 0.1321 0.1642 0.8797 0.0615 0.5850 0.5387 0.0062 0.0083 0.5791 0.0163 0.6077 0.0850 0.1417 0.0529 0.0643 |
| 75 405 ribosomal protein 511 Rps11 76 ATP synthase subunit bela, ribo: Ap5b 77 Heteropeneous nuclear ribonucle Hempin 78 Fibrinogen gamma chain Figg | RS11_MOUSE 18 KDs ATPS_MOUSE 55 KDs HNRPM_MOUSE 78 KDs FIRS_MOUSE 49 KDs | 23% 17% 2 69% 76% 7 2% 11% 5% 19% 1 | 15% 18.2% 72% 74.1% 8% 7.1% 11% 11.9% | 61% 67% 25% 21% 87% 79% 72% 51% | 65% 64.2% 19% 21.7% 80% 82.0% 75% 66.2% | 16% 17% 5% 4% 10% 11% 22% 30% | 20% 17.6% 2% 4.2% 12% 10.9% 14% 21.9% | 21% 18% 77% 78% 12% 6% 20% 17% | 15% 18.0% 82% 78.9% 6% 7.3% 9% 15.5% | 62% 64% 21% 20% 82% 86% 68% 58% | 70% 65.9% 15% 18.6% 87% 85.5% 63% 63.0% | 15% 18% 2% 1% 5% 8% 12% 25% | 15% 95.1% 2% 2.4% 8% 7.1% 28% 21.5% | 16% 12% 76% 76% 18% 12% 22% 25% | 22% 16.2% 77% 77.4% 12% 14.1% 23% 23.2% | 72% 749 21% 189 76% 769 57% 489 | 6 71% 72.8% 6 22% 20.3% 6 82% 78.9% 6 50% 51.6% | 12% 129 2% 29 6% 99 21% 289 | 8% 11.0% 1% 2.3% 6% 7.0% 27% 25.1% | 18% 21% 81% 72% 12% 13% 30% 29% | 18% 18.7% 8e% 79.5% 1e% 13.0% 25% 28.2% | 72% 77% 7 14% 22% 1 79% 80% 7 18% 52% 5 | 9% 76.6% 91 2% 15.8% 51 7% 78.8% 81 1% 50.6% 221 | N 2% 2% 4.7 N 5% 4% 4.7 N 7% 10% 8.2 N 18% 24% 21.3 | % 0.9706 0.40 % 0.1726 0.50 % 0.9572 0.60 % 0.5323 0.00 | 0.5158 H9 0.2953 H9 0.0907 H51 0.1073 | 0.7478 0.50 0.8844 0.30 0.1413 0.3 0.0366 0.7 | 000 0 0000 180 0 2325 183 0 1575 184 0 2541 140 0 5447 185 0 7633 171 0 3455 367 0 3237 368 0 700 | 1.5381 0.4906 1.5381 0.4906 1.3815 0.0133 1.1945 0.0411 | 0.4282 0.0786 0.0349 0.0165 0.1223 0.0121 0.0780 0.0471 0.0239 0.3872 0.0341 0.5478 0.9591 0.2225 0.5672 0.9684 |
| March Select Selec | TLNI_MOUSE 270 kDa HNRPU_MOUSE 85 kDa EIF3A_MOUSE 162 kDa LIPRI_MOUSE 53 kDa | 42% 46% 4 14% 19% 1 25% 24% 2 79% 88% 8 | 62% 43.9% 11% 14.7% 27% 25.3% 82% 83.2% | 62% 22% 66% 66% 51% 50% 17% 11% | 42% 39.1% 70% 67.4% 56% 52.7% 15% 14.3% | 15% 21% 20% 15% 23% 26% 4% 1% | 15% 17.0% 18% 17.9% 17% 22.0% 2% 2.5% | 64% 32% 16% 15% 26% 27% 79% 92% | 61% 45.0% 18% 16.3% 29% 27.4% 92% 87.6% | 22% 51% 71% 62% 42% 42% 26% 7% | 15% 32.9% 69% 67.8% 28% 40.7% 7% 10.2% | 26% 15% 12% 22% 22% 32% 4% 2% | 24% 21.1% 12% 15.9% 22% 31.9% 1% 2.2% | 55% 50% 22% 22% 32% 38% 95% 94% | 52% 52.8% 21% 21.8% 29% 33.2% 92% 93.9% | 27% 229 60% 549 45% 239 5% 49 | 6 30% 25.4% 6 59% 57.4% 6 49% 39.0% 6 6% 5.2% | 18% 289 18% 259 23% 289 0% 29 | 17% 20.9% 20% 21.0% 22% 27.8% 1% 1.0% | 50% 52% 22% 22% 50% 20% 100% 100% 2 | 72% 63.5% : 29% 24.8% ! 62% 50.0% 100% 100.0% | 15% 31% 17% 64% 5 7% 27% 0% 0% | 9% 18.2% 191 2% 56.7% 201 4% 12.5% 421 0% 0.0% 01 | N 16% 20% 18.3 N 16% 20% 18.5 N 22% 26% 37.5 N 0% 0% 0.0 | % 0.8122 0.11 % 0.5448 0.24 % 0.1907 0.05 % 0.4291 0.01 | 0.000 0.0007 0.000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 | 0.1524 0.6 0.0337 0.9 0.0027 0.00 0.0971 0.3 | | 10004 0.3109 10141 0.0054 12165 0.0097 10033 0.0799 | 0.0007 0. |
| 84 Biglycan Bgn 85 Deamophiún Dap 86 Clusterin Clu 87 605 ribosomal protein LB Padil | RESA MOURE 23 SUB- REST MOURE 23 | 235 265 2 285 205 05 05 596 445 6 126 245 3 | 4% 14.1% 0% 0.0% 63% 55.2% | 64N 60N 22N 29N 27N 50N 74N 65N | 885 73.45 425 28.15 285 41.55 554 64.35 | 18% 20% 28% 81% 4% 6% 14% 12% | 9% 15.5% 52% 71.9% 9% 3.2% 15% 13.5% | 205 265 17% 18% 0% 0% 42% 44% 20% 34% | 11% 15.0% 0% 0.0% 50% 45.8% 21% 28.0% | 72% 71% 11% 7% 57% 50% 65% 68% | 84% 75.5% 8% 8.9% 44% 50.2% 58% 56.8% | 275 285 115 125 895 925 05 65 155 195 | 28 9.4% 92% 91.1% 98 3.9% | 275 285 226 205 206 205 285 295 226 196 | 21% 21.2% 21% 21.2% 21% 30.2% 21% 24.2% | 60% 603 20% 229 52% 529 50% 600 | 6 60% 53.2% 6 12% 19.9% 6 52% 52.9% 6 50% 55.9% | 125 119 125 189 805 779 95 99 80 129 | 10% 15.0% 16% 15.0% 83% 80.1% 9% 8.0% | 205 205 205 215 05 05 205 205 205 115 | 205 23.4% 206 0.0% 276 31.8% | 27% 64% 6 18% 11% 2 12% 59% 5 | 75 52.4% X 25 51.0% 181 75 18.8% 821 65 54.0% 141 76 72.7% 91 | 5 15% 14% 15.5 8 15% 14% 15.5 8 89% 22% 81.2 8 11% 12% 14.2 8 5% 2% 5% 5% 5.5 | % 0.6354 0.20 % 0.8768 0.20 % 0.2407 0.21 % 0.4174 0.75 | 93 0.1000 93 0.7774 | 0.0387 0.50 0.11 0.0418 0.21 0.4027 0.31 | 192 0.4146 187 0.8303 1015 0.8010 154 0.3739 | 1.4907 0.0534 1.3850 0.1499 1.1150 0.5327 1.8089 0.1010 | 0.2354 0.9873 0.9805 0.0729 0.1167 0.3303 0.3850 0.1469 0.8225 0.0827 0.0934 0.017 0.5154 0.1187 0.0738 0.0228 |
| 20 Treiter desiriée incresses A.2 Pais A.2 | PALACUSE 23 HOS PORA MOUSE 27 HOS CERAL MAUSE 25 HOS COPAL MOUSE 25 HOS LANGU MOUSE 25 HOS LANGU MOUSE 25 HOS PROPERTY MAUSE 27 HOS PROPERTY MAUSE 27 HOS PROPERTY MAUSE 27 HOS PROPERTY MOUSE 27 HOS NOT MOUSE 27 HOS SCHAM MOUSE 27 HOS COMMO MOUSE 27 HOS COM | 85% 91% 8 76% 75% 7 0% 0% 0% 0% | 87 87.7% 38% 75.9% 0% 0.0% 0% 0.0% | 15% 9% 21% 21% 50% 50% 70% 61% | 12% 12.3% 20% 20.7% 50% 50.0% 71% 67.2% | 9% 9% 4% 4% 59% 50% 32% 39% | 0% 0.0% 2% 3.2% 50% 50.0% 29% 32.8% | 91% 95% 82% 84% 0% 0% 0% 0% | 92% 92.8% 92% 82.8% 0% 0.0% 0% 0.0% | 9% 5% 17% 12% 59% 20% 65% 67% | 7% 7.2% 14% 14.8% 50% 40.0% 50% 51.1% | 0% 0% 2% 2% 50% 80% 35% 22% | 0% 0.0% 3% 2.4% 50% 60.0% 50% 38.9% | 86% 86% 68% 78% 6% 0% 0% 1% | 88% B5.8% 64% 69.8% 0% 0.0% 0% 0.4% | 20% 229 0% 509 60% 459 | 6 12% 12.8% 6 36% 29.3% 6 18% 22.7% 6 60% 55.0% | 2% 29 2% 09 100% 509 40% 529 | 0% 0.4% 0% 0.9% 82% 77.2% 40% 44.6% | 995 975 100% 100% 1 0% 0% 0% 0% | 925 56.7% 1006 100.0% 06 0.0% | 11% 12% 0% 0% 12% 12% 16% 41% 3 | 8% 19.7% 01 0% 0.0% 01 5% 19.0% 82 2% 33.5% 24 | N 1% 1% 0.5 N 0% 0% 0% 0.0 N 88% 95% 90.0 N 59% 67% 65.5 | % 0.0002 0.25 % 0.0000 0.05 % 0.40 | 22 0.5199 03 0.2944 25 0.4225 24 0.0392 | 0.0000 0.00 0.0018 0.0 0.40 0.30 | 140 | 17672 0.0095 1.1790 0.0041 1.2029 0.0672 1.1117 0.0177 | 0.2085 0.4226 0.0979 0.0035 0.4226 0.4795 0.2029 0.0072 0.2919 0.0246 0.1014 0.0177 |
| 405 ribosomal protein SS Rps6 54 Serpin H1 Serpin H2 55 405 ribosomal protein S9 Rps6 55 405 ribosomal protein L18a Rp18a 57 Metrown H2 | RSS MOUSE 29 KGs 1 SERPH MOUSE 47 KGs RSS MOUSE 23 KGs RSSA MOUSE 21 KGs ND1 MOUSE 137 KGs | 20% 20% 2 12% 19% 21% 28% 3 21% 22% 2 | 29% 29.8% 6% 12.6% 22% 25.4% 22% 21.8% | 59% 58% 76% 69% 45% 45% 63% 64% | 615 59.5% 805 74.7% 665 45.2% 668 63.7% | 11% 12% 11% 12% 25% 17% 16% 17% | 10% 10.8% 14% 12.7% 17% 19.4% 11% 14.5% | 20% 28% 5% 5% 28% 26% 21% 21% | 205 34.45 8% 5.9% 22% 35.4% 25% 22.1% | 57% 50% 95% 90% 45% 41% 64% 56% | 60% 55.7% 92% 92.4% 47% 44.2% 58% 59.4% | 76 128 05 58 176 228 156 248 | 11% 9.9% 0% 1.7% 20% 20.4% 17% 18.5% | 18% 24% 15% 19% 26% 20% 18% 11% | 23% 21.7% 12% 15.5% 21% 28.8% 11% 13.7% | 20% 629 67% 629 60% 529 72% 779 | 6 676 66.7% 6 206 66.7% 6 526 54.5% 6 286 76.0% | 12% 139 18% 189 14% 199 8% 119 | 10% 11.0% 17% 17.0% 17% 95.7% 11% 90.2% | 22% 22% 15% 9% 28% 24% 15% 7% | 226 22.05 166 13.25 266 25.75 166 11.85 | 998 208 7 688 808 7 588 648 5 708 828 7 | 25 70.7% 90 05 71.4% 20 65 57.4% 12 26 76.2% 12 | N 11% 6% 7.4 N 11% 14% 15.1 N 15% 18% 16.5 N 10% 14% 11.9 | % 0.2003 0.52 % 0.2003 0.52 % 0.9970 0.25 % 0.8726 0.65 | 06 0.000 05 0.000 00 0.0794 | 0.0005 0.0 0.0003 0.6 0.0412 0.2 | 199 0.4311 197 0.4455 121 0.9483 | 1.1276 0.0340 1.0724 0.0073 1.0046 0.0214 1.2286 0.0336 | 0.5124 0.0860 0.5126 0.2145 0.0001 0.4510 0.0211 0.0220 0.7681 0.9249 0.4196 0.1434 0.2770 0.3142 0.1312 0.1068 0.8307 0.9374 0.2296 0.9308 |
| 90 Transitional endoclasmic neticular Vicp 99 Protein transcort protein Sec31A Sec31a 100 Collegen alpha-6(VI) chain College 101 605 ribosomal protein L13 Rpt13 | TERA MOUSE 89 KGs SC31A MOUSE 134 KGs C08A6 MOUSE 246 KGs RL13 MOUSE 24 KGs | 72% 80% 8 31% 27% 2 0% 0% 14% 22% 1 | 82% 77.1% 22% 26.4% 0% 0.0% 17% 18.2% | 26% 18% 51% 50% 42% 42% 71% 61% | 17% 20.7% 59% 53.0% 42% 42.4% 68% 65.8% | 2% 2% 18% 24% 58% 57% 15% 16% | 2% 2.2% 20% 20.6% 58% 57.6% 15% 15.1% | 79% 84% 27% 21% 0% 0% 24% 28% | 86% 82.7% 36% 28.0% 0% 0.0% 26% 25.6% | 20% 15% 29% 51% 22% 17% 60% 58% | 14% 15.4% 34% 41.4% 17% 22.2% 63% 50.2% | 1% 1% 26% 29% 67% 82% 16% 14% | 1% 0.9% 29% 30.5% 82% 77.8% 12% 14.2% | 76% 72% 36% 22% 2% 6% 22% 27% | 72% 73.9% 19% 25.0% 6% 4.0% 18% 22.5% | 20% 229 28% 219 27% 209 60% 579 | 5 22% 21.3% 5 51% 39.9% 6 32% 34.8% 6 66% 60.2% | 4% 69 22% 479 61% 649 18% 169 | 4% 4.8% 20% 34.5% 56% 60.6% 18% 17.3% | 89% 76% 42% 38% 0% 0% 17% 15% | 82% 82-4% 62% 49.0% 12% 3.7% 25% 19.0% | 9% 29% 1 18% 33% 12% 30% 2 30% 78% 6 | 4% 14.2% 21 0% 17.1% 291 2% 21.4% 881 9% 71.6% 141 | 5 5% 4% 3.4 5 29% 22% 33.9 6 70% 62% 75.0 8 8% 6% 9.3 | % 0.1561 0.15 % 0.7709 0.10 % 0.0945 0.45 | 55 0.3444 35 0.9102 115 0.0702 187 0.3028 | 0.9525 0.2 0.1293 0.12 0.4226 0.0 0.1527 0.13 | 861 0.1216 1 868 0.1273 1 881 0.0967 1 871 0.0389 1 | 1.8500 0.5585 1.1337 0.1104 1.0785 0.9129 1.1290 0.0412 | 0.0352 0.03600 0.5156 0.5146 0 |
| 902 acidic ribosomal protein PO Rpipi 903 Heat shock protein HSP 90-bets HepSchol 104 Receipt of activated crotein C is Rack1 905 showomal protein L14 Rpi14 | RAO MOUSE 34 KDs b1 HESSE MOUSE 63 KDs RACK1 MOUSE 35 KDs RL14 MOUSE 24 KDs | 57% 54% 5 69% 77% 6 62% 72% 7 26% 35% 3 | 50% 53.9% 50% 71.9% 71% 69.0% 32% 31.6% | 27% 25% 27% 17% 31% 22% 61% 51% | 26% 29.2% 26% 24.0% 24% 25.0% 55% 55.6% | 17% 19% 4% 6% 7% 2% 12% 14% | 15% 16.8% 2% 4.1% 5% 4.9% 12% 12.8% | 58% 55% 74% 80% 75% 76% 32% 28% | 57% 57.1% 96% 79.9% 78% 76.5% 31% 30.4% | 18% 22% 18% 17% 19% 19% 57% 58% | 18% 19.4% 6% 13.5% 18% 18.8% 54% 56.3% | 26% 22% 8% 2% 6% 5% 11% 14% | 25% 23.5% 9% 6.6% 4% 4.7% 15% 13.4% | 62% 60% 80% 84% 82% 82% 15% 14% | 59% 60.2% 77% 80.3% 82% 82.4% 34% 21.1% | 22% 219 15% 109 18% 159 76% 229 | 6 22% 22.1% 6 17% 14.0% 6 17% 15.7% 6 19% 60.0% | 16% 199 6% 69 0% 29 9% 129 | 18% 17.7% 6% 5.8% 1% 1.0% 6% 9.3% | 90% 84% 90% 96% 9 94% 90% 1 | 75% 67.8% 92% 88.2% 100% 94.8% 26% 20.6% | 11% 18% 2% 11% 4% 20% 5% 72% 6 | 2% 10.4% 241 2% 5.9% 71 0% 4.6% 21 9% 72.3% 111 | N 20% 22% 21.9 N 5% 6% 5.9 N 0% 0% 0.7 N 6% 5% 7.1 | % 0.2259 0.17 % 0.1370 0.05 % 0.1513 0.09 % 0.7249 0.32 | 36 0.0919 36 0.0737 58 0.0566 82 0.2510 | 0.0009 0.0 0.1105 0.1 0.0163 0.0 0.0006 0.8 | 152 0.002 152 0.0007 104 0.0417 108 0.0641 | 1.1546 0.1402 1.0051 0.1856 1.0454 0.0346 1.0073 0.0027 | 0.0125 0.0443 0.6122 0.2025 0.2673 0.8693 0.1755 0.6695 0.8694 0.7439 0.0384 0.0160 0.7039 0.4286 0.1925 0.0485 0.7039 0.4286 0.1925 0.0485 |
| Description Control | SCHA MANUEL MAN SIGN RELATIONS AND SIGN RELATIONS A | 0% 0% 0% 0 72% 72% 72% 82% 72% 66% 66% 66% | 0% 0.0% 77% 70.5% 36% 78.7% | 67% 67% 29% 36% 12% 20% 32% 29% | 75% 69.4% 23% 25.2% 19% 13.8% 21% 30.7% | 22% 22% 8% 5% 9% 9% 8% 5% | 25% 30.6% 0% 4.3% 5% 7.5% 1% 4.6% | ON ON 66N 80N 72N 82N 59N 62N | 0% 0.0% 76% 74.3% 86% 79.8% 66% 62.2% | 50% 64% 31% 20% 12% 8% 32% 29% | 50% 48.1% 17% 22.6% 4% 8.0% 23% 31.7% | 50% 56% 2% 0% 15% 12% 9% 8% | 50% 51.9% 7% 3.2% 11% 12.2% | 5% 9% 80% 74% 82% 66% 67% 62% | 5% 6.3% 36% 76.5% 26% 75.6% 62% 64.1% | 56% 500 17% 199 8% 109 28% 339 | 6 57% 54.1% 6 29% 18.0% 6 11% 9.4% 6 35% 32.2% | 20% 419 2% 69 10% 249 4% 49 | 28% 20.0% 5% 4.8% 11% 54.9% | 23% 21% 84% 82% 83% 77% 73% 72% | SN 15.4% 84% 83.1% 86% 81.9% 72% 74.4% | 18% 45% 3 13% 16% 1 6% 7% 15% 25% 2 | 8% 40.0% 601 5% 14.6% 21 2% 5.1% 111 0% 23.2% 31 | N 24N 57N 43.6 N 28N 1N 23 N 16N 12N 130 N 18N 2N 24 | % 0.5400 0.00 % 0.8126 0.34 % 0.4507 0.00 | 01 0.0440 07 0.2550 115 0.5659 98 0.8560 | 0.0968 0.00 0.1672 0.6 0.6886 0.11 0.0112 0.5 | 949 0.0126 130 0.0124 1 155 0.0665 124 0.0309 | 1,0459 0.2047 1,2333 0.4121 1,5565 0.0244 | 0.50 |
| 110 Historic FGB type 1-H Historic FGB 111 Prolegin Prelig 112 Complement G3 G3 113 Carricon Lum | 25 HOSHH MOUSE 14 KDs PRELP MOUSE 43 KDs CCG MOUSE 186 KDs LUM MOUSE 36 KDs | 60% 66% 6 17% 38% 96% 100% 10 46% 63% 4 | 68% 54.7% 9% 18.1% 99% 98.8% 65% 51.5% | 22% 29% 75% 50% 4% 0% 66% 26% | 315 30.7% 100% 75.0% 0% 1.2% 45% 39.2% | 8% 5% 8% 12% 0% 0% 8% 11% | 25 4.05 05 5.95 05 0.05 95 9.75 | 59% 62% 25% 32% 100% 100% 65% 45% | 66% 62.2% 19% 25.0% 100% 100.0% 66% 52.1% | 32% 29% 62% 58% 9% 0% 27% 39% | 22% 31.7% 67% 62.4% 6% 0.0% 49% 38.1% | 9% 8% 12% 11% 0% 0% 8% 16% | 1% 6.1% 15% 12.6% 0% 0.0% 6% 9.8% | 67% 62% 24% 24% 92% 94% 42% 42% | 62% 54.1% 22% 23.2% 89% 91.9% 22% 38.7% | 28% 229 60% 629 2% 09 50% 689 | 6 35% 32.2% 6 66% 62.1% 6 5% 2.9% 6 52% 51.0% | 4% 49 17% 159 5% 59 9% 109 | 28 3.7% 128 94.7% 58 5.2% 108 9.6% | 725 725 255 255 895 925 455 285 | 726 74.4% 268 25.2% 926 90.7% 426 41.7% | 5% 25% 2 6% 60% 5 6% 1% 6% 53% 5 | 0% 23.2% 20 8% 57.9% 190 0% 0.2% 110 0% 49.2% 90 | N 1% 2% 2.4 N 15% 16% 16.7 N 6% 2% 6.5 N 10% 10% 9.5 | % 0.4587 0.00 % 0.5946 0.00 % 0.4226 0.00 % 0.9400 0.54 | 98 0.8500 173 0.6026 171 0.0223 53 0.1475 | 0.0112 0.5 0.9204 0.45 0.0915 0.45 0.2364 0.96 | 124 0.0309 1 145 0.1600 1 126 0.1864 1 187 0.5197 1 | 1.5555 0.0244 1.4653 0.2125 1.3944 0.4226 1.1837 0.2099 | 0.6614 0.1217 0.6846 0.2461 0.2991 0.3677 0.1550 0.1000 0.5756 0.0001 0.064 0.8551 0.9267 0.7236 0.9037 |
| 116 sus posterna promis L15 (1901) 115 Adenosylvenocysteinase Ahry 116 Hyposta up-regulated protein 1 Hypus 117 Delichté-dehoesinoloossocheri Deles 118 405 ribosomi ontein SA Ross | 53.5 MOUSE 24 KGs 5491 MOUSE 46 KGs HYOUR MOUSE 111 KGs OST46 MOUSE 49 KGs RSSA MOUSE 33 KGs | 235 225 3 885 925 5 825 875 9 275 515 4 476 515 4 | 90.0% 90.0% 90.0% 90.0 90.0 90.0 90.0 90 | 9% 6% 17% 12% 21% 25% 28% 27% | 85 7.55 65 11.85 265 30.55 365 37.65 | 28 18 18 08 28 28 258 158 128 | 25 1.8% 25 1.8% 26 0.5% 265 27.0% 125 13.2% | 94% 97% 92% 99% 49% 50% 47% 51% | 995 95.7% 965 91.4% 965 51.0% 975 49.9% | 25 25 26 45 28 215 28 215 28 225 | 9% 1.6% 4% 8.2% 22% 23.9% 22% 34.2% | 2% 2% 2% 2% 1% 0% 22% 29% 15% 17% | 25 275 05 0.55 26 25.15 | 100% 100% 95% 88% 32% 31% 44% 52% | 100 10.0% 100% 100.0% 94% 92.3% 34% 32.4% 42% 46.6% | 0% 09 5% 129 22% 159 29% 279 | 6 98 9078 6 98 7.7% 6 98 7.7% 6 22% 21.3% 6 50% 41.8% | 0% 09 0% 09 45% 559 17% 109 | 0% 0.0% 0% 0.0% 0% 0.0% 29% 46.4% | 100% 100% 1 100% 95% 1 21% 29% 55% 55% | 100 100.0% 100 90.2% 110 33.9% | 2% 2% 5 2% 2% 5 2% 5 2% 5 2% 1 2% 1 2% 1 | 65 6235 20 05 9.05 0 05 1.75 0 45 11.25 62 95 34.15 10 | N ON | % 0.0477 % 0.5636 0.00 % 0.1626 0.00 % 0.6723 0.00 | 0.0240 139 0.3307 146 0.1243 | 0.1632 0.0 0.2591 0.5 0.0116 0.11 0.0957 0.11 | 131 0.0039 1 101 0.0039 1 107 0.0062 1 102 0.2125 1 | 10172 0.2322 1.3354 0.2452 1.1297 0.0142 1.4239 0.9937 | 0.5565 0.0092 0.0966 0.9859 0.4226 0.4226 0.9971 0.2401 0.0002 0.0000 0.0016 0.3709 0.0352 0.0004 |
| 119 Collegen alpha-1(II) chain CoGarl 120 Keratin, type I cylorideletal 20 Kr20 121 495 ribosomi protein Sila Ryadia 122 Caterio alpha-1 Chrari | CCDA1 MOUSE 142 KDs K1C20 MOUSE 49 KDs RS3A MOUSE 30 KDs CTNA1 MOUSE 100 KDs | 0% 0% 64% 69% 7 12% 9% | 0% 0.0% 30% 67.8% 6% 9.1% | 28% 94% 24% 29% 67% 62% | 67% 85.2% 28% 30.1% 72% 67.5% | 62% 6% 2% 2% 21% 28% | 22% 33.8% 26 2.0% 21% 23.4% | 0% 0% 57% 66% 11% 11% | 0% 0.0% 62% 01.0% 24% 15.3% | 0% 100% 2% 100% 37% 29% 46% 61% | 0% 33.3% 34% 33.6% 35% 47.5% | 100% 0% 1 6% 5% 42% 28% | 00% 65.7% 6% 4.8% 41% 27.2% | 9% 9% 9% 9% 64% 74% 16% 19% | 0% 0.0% 0% 0.0% 65% 67.0% 21% 18.7% | 0% 09 92% 923 36% 223 49% 283 | 6 06 0.0% 6 976 93.2% 6 356 31.0% 6 426 44.0% | 200% 2009 8% 99 6% 39 24% 439 | 200% 100.0% 2% 5.8% 0% 0.9% 23% 35.7% | 9% 9% 9% 1% 93% 80% 46% 42% | 0% 0.0% 5% 2.7% 90% 07.8% 54% 47.2% | 0% 0% 0% 87% 8 7% 20% 1 14% 25% | 0% 0.0% 200 0% 03.4% 141 0% 12.2% 01 9% 15.7% 411 | N 100% 100% 100.0 N 12% 16% 14.0 N 0% 0% 0.0 N 22% 27% 37.0 | % 0.1309 0.01 % 0.2987 0.00 | 55 86 0.9406 174 0.0148 | 0.1355 0.40 0.0082 0.30 0.0089 0.00 | 000 0.0294 1005 0.0000 1 | 1.2410 0.2720 1.7734 0.0162 1.0089 0.0304 | 0.4433 0.0278 0.2410 0.2546 0.0354 0.4226 0.3116 0.0207 0.0750 0.9500 0.0379 0.9717 |
| 124 Dascerin Con 125 Peoblyf-croki cis-trans isomeras Ppia 126 Polyadenylate-bildning protein i Pabpot 127 905 ribosperal protein 1 (10s R010s) | SHIP MARKE SHIP | 78% 25% 78% 82% 8 29% 42% 4 58% 56% 4 | 5% 14.4% 6% 81.7% 62% 41.4% 68% 53.8% | 81% 70% 19% 12% 55% 44% 25% 28% | 90% 80.5% 12% 15.0% 50% 49.7% 38% 30.4% | 5% 5% 5% 5% 2% 4% 6% 12% 17% 16% | 5% 5.7% 5% 5.7% 2% 3.2% 8% 8.8% 14% 15.7% | 26% 22% 80% 84% 25% 46% 55% 57% | 26% 23.2% 26% 23.2% 26% 82.6% 26% 40.0% 56% 57.2% | 22% 22% 32% 36% 17% 12% 60% 47% 36% 26% | 185 2005 698 7245 128 1375 528 5335 228 2475 | 2% 2% 2% 4% 5% 7% 18% 17% | 7% 4.5% 6% 3.7% 8% 6.7% | 15% 21% 87% 88% 32% 25% 76% 82% | 17% 17.7% 17% 87.3% 26% 87.3% 28% 35.4% 71% 76.7% | 80% 729 12% 119 64% 589 12% 109 | 6 29% 77.2% 6 29% 77.2% 6 12% 12.0% 6 56% 50.4% 6 20% 14.5% | 2% 69 6% 19 2% 79 11% 79 | 5% 5.1% 1% 0.7% 6% 5.2% 9% 0.8% | 22% 19% 84% 80% 42% 28% 100% 82% 1 | 22% 21.9% 86% 83.1% 52% 44.0% | 905 72% 36% 7 15% 20% 1 16% 59% 4 | 0% 72.7% 61 2% 16.3% 11 7% 53.7% 11 0% 5.9% 01 | N SN 7N 54 N ON 1N 0.6 N 2N 2N 2N 2.3 N ON 0N 0N 0.0 | % 0.2729 0.15 % 0.7351 0.13 % 0.6949 0.94 % 0.3824 0.03 | 30 0.5433 38 0.1104 05 0.0379 80 0.0075 | 0.4944 0.30 0.8390 0.60 0.4059 0.50 0.0212 0.20 | 014 0.1787 1 542 0.1639 1 015 0.2789 1 86 0.2822 | 1.6387 0.9069 1.2756 0.3810 1.0722 0.9435 1.0724 0.0784 | 0.6755 0.8393 0.7333 0.5668 0.5434 0.8911 0.0238 0.0027 0.3791 0.1671 0.1864 0.0340 0.0971 0.0140 0.0076 0.0004 |
| 127 635 ribosomal protein L10s | EPIPL_MOUSE 725 kDs LAME2_MOUSE 197 kDs TGM2_MOUSE 77 kDs RS13_MOUSE 17 kDs | 0% 0% 0% 0% 29% 79% 4 52% 55% 4 | 0% 0.0% 0% 0.0% 62% 53.3% 62% 49.9% | 50% 32% 67% 52% 30% 17% 36% 37% | 63% 42.1% 67% 62.2% 43% 30.0% 52% 41.7% | 50% 67% 22% 48% 20% 6% 11% 8% | 57% 57.9% 22% 37.8% 14% 15.8% 6% 8.4% | ON ON ON SAN SON 48% 52% | 0% 0.0% 0% 0.0% 70% 57.9% 47% 49.1% | 32% 20% 57% 55% 31% 31% 42% 25% | 20% 24.4% 43% 51.8% 20% 27.3% 44% 40.3% | 67% 80% 42% 45% 15% 19% 10% 12% | 90% 75.6% 57% 48.2% 10% 14.7% 9% 10.6% | 0% 0% 0% 0% 30% 26% 48% 34% | 0% 0.0% 0% 0.0% 23% 25.1% 47% 43.3% | 36% 309 48% 369 27% 349 48% 559 | 6 22% 29.3% 6 42% 42.2% 6 29% 29.9% 6 38% 47.3% | 64% 709 52% 649 42% 509 3% 109 | 78% 70.7% 58% 57.8% 29% 44.0% 15% 9.4% | 2% 0% 2% 29% 62% 52% | 2% 0.9% 0% 0.0% 44% 39.1% 59% 58.1% | 19% 29% 2 17% 29% 2 17% 21% 2 | 1% 23.0% 811 1% 22.4% 821 2% 20.4% 691 6% 35.5% 41 | N 71% 77% 76.1 N 71% 79% 77.6 N 40% 22% 40.5 N 11% 5% 6.4 | % 0.7556 8.05 % 0.7556 0.05 | 36 0.1550 84 0.3362 | 0.2538 0.00 0.11 0.0741 0.77 0.0733 0.80 | 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 | 11124 0.8123 10353 0.0070 19925 0.1923 14804 0.2124 | 0.0503 0.3337 0.1124 0.9241 0.1919 0.0167 0.0053 0.0070 0.8113 0.5748 0.0465 0.0139 0.3075 0.4940 0.7952 0.1778 |
| 132 due nosaema proma L16 i repta 133 Sheanharantain rashanida Pol2 134 Costoner suburit sipha Copa 135 Visculin Vol 135 Artin sibha coolae marcia 1 | PORCEA MOUSE 71 KDs COPA MOUSE 108 KDs VINC MOUSE 117 KDs ACC MOUSE 177 KDs | 51% 51% 5 68% 76% 7 26% 23% 3 | 25.4% 51% 51.1% 71.6% 21% 71.6% 21% 30.2% | 26% 42% 12% 24% 68% 59% | 415 38.95 215 17.45 655 54.15 | 176 206 128 98 158 108 68 78 | 8% 10.0% 2% 11.0% 4% 5.7% | 20% 20% 57% 55% 78% 82% 22% 22% 57% 66% | 60% 58.8% 89% 82.6% 30% 27.9% | 21% 22% 9% 8% 58% 72% | 18% 25.8% 2% 5.4% 52% 50.6% | 10% 17% 12% 14% 12% 11% 10% 6% | 176 14.4% 96 11.0% 196 11.5% | 23% 22% 22% 92% 92% 92% 22% 24% | 89% 83.2% 92% 92.3% 35% 34.2% | 22% 99 22% 99 25 09 58% 669 | 6 28 1278 6 28 1278 6 48 1878 6 508 5278 | 4% 49 2% 29 9% 199 | 4% 5.8% 4% 5.8% 11% 13.1% | 100% 94% 1 97% 97% 1 58% 41% | 100% 97.9% 100% 98.0% 57% 52.7% | 0% 6% 0% 0% 0% 0% 0% 0% | 15 48.7% 12 0% 2.1% 01 0% 0.0% 21 6% 34.1% 141 | N 0% 0% 0.0 N 2% 0% 2.0 N 11% 12% 13.0 N 10% 15% 10.0 | % 0.1271 0.00 % 0.0500 0.01 % 0.5785 0.00 | 01 0.4559 114 0.0231 90 0.0103 36 0.1747 23 0.1406 | 0.0008 0.00 0.0287 0.00 0.0301 0.60 0.1037 0.75 | 992 0.1442 1984 0.2407 178 0.1041 1986 0.0006 | 10045 0.0163 10092 0.0952 1.0549 0.0479 1.3531 0.2197 | 0.915 0.0945 0.0423 0.0096 0.9967 0.0526 0.1328 0.0096 0.9967 0.0526 0.1328 0.0096 0.2513 0.5941 0.1444 0.0003 0.0408 0.2439 0.0097 0.2443 |
| 137 Calredouln Calr 138 Trifunctional experse subunit sici Hadha 139 435 ribasonal protein 58 Rpsil 140 Desmin Des | CALR MOUSE 48 KGs ECHA MOUSE 53 KGs RSB MOUSE 24 KGs DESM MOUSE 53 KGs | 94% 97% 9 51% 52% 4 30% 36% 3 0% 0% | 95.2% 66% 50.0% 38% 34.9% 0% 0.0% | 6% 2% 41% 32% 56% 48% 88% 95% | 25 3.8% 445 29.6% 476 50.5% 985 93.6% | 0% 0% 8% 14% 14% 16% 12% 5% | 0% 0.0% 10% 10.4% 14% 14.7% 2% 0.4% | 97% 96% 48% 52% 20% 32% 0% 0% | 97% 95.5% 53% 50.6% 30% 31.0% 0% 0.0% | 25 45 295 405 545 465 1005 975 | 28 3.5% 218 36.2% 50% 50.0% 97% 97.9% | 0% 0% 16% 9% 16% 21% 0% 2% | 0% 0.0% 12% 13.1% 20% 19.0% 26 2.1% | 96% 95% 60% 52% 27% 28% 0% 0% | 96% 95.8% 49% 53.9% 49% 35.9% 9% 0.0% | 4% 50 31% 369 52% 539 85% 809 | 6 4% 4.4% 6 36% 34.5% 6 49% 51.4% 6 92% 85.7% | 9% 9% 119 9% 119 11% 199 15% 209 | 0% 0.0% 15% 11.6% 8% 12.6% 8% 14.3% | 95% 97% 55% 51% 44% 30% 0% 0% | 98% 96.6% 61% 55.8% 41% 36.5% | 5N 2N HN 41N 2 11N 65N 5 | 25 3.4% 0: 95 34.7% 111 65 57.3% 5: 75 84.9% 15: | N 0% 0% 00 N 8% 9% 95 N 5% 2% 42 N 17% 12% 15.1 | % 0.7723 0.30 % 0.8011 0.65 % 0.2763 0.70 | 005 0.00379 00 0.0075 00 0.0075 00 0.1500 00 0.1500 01 0.4500 | 0.9484 0.7: 0.2253 0.46 0.2231 0.90 0.22 | 723 0.3673 (135 0.9504 (162 0.2604 (147 0.8438 (| 1.5514 0.9484 1.2602 0.7491 1.7875 0.2085 1.1600 0.0015 | 0.4980 0.3338 0.6310 0.2016 0.0870 0.1079 0.5634 0.0041 0.2747 0.8436 0.1600 0.0015 |
| Protein framscort postein Sec238 Sec23b Voltace-decendent anion-selecti, Vdac 1 Perceinschale 1 Perceinschale 1 Pedel Serios protease inhibitor ASK Serginalis | SC238 MOUSE 86 KDs VDAC1 MOUSE 32 KDs PROX1 MOUSE 22 KDs 3k SPAIK MOUSE 47 KDs | 20% 25% 2 24% 22% 2 80% 85% 8 90% 92% 9 | 28% 27.8% 26% 23.8% 86% 82.6% 86% 92.0% | 46% 47% 59% 64% 17% 54% 10% 8% | 54% 48.9% 59% 60.9% 15% 15.3% 5% 8.0% | 24% 27% 16% 14% 2% 1% 0% 0% | 18% 23.2% 15% 15.2% 2% 2.1% 0% 0.0% | 22% 25% 25% 25% 86% 86% 100% 200% | 50% 29.5% 20% 25.7% 86% 54.7% 100% 100.0% | 30% 32% 62% 58% 16% 11% 0% 0% | 19% 27.2% 57% 59.2% 11% 11.7% 0% 0.0% | 27% 22% 12% 16% 2% 5% 0% 0% | 31% 33.2% 12% 14.1% 4% 3.0% 0% 0.0% | 276 276 85 76 828 858 898 925 | 32% 35.2% 8% 7.8% 77% 81.0% 92% 90.1% | 14% 109 71% 729 17% 129 8% 29 | 6 36% 19.5% 6 22% 71.8% 6 32% 15.2% 6 26 7.4% | 49% 529 20% 219 2% 49 2% 29 | 26% 45.2% 20% 20.4% 6% 3.8% 2% 2.5% | 95 45 85 70 100 91 1 | 25% 51.2% 20% 7.2% 36% 51.7% 36% 97.7% | 2% 8% 6% 28% 5 12% 18% 2% 9% | 0% 2.5% 451 8% 64.2% 251 9% 13.0% 61 0% 2.5% 01 | N 28% 25% 35.2 N 19% 21% 28.4 N 6% 5% 5.3 N 0% 0% 0.0 | % 0.1468 0.00 % 0.1745 0.80 % 0.2884 0.80 % 0.0009 0.15 | 25 0.5896 | 0.3961 0.00 | 733 0.3624 515 0.5305 (809 0.2614 (| 1.0075 0.0094 1.0007 0.5431 1.9645 0.0911 1.7019 0.4225 | 0.436 0.325 0.048 0.6758 0.4369 0.2376 0.0059 0.1002 0.2950 0.2326 0.2646 0.2326 0.0329 0.0329 |
| 146 Heterconneau nuclear ribonucia Hermach 147 Voltase-dependent anion-selectis Voltac2 148 Eukaroots transition initiation fo EMg1 149 Protein EMG2-53 Lument | 201 ROBA MOUSE 37 KDs VDAC2 MOUSE 32 KDs IF4G1 MOUSE 176 KDs LMANT MOUSE 58 KDs | 24% 26% 4 27% 24% 2 25% 24% 2 22% 47% 2 | 61% 36.9% 27% 29.4% 31% 33.5% 34% 37.7% | 61N 52N 52N 42N 26N 28N 10N 6N | 52% 55.6% 52% 48.5% 35% 25.7% 17% 10.9% | 5% 11% 22% 22% 28% 48% 58% 47% | 76 7.0% 21% 22.1% 22% 30.0% 50% 51.4% | 40% 40% 20% 26% 21% 29% 57% 26% | 36% 37.9% 36% 31.5% 43% 37.8% 55% 49.2% | 57% 50% 47% 47% 34% 16% 5% 6% | 57% 54.7% 37% 43.7% 17% 15.7% 10% 6.9% | 2% 20% 22% 27% 54% 45% 28% 58% | 9% 7.4% 25% 24.8% 60% 45.5% 25% 43.8% | 56% 51% 22% 15% 45% 50% 56% 52% | 66% 57.7% 12% 16.8% 52% 49.1% 52% 53.2% | 40% 433 48% 513 15% 83 0% 00 | 6 30% 37.7% 6 55% 51.5% 6 29% 14.1% 6 0% 0.0% | 4% 59 29% 259 40% 429 44% 489 | 5% 4.6% 21% 31.7% 29% 36.7% 48% 46.8% | 65% 58% 14% 14% 56% 67% 31% 20% | 64% 52.4% 16% 14.7% 80% 57.4% 50% 33.0% | 0% 39% 3 9% 52% 3 0% 11% | 2% 33.8% St 9% 43.2% 471 0% 3.7% 441 0% 0.0% 691 | N 2N 4N 38 N 34N 45N 421 N 22N 20N 289 N 80N 50N 56.4 | % 0.7544 0.30 % 0.6697 0.52 % 0.3416 0.11 % 0.2450 0.16 | M4 0.0220 1 67 0.0239 1 21 0.0074 1 22 0.0724 | 0.4205 0.00 0.1414 0.32 0.0000 0.0 0.0400 0.0 0.0400 0.0 0.0347 0.15 0.2350 0.32 0.2350 0.15 0.2507 0.5 0.0514 0.30 0.0059 0.5 0.1104 0.31 0.2360 0.2 | 080 0.4820 179 0.2021 103 0.0968 | 1.4212 0.9056 1.4212 0.9076 1.1087 0.0720 1.0750 0.0547 | 0.9995 0.4438 0.2053 0.2023 0.9997 0.1112 0.0175 0.0099 0.3202 0.4381 0.6276 0.1383 0.4226 0.1322 0.2788 0.1221 |
| 150 Ras GTPase-achadino-like ordis Iggap1 151 Pyrusite kinase PRM Plen 152 Nucleoprolein TPR Tpr 153 Delichyl-dehosehoolioosacchari Rpn2 | IOGA1 MOUSE 189 KDs KPYM MOUSE 58 KDs TPR_MOUSE 274 KDs RPN2_MOUSE 69 KDs | 69% 66% 5 82% 88% 9 0% 0% 52% 62% 4 | 56% 62.7% 81% 87.4% 0% 0.0% 68% 53.6% | 25% 25% 17% 12% 100% 99% 16% 12% | 62% 30.8% 9% 12.6% 99% 99.0% 26% 18.3% | 6% 9% 0% 0% 0% 1% 32% 26% | 6% 5.5% 0% 0.0% 1% 1.0% 26% 28.1% | 59% 70% 88% 92% 0% 0% 60% 49% | 85% 71.8% 92% 90.3% 0% 0.0% 61% 56.7% | 22% 19% 12% 9% 99% 100% 12% 16% | 5% 15.1% 8% 9.7% 98% 98.9% 12% 13.9% | 19% 11% 0% 0% 1% 0% 27% 25% | 10% 13.3% 0% 0.0% 2% 1.1% 26% 29.4% | 70% 69% 92% 99% 0% 0% 40% 49% | 67% 68.7% 86% 89.2% 6% 0.0% 49% 48.2% | 12% 79 7% 99 99% 989 2% 49 | 6 96% 12.0% 6 12% 9.7% 6 95% 97.2% 6 11% 6.0% | 17% 249 0% 29 1% 29 51% 479 | 17% 19.3% 1% 1.1% 5% 2.8% 29% 45.9% | 81% 80% 94% 88% 0% 0% 42% 48% | 85% 82.3% 92% 91.7% 0% 0.0% 1 | 5% 4% 5% 12% 9% 10% 10 10% 4% 1 | 2% 3.6% 141 7% 8.0% 11 0% 99.7% 11 1% 8.1% 481 | N 16% 12% 14.1 N 0% 0% 0.3 N 0% 0% 0.3 N 48% 52% 49.5 | % 0.3779 0.00 % 0.3406 0.45 % 0.6180 0.22 | 98 0.5987 19 0.5987 | 0.2850 0.1 0.5677 0.3 0.85 0.0514 0.3 | 003 0.0968 128 143 0.0671 186 0.5749 149 0.1389 182 0.5696 | 1.4212 0.9376 1.1087 0.0733 1.0750 0.0547 1.0655 0.1514 1.3005 0.5234 1.2239 0.3258 1.0752 0.1997 | 0.9996 0.4408 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2003 0.2004 0.2005 0.2004 0. |
| 154 Pregnancy around the state anomaria in pro- 155 Tensacio Tro 156 Pregnancy zone prolein Pap 157 Valino-676A Igassa Vars | TENA_MOUSE 232 KOs PEP_MOUSE 165 KOs SYVC_MOUSE 140 KOs SYVC_MOUSE 140 KOs | 97% 96% 9 85% 92% 8 | 6% 96.5% 8% 87.9% | 200 4% 20 4% 20 2% | 4% 3.5% 7% 4.0% | 0% 0% 0% 0% 12% 6% | 0% 0.0% 5% 8.1% | 100% 96% 91% 92% | 100% 98.8% 97% 93.2% | 0% 4% 1% 2% | 0% 1.2% 1% 1.4% | 2% 2% 0% 0% 8% 6% | 0% 0.0% 2% 5.5% | 976 956 98 1% 926 926 956 946 | 90% 90.0% 90% 91.7% 92% 93.7% | 81% 809 7% 59 0% 09 | 6 25% 78.8% 6 4% 5.1% 6 4% 5.1% | 29% 299 2% 49 5% 69 | 25% 21.0% 4% 3.3% 6% 5.7% | 976 976 9 926 926 976 976 | 0% 0.0% 9% 94.5% 94% 96.2% | 3% 3% 7 9% 71% 7 3% 6% 0% 0% | 0% 2.1% 01 5% 74.9% 2.11 2% 3.9% 2.1 0% 0.0% 3.1 | N 29% 25% 25.1 N 1% 0% 1.6 N 2% 6% 3.8 | % 0.428 0.25 % 0.1928 0.25 % 0.1955 0.15 | 26 95 0.0001 90 0.0724 | 0.1104 0.11 0.2308 0.2 0.0309 0.00 | 0.2640 028 0.4664 126 0.4226 104 0.1534 | 1.1887 0.1770 1.1479 0.0657 | 0.2903 0.2403 0.0446 0.2032 0.4370 0.1510 0.4304 0.4677 0.8327 0.2005 0.8046 0.8077 |
| 199 Churenturain-Ilia alsatesa famili Calabb 190 Annain A2 191 Eukanyoli: Iniliation factor 4A-1 192 Heterosenaus nuclear ribonucia Hompali | CELSE MOUSE 29 KGs ANKAZ MOUSE 39 KGs IF4A1 MOUSE 46 KGs I ROAJ MOUSE 40 KGs | 80% 85% 8 71% 79% 8 77% 71% 7 22% 21% 2 | 86% 83.7% 86% 78.5% 77% 75.0% 30% 21.2% | 16% 12% 21% 18% 19% 21% 58% 65% | 12% 54.0% 12% 17.2% 20% 20.0% 69% 54.1% | 4% 1% 7% 2% 2% 9% 19% 15% | 25 2.25 26 4.25 26 5.05 20 14.75 | 86N 89N 76N 89N 70N 87N 14N 18N | 92% 89.6% 92% 82.8% 91% 82.4% 26% 18.8% | 11% 9% 18% 4% 29% 8% 72% 62% | 6% 8.6% 7% 9.8% 2% 10.0% 62% 65.8% | 25 25 55 25 115 55 145 205 | 1% 1.9% 10% 7.4% 7% 7.6% 12% 15.3% | 98% 100% 26% 77% 96% 92% 26% 32% | 92% 96.6% 76% 76.4% 92% 93.5% 22% 30.7% | 2% 09 20% 179 4% 49 59% 529 | 88 34% 6 286 152% 6 86 52% 6 508 553% | 0% 09 4% 69 0% 29 15% 169 | 0% 0.0% 6% 5.4% 2% 1.2% 12% 14.1% | 100% 100% 1 90% 79% 98% 96% 1 41% 25% | 100% 100.0% 81% 79.9% 100% 97.9% 41% 39.7% | 0% 0% 6% 16% 1 2% 6% 6% 55% 5 | 0% 0.0% 01 2% 14.1% 51 0% 2.1% 01 2% 51.0% 121 | N 0% 0% 0.0 N 6% 2% 5.0 N 0% 0% 0.0 N 9% 2% 9.7 | % 0.0882 0.25 % 0.4618 0.05 % 0.3893 0.11 % 0.5208 0.09 | 778 0.0159 1776 0.6354 22 0.0025 160 0.0433 | 0.0006 0.00 0.5138 0.20 0.1314 0.10 0.0001 0.77 | 0.2978 130 0.0577 195 0.1580 195 0.2919 | 1.7553 0.4350 1.7553 0.4350 1.0054 0.2349 1.0062 0.0283 | 0.7387 0.1575 0.1019 0.1924 0.5899 0.5165 0.4205 0.3761 0.1942 0.1526 0.092 0.8544 0.1130 0.8434 0.1314 |
| 953 Laminin subunit alabha-4 Lamael 1954 Nacionale dichenhale kinasa A New 1 955 Helercomenas suclear ribonacia Syncis 1956 Prohibitin 957 Debt and subh | COLUMN C | 05 05 205 205 205 245 245 245 2 | 0% 0.0% 71% 77.6% 26% 22.1% 26% 24.1% | 82N 78N 14N 26N 67N 62N 58N 60N | 80% 78.7% 22% 17.3% 65% 64.8% 60% 59.6% | 17% 26% 6% 2% 12% 17% 18% 16% | 20% 21.2% 2% 5.1% 9% 13.1% 14% 16.2% | 0% 0% 84% 72% 19% 26% 28% 28% | 0% 0.0% 72% 75.8% 25% 23.2% 26% 27.1% | 26% 72% 26% 25% 72% 58% 49% 50% | 22% 73.4% 24% 21.0% 60% 63.6% 28% 45.8% | 265 285 25 25 85 165 225 225 | 285 25.0% 26 2.2% 15% 13.3% 36% 27.1% | 0% 0% 65% 65% 28% 27% 11% 16% | 0% 0.0% 64% 64.5% 29% 28.1% 11% 12.6% | 71% 603 22% 213 67% 660 68% 553 | 6 69% 57.7% 6 31% 31.6% 6 62% 55.5% 6 62% 52.0% | 29% 279 2% 49 4% 79 21% 289 | 21% 32.3% 5% 3.9% 8% 5.4% 27% 25.4% | 0% 0% 62% 61% 41% 20% 14% 12% | 0% 0.0% 20% 64.2% 22% 35.0% 15% 13.8% | 9% 51% 3 9% 35% 2 9% 60% 6 6% 58% 5 | 75 29.05 711 85 30.55 101 85 58.45 71 85 60.05 211 | 8 49% GN 510 8 4% 2% 52 8 9% 4% 57 8 19% 27% 257 | % 0.8724 0.94 % 0.7226 0.11 % 0.9422 0.50 % 0.1997 0.44 | 24 0.0507 25 0.0730 179 0.0165 | 0.0550 0.40 0.0485 0.80 0.0055 0.00 | 130 0.6634 137 0.1406 134 0.7994 | 10040 0.0012 10040 0.0086 17325 0.4077 15044 0.0423 | U.1747 0.0366 0.0406 0.0312 0.1905 0.6293 0.3740 0.3216 0.9565 0.8795 0.0335 0.1040 0.1321 0.9532 0.0402 0.8121 0.4225 0.4409 0.7790 0.0812 |
| 150 Protein destitute increase A4 Pda4 159 La-related potein 1 Larp1 170 Mirecian Ogn 171 Accesso A6 Access | PDIA4 MOUSE 72 KDs LARP1 MOUSE 121 KDs MME MOUSE 34 KDs ANK46 MOUSE 76 KDs | 895 925 5 175 165 2 85 365 1 885 925 5 | 95% 92.2% 20% 17.9% 14% 19.7% 96% 92.4% | 11% 7% 76% 72% 92% 64% 9% 5% | 5% 7,8% 73% 73,8% 86% 80,3% 4% 5,0% | 2% 2% 7% 11% 2% 2% | 0% 0.0% 6% 8.2% 0% 0.0% 0% 1.7% | 96% 96% 18% 20% 18% 17% 92% 100% | 96% 95.9% 26% 21.4% 18% 17.7% 190% 97.7% | 6% 6% 20% 68% 82% 83% 2% 0% | 4% 4.1% 57% 65.0% 27% 80.8% 0% 0.9% | 0% 0% 12% 12% 0% 0% 4% 0% | 05 0.05 175 13.05 55 1.05 05 1.45 | 100% 97% 0% 0% 15% 13% 100% 92% | 92% 96.7% 9% 3.0% 2% 11.6% 99% 97.0% | 0% 29 100% 1009 72% 729 0% 29 | 5 7% 3,3% 6 77% 92,4% 6 28% 74,5% 6 28 1,5% | 0% 09 0% 09 12% 149 0% 59 | 0% 0.0% 14% 4.5% 15% 13.8% 0% 1.5% | 97% 98% 1 17% 17% 12% 8% 100% 100% | 00% 98.2% 9% 11.1% 12% 11.0% 98% 99.4% | 2% 2% 12% 82% 10 19% 72% 7 2% 2% | 0% 1.7% 01 0% 88.9% 01 1% 70.6% 191 0% 0.0% 0 | N 0% 0% 00 N 0% 0% 00 N 20% 16% 18.4 N 0% 2% 0.5 | % 0.1610 0.51 % 0.3065 0.26 % 0.8378 0.83 % 0.1794 0.41 | 32 0.1696 90 0.0249 80 0.4453 52 0.2374 | 0.1201 0.10 0.1967 0.15 0.0343 0.96 0.5467 0.00 | 334 0.7984 1926 1910 0.5132 1977 0.72274 1916 0.1291 1926 0.2317 | 1.1095 0.1201 1.1314 0.0294 1.5715 0.0191 1.0061 0.4226 | 0.0789 0.4226 0.5014 0.0125 0.4226 0.0402 0.0018 0.0012 0.8581 0.6269 0.9404 0.6548 |
| 172 Caterin delta-1 Chrodi 173 00 kTo hast shock protein, miloc Hepdi 174 Nucleolin Noi 175 Stitunctional distantal for oline-191 Epps | CTND1 MOUSE 105 KDa CH60 MOUSE 61 KDa NUCL MOUSE 77 KDa SYEP MOUSE 170 KDa | 9% 5% 82% 8 45% 45% 45% 25% 52% 7 | 5% 6.2% 6% 83.5% 6% 45.1% 36% 79.4% | 65% 68% 18% 16% 48% 49% 12% 8% | 74% 59.1% 15% 55.1% 52% 49.7% 17% 12.3% | 26% 27% 0% 1% 7% 6% 8% 10% | 215 24.7% 05 0.4% 25 5.2% 26 8.2% | 8% 5% 82% 92% 40% 35% 89% 92% | 2% 5.2% 91% 55.4% 29% 35.2% 94% 91.0% | 62% 68% 17% 9% 55% 60% 2% 1% | 9% 11.0% 9% 11.0% 59% 50.1% 9% 1.3% | 21% 27% 0% 0% 5% 4% 9% 8% | 25% 21.0% 0% 0.0% 2% 3.7% 6% 7.7% | 8% 6% 94% 88% 56% 58% 98% 97% | 15% 9.7% 88% 90.3% 56% 56.8% 94% 96.3% | 77% 779 6% 113 42% 429 0% 09 | 6 20% 74.5% 6 12% 9.7% 6 46% 42.5% 6 0% 0.0% | 15% 179 0% 09 1% 09 2% 29 | 15% 15.8% 0% 0.0% 0% 0.4% 6% 3.7% | 22% 22% 94% 92% 66% 67% 100% 100% 1 | 265 25.0% 985 25.1% 626 05.2% 000 100.0% | 2% 52% 4 5% 7% 6% 22% 2 0% 0% | 1% 53.6% 201 2% 4.9% 01 7% 34.7% 01 0% 0.0% 01 | N 15% 24% 19.8 N 0% 0% 0.0 N 0% 0% 0.0 N 0% 0% 0.0 | No. 0.6011 0.05 No. 0.2303 0.13 No. 0.0368 0.00 No. 0.0063 0.10 | 0.3485 47 0.0571 47 0.0019 00 0.0017 | 0.0196 0.2 0.1337 0.2 0.0002 0.0 0.0226 0.0 | 05 0.0555 364 0.1347 163 0.0058 | 1.2103 0.2408 1.0654 0.1337 1.0166 0.0005 1.0424 0.2164 | 0.1125 0.2940 0.0363 0.0385 0.4226 0.4226 0.0751 0.0706 0.6411 0.1008 0.0075 |
| 177 605 ribosomal prolein acreama i Ubal 1 177 605 ribosomal prolein L19 Rp128 178 605 ribosomal prolein L17 Rp117 179 Libicultin-405 ribosomal prolein 1 Rps27s 190 405 ribosomal prolein 516 Rps16 | RL28 MOUSE 16 KDs RL17 MOUSE 21 KDs RS17 MOUSE 18 KDs RS27A MOUSE 18 KDs RS16 MOUSE 16 KDs | 16% 18% 2 45% 42% 4 55% 65% 6 51% 40% 4 | 20% 20.9% 43.2% 60% 60.3% 67% 46.4% | 2% 20% 46% 49% 27% 29% 27% 44% | 2% 52.4% 52% 52.4% 52% 48.7% 24% 33.5% 28% 32.6% | 9% 12% 9% 8% 9% 8% 2% 6% 12% 15% | 9% 9.7% 9% 8.9% 5% 8.2% 15% 14.1% | 15% 23% 48% 42% 57% 45% 42% 55% | 20% 19.5% 47% 45.9% 58% 53.2% 49% 42.0% | 5% G2% 46% 47% 36% 20% 42% 21% | 71% 69.8% 42% 64.9% 36% 35.9% 35% 36.4% | 9% 16% 10% 14% 8% 10% 9% 16% 14% 14% | 9% 10.7% 10% 9.2% 8% 10.9% 16% 14.6% | 10% 14% 16% 29% 42% 29% 48% 42% 49% 42% | 15% 15.0% 42% 37.7% 42% 44.5% 42% 44.5% | 90% 939 52% 649 44% 409 40% 479 | 6 82% 81.5% 6 52% 55.3% 6 42% 41.7% 6 42% 44.5% | 9% 29 6% 79 8% 189 11% 129 | 0.0% 30 3.5% 50 6.0% 150 13.9% 100 10.8% | 7% 11% 46% 28% 67% 56% 55% 45% | 12% 10.4% 1 46% 39.8% 1 52% 58.5% 1 | 0% 89% 8 89% 66% 5 12% 89% 3 16% 48% 3 | 7% 88.4% 41 0% 54.7% 61 2% 31.8% 101 1% 38.3% 101 | 0% 0% 0% 1.2 % 7% 4% 5.5 % 5% 54% 9.8 % 6% 8% 7.8 | % 0.7836 0.10 % 0.1863 0.75 % 0.2326 0.01 % 0.6281 0.11 | 08 0.0017 26 0.0511 67 0.2853 63 0.3510 36 0.0136 | 0.0405 0.9 0.4272 0.0 0.4336 0.4 0.4363 0.5 | 173 0.0003 162 0.0200 186 0.1811 124 0.3587 | 1992 0.2094 1992 0.2094 10544 0.5050 11772 0.7822 | 0.6144 0.1877 0.0155 0.0055 0.2994 0.6341 0.0515 0.0029 0.1785 0.3654 0.1090 0.7670 0.8784 0.0756 0.0000 0.0000 |

| 982, Solicins Indica, reoline- and salar Step. SPEP_MOUSE, 73-60s. 128. 148. 98. 1179. 99. 1930, Conformers best Consistant March 1992, GPEP_MOUSE, 64-80s. 57-8, 529. 59. 53-25. 259. 53-25. 269. 1994. Collagon alphin-12XV chain. collistal. COPEA_MOUSE, 149-80s. 09. 09. 09. 09. 09. 09. 09. 09. 10079. 699. 1995. HORD MOUSE, 51-80s. 1009. 1009. 1009. 10079. 699. | 2785 2782 73.278 288 1575 488 9.775 1285 288 881 92.478 2888 569 42.575 488 68 69 1.728 569 5488 569 52.678 2288 2288 2278 2278 2289 1588 1288 17.758 69 69 69 60.578 1288 1288 1288 1289 | 88% 92% 87.7% 28 48 09 2.2% 540 128 89 11.09 48% 548 3875 28 48 22 2.5% 540 25 55 55 55 55 55 55 55 31% 548 72.5% 52% 52% 52% 72.5% 72.5% 72.5 28 09 14.5% 50% 50% 0.0% 0.0% 0.0% 0.0 0.0 0.0% 99 99 99 99 89 80 80 80 80 80 80 80 80 80 80 80 80 80 | 288 288 859 8595 8595 8 98 78 7278 228 148 228 220.05 728 228 278 528 569 5595 569 578 528 569 5595 569 578 528 569 569 578 582 569 569 578 582 569 569 578 582 569 569 578 582 569 569 578 582 569 578 582 569 578 582 569 578 582 569 578 582 569 578 582 582 569 578 582 569 578 582 569 578 582 569 578 582 569 578 582 582 569 578 582 569 578 582 569 578 582 569 578 582 569 578 582 582 569 578 578 578 578 578 582 569 578 578 578 578 578 578 578 578 578 578 | 758 7285 68 58 28 28 428 04409 0.004 0.0050 0.0019 0.0077 0.1005 0.2209 0.7273 0.0477 0.1054 0.020 0.0205 0.0255 0.0057 0.0057 0.0057 0.0057 0.0257 0.0057 0 | 0.3739 0.1384 0.6900 |
|---|---|---|--|--|--|
| 986 Luminin suburst alpha-5 Lamed LAMAG SUKUSE 604 M2s 05 05 05 00 205 205 987 Problembre 2 Phica Phica 208 <td< td=""><td>20% 15% 194.57 20% 20% 80% 80% 80.0 50.0 0% 0% 0% 0.0 50.5 12% 50% 50% 50% 50.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0</td><td>18% 12% 15.0% 82% 82% 88% M-4% 0% 0% 0% 0.00 0.00 0.00 0.00 0.00 0.0</td><td>258 188 289 242% 258 258 262 269 75.87 08 08 08 08 09.0% 128 268 258 638 259 645 259 645 259 645 259 645 259 650 259 6</td><td> 1568 1775 888 298 858 8228 858 8228 858 8228 828 </td><td>0.5923 0.2221 0.5611 0.0126</td></td<> | 20% 15% 194.57 20% 20% 80% 80% 80.0 50.0 0% 0% 0% 0.0 50.5 12% 50% 50% 50% 50.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 | 18% 12% 15.0% 82% 82% 88% M-4% 0% 0% 0% 0.00 0.00 0.00 0.00 0.00 0.0 | 258 188 289 242% 258 258 262 269 75.87 08 08 08 08 09.0% 128 268 258 638 259 645 259 645 259 645 259 645 259 650 259 6 | 1568 1775 888 298 858 8228 858 8228 858 8228 828 | 0.5923 0.2221 0.5611 0.0126 |
| 990 Sercontemicindosteric refox Asbitz Arabitz 175 150 500 750 750 750 750 750 950 915 Sercontemicindosteric refox Asbitz 175 150 500 750 750 750 750 750 950 915 Sercontemicindosterial Header GPPT MINISTER 774 500 450 570 550 550 550 550 950 950 950 950 950 95 | 98 | 08 00 029 278 228 228 279 2705 528 528 528 572 5728 526 227 5055 48 48 48 4 475 528 528 528 500 501 502 58 88 7.0% 08 08 00 00 88 92 928 928 928 928 928 500 528 528 528 528 528 528 528 528 528 528 | 08 08 08 075 448 478 328 328 328 728 528 528 528 528 60.08 418 328 328 328 58 58 58 48 328 328 328 328 328 328 328 328 328 32 | | 0.0563 |
| 10 10 10 10 10 10 10 10 | 4N 4N 75% 2N 2N 2N 2N 50% 90% 90% 90% 925% 7% 9N 0N 00 05% 12N 8N 15N 120% 86% 92% 86% 955% 0N 20N 25N 220% 2N 2N 0N 15% 66% 66% 61% 64.5% 38 20N 25N 220% 2N 2N 0N 15% 66% 66% 61% 64.5% 38 2N 2N 2N 2N 2N 2N 2N 0N 15% 66% 66% 61% 64.5% 38 2N 2N 2N 2N 2N 2N 2N 2N 0N 15% 66% 66% 61% 64.5% 38 2N 2N 2 | 68 296 3295 229 226 28 2295 9696 10000 6010 95.796 095 316 0.575 1696 896 1696 12776 9696 10000 10000 50.796 280 281 33.275 118 496 276 2275 5696 5696 5696 56.455 | 0% 0% 0% 2.2% 4% 0% 0% 1.4% 1.5% 1.00% 1.60% 1.00% 1.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 1.20% 1.00% 1.00% 1.00% 0.00% 0.00% 0.00% 1.00% 1.00% 1.00% 1.00% 0.00% 0.00% 0.00% 1.00% 1.00% 1.00% 1.00% 1.00% 0.00% 0.00% 1.00% 1.00% 1.00% 1.00% 1.00% 1.00% 0.00% 0.00% 1.00% 1.00% 1.00% 1.00% 1.00% 1.00% 0.00% 0.00% 0.00% 1.00% 1.00% 1.00% 1.00% 1.00% 1.00% 0.00% 0.00% 0.00% 1.00% 1.00% 1.00% 1.00% 1.00% 0.0 | . 8 64. 8 6 6 7 8 6 7 8 6 7 8 7 8 7 8 7 8 8 8 7 8 8 8 8 | 0.0376 |
| 19 State | 25% 57% 50.0 50.0 8% 57% 7.0% 40% 48% 51% 47.4% 49% 25% 57% 50% 60% 67.00% 00% 00.0 00% 00% 50% 50% 50% 50% 50% 50% 50% 50 | 110 10 17.50 18 17.50 20 20 20 20 20 20 20 20 20 20 20 20 20 | 500 250 550 553.75 70 100 90 40 475 420 400 400 420 420 520 220 220 220 220 220 220 220 220 2 | SN 5.7% 900K 85% 918 91.8% 0.0427 0.000M 0.1000 0.0238 0.040M 0.1007 0.2400 0.0238 0.000M 0.5729 | 0.0341 0.2767 0.7456 |
| 201 Microbabele actin cross-linking fil Micrif LMCCF LMCLEE 022 (20) 0% 0% 0% 0% 0% 0% 0% 022 Transistations Tit TOT, AUCLEE 03 (20) 0% 0% 09% 05% 06% 05.2% 06% 05.2% 06% 05.2% 06% 05.2% 06% 05.2% 05% 05.2% 06% 05.2% | 7% 12% 6.5% 200% 92% 88% 20.5% 14% 0% 0% 48% 0% 5% 5% 22% 4.8% 0% 0% 0.0% 100% 100% 100% 100% 100% 10 | 0% 0% 0.0% 86% 100% 100% 155.2% 17% 0% 0% 5.6% 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0 | 1791 20% ON 12.27% C7% 80% 100% 102.7% ON 00% ON 0.0% 23% ON 20% 20% ON 0.27% ON 0.27% ON 0.28% ON 0.27% ON 0.28% ON 0.2 | 006 9775 88 65 16 597 0000 0000 0000 0000 0000 0000 0000 | 0.0320 |
| 205 Dynamics 2 Direct Direct State | 268 918 83.26 118 128 58 9.09 68 148 228 56.05 80 278 488 480 49.05 208 178 178 18.07 18.07 428 428 418 418 598 618 581 128 128 128 128 128 128 128 228 228 2 | 28% 56% 73.3% 11% 56% 22% 12.7% 14% 15% 15% 15% 15.4% 15% 15% 15% 15% 15% 15% 15% 15% 15% 15 | 70% 68% 68% 68.7% 52% 16% 16% 15% 15.5% 36% 20% 48% 34.7% 48% 56% 51% 48% 55% 48% 55% 48% 56% 30% 20% 55% 15% 20% 12% 17.7% 52% 68% 55% 20% 55% 55% 20% 55% 55% 20% 55% 55% 55% 55% 55% 55% 55% 55% 55% 5 | 265 4425 228 156 268 268 268 03301 0.147 0.0000 0.1170 0.3019 0.1447 0.0000 0.0347 0.1420 0.00000 0.0000 0.00000 0.0000 0.00000 0.0000 0.0000 0.0000 0.00000 | 0.2158 0.0154 0.0019 0.0093 |
| 200 (05) ribosomi protein 1.32 R632 R632 M53.05 (6 6 6 6 8 18) 229 599 729 729 720 (7 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | \$80 569 515% 109 109 88 9.5% 228 228 278 255.55 528 628 5125 28 128 28 278 278 288 288 288 288 288 288 28 | 48% 59% 56.2% 6% 15% 6% 8.4% 26% 17% 25% 22.9% 55% 53.8% 7% 13.8% 7% 17.5% 26% 25% 25% 25% 55% 18% 24.8% 45% 45% 26% 26% 26.7% 45% 45% 45.8% | 785 287 758 77.15 98 98 98 0.055 279 218 199 1925 278 298 698 77 1925 278 298 698 77 1925 278 278 278 278 278 278 278 278 278 278 | 905 2025 05 00 00 05 00 09 0327 0.327 0.525 0.415 0.010 0.415 0.010 0.022 0.025 0.007 0.020 0.025 0.02 | 0.1289 0.4804 0.7744 |
| 22 Seguin for largers Sefu | 90 256 1945 00 05 05 05 0.055 800 200 200 200 200 200 200 200 200 200 | 00 00 6.75 0.70 00 00 00 00 00 00 00 00 00 00 00 00 0 | 58 | 88 84% 08 08 08 08 09 0.2550 0.8877 0.1917 0.0204 0.2021 0.2021 0.007 0.1917 0.0204 0.2021 0.2021 0.007 0.00 | 0.1459 |
| 216, Collegen alpha-UAXVIII chain. Colfdel. COAA-MACUSE. 100 kBp. 0%. 0%. 0%. 0%. 0%. 0%. 0%. 127. 2-2 | 57% 100% 55.65% 200% 22.8 0% 44.6% 0% 0% 0% 0.5 0.5% 50% 10% 10% 10% 10% 10% 10% 10% 10% 10% 1 | \$278, 256, 57,296, 4606, 3239, 2206, 32,295, 00, 006, 006, 0,006, 27276, 276, 12076, 276, 286, 287, 287, 3,295, 496, 1009, 1009, 1009, 20,75, 48, 236, 5,096, 1009, 1009, 1009, 1009, 1009, 1009, 48, 216, 5,096, 1009, | 98% 92% 88% 97.2% 68 98 12% 0.5 0.5 0.5 0.5 0.5 68 48 2.7% 68% 68% 6.8 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 | MRS 2756 48 175 275 975 0.000 | 0.0401 0.8023 0.9391 |
| 220 Profile-1 Phot PROFILE-1 SIX to SiX 86K 29K 72K 22K 22K Conformers b-c1 correlate subshort (upper CQF1 MOUDE SIX to SiX 646K SIX 50K 50K 646K 22Z Polementum I and transcript relies (PM PFEP MOUDE 44 k to SiX 646K SiX 53K 546K 546K 246K 22K 22K 646K | \$68 168 58.05 28 08 28 1.75 808 828 809 80.25 205 208 448 428 427 5 68 108 75 7.598 428 528 658 52.05 448 868 858 85.05 128 858 128 128 10.78 08 08 28 0.25 668 668 668 52.05 128 668 128 128 10.7 | 27% 18% 16.2% 0% 0% 2% 0.2% 5.2% 8.2% 8.5% 8.5% 8.5% 8.5% 85.2% 27% 2.2% 2.2% 2.2% 2.2% 2.2% 2.2% 2. | 20% 20% 20% 20% 20% 4% 5% 6% 4.5% 86% 86% 85% 54.5% 9% 20% | 7% 8.0% 7% 5% 8% 86 60% 0.6728 0.2027 0.1015 0.0020 | 0.0017 0.3468 0.0967 |
| 224 Tight Junction proteix 20-1 Tight 201 JUNUSE 105 SCIs 0% 0% 0% 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | 96N 500N 97.7% 5N 4N 0N 2.29N 0N 0N 0N 0N 0.07N 500N 0N | 9485 10006 90.1% 0% 0% 0% 0% 1.5% 0% 0% 0% 0% 0% 0.0% 0% 0% 0.0% 0% 0% 0.0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 55% 56% 56% 55% 55% 58% 48% 48 4.1% 28 28 28 108 7.4% 59% 52% 22% 17% 55% 55% 56% 57% 48% 38% 59% 56% 56% 56% 56% 57% 56% 55% 55% 56% 57% 57% 57% 57% 57% 57% 57% 57% 57% 57 | 15 | 0.0817 0.3466 0.0927 0.2106 0.0466 0.9046 0.4120 |
| 202 Accounted tradecisions enterchannel Accounted (Accounted to Station) 88% 66% 66% 92% 12% 202 Accounted tradecisions included Post of Control (Accounted to Station) 96% 96% 96% 96% 12% 12% 202 Recognitions included Red in 180% ACCounted (Accounted to Station) 96% 96% 96% 96% 12% 12% 202 Recognition in control (Accounted to Station) Red in Control (Accounted to Station) 10% ACCounted (Accounted to Station) 12% 22% <td>5% 5% 7.4% 0% 0% 0% 0.0% 8.7% 100% 98% 55.2% 12% 5% 11% 8.7% 0% 0% 0% 0.07% 91% 92% 100% 94.6% 98 92% 120% 94.6% 91% 128% 12% 22% 12% 0.0% 0.0% 0.0% 92% 98% 92% 100% 94.6% 11%</td> <td>0% 2% 4.7% 0% 0% 0% 0% 0.0% 98% 98% 96% 97.4% 7% 0% 5.4% 0% 0% 0% 0% 0.0% 88% 90% 90% 90% 90.7% 90% 90% 90% 90% 90% 90% 90% 90% 90% 90</td> <td>28 28 68 20% 08 08 08 08 0.05 978 1008 2008 20% 28 08 08 08 08 08 278 128 92% 28 28 28 28 20 20% 20% 20% 20% 20% 20% 20% 20% 20%</td> <td>26 7.95 05 05 25 1.95 0.3330 0.3330 0.3076 0.4377 0.3620 0.7535 0.7989 0.6116 0.4460 0.0219</td> <td>0.4226 0.4226</td> | 5% 5% 7.4% 0% 0% 0% 0.0% 8.7% 100% 98% 55.2% 12% 5% 11% 8.7% 0% 0% 0% 0.07% 91% 92% 100% 94.6% 98 92% 120% 94.6% 91% 128% 12% 22% 12% 0.0% 0.0% 0.0% 92% 98% 92% 100% 94.6% 11% | 0% 2% 4.7% 0% 0% 0% 0% 0.0% 98% 98% 96% 97.4% 7% 0% 5.4% 0% 0% 0% 0% 0.0% 88% 90% 90% 90% 90.7% 90% 90% 90% 90% 90% 90% 90% 90% 90% 90 | 28 28 68 20% 08 08 08 08 0.05 978 1008 2008 20% 28 08 08 08 08 08 278 128 92% 28 28 28 28 20 20% 20% 20% 20% 20% 20% 20% 20% 20% | 26 7.95 05 05 25 1.95 0.3330 0.3330 0.3076 0.4377 0.3620 0.7535 0.7989 0.6116 0.4460 0.0219 | 0.4226 0.4226 |
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| 278 Louche-rich neueroconteins or Limite LIMITE SUBJECT 50% 60% </td <td>99% 17% 20.1% 19% 16% 19% 17.9% 56% 65% 67% 63.25% 20% 0% 0% 0.0% 6% 0% 4% 3.27% 92% 85% 100% 95.65% 0%</td> <td>18% 15% 16.3% 21% 27% 50% 15.2% 75% 72% 67% 71.0% 0% 0% 0% 0.0% 8% 5% 0% 4.4% 85% 88% 92% 05.0%</td> <td>13% 9% 28% 12.0% 34% 20% 15% 10.3% 84% 81% 79% 81.5% 5% 12% 9% 9% 90% 100% 100% 500% 61% 41% 20% 50% 50% 100% 500% 60% 00% 00% 00% 00% 00% 00% 00% 00%</td> <td>115 945 115 64 115 675 67306 0.0000 0.0000 0.0007 0.5227 0.4286 0.1149 0.0007 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000</td> <td>0.0134</td> | 99% 17% 20.1% 19% 16% 19% 17.9% 56% 65% 67% 63.25% 20% 0% 0% 0.0% 6% 0% 4% 3.27% 92% 85% 100% 95.65% 0% | 18% 15% 16.3% 21% 27% 50% 15.2% 75% 72% 67% 71.0% 0% 0% 0% 0.0% 8% 5% 0% 4.4% 85% 88% 92% 05.0% | 13% 9% 28% 12.0% 34% 20% 15% 10.3% 84% 81% 79% 81.5% 5% 12% 9% 9% 90% 100% 100% 500% 61% 41% 20% 50% 50% 100% 500% 60% 00% 00% 00% 00% 00% 00% 00% 00% | 115 945 115 64 115 675 67306 0.0000 0.0000 0.0007 0.5227 0.4286 0.1149 0.0007 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 | 0.0134 |
| 202 455 ribuscost protein 556 Papidis RSSS-MAUSE 13150s 218 46% 229 34-29 56% 231 Tearnestones protein 55 Tearnest 5 Tearnest 23 KDR 86% 100% 09 51.9% 14% 236 24 Paraules carbonoleum entechnical per PMC (MASSE 128 26 50 86% 16% 15% 15% 15% 15% 15% 15% 15% 15% 15% 15 | 276 578 532% 126 126 138 1275 250 360 438 428 4105 518 00 00 44% 40% 00 00 100 3375 600 1008 322% 00 110 110 110 110 110 110 110 110 110 | 66% 48% 48.4% 11% 11% 10% 126% 41% 16% 25% 25.6% 66% 05% 05% 00% 00% 67% 100% 100% 28 68 46% 08 50 68 68 25% 100% 100% 17% 160% 17.5% | 538 688 678 5128 68 188 130 2.25 208 558 238 2838 7.0 65 60 58 50 50 50 50 50 50 50 50 50 50 50 50 50 | 0. 00 00 00 00 00 00 00 00 00 00 00 00 0 | 0.2996 |
| ALC 490 Information profits 12 Page 15 | 90 | 505 289 4128 005 58 18 2278 885 718 726 726 776 8 175 909 87707 105 228 105 1305 25 005 00 0.75 22 00 2075 15 00 005 100 100 100 100 100 100 100 | 228 296 230 22.05 08 08 08 00 00 005 298 888 889 889 78 78 228 882 883 887 78 228 228 228 228 228 228 228 228 | 1 | 0.2955 |
| .202 (Stochast Sethioropassinas (MALP) (Stoch LIMP) MALOR. 2515.08. 896. 905. 907. 905.27. 1655. 2020 (Stochast Sethioropassinas (MALP) (Stoch | 225, 105, 13,67, 05, 05, 05, 06, 0,07, 86, 125, 165, 165, 165, 165, 165, 165, 165, 16 | 76. 28. 6.87% 25% 25% 25% 25% 25% 25% 50% 60% 60% 60% 60% 60% 60% 60% 60% 60% 6 | .00, 48, 48, 22% 50, 08, 09, 005, 005, 008, 078, 200, 40,75, 50, 48, 200, 110, 22% 50, 28, 200, 110, 25% 500, 100, 500, 500, 500, 500, 500, 500, | 0. 27% 0. 00 0. 00 0. 00% 0. 0 | 0.0023 |
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| 207 Ex SAMD-ordine beams RestREP, Reshpit PROPE, MIXTURE 241 M/Sn OK OK OK OK OK OX 224 M/Sn 200 Leuten-ePAN Assess rechebered Law SYLC, MAJOUR 214 M/Sn 276 S1 S1 S75 S1 M/Sn 247 S1 M/Sn 200 Exhauved translation initiation in Elifs 1974 MOURE 17 M/Sn 91% 64% 92% 64% 92% 65.07% 95 M/Sn 200 005 Feboussering prints 1.54 PgCN4 MOURE 17 M/Sn 200 105 64% 92% 126% 226% 200 105 M/Sn 200 M/Sn 200 105 M/Sn 200 M/Sn 200 M/Sn 200 | \$495 GON \$22.275 7795 \$605 4005 G7.775 GN 605 GN 605 GN 50.075 5055 5055 5055 5055 5055 5055 50 | ABM CON EDD/S SEM LODE CON CON< | 20% 0% 21% 13.7% 80% 200% 79% 86.3% 0% 0% 0% 25% 8.3% 11% 20% 0% 0% 0% 0 % 0.0% 0% 0% 0 % 0.0% 0 % 0 | 08 12.7% 98% 70% 75% 78.0% 0-000 0-0 | 0.1152 0.1152 0.0039 0.1300 |
| 200 Continues and Continues Continue | 22% 20% 20.5% 4% 4% 5% 4% 5.7% 50% 50% 70% 54.4% 20% 70% 50% 5.8% 77.4% 59% 7% 10% 8.2% 15% 12% 18% 17.7% 77% 20% 11% 2.1% 2% 2% 2.1% 5.2% 50% 50% 50% 50% 50% 50% 4% 50% 50% 50% 50% 50% 50% 50% 4% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50 | 26% 26% 26.3% 12% 12% 6% 9.3% 72% 6% 9.4% 71.2% 50% 72% 73.4% 6% 6% 9% 7.6% 26% 25% 25% 25.0% 21.6% 28 28 27 27% 28 28 28 27 20% 100% 95% 93% 93.0% 10.5% | 22% 26% 26% 28% 22.0% 26% 7% 56 78 58 5.6% 80% 66% 70.0 71.4% 16% 23% 67% 66% 6.5% 65% 65% 13% 13% 12% 12% 22% 22% 20% 13% 15% 12.0% 22% 20% 15% 15% 15% 15% 15% 12% 22% 22% 22% 25% 66% 66% 66% 66% 66% 66% 26% 26% 26% 26 | 1 | 0.2536 0.9347 0.7608 |
| Sec Secretaria Belanda Maria Sec S | 00 05 05 005 005 00 05 00 005 00 005 000 0 | An O. | . 00 | 00 00% 00 00 00 00 00 00 00 00 00 00 00 | 0.0663 |
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| 317. Myoferin. 318. M | 2% 0% 2.4% 0% 0% 0% 0.0% 56% 100% 96% 97.7% 5% 40% 50% 41.8% 29% 24% 17% 22.4% 27% 27% 20% 24.8% 56% | 0% 0% 1.7% 0% 0% 2% 0.5% 10% 50% 100% 1000.5 65% 50% 50.0% 110% 27% 20% 25.2% 45% 45% 45% 100% 1000.5 65% 50% 50.0% 110% 27% 20% 25.2% 47% 4.2% 23.8% 24.2% | .0% 08 29 0875 55% 46% 55% 32.0% 72% 66% 56% 57.0% 00% 00% 00% 00% 00% 00% 00% 00% 00% | A | 0.4226 |
| 221 Nucleolar protein 56 Nuppide | 278 248 248 248 248 248 279 278 158 368 2245 278 | 21% 24% 200.4% 6.7% 5.6% 28% 46.2% 24% 60% 60% 25% 31.6% 60% 50% 00% 00% 00% 00% 00% 00% 00% 00% 0 | 26% 1.2% 28% 2.2% 2.2% 28% 4.7% 4.7% 4.7% 4.5% 4.8% 3.2% 9.2% 56.0% 1.0% 29% 0.0% 0.0% 0.0% 1.00 | 0.5 9.5% 48% 46% 59% 59.5% 50.00% 0. | 0.4226 |
| 205 Eukarvotic transition iritiation in ELEDia ELETIS (MCUSEE 91 KDa 206 594 594 502 504 502 504 205 205 205 205 205 205 205 205 205 205 | 28% 41% 45.9% 5% 48 28 4.0% 628 56% 21% 65.0% 29% 56% 56% 56% 56% 56% 56% 56% 56% 56% 56 | 26% 27.4% 5% 6% 6% 6% 5.7% 6.9% 6.9% 22.0 26.7% 0% 0.0 1.7% 0.0 0% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 | 26% 22% 22% 224.5% 5% 5% 1.4% 5% 7.5% 92% 75% 92% 65.5% 8% 25% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5 | 08 1115 08 08 08 98 20% 0.991 0.000 0.1919 0.0000 0.1277 0.1000 0.1255 0.2555 0.0253 0.1777 0.1837 0.3802 0.4165 0.1837 0.3802 0.4165 0.1837 0.1837 0.3802 0.4165 0.1837 0.1837 0.1837 0.3802 0.4165 0.1837 0 | 0.4284 |
| 220 ATT-claims synthesis Adv ACLY-MCUSE 120 ASts 100% 100% 100% 100% 100% 100% 100% 100 | 0% 0% 0.0% 0% 0% 0% 0% 0.0% 100% 100% 10 | 0% 0% 0.0% 0% 0% 0% 0.0% 0.0% 0.0% 0.0% | 0% 0% 0% 0.0% 2.0% 3% 0% 0% 1.0% 1.0% 100% 100% 100% 100.0% 0% 0% 1.0% 100% 10 | 05 0.0% 08 08 08 00 0.0% 0-0.026 0-0.2 | 0.0206 0.4226 0.1882 |
| 333 ATE sombrom orbital of mischin Aggle, ATPGLACUSE, 1930a, 48% 51% 50% 50% 52% 55% 52% 53% 324 145-53 peninin rathicides. Vehicus 14032/ACUSE, 2830a, 88% 50% 68% 88% 57% 51% 51% 32% 320 Feu uninisam niemen-bioriforus (Natur. FLAPEZ/ACUSE 77 KGR. 8% 7% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50 | 48% 50% 48.5% 0% 0% 0% 0.0% 50% 32% 50% 52.5% 50.5% 1.0% 1.0% 1.0% 1.0% 1.0% 1.0% 1.0% 1.0 | 27% 44% 40.5% 0% 0% 0% 0.0% 2.0% 2.1% 2.8% 24% 27.5% 28% 38% 0.0% 0.0% 8.1% 2.8% 28% 28% 0.4.5% 0.0% 0.0% 8.1% 8.1% 8.1% 8.1% 8.1% 8.1% 8.1% 8.1 | 696 725 368 72255 08 08 08 08 0.055 268 176 398 22.055 218 818 818 825 725 818 818 825 725 818 818 825 725 818 818 825 725 818 818 825 725 818 818 825 725 818 818 825 725 818 818 825 725 818 818 825 725 818 818 825 | 56, 3575, 56, 158, 58, 775, 50, 50, 775, 50, 50, 775, 50, 50, 50, 50, 50, 50, 50, 50, 50, 5 | 0.0048 0.0026 0.4226 |
| 337. 492 cell-surface antiom haravic. Sicha2. 492, MCMSE. 50 MCB. 42% 69% 649% 64.9% 15% 308. 492 chosenal prolein 517 Pay17 Pay17 MAXEE 69 MCB. 54% 64% 64% 64% 51.7% 64% 320 Deaths. Dots. 0651 MAXEE 193.06 193.06 29% 79% 193.00% 157.00% 6551 MAXEE 193.06 193.06 29% 79% 193.00% 157.00% 157.00% | 75 145 1525 246 246 216 2295 718 728 727 7245 96 475 265 437 50 65 75 475 475 476 486 527 528 528 528 528 528 528 528 528 528 528 | 56 58 60% 20% 22% 19% 20% 20% 52% 52% 52% 52% 52% 52% 54% 54% 54% 54% 54% 54% 54% 54% 54% 54 | 06 05 08 07 20% 25 25 27 26 27 26 27 27 28 27 28 27 28 27 28 27 28 28 28 28 28 28 28 28 28 28 28 28 28 | 06 0.0% 06 06 09 009 0090 0090 0090 0090 0090 | 0.0039 0.0233 0.1903 |
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| em powerable - 200 MSBB, CYXXXI (1988) | .en .en .6426 .en .655 .en .en .655 .en .en .655 .en .en .655 .en .655 .en .en .655 .en .en .655 .en . | .vm vm 90.00% cm 2n 2n 2n 2005 100% 1000 1000 52 12 12 12 12 12 12 12 12 12 12 12 12 12 | | AN AND AND AND AND AND AND AND AND AND A | 0.4226 |
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| 202 Protein PRRICE Prof. PRRICE AUGUSE 46 K/bs 55% 55% 55% 54% 14.1% 65% 55% 55% 64% 64% 64% 65% 64% | 66% 72% 65.2% 17% 20% 16% 17.7% 10% 28 28 26 54% 69% 27% 5 28 5 32% 5 54% 69% 6 50% | \$68% \$23% \$55.0% \$21% \$29% \$48% \$21% \$48 \$17% \$48 \$17% \$6.00% \$0.00% \$0.00% \$0.00% \$0.00% \$0.00% \$0.00% \$1.00% \$1.000% | 20% (26%) 75% (26.97%) 45% (25%) 22% (21.7%) 0% (0% 15%) 3.7% 72% 80% 0% 0% 0% 0.0% 0.0% 0.0% 0.0% 0.0% | 50 17.7 0.1 0.1 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 | 0.2907 0.0018 0.9400 0.2524 |
| December | 95 | 281 991 1.275 991 991 991 991 997 1.070 1.000 1. | 091 991 995 905 905 995 995 995 095 095 0095 10005 100 | 0. 055 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. | 0.0064 |
| 301 Stread resconding particle second Stream SPEPA_ASSUE 773 Mon. 595. 756. 757. 752.752 J335 J335 J335 J335 J335 J335 J335 J3 | 200 200 14.2% 18% 15% 15% 15.0% 72% 72% 65% 77.1% 66 22% 15% 33.0% 15% 15% 78 8.2% 16% 25% 25% 55% 55% 55% 55% 55% 55% 55% 55 | 58 46 4.525 218 228 118 3025 208 1008 1008 68 55.28 58 80 2025 118 72 108 248 28 128 118 1008 1008 60 1008 60 55.28 100 446 11.55 360 448 28 28 27 52 32 28 20 28 20 20 20 20 20 20 20 20 20 20 20 20 20 | 08 | 06 08 08 075 0775 0775 0775 0775 0775 0775 | 0.0325 0.0180 0.0071 0.4276 |
| Description | \$25. 566, \$1.075, \$285, \$285, \$285, \$285, \$285, \$685, \$285, | 525, 346, 4975, 128, 275, 286, 518, 527, 528, 518, 487, 775, 528, 548, 549, 549, 549, 549, 549, 549, 549, 549 | 505 451 226 245 227 25 25 27 26 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28 | 69 54.75 288 228 469 2275 0.385 8888 0.325 0.525 0.505 | 0.1056 0.7687 0.4544 |
| most process SHYSTOSTORISMER EXECUTOR (1982) A. PRIAD (2015) A. 2015 255 355 231 231 231 231 232 232 232 233 233 234 235 234 235 234 235 234 235 234 235 234 235 234 235 234 236 237 | 3500, 3500, 454.75, 4070, 4270, 4270, 40.25, 4695, 2496, 2496, 2496, 2415, 2416, 2415, 2416, 2415, 2416, 241 | ome ann 13.00% 1.0% 00% 00% 20% 22% 22% 25% 16% 16% 22.0% 25% 25% 16% 22.0% 25% 25% 25% 25% 25% 25% 25% 25% 25% 25 | men en e | 126 2075 5276 438 1738 2075 0010 0.7715 0.1310 0.0000 0.0040 0.1110 0.4000 0.0040 0.1110 0.4000 0.0040 0.1010 0.0000 0.00 | 0.4963 |
| arz rement-C Finc FENC, MICUSE 291 M/m 06; 100% 100% 373 Penciredosin-4 Podrá PPDOM, MUCES 311 K/m 5/0% 47% 48% 48.4% 38% 374 Transgelin-2 Tagin-2 TAGL2, MOUSE 22 K/m 92% 96% 100% 50.0% 50.0% 7% | 41% 41% 40.7% 8% 11% 20% 5.0% 45% 52% 51% 49.5% 42% 5% 0% 4.0% 0% 0% 0% 0.0% 100% 100% 100% 100% 10 | 27% 27% 36.1% 12% 20% 11.4% 9% 5% 7% 6.6% 00% 00% 00% 0.0% 99% 50% 50% 69% 70.0% 00% 00% 0.0% 99% 74% 89% 65.2% | 2895, 3479, 2479, 2479, 2286 8236 7287, 75,075 4488 1486 29 15,475, 90 15,475 | Section Sect | 0.0030 |

| 375 T-complex protein 1 subunit beta CcQ 376 Dermatoponin Dpt | TOPS MOUSE DESN MOUSE | 57 kDa 72% 24 kDa 0% | 795 365 76.0° 65 05 05 0.0° | % 22% 29% 24% % 100% 200% 85% | S 2185 48 S 9655 08 | 2% 0% 2.3 0% 13% 3.5 | 75. 725. 885. 75. 05. 05. | 92% 54.4% 0% 9.0% | 23% 12% 95% 92% | 85 14.45 915 94.25 | 25 05 55 25 | 05 1.75 65 5.85 | 87% 2% | 81% 78% 82 0% 0% 0 | 0% 11% 0% 98% | 12% 15% 92% 92% | 12.7% 2% 95.3% 2% | 7% 8% | 76 5.3% 26 4.7% | 18% 86% 0% 0% | 92N M.ON ON 0.0N | 5N 9N 96N 98N | 0% 4.7% 98% 97.5% | 78 58 48 28 | 9% 6.7 2% 2.5 | % 0.2715 % 0.2794 | 0.0979 0.12 | 57 0.5434 | 0.2446 0.5868 0.3678 | 0.0786 0.0088 0.3403 0.7829 | 0.1954 0.5 0.0293 0.5 0.7381 0.9 | 625 0.4992 0 668 0.3403 0 166 0.0992 0 | 0.1920 0.0042 0.7829 0.0293 0.4226 0.1967 |
|--|--|--|--|---|--|--|--|--|---|--|--|--|---|--|--|--|---|---|---|--|--|--|--|---|--|--|--|---|--|--|--|--|---|
| 279 495 ribosomai protein 521 Rps21 279 495 ribosomai protein 514 Rps14 280 Galectin-1 Lgaliti 381 Indiscrine-6954 licase, cylcolar (alexandra) 382 Colifie-1 Cff | RS21 MOUSE RS14 MOUSE LEG1 MOUSE SYIC MOUSE COF1 MOUSE | 9 kDa 52% 16 kDa 48% 15 kDa 29% 144 kDa 24% 19 kDa 74% | 58% 50% 53.4° 55% 56% 52.9° 87% 81% 52.1° 56% 50% 50.0° 90% 31% 54.9° | 5 66N 27N 509 S 66N 27N 34N S 60N 25N 24N S 22N 22N 199 S 20N 20N 20N S 20N 20N 99 | 5 44.2% 2% 5 35.2% 12% 5 17.9% 0% 5 0.0% 16% 5 15.1% 0% | 5% 0% 23 10% 10% 10.8 0% 0% 0.5 4% 10% 10.5 0% 0% 0.0 | PN 61N 60N PN 60N 57N PN 82N 82N PN 98N 96N PN 92N 96N | 695 57.0% 56% 57.0% 80% 81.2% 97% 97.1% 96% 90.9% | 29% 27% 30% 24% 28% 18% 0% 0% 18% 5% | 51% 42.0% 25% 33.1% 20% 18.8% 0% 0.0% 5% 9.1% | 0% 2% 10% 9% 0% 0% 2% 4% 0% 0% | 0% 1.0% 9% 9.3% 0% 0.0% 2% 2.9% 0% 0.0% | 62% 24% 50% 100% 1 | 52% 56% 51 75% 65% 71 52% 66% 50 90% 100% 100 87% 85% 85 | 2% 22% 2% 26% 5% 26% 5% 0% 5% 0% | 28% 46% 25% 25% 42% 22% 0% 0% 11% 12% | 36.7% 0% 26.7% 0% 37.0% 2% 0.0% 0% 11.9% 2% | 9% 9% 2% 9% 2% | 0% 0.0% 0% 0.0% 2% 2.4% 0% 0.0% 1 2% 2.0% | 5% 67% 12% 78% 17% 65% 10% 100% 12% 84% | 57% 65.2% 92% 54.2% 72% 71.0% 100% 100.0% 90% 65.0% | 25% 22% 17% 22% 22% 32% 0% 0% 17% 24% | 695 33.7% 895 15.7% 2095 27.4% 095 0.0% 995 13.2% | 0% 0% 0% 0% 2% 2% 2% 0% 0% | 9% 0.0 9% 0.0 9% 1.5 9% 0.0 2% 1.1 | % 0.4794 % 0.2053 % 0.7648 % 0.1018 | 0.4638 0.12 0.0685 0.01 0.1374 0.01 0.10 0.8635 0.85 | 82 0.0514 | 0.5868 0.2676 0.7159 0.2394 0.7648 | 0.4638 0.3334 0.0685 0.1231 0.1291 0.0179 0.6673 0.6272 | 0.2869 0.5 0.0367 0.2 0.1126 0.1 0.4731 0.0545 | 005 0 202 0 0.5083 0 915 0.2728 0 | 0.2039 0.4226 0.0064 0.0002 0.0437 0.2254 0.1002 0.0514 0.0018 0.1035 |
| 303 192 kGs tankrusse-1-binding on: Trike18 384 Tight junction protein ZG-2 Tigs 385 Eukanvolic translation initiation fs Editi 385 Ademyt cyclasse sssociated and Cap1 387 Calcium-binding mitochondrial cs Sci253 387 Calcium-binding mitochondrial cs Sci253 | 202 MOUSE EIFSF MOUSE CAP1 MOUSE CAP1 MOUSE CMC1 MOUSE | 182 MOs ON 131 MOs ON 38 MOs 29% 52 MOs 76% 75 MOs 41% | 0% 6% 2.0° 0% 0% 0.0° 29% 31% 29.0° 68% 34% 72.5° 68% 25% 37.3° | \$ 100% 100% 94% \$ 100% 100% 100% \$ 50% 47% 48% \$ 24% 32% 26% \$ 31% 27% 66% | \$ 98.0% 08 5 500.0% 08 5 500.0% 08 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 0% 0% 0.5 0% 0% 0.5 24% 22% 21.5 0% 0% 0.5 27% 9% 21.5 | 75 25 25 25 25 25 25 25 25 25 25 25 25 25 | 05 1.75 05 0.05 65 34.05 895 74.55 675 53.85 | 95% 100% 100% 100% 41% 42% 32% 32% 7% 16% | 100% 98.3% 100% 100.0% 18% 34.0% 11% 25.5% 5% 9.0% | 0% 0% 0% 0% 20% 20% 0% 0% 20% 52% | 0% 0.0% 0% 0.0% 27% 32.0% 0% 0.0% 29% 37.2% | 2% 0% 40% 72% 19% | 2% 0% 1 6% 4% 3 66% 61% 42 71% 26% 73 9% 6% 11 | 7% 90% 1% 100% 5% 60% 5% 24% 5% 14% | 92% 88% 94% 96% 22% 41% 24% 18% 9% 25% | 86.7% 2% 96.9% 0% 37.8% 20% 21.9% 4% 19.6% 62% | 16% 1 9% 21% 1 5% 82% 5 | 25 11.05 05 0.05 85 19.75 45 4.25 95 09.15 | 0% 10% 6% 2% 17% 36% 98% 72% 5% 24% | 12% 10.8% 21% 13.0% 52% 46.4% 76% 75.9% 12% 18.5% | 82% 88% 88% 96% 12% 41% 16% 25% 0% 0% | 28% 82.8% 29% 85.2% 14% 22.9% 17% 19.2% 11% 3.7% | 8% 2% 9% 2% 62% 24% 65% 4% 85% 76% | 9% 6.4 9% 0.7 29% 30.7 5% 4.9 72% 77.8 | % 0.4258 % 0.4258 % 0.8151 % 0.2887 | 0.0017 0.90 0.2223 0.15 0.6121 0.01 0.5131 0.60 0.2194 0.03 | 13 0.0166 67 0.1516 35 0.2125 01 0.8549 36 0.0018 | 0.9147 0.2019 0.8151 0.1102 | 0.3689 0.0304 0.1652 0.1967 0.2408 0.0541 0.4457 0.1457 0.1762 0.2230 | 0.0145 0.1151 0.4107 0.0 0.4812 0.3470 0.1 | 0.2728 6 0.1887 6 0.4226 0.425 0 0.402 0 0.402 0 | 0.0056 0.0256 0.4225 0.1937 0.8261 0.0061 0.0189 0.0065 0.0214 |
| 300 Percentific lease-related protein 300 Lithostathine-1 301 Colleges alpha-1(XXVIII) chain CoStat 302 Straid contidess correlate called 303 17-beta-hydrossateroid dehydroc Held? | p2 LIPR2 MOUSE LITT MOUSE at COSA1 MOUSE to SCITC MOUSE bt3 DHB13 MOUSE | 73 800 296 196 197 197 197 197 197 197 197 197 197 197 | 92% 88% 87.4° 97% 200% 95.3° 28% 49% 41.7° 91% 89% 88.5° | % 12% 8% 12% % 11% 2% 0% % 16% 21% 23% % 26 0% 23% | % 12.5% ON % 4.7% ON % 12.5% 28% % 12.5% 12% | 0% 0% 0.0 0% 0% 0.0 40% 28% 30.5 9% 9% 10.3 | 7% 87% 95% 7% 97% 99% 7% 56% 47% 7% 82% 82% | 98% 93.3% 98% 97.9% 46% 49.5% 88% 84.5% | 12% 5% 2% 1% 11% 6% 2% 2% | 2% 6.7% 2% 2.1% 15% 11.8% 2% 1.9% | 22% 44% 16% 16% | 0% 0.0% 0% 0.0% 28% 38.7% 9% 13.5% | 200% 1 200% 1 200% 1 | 00% 100% 500 00% 100% 500 0% 29% 22% 34 00% 97% 98 | 0% 0% 0% 0% 0% 0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0.0% 0% 0.0% 0% 5.6% 60% 0.0% 3% | 0% 0% 0% 20% 71% S 0% | 0% 0.0% 1/2 0% 0.0% 1/2 0% 00.5% 2% 2.0% 1/2 | 100% 10% 100% 0% 0% 0% 100% | 90% 100% 100.0% 0% 0.0% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 20% 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 200% 200% 0% 0% | 0% 0.0 0% 100.0 0% 0.0 | 0.2387 % 0.5040 % 0.1278 % 0.1583 | 0.2194 0.00 0.40 0.5000 0.00 0.21 0.0094 0.14 0.1039 0.01 | 79 0.8008 76 0.0383 83 0.0038 07 0.0123 | 0.2387 0.5040 0.0488 0.3613 | 0.5000 0.6079 0.2776 0.4226 0.1098 0.1836 | 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 | 436 0.0237 0 925 0.1930 0 | 0.0027 0.0072 0.0027 |
| 394 Heterosensous nuclear riboraule Hemp 365 9194-spicino licase RicS homoi: Rich 395 905 ribosomal protein L30 Rgi30, 397 Serpin I2 Serpin 398 Protein PRRICEC Process | | | 06 12% 8.1° 296 40% 33.9° 52% 64% 57.1° 94% 93% 92.1° 6% 9% 0.0° | % 88% 92% 76% % 62% 62% 55% % 64% 64% 223 % 100% 55% 79 % 100% 200% 100% | % 85.6% 0% % 60.3% 5% % 40.4% 2% % 7.4% 0% % 100.0% 0% | 7% 12% 6.3 7% 5% 5.8 2% 2% 2% 0.5 0% 0.5 0% 0.5 | PN 0N 12N PN 20N 32N PN 45N 64N PN 94N 95N PN 0N 0N | 0% 3.7% 90% 37.9% 66% 58.2% 90% 95.9% 0.0 0.0% | 100% 89% 67% 64% 52% 21% 6% 5% 100% 100% | 90% 93.0% 44% 50.3% 34% 39.2% 0% 3.6% 100% 100.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 10% 3.3% 6% 3.8% 0% 2.6% 2% 0.6% 0% 0.0% | 11% 38% 64% 200% 1 | 9% 16% 12 44% 29% 40 56% 62% 50 00% 100% 100 0% 0% 0% | 0% 90% 6% 62% 4% 36% 0% 0% 0% 100% | 79% 76% 48% 57% 44% 38% 0% 0% 100% 100% | 78.4% 9% 55.7% 0% 39.5% 0% 0.0% 0% 100.0% 0% | 12% 7% 9% 9% 9% | 8% 9.6% 6% 3.7% 6% 0.0% 6% 0.0% 6% 0.0% | 1% 12% 0% 57% 6% 22% | 16N 13.0% 60N 52.4% 42N 45.7% 100N 0.0% | 81% 82% 30% 42% 44% 62% | 78% 80.3% 40% 37.6% 53% 54.3% 0% 100% 100.0% | 9% 6% 9% 0% 9% 0% | 5% 6.7 0% 0.0 0% 0.0 0% 0.0 | % 0.6065 % 0.6065 % 0.0960 | 0.7123 0.44 0.0162 0.10 0.1469 0.45 0.01 | 61 0.1123 20 0.0359 62 0.2558 92 0.0477 | 0.2918 0.8148 0.8849 0.1858 | 0.2416 0.2711 0.0321 0.4053 0.1409 0.8733 0.0407 | 0.4731 0.6965 0.1536 0.4907 0.4907 0.4902 0.4902 0.4902 0.0003 0. | 579 0.1180 0 552 0.2292 0 554 6 680 0 | 0.4442 0.4237 0.4332 0.0054 0.0010 0.2227 0.4226 |
| 400 Collegen alpha-1/X) chain Colfor 401 Perceiredoste-2 Proto2 402 Branched-chain-amino-acid amis Boat2 403 Keratin, fipe I cytoskeletal 10 Krt10 404 Storal osofidase corrollox saburti Sopol2 | PROXE MOUSE PROXE MOUSE BCATE MOUSE K1C10 MOUSE SPCSE MOUSE | 57 kDa 57 kDa 52 kDa 52 kDa 52 kDa 58 | 89% 98% 91.0° 99% 98% 98.7° 18% 14% 10.0° 85% 88% 53.0° 2% 5% 3.0° | N 12N 8N 20 N 5N 1N 23 N 6N 20 20 N 0N 0N 00 | \$ 60.5% SX \$ 42.4% SX \$ 7.4% OX \$ 190.0% OX \$ 45.2% OX \$ 7.2% OX \$ 2.2% SX \$ 35.9% S2X \$ 05.9% S2X | 7% 5% 5.0 2% 28 20 20 2% 9% 0.0 6% 9% 0.0 5% 9% 0.0 6% 9% 0.0 6% 9% 0.0 6% 57% 53.1 15% 12% 17.5 26% 28% 30.1 | 0% 08% 97% 98% 97% 98% 98% 98% 98% 98% 98% 98% 98% 98% 98 | 985 96.255 985 96.255 245 30.855 985 94.95 985 96.75 58 19.455 985 79.255 985 1.275 985 96.75 985 1.275 | 9% 6% 2% 1% 2% 25% 42% 9% 0% | 6% 5.1% 6% 1.1% 8% 37.7% 6% 0.0% | 100% 0% 0% 5% 0% 55% 42% 28% 27% | 0% 0.0% 2% 2.2% 50% 51.9% 20% 29.5% | 97% 97% 100% 1 6% | 0% 0% 0 90% 86% 91 90% 100% 90 22% 18% 15 90% 100% 94 | 0% 10% 2% 2% 2% 0% 0% 2% 56% 4% 0% | 0% 20% 10% 14% 0% 0% 52% 27% 0% 0% | 10.0% 90% 8.8% 0% 0.0% 0% 45.0% 29% 0.0% 7% | 200% 8 0% 0% 0% 26% 5 10% | 0% 90.0% 0% 0.0% 0% 0.0% 10 0% 0.0% 10 0% 30.0% | 0% 0% 62% 92% 62% 100% 8% 5% 62% 100% | 0% 0.0% 100% 95.9% 100% 100.0% 0% 4.4% 100% 100.0% | 0% 0% 0% 7% 0% 0% 58% 32% 0% 0% | 0% 0.0% 0% 2.3% 0% 0.0% 40% 45.4% 0% 0.0% | 200% 100% 2% 0% 0% 0% 32% 62% 0% 0% | 100% 100.0 0% 0.8 0% 0.0 56% 50.3 0% 0.0 | % 0.2967 % 0.9783 % 0.9526 % 0.0837 | 0.2234 0.90 0.15 0.1458 0.58 0.1994 0.01 | 44 0.4451 80 0.1057 94 0.2374 49 0.0179 | 0.4970 0.3121 0.7304 | 0.2254 0.1856 0.7490 0.1453 0.9759 0.4280 | 0.3572 0.4 0.2219 0.3 0.4007 0.8 | 0.2254 226 0.4226 0 377 0 500 0.4323 0 137 0.1994 0 | 0.4225 0.4225 0.4225 0.2335 0.2416 0.8756 0.0749 0.0179 |
| 405 SEC23-Interacting protein Sec23 405 Ecsimophi perceidase Epc 407 Integrin beta-4 light 400 Janiscoppidase N Arpag 400 E3 URM protein ligase 1 UR 444 August Armania August 1 URM 444 August August 1 URM 444 August 1 URM | PERE_MOUSE PERE_MOUSE ITEM_MOUSE AMPN_MOUSE UFL_MOUSE | 111 MDa 2% 81 MDa 202 MDa 0% 110 MDa 100% 90 MDa 61% | 2N 5N 3B 2N 0N 0D 100N 100N 100D 58N 44N 54-0 60N 2N 54-0 10N 0N 0D 10N 0N 0D 10N 52N 54-1 10N 0N 0D | \$ 63% 69% 66% \$ 8% 0% 10% \$ 0% 0% 0% \$ 16% 21% 24% | S 65.9% 22% S 6.1% 92% S 0.0% 0% S 23.8% 22% | 29% 29% 30.1 100% 90% 93.5 0% 0% 0.5 21% 22% 21.8 29% 21% 22.5 0% 0% 0.5 0% 0% 0.5 0% 0% 0.5 | PS 4% 0% PS 0% 0% PS 100% 100% PS 64% 52% | 0% 1.2% 0% 0.0% 100% 100.0% 24% 64.0% | 8% 0% 8% 0% 0% 0% 2% 18% | 22% 38.6% 6% 14% 7.2% 6% 0.0% 6% 8.7% | 92% 100% 0% 0% 29% 29% | 28% 60.0% 200% 86% 92.7% 0% 0.0% 26% 27.8% | 12% 18% 2% 92% 55% | 0% 0% 3 19% 6% 14 0% 0% 0 91% 82% 88 50% 54% 56 | 7% 56% 1% 67% 5% 6% 1% 0% 2% 6% | 57% 77% 48% 57% 7% 9% 0% 0% 12% 8% | 53.2% 23% 50.7% 25% 8.0% 92% 0.0% 10% 8.7% 28% | 42% 2 22% 2 92% 9 9% 1 28% 2 | 25 23.15 75 25.25 15 22.05 75 11.95 85 25.15 | 0% 0% 0% 6% 0% 10% 9% 82% | 50% 15.7% 20% 15.0% 20% 9.8% 85% 52.7% | 20% 22% 20% 56% 22% 42% 0% 0% | 0% 22.0% 60% 44.8% 60% 34.6% 0% 0.0% | 52% 71% 42% 29% 79% 48% 21% 17% 32% | 50% 61.3 40% 40.2 40% 55.5 15% 17.9 | % 0.1979 % % % 0.2970 | 0.5207 0.97 0.8942 0.2305 0.1397 0.04 0.3372 0.80 | 0.4549 0.2305 49 0.0100 74 0.4411 | 0.1155 0.8262 0.1019 | 0.0485 0.7361 0.4112 0.0587 0.6017 0.0479 0.087 | 0.3394 0.0 0.0305 0.8 0.2507 0.0 | 552 0.2202 0.655 0 | 0.6767 0.9210 0.6017 0.0764 0.0440 0.0100 0.0412 0.6348 0.1136 0.046 |
| 412. Transcription intermediary factor. Trins1 413. PNN-binding protein EWS Exert 414. Complement C4-5. C4b. 415. 405 ribosomal protein 525. Rps25 417. Sicide tail protein. S8t. | TIFIB MOUSE EWS MOUSE CORE MOUSE RS25 MOUSE SKT MOUSE | 89 kDa 20% 68 kDa 0% 193 kDa 100% 14 kDa 100% 213 kDa 0% | 20% 15% 18.37 0% 0% 0.0 100% 40% 52% 54.17 0% 0% 0.0 | 55 80% 82% 85% 55 96% 100% 96% 96 00 0% 55 32% 60% 36% 55 88% 100% 100% | S 81.7% ON S 95.0% GN ON S 35.9% SN S 95.8% 12% | 0% 0% 0.5 0% 6% 4.5 0% 11% 12% 10.1 0% 0% 4.3 | 7% 22% 36% 7% 0% 0% 100% 7% 45% 48% 7% 0% 0% | 27% 32.1% 9% 3.0% 52% 48.5% 0% 0.0% | 67% 64% 200% 92% 0% 45% 42% 100% 100% | 72% 67.9% 91% 94.6% 34% 40.8% 100% 100.0% | 0% 0% 0% 7% 0% 10% 9% 0% 0% | 0% 0.0% 0% 2.4% 12% 10.7% 0% 0.0% | 47% 12% 27% 59% 0% | 51% 62% 45 0% 7% 5 82% 62% 74 54% 65% 59 0% 0% 0 | 9% 51% 6% 82% 5% 11% 4% 41% 6% 100% | 60% 55% 96% 93% 5% 17% 66% 25% 100% 100% | 50.7% 2% 50.1% 4% 10.9% 12% 40.6% 0% 100.0% 0% | 2% 6% 12% 1 0% | 26 2.3% 06 3.3% 96 14.6% 06 0.0% | 226 57% 206 60 206 62% 126 62% 126 52% 006 006 | 60% 62.9% 5% 6.9% 62% 65.8% 55% 55.9% 0% 0.0% | 25% 42% 86% 88% 0% 22% 29% 48% 100% 100% | 60% 35.2% 89% 87.8% 3% 4.1% 45% 44.1% 100% 100.0% | 2% 0% 5% 6% 27% 29% 0% 0% 0% 0% | 0% 0.9 5% 5.3 24% 30.0 0% 0.0 | % 0.0139 % 0.4226 % 0.2351 | 0.0583 0.00 0.9422 0.25 0.2029 0.04 0.4286 0.25 0.0075 0.33 | 74 0.4411 00 0.0146 13 0.0103 31 0.3348 79 0.0981 41 0.0764 20 0.6973 | 0.0139 0.7120 0.2968 0.4226 | 0.1001 0.8000 0.8071 0.2051 0.2215 0.0609 0.4285 0.2772 0.4285 | 0.0177 0.1127 0.6 0.4816 0.7 0.4 | 0.2036 0 235 0.3571 0 0.0082 0 273 0 | 0.0006 0.4226 0.7924 0.3443 0.0240 0.0104 0.0135 0.4226 |
| 418 Procional-CoA carbonistes alpha Poca 419 T-corrolas protein 1 subunit sosii CcS 430 C-1-latrahychololas svriftass. ci Mithidi 421 Ras-related protein Rab-LA Rab-LA 422 T-corrolas protein 1 subunit care CcS | POCA MOUSE TOPE MOUSE I C1TC MOUSE RABIA MOUSE TOPG MOUSE | 13100. 569. - 150. - | 78% 65% 65.9° 66% 75% 72.3° 86% 95% 92.0° 89% 88% 85.2° 88% 95% 80% 80.4° | % 63% 22% 35% % 22% 31% 22% % 5% 54% 5% % 3% 0% 0% 0% 6% 6% 7% | N 5525 225 N 5.15 926 N 5.15 926 N 5.15 926 N 5.25 | 0% 0% 0.0 2% 2% 2.5 0% 0% 0.0 11% 12% 12.5 6% 2% 4.3 | 700 200 880 70 680 880 70 1000 2000 70 860 880 70 900 920 | 95% 81.2% 100% 82.6% 100% 100.0% 90% 87.7% 94% 91.7% | 30% 12% 32% 16% 0% 0% 2% 0% 7% 5% | 15% 18.8% 0% 15.9% 0% 0.0% 3% 2.9% 0% 5.3% | 0% 0% 5% 0% 0% 0% 11% 12% 2% 0% | 0% 0.0% 0% 1.5% 0% 0.0% 7% 10.1% 6% 3.1% | 200% 1 70% 200% 1 92% 82% | 00% 100% 100 69% 65% 67 00% 100% 100 94% 66% 93 82% 68% 78 | 0% 0% 9% 27% 0% 0% 8% 0% 1% 12% | 0% 0% 26% 26% 0% 0% 0% 0% 20% 26% | 0.0% 0% 25.8% 3% 0.0% 0% 0.0% 9% 15.7% 5% | 0% 7% 0% 6% 7% | 0% 0.0% 1/ 9% 6.4% 1 0% 0.0% 1/ 4% 6.2% 1 7% 6.2% 1/ | 10% 100% 18% 82% 10% 100% 11% 89% 10% 86% | 92% 87.4% 92% 87.4% 100% 100.0% 100% 93.3% 92% 92.9% | 0% 0% 8% 12% 0% 0% 2% 7% 0% 11% | 0% 0.0% 4% 9.9% 0% 0.0% 0% 3.4% 0% 3.8% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0 4% 2.7 0% 0.0 0% 3.3 7% 3.3 | % 0.4339 % 0.4339 % 0.9003 % 0.6021 % 0.2474 | 0.0075 0.33 0.10 0.9077 0.00 0.0760 0.13 | 41 0.0764 20 0.6973 00 0.2360 59 0.8061 45 0.1232 | 0.1667 0.4357 0.1603 0.4266 0.7278 | 0.4295 0.5500 0.8000 0.8000 0.8000 0.8000 0.8000 0.8000 0.4000 0. | 0.0794 0.5982 0.4 0.6999 0.2 0.7747 0.6 0.1446 0.4226 0.7 0.2236 0.1 0.1133 0.6 | 939 0.1958 0 911 0.3007 0 932 0.2956 0 | 0.1502 0.5085 0.0419 0.0485 0.1807 0.9273 0.7742 0.2312 |
| Matristratorionne M. sodratine Cybb. Matristratorionne M. sodratine Cybb. Matristratorionne M. sodratine Cybb. Model modulator 1 Nome Model modulator 1 Nome Model modulator 1 Nome Model modulator 2 Nome Model modulator 3 Nome M | DPTES MOUSE DPSPS MOUSE PRO MOUSE INDIVIDUAL MOUSE DID I MOUSE ODO! MOUSE | 52 808 785 34 80a 975 274 80a 1005 133 80a 54% 41 80a 495 116 80a 965 | 97% 90% 94.6° 92% 100% 97.2° 72% 52% 59.8° 50% 52% 50.4° 96% 96% 95.7° | 5 225 05 95 5 08 08 08 09 5 08 08 08 09 5 28 28 28 60 5 658 428 428 5 08 08 53 | 5 0.0% 28 5 0.0% 28 5 0.0% 08 5 28.0% 14% 5 43.0% 68 5 1.0% 48 | 2% 12% 5-4 2% 26% 5-2 12% 8% 11.8 7% 5% 5-1 | 75. 1005. 2005. 75. 775. 1005. 75. 805. 805. 75. 815. 645. 75. 1005. 1005. | 96% 91.1% 100% 85.7% 86% 75.8% 60% 55.2% 100% 100.0% | 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9 | 0% 1.2% 0% 0.0% 0% 5.1% 28% 39.7% 0% 0.0% | 19% 0% 20% 20% 16% 24% 5% 8% 0% 0% | 6% 7.6% 6% 7.6% 6% 13.3% 14% 18.1% 2% 5.0% 6% 0.0% | 96% 1 96% 1 56% 56% | 200 220 220 220 220 220 220 220 220 220 | 25 25 25 25 25 25 25 25 25 25 25 25 25 2 | 0% 0% 0% 0% 0% 0% 0% 21% 28% 41% 0% 0% | 0.0% 48 0.0% 10% 7.0% 50% 39.5% 0% 1.5% 0% | 95 95 1 625 5 95 75 | 05 2.05 76 4.95 05 6.75 25 25.05 05 0.05 1 | 05 825 05 885 95 925 95 95 05 675 65 885 | 925 00.25 926 00.75 928 11.75 1205 00.95 966 90.45 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 11.1% 0% 0.0% | 15% 12% 5% 8% 20% 100% 0% 0% 4% 12% | 2% 11.3 20% 11.3 52% 88.9 0% 0.0 4% 6.6 | 5 0.6021 5 0.2474 5 0.5212 5 0.6000 5 0.2505 6 0.1508 6 0.4022 7 0.0538 | 0.1045 0.84 0.4480 0.45 0.1230 0.00 0.1241 0.00 | 01 0.7922 23 0.8143 60 0.0118 20 0.0780 96 0.1220 | 0.4226 0.0801 0.3450 0.4226 | 0.4226 0.1124 0.1241 0.0301 0.4226 0.9229 | 0.4226 0.7 0.2 0.2236 0.1 0.1133 0.6 0.1 | 520 0.1045 0 505 0.4460 0 704 0.0802 0 865 0 848 0.6807 0 | 0.8401 0.6256 0.4223 0.8143 0.0024 0.0176 0.0129 0.0819 0.4401 0.1220 |
| 409 Extended symplotagemin-1 East1 400 Hord cell factor 1 Hidde 401 Complement factor H Cith 402 Accessio induction factor 1 mits Affm1 403 Accessio Aff Accessio Acc | ESYTI MOUSE HOFCI MOUSE CFAH MOUSE AIRMI MOUSE ANNA MOUSE | 122 KDa 50% 210 KDa 0% 139 KDa 22% 57 KDa 22% 35 KDa 100% | 75% 17% 47.2° 0% 0% 0.0° 100% 100% 36% 48% 29.3° 100% 100.0° | \$ 10% 0% 23% \$ 100% 100% 100% 0% 0% \$ 68% 63% 52% \$ 0% 0% 0% | 5 14.4% 40% 5 100.0% 0% 5 60.7% 0% 5 0.0% 0% | 25% 50% 28, 20, 20, 20, 20, 20, 20, 20, 20, 20, 20 | PS 60% 72% PS 0% 0% 100% 100% PS 29% 45% PS 100% 100% | 100% 77.1% 0% 0.0% 100% 100.0% 62% 45.0% 100% 100.0% | 0% 0% 100% 100% 0% 0% 71% 55% 0% | 0% 0.0% 100% 100.0% 0% 0.0% 38% 54.4% 0% 0.0% | 60% 29% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 22.9% 0% 0.0% 0% 0.0% 0% 0.0% | 52% 19% 85% 17% 92% 1 | 61% 52% 55 0% 0% 6 95% 88% 89 65% 22% 28 00% 92% 96 | 5% 5% 2% 62% 5% 15% 4% 71% 5% 2% | 9% 2% 90% 96% 5% 12% 45% 72% 9% 72% | 2.7% 42% 52.6% 19% 10.4% 0% 62.6% 11% 3.4% 0% | 20% 4 10% 0% 9% 0% | 4% 41.8% 4% 11.1% 6% 0.0% 6% 9.0% 6% 9.0% | 2% 66% 5% 10% 9% 71% 9% 26% 8% 91% | 71% 65.7% 8% 7.8% 85% 78.4% 12% 29.5% 95% 93.7% | 98 28 798 298 228 228 628 698 28 58 | 0% 1,0% 60% 75,8% 12% 18,8% 52% 54,1% 2% 31% | 28% 21% 16% 10% 0% 6% 9% 6% 5% 4% | 29% 32.9 22% 16.4 2% 2.9 5% 6.4 2% 3.8 | % 0.2289 % % % 0.6047 | 0.0514 0.67 0.8462 0.42 0.0931 0.00 0.9128 0.34 0.2377 0.25 | 42 0.4548 26 0.0339 82 0.0329 89 0.2335 22 0.0192 94 0.0339 | 0.8047 | 0.3995 0.3555 0.5922 0.2382 0.1300 0.0682 0.8525 0.8541 0.9150 0.2522 | 0.4226 0.3 0.0081 0.0285 0.4237 0.0887 | 0.0029 0 0.4028 0 0.2000 0 0.2400 0 | 0.5024 0.4000 0.1249 0.0470 0.2000 0.0245 0.0345 0.0245 |
| 435 Carbonyl reductine (NADPH) 1 Cbr1 436 Unconvertional myonin-is Myoto 437 Spicing factor 3A subunit 1 SSBs1 438 Assortation enricotransferans. mito Go2 439 Profiterator-associated protein 2 Psi2g4 | CORT MOUSE MYOIC MOUSE SEAR MOUSE AATM MOUSE PASSA MOUSE | 31 kDa 90% 122 kDa 36% 59 kDa 0% 47 kDa 66% 44 kDa 100% | 91N 91N 90.37 52N 32N 41.07 0N 0N 0.07 75N 68N 59.7 100N 100N 100.07 | 5 100 90 90 N 55N 27N 580 N 56N 100N 100N N 56N 100N 100N N 96N 100N 100N | 5 975 05 5 4555 95 5 9555 55 5 2595 65 5 005 05 | 0% 0% 0.5 20% 8% 12.7 0% 0% 1.7 2% 5% 4.7 0% 0% 0.5 | 75 815 965 75 555 865 75 556 860 75 05 05 75 758 758 75 1005 1005 | 97% 91.3% 99% 75.4% 9% 0.0% 82% 77.8% 100% 900.0% | 29% 4% 28% 14% 20% 100% 20% 20% 0% 0% | 2% 8.7% 0% 10.8% 100% 100.0% 8% 16.4% 0% 0.0% | 0% 0% 27% 0% 0% 0% 5% 5% 0% 0% | 0% 0.0% 11% 12.8% 0% 0.0% 8% 5.8% 0% 0.0% | 90% 1 47% 9% 92% 1 100% 1 | 90% 100% 900 41% 24% 40 5% 10% 7 90% 86% 92 90% 100% 100 | 2% 0% 2% 34% 2% 91% 2% 91% 2% 0% | 9% 9% 22% 27% 96% 87% 9% 14% 9% 9% | 0.0% 0% 31.2% 19% 91.2% 0% 7.2% 0% 0.0% 0% | 9% 37% 2 9% 9% 9% | 0% 0.0% 1/ 5% 28.0% 2% 1.1% 0% 0.0% 1/ 0% 0.0% 1/ | 00% 96% 10% 62% 2% 96% 17% 96% 10% 100% | 20% 98.8% 20% 70.2% 19% 13.2% 95% 95.7% 100% 100.0% | 05 45 75 185 885 915 25 25 05 05 | 0% 1,2% 0% 7,0% 81% 85,8% 5% 3,5% 0% 0,0% | 0% 0% 14% 24% 0% 0% 0% 2% 0% 0% | 0% 0.0 20% 22.5 0% 0.0 0% 0.8 0% 0.0 | % 0.8721 % 0.0533 % 0.1075 % 0.1075 | | | | | | 733 0.4787 0 226 0.4226 0 342 0.4226 0 | 0.0782 0.3656 0.8257 0.0363 0.0363 |
| 440. Reculator of nonsense transcribt Upf1 441. Aceth4CoA acethfransferase, ml 442. Twosine-978A losses, cybolaser Yars 443. 6-shosshoolucorate dehvdroom; Pgd 444. T-complex protein 1 subunit zeta. College 445. ACP worthase subunit camma, ml Addiction. | RENT! MOUSE THE MOUSE SYYC MOUSE SPEC MOUSE TOPZ MOUSE 1 ATPG MOUSE | 124 KDs 9% 45 KDs 91% 59 KDs 97% 53 KDs 100% 58 KDs 64% 33 KDs 60% | 12% 50% 11.0° 96% 97% 94.9° 100% 98% 98.2° 100% 100% 100.0° 82% 80% 75.4° 60% 58% 52.2° | 56 88% 76% 76% 56 9% 4% 2% 56 2% 0% 2% 56 0% 0% 0% 57 29% 28% 17% 56 58% 28% 28% 26% | % 81.9% 2% % 5.1% 0% % 1.8% 0% % 0.0% 0% % 21.1% 2% | 8% 20% 7.0 0% 0% 0.0 0% 0% 0.0 0% 0% 0.0 0% 2% 3.5 2% 2% 2.6 | PN 0N 12N PN 97% 97% 97% PN 100N 200N PN 100N 200N PN 50N 92N PN 630 72N | 985 6.1% 985 96.3% 100% 900.0% 100% 900.0% 100% 80.3% 71% 68.9% | 96% 82% 2% 2% 0% 0% 0% 0% 36% 9% 35% 24% | 81% 86.4% 6% 3.7% 6% 0.0% 6% 0.0% 6% 14.9% 26% 28.5% | 6% 7% 0% 0% 0% 0% 0% 0% 14% 0% 2% 2% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 4.8% | 95% 1 100% 1 100% 1 72% | 10% 8% 9 00% 100% 98 00% 100% 100 00% 100% 100 75% 58% 68 | 0% 84% 4% 5% 0% 0% 0% 0% 8% 21% 8% 22% | 72% 82% 0% 0% 0% 0% 0% 0% 20% 22% 42% 28% | 78.7% 6% 1.6% 0% 0.0% 0% 0.0% 0% 24.2% 7% 34.2% 0% | 19% 1 0% 0% 0% 5% | 2% 12.3% 20% 20% 20% 0.0% 20% 20% 20% 20% 20% 20% 20% 20% 20% 2 | 12% 6% 10% 100% 10% 100% 10% 100% 10% 86% | 40% 21.9% 100% 100.0% 100% 100.0% 100% 100.0% 95% 89.4% 20% 66.8% | 72% 92% 0% 0% 0% 0% 0% 0% 6% 12% 36% 34% | 60% 74.4% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 33.2% | 7% 6% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 3.8 0% 0.0 0% 0.0 0% 0.0 5% 4.7 | % 0.5375 % 0.5375 % 0.1872 % 0.7860 | 0.0316 0.40 | 98 0.6154 | 0.6299 | 0.6018 | 0.3324 0.9 0.0994 0.9 0.4917 0.8 0.2899 0.8 | 230 0.1224 0 | 0.202 0.906 0.0076 0.0079 |
| 446 Threorine-PRVA brass. cvlooks Tars 447 Junction piskoglobin Jup 448 Selbolin Gen 449 Gastookne-2 Ginz 450 Cingulin Cgn | SYTC MOUSE PLAK MOUSE GELS MOUSE GROW MOUSE CING MOUSE | 83 kDs 100% 82 kDs 0% 85 kDs 100% 20 kDs 136 kDs 0% | 100% 91% 97.0° 5% 4% 2.8° 100% 100% 100.0° 0% 0% 0.0° | % 0% 0% 9% % 18% 22% 65% % 0% 0% 0% % 90% 96% 100% | N 30% ON N 383% 82% N 90% ON N 97.7% 28 | 0% 0% 0.0 64% 32% 58.5 0% 0% 0.0 | 7% 100% 100% 7% 12% 11% 7% 100% 100% | 100% 100.0% 18% 13.9% 100% 100.0% | 0% 0% 12% 22% 0% 0% 100% 100% | 0% 0.0% 18% 17.6% 0% 0.0% 100% 100.0% | 0% 0% 75% 67% 0% 0% | 0% 0.0% 64% 68.4% 0% 0.0% | 92% 92% 92% 93% 93% | 00% 100% 100 17% 11% 16 80% 82% 84 67% 53% 63 0% 0% 0 | 0% 0% 5% 17% 6% 9% 5% 18% 0% 100% | 0% 0% 25% 16% 20% 18% 17% 20% 100% 96% | 0.0% 0% 19.2% 61% 15.4% 0% 18.1% 12% 58.7% 0% | 9% 58% 7 9% 17% 2 9% | 0% 0.0% 1/ 4% 64.4% 0% 0.0% 7% 18.4% | 10% 100% 15% 24% 15% 89% 15% 64% | 100% 100.0% 30% 29.7% 92% 91.2% 26% 67.1% 26 5.5% | 0% 0% 17% 29% 6% 11% 19% 18% 94% 92% | 0% 0.0% 12% 16.5% 9% 0.8% 7% 14.4% 92% 92.2% | 0% 0% 48% 57% 0% 0% 20% 18% 0% 4% | 6% 0.0 57% 53.8 6% 0.0 17% 18.5 6% 1.3 | % 0.4226 % 0.0173 % | 0.0470 0.04 0.1063 0.04 0.6412 0.0228 | 26 05 0.0195 10 0.0292 0.0228 | 0.2802 | 0.8649 0.2417 0.4226 0.4800 0.3078 0.1663 0.8410 0.4523 0.8414 0.6213 0.2500 0.1022 0.4226 | 0.7529 0.5 0.0292 | 957 0.1454 0 0.9832 054 0.9792 0 | 0.7579 0.0330 0.6213 0.4226 |
| 401 - 905 recogning protein 515 PSP 13 402 Symmin 59 mm 59 mm 643 Periode Pro | SYNEM MOUSE PRAY MOUSE PRAY MOUSE SPRINT MOUSE REAN MOUSE EIFSL MOUSE | 173 KDs 925, 173 KDs 95, 146 KDs 1995, 167 KDs 95, 25 KDs 175, 67 KDs 625, | 0% 0% 0% 0.07 0% 0% 0% 0.07 0% 0% 0% 0.07 0% 0% 0% 0.07 | 5 600 200 200 200 5 500 500 500 500 500 500 | 95 91.9% 98 98 93.9% 59% 5 76.1% 25% 8 92% 92% | 0% 0% 0% 15.7 0% 0% 15.7 2% 2% 2% 20.5 | 75 225 225 25 25 25 25 25 25 25 25 25 25 | 100% 0% 0.0% 11% 3.7% 57% 57.3% | 27% 17% 57% 100% 100% 100% 77% 50% 0% 8% | 0% 100% 100.0% 78% 68.2% 4% 4.2% | 0% 0% 0% 0% 22% 50% 42% 22% | 0% 0.0% 0% 0.0% 11% 28.1% 29% 38.4% | 200 200 200 200 200 820 | 0% 0% 0 100% 0% 0% 0% 7% 2% 12 7% 7% 77 | 25 205 25 1005 26 65 25 05 | 100N 100N 0N 200N 200N 86N 87N 0N 8N | 79.1% 10% 2.0% 18% | 9% 9% 2% 25% 1 | 08 0.0% 0 08 0.0% 08 0 08 7.9% 7 | 95 95 95 95 95 95 | 20% 14.9% 82% 50.7% | 95 95% 100% 96% 82% 24% 0% 0% | 72% 75.0% 0% 9.0% | 0% 6% 0% 4% 5% 16% 0% 14% | 2% 9.1 2% 9.1 12% 10.3 | v 02308 | 0.50 | 00 0.0770 | 0.4226 | 1.0000 | 0.4 | 0.4226 226 0 373 0.7755 0 300 0.1260 0 | 0.4225 0.4549 0.2357 0.1202 0.0169 |
| 457 Cylochrome b - cl. comeiex subur. Ugorle 458 Dihedrolloori dehvidroomase. mi Did 459 E3 subsultin-crotein licese RNF2 Rvf21; 450 ATPass family AAA domain-cont Alaco. 461 Cathepsin D. Clad. | DLDH MOUSE DLDH MOUSE DRIPT MOUSE ATADS MOUSE CATO MOUSE | 2910a 28% 5410a 74% 52510a 9% 6710a 9% 4510a 72% | 26% 31% 27.5° 79% 82% 78.6° 18% 9% 11.5° 86% 85% 80.4° | \$ 698 228 658 \$ 268 218 179 \$ 828 268 889 \$ 208 168 159 | S 68.8% 2% S 21.4% 0% S 61.2% 9% S 18.2% 2% | 6% 6% 53 6% 6% 53 6% 6% 53 | PS 68 22% PS 758 92% PS 48 80 PS 768 90% | 25% 19.5% 91% 85.0% 12% 7.8% 92% 85.1% | 91% 68% 25% 8% 92% 85% 24% 65% | 25% 77.9% 9% 14.0% 88% 88.4% 8% 12.8% | 2% 5% 0% 0% 4% 8% 0% 2% | 0% 2,0% 0% 0,0% 0% 1,0% 0% 1,1% | 4% 100% 1 100% 0% 88% | 0% 10% 4 00% 100% 500 0% 0% 0 89% 85% 87 | 8% 87% 0% 0% 0% 0% 6% 4% 12% | 98% 90% 0% 0% 200% 92% 90% 11% 15% | 95.7% 9% 0.0% 0% 0.0% 92.7% 5% 12.5% 0% | 2% 9% 7% 1 | 0% 6.9% 0% 0.0% 1/ 0% 7.3% 1/ 0% 0.0% | 6% 10% 10% 100% 0% 0% 12% 89% | 14% 13.7% 100% 100.0% 100% 7% 2.4% 100% 94.2% | 0% 82% 0% 0% 0% 88% 91% 2% 11% | 92% 79.1% 0% 9.0% 0% 0% 50% 0% 50% 0% 50% | 16% 2% 0% 0% 0% 12% 9% 0% 0% | 5% 7.8 6% 0.0 6% 11.7 6% 0.0 | % 0.3259 % 0.3259 % 0.3256 % 0.4254 | 0.0036 0.00 0.01 0.5000 0.4226 0.05 0.1492 0.20 | 45 0.4389 20 0.1349 49 0.1781 64 0.2591 | 0.3055 0.3299 0.0657 0.4307 | 0.2240 0.0033 0.0120 0.5000 0.2134 0.0249 0.1492 0.1608 | 0.9002 0.4 0.1349 0.6 0.6163 0.3 0.3509 0.9 | 222 0.1046 0 509 0 | 0.4736 0.3088 0.7995 0.0519 0.4226 0.4226 0.7201 0.1940 |
| 463 AP-2 complex suburit bets Ap3h 1 464 Annuin A7 Ansu7 465 Sec1 family domain-containing o Sch1 466 AP-2 complex suburit sights-2 Ap3h2 467 Sideroflatin-3 Stes3 | AP281 MOUSE SOFD! MOUSE SOFD! MOUSE AP2A2 MOUSE SFXNG MOUSE | 105 kDa 75% 50 kDa 60% 72 kDa 34% 104 kDa 72% 35 kDa 28% | 80% 52% 69.3° 27% 30% 32.2° 27% 32% 34.0° 60% 64% 65.5° 26% 29% 24.3° | 5 0N 0N 12N 5 0N 0N 12N 5 52N 57N 60N 5 42N 42N 52N 5 9N 20N 9N 5 56N 52N 75N | % 3.9% 25% % 60.0% 7% % 45.8% 24% % 9.4% 18% % 61.1% 17% | 20% 25% 25.5 7% 20% 7.5 21% 12% 19.4 20% 27% 25.1 21% 6% 14.1 | 7% 67% 60% 7% 23% 25% 25% 7% 42% 40% 7% 67% 72% 7% 47% 46% | 100% 75.6% 21% 29.7% 57% 46.3% 100% 79.4% 53% 48.6% | 0% 0% 32% 60% 29% 27% 0% 0% 29% 21% | 0% 0.0% 28% 43.9% 2% 19.9% 0% 0.0% 6% 18.7% | 23% 40% 23% 15% 28% 23% 28% 23% 22% 29% 24% 22% | 0% 24.4% 21% 25.4% 62% 33.8% 0% 20.6% 41% 32.7% | 59% 59% 40% 67% 20% | 56% 60% 61 22% 24% 25 50% 42% 44 56% 56% 60 22% 22% 21 | 0% 0% 0% 61% 0% 22% 4% 2% 8% 22% | 9% 9% 52% 59% 6% 52% 2% 7% 35% 44% | 0.0% 41% 57.5% 19% 28.2% 28% 4.3% 21% 37.0% 48% | 36% 6 16% 1 50% 29% 2 42% 2 | 0% 39.0% 7% 17.5% 5% 27.8% 7% 35.3% 2% 41.2% | 985 795 135 355 006 806 126 756 176 665 | 82% 80.0% 42% 33.4% 75% 78.7% 82% 79.7% 28% 40.7% | 0% 0% 68% 56% 0% 0% 0% 4% 15% 26% | 0% 0.0% 30% 47.9% 0% 0.0% 0% 1.4% 11% 17.3% | 22% 21% 29% 9% 20% 20% 19% 21% 48% 20% | 17% 20.0 18% 18.7 25% 21.7 18% 19.5 50% 42.6 | % 0.6267 % 0.6267 % 0.1528 % 0.3130 | 0.0013 0.45 0.2970 0.25 0.0019 0.05 0.0120 0.35 0.0070 0.46 | 52 0.7543 11 0.5998 05 0.0179 49 0.9811 90 0.0532 | 0.4226 0.1782 0.1032 0.0010 0.0126 | 0.4226 0.1713 0.6233 0.2067 0.3688 0.2310 0.0725 0.0553 | 0.2211 0.000 | 733 0.0013 0 783 0.8554 6 913 0.6548 0 145 0.0180 0 567 0.8092 0 | 0.0000 0.7543 0.0002 0.4006 0.5860 0.1486 0.0071 0.9251 0.0123 0.3001 |
| 460 Glucine amidinotransferase, milo Galtin 460 Eukarvolic transistion initiation fo ElDh 470 LIM domain and actin-binden on Limst 471 Inocitate deliverocenase INADP (bht 472 Cutodrome c1, heme cristein, m Cycl. 473 Streetin-1 bene cristein | EIF3H MOUSE LIMAT MOUSE LIMAT MOUSE CYT_MOUSE CYT_MOUSE | 48 kDs 82% 40 kDs 22% 84 kDs 0% 47 kDs 100% 35 kDs 52% 110 kDs 42% | 92% 94% 89.5° 21% 21% 27.9° 0% 0% 0.0° 100% 100% 100.0° 50% 47% 50.0° 50% 47% 40.1° | % 17% 8% 6% % 62% 56% 58% % 100% 100% 100% % 0% 0% 0% % 35% 32% 35% | % 10.5% 0% % 58.3% 17% % 100.0% 0% % 0.0% 0% % 34.6% 12% | 0% 0% 0.0 12% 12% 12% 13.8 0% 0% 0.0 17% 12% 15.4 | PN 94N 95N PN 24N 34N PN 0N 0N 100N 100N PN 150N 44N PN 45N 44N | 97% 95.4% 41% 29.7% 0% 0.0% 100% 100.0% 61% 46.9% | 5% 5% 52% 57% 100% 100% 0% 0% 34% 28% | 3% 4.8% 34% 47.5% 100% 100.0% 0% 0.0% 11% 20.8% | 0% 0% 28% 29% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 25% 22.7% 0% 0.0% 0% 0.0% 28% 32.2% | 92% 1 45% 22% 500% 1 25% | 00% 94% 95 42% 55% 47 20% 8% 17 00% 97% 99 27% 50% 34 | 0% 55% 0% 55% 0% 77% 0% 0% 1% 56% | 0% 6% 57% 36% 80% 92% 0% 2% 45% 42% | 5.0% 0% 49.4% 0% 82.9% 0% 1.0% 0% 48.2% 19% | 0% 0% 0% 0% 27% | 0% 0.0% 1 9% 3.0% 0% 0.0% 0% 0.0% 7% 17.7% | 00% 12% 12% 12% 12% 12% 12% 12% 12% 12% 12 | 50% 37.5% 22% 24.5% 100% 58.8% 30% 25.9% | 20% 25% 22% 25% 28% 22% 2% 2% 25% 64% 25% 54% | 0% 52.8% 75.9% 0% 1.2% 20% 39.8% 15.7% | 0% 12% 12% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 9.7 0% 0.0 0% 0.0 50% 33.3 | % 0.7835 % 0.7835 % 0.7286 % 0.7286 | 0.5077 0.01 0.2706 0.00 0.8429 0.43 0.4640 0.17 0.1507 0.00 | 50 0.0510 50 0.6123 57 0.0050 26 0.1852 59 0.1073 57 0.0404 | 0.1072 | 0.1942 0.2586 0.8190 0.3033 0.2706 0.0007 0.8429 0.4226 0.5901 0.0772 | 0.7502 0.0 0.7502 0.0 0.0050 0.1852 0.2757 0.0 0.0119 0.9 | 988 0.3292 0 480 0.3559 0 524 0.4530 0 | 0.7309 0.9434 0.7102 0.7270 |
| 474 Palladin Pald 475 Chillinamovinish NETUR-Invoic Capil 476 Verenbe renish sortinamovini Vgs.18 477 Helerocensous mucker riborucis Hompl 478 Accinine—659A Josep, cytochem Rans | PALLD MOUSE CANDI MOUSE VPS18 MOUSE HNRPL MOUSE SYRC MOUSE | 152 KDs 0% 136 KDs 100% 110 KDs 0% 54 KDs 25% 76 KDs 92% | 0% 99% 95.11 0% 0% 0.07 35% 44% 34.07 89% 87% 89.7 | \$ 000 000 000 000 000 000 000 000 000 0 | 95 955 95 5 41.15 525 5 29.55 65 5 1.55 45 | 0% 4% 11% 4.5 67% 60% 58.5 5% 6% 5.8 11% 11% 8.8 | 0% 95% 95% 95% 95% 95% 95% 95% 95% 95% 95 | 0% 100% 97.0% 0% 0.0% 38% 41.1% 94% 91.9% | 200% ON ON 67% 60% 60% ON ON ON | 100% 0% 0.0% 60% 62.2% 62% 58.9% 0% 0.0% | 0% 4% 5% 2% 40% 0% 0% 14% 5% | 0% 3.0% 0% 37.8% 0% 0.0% 6% 8.1% | 2% 100% 1 0% 45% 96% | 5% 5% 5 90% 100% 900 0% 0% 0 54% 52% 52 95% 92% 94 | 7% 90% 0% 0% 0% 57% 1% 62% 7% 0% | 88% 88% 0% 0% 42% 56% 42% 36% 0% 0% | 55.7% 2N 0.0% 0N 51.9% 42N 40.3% 12N 0.0% 4N | 7% 9% 57% 4 4% 5% | 7% 5.5% 0% 0.0% 1/2 1/2 1/2 1/2 1/2 1/2 1/2 1/2 1/2 1/2 | 2% 8% 10% 100% 0% 0% 6% 62% 100% | 0% 5.7% 100% 100.0% 0% 0.0% 44% 59.4% 100% 100.0% | 80% 90% 0% 0% 55% 56% 25% 22% 0% 0% | 88% 85.8% 0% 9.0% 71% 60.5% 50% 39.5% 0% 9.0% | 8% 2% 0% 0% 45% 44% 9% 4% 0% 0% | 12% 7.5 0% 0.0 29% 39.5 6% 6.0 0% 0.0 | % 0.6292 % 0.4104 % 0.5391 | 0.7942 0.01 0.20 0.7329 0.00 0.0333 0.00 | 0.1979 97 0.1986 33 0.1392 91 0.0992 | 0.0324 0.9305 0.1836 | 0.4252 0.6018 0.2915 0.1806 0.9062 0.0542 0.1835 | 0.5495 0.7929 0.0500 0.8 | 0.6072 0 202 0 204 0.2915 0 351 0.6193 0 545 0.0333 0 | 0.0356 0.1313 0.2697 0.1956 0.1806 0.7929 0.5492 0.0565 0.2409 0.0992 |
| 401 JOSEPH AL JO | SYSC MOUSE 1 B3AT MOUSE 214 TM214 MOUSE 1 BMOUS MOUSE 1 BMOU MOUSE | 30 kDa 92k 55 kDa 92k 103 kDa 52k 76 kDa 74k 42 kDa 19k 34 kDa 21k | 97% 190% 95.7 47% 41% 45.9 91% 88% 84.3 19% 0% 12.7 21% 22% 28.1 | 5 28 28 28 28 5 5 5 28 28 28 28 28 28 28 28 28 28 28 28 28 | 5 24.15 135 5 2.05 428 5 1.05 248 5 1.05 58 5 22.05 58 5 22.05 68 | 0% 0% 05 52% 52% 51. 9% 20% 14. 5% 5% 43 50% 22% 42. | 75. 925. 925. 75. 925. 925. 75. 205. 95. 75. 805. 805. 75. 185. 55. | 905 47.55 1005 95.85 505 25.45 805 82.45 85 10.05 275 30.55 | 975 25 5% 28 98 98 28 98 82% 91% 21% 12% | 0% 24% 0% 0.0% 0% 0.0% 0% 0.0% 92% 00.5% 11% 15.1% | 2% 0% 80% 92% 18% 20% 0% 5% 57% 52% | 935 24.25 93 2.85 935 73.65 145 17.05 93 1.25 525 54.45 | 100% 1 100% 1 100% 20% 22% | 925 895 91 926 1006 900 526 256 41 826 926 88 126 126 15 76 66 4 | 25 05 05 25 05 25 25 215 | 0% 0% 0% 2% 0% 2% 0% 0% 75% 86% 75% 38% | 0.0% 0% 1.1% 61% 0.0% 10% 78.2% 4% 22.0% 78% | 25 25 495 6 175 75 26 855 5 | 05 0.0% 1 15 57.0% 95 11.9% 45 5.0% 65 73.5% | 0% 100% 12% 57% 16% 14% 5% 6% | 20% 100.0% 52% 44.0% 21% 23.9% 12% 11.4% | 9% 9% 9% 9% 9% 9% 54% 86% 5% 6% | 0% 0.0% 11% 3.0% 26% 75.1% 0% 3.7% | 9% 9% 78% 42% 9% 9% 9% 9% | 9% 0.0 37% 52.5 9% 0.0 88% 84.9 | 0.7897 0.7897 | 0.8721 0.44 0.57 0.4016 0.60 | 45 0.3441 34 80 0.1571 | 0.4226 0.3923 0.4703 | 0.5659 0.7178 0.1900 0.7967 0.5931 | 0.4226 0.2 0.6 0.1887 0.1 | 0.7620 0 238 0 709 0.0436 0 | 0.4226 0.2031 0.2078 0.7080 0.7893 0.4226 0.0528 0.0003 |
| 465 Accessio A1 Asset 466 Cytosel swrinopoptidase Lap3 467 ADC-sbowylation factor 1 Art 468 Carbowylations of C Cests 469 Gold researchite-stacking proteil Gorag | ANKAL MOUSE AMPL MOUSE APPL MOUSE ESTIC MOUSE GORSO MOUSE ANGAL M | 3910a 82% 5510a 98% 2110a 97% 5110a 100% 4710a 20% | 98% 100% 90.7 97% 100% 98.7 97% 92% 95.4 100% 100% 100.0 15% 25% 19.7 | \$ 12% 12% 09 \$ 2% 2% 2% 09 \$ 0% 0% 09 \$ 0% 0% 09 \$ 50 0% 09 | \$ 9.7% 0% \$ 1.7% 0% \$ 0.0% 2% \$ 0.0% 0% \$ 47.9% 20% | 0% 0% 0.0 0% 0% 0.0 2% 8% 4.6 0% 0% 0.0 26% 23% 32% | 75 1005 1005 75 945 1005 75 925 925 75 1005 1005 75 225 100 | 100% 100.0% 100% 98.1% 100% 95.0% 100% 100.0% 26% 22.9% | 0% 0% 6% 0% 0% 0% 0% 0% 40% 46% | 0% 0.0% 0% 1.9% 0% 0.0% 0% 0.0% 27% 41.0% | 0% 0% 0% 0% 8% 7% 0% 0% 27% 32% | 0% 0.0% 0% 0.0% 0% 5.0% 0% 0.0% 2% 35.3% | 200% 1 200% 1 200% 1 200% 1 | 98% 92% 85 90% 100% 900 90% 96% 98 90% 100% 90 22% 12% 22 | 5% 10% 5% 0% 8% 0% 5% 0% 1% 66% | 12% 11% 0% 0% 0% 0% 0% 0% 46% 62% | 11.4% 2% 0.0% 0% 0.0% 0% 0.0% 0% 50.2% 22% | 2% 9% 9% 9% 2% 2% 2 | 28 2.1% 08 0.0% 10 48 1.2% 08 0.0% 10 7% 27.7% | 0% 86% 0% 100% 17% 100% 0% 100% 5% 100% | 88% 88.7% 100% 100.0% 100% 99.0% 100% 100.0% 20% 10.0% | 6% 12% 0% 0% 0% 0% 0% 0% 28% 62% | 10% 9.3% 0% 9.0% 0% 9.0% 0% 9.0% 0% 9.0% | 4% 2% 9% 9% 9% 9% 9% 9% 46% 25% | 2% 2.5 6% 0.0 6% 1.0 6% 0.0 40% 37.1 | % 0.9354 % 0.9354 % 0.8891 % 0.4255 | 0.3072 0.53 0.18 0.8657 0.13 0.3515 0.73 0.1319 0.43 | 92 0.0771 | 0.2144 | 0.7013 | 0.5883 0.2 | 296 0.2753 0 | 0.2775 0.8117 |
| 491 Electron transfer flavorotein sub Effi 492 495 ribosomal protein 523 Rps23 493 Drau homolos subfamily C ment Dray; 494 Desmoglén-2 495 Probable ATP-dependent RNA hy Didn't | ETFB MOUSE RS23 MOUSE DNIC3 MOUSE DSG2 MOUSE DOX17 MOUSE | 28 kDs 92% 16 kDs 45% 57 kDs 77% 122 kDs 0% 72 kDs 14% | 92% 97% 94.1° 52% 47% 47.9° 80% 86% 81.1° 0% 0% 0.0° 14% 20% 15.8° | % 8% 8% 2% % 89% 44% 47% % 89% 44% 47% % 0% 0% 0% 0% % 77% 82% 76% | % 5.9% 0% % 46.5% 6% % 18.2% 2% % 0.0% 200% % 78.7% 9% | 0% 0% 0.0 4% 6% 5.0 0% 0% 0.1 20% 90% 100.0 2% 4% 5.5 | 7% 92% 98% 7% 52% 52% 52% 7% 78% 86% 7% 0% 0% | 98% 95.1% 52% 52.1% 89% 84.4% 0% 0.0% 7% 7.3% | 7% 2% 42% 40% 22% 14% 0% 0% 82% 86% | 2% 3.9% 28% 40.4% 11% 15.6% 0% 0.0% 79% 82.8% | 0% 0% 5% 8% 0% 0% 100% 100% 11% 5% | 0% 0.0% 10% 7.5% 0% 0.0% 200% 100.0% 14% 10.0% | 900% 1 36% 92% 0% | 00% 100% 900 28% 42% 39 92% 94% 92 0% 0% 0 9% 16% 13 | 0% 0% 0% 55% 8% 6% 0% 20% 7% 72% | 0% 0% 54% 47% 7% 6% 25% 25% 79% 75% | 0.0% 0% 51.9% 9% 7.2% 0% 23.3% 80% 75.3% 12% | 0% 8% 1 0% 75% 7 | 0% 0.0% 1 1% 9.1% 1 0% 0.0% 1 5% 76.7% 9 9% 11.0% | 17% 97% 15% 32% 10% 91% 6% 6% 12% 26% | 100% 97.9% 67% 41.7% 90% 93.6% 12% 7.9% 29% 31.8% | 2% 2% 75% 67% 0% 9% 22% 72% 52% 69% | 0% 2.1% 22% 58.3% 10% 6.4% 62% 57.9% 50% 56.9% | 0% 0% 0% 0% 0% 0% 61% 17% 16% 7% | 0% 0.0 0% 0.0 0% 0.0 25% 34.3 11% 11.4 | % 0.4173 % 0.1224 % 0.4608 % 0.4608 | 0.1835 0.00 0.8529 0.00 0.8194 0.00 0.0767 0.0322 0.55 | 97 0.3920 59 0.4994 94 0.1146 0.0767 83 0.0239 | 0.4173 0.0466 0.5293 | 0.1835 0.0097 0.8685 0.1295 0.8194 0.0175 0.1156 0.6651 0.0620 0.2994 | 0.3920 0.2945 0.2 0.1146 0.4 0.6472 0.0376 0.2 | 732 0.0080 0 226 0.0876 0 926 0.9134 0 | 0.0354 0.0244 0.4225 0.0051 0.0405 0.0730 0.7363 |
| #86 Peripitation Ppi #87 Calmodulin Ppi #88 MATH Ashovimensus Inhimitore Nglyfal #89 Evenims (**Child merhandess hale Pccb #80 MATH Ashovimensus Inhimitore Nglyfal #81 Annal Ashovimensus | PEPL MOUSE CALM MOUSE NOUAL MOUSE POOR MOUSE NOUSE MOUSE ADDAM MOUSE | 204 KDs 0% 17 KDs 74% 20 KDs 42% 58 KDs 67% 53 KDs 54% 45 KDs 100% | 0% 30% 6.P 72% 36% 74.2° 36% 47% 42.0° 77% 66% 69.0° 59% 48.3° 100% 100% 100.0° | % 100% 100% 80% % 35% 28% 28% 28% % 50% 55% 47% % 30% 22% 32% % 30% 30% 30% 60% | N 93.3% ON N 25.8% ON N 90.6% RN N 28.2% AN N 27.9% 21% | 0% 0% 0.0 0% 0% 0.0 9% 5% 7.3 0% 2% 2% 2.3 0% 0% 0.0 | 7% 0% 0% 0% 7% 82% 89% 7% 27% 42% 7% 56% 85% 7% 54% 52% | 0% 0.0% 85% 85.9% 25% 35.1% 96% 85.0% 53% 53.1% | 100% 100% 17% 11% 62% 48% 15% 15% 0% 14% | 200 100.0% 25% 14.1% 75% 62.0% 0% 10.1% 12% 8.7% | 0% 0% 0% 0% 0% 9% 10% 0% 66% 22% | 0% 0.0% 0% 0.0% 0% 2.9% 2% 3.9% 2% 38.3% | 200 220 220 240 120 120 | 0% 9% 3 61% 62% 64 4% 9% 8 00% 100% 97 42% 18% 34 | 0% 100% 1% 26% 8% 26% 9% 6% 2% 0% | 20% 91% 26% 28% 88% 82% 0% 0% 8% 0% | 97.0% 8% 34.0% 3% 82.5% 9% 2.1% 6% 2.8% 52% | 9% 9% 9% 9% 52% 8 | 0% 0.0% 0% 1.9% 9% 8.7% 0% 0.0% 1/ 2% 63.0% | 6% 2% 6% 76% 6% 20% 10% 100% 9% 12% | 0% 2.7% 75% 75.8% 6% 13.7% 100% 100.0% 50% 27.1% | 92% 97% 26% 26% 82% 22% 9% 9% 9% 9% | 98% 95.5% 26% 24.2% 99% 90.7% 0% 0.0% 0% 0.0% | 2% 2% 0% 0% 2% 8% 0% 0% 81% 88% | 2% 1.8 0% 0.0 6% 5.5 0% 0.0 50% 72.9 | % 0.425 % 0.0001 % 0.3458 % 0.1169 % 0.6204 | 0.9433 0.04 0.3877 0.00 0.4226 0.00 0.5420 0.20 | 45 0.0005 15 0.0007 43 0.1668 70 0.1543 | 0.0091 0.2832 0.0492 0.1603 | 0.0752 0.0919 0.0750 0.0919 0.7656 0.0010 0.4226 0.0016 0.4226 0.1015 | 0.0255 0.1270 0.2 0.1836 0.5 0.1873 0.0 | 0.1953 0 912 0.1919 0 942 0 956 0.5474 0 | 0.1863 0.3482 0.4714 0.2177 0.3075 0.0511 0.0034 |
| 502 Cytichromic ciddae subunit 6: Costo 503 Serinelassinine-rich solcino fact Srsf7 504 Apha-1-anthypsis 1-3 Septi 505 T-combia scelein 1 subunit field Cost 505 GTP-AMP choshotosinferase A Ak3 | SRSF7 MOUSE SRSF7 MOUSE WIS ASATS MOUSE TOPO MOUSE KADS MOUSE | 8 kDa 44% 31 kDa 9% 45 kDa 82% 50 kDa 97% 25 kDa 54% | 45% 52% 47.0° 4% 11% 5.2° 82% 89% 55.1° 97% 95% 96.0° 48% 28% 46.7° | % 56% 55% 47% % 77% 28% 24% % 12% 18% 11% % 0% 0% 20 % 66% 52% 62% | S 52.4% ON S 76.5% 14% S 14.9% ON S 0.9% 2% S 53.3% ON | 0% 0% 0.0 17% 15% 15.1 0% 0% 0.0 2% 2% 3.1 | 7% 47% 58% 7% 0% 0% 7% 86% 100% 7% 100% 100% 7% 47% 51% | 995 57.9% 75 2.4% 82% 89.4% 100% 100.0% No. 58.1% | 52% 42% 28% 92% 54% 0% 0% 0% 52% 46% | 31% 42.1% 86% 85.4% 18% 10.6% 0% 0.0% 24% 41.9% | 0% 0% 22% 7% 0% 0% 0% 0% | 0% 0.0% 7% 12.2% 0% 0.0% 0% 0.0% | 25% 8% 82% 100% 1 82% 1 | 17% 25% 22 12% 10% 10 29% 86% 85 00% 97% 98 00% 79% 86 | 2% 76% 4% 84% 0% 12% 5% 0% | 82% 75% 72% 81% 8% 92% 0% 0% 0% 21% | 77.8% 0% 79.3% 8% 10.4% 4% 0.0% 0% 13.4% 0% | 0% 13% 1 3% 0% | 0% 0.0% 0% 10.4% 2% 3.6% 2% 1.1% 1/ 0% 0.0% | 7% 20% 12% 12% 12% 62% 10% 100% 17% 79% | 14% 17.0% 18% 17.0% 67% 70.0% 100% 100.0% 82% 77.2% | 82% 82% 68% 77% 10% 21% 0% 0% 22% 21% | 86% 83.0% 82% 76.0% 17% 19.1% 0% 0.0% 12% 22.7% | 9% 0% 9% 10% 7% 8% 0% 0% | 0% 0.0 0% 6.3 12% 10.3 0% 0.0 | % 0.2434 % 0.1378 % 0.5216 % 0.0004 % 0.3387 | 0.1964 0.00 0.1037 0.43 0.1351 0.75 0.4226 0.00 0.3559 0.01 | 28 0.0182 39 0.0151 50 0.0039 66 0.0039 | 0.2434 0.1697 0.5216 0.4226 0.3387 | 0.1964 0.8028 0.5648 0.4629 0.2883 0.1799 0.4226 0.3559 0.0999 | 0.0102 0.1910 0.5 0.3577 0.1567 | 0.3257 0 0.1005 0 0.4226 0 | 0.0678 0.3646 0.0628 0.0628 0.1976 |
| 500 Cultomic annyotise 3 Cab 500 Agrin Agrin Stoschalase Rho-Interes; Myrip 510 E3 ubiquito-protein ligase URPH Ubr4 511 Septin-7 Capric | AGRIN MOUSE MPRIP MOUSE URRY MOUSE 7-Sep SEPTY MOUSE 11 CAPRI MOUSE | 2018 MDa 88 116 MDa 98 572 MDa 75% 51 MDa 54% 78 MDa 12% | 0% 0% 287 0% 0% 0.07 5% 100% 83.37 5% 100% 83.37 5% 5% 46% 50.97 | 55 58 50 50 50 50 50 50 50 50 50 50 50 50 50 | 5 55.1% 22% 5 59.9% 14% 5 5.2% 0% 5 44.0% 2% | 50% 40% 41.1 8% 8% 10.1 25% 0% 8.3 0% 6% 4.4 | 7% 0% 0% 0% 7% 0% 0% 0% 7% 0% 0% 100% 7% 50% 100% 7% 50% 100% | 0% 0.0% 0% 0.0% 100% 06.7% 67% 55.0% 11% 12.8% | 28% 71% 200% 100% 50% 0% 50% 50% 91% 81% | 71% 73.5% 78% 92.6% 9% 16.7% 22% 44.4% 89% 87.2% | 22% 29% 0% 0% 50% 0% 0% 0% 0% 0% | 295 25.5% 225 7.4% 25 95.7% 25 95.7% 26 9.0% | 28 28 28 20 20 50 50 75 | 26 28 3 06 08 0 808 1008 9 518 548 55 78 108 7 | 0% 26% 0% 100% 2% 0% 1% 26% 2% 82% | 95 05 92 89 99 20 99 465 415 825 775 | 79.3% 19% 93.3% 0% 6.7% 0% 40.0% 5% 80.7% 10% | 9% 1 9% 1 9% 1 9% 2 11% 1 | 08 0.0% 1 18 17.7% 18 6.7% 08 0.0% 58 4.2% 28 11.2% | 75 115 95 95 75 505 75 625 45 95 | 6% 7.8% 6% 0.0% 82% 00.7% 68% 00.2% | 25 | 72% 75.4% 100% 93.5% 17% 23.6% 26% 28.9% 77% 83.8% | 21% 22% 12% 7% 12% 12% 12% 12% 12% 12% 2% 6% | 22% 21.8 2% 5.5 2% 9.7 6% 5.8 5% 2.7 | % 0.4225 % 0.6708 % 0.5224 % 0.3399 | 0.0000 0.94 0.0032 0.46 0.0358 0.33 0.1665 0.83 | 70 0.0372 42 1.0000 50 0.2139 12 0.8585 | 0.0129 0.7555 0.6556 0.9778 0.8495 | 0.0435 0.0049 0.9688 0.4570 0.1533 0.8838 0.0439 0.4249 0.5512 0.3641 | 0.2955 0.0 0.9219 0.7 0.7290 0.6 0.0973 0.1 0.5423 0.2 | 770 0.2406 0 555 0.9688 0 196 0.1917 0 209 0.1741 0 552 0.0087 0 | 0.0234 0.1550 0.4570 0.9219 0.4225 0.7232 0.9738 0.0039 0.2273 0.1911 |
| 513. T-complex protein 1 suburat eta. Cc7 514. 3-lestoarci-CoA triciase, mitocho Acasa2 515. Heat shock 70 kDs protein 4. Hepsel 516. 605 ribosomal protein L11. Rpi11 517. Prosporin Pasp 518. Cotracio: Silvermidetabutani | TOPH MOUSE THIM MOUSE HSP74 MOUSE RL11 MOUSE SAP MOUSE ALI I MOUSE | 50 kDa 81% 42 kDa 69% 94 kDa 96% 20 kDa 68% 61 kDa 100% | 895 90% 87.1° 796 796 75.7° 1006 200% 98.6° 71% 80% 72.8° 1006 200% 100.0° | % 19% 11% 10% % 23% 18% 14% % 4% 0% 0% 0% 30% 26% 18% % 0% 0% 0% | 5 12.9% ON 5 18.2% SN 5 1.4% ON 5 24.9% 26 6 0.0% ON | 0% 0% 0.5 6% 7% 6.1 0% 0% 0.0 2% 2% 2.1 0% 0% 0% 0.0 | PN 94% 95% PN 81% 100% PN 100% 100% PN 68% 80% PN 100% 100% | 100% 95.3% 92% 87.8% 100% 100.0% 94% 77.2% 100% 100.0% | 9% 5% 29% 0% 0% 0% 30% 18% 0% 0% | 0% 3.8% 14% 11.0% 0% 0.0% 12% 20.6% 0% 0.0% | 0% 0% 0% 0% 0% 0% 3% 2% 0% 0% | 0% 0.0% 2% 1.1% 0% 0.0% 2% 2.3% 0% 0.0% | 100% 1 100% 1 100% 1 82% 1 | 99% 92% 98 90% 100% 900 90% 100% 900 70% 78% 79 90% 95% 98 | 7% 0% 0% 0% 7% 18% 3% 0% | 4% 7% 9% 9% 9% 9% 9% 16% 17% 9% 9% | 3.9% 0% 0.0% 0% 0.0% 0% 17.1% 0% 0.9% 0% | 0% 0% 0% 5% 0% | 0% 0.0% 1/0 00 0.0% 1/0 00 0.0% 1/0 1/0 1/0 1/0 1/0 1/0 1/0 1/0 1/0 1/0 | 10% 100% 17% 96% 10% 100% 12% 92% 10% 100% | 100% 100.0% 100% 97.7% 100% 100.0% 82% 85.6% 100% 100.0% | 0% 0% 2% 0% 0% 0% 17% 8% 0% 0% | 0% 0,0% 0% 1,0% 0% 0,0% 18% 14,4% 0% 0,0% | 0% 0% 0% 4% 0% 0% 0% 0% 0% 0% | 0% 0.0 0% 1.3 0% 0.0 0% 0.0 | % 0.0026 % 0.1783 % 0.4226 % 0.5247 | 0.2137 0.00 0.1092 0.01 0.42 0.1837 0.18 0.4226 0.42 | 72 0.1885 74 0.2450 25 77 0.2403 26 52 0.4226 | 0.0626 0.3440 0.4226 0.5195 | 0.2137 0.0072 0.4226 0.0290 0.4226 0.4226 0.4226 0.1475 0.4226 0.4226 | 0.1985 0.2205 0.0 0.3586 0.7 | 658 0.4226 6 963 0.1872 0 0.4226 0 | 0.0408 0.9423 0.0367 0.0035 0.4226 |
| 519 Assartate—FRA licase, cylopias Dars 520 Colleges alpha—1/VIII) chain Collia 521 NADH dehydroossas fubiculion Side 522 Actin-related protein 3 Actin 523 Fibrillin-2 Fbr2 | SYDC MOUSE 1 COBAL MOUSE 10 NDUAA MOUSE APP3 MOUSE FEN2 MOUSE | 57 kDa 87% 74 kDa 27% 41 kDa 27% 47 kDa 89% 314 kDa 0% | 89% 34% 83.0° 21% 22% 30.0° 97% 94% 93.3° 0% | % 58% 56% 53% % 58% 56% 53% % 11% 2% 6% | % 15.4% 0% % 54.9% 15% % 6.7% 0% | 0% 0% 0.0 14% 16% 15.3 0% 0% 0.0 | 7% 100% 100% 7% 43% 50% 7% 65% 100% | 200% 900.0% 22% 42.2% 96% 95.4% | 0% 0% 32% 29% 5% 0% | 0% 0.0% 28% 34.4% 6% 3.6% | 20% 21% 0% 0% | 0% 0.0% 29% 23.3% 0% 0.0% | 200N 1 0N 27N 92N 92N | 00% 100% 100 0% 0% 0 60% 28% 35 92% 92% 93 0% 0% 0 | 0% 0% 0% 25% 2% 55% 2% 4% 0% 0% | 0% 0% 14% 22% 22% 21% 4% 5% 0% 11% | 0.0% 0% 24.2% 75% 39.5% 18% 4.6% 2% 3.5% 100% | 0% 86% 6 27% 3 2% 20% 8 | 0% 0.0% 1/7% 75.8% 11% 25.2% 12% 12.3% 19% 19.5% | 0% 100% 0% 0% 9% 42% 60% 96% | 000 100.0% 01 0.0% 691 55.4% 951 95.4% | 0% 0% 7% 11% 18% 42% 2% 2% 0% 0% | 0% 0.0% 20% 12.6% 12% 23.9% 2% 2.3% 0% 0.0% | 0% 0% 92% 89% 24% 17% 2% 2% 200% 100% | 206 0.0 806 87.4 196 19.6 316 2.3 1006 100.0 | % 0.0736 % 0.1966 % 0.3313 | 0.01 0.0901 0.33 0.0130 0.93 | 36 02 0.2150 87 0.6624 | 0.0738 | 0.0738 0.1688 0.2580 0.1749 0.0011 0.4110 0.4226 0.4226 | 0.3646 0.0 0.5395 | 0.908 870 0.2773 0 0.9731 0 0.4226 0 | 0.1112 0.3387 0.0005 0.0061 0.4226 |
| 524. Mysatin-10. Myhtil. 525. KH Areminumeteininn Billik-hind Khida 526. 495 ribosomal protein 527. Rps27. 527. Ig.mu chain C. region. Ighm. 528. 695 ribosomal protein 1,27a. Rps27. 529. 695 seider ribosomal protein P. Rps2. | MYNYO MOUSE NOORI MOUSE RS27 MOUSE IGHM MOUSE RL37A MOUSE RLA2 MOUSE | 350.0. 1001 351.0. | 0% 0% 0.07 16% 26% 24.57 100% 71% 90.57 24% 24% 20.97 72% 77% 75.97 | N 100% 80% 92% N 49% 60% 50% N 0% 0% 20% N 56% 30% 20% N 28% 20% 20% | S 91.0% ON S 55.9% 20% S 95% ON S 77.7% ON S 22.5% ON | 20% 7% 9.0 24% 15% 19.5 0% 0% 0.5 2% 2% 1.5 | PS 08 08 PS 226 178 PS 678 1008 PS 208 388 PS 730 828 | 0% 0.0% 28% 22.0% 100% 88.9% 28% 28.5% 28% 76.4% | 100% 100% 54% 65% 32% 0% 28% 62% 24% 19% | 98 93.3% 998 93.3% 998 59.7% 98 11.1% 228 70.7% 268 23.0% | 0% 0% 14% 17% 0% 0% 2% 0% | 20% 6.7% 22% 17.7% 2% 0.0% 0% 0.7% 0% 0.7% | 28% 28% 32% 52% 29% 82% | 298 228 29 88 08 2 228 128 23 628 628 50 78 258 23 | 4% 21% 8% 87% 4% 69% 8% 36% 7% 71% 2% 18% | 26% 21% 82% 85% 28% 82% 20% 28% 92% 65% 21% 20% | 21.9% 53% 84.9% 12% 76.6% 0% 31.2% 12% 76.3% 0% 19.8% 0% | 9% 1 9% 1 9% 1 | 6% 48.7% 5% 12.4% 0% 0.0% 0% 10.2% 0% 0.0% | 25 825 25 05 75 225 05 725 115 225 05 865 | 92% 74.0% 14% 10.0% 18% 20.7% 68% 67.0% 17% 20.4% | 8% 5% 55% 29% 72% 23% 35% 22% 89% 62% 10% 16% | 58 5.0% 71% 68.2% 50% 64.7% 22% 28.3% 82% 79.6% 14% 13.2% | 21% 24% 27% 21% 2% 2% 5% 0% 5% 0% 0% 0% | 14% 19.5 14% 21.0 12% 6.5 9% 4.7 9% 0.0 | % 0.7519 % 0.9190 % 0.9990 % 0.2995 | 0.2857 0.45 0.4460 0.83 0.1775 0.00 0.7760 0.78 0.0532 0.11 | 26 0.1863 12 0.3444 46 0.1787 24 0.3949 60 0.0310 | 0.8019 0.5739 0.9190 0.3084 0.8935 | 0.1415 0.4083 0.2509 0.6021 0.5559 0.1422 0.7780 0.8074 0.0532 0.3992 | 0.0517 0.5 0.0047 0.5 0.2574 0.3435 0.5 0.0272 0.4 | 0.0383 0.1340 0 212 0.2123 0 0.1597 0 | 0.6386 0.1533 0.0179 0.0707 0.0104 0.2159 0.1036 0.4226 0.1840 0.4226 |
| 530 Collagen alpha-2(VIII) chain Collisi 531 Reland sithydrogenase 1 Alphi) 532 Perceiredoile-5, mischondrial Printi 533 Prosphodycerale mutase 1 Papani 534 Leukotriene A-4 hydrolase Litelih | 2 COBAC MOUSE proxi AL1A1 MOUSE proxi MOUSE 1 PGAMI MOUSE LISTAL MOUSE | 67 kDa 92% 54 kDa 92% 22 kDa 92% 29 kDa 100% 59 kDa 100% | 94N 92N 92.67 95N 100N 96.07 100N 100N 100.07 100N 100N 100.07 | N 5% 6% 8% N 7% 5% 0% N 0% 0% 0% 0% | S 55% 28 S 40% 08 S 00% 08 S 00% 08 | 0% 0% 0.5 0% 0% 0.5 0% 0% 0.5 0% 0% 0.5 | 7% 97% 100% 7% 86% 100% 7% 100% 100% 7% 100% 100% | 100% 99.1% 96% 94.2% 100% 100.0% | 28 08 24% 08 08 08 08 08 | 0% 0.9% 4% 5.8% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 9% 100% 1 97% 97% 100% 1 | 0% 0% 0 00% 100% 100 92% 92% 94 97% 100% 98 90% 100% 100 | 0% 0% 0% 0% 2% 2% 2% 2% 0% 0% | 0% 0% 0% 0% 7% 7% 2% 0% 0% 0% | 0.0% 100% 0.0% 0% 5.7% 0% 1.8% 0% 0.0% 0% | 900% 50 9% 9% 9% 9% | 0% 100,0% 3 0% 0,0% 3 0% 0,0% 0% 0,0% 0% 0,0% 3 | 0% 0% 10% 100% 18% 89% 17% 97% 10% 100% | 0% 0.0% 100% 100.0% 97% 91.2% 100% 98.1% 100% 100.0% | 0% 0% 0% 0% 12% 11% 2% 2% 0% 0% | 0% 0.0% 0% 0.0% 2% 0.7% 0% 1.9% 0% 0.0% | 900% 200% 9% 0% 9% 0% 9% 0% | 200% 100.0 20% 0.0 20% 0.0 20% 0.0 20% 0.0 | % 0.0053 % 0.7176 % 0.7176 | 0.01 0.4431 0.53 0.9402 0.18 | 03 0.4226 59 0.6114 54 0.1856 | 0.0120 | 0.0002 0.4431 0.5359 0.9402 0.1854 | 0.4226 0.4 0.6194 0.1896 | 226 6 | 0.4226 |
| 336 PSN-binding potein 14 PSm1- 337 Protectin recutatory element-bind Preb 338 Succinate-CoA licase (GCP-for) Sucigi- 339 Cytoplasmic aconitate hydratase Aco1 540 Fathy acid-binding protein, adico (Fatip- | FABRY MOUSE | 15 kDa 100% | 0% 0% 0.0° 35% 31% 35.4° 88% 95% 90.4° 100% 100% 98.7° 100% 100% 100.0° | 5 100% 100% 100% S 00% 4% 4% S 12% 12% 5% S 4% 0% 0% S 0% 0% 0% | S 100.0% ON S 2.5% S9% N 9.5% ON N 1.3% ON N 0.0% ON | 0% 0% 0.0 62% 65% 62.0 0% 0% 0.0 0% 0% 0.0 | 75 05 05 75 295 275 75 885 975 75 965 1005 76 915 1005 | 0% 0.0% 66% 33.6% 100% 95.0% 100% 96.6% 100% 97.0% | 200% 100% 4% 0% 12% 2% 4% 0% 9% 0% | 100% 100.0% 11% 51% 0% 50% 0% 1.4% 0% 3.0% | 0% 0% 67% 23% 0% 0% 0% 0% 0% 0% | 0% 0.0% 46% 51.3% 0% 0.0% 0% 0.0% | 2% 25% 100% 1 100% 1 | 0% 2% 1 50% 42% 39 50% 100% 900 50% 100% 90% 90 50% 96% 90 | 4% 96% 2% 12% 0% 0% 0% 0% | 100% 96% 0% 0% 0% 0% 0% 0% 0% 0% | 97.2% 2% 4.2% 62% 0.0% 0% 0.0% 0% 1.2% 0% | 0% 50% 5 0% 0% | 25 1.4% 7% 56.5% 1/ 0% 0.0% 1/ 0% 0.0% 1/ 0% 0.0% 1/ | 0% 0% 10% 67% 10% 100% 10% 100% | 26 1.7% 2006 88.9% 2006 100.0% 2006 100.0% | 97% 100% 0% 0% 0% 0% 0% 0% 0% 0% | 97% 97.9% 0% 9.0% 0% 9.0% 0% 9.0% 0% 9.0% | 2% 0% 0% 22% 0% 0% 0% 0% | 0% 0.9 0% 11.1 0% 0.0 0% 0.0 | % 0.7892 % 0.3659 % 0.9784 % 0.4226 | 0.8613 0.18 0.0262 0.60 0.02 0.42 0.4226 0.43 | 35 0.4225 73 0.0223 80 0.3062 26 0.4225 26 0.4225 | 0.5277 0.3659 0.9784 0.4226 | 0.6998 0.1635 0.4226 0.7434 0.0580 0.4226 0.4226 | 0.1882 0.2567 0.9 0.3062 0.4226 0.4226 | 0.7035 0 412 0.0439 0 | 0.1835 0.4226 0.2724 0.0259 |
| 341 MADH dehvdroomsee fubiosinor Nduh/ 542 Myb-binding protein 1A Mybby 543 ATP-binding casselle sub-territy Abos 1 544 Selenium-binding protein 1 Selenti 545 Amesin A11 Assa1 546 Adenosine kinase A-6 | NDUVI_MOUSE ola MEBIA_MOUSE ABCE1_MOUSE pt SEP1_MOUSE 1 ANX11_MOUSE ADK_MOUSE | 51 KDa 52% 152 KDa 88% 67 KDa 72% 52 KDa 100% 54 KDa 22% 40 KDa 100% | 80% 52% 54.9° 86% 90% 87.9° 74% 60% 58.9° 100% 100.0° 15% 27% 21.0° 100% 100% 100.0° | 75 45% 27% 47% % 0% 0% 3% % 17% 20% 22% % 0% 0% 0% % 0% 0% 0% % 0% 0% 0% | 5 43.1% 2% 5 1.1% 12% 5 23.5% 10% 6 0.0% 0% 78.4% 0% 6 0.0% 0% | 2% 0% 2.0 14% 7% 11.0 6% 7% 7.6 0% 0% 0.0 0% 0% 0.0 | Ph. 65% 62% Ph. 87% 94% Ph. 75% 75% Ph. 100% 100% Ph. 22% 29% Ph. 100% 100% | 94% 73.9% 100% 93.6% 88% 79.4% 100% 100.0% 23% 24.6% 100% 100.0% | 29% 27% 0% 0% 9% 19% 0% 0% 78% 71% 0% 0% | 6% 24.2% 6% 0.0% 2% 10.6% 6% 0.0% 62% 70.2% 6% 0.0% | 6% 0% 12% 6% 16% 6% 0% 0% 0% 0% | 0% 2.0% 0% 6.4% 9% 10.0% 0% 0.0% 15% 5.1% 0% 0.0% | 29% 95% 1 95% 1 100% 1 100% 1 12% | 88% 38% 38 90% 89% 94 90% 100% 900 90% 100% 900 24% 17% 17 90% 100% 900 | 50% 56% 7% 0% 0% 0% 0% 0% 6% 88% 0% 0% | 54% 57% 0% 5% 0% 0% 0% 0% 72% 78% 0% 0% | 1.8% 5% 0.0% 0% 0.0% 0% 78.6% 0% 0.0% 0% | 9% 0% 0% 0% 6% | 5% 5.0% 5 5% 3.5% 20 6% 0.0% 20 6% 0.0% 20 6% 3.8% 5 6% 0.0% 4 | 00% 100% 100% 100% 100% 100% 100% 100% 17% 14% 10% 100% | 6.76 58.2% 100% 100.0% 100% 100.0% 100% 100.0% 100% 17.9% 100% 100.0% | 62% 22% 0% 0% 0% 0% 0% 0% 70% 72% 0% 0% | 25% 33.5% 0% 0.0% 0% 0.0% 0% 0.0% 66% 71.4% 0% 0.0% | 9% 8% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 9% 8.3 0% 0.0 0% 0.0 0% 0.0 11% 10.6 | % 0.2752 % 0.2752 % 0.1700 % 0.5026 | 0.2254 0.14 0.2254 0.05 0.00 | 0 2579 19 0 2387 01 0 0430 76 0 1120 | 0.1079 0.4226 0.1345 0.2432 | 0.4225 0.7749 0.6418 0.3125 0.9691 | 0.440M 0.9 0.3 0.1583 0.5 0.8553 0.4 | 100 | 0.0913 0.0920 0.2387 0.0330 0.0778 0.1838 0.3985 |
| 547 GSP-binding rusteer crotein Ren Ren 548 Bitroner leconomien D'Ell-binding 1 Rent 549 E'l shirt internation brane 14 MV Haser 550 Kinedin 551 Sorbibl dehydrogenase Sord | RAN MOUSE 1 RAVRI MOUSE HUWE! MOUSE KTN1 MOUSE DHSO MOUSE | 51 M/m 528 151 M/m 528 157 M/m 528 157 M/m 528 157 M/m 728 151 M/m | 000 72% 00.3° 0% 0% 0.0° 100% 22% 11% 11.1° 96% 97% 96.0° 40% 0% 21.7° 100% 100% 100.0° | % 31% 34% 27% % 100% 200% 100% 9% 0% % 17% 11% 22% % 5% 4% 23% | X 30.7% OX X 900.0% OX 22.6 X 20.4% 82% X 4.0% OX | 0% 0% 0.0 0% 0% 0.0 0% 67% 56% 00.5 0% 0% 0.0 | 7% 72% 82% 7% 0% 0% 0% 7% 20% 20% 2% 96% 200% | 95% 79.9% 0% 9.0% 0% 20.0% 100% 98.7% | 36% 17% 190% 100% 0% 20% 10% 4% 0% | 14% 19.1% 100% 100.0% 0% 10.0% 0% 1.3% | 3% 0% 0% 0% 100% 50% 60% 0% 0% | 0% 1.0% 0% 0.0% 100% 70.0% 0% 0.0% | 78% 2% 50% 12% 200% 1 | 81% 72% 76 0% 0% 0 0% 50% 33 8% 29% 15 00% 95% 98 | 7% 22% 5% 100% 3% 0% 5% 60% 5% 00% | 16% 29% 100% 100% 0% 0% 23% 21% 0% 5% | 22.3% 0% 100.0% 0% 0.0% 50% 28.2% 42% 1.5% 0% | 2% 0% 200% S 69% S | 0% 1.0% 1 0% 0.0% 0% 65.7% 0% 55.3% 0% 0.0% 1 | 7% 75% 0% 0% 0% 0% 0% 0% 0% 0% | 92% 81.7% 0% 0.0% 100% 0% 0.0% 100% 100.0% | 12% 22% 100% 100% 0% 22% 44% 0% 0% | 12% 16.0% 100% 100.0% 0% 26% 34.7% 0% 0.0% | 0% 2% 0% 0% 100% 78% 56% 0% 0% | 4% 2.3 9% 0.0 9% 62% 65.3 9% 0.0 | % 0.5442 % 0.5027 % 0.5027 % 0.1703 | 0.3400 0.12 0.7971 0.13 0.1177 0.53 0.4226 0.24 | 49 0.7813 53 73 0.1835 00 0.4226 | 0.0743 0.3065 0.1783 | 0.2780 0.1492 0.5004 0.4326 0.4226 0.2400 | 0.5651 0.4 0.6483 0.9 0.4226 | 220 0.0915 0.0220 0.4720 0.0220 0.4720 0.0220 0.4720 0.0220 0.0271 0.0220 0.0272 0.0220 0.0272 0.0220 0.0272 0.0220 0.0272 0.0220 0.0272 0.0220 0.0272 0.0220 0.022 | 0.4226 0.4451 0.1353 0.2856 0.7967 |
| 252 Vacuolar protein sortino-associal Vps 13 253 Kininogen-1 Krg1 554 Nuclear receptor corepressor 2 Noor2 555 Tubulin beta-5 chain Tubb5 256 Malectin Mac. 557 Tubb Noor2 Tubb5 | K VP13C MOUSE KNG1 MOUSE NCOS2 MOUSE TRIS MOUSE MARC MOUSE P. TACKP MOUSE | 60 KDa 25% 73 KDa 100% 270 KDa 25% 50 KDa 25% 32 KDa 66% 45 KDa 29% | 40% 0% 21.7 100% 100% 100.0 0% 21% 14% 22.4 64% 60% 55.8 28% 24% 76.2 | 5 08 08 258 S 08 08 08 08 5 588 288 299 S 08 08 208 S 738 578 719 | \$ 20.45 828 8 4.05 08 8 8.25 758 8 9.05 08 8 9.05 08 8 50.55 178 8 575 548 8 65.45 08 | 60% 75% 70.0 0% 0% 0.0 0% 21% 7% 18.2 50% 20% 36.5 50% 50% 3.2 | Th 57% 0% Th 100% 100% Th 18% 40% Th 52% 62% Th 29% 27% | 20% 20.0% 27% 20.5% 65% 59.7% 27% 29.5% | 0% 0% 0% 0% 66% 40% 0% 7% 71% 60% | 0% 0.0% 36% 46.7% 0% 2.4% 60% 63.8% | 43% 100% 0% 0% 18% 20% 47% 32% 0% 7% | 0% 0.0% 26% 24.0% 25% 27.9% 12% 6.7% | 678 908 08 268 268 278 | 70% 0% 47 89% 94% 91 0% 0% 0 12% 26% 21 50% 40% 50 30% 39% 34 | 25 05 05 105 05 1005 75 595 85 05 85 05 | 0% 0% 11% 6% 100% 100% 60% 54% 0% 0% 60% 50% | 0.0% 22% 9.0% 0% 100.0% 0% 57.7% 15% 0.0% 28% 58.2% 12* | 25% 10 9% 9% 27% 2 59% 6 76 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 20.6% 0% 49.2% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 97% 98.2% 0% 0.0% 45% 27.4% 80% 60.0% 52% 51.2% | 0% 0% 2% 0% 100% 100% 35% 46% 0% 0% 46% 41° | 2% 1.7% 100% 100.0% 26% 35.4% 0% 0.0% 46% 43.4% | 50% 100% 0% 0% 0% 0% 26% 26% 50% 50% | 0% 0.0 0% 0.0 30% 27.2 20% 40.0 4% 5.3 | 5. 0.5564 5. 0.5564 5. 0.5567 | 0.0700 0.81 0.0200 0.03 0.0700 0.81 0.4917 0.53 0.0265 0.83 | 0.9338 55 0.1845 04 0.3270 17 0.9782 27 0.0014 | 0.4625 0.5653 0.6902 | 0.4225 0.0000 0.0055 0.0556 0.9518 0.4225 0.0585 0.2005 | 0.1945 0.3475 0.5 0.4226 0.9 0.0217 0.4 | 9.5720 0 906 0.1774 0 943 0.4917 0 702 0.0517 6 | 0.7711 0.7301 0.3505 0.8642 0.0317 0.7618 |
| 550 Galaxine-fractos-6-choschale Glyt 550 Colorbone c coldans subunit 55 color 550 Res GTPase-acharina crotein-b GRyb 551 Gasnine nucleotide-binding crote Grob 552 T-corrolles protein 1 subunit alch Top | GPPTI MOUSE COSSI MOUSE GREY MOUSE GREZ MOUSE TOPA MOUSE | 79 kDa 96% 10 kDa 36% 52 kDa 22% 37 kDa 55% 60 kDa 77% | 100% 97% 97.07 36% 25% 32.22 32% 36% 34.11 82% 64% 67.37 79% 82% 79.97 | S 08 08 28 S 468 608 723 S 678 678 648 S 658 178 369 S 238 238 178 | 5 1.15 4% 5 59.35 18% 6 65.95 0% 5 32.75 0% 5 20.15 0% | 0% 0% 1.7 4% 4% 8.7 0% 0% 0.0 0% 0% 0.0 | PS 100% 100% PS 42% 34% PS 9% 44% PS 75% 82% PS 50% 92% | 100% 100.0% 26% 38.4% 26% 26.2% 86% 82.6% 100% 94.6% | 9% 9% 58% 62% 91% 56% 25% 17% 20% 7% | 0% 0.0% 62% 60.4% 75% 73.8% 11% 17.4% 0% 5.4% | 0% 0% 0% 2% 0% 0% 0% 0% | 0% 0.0% 0% 1.1% 0% 0.0% 0% 0.0% | 20% 1 29% 27% 82% 88% | 00% 100% 500 26% 19% 24 45% 28% 39 85% 88% 85 88% 89% 85 | 0% 0% 7% 65% 8% 63% 9% 10% 5% 12% | 9% 9% 62% 22% 55% 62% 15% 12% 12% 11% | 0.0% 0% 68.1% 6% 60.2% 0% 12.3% 2% 11.5% 0% | 9% 7% 9% 9% 9% | 0% 0.0% 8% 7.2% 0% 0.0% 0% 0.9% 0% 0.0% 1 | 7% 100% 10% 18% 18% 25% 12% 82% 10% 100% | 22N 58.9% 22N 19.4% 52N 45.7% 82N 53.0% | 9% 9% 77% 29% 52% 65% 17% 17% 9% 9% | 0% 9,0% 76% 75,5% 62% 53,3% 16% 55,0% 0% 9,0% | 28 08 28 28 08 08 08 08 | 0% 1.1 6% 4.1 0% 0.0 2% 1.0 0% 0.0 | % 0.1856 % 0.2342 % 0.5185 % 0.2061 % 0.0178 | 0.4226 0.18 0.2006 0.18 0.4000 0.15 0.0071 0.14 0.0010 0.00 | 96 0.4226 39 0.0070 46 0.1775 96 0.9286 76 0.1959 | 0.4226 0.8895 0.5185 0.2061 0.0178 | 0.4225 0.0607 0.3491 0.4000 0.1545 0.0908 0.1342 0.0010 0.6276 | 0.0021 0.2 0.1775 0.7743 0.1259 | 225 0.4225 0 536 0.0010 0 0.9429 0 | 0.4225 0.4226 0.8091 0.1235 0.4226 0.4226 |
| 563 Citale synthase, mischondrial Cs 564 Dystrophin Dmd 565 Fibulin-5 Fibris 566 Earninin subunit alpha-3 Lamad | DMD_MOUSE FBLNS_MOUSE FBLNS_MOUSE LAMAS_MOUSE | 52 KUB 100% 425 KUB 20% 50 KUB 0% 365 KUB | 0% 20% 13.3° 0% 0% 0.0° | 5 08 08 08 5 608 608 808 5 728 828 678 | 5 0.0% 0% 5 05.7% 20% 5 74.2% 27% | 0% 0% 0.0 40% 0% 20.0 17% 32% 25.0 | 7% 60% 20% 7% 60% 20% 7% 0% 0% | 100% 98.7% 50% 36.7% 0% 0.0% | 40% 0% 40% 20% 86% 0% | 0% 0.0% 0% 36.7% 63% 49.4% | 4% 0% 20% 10% 14% 100% | 0% 1.3% 50% 25.7% 28% 50.6% | 4% 0% | 00% 100% 500 0% 100% 7% 0% 3 0% 0% 0 | 0% 74% 0% 64% | 0% 0% 0% 0% 56% 62% 75% 67% | 0.0% 0% 64.1% 22% 68.4% 36% | 200% 200% 27% 2 25% 2 | 0% 0.0% 1 0% 1 8% 32.3% 2% 31.6% | 0% 100% 0% 100% 0% 2% 0% 0% | 200% 100.0% 200% 100.0% 2% 2.1% 0% 0.0% | 0% 0% 0% 0% 48% 54% 52% 65% | 0% 0.0% 0% 0.0% 57% 52.9% 67% 61.2% | 0% 0% 0% 0% 52% 42% 48% 25% | 0% 0.0 0% 0.0 40% 45.0 32% 38.8 | % 0.1076 | 0.5000 0.56 0.5565 0.21 | 64 0.0188 93 0.1859 | 0.2742 0.4352 | 0.0099 0.1587 0.2345 0.2794 | 0.1959 0.4 0.2123 0.9034 0.4 | 095 0.5000 0 352 0.1102 0 0.2794 | 0.4226 0.6553 0.1567 0.4030 0.8483 |

| S67 Eukarcotic translation initiation to E1556 IF2P_MCUSE 128 kDa G S68 Plannincoan activatic inhibitor 1 Serbot PARIS_MCUSE 45 kDa J S69 Oalst 1-curstines-curbonisties at Abstration 1 Serbot S7 kDa J S69 Oalst 1-curstines-curbonisties at Abstration 1 S69 Oalst 1-curstines-curbonisties at Oalst 1-curbonisties at Oalst 1-curbonistie | 65% 72% 72% 70.3% 19% 26% 29% 24.5% 82% 74% 82% 80.1% | 178 348 208 17.15 178 148 78 12.05 509 288 288 688 668 668 70.45 08 09 68 5.07 368 348 218 348 3 | 73.4% 55% 7% 31% 15.1% 26% 55% 15% 18.5% 160% 10.0% 34.7% 34% 56% 55% 55.5% 58 4% 6% 42.7% 46% 27.54.5% 35% 36% 36.7% 36% 37% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 36% 37% 37% 37% 37% 37% 37% 37% 37% 37% 37 | 1008 90.075 08 48 09 0.075 08 08 08 09 0.075 1008 1008 1008 100.075 08 08 0.05 | 05 |
|--|--|---|--|--|--|
| Description Proceedings Procedings Proceedings Procedings Proceedings Proceedings Procedings Proceedings Proceedings Procedings P | 805 818 919 54.15 826 786 919 54.25 915 950 850 90.35 06 128 46 5.35 | 20% 29% 9% 155% 9% 0% 0% 0.0% 0.0% 20% 100% 100% 12% 12% 9% 56% 56% 1.0% 1.0% 1.00% | 94.1% 22% 0% 0% 5.9% 0% 0% 0% 0.0% 44% 86 200.0% 0% 0% 0.0% 0% 0.0 0% 0.0 0.0 0.0 0 | 588 589 505 561 548 518 518 518 518 508 508 508 508 518 518 508 505 508 | 68 |
| SF4 Apolipoprotein B 100 | 95 925 825 87.05 125 95 215 14.25 | 100% 500% 0% 0% 0% 0.0% 18% 84% 96% 18% 53.07% 0% 0% 0% 0% 0.07% 78% 84% 96% 15% 57% 72% 72.87% 13% 18% 5% 12.0% 0% 16% 14% 13% | 55.2% 22% 16% 4% 13.8% 0% 0% 0% 0.7% 92% 93 9.2% 82% 72% 80% 78.2% 17% 14% 7% 12.5% 26% 19 | 1506 1505 1505 1506 | 05 1.2% 0.8972 0.5544 0.1000 0.5400 0.8872 0.7552 0.1000 0.422 0.422 0.4226 0.4722 05 5.7% 0.4472 0.4712 0.000 0.88027 0.3355 0.9118 0.1712 0.88026 0.9133 0.2400 0.7007 0.1732 |
| Sri | 885 875 875 87.15 655 786 915 78.05 465 406 281 40.45 | 108 128 108 1295 08 08 08 08 005 2075 928 928 928 128 128 1295 08 08 08 08 1275 208 928 928 228 128 128 128 128 128 128 128 128 1 | \$6.55. 228, 165. 65, 1345. 05, 68, 08, 08, 08, 08, 183. 193. 255. 184. 135. 145. 155. 155. 155. 155. 155. 155. 15 | 1300 (30.0%) (50.0%) (| 50 17.5 1887 19 |
| 533 Glycine-690A Igase Gars 5YG MOUSE 02 KDs 8: 564 Protein transcort ordein Sec23A Sec23a SC23A MOUSE 66 KDs 565 Glycer61-3-choschais defindroos Gpd2 GPDM, MOUSE 61 KDs 1 566 Hescikrase-1 Hd 190K1 MOUSE 100 KDs | 84% 94% 92% 90.0% 6% 30% 0% 5.3% 92% 83% 86% 87.1% 0% 0% 0% 0.0% | 60 10 30 35 515 10 10 20 20 10 | 5 | 1001 100 101 08 08 08 07 08 08 08 08 | 8. 0.0 4.00 2.00 2.00 2.00 2.00 2.00 2.00 |
| S07 Aquatyl aminopepidase | 97% 100% 97% 98.0% 6% 16% 5% 9.0% 68% 76% 66% 58.0% 27% 26% 26% 25.0% | 3% ON 3% 2.0% ON OK OK 0.0% 100% 100% 100% 100% 100% 100% 100% | 000.0% ON ON ON O. 0.0% ON ON ON O. 0.0% 1000 100 3.0% 92% 92% 22% 03.2% 98 12% 188 13.3% 26 0 75.0% 12% 12% 18 0% 0.2% 12% 198 18 13.3% 26 53 3.34% 42% 26% 26% 36% 30.5% 20% 20% 20% 27% 57% 57% | \$ 1000 100.076 ON ON ON ON ON ON ON ON ON O | A |
| 201 Disconsisteriors. IPMA Entress sinto Fanta SYFA MOLESE 20 kDs 7: | 705 826 776 75.5% 925 976 956 94.8% 966 1006 1006 98.5% 846 946 866 88.2% | 22N 120S 150S 17.7NS 78S 68S 48S 5.7NS 78SS 82NS 850S 88S 28S 58S 5.2NS 50S 50S 50S 50S 50S 88S 89S 89S 48S 50S 50S 1.47S 50S 50S 50S 50S 50S 50S 89S 100S 48S 60S 148S 11.27S 28S 50S 50S 5.7NS 86S 20SS 94S 148S 60S 148S 11.27S 28S 50S 50S 5.7NS 86S 20SS 94SS | \$1.1% 12% 15% 12% 14.2% 6% 4% 4% 4.4% 92% 83 93.2% 2% 11% 8% 6.8% 0% 0% 0% 0.7% 100% 100 93.2% 4% 0% 2.4% 0% 0% 0% 0.5% 100% 100 93.2% 4% 0% 2.4% 0% 0% 0% 0.5% 100% 100 93.2% 4% 0% 9.1% 0% 0% 0% 0.5% 100% 100 | \$ 888 57.5% 881 886 681 7.5% 581 881 681 4.5% 888 7.5% 2.5% 5.0% 5.0% 881 7.5% 981 11.5% 981 18.5% 5.0% 5 | 99; 8,4% 0.3367 0.1362 0.0000 0.8772 0.4446 0.3341 0.0077 0.338 0.3491 0.2348 0.7774 0.00005 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 |
| 565 INADH dehrydcomman Lubisuinor (Nathril) INADH DAUGE 17 kDa 2 566 Mitochordeid erriddorine reducin 2-Mar MAPICZ MCUSE 28 kDa 2 577 Missenceshalic unbook-derived March MANY MOUSE 20 kDa 10 568 Lisosokvasccharide-responste a Lirba LIRBA MCUSE 317 kDa 5 | 25% 22% 29% 29.2% 59% 79% 72% 69.9% 100% 100% 100% 100.0% 50% 32% 50% 44.4% | 72N 58% 67% 95.7% 4% 6% 4% 5.5% 30% 50% 20% 20% 20% 4% 5.5% 30% 50% 20% 20% 6% 10.7% 8.8% 7.2% 8% 10.7% 50% 20% 50% 20% 50% | 35.2% 52% 63% 57% 57.2% 7% 7% 6% 5.2% 18% 12.7 200.0% 60% 7% 60% 0.0% 60% 60% 60% 60% 10% 120% 120% 120% 120% 120% 120% 120 | \$\\ \begin{array}{cccccccccccccccccccccccccccccccccccc | 12% 14.4% 0.44% 0.2000 0.003 0.2044 0.4252 0.4173 0.4602 0.2035 0.7250 0.2272 0.004 0.0018 0.2018 0 |
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| 600 WD repeat-containing protein 1 Wdr1 WDR1_MDUSE 65 kDs 10 600 Pancesate secretory cransis ess Gp2 GP2_MDUSE 50 kDs 6 610 605 ribosomal protein L31 Rp31 RL31_MDUSE 21 kDs 6 611 Rh0 GP2-dissociation inhibitor 1 Amgdis GDR1_MDUSE 23 kDs 6 611 Rh0 GP2-dissociation inhibitor 1 Amgdis GDR1_MDUSE 23 kDs 6 611 Rh0 GP2-dissociation inhibitor 1 Amgdis GDR1_MDUSE 23 kDs 6 611 612 612 612 613 | 100% 100% 100% 100.0% 61% 56% 64% 60.6% 68% 56% 69% 64.3% 88% 88% 95% 90.1% | 06 ON 08 GUN 08 ON 08 ON 08 D.ON 1000 1000 1000 1000 1000 1000 1000 10 | 000.0% ON ON ON O. 0.0% ON ON ON ON 0.0% 1000 1000 52.4% 32N 25% 28N 32.5% 20N 15.0% 15N 15N 15.5% 94N 100 61.7% 50N 25N 28N 32.7% ON 5N ON 15N 69N 69N 64N 96.3% 6N 5N ON 3.7% ON ON ON 0.0% 92N 92N 64 | \$ 97% \$9.7% \$0.8 \$0.8 \$0.8 \$0.9 \$0.9 \$0.9 \$0.8 \$0.8 \$0.8 \$0.9 \$0.9 \$0.9 \$0.9 \$0.9 \$0.9 \$0.9 \$0.9 | 6% 0.0% 0.4465 0.4226 0.227 0.2277 0.2277 0.4226 0. |
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| 565 Enteronitir mentific rhain relations Gapt EPFIA, MILUSE 50 kDs 6 | 67% 63% 68% 55.9% 100% 100% 100% 100.0% 55% 55% 42% 50.5% 100% 100% 100% 100.0% | 22% 34% 22% 33.2% 0% 28 0% 0.0% 70% 50% 50% 50% 00 0 0 0 0 0 0 0 0 0 0 0 | 51.1% John 20% 46% 502% 4% 4% 4% 37.7% 100% 100 100.0% 0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 0.0% 97% 97% 51.5% J2W 12% 15% 156.5% 25% 35% 25% 37% 100% 100 100.0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 27% 72% 76 | 1000 100078 05 06 08 08 075 05 08 08 08 05 05 08 08 105 105 105 105 105 105 105 105 | 0.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 |
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| GSD Inter albite-Investin Inhibitor, Isses 1894 CTINN MOUSE 105 KDa 6 | 67% 100% 100% 100% 100% 100.0% 100% 100% 100% 100.0% 17% 28% 18% 21.0% | 10 | 0% 100% 0% 0% 0% 0% 0% 0% 0% 100% 09 000 00 000 00 00 00 00 00 00 00 00 0 | \$ 568, 568% 228, 228, 288, 389, 569, 58, 58, 58, 58, 58, 58, 58, 58, 58, 58 | 6% 05% 02%4 83022 03700 05977 05048 83022 03700 05977 05048 83002 04700 05977 63025 85020 650 050 050 050 050 050 050 050 050 05 |
| 633 Phosphogloconsisse-1 Pgm1 PGM1 MOUSE 61 kDs 10 534 265 ordinase recubitory subunit Psmc2 PRS7 MOUSE 49 kDs 7 635 PDZ and LIM domain protein 1 Pdint PGL11 MOUSE 36 kDs 6 636 ATP synthase subunit f milochor ApSQ ATPK MOUSE 10 kDs 1 | 100% 100% 100% 100.0% 72% 92% 87% 84.1% 48% 65% 52% 55.1% 52% 626 52% 58.1% | 0N 0 0 0 0 0 | 00.07% | 1001 100.076 051 056 051 057 058 058 058 058 058 059 1005 1005 100.076 050 | 6% 0.0% 0.522 0.000 0.5201 0.000 0.5201 0.000 0.5202 0.000 0.5202 0.000 0.5201 0.5201 0.52 |
| 27 Anick Co. enterprises Access A. ACCA, MACRE 266 Cbs 1 | 0% 6% 5% 35% 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 061 081 081 0.005 2881 80% 1000 80.255 0% 061 208 529 779 09295 200 1215 185 20.75 08 88 155 1008 1008 1008 0005 0005 08 08 0.005 08 08 08 208 500 808 51.78 750 508 208 40.29 08 08 08 | 0% 0% 100% 100% 50% 52% 75 7.9% 47% 42% 31% 30.8% 51% 50% 56% 52.7% 0% 0 0.0% 100% 100% 100.0% 00 0% 0% 0.0% 0 0.0% 25% 26% 0% 17.9% 75% 71% 100% 52.1% | 0.00 | 0.0 |
| 991 Syrtosin Syrtosin homolog Sib LA MOUSE 13 500 5 592 Liupus La prolein homolog Sib LA MOUSE 49 600 2 593 005 ribosomi prolein L35 Rp35 RL35 MOUSE 15 600 3 594 Sorbin and SP3 domain-contains Sorbest SRB51 MOUSE 13 500 5 594 Sorbin and SP3 domain-contains Sorbest Serbest MOUSE 13 500 6 595 Centropour protein city Taylor La Central MOUSE 13 500 6 | 905 805 805 807 80.25 21% 50% 59% 46.7% 54% 46% 54% 51.2% 0% 0% 0% 0.0% | 78 | 30.15% 30% 40% 40.05% 40% 41.05% 40% 40% 40% 40% 40% 40% 40% 40% 40.05% 40.05% 4 | | 27 44% 5-676 9384 5716 9384 000 968 000 968 000 968 000 000 000 000 000 000 000 000 000 0 |
| Self Splicing Sector 30 subunit ST301 SF301 MCUSE 146 KDa | 08 88 128 5.78 178 388 298 28.08 1008 1008 1008 100.08 08 48 48 2.78 | ON ON 12N 4.2% 200% 92% 75% 80.7% 0% 0% 24N 52N 62N 62.7% 9% 10% 10% 9.2% 20% 25% 24% 0% 0% 0% 0.0% 0.0% 0.0% 100% <td>0% 0% 100% 100% 100% 70% 44 25.5% 44% 63.5% 6% 12% 12% 10.2% 50.6% 9 90.0% 0% 0% 0% 0.0% 0% 0.0% 0% 0.0% 0.0%</td> <td>281, 48, 15, 06, 06, 07, 07, 286, 569, 706, 15, 07, 08, 15, 07, 15, 08</td> <td> Sec. 25/56 0.2007 0.2004 0.0004 0.0005 0.4206</td> | 0% 0% 100% 100% 100% 70% 44 25.5% 44% 63.5% 6% 12% 12% 10.2% 50.6% 9 90.0% 0% 0% 0% 0.0% 0% 0.0% 0% 0.0% 0.0% | 281, 48, 15, 06, 06, 07, 07, 286, 569, 706, 15, 07, 08, 15, 07, 15, 08 | Sec. 25/56 0.2007 0.2004 0.0004 0.0005 0.4206 |
| 600 Alpha-2-RS-glycopolain Alag FETUA_MOUSE 37 kCa 9 651 Computation factor XIII A chain F13a1 F13a MOUSE 63 kDa 652 Libratin-sancciated crosin 2-bis Libratin-sancciated crosin 2-bis USP21_MOUSE 117 kDa 653 505 chosenul protein 125 Rg29 RL29 MOUSE 18 kDa | 90% 92% 94% 92.1% 100% 0% 4% 0% 0% 1.4% 26% 20% 20% 22.0% | 10% 8% 6% 7.9% 0% 0% 0.0% 0.0% 9.2% 9.2% 9.2% 9.2% 0.0% 0.0% 0.0% 0.0% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.0 | 050.0% 0% 0% 0.0% 0.0% 0.0% 0.0% 0.0 0.0% 0.0 0.0 | \$ 998, 91.85 96 56 78 72 72 72 72 72 72 72 72 72 72 72 72 72 | 15% |
| 564 Phenylidarine-4-hydroxylase Path PHMI_MOUSE 52 kDs 5. | 52% 52% 42% 48.7% 92% 92% 100% 94.9% 100% 100% 100% 100.0% 0% 0% 0% 0.0% | 64% 39% 51% 44.9% 4% 10% 5% 6.4% 52% 62% 62% 62% 62% 62% 62% 62% 62% 62% 6 | 64.2% 26% 26% 32% 25.4% 9% 9% 12% 19.3% 67% 100 95.2% 5% 0% 6% 3.8% 0% 0% 0% 0.0% 0.0% 95.0% 0% 0% 0% 0.0% 0% 0.0% 100 0.0% 100% 100% 100% 100.0% 0% 0% 0% 0.0% 0% 0.0% | \$ 600, \$ 62.76 \$ 288, \$ 0% \$ 208, \$ 17.87 \$ 0% \$ 0% \$ 0% \$ 0.05 \$ | 05 0.0% 0.0003 0.0205 0.4106 0.1005 0.0004 0.4205 0.4000 0.1005 0.00070 0.0007 |
| 200 200 OF CREMINISTRE HOTO PLATE PERMICA MULCISE 100 KUR | 500 500 500 500 500 500 500 500 500 500 | on 49 (10 144) on 05 (05 00 0.07) 1000 1000 1000 1000 1000 1000 1000 1 | 000 DW 0W | 1 200 | 00 00% C-000 |
| 003 Constitution restriction of EOMS FAMISSA FISSA ADDISSE 122 kBs | 0% 12% 0% 4.2% 100% 97% 100% 58.9% 100% 100% 100% 100.0% | 20% 12% 50% 27.75% 80% 75% 50% 60.75% 00% 00% 00% 00% 00% 00% 00% 00% 00% 120% 12 | 96.7% 9% 9% 9% 120% 6.7% 160% 100% 90% 93.7% 9% 99.7% 100% 100% 90% 90% 10.7% 100% 100% 100% 100% 100% 100% 100% 10 | 08 0 025 05 05 05 06 06 07 08 07 08 0 08 07 08 0 08 0 08 | A. |
| 607 605 ribosomal prolein LNSa RpDSa RLSSA MOUSE 12 kCa 2 608 Hatone HH A Healthile HHA MOUSE 22 kGa 9 609 Haptopichin Hp HPT MOUSE 20 kGa 9 670 Chromodomaio-helicase-DNA-bit Ch64 Ch64 MOUSE 218 kGa | 25% 21% 42% 32.9% 95% 95% 92% 94.2% | 65K 52K 57K 54.9% 20K 17K 0K 12.2% 20K 12K 86K 55K 55K 77K 5.7% 0K 0K 0K 0.0% 86K 82K 82K 120K 80K 57K 57K 0K 0K 0K 0K 0K 0K 0K 0K | 22.5% 57% 68% 50% 51.6% 14% 14% 14% 15.9% 29% 0 33.6% 14% 15% 17% 15.4% 0% 0% 0% 0.0% 52.0% 52.0 0.0% 0% 0% 0.0% 10.0% 10.0% 10.0 0.0% 0% 0% 0% 0.0% 10.0% 10.0% 10.0 0.0% 10.0 0.0% 0% 0% 0% 0.0 0.0% 10.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 | 4 64 24.75 72.8 1008 568 72.75 68 08 08 60.55 568 22.8 25.8 | 65 0.075 0.0902 0.4605 0.5972 0.0605 0.0151 0.4405 0.2460 0.2505 0.6162 0.1600 0.0006 |
| ST1 Protein ELYS Abc#1 ELYS MOUSE 248 KDs | 0% 0% 0% 0.0% 22% 22% 22% 21% 21.3% 81% 89% 92% 87.4% 77% 87% 85% 83.1% | 0% 0% 0% 0.5% 200% 120% 120% 100.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 50 | CS 0.755 CS 238 238 444.9 238 278 278 2555 08 28 0.98 228 238 0.98 278 2 | 300% 0.20% 0.20% 0.20% 0.20% 0.20% 0.20% 0.20% 0.00% 0.20% 0.00% |
| STS Transforming protein PhoA Broad BFOA MOUSE 22 kGa 8 kTo Mouse Color Colo | 998 938 1008 94.75 1008 1008 1008 100.0% 1008 1008 1008 100.0% | SN ON ON US 1055 SN 7% SN 4175 880 100% 100% ON ON ON ON ON ON 0.00% 100% 100% 100% 100% 100% 100% 100 | 25.0% 12% 0% 0% 4.2% 0% 0% 0% 0% 0.0% 160% 100 000.0% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 1500 15078 051 054 054 055 055 451 054 051 1258 0591 1505 1505 1505 1507 451 056 051 1258 0591 1505 | 95 0/5 U/301 13000 U/301 U3000 U4200 |
| | 100% 100% 100% 100.0% 95% 100% 100% 98.4% 0% 0% 0.0% | 0% 0% 0% 0.0% 0.0% 0% 0% 0% 0.0% 100% 10 | 000 07% 0% 0% 0% 0.07% 0% 0% 0% 0.07% 1000 100 000 07% 0% 0% 0.07% 0 0% 0 0% 0 0% 0.07% 1000 100 000 07% 1000 1000 1000 100 07% 0 0% 0 0% | \$1000 \$5250 00 \$2 \$00 \$00 \$00 \$00 \$00 \$00 \$00 \$00 | 64-005 0-4226 0- |
| 654 Cacherin-1 Coh-1 CADHT MDUSE 55 kDa 1 | 0% 8% 12% 5.9% 82% 82% 81% 82.0% 69% 82% 75% 75.2% 100% 100% 100% 100.0% | 22% 32% 19% 24.8% 7.8% 58% 69% 68.7% 14% 17% 32% 6% 60% 00 00 00 00 00 00 00 00 00 00 00 00 0 | 21.4% 21% 8% 22% 17.2% 64% 75% 46% 61.2% 62% 64 64.7% 0% 0% 0% 0.0% 18% 22% 6% 15.3% 75% 62 62.2% 26% 26% 29% 30.8% 0% 00 0% 0.0% 0.0% 72% 500.0% 0% 0% 0% 0.0% 0% 0% 0.0% 0.0% 10.0% 10.0% | \$\text{51.0}51 | 17% 2.70% 0.1226 0.2009 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.000 |
| 1 | 805 865 75% 80,2% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% | 0% 0% 4% 1.4% 20% 1.4% 22% 18.4% 72% 72% 66% 1.00% 100% 100% 502.0% 0% 0% 0% 0% 0.0% 0.0% 0% 0% 100% 100 | 0.00 | 10 10 10 10 10 10 10 10 | 2281 2085 0.00512 0.0000 0.0000 0.0000 0.4467 0.4225 0.4226 0.4220 0.0000 0.0400 0.1223 0.0000 0.000 |
| 503 Cell distriction confort enterin 42 bit Col-12 CDC42 MDUSE 21 60a 2 504 Puri found-fromerinent decarboxis Protect PDISD1 MDUSE 87 60a 6 505 Incolated 1-4.5-trice/bosolated record [bpz 2 TTP92 MDUSE 307 60a 6 505 Incolated 1-4.5-trice/bosolated record [bpz 2 TTP92 MDUSE 307 60a 6 506 Incolated 1-4.5-trice/bosolated record [bpz 2 TTP92 MDUSE 31 60a 6 506 Incolated 1-4.5-trice/bosolated record [bpz 2 TTP92 MDUSE 31 60a 6 506 Incolated 1-4.5-trice/bosolated in the Incolated I | 795 925 825 84.75 625 425 385 45.85 05 05 05 0.05 885 958 928 91.85 | 08 | 22.25% ON OS OS OS OS 17% SS OS 7.25% 90% 85 53.1% 20% 22% 10% 17.4% 10% 10% 30% 30% 12.5% 90% 100 05. 0% 0% 0% 100% 0% 0% 0% 0.0 0% 0% 0.0 0.5% 100% 100 00.00% 0% 0% 0% 0.0% 0% 0% 0.0 0.0 0.0 0 | 278 278 08 08 08 078 268 248 248 258 268 268 278 268 268 278 268 278 2 | 35 (0.5% 0.7%) 0.594 |
| 1985 | 100% 100% 100% 12% 5% 12% 9.4% 100% 100% 100% 100.0% 0% 0% 0% 0.0% | 10 | 13.2% 82% 56% 75.5% 58 8% 12% 13.2% 100.5% 100 100 100 100 100 100 100 100 100 10 | 338, 4555, 458, 606, 606, 738, 4575, 50 1391, 1505, 607, 607, 607, 607, 607, 607, 607, 607 | 1 |
| 702 Tropomyosin bela chain Tjm2 TPM2 MOUSE 23 kGs 8 | 82% 100% 100% 94.4% 22% 36% 31% 29.5% 20% 29% 29% 22.4% 100% 100% 100% 100.0% | 081 081 085 9.075 1731 085 081 5.078 1008 10095 10095 1118 79 1158 11.275 6.775 5.795 5.085 50.275 2.285 1118 608 608 628 6285 6218 55.575 209 209 1198 22.475 1198 22.825 218 09 09 09 08 0.075 0.075 0.08 0.075 1008 10095 1 | 000.07% ON 0% 0.0 0.05% ON 0% 0% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0 | 778 778 568 668 228 279 58 68 68 68 68 68 68 68 | 981 0/55 U4-4409 U.1746 0.1001 0.0001 0.1146 0.0054 0.0001 0.4220 |
| 2017 205 columnar reculators suburel Parce 5 PRES MUDUE 46 KDs 5 707 205 columnar reculators suburel Parce 5 PRES MUDUE 46 KDs 5 708 Cytlochroma c-c cordans suburel NA NAUHA | 526 526 526 5276 55.3% 226 366 2276 51.5% 226 576 566 54.9% 866 926 1000 52.7% | 27% 48% 27% 42.7% 0.9% 0.0% 0.0% 0.0% 0.0% 5.0% 5.0% 5.0% 5.0% 6.0% 0. | | 77 (20 5) 20 5 (20 5) 20 6 (20 | 201 0.541 0.540 |
| 711 Protein RCC2 RCC2 RCC2 RCC2 SS 40s 1. 712 Eukarvolic translation initiation is Eliforn Eliforn Eliforn ARCUSE 42 40s 6 713 Palaciphilin-4 Pkp4 PkP4 MCUSE 132 kDs 714 Glacapon Gog GLUC MCUSE 21 40s | 12% 5% 17% 11.0% 60% 68% 56% 61.3% 0% 0% 0% 0.0% 47% 35% 42% 40,8% | 88% 86% 82% 85.0% 0% 0% 0% 3.0% 0% 22% 0% 020 20% 20% 22% 0% 12% 18% 16.0% 60% 5.0% 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% | 7.4% 89% 76% 300% 80.9% 11% 0% 0% 3.7% 46% 17 62.2% 12% 21% 21% 15% 16.5% 22% 21% 20% 21.1% 86% 60 0.0% 0% 0% 0% 0.0% 10.0% 10.0% 10.0% 100.0 10 | 381 2875 468 C78 586 6285 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 178 68 68 68 68 68 68 68 | 66 3.95 0.6000 0.7276 0.777 0.777 1.0079 2.0099 0.0004 0.0021 0.000 0.0023 0.000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 |
| 715 Condon-bleu protein-bleu 1 Cobbt COBLI MOUSE 137 M/m 716 Protein capicus homolog Cic CIC MOUSE 228 M/m 717 R98-bindrog protein 47 R9m47 R9m47 MOUSE C48 M/m 718 255 colesses recolators valuated Perco | 0% 0% 0% 0.0% 17% 10% 4% 10.2% 52% 80% 80% 71.0% | 100% 100% 100% 90.075 0% 0% 0.00% | 72.75, 154, 156, 157, 157, 157, 158, 158, 158, 159, 159, 159, 159, 159, 159, 159, 159 | Graph Grap | 68 0.0% 0.0% 0.000 1.0000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.4226 0.2105 0.4226 0.2105 0.000 0.000 0.4226 0.2105 0.4226 0.2105 0.000 0.000 0.000 0.4226 0.2105 0.000 0. |
| 791 (James suinone coldoreductess - Serdi SCRD MCUSE 50 kGs 10 720 (Cathrin Interactor 1 Circl EPN MCUSE 00 kGs 10 721 (Searn-secrific artifice 2 horrois) Sinta SSFA2 MCUSE 137 kGs 7 722 (Searceates dehydrocensus mice Sinch SARDH MCUSE 102 kGs 3 | 000 900 900 9005 00 110 60 7,05 00 00 00 00 910 940 940 93,05 | \$\text{cm}\$ \text{200}\$ \text{500}\$ | 99-27- 17% 0% 6% 5.0% 0% 0% 0.0% 0.0% 82% 82 3.2% 92% 82% 100% 21.0% 7% 12% 0% 5.7% 6% 9 11/15 52% 07% 82% 79.2% 96 0% 22% 27% 6% 0 94-67% 72% 12% 22% 27% 0% 0 94-67% 72% 12% 22% 27% 0% 0 94-67% 72% 12% 12% 0.0% 0% 1.7% 100% 100% | 881 805 125 05 05 505 505 08 113 128 725 706 707 508 0.25 05 128 75 505 248 120 12 | AST AST Control Co |
| 1995 | 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 6% 2.1% 58% 68% 68% 54.8% | NS USA | | | \(\frac{\pi_0}{15}\), \(\frac{\pi_0}{66}\), \(\frac{\pi_0}{660}\), \(\frac{\pi_0}{6600}\), \(\frac{\pi_0}{6600}\), \(\frac{\pi_0}{660}\), \(\frac{\pi_0}{6600}\), \(\frac{\pi_0}{660 |
| 23 State-trained protein roles to 100 State 10 | 89% 95% 91% 91.7% 57% 58% 68% 60.67% 0% 0% 8% 2.87% 0% 0% 0% 0.07% | 05 05 05 05 115 55 36 127 565 565 675 685 565 685 685 685 685 685 68 | 91.0% ON ON ON ON O.S 0.0% O.S 0.0% ON | 1001 500.05 | 77 85% GRBFG G.2505 GRBFT G.5505 GRBFT G.5505 GRBFT G.5505 G.5215 GRBFT G.5505 GRBFT G. |
| 732 Importin subunit bela-1 Kprb1 IMB1 MCUSE 97 kDa 7; 733 Endocksamic relicular nesider is Erp44 ERP44 MCUSE 47 kDa 8; 744 Vesich-associated membrane or Vapa VAPA MCUSE 28 kDa 1; 755 MicroBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MicroBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 MincoBert-associated divisionals Minp4 M/PAP4 MCUSE 20 kDa 1; 755 Mi | 78% 80% 94% 83.8% 82% 95% 94% 90.9% 54% 75% 58% 62.4% 0% 0% 0% 0.0% | ON ON ON ON 22N 20N 6N 16.2% 6N 100N 100N 27% 5N 6N 9.1% 0N 6N 60 0.0% 82N 94N 92N 8N 6N 8N 5.3% 28N 25N 23N 32.7% 50N 55N 55N 92N 80N 75N 75N 76.7% 20N 25N 22.3% 0N 0N 0N 0N | 97.5% ON ON ON ON O.O. GN ON ON ON 2.1% SIN 93. 90.0% 17% GN SN 10.0% ON ON ON O.O. 5. 92.3% ON SN ON 1.7% 10% 40% 7% 19.0% Sek 90. 0.0% GN GN GN G2.2% 40% 32% 40% 37.5% ON ON | \$\ \text{50.8} \ \text{50.95} \ \text{60.95} \ \text{60.95} \ \text{60.95} \ \text{60.95} \ \text{60.95} \ \text{50.95} \ \text{60.95} \ \text{50.95} \ \tex | 6% 0.9% 0.0000 0.83848 0.3461 0.4206 0.600 0.000 0.0000 0.63648 0.3461 0.4206 0.600 0.000 0.0000 0.63648 0.3461 0.4206 0.600 0.000 0.0000 0.60 |
| 735 U1 small nuclear ribonucleocrete Smmg/70 RU17 MOUSE 52 kDs 1737 Sperridine synthase Smm SPEE MOUSE 34 kDs 2738 Transformer-2 crotisis homoloob Tra25 TRA03 MOUSE 34 kDs 2738 Transformer-2 crotisis homoloob Tra25 TRA03 MOUSE 34 kDs 738 Transformer-2 crotisis homoloob Tra25 TRA03 MOUSE 35 kDs 7 | 0% 0% 6% 2.0% 88% 90% 95% 91.1% 0% 0% 0% 0.0% 82% 90% 86% 86.0% | 100N 940N 985 M 985 M 0.0% 00% | 0.0% 0.0% 1.00% 1.00% 1.00% 0% 0% 0% 0.0% 0% 0.0% 0.0% 0.0% 0.00% 0.00% 0.00% 0.0% | 1 751 6756 8051 8885 9875 80575 65 65 65 65 65 65 65 65 65 65 65 65 65 | 95 4.7% UA-469 UA-56 TO 2008 - 0.000 - |
| Type The American State Type | 828 900 865 85.5% 1005 1006 1000 100.0% 905 896 1000 93.2% 90 00 00 0.0% 968 968 870 95.1% | 12% 20% 14% 1.24% 08 0% 0.05 0.05 0.08 30.03 0.00 0.05 1.00 3.00 | 1001 17% (7% (7% (7% (7% (7% (7% (7% (7% (7% (| . 500 505.00 50 50 518. | 98 0.058 1.11 |
| 20 | 96% 95% 95% 96.7% 82% 96% 96% 54.0% 0% 5% 6% 4.0% 100% 100% 25% 29% 27% 26.0% | 50 30 40 40 40 40 40 40 40 40 40 40 40 40 40 | 250 | 100 1 200 1 | 20 1275 0.000 0.00 |
| 752 Calcium-binding mitochondrial cr Stc25a24 SCMC1 MOUSE 53 kDa | 94% 96% 90% 93.5% 96% 96% 100% 97.7% 41% 42% 54% 45.8% 0% 0% 0% 0.0% | 120 120 110 1105 150 | 94.2% 6% 2% 8% 5.8% 0% 0% 0% 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. | \$60, \$62.50 \qquad \qquad \qquad \qquad \qquad \qquad \qqqqq\qqqqqqqqqqqqqqqqqqqqqqqqqqqqqq | 13 |
| 753 6-phosphogluconolectorase Pgis 6PGL MCUSE 27 kDs 8 754 Fibronecin troe-III domain-conta Findc2s FND3A MOUSE 132 kDs 2 | 81% 78% 82% 80.4% 29% 18% 0% 15.6% | 100% 100% 100% 1000075; 00% 00% 00.075; 00% 00.075; 00% 00.075; 00% 00.075; 00% 00.075; 00% 00.075; 00% 00% 00.075; 00% 00% 00.075; 100% | 90.7% Jen en on 9.2% on on on 0.0% Jen en 92.2% on on on 0.0% Jen 92.2% on on on 0.0% Jen 92.20% on on on 0.0% Jen 100% | 88 00 TN 160 5N 12N 10.9% ON ON ON ON ON ON 000 950 950 1000 07.0% 4N 5N ON 20% ON | 0% 0.0% U.MG3 0.1154 0.0076 0.4800 0.2963 0.1154 0.0076 0.4800 0.2963 0.1154 0.0076 0.4800 0.4800 0.2029 0.1917 |

| 750 (1980co;191.0. 1910 1913 MCASS 21 MSs 885 885 82.255 1915 | 17N 16N 17.7N 0N 0N 0N 0N 0.0N 12N 12N 12N 12N 152.7N | 28% 9% 12% 14.8% 0% 0% 0% 0.0% 100% 84% 76% 85. | S | 98 08 08 0.008 0.0114 0.8851 0.009 0.301 0.5114 0.885 0.009 0.301 |
|--|---|--|---|--|
| 760 Ver. bros-thin seeffic section AGEN_MISSES 71 MSn 1000s 1000 | 08 | 0% 0% 0% 0.0% 0% 0.0% 0% 0% 0% 0.0% 100% 10 | 55 050 268 078 078 078 078 078 078 078 078 078 100 100 100 100 100 100 100 100 100 10 | 50. Do. So. So. So. So. So. So. So. So. So. S |
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| 700 Los continues horrollos, milectivos Lory 1 LSMA MAJURE 50 KSDs 93% 150% 29.5 F7.7% 79. 770 Saminiferentin chancelle Program Pop fica 30 MSDs 300% 300% 500% 500% 500% 500% 500% 500% 500% 500% 500% 500% 500% 500% 500% 500% 500 500% 500 500% 500 500% 500 500% | | 0% 0% 0% 0.0% 0.0% 0% 0% 0.0% 100% 100% | 55 ON 105 181 37% 051 ON 105 ON 105 100 100 100 100 100 100 100 100 0 0 0 | .09 |
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| Th2 ding chain-associated in Transi | TLN2 MOUSE 25 TRAMI MOUSE 43 | 1 KDs 1 KDs 1 KDs 1 KDs | 905 995 80.2 906 795 80.2 | 75 05 05 PS 105 105 | 100% 0% 0.07 | % 18% 20% | 0% 0% 19.7% | 205 205 76% 69% | 62% 69.0% 100% 79.2% | 0% 0% 5% 0% 0% 5% | 1.0% 24% | 100% 31% 32% 2 | 25% 0 25% 50 29.4% 62% 50 | S 29% 17.9% S 75% 63.9% | 25% 0% 0% 0% | 9% 17.9% 50% 0% 0.0% 33% | 200% 431 50% 251 | 5 64.3% 60% 5 36.1% | 0% 50% 100% 0% | 6.7% 0% 0 | N 0% 0.0% 40% N 0% 5.7% *** | 100% 50% 63.3% 0% 100% | 0.1075 0.82 0.9910 0.99 | 13 0.1859 78 0.1523 0.7684 76 0.0561 0.4489 | 0.4226 0.9910 | 0.1853 0.1875 0.0551 | 0.4226 0.0091 0.4489 | 0.9724 0.8278 |
| s-CoA licese (ADP-for: Sucis2 - like protein Cot1 | SUCBI_MOUSE 50 COTLI_MOUSE 16 | KDs 92% KDs 100% | 92% 94% 92.5 80% 100% 92.5 | 75 26 115 25 25 25 25 25 05 225 | 6% 6.57 0% 6.75 | 5 95 95 5 95 95 | 5 05 0.0% | 100% 100% | 100% 100.0% | 0% 0% 0% | 0.0% 0% | 9% 9% 9% 9% | 0.0% 100% 100 9.0% 9.0 9.0% 9.3 | 5 1005 100.0% 5 1005 100.0% | 0% 0% 10% 7% | 0% 0.0% 0% 0% 0.0% 0% 2% 7.9% 0% | 9% 01 9% 01 | 6 0.0% 100% 6 0.0% 100% 6 0.0% 90% | 100% 100% 1 93% 100% | 0.2% 0% 9 0.0% 0% 0 0.8% 10% 9 | N ON 0.0% ON N ON 5.2% ON | 0% 0% 0.0% 0% 0% 0.0% | 0.0005 0.64 0.4229 0.30 | 0.0005 25 0.8591 | 0.0005 | 0.0005 0.6425 0.8691 | | 0.2697 |
| roiso subfamily A ment Draja2 de-associated tumor sur Mtus1 incedicic semialdehyde Asso | MILIST MOUSE 13 AASS MOUSE 10 | KDs 295 KDs 05 KDs 885 | 64N 22N 31.5 0N 0N 0.0 82N 25N 81.5 | 75 725 565 75 1005 1005 75 125 165 | 25% 17.35 | 5 95 95 5 95 45 | 5 05 0.05 0 05 1.25 | 17% 14% 0% 0% 93% 100% | 0% 0.0% 10 100% 97.8% | 200 960 600 7 000 1000 1000 10 70 00 00 | 0.0% 0% 2.2% 0% | 9% 9% 9% 9% | 0.0% S0% 29 0.0% 0.0% | S 50% 41.7% | 50% 50% | 25 47.25 05 05 | 25% 8 | 6 11.1% 71% 6 0% | 44% S0% 0% | 5.2% 29% 50 100% 100 | S 50% 44.7% 0% S 9% | 0% 0% 0.0% 0% | 0.0264 | 25 0.8591 23 0.3918 0.0528 28 0.095 | 0.0406 | 0.0025 | 0.0528 | 0.2697 |
| shydrogenase 1 Adh1 zona pellucida-like donr Cuzd1 isrbutun/LCoA buttela 18brth | ADHI_MOUSE 40 CUZDI_MOUSE 68 HIRCH MOUSE 43 | kDa 100% kDa 80% | 100% 100% 100.0 55% 82% 72.3 96% 100% 58.6 | 75 05 05 75 205 275 | 0% 0.07 11% 19.35 | % 0% 0% % 0% 189 | 5 05 0.0% & 25 8.4% | 100% 100% 82% 78% 94% 100% | 100% 100.0% 90% 83.4% 100% 98.0% | 0% 0% 0% 6% 6% 0% | 0.0% 0% 3.8% 12% 2.0% 0% | 2% 2% 17% 12% 1 | 0.0% 100% 100 12.8% 100% 100 0.0% 100% 100 | 5 1005 100.0% 5 1005 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 0% | 0% 00 0% 00 | 6 0.0% 99% 6 0.0% 100% | 96% 97% 100% 100% 1 | 6.4% 0% 2 0.0% 0% 0 | N 0% 0.7% 4% | 25 25 295 | 0.3381 0.8307 | 0.0005 0.4225 0.4225 | 0.0581 | 0.4226 0.0563 0.4225 | 0.4226 | 0.0223 |
| Abrú2 Vin | ATIC MOUSE 13 VTNC MOUSE 55 | KDs 0% | 0% 0% 0.0 22% 22% 24.8 | 7% 100% 100% 9% 70% 78% | 100% 100.01 78% 75.21 | % 0% 0% | A 0% 0.0% | 0% 0% 12% 25% | 0% 0.0% 10 20% 19.2% 8 | 20% 100% 100% 10 18% 75% 80% 8 | 00.0% 0% 00.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0 0.0% 41% 49 | % 0% 0.0% % 46% 45.0% | 100% 100% 1 48% 42% | 0% 100.0% 0% 2% 44.2% 11% | 9% 01 9% 12 | 6 0.0% 0% 6 10.7% 29% | 0% 21% 22% | 100% 100 0.9% 71% 69 | K 0% 69.1% 0% | 0% 0% 0.0% | 0.2810 0.01 | 0 00045 0.0005 | 0.2810 | 0.0009 | 0.0095 | 0.0113 |
| pha-V ligav suctase (NADPH) Blab | ITAV_MOUSE 11 BLVRB_MOUSE 22 | KDa KDa 100% | 100N 100N 100.0 | 9% ON ON | 0% 0.01 | % 0% 0% | n on 0.0% | 100% 100% | 100% 100.0% | 0% 0% 0% | 0.0% 0% | on on | 200% 100% 0.0% 100% 96 | % 0% 0.0% % 100% 100.0% % 100% 98.7% | 92% 100% 0% 0% 0% 4% | 2% 88.1% 8% 0% 0.0% 0% 0% 1.3% 0% | 0% 27 0% 00 0% 00 | 6 0.0% 100% 6 0.0% 100% | 200% 200% 1 100% 200% 1 | 2.4% 63% 48 0.0% 0% 0 0.0% 0% 0 | N 26% 48.9% 28% N 0% 0.0% 0.0 N 0% 0.0% 0.0 | 52% 57% 48.8% 0% 0% 0.0% 0% 0% 0.0% | 0.42 | 85 0.4226 | _ | 0.4226 0.4226 | | 0.0245 |
| ome allonment-maintain Champ sase regulatory subunit PamoS racting protein 13-bets Apol2 | 1 CHAP1_MOUSE 88 PRS10_MOUSE 44 DP138_MOUSE 74 | kDa 0% kDa 71% kDa 45% | 93% 82% 82.4 38% 36% 39.8 | 7% 100% 100% 8% 29% 7% 9% 55% 56% | 18% 17.67 64% 58.11 | % 0% 0% % 0% 0% | 4 0N 0.0% N 0N 0.0% | 0% 0% 80% 92% 56% 82% | 100% 90.8% 2 83% 74.1% 3 | 10% 200% 10% 8% 0% 12% 17% 8% 1 | 9.2% 0% 19.4% 11% | 0% 0% 0% 8% | 0.0% 76% 89 6.5% 100% 100 | % 0% 0.0% % 71% 78.6% % 100% 100.0% | 20% 10% 5 24% 11% 0% 0% | 0% 100.0% 0% 9% 21.4% 0% 0% 0.0% 0% | 0% 00 0% 00 | 6 0.0% 0% 6 0.0% 94% 6 0.0% 100% | 93% 90% 93% 100% | 0.0% 100% 100 0.4% 6% 7 5.2% 0% 16 | N 100% 100.0% 0% N 10% 7.6% 0% N 0% 4.8% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.3843 0.12 0.0551 0.42 | 01 0.6780 0.8122 06 0.0022 0.1353 01 0.3662 0.003 06 0.6456 0.5681 11 0.5716 0.0017 | 0.3843 0 | 0.1201 0.6780 | 0.8122 0.1907 0.3374 | |
| domain, containing rank Effet2 all destant factor 7.8km 5:(2)1 | EFHEQ MOUSE 27 SDF2L_MOUSE 24 | KDs 100% KDs 71% | 100% 86% 95.2 67% 66% 67.3 | 75 05 05 75 295 225 | 14% 4.87 24% 32.35 | % 9% 9% % 9% 9% | 6 05 0.0% 6 05 0.0% | 100% 100% 66% 71% | 100% 100.0% 77% 71.2% 3 | 0% 0% 0% M% 29% 22% 2 | 0.0% 0% 08.8% 0% | 0% 0% 0% 0% | 0.0% 92% 76 0.0% 62% 56 | S 99% 87.7% S 79% 65.0% | 7% 24% 22% 64% | 2% 12.3% 0% 2% 35.0% 0% | 9% 01 9% 01 | 6 0.0% 100% 6 0.0% 100% | 94N 92N 62N | 5.7% 0% 6 0% | N 9% 4.9% 9% 22% 9% | 0% 0% 0.0% 0% | 0.4226 0.32 0.4265 0.46 | 01 0.3662 0.2063 06 0.6456 0.5981 | 0.4225 0 0.4255 0 | 0.3231 0.3662 0.4606 0.6456 | 0.2053 0.5981 | |
| ATPase 1 Clari port factor Ree 1 3-ohosphale dehidroos Gpd 11 | RAE IL MOUSE 45 GPD IL MOUSE 36 | KDs 94% KDs 0% KDs 100% | 99% 94% 92.6 9% 9% 0.0 100% 100% 100.0 | 75 65 115 75 1005 1005 75 05 05 | 6% 7.45 100% 100.05 0% 0.05 | 5 05 05 5 05 05 | N 05 0.05 N 05 0.05 | 95% 95% 0% 0% 100% 100% | 955 95.4% 05 0.0% 10 1005 100.0% | 5% 5% 4% 0% 100% 100% 10 0% 0% 0% | 4.6% 0% 0.0% 0% | 9% 9% 9% 9% | 0.0% 92% 67 0.0% 0% 0 0.0% 100% 100 | 5 1005 85.9% 5 05 0.0% 5 1005 900.0% | 9% 23% 100% 88% | 95 14.1% 95 65 93.9% 95 95 9.0% 95 | 0% 0 13% 6 0% 0 | 6 0.0% 100% 6 0.1% 0% 6 0.0% 100% | 200% 200% 1 20% 20% 1 200% 200% 1 | 0.0% 0% 0 0.0% 100% 92 0.0% 0% 0 | N 0% 0.0% 0% N 100% 97.4% 0% N 0% 0.0% 0.0 | 9% 9% 2.5% 9% 9% 2.5% | 0.2105 0.29 | 0.5/16 0.0017 | 0.2105 | 0.4707 0.2318 | 0.4226 | 0.4707 |
| eta-1 (tgb1 subunit 2 Dcts2 | DOTTO MOUSE 66 DOTTO MOUSE 44 AVII MOUSE 92 | kDa 75% kDa 50% | 100% 100% 91.7 81% 60% 53.8 | TS 50% 29% | 60% 35.25 | % 25% 0% % 0% 0% | 5 05 8.75 N 05 0.05 | 100% 100% 46% 57% | 100% 100.0% 89% 64.1% S | 0% 0% 0% 4% 49% 11% 2 | 0.0% on 05.9% on | 0% 0% 0% 0% | 0.0% 92% 86 0.0% 47% 59 | S 998 90.7% S 628 55.9% | 0% 0% 53% 42% | 0% 0.0% 7% 8% 44.1% 0% | 14% 7 0% 0 | 6 9.3% 96% 6 0.0% 100% | 97% 97% 90% 93% | 0.7% 0% 0 1.2% 0% 22 | N 0N 0.0% 4% N 17% 8.7% 0N | 12% 12% 9.9% 0% 0% 0.0% | 0.4225 0.87 0.9853 0.00 | 53 0.9192 0.0024 57 0.5003 0.1568 | 0.9853 | 0.0057 0.5003 | 0.4220 | 0.8763 |
| schwied protein kinsee Mapk3 spe I cytoskeletal 14 Krt14 | MKG3_MOUSE 43 K1C14_MOUSE 53 | kDa 100% kDa 0% | 100% 100% 100.0 0% 9% 3.0 | 75 05 05 75 225 225 | 0% 0.07 26% 34.35 | % 0% 0% % 62% 62% | 8 08 0.0% 8 558 62.6% | 100% 100% 0% 27% | 100% 100.0% 10% 12.4% 4 | ON ON ON MN 27% 40% 2 | 0.0% 0% 57.2% 56% | 0% 0% 45% 50% 5 | 0.0% 100% 100 0.3% 0% 0 | % 100% 100.0% % 0% 0.0% | 0% 0% 17% 57% 1 | 0% 0.0% 0% 0% 57.9% 83% | 0% 0 43% 0 | 6 0.0% 100% 6 42.1% 0% | 100% 100% 1 0% 0% | 0.0% 0% 0 0.0% 71% 25 | N 0% 0.0% 0% N 82% 59.5% 29% | 0% 0% 0.0% 75% 12% 40.1% | 0.3629 | 0.4226 0.2592 | 0.6328 0 | 0.9506 0.4302 | 0.3300 0.0750 | |
| A-processing factor 40 PrpHOs rich with DGF-like dom; Creid2 | PRIOR MOUSE 10 CREL2 MOUSE 36 | \$00 1005 1005 | 0% 0% 4.2 100% 100% 100.0 | 75 75 100 N 75 05 05 | 100% 91.75 0% 9.05 | % 12% 0% % 0% 0% | S 05 4.25 N 05 0.05 | 0% 0% 100% 100% | 0% 0.0% 10 100% 100.0% | 0% 20% 100% 10 0% 0% 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% 17% 8 0.0% 100% 100 | S 0N 8.2% N 100N 100.0% | 83% 92% 2 0% 9% | 0% 91.7% 0% 0% 0.0% 0% | 0% 01 0% 01 | 6 0.0% 12% 6 0.0% | 14% 0% 10% 100% | 5.7% SSN SG | 8 100% 91.3% 0% 8 0% | 0% 0% 0.0% 0% 0% | 0.4226 0.95 | 38 0.5491 0.1873 20 0.2433 0.4226 26 0.3846 0.5444 | 0.4226 0 | 0.9568 1.0000 | 0.1873 0.4228 | 5 |
| ing protein 25 Rbm25 odin-2 Sympol ed protein Rep-1A Rep1a | REMOS MOUSE 10 SYNP2 MOUSE 11 RAP1A MOUSE 21 | RDs 0% RDs 57% | 0% 0% 0.0 0% 94% 73.0 | 75 100% 86% 100% 100% 75 14% 22% | 100% 95.25 6% 10.25 | 55 0% 14% 0% 0% 55 29% 20% | N 05 15.25 | 0% 0% 0% 70% 92% | 0% 0.0% 8 0% 82.7% 1 | 2% 88% 100% 8 100% 100% 0% 0% 14% | 8.1% 20% | 235 05 1 25 05 85 05 | 9.2% 9% 18 9.2% 89% 81 | 5 95 0.05 5 95 0.55 5 865 05.55 | 100% 94% 2 5% 6% | 26 74.4% 85 05 98.1% 05 26 6.2% 55 | 27% 19 6% 01 12% 7 | 6 17.0% 0% 6 1.9% 0% 6 8.3% 90% | 20% 20% 20% 20% 88% 85% | 3.2% 72% 80 0.0% 100% 100 7.5% 5% 8 | N 90% 77.8% 27% N 100% 100.0% 0% N 5% 6.1% 5% | 0% 0% 0.0% 4% 10% 6.4% | 0.5200 0.51 | 55 0.3848 0.5444 | 0.6943 | 0.4225 0.4225 0.9363 0.2253 | 0.5393 0.5393 | 0.4226 0.5374 |
| tional regulator ATRX Ahx aminotransferase, milo Cet brand factor A domain-: VeeSe | OAT_MOUSE 27 OAT_MOUSE 46 VMASA MOUSE 87 | KDs 100% KDs 100% | 100% 100% 100.0 100% 100% 100.0 | 7% 0% 0% 7% 0% 0% | 0% 0.05 0% 0.05 | % 0% 0% % 0% 0% | N 0N 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | ON ON ON | 0.0% 0% | 0% 0% 0% 0% | 0.0% 100% 100 0.0% 100% 100 | % 100% 100.0% % 100% 100.0% | 0% 0% 0% 0% | ON 0.0% ON ON 0.0% ON | 0% 00 0% 00 | 6 0.0% 100% 6 0.0% 100% | 100% 100% 1 | 0.0% 0% 0 0.0% 0% 0 | N ON 0.0% ON N ON 0.0% ON | 0% 0% 0.0% 0% 0% 0.0% | | | | | | |
| protein 4 Larp4 se 2 subunit beta Priccah | GLUDE MOUSE 59 | kDa 4% kDa 100% | 0% 0% 1.3 100% 100% 100.0 | 9% 92% 100% 9% 0% 0% | 96% 95.11 0% 0.01 | % 4% 0% % 0% 0% | 6 4% 2.0% 6 0% 0.0% | 4% 0% 100% 100% | 0% 1.3% 9 100% 100.0% | 6% 100% 100% 5 0% 0% 0% | 0.0% on | 0% 0% 0% 0% | 0.0% 0% 0 0.0% 100% 100 | % 0% 0.0% % 94% 98.1% | 100% 100% 1 0% 0% | 0% 100.0% 0% 6% 1.9% 0% | 0% Of | 6 0.0% 0% 6 0.0% 100% | 0% 0% 100% 100% 1 | 0.0% 100% 100 0.0% 0% 0 | N 100% 100.0% 0% N 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 1.0000 | 0.4226 0.4226 0.4226 0.0648 04 0.4216 0.0691 04 0.4216 0.0691 | 0.4029 | 0.2335 0.4226 0.4226 | 0.4226 0.1541 | |
| mbrane emp24 domain+ Tmed5 EA.V HSafv | TMEDS_MOUSE 28 HGAV_MOUSE 13 | kDa 676 kDa 786 | 70% 62% 66.2 89% 92% 86.2 | 7% 7% 27% 2% 6% 99% 9% 22% 11% | 24% 13.25 8% 13.75 | % 28% 20% % 0% 0% | s 14% 20.5% n 0% 0.0% | 55N 57N 55N 57N | 72% 61.7% 80% 72.4% 1 | ON 5N ON 2N 2N 2 | 1.6% 45% 20.6% 0% | 28% 27% 2 0% 0% | 15.8% 100% 100 15.7% 100% 0.0% 100% 88 | s 88% 91.7% | ON 13% | 0% 0% 3% 8.3% 0% | 0% 0 | 6 0.0% 86% | 100% S4% | 0.2% 14% O | N 6% 5.8% ON | 0% 0% 0.0% | 0.5286 0.2553 0.81 | N 0.4218 0.0501 | 0.1657 0.2553 0 | 0.1319 | 0.0591 | |
| EAZ HOstz minina dalminasa h.ma. Pad2 na narnaidasa 3 Grafi | PACIZ MOUSE 14 PACIZ MOUSE 76 GENO MOUSE 25 | kDa 78% kDa 100% | 99% 92% 85.3 100% 100% 100.0 100% 100% 100.0 | 9% 22% 11% 2% 0% 0% 9% 0% 0% | 8% 13.79 0% 0.09 | % 0% 0% % 0% 0% | 4 0% 0.0% N 0% 0.0% | 93% 75% 100% 100% 100% 100% | 90% 79.4% 1 100% 100.0% | 27% 25% 20% 2 9% 9% 9% 9% 9% 9% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 100% 88 0.0% 0.0% 90% 70 | % 88% 91.7% % 75% 76.7% | 20% 12% | 3% 8.3% 0% 9% 18.5% 0% | 9% 67 | 6 0.0% 86% 6 4.9% 63% | 100% 94% 64% 93% | 0.2% 14% 0 0.4% 15% 14 | K 6% 5.8% 0% | 12% 9% 11.2% | | | | | | |
| s protein cut-like 1 Cus1 remiletore fer tor 3.him [rf2bp2 | CUX1_MOUSE 16 128P2_MOUSE 59 | KDs 0% | 9% 9% 9.0 9% 9% 9.0 | 7% 0% 0% 7% 100% 100% | 50% 15.75 100% 100.05 | % 200% 100% % 0% 0% | A 50% 83.7% (% 0% 0.0% | 0% 0% 0% 0% | ON 0.0% 10 | 0% 0% 0% 100% 100% 10 | 100% 00.0% 0% | 100% 0% 0% | 0.0% 0% 0 | 0% % 0% 0.0% | 100% 100% 1 | 0% 0% 100,0% 0% | 9% O | 0.0% 0% | 0% 0% | 0.0% 100% 100 | N 100% 100.0% ON | 0% 0% 0.0% | | 17 0.0051 0.0388 | 0.4226 | | 0.4220 | 1 |
| brand factor A domain-: VeelS en reductase 1, cylopia, Txerd1 | VWAS MOUSE 21 TRURI MOUSE 67 | 1 KDs 67% KDs 100% | 40% 25% 43.5 100% 100% 100.0 | 2% 23% 62% 2% 0% 0% | 75% 56.11 0% 0.01 | % 0% 0% % 0% 0% | N 0N 0.0% | 75% 100% 100% 100% | 100% 91.7% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 25% 0.0% 0% | 0% 0% 0% 0% | 8.3% 0.0% 100% 100 | N 100N 100.0% | 0% 0% | 0% 0.0% 0% | 0% 0 | s 0.0% 100% | 100% 100% 100% 100% 1 | 0.0% 0% 0 | 5 05 0.0% 0.0% | 0% 0% 0.0% | 0.0380 | 0.4226 | 0.0441 | | 0.4220 | 5 |
| protein 58 Nop58 dducin Add3 ransfer flavoprotein-ubi Effdh | ADDG_MOUSE 79 ETFD_MOUSE 68 | kDs 78% kDs 0% kDs 67% | 61N 52N 63.7 0N 0N 0.0 64N 72N 68.1 | PS 17% 28% 2% 100% 100% 1% 23% 36% | 29% 27.95 100% 100.05 27% 31.95 | 75 6% 11% 75 0% 0% | 6 98 8.5% N 98 0.0% | 64N 82N 82N 92N | 98% 78.2% 1 | 2% 2% 0% 1 2% 8% 0% | 8.1% 0% | 0% 13% 1 | 0.2% 72% 100 28% 100 0.0% 100% 100 | 5 55% 76,0% 5 20% 52,5% 5 100% 100,0% | 20% 0% 28% 0% 0% 0% | 8% 12.7% 7% 0% 25.8% 25% 0% 0.0% 0% | 0% 27 0% 40 0% 0 | 6 11.2% 100% 6 21.7% 50% 6 0.0% 100% | 89% 100% 80% 83% 100% 100% 1 | 6.2% 0% 0 1.1% 0% 20 0.0% 0% 0 | N 0% 0.0% 0% N 0% 6.7% 50% N 0% 0.0% 0% | 11% 0% 3.7% 0% 17% 22.2% 0% 0% 0.0% | 0.2406 0.25 0.53 | 0.1631 0.0071 0.2338 | 0.1367 0 | 0.1844 0.1717 0.2796 0.0291 0.0071 | 0.1843 0.7770 | 0.9779 |
| saome non-ATPase rec Pand S isohosohale nucleotidas (Spnt) | BPNT1_MOUSE 43 | KDs 100% KDs 100% | 100% 94% 97.5 100% 100% 100.0 | 25 05 05 25 05 05 | 6% 2.11 0% 0.01 | % 0% 0% % 0% 0% | 5 05 0.0% & 05 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% 100% 100 0.0% 100% 100 | 5 1005 100.0% 5 1005 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 0% | 0% 0 0% 0 | 6 0.0% 100% 6 0.0% 100% | 100% 100% 1 100% 100% 1 | 0.0% 0% 0 0.0% 0% 0 | N 0% 0.0% 0% N 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.4226 | 0.4225 | 0.4226 | 0.4225 | 0.4236 0.0521 | 0.8300 |
| Ichosphooloosacchari Dad1 hydrosenass lubiquinor Ndufs5 | DAD1_MOUSE 12 NDUSS_MOUSE 13 | KDs 56% KDs 22% | 87% 28% 73.2 23% 25% 27.1 | 75 05 05 15 605 695 | 6% 1.97 69% 95.07 | % 66% 123 % 7% 83 | 5 175 24.8% % 65 6.9% | 82% 77% 27% 18% | 785 79.2% 145 19.9% 7 | 0% 0% 4% 2% 72% 86% 7 | 1.4% 17% 77.1% 0% | 225 175 1 95 05 | 19.3% 72% 67 3.0% 9% 0 | S 52% 66.9% S 12% 8.6% | 0% 0% 73% 100% | 0% 0.0% 23% 3% 85.4% 18% | 22% 42° | 5 23.1% 60% 5 6.1% 20% | 86N 50N 8N 13N | 8.6% 0% 0 2.9% 80% 92 | 8 25% 8.2% 60% 8 89% 87.1% 0% | 14% 25% 33.1% 0% 0% 0.0% | 0.5893 0.62 0.2226 0.51 | 17 0.5924 0.2735 50 0.0398 0.2596 | 0.8728 0 0.1121 0 | 0.4225 0.4225 0.8580 0.1219 | 0.4970 0.6336 0.1544 0.3325 | 0.9997 |
| ore complex protein Nu Nup155 viochrome P450 redux Por didvinositol 4.5-bispho Plos2 | NUISS MOUSE 15 NCPR MOUSE 77 PLOGS MOUSE 14 | KDs 100% KDs | 100% 100% 100.0 | 2% 0% 0% | 50% 0% 0.01 | % 0% 0% | S 0N 0.0% | 0% 100% 100% | 100% 100.0% | 0% 0% 0% | 0.0% 0% | 0% 0% | 0.0% 200% 200 2,0% 200% 200 | 98 98 95.8% 8 88% 95.8% 8 100% 900.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 0% 0% 0.0% 0% | 900% 100° 0% 12° 0% 0° | 6 4.2% 92% 6 0.0% 100% | 67% 100% 90% 100% 89% 100% | 2.2% 0% 0 H.2% 0% 0 6.2% 0% 0 | N 0% 0.0% 50% N 0% 0.0% 7% N 0% 0.0% 0.0 | 10% 0% 27.8% 10% 0% 5.7% 11% 0% 3.7% | 0.03 0.77 0.42 | 0.0360 0.4226 0.1946 | | | | 0.7790 0.4225 |
| arrinopeptidase 2 Metap2 rdon-bleu Cobi ssome non-ATPase rec Perest1 | COBL MOUSE 53 COBL MOUSE 14 PSMD3 MOUSE 61 | kDa S9% kDa 93% | Sen Sen 58.5 | 7% 41% 42% 1% 7% 0% | 66% 42.11 16% #.04 | % 0% 4% | 6 0% 1.4% | 26% 57% 0% 100% 100% | 73% 62.2% 4 100% 100.0% | 0% 42% 27% 2 0% 0% 0% | 95.5% e% 0% 0.0% 0% | 0% 0% 0% 09 | 1.3% 100% 100 0.0% 100% 100 | % 100% 100.0% | 0% 0% | 0% 0.0% 0% 0% 0.0% 0% | 0% 0t | 6 0.0% 100% | 90% 100% 100% 100° | 0.3% 0% 20 0.4% 8% 0 | N 0% 5.7% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.4204 0.42 | 0.4206 0.4206 0.4206 0.4206 0.4108 0.4108 0.4108 0.4007 | 0.3783 0 | 0.4226 0.0004 | 0.4226 | |
| ke protein 2. mitochon StomQ ubiouitin carboxul-termi Uap9x | STML2_MOUSE 36 USPSX_MOUSE 29 | kDa 22% kDa 100% | 66% 50% 43.3 80% 500% 93.3 | 2% 67% 46% 9% 0% 0% | 63% 51.95 0% 0.05 | % 0% 8% % 0% 20% | 6 76 4.9% 6 06 6.7% | 54% 54% 100% 50% | 25% 44.8% 4 | 65% 66% 62% 5 0% 0% | 51.0% ons ons | 0% 12% 50% | 4.2% 21% 20 75% 50 | % 12% 18.1% % 100% 75.0% | 68% 60% 0% 0% | 0% 69.5% 11% 0% 0.0% 25% | 20% 71 50% 01 | 6 12.4% 11% 6 25.0% | 12% 20% 100% 100% | 4.1% 74% 76 0 | N SON 88.7% 16% N ON | 12% 30% 19.2% 0% 0% | 0.8923 0.35 0.5950 0.22 | 54 0.3373 0.5000 54 0.3373 0.5000 53 0.7442 0.3959 | 0.9319 0 | 0.8021 0.1403 | 0.2073 0.8819 | 0.3803 |
| deceide chosphorytase Pro receide chosphorytase Pro recementaries revision Legad3 | PNPH_MOUSE 32 MAN1_MOUSE 10 | kDa 100% kDa 0% | 100% 100% 100.0 | 7% 11% 11% 7% 0% 0% | 0% 0.01 | % ON ON | s on 0.0% | 100% 100% | 100% 100.0% | 0% 0% 0% | 0.0% 0% | 0% 0% | 0.0% 100% 100 0.0% 100% 100 | N 100N 100.0% | 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 0% | 0% 00 100 | 6 0.0% 100% | 100% 100% 1 | 0.0% 0% 0 | K 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | |
| a Asilta intersection rend Poldigij Asilta innovareas 1 mi Egil sin 2 Sm2 | PDP3 MOUSE 46 ECH MOUSE 32 SNO2 MOUSE 50 | kDa 0% kDa 29% | 90% 90% 90.2 90% 99% 90.2 | 75 100% 100% 75 11% 8% | 100% 100.05 11% 9.85 15% 12.55 | 75 0% 0% 75 0% 0% | 5 05 0.0% N 05 0.0% | 95% 94% 100% 100% | 0% 0.0% 10 100% 95.6% | 0% 67% 100% E 5% 6% 0% | 3.4% 0% 0.0% 0% | 22% 0% 1 0% 0% | 0.0% 100% 100 0.0% 100% 100 | 5 05 0.0% 5 1005 500.0% | 100% 100% 2 0% 0% | 0% 100.0% 0% 0% 0.0% 0% | 0% 00 0% 00 | 6 0.0% 0% 6 0.0% 100% | 0% 0% 100% 100% 1 | 0.0% 100% 100 0.0% 0% 0 0.0% 0% 0 | N 100N 100.0% ON N ON 0.0% ON | 0% 0% 0.0% 0% 0% 0.0% | 0.0429 | 0.0115 0.1876 0.2254 | 0.4226 0.0429 0.2254 | 0.0115 | 0.4225 0.4225 0.1876 | 5 |
| ooing protein subunit s CapzaG e subunit sloha type-4 Pame4 | PSA4_MOUSE 29 | kDa 100% kDa 92% | 100% 100% 100.0 92% 94% 93.0 | 75 05 05 75 85 75 | 6% 7.05 | % 0% 0% % 0% 0% | A 0N 0.0% (N 0N 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 92% 74 0.0% 100% 94 | 5 77% 80.6% 5 100% 97.9% | 9% 26% 0% 6% | 2% 19.4% 0% 0% 2.1% 0% | 0% 00 0% 00 | 6 0.0% 78% 6 0.0% 100% | 83% 95% 89% 100% | 5.2% 22% 17 6.5% 0% 11 | N 5% 54.8% 0% N 0% 3.5% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.0129 0.74 | 12 0.1288 0.4226 | 0.0129 | 0.5554 0.0651 0.7482 0.1288 | 0.0954 0.4226 | |
| in-binding protein 11 Wbp11 Rei14 | WBP11_MOUSE 70 RA14_MOUSE 10 | KDs 0% | 0% 0% 0.0 00 00 00 | 7% 100% 100% 7% 100% 100% | 100% 100.07 | 7% 0% 0% 7% 0% 0% | 5 05 0.05 5 05 0.05 | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 10 0% 100% 100% 10 | 00.0% 0% 00.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0 0.0% 0% 0 | S 05 0.05 S 05 0.05 | 100% 100% 2 100% 100% 2 | 0% 100,0% 0% 0% 100,0% 0% | 0% 00 0% 00 | 6 0.0% 0% 6 0.0% 0% | 0% 0% 0% 0% | 0.0% 100% 100 1.0% 89% 100 | 65 005 05 8 67% 55.9% 0% 8 100% 95.5% 5% | 0% 22% 11.1% 0% 0% 1.8% | 0.42 | 26 0.4226 26 0.6604 0.4226 | 0 | 0.4225 0.4225 | 0.4225 0.4225 | 0.4226 0.4226 |
| some non-ATPase rec Pared 1 domain-containing on Glod4 ear ribonucleoprolein 1 Smod1 | GLODI_MOUSE 13 SMD1 MOUSE 13 | KDs 100% KDs 100% KDs 7% | 100% 92% 97.4 100% 100% 100.0 0% 8% 5.0 | 7% 0% 0% 7% 0% 0% 7% 87% 92% | 0% 0.05 0% 0.05 83% 07.25 | % 0% 0% % 0% 0% | 6 85 2.05 N 05 0.05 O 85 7.05 | 100% 100% 100% 100% 0% 0% | 100% 100.0% 100% 100.0% 0% 0.0% 9 | 0% 0% 0% 0% 0% 0% 12% 88% 100% 5 | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 100% 83 0.0% 100% 100 6.9% 29% 9 | % 100% 94.4% % 100% 100.0% % 15% 17.7% | 0% 0% 0% 0% 64% 82% | 0% 0.0% 0% 0% 0.0% 0% 7% 74.3% 7% | 17% 01 0% 01 9% 81 | 6 5.6% 100% 6 0.0% 100% 6 8.0% 28% | 100% 100% 1 100% 100% 1 15% 16% | 0.0% 0% 0 0.0% 0% 0 9.7% 61% 77 | N 0% 0.0% 0% N 0% 0.0% 0% N 79% 72.3% 11% | 0% 0% 0.0% 0% 0% 0.0% | 0.1885 0.79 | 25 0.5504 19 0.1447 0.0402 | 0.2657 0 | 0.8062 0.1109 | 0.4220 | 5 0.4226 5 0.9811 0 0.9509 |
| brane 9 superfamily m Tm9xD subunit 1 Doin1 | DCTNI_MOUSE 68 | KDs 50% | 22% 22% 28.5 80% 55% 69.5 | PS 0N 0N PS 25N 20N | 0% 0.05 45% 30.25 | % SON 679 % ON ON | 6 67% 61.1% 6 0% 0.0% | 64% 20% 83% 100% | 43% 29.1% 100% 94.4% 1 | 0% 0% 0% 12% 0% 0% | 0.0% S6% 5.6% 0% | 70% 57% 6 0% 0% | 0.9% 22% 14 0.0% 89% 100 | % 23% 27.0% % 86% 91.5% | 0% 0% 11% 0% | 0% 0.0% 67% 0% 3.7% 0% | 96% 67 9% 141 | 5 73.0% 14% 5 4.8% 100% | 20% 22% 92% 200% | 2.5% 0% 0 7.0% 0% 9 | N 11% 3.7% 86% N 0% 3.0% 0% | 80% S6% 73.8% 0% 0% 0.0% | 0.9780 0.62 0.0583 0.36 | 00 0.1447 0.0402 00 0.2322 0.0076 02 0.0095 0.7158 04 0.0779 0.0005 | 0.0683 | 0.4225 0.8951 0.0582 0.2164 0.0779 | 0.4226 0.9780 0.7158 | 0.9509 |
| odin Syngo e reductase, mitochon; Gar | SYNPO_MOUSE 10 GSHR_MOUSE 54 | KDs 100% KDs 100% | 100% 100% 100.0 100% 100% 100.0 | 75 05 05 75 05 05 | 100% 0% 0.07 | % 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 0% 100% 100% | 100% 100.0% | 200% 20% 20% 200% 20% 20% | 0.0% 0% | 0% 0% 0% 0% | 0.0% 20% 20 0.0% 100% 100 | % 0% 0.0% % 100% 100.0% | 21% 16% 100% 100% 2 0% 0% | 0% 100.0% 0% 0% 0.0% 0% | 0% 00 0% 00 | 6 0.0% 0% 6 0.0% 100% | 0% 0% 96% 100% | 0.4% 5% 8 0.0% 100% 100 8.6% 0% 4 | N 100% 100.0% 0% N 0% 1.4% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.42 | 26 0.8880 0.083 | | 0.4226 | 0.4226 | |
| late transport protein. Sic2Sa mplex subunit Mic27 Appol lonal myosin-Va MyoSa | MIC27_MOUSE 29 MYOSA_MOUSE 21 | kDa Son kDa on | 60% S0% 46.7 0% 0% 0.0 | PS 28% 42% 2% 92% 92% | 92% 91.57 | % 12% 20% % 8% 10% | 4 7% 13.2% N 7% 8.5% | 50% 75% 0% 0% 0% 0% | 63% 62.5% 0% 0.0% 8 | ON SN ON SON E | 2.8% S0% 95.3% 11% | 17% 28% 3 40% 50% 3 100% | 94.7% SON S7 13.7% ON O | % 29% 45.2% % 0% 0.0% | 17% 0% 80% 77% 0% | 9% 15.1% 22% 2% 80.1% 20% | 42% 42° 22% 17° 200% | 5 29.7% 22% 5 19.9% 0% | 62% 42% 0% 0% | 0.0% 0% 29 0.0% 82% 82 | N 25% 17.9% 67% N 78% 80.6% 18% | 29% 22% 42.9% 18% 22% 19.4% 100% | | | | | | 0.8192 |
| core protein Voan am element-binding on Fubp1 corretein 1 Annh | CSPG2_MOUSE 36 FUEP1_MOUSE 69 ADON MOUSE 10 | KDa (%) | 18% 8% 8.6 100% 100% 100.0 | 5% 100% 82% 9% 0% 0% | 92% 91.45 | % on on | N 0N 0.0N | 0% 0% | ON 0.0% 10 | 00% 100% 100% 10 | 00.0% on | 0% 0% 0% 0% | 7% 21 0.0% 24% 25 0.0% 97% 90 | N 12N 13.7% N 28N 25.5% N 60N 95.9% | 92% 79% : 76% 75% : | 8% 85.3% 0% 2% 74.5% 0% 5% 4.1% 0% | 0% 01 0% 01 | 6 0.0% S0% 6 0.0% 25% 6 0.0% 100% | 0% 25% 9% 44% 100% 100% 1 | 5.0% S0% S00 6.2% 75% 90 0.0% 0% 0 | N 75/N 75/0% ON N 56/N 73/8% ON N ON 0.0% ON | 0% 0% 0.0% 0% 0% 0.0% | 0.52 0.2433 0.95 | 02 03 0.0785 0.1246 06 0.0136 | 0.2423 | 0.5202 0.5553 0.0765 0.0136 0.0136 | 0.1246 | |
| binding protein Dbi dehydrogenase, cylosi Aldhilai | ACBP_MOUSE 10 7 AL1A7_MOUSE 55 | 100 | 100% 100% 100.0 100% 91% 97.1 | 7% 0% 0% 1% 0% 0% | 0% 0.07 4% 1.45 | % 0% 0% % 0% 0% | 6 0% 0.0% 6 4% 1.4% | 100% 100% 96% 100% | 100% 100.0% 100% 98.7% | 0% 0% 0% 4% 0% 0% | 0.0% ons 1.3% ons | 0% 0% 0% 0% | 0.0% 100% 100 0.0% 82% 100 | % 100% 100.0% % 100% 94.4% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 17% | 0% Of | 6 0.0% 100% 6 5.6% 0% | 100% 100% 1 0% 0% | 0.0% 0% 0 0.0% 0% 0 | N 0% 0.0% 0% N 100% 33.3% 100% | 0% 0% 0.0% 100% 0% 66.7% | 0.6595 0.00 | M 0.7000 0.0002 | 0.9559 | 0.4226 0.4226 | 0.4384 0.4226 | 0.2056 |
| in aracilir sout l'oit is Agada sin alpha Pless sa hurt commisse subun Ligging | PTMA_MOUSE 12 QCR8_MOUSE 10 | KDs 90% KDs 100% KDs 50% | 100% 100% 96.7 100% 100% 100.0 55% 60% 54.8 | 75 105 05 75 05 05 75 505 455 | 0% 0.07 60% 45.27 | 5 95 05 5 95 05 | N 05 0.05 N 05 0.05 | 92% 200% 100% 200% 22% 67% | 100% 97.8% 100% 100.0% 22% 44.4% 5 | 7% 0% 0% 0% 0% 0% 0% 17% 67% 4 | 0.0% 0% 0.0% 0% | 9% 9% 9% 9% 17% 9% 1 | 0.0% 100% 100 0.0% 100% 100 11.1% 22% 28 | 5 1005 900.0% 5 975 99.0% 5 425 30.0% | 0% 0% 67% 75% | 0% 0.0% 0% 3% 1.0% 0% 2% 66.3% 11% | 0% 0 0% 0 | 6 0.0% 94% 6 0.0% 100% 5 3.7% 30% | 100% 100% 1 100% 100% 1 50% 14% | 8.7% 6% 0 0.0% 0% 0 1.4% 50% 42 | N 0% 1.9% 0% N 0% 0.0% 0.0 N 57% 49.0% 20% | 0% 0% 0.0% 0% 0% 0.0% 10% 29% 19.5% | 0.4505 0.91 | 94 0.7000 0.0002 25 0.4226 0.9045 25 0.4226 50 0.0446 0.4366 | 0.9884 | 0.4226 0.4226 0.4226 0.4226 0.0741 0.0348 | 0.7900 0.1832 | 5 0.0803 |
| In-dependent perceide Proble Variety & marrier & Colonal | PROX MOUSE 25 PROX MOUSE 26 GOGGA MOUSE 25 | KDa 90% | 76% 76% 81.1 | 1% 10% 18% 1% 100% 100% | 24% 15.97 67% 88.99 | % 0% 6% % 0% 0% | N 0N 2.0% | 86N 92N | 0% 92.5% 0% 0.0% 10 | 7% 0% 0% 0% | 24% 7% | 8% 0% | 5.2% 86% 100 0.0% 0% 0 | N 0N 0.0% N 75N 86.9% | 100% 100% 2 14% 0% | 0% 100,0% 0% 5% 13,1% 0% | 9% 01 9% 01 | 6 0.0% 0% 6 0.0% 92% 6 0.0% 100% | 0% 0% 100% 92% | 0.0% 100% 100 H.9% 0% 0 | N 100% 100.0% ON N ON 0.0% SN | 0% 0% 0.0% 0% 8% 5.1% | 0.1449 0.38 | 0.5458 0.6514 0.4226 | 0.0489 0 | 0.2123 0.6766 0.4226 | 0.4225 0.3858 | 0.1835 |
| ndent RNA helicase Dt Dhs29 sge-binding protein 1 Ddb1 | D19G9_MOUSE 15 D081_MOUSE 12 | KDs 100% | 90 90 93.0 | 75 05 05 | 10% 3.35 | % 9% 11% | 0% 1% 0% 3.7% | 100% 100% 100% 100% | 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 0% | 0% 0% 0% | 0.0% 100% 100 | 100% % 100% 100.0% | 0% 0% | 9% 9% 0.0% 9% | 0% O | 0.0% 89% | 100% 100% | 6.2% 0% 0 | N 0% 9.0% 11% | 0% 0% 3.7% | 0.1846 0.42 | 06 0.5458 0.6514 0.4226 0.4226 0.1846 0.4226 0.1846 0.4226 0.00 0.0720 0.0720 0.0720 0.0720 0.0720 0.0720 | 0.4226 | 0.4225 | 0.4220 | 0.4226 |
| e 5-transferane A3 Geta3 RNA helicane 2 Dds21 | GSTA3_MOUSE 25 DDX21_MOUSE 94 | KDs 100% KDs 27% | 100% 100% 100.0 22% 22% 21.2 | 75 05 05 75 725 675 | 67% 58.75 | % 0% 0% % 0% 0% | s os 0.0% | 100% 100% 23% 20% | 100% 100.0% 0% 17.8% 6 | ON ON ON 27% 80% 100% E | 0.0% 0% 12.2% 0% | 0% 0% 0% 0% | 0.0% 100% 100 0.0% 22% 42 | 5 100% 100.0% 5 42% 39.7% | 0% 0% 58% 57% | 25 27.2% 25 26 0.0% 26 26 57.2% 85 | 0% 00 0% 00 | 6 0.0% 95% 6 0.0% 95% 6 2.8% 33% | 90% 96% 60% 96% 45% 100% | 0.9% SN 22 0.9% SN 45 | 8 4% 5.1% 0% 8 0% 31.8% 17% | 0% 0% 0.0% 9% 0% 0.0% | 0.07 | 0.0720 44 0.1023 0.1672 | 0.2956 | 0.0720 0.2484 0.0275 | 0.0720 0.0666 | 0.3688 |
| SA effector molecule hi Stri me transmission fidelit Chttli Erbin | STRT_MOUSE 10 CTFSA_MOUSE 52 EPBIN_MOUSE 15 | KDs 0% | 25% 25% 16.7 0% | PS 100% 75% | 75% 83.25 | N 0% 0% | 6 05 0.0% | 12% 17% | 60% 23.1% s | 88% 88% 60% 7 | PE.9% 0% | on on | 0.0% 21% 40 0% 0% | S 27% 29.8% 9% 5 9% 0.0% | 79% 60% 100% 0% | 3% 70.4% 0% 0% 0% 7% 55.6% 0% | 0% 0° 0° 200% 22° | 6 0.0% 20% 6 44.4% 0% | 25% 50% 0% 0% | 0.0% 82% 50 0.0% 82% 50 | N 50% 58.3% 0% N 50% 51.1% 17% | 0% 0% 0.0% 50% 50% 38.9% | 0.6211 0.85 | N 0.2755 0.5328 | 0.6211 0 | 0.8571 0.2755 | 0.5328 | 0.8727 |
| d C3 betalinum tesin si Rac I 00-A5 5100at | RAC1_MOUSE 21 5 510A6_MOUSE 10 | KDs 100% KDs 100% | 93% 100% 97.6 100% 100% 100.0 | 7% 0% 0% 7% 0% 0% | 0% 0.05 0% 0.05 | % 0% 79 % 0% 0% | 5 05 2.4% & 05 0.0% | 92% 100% 100% 100% | 100% 97.4% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 8% | 0% 0% 0% 0% | 2.6% 96% 100 0.0% 89% 100 | 5 100% 98.8% 5 92% 93.3% | 0% 0% 11% 0% | 0% 0.0% 4% 9% 6.7% 0% | 0% 01 0% 01 | 5 1.4% 100% 5 0.0% 86% | 100% 100% 1 88% 95% | 0.0% 0% 0 0.0% 14% 12 | N 0% 0.0% 0% N 5% 10.4% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.9608 0.42 0.44 | 26 0.7583 0.4226 87 0.1876 0.0004 | | 0.4447 0.1876 | 0.9608 | 0.4226 |
| splex subunit mu Ap2m1 splex subunit delta-1 Ap3d1 | AP301_MOUSE 50 AP301_MOUSE 13 | KDs 100% KDs 67% | 100% 42% 81.0 60% 75% 67.2 | 7% 0% 0% 2% 0% 0% | 57% 19.01 12% 4.21 | % 0% 0% % 22% 40% | 6 0% 0.0% % 12% 28.0% | 100% 50% 44% 67% | 100% 83.3% 67% 59.3% 1 | 0% 0% 0% 11% 0% 0% | 0.0% 0% 3.7% 44% | 50% 0% 1 22% 22% 2 | 15.7% 69% 78° 17.0% 0% 0 | % 45% 54.2% % 100% 33.3% | 15% 0% 0% 0% | 8% 11.2% 15% 0% 0.0% 100% | 22% 36° 200% 0° | 5 24.7% 78% 5 66.7% 100% | 75N 82N 100N 100N 1 | 8.7% ON O | N 0% 0.0% 22% N 0% 0.0% 0% | 25% 17% 21.3% 0% 0% 0.0% | 0.9297 0.26 0.4176 0.16 | 55 0.4896 0.8083 55 0.4165 0.0315 | 0.4226 0.9379 | 0.1863 0.7255 0.4226 | 0.4226 0.4251 | 0.6526 F 0.1835 |
| cisted protein kinase 2 Rock2 c translation initiation to Elf2s2 A carboxylase 2 Acacb | F2B_MOUSE 16 F2B_MOUSE 36 ACACB_MOUSE 27 | kDa 88% kDa 0% | 90% 89% 89.1 50% | 1% 12% 10% 0% 0% | 11% 10.91 | ns on on | 26 28 28.0% 26 06 0.0% 26 06 0.0% | 82% 90% 0% 0% | 94% 89.0% 1 0% 0.0% 78% 83.5% 1 100% 900.0% | 17% 10% 6% 1 0% 0% 0% | 11.0% ON 0.0% 100% | 0% 0% 100% 100% 10 | 0.0% 100% 100 0.0% 100% 100 | 100% % 100% 100.0% | 0% 0% | 0% 0.0% 0% | ON O | 6 0.0% 100% | 100% 100% 1 100% 100% 1 | 0.0% 0% 0 0.0% 0% 0 | N 0% 0.0% 0% N 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.9723 | 0.0064 0.0662 | 0.9723 | 0.0064 | 0.0692 | , |
| neous nuclear ribonucle Himnpa grading enzyme Ide ne activator complex su Deme t | b ROAA_MOUSE 31 IDE_MOUSE 11 PRME1 MOUSE 20 | kDa 87% kDa 100% kDa 100% | 91% 92% 90.1 100% 100% 100.0 100% 100% 100.0 | 1% 12% 9% 5% 0% 0% 5% 0% 0% | 7% 9.95 0% 0.05 | 7% 01% 01% 7% 01% 01% | 6 0N 0.0% N 0N 0.0% | 92% 92% 100% 100% 100% 100% | 78% 83.5% 1 100% 100.0% 100% 100.0% | 18% 9% 22% 1 0% 0% 0% 0% 0% 0% | 0.0% ON ON | 0% 0% 0% 0% | 0.0% 88% 88 0.0% 100% 100 0.0% 100% 100 | N 80N 85.2% N 100N 100.0% | 12% 13% 0% 0% | 0% 14.8% 0% 0% 0.0% 0% 6% 2.1% 0% | 0% 00 0% 00 | 6 0.0% 92% 6 0.0% 100% 6 0.0% 100% | 92% 92% 100% 100% 1 | 0.8% 7% 7 0.0% 0% 0 0.0% 0% 0 | N 8% 7.2% ON N ON 0.0% ON N ON 0.0% ON | 0% 0% 0.0% 0% 0% 0.0% | 0.2243 0.09 | 76 0.2094 0.1368 NI 0.4726 | 0.2243 0 | 0.0076 0.2094 | 0.1368 | |
| notonemen Interview Ndutc2 | NDUCZ MOUSE 14 STATO MOUSE 00 | KDs 27% KDs 100% | 33% 22% 27.6 83% 0% 51.1 | 2% 55% 44% 1% 0% 0% | 67% 55.25 0% 0.05 | % 18% 22% % 0% 17% | 5 125 17.25 % 1005 36.95 | 26% 22% 0% 200% | 60% 43.2% 3 | 6% 33% 20% 2 0% 0% | 29.9% 27% 100% | 225 225 2 25 | 85.9% 32% 0 92% 82 | 5 295 20.8% 5 295 83.8% | 22% S0% | 2% 42.1% 22% 2% 0.0% 8% | 50% 29° 20% 21° | 5 37.3% 0% 6 95.4% 71% | 20% 0% 100% 100% | 5.7% 28% 60 0.5% 0% 0 | N 67% 54.7% 63% N 0% 0.0% 29% | 20% 22% 38.6% 0% 0% 9.5% | 0.1969 0.33 0.8694 0.56 | 05 0.4226 17 0.5783 0.0085 28 0.5434 0.5645 55 0.1182 0.2183 | 0.0389 | 0.2945 0.1824 | 0.0874 0.1287 0.8694 | 0.9320 6 0.9528 |
| risentialise inhibitor al Gd1 se-activating protein 1 Artigap | GENA MOUSE 51 1 RHG01 MOUSE 50 | KDs 88% KDs 100% KDs 100% | 92% 60% 76.4 100% 100% 100.0 100% 100% 100.0 | 75 125 125 75 05 05 75 05 05 | 60% 23.65 0% 0.05 0% 0.05 | 5 95 05 5 95 05 | N 05 0.05 N 05 0.05 | 100% 100% 100% 100% | 100% 75.9% 3 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 9% 9% 9% 9% | 2.8% 92% 100 0.0% 100% 100 0.0% 100% 100 | 5 100% 97.6% 5 100% 900.0% 5 100% 900.0% | 7% 0% 0% 0% 0% 0% | 95 24% 95 95 9.0% 95 95 9.0% 95 | 9% 01 9% 01 | 6 0.0% 100% 6 0.0% 100% 6 0.0% 100% | 92% 100% 100% 100% 1 100% 100% 1 | 7.8% 0% 7 0.0% 0% 0 0.0% 0% 0 | N 0% 2.2% 0% N 0% 0.0% 0% N 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.9/11 0.96 | IS 0.1162 0.2163 | 0.8801 | 0.1182 | 0.2121 0.4226 | |
| tidase complex subunit Spcs3 rier family 12 member Sic12si constitution reporter Ene 15 | SPCS3_MOUSE 20 2 S12A2_MOUSE 13 EDS15_MOUSE 00 | kOs 67% 1kOs 0% | 61% 76% 67.1 0% 0% 0.0 | 75 295 325 75 05 05 75 1005 1005 | 21% 25.75 0% 0.05 | % 5% 99 % 100% 100% | 5 5% 6.2% N 100% 100.0% | 88% 71% 0% 0% | 79.0% | 8% 17% 14% 1 9% 0% | 13.1% 4% 100% | 12% 7% 100% | 7.9% 80% 80 0% 60 23% 0 | 5 60% 73.3% 5 0% 20.0% | 0% 0% 0% 0% 73% 73% | 0% 10.0% 20% 0% 0.0% 100% 0% 77.4% 6% | 20% 10° 40% 100° | 6 95.7% 6 80.0% 79% | 100% 100% 57% 50% | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | N 0% 0.0% 21% N 0% 0.0% 10% | 0% 0% 43% 50% 38.1% | 0.1265 0.05 0.15 0.16 | 72 0.4697 0.0485 0.4226 0.0187 00 0.0665 | 0.0239 | 0.1007 0.0005 | 0.0340 0.5723 | 0.0377 0.1595 0.8891 |
| er-associated protein 2 Mfsp2 induced very large GT Gwin1 | MFAP2_MOUSE 21 GVIN1_MOUSE 28 | kDa I kDa | 9% | | 75% | | 25% | 0% 0% | os 0.0% | on on on | 0.0% 100% | 100% 100% 10 | 0.0% 0% 0 | s os 0.0% | 75% 79% | 1% 78.3% 25% | 21% 19 | 5 21.7% 0% 67% | 0% 0% | 0.0% 74% 80 0% | N 87% 80.2% 26% 33% | 20% 12% 19.8% | | | | 0.6638 | 0.0020 | 0.6638 |
| lex subunit 4 Alynef well medium polypeptic Nefm | THOCA_MOUSE 27 NFM_MOUSE 96 | KDs 20% KDs | 0% 0% 0.0 20% 21% 25.5 0% 100% 0% 55.7 | 25 80% 20% 20% 200% | 69% 73.11 | % 0% 0% | A 0% 0.0% | 11N 11N 0% | 16% 12.2% S 0% 10 | 9% 99% 86% 8 0% 100% | 57.8% ON ON | 9% 9% 9% | 0.0% 45% 43 0% 0 | S 55% 47.5% S 0% 0.0% | 55% 57% 100% 100% 2 | 5% 52.5% 0% 0% 100.0% 0% | 0% 00 0% 00 | 0.0% 64% 6 0.0% | 50% 50% 0% 0% | 4.5% 36% 50 100 | N 50% 45.5% 0% N 100% | 0% 0% 0.0% 0% 0% | | 22 0.0147 0.0085 0.4225 | | | | 0.4226 |
| se-activating protein 1 Rangag tivated protein kinase i Privag2 vdrocenase lubiculnor Ndurb4 | AAKG2 MOUSE 63 NOUBA MOUSE 15 | KDs 25% | 100% 0% 65.7 100% 50% 30% 35.0 | 75 755 385 | 0% 33.35 60% 57.55 | 06 08 09 76 08 129 | 05 0.05 05 7.55 | 75% 42% | 100% 62% 37.8% 6 | 978 978 978 978 978 978 978 978 978 978 | 25% 53.3% 10% | 25 25 | 100% 100 100% 100 8.9% 0% 0 | 5 100% 100.0% S 100% 100.0% S 25% 8.2% | 0% 0% 0% 0% 91% 100% | 28 0.0% 0% 0% 0.0% 0% 5% 88.6% 9% | 9% 01 9% 01 | 0.0% 100% 6 0.0% 6 3.0% 20% | 100% 100% 1 100% 17% | 8.9% 80% 70 | 0% 0.0% 0.0 8 83% 77.8% 0% | 0% 0% 0.0% 0% 10% 0% 3.3% | | 0.4225 N 0.0702 0.0319 N 0.3545 0.3464 | | | | 0.9495 |
| Xpo1 otein thioesterase 1 Ppt1 | PPT1_MOUSE 12 | KDs 23% KDs 100% | 100% 0% 44.4 100% 100% 100.0 | PS 0% 0% 2% 0% 0% | 0% 0.05 0% 0.05 | % 67% 0% % 0% 0% | 6 100% 55.6% & 0% 0.0% | 50% 50% 100% 100% | 100% 65.7% 1 100% 100.0% | 2% 0% 0% 0% 0% 0% | 5.6% 22% 0.0% 0% | 50% 0% 2 0% 0% | 77.8% 77% 80 0.0% 100% 100 | 5 82% 79.8% 5 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 22% 0% 0.0% 0% | 20% 18° | 5 20.4% 78% 6 0.0% 100% | 83% 100% 100% 100% 1 | 7.0% 11% 0 0.0% 0% 0 | N 0% 3.7% 11% N 0% 0.0% 0% | 17% 0% 9.3% 0% 0% 0.0% | | 35 0.8576 0.7193 | | | | |
| and factor Vell use C delta-binding or Pricob | VWF_MOUSE 30 p PROSP_MOUSE 28 | kDa on | 0% 0% 0.0 | 0% 0% 0% 100% 100% | 100% 100.01 | 900% 100% % 0% 0% | A 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 10 | 0% 0% 0% 100% 100% 10 | 00.0% 0% | 100% 0% 0% | 0% 0 0.0% 0% 0 | % 0% 0.0% % 0% 0.0% | 0% 0% 100% 100% 1 | 0% 0.0% 100% 0% 100.0% 0% | 200% 100° | 6 0.0% 0% | ON ON | 0.0% 0% 0 3.0% 100% 100 | N 0% 0.0% 200% N 91% 97.0% 0% | 100% 100% 100.0% 0% 0% 0.0% | 0.42 | 0.4226 | | 0.4226 | 0.4226 | |
| terase 1D Ces1d associated procester: Pgrmc1 1 (tan1) | CESTD_MOUSE 62 PGRC1_MOUSE 22 ITSN1_MOUSE 19 | kDa 100% kDa 42% | 100% 100% 100.0 56% 29% 42.3 | 7% 0% 0% 9% 29% 32% | 63% 34.95 | % 0% 0% % 29% 11% | 5 0% 0.0% % 29% 22.8% | 78% 50% | 78% 68.5% 1 | 0% 0% 0% 11% 12% 11% 1 | 0.0% 0% 11.6% 11% | 28% 11% 1 | 0.0% 100% 100 19.9% 50% 50 0% 0 | % 20% 40.0% % 20% 40.0% | 25% 17% 100% 100% 1 | 0% 0.0% 0% 0% 20.6% 25% 0% 100.0% 0% | 23% 60° | 6 0.0% 100% 6 39.4% 32% 6 0.0% 8% | 72% S8% 0% 0% | 0.0% 0% 0 4.8% 11% 18 2.8% 92% 100 | N 9% 12.5% 56% N 100% 97.2% 0% | 0% 0% 0.0% 9% 32% 32.7% 0% 0% 0.0% | 0.0984 0.38 | 77 0.8637 0.4078 | 0.036 | 0.1053 0.0548 | 0.7740 0.8027 | 0.7524 |
| e I cytoskeletal 13 Krt13 se subunit o milorbo AlpSI | ATPS_MOUSE 48 | kDs 60% | 25% 25% 16.7 62% 62% 63.1 | PN 50% 50% PN 20% 13% | 50% 50.01 0% 10.81 | % 50% 25% % 20% 25% | 6 25% 33.3% & 22% 25.1% | 0% 27% 83% 75% | 12% 13.3% S 71% 76.6% 1 | 20% SS% 63% 5 (2% 0% 0% | 55.7% SON 5.6% ON | 18% 25% 2 25% 29% 1 | 01.1% 0% 12 17.9% 40% 50 | 5 25% 12.5% 5 40% 43.2% | 75% 63% 0% 0% | 0% 62.5% 25% 0% 0.0% 60% | 25% 25° | 5 25.0% 0% 5 25.7% 33% | 0% 0% 42% 75% | 0.0% SON 80 0.4% ON 0 | N SON 60.0% SON N ON 0.0% 67N | 20% S0% 40.0% 57% 25% 49.6% | 0.7811 0.22 0.0414 0.63 | 54 0.7250 0.2346 54 0.0122 0.1659 | 0.2601 0 0.5482 | 0.8502 0.2254 0.2044 | 0.7169 0.8675 0.4226 0.4665 | 0.2724 |
| Manufalmining D Pulso Manufalmining Pulso Manufal | GALTZ MOUSE 64 PLF60 MOUSE 60 | KDs 20% KDs 0% | 45% 0% 21.8 8% 22% 5.1 | 7% 0% 0% 1% 100% 92% | 29% 9.55 90% 93.95 | % 80% 55% % 0% 0% | 5 72% 68.7% 6 96 9.9% | 100% 25% 0% 0% | 100% 75.0% 0% 0.0% 10 | ON ON ON ON ON 100% 10 | 0.0% 0% 00.0% 0% | 75% 0% 2 0% 0% | 25.0% S0% 0 0.0% 6% 11 | S 22% 27.8% S 12% 11.1% | 0% 0% 94% 89% | 0% 0.0% 50% 2% 85.2% 0% | 200% 67 0% 11 | 5 72.2% 0% 5 3.7% 10% | 0% 10% 50% | 0% 0 0.2% 20% 90 | N 50% 70.0% 20% | 100% 0% 0% 5.7% | 0.1954 0.19 0.1959 0.45 | 86 0.7250 0.2346 94 0.7250 0.2346 94 0.7776 0.0055 33 0.3047 0.2222 95 0.0032 0.4226 13 0.4226 0.1849 | 0.4226 0.1869 0 | 0.4226 | 0.1217 | 0.1994 0.7226 |
| containing protein 1 Ehd1 NuPS3 Nup35 protein Rab-15 Ryb to | NLP53 MOUSE 55 RAB18 MOUSE 22 | 60s 0% 60s 0% | 75% 92% 80.2 0% 0% 0.0 100% 100% 100.0 | 75 125 225 75 1005 1005 75 05 05 | 17% 15.45 100% 100.05 0% 0.05 | 75 9% 10% 75 9% 0% | 5 05 0.0% 5 05 0.0% | 90% 100% 0% 0% 100% 100% | 0% 0.0% 10 100% 100.0% | 976 0% 0% 976 100% 100% 10 976 0% 0% | 0.0% 20% 0.0% 0% | 0% 0% 0% 0% | 9.7% 92% 94 9.0% 96 9 9.0% 100% 88 | 5 100% 95.8% 5 0% 0.0% 5 100% 95.8% | 75 6% 100% 88% 3 0% 0% | 23 42% 0% 0% 95.8% 0% 0% 0.0% 0% | 2% 0 12% 0 12% 0 | 6 4.2% 0% 6 4.2% 0% | 2005 2005 1 205 205 895 885 | 0.0% 91% 100 0.0% 91% 100 0.1% 9% 0 | N 99% 93.3% 9% N 99% 93.3% 9% N 9% 9.0% 9% | 0% 0% 0.0% 0% 11% 5.7% 11% 12% 7.9% | 0.55 | U.0832 0.4228 U.0832 0.1849 | 001/1 | 0.6565 0.4226 | 0.1876 | 0.6595 0.5543 |
| receyborrocysteinus AhcyG ra vesicle-associated Phap amal rucieur ribonu Eff+47 | PLYAP MOUSE 50 USS1 MOUSE 10 | KDs 100% KDs 0% | 100% 100% 100.0 14% 0% 4.8 100% 71% 50.* | 75 05 05 75 05 05 75 05 0° | 0% 0.07 0% 0.07 29% 9.55 | % 0% 0% % 100% 86% | 1 05 0.05 N 100N 95.25 N 0N 0 PA | 100% 100% 32% 8% 100% 100% | 100% 100.0% 0% 13.9% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 0% 0.0% 67% 0.0% 0% | 92% 100% E | 0.0% 100% 100 8.1% 0% 0 0.0% 94% 0 | 5 100% 100.0% 5 0% 0.0% 5 88% 91.4% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 100% 0% 0.0% FM | 200% 100° | 6 0.0% 100% 6 100.0% 0% 6 0.6% 92* | 100% 100% 1 22% 0% 90% 88% | 0.0% 0% 0 1.1% 0% 0 0.2% 0% 0 | N 0% 0.0% 0% N 0% 0.0% 20% N 0% 0.0% 20% | 0% 0% 0.0% 67% 100% 88.9% 10% 12% 9.7% | 0.4226 0.65 | 77 0.9287 0.0289 | 0.4226 | 0.4225 | | 0.6597 |
| ng LIM protein 1 Ablim1 nubunit aloha type-2 Parra2 | PSA2 MOUSE 25 | KDs 0% | 0% 0% 0.0 78% 92% 82.5 | 75 100% 100% 75 21% 22% | 100% 100.05 8% 17.15 | % 0% 0% % 0% 0% | 6 05 0.0% N 05 0.0% | 0% 0% 67% 100% | 0% 0.0% 10 100% 88.9% 3 | 00% 100% 100% 10 12% 0% 0% 1 | 00.0% 0% 11.1% 0% | 0% 0% 0% 0% | 0.0% 0% 0 0.0% 94% 87 | S 85% 88.6% | 100% 100% 1 6% 12% | 0% 100.0% 0% 5% 11.4% 0% | 0% 00 0% 00 | 6 0.0% 0% 6 0.0% 90% | 0% 0% 90% 100% | 0.0% 100% 100 0.2% 10% 10 | N 100% 100.0% ON N ON 5.7% ON | 0% 0% 0.0% 0% 0% 0.0% | 0.6566 0.34 0.2788 | 98 0.3756 0.7335 0.1939 0.4754 | 0.6566 | 0.3488 0.3756 | 0.7335 | |
| ne Galt 1 nucleoprotein comple Dic 1 | GALKI MOUSE 42 DNC1 MOUSE 57 | KDs 100% KDs 0% | 95N 100N 98.2 0N 6N 20 | 75 95 55 75 925 735 | 0% 1.57 82% 82.75 | % 0% 0% % 8% 27% | 5 05 0.05 5 125 15.45 | 100% 100% 0% 12% | 100% 100.0% 0% 4.2% 6 | 0% 0% 0% 2% 50% 52% | 0.0% 0% 95.5% 28% | 0% 0% 28% 42% 2 | 0.0% 100% 100 9.3% 25% 0 | 5 100% 100.0% 5 100% 11.7% | 0% 0% 50% 62% | 0N 0.0% 0N 0N 65.6% 25% | 0% 0 32% 10 | 0.0% 100% 5 22.8% 100% | 100% 100% 1 0% 50% | 0.0% 0% 0 0.0% 0% 2 | N 0% 0.0% 0% N 0% 11.1% 0% | 0% 0% 0.0% 67% 50% 38.9% | 0.4226 0.6963 0.31 | 0.3756 0.7335 0.1939 0.4226 0.4226 12 0.3120 0.2518 10 0.0104 0.0024 | 0.4226 0.0217 0 | 0.4225 0.0002 0.1839 | 0.0439 0.0435 | 0.5128 |
| ssea protein Cd2ap fein Tcof1 onine-crotein kinase F Psk2 | TCOF_MOUSE 13 PAK2_MOUSE 58 | KDs 100% | 17% 0% 5.6 100% 100% 100.0 | 7% 100% 82% 9% 0% 0% | 100% 94.45 0% 0.05 | 0% 0% 0% 0% 0% 0% | 5 0N 0.0% | 14% 20% 100% 100% | 20% 58.1% 8 100% 100.0% | 0% 0% 0% 0% | 0.0% 0% | 0% 0% 0% 0% | 9.0% 44% 50 9.0% 100% 100 9.0% 100% 100 | % 50% 48.1% % 100% 100.0% % 100% 100.0% | 0% 0% 0% 0% | 0% 51.9% 0% 0% 0.0% 0% 0% 0.0% 0% | 0% 00 0% 00 | 6 0.0% 50% 6 0.0% 100% 6 0.0% 100% | 67% 78% 100% 100% 1 100% 100% 1 | 86.4% 36% 33 0.0% 0% 0 0.0% 0% 0 | N 0% 0.0% 0% N 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% 0% 0% 0.0% | | | | | | |
| associated protein MT Mts1 on elonoation factor Si SupiSh ne applytransference North | MTA1 MOUSE 81 SPTSH MOUSE 12 NAT10 MOUSE 12 | KDs On KDs On | 10% 0% 3.3 100% 32% 40.4 | 9% 100% 80% 1% 0% 0% | 100% 93.35 67% 22.56 | % 0% 10% % 75% | N 0N 3.7% | 0% 0% | 0% 0.0% 10 100% 65.7% | 30% 100% 100% 10 | 0.0% 0% | 0% 0% 0% 0% | 0.0% 8% 0 0.3% | % 0% 0.0% % 14% 7.5% | 100% 100% 1 83% 100% | 0% 100.0% 0% 6% 89.7% 8% | 0% 01 0% 01 | 6 0.0% 0% 6 2.8% 0% | ON ON 22% | 0.0% 100% 100 1.1% 100% 100 | N 100% 100.0% ON N 67% 88.9% ON | 0% 0% 0.0% 0% 0% 0.0% | 0.4226 0.78 | 52 0.4751 0.4226 | 0.4226 0 0.4226 | 0.5527 0.5895 | 0.4226 0.4226 0.919 | 0.4226 |
| 10 Arxer10 1 reductase Spr | ANX10 MOUSE 37 SPRE_MOUSE 28 | kDs 100% | 100% 100% 100.0 | 7% 0% 0% | 0% 0.01 | % 0% 0% | ns 0% 0.0% | 100% 100% | 100% 100.0% | 0% 0% 0% | 0.0% 0% | 0% 0% | 90% 100 0.0% 100% 100 | % 100% 96.7% % 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 10% 0% 0.0% 0% | 0% 01 0% 01 | 5 3.3% 94% 6 0.0% 100% | 90% 96% 100% 100% 1 | 0.7% 6% S 0.0% 0% 0 | N 2% 4.1% ON N ON 0.0% ON | 5% 2% 2.2% 0% 0% 0.0% | 0.48 | 52 0.4751 0.4226 57 | - | 0.0642 | | 0.7841 |
| nopy homolog 2 Cripy 2 Plin4 cyde dehydrogenase APANA | PLINA MOUSE 13 2 ALSAS MOUSE 44 | KDs 91% | 100% 100% 100.0 0% 0% 0.0 100% 100% 977 | 7% 0% 0% 2% 67% 75% 2% 05 0% | 0% 0.01 0% 47.21 0% 0.00 | % 0% 0% % 32% 25% | 6 100% 52.8% (6 0) 3.0% | 100% 100% 0% 0% 83% 100% | 100% 100.0% 6 0% 0.0% 6 100% 94.4% | UN 0% 0% 2% 100% 60% 3 0% 0% 0% | 0.0% 0% PS.6% 22% 0.0% 17% | 0% 0% 2 0% 40% 2 | U.U% 100% 100 M.4% 100% 0 5.6% 100% 400 | n 100% 100.0% n 86% 95.2% | 0% 0% 0% 72% 0% 0% | UN 0.0% 0% 0% 0% 0.0% 0% | 0% 01 29% 0% 141 | 6 4.8% 20% | 100% 100% 1 0% 0% 88% 87% | 0.0% 0% 0 100 4.7% 0% 0 | N 006 0.0% 0% N 100% N 006 0.0% XW | 0% 0% 0.0% 0% 0% 12% 12% 15.3% | 0.50 | 00 0.5000 IS 0.7769 0.2156 | 0.3672 0 | 0.3228 0.8148 | 0.1869 0.3672 0.7156 | 0.5000 |
| teine oxidase Poyod synaptotagmin-2 Eayt2 | PCYCK MOUSE 56 ESYT2 MOUSE 94 | KDs 100% KDs 100% | 100% 100% 100.0 100% | 75 05 05 05 05 | 0% 0.05 | 75 95 95 95 95 | s 0x 0.0% | 100% 100% | 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0.0% 0% | 0% 0% 0% | 0.0% 100% 100 9.2% 7.1 0.0% (*** | 5 100% 100.0% 5 67% 73.8% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 12% | 0% 00 29% 23° | 0.0% 100% 5 25.2% 60% | 100% 100% 1 73% 100% | 0.0% 0% 0 7.6% 0% 0 | N 0% 0.0% 0% N 0% 0.0% 40% | 0% 0% 0.0% 27% 0% 22.4% | 0.0447 | 0.0340 | 0.0647 | 0.5983 0.8904 | 0.0059 | 0.7898 |
| containing protein 1 Yipm1 neducer and activator o Stat1 | YLPMI MOUSE 15 STATI MOUSE 87 | KDs 0% | 0% 0% 0.0 82% 100% | 7% 100% 100% 9% | 100% 100.05 0% | % 0% 0% 17% | A 05 0.05 | 0% 0% | 25 | 0% 100% ⁵⁰⁸ | 0% | 0% US | 94% 100 | 5 0% 0.0% 5 70% 88.0% | 100% 100% 1 0% 0% | 0N 100.0% 0N 0N 0.0% 6N | 0% 00 0% 20 | 6 0.0% 0% 6 12.0% 100% | 0% 100% 100% 92% | 0.7% 100% 100 7.4% 0% 0 | N ON 55.7% ON N ON 55.7% ON | 0% 0% 0.0% 0% 8% 2.6% | 0.42 0.41 | 00 0.5000 15 0.7769 0.2156 26 0.0340 27 0.8004 0.0350 28 0.7900 | | 0.4226 | 0.4226 | 0.4159 |
| cussed protein kinase 1 Ask1 s sulfurbaneferase Tat me.c. sometic Cvcs | THER MOUSE 33 CYC_MOUSE 33 | HDs 100% HDs 100% | 0% 0% 0.0 100% 100% 100.0 100% 100% 100.0 | 7% 100% 100% 7% 0% 0% 7% 0% 0% | 0% 0.05 0% 0.05 | 06 05 05 5 06 05 | 5 05 0.05 5 05 0.05 | 0% 0% 100% 100% 100% 100% | 0% 0.0% 10 100% 100.0% 100% 100.0% | 82% 500% 100% 10 0% 0% 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 00% 0 0.0% 100% 100 0.0% 100% 100 | 5 100% 100.0% 5 100% 100.0% | 0% 0% 0% 0% | 77.8% 9% 9% 9.0% 9% 9% 9.0% 9% | 23% 23 0% 0 0% 0 | 5 0.0% 100% 6 0.0% 100% | 100% 100% 1 100% 100% 1 | 0.0% 0% 0 0.0% 0% 0 | N 0% 0.0% 0% N 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | 0.1835 | | |
| ensport protein Sectil a Sectilg actor LDAF 35 kDs sub LDaf1 mail subunit 1 | SOSIG MOUSE 89 LIGAT I MOUSE 28 CPNS1 MOUSE 29 | Da 62% KDa 11% KDa 92% | 71% 41% 58.0 22% 9% 14.1 67% 40% 83.7 | 75 15% 22% 1% 89% 67% 1% 17% 22% | 18% 54.25 82% 79.15 60% 34.75 | 5 23% 199 5 0% 119 | 6 41% 27.8% N 98 5.7% | 53% 50% 10% 0% 80% 100% | 43% 45.5% 1 14% 5.1% 5 100% 93.3% 7 | 13% 12% 14% 1 0% 88% 71% 7 0% 0% 0% | 12.4% 27% 19.6% 10% 6.7% 0% | 28% 42% 2 12% 14% 1 | 99.1% 86% 79 12.3% 26% 21 0.0% 72% 72 | 5 625 74.45 5 185 22.05 5 725 74.95 | 0% 0% 63% 64% | 3% 4.2% 14% 2% 69.8% 11% 8% 11.7% 19% | 25% 25° 14% 0° 15% 0° | 5 21.4% 62% 5 8.3% 25% 5 54.2% 5% | 100% 100% 18% 27% 42% 28% | 8.9% 0% 0 3.5% 75% 73 3.5% 19% 22 | N 0% 0.0% 22% N 72% 73.5% 0% N 19% 23.6% 21% | 0% 0% 11.1% 9% 0% 3.0% 24% 44% 32.9% | 0.3650 0.33 0.3620 0.69 0.1253 0.00 | 03 0.2215 0.0556 09 0.1855 0.0455 01 0.4830 0.0055 0.9790 0.0050 0.4225 04 0.4916 0.8584 00 0.8417 0.0259 | 0.5605 0 0.9520 0 0.1253 0 | 0.4226 0.1231 0.6007 0.3526 0.1210 0.1798 | 0.0075 0.2341 0.3151 0.2422 0.1150 | 0.4550 0.3795 0.0564 |
| I FRA synthase compi. Aimp1 ssome non-ATPase rec. Pamd5 | AIMP1_MOUSE 34 PSMD6_MOUSE 46 | kDa 75% kDa 91% | 71% 72% 72.6 100% 100% 97.0 | 75 258 298 75 98 98 | 28% 27.45 0% 3.05 | % 0% 0% % 0% 0% | 5 05 0.0% 6 05 0.0% | 88% 82% 100% 100% | 78% 82.9% 1 100% 100.0% | 12% 17% 22% 1 0% 0% 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% 86% 72° 0.0% 100% 100° | 5 60% 72.4% 5 100% 100.0% | 14% 29% 0% 0% | 0% 27.6% 0% 0% 0.0% 0% | 9% Of | 6 0.0% 100% 6 0.0% 100% | 100% 100% 1 100% 100% 1 | 0.0% 0% 0 0.0% 0% 0 | N 0% 0.0% 0% N 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.0499 0.06 0.4226 | 0.9790 0.0260 0.4225 | 0.0499 0 | 0.0055 0.9790 0.4225 | 0.0260 | |
| | ALITE MANUEL 14 | kDs 17% | 0% 0% 5.0 | 5% SON SON | 70% 56.75 | % 33% S0% | 66 306 37.8% | ON 20% | 25% 17.9% S | 29% 29% 25% 2 | MAN CON | 439 709 4 | 200% 100° | 100% 100.0% | 200 FAN | 6% 34.6% 63% | GW 22 | 0.0% 100% | 4445 2005 1 | 50 00 0 | N 0% 0.0% 0% | MA 98 0.0% | 0.7208 0.83 | TAL O SOME DIRECT | 0.0000 | 0.1021 0.1925 | 0.0675 0.2454 | 0.0589 |

| instruction of the control of the co | CPT2 MOUSE HTRA1 MOUSE 513AB MOUSE PTN23 MOUSE | 130 KDa 74 kDa 8 51 kDa 11 kDa 10 | 9% 100% 9% 67% 9% 0% | 93% 93.0% 9% 9% 77.8% 9% 0.7% | N 0% N 000 | 9% 32% 3 100% 17 | 7% 7.0% 0% 33% 22.2% 00% 100.0% | 9% 0 9% 0 | 000 0.0 | 0% 100% 0% 0% 0% 100% | 100% 1009 00 100% 1009 25% 00 | 100.0% | 0% 0% 0% 0% 0% 75% | 0% 0.0 0% 0.0 100% | % 0% 100% % 0% | 0% 0% 200% 0% 0% 0% /** | 0.0% 10 | 0% 0% 00% 100% 0% 0% 79% 72% 0% 0° | 0% 0.05 100% 100.05 0% 0.05 82% 78.35 0% 0.76 | S 96% S 67% S 16% S 22% | 86% 77% 6% 6% 75% 6% 12% 14% 50% 85% | 82.8% 1 0.0% 47.2% 3 14.3% 73.0% | 4% 14% 9% 9% 2% 25% 5% 12% 2% 50% | 22% 17.2% 0% 0.0% 100% 52.8% 2% 7.3% 14% 27.0% | 0% 0% 100% 100% 0% 0% 86% 82% 0% 0% | 0% 0.05 100% 100.05 0% 0.05 89% 00.15 | 71% 611 9% 91 50% 501 11% 121 50% 94 | 25% 58.9% 0% 0.0% 23% 44.4% 7% 10.4% 100% 56.7% | 29% 29% 9% 0% 50% 50% 4% 2% 50% 50% | 25% 31. 9% 0. 67% 55. 4% 3. 9% 33 | 9% 0.2327 9% 0.1835 5% 0.1835 3% 0.5000 | 0.0864 | 0.2327 0.9644 0.0 0.5 0.8513 0.1 0.0572 0.4 | 0.2327 0.1835 000 0.5000 | 0.0570 0.9185 0.1485 0.5 0.7715 0.1 0.3754 0.9 0.6728 0.0 | 2327 0.0153 5503 0.0285 1441 0.3912 | 0.05 0.91 0.33 0.77 | 188 0. 715 0. |
|--|--|--|-----------------------------------|---|--------------------------|----------------------------|---|---|---|-------------------------------|--|---|--------------------------------|--|------------------------|----------------------------------|-------------------------------|--|---|----------------------------------|--|--|---|--|---|--|--|---|---|---|--|----------------------------|---|---|--|--|---|----------------------|
| Plin 1 ociated protein MT Mts2 olein 14 Ptr 14 | PLINI MOUSE MTA2 MOUSE PRR14 MOUSE | 11 150a 10 105 100 105 100 105 100 105 100 105 100 105 100 105 100 105 105 | 0% 8% 0% 0% 0% 0% 17% | 22% 13.7% 0% 0.0% 0% 12% 18.8% | N 88% N 100% 100% | 77% 6 89% 10 | 67% 77.0% 00% 95.3% 00% 83% 70.5% | 13% 15 9% 11 9% | N 0% 9.7 N 0% 3.7 | 25 258 75 05 | 9% 00 9% 00 | 9.2% | 0% 100% 0% 100% | 67% 72.2 50% 50.0 | % 25% % 100% | 0% 33% 0% 50% | 19.4% 50.0% 2 | 9% 42% 20% 10% 9% | 0% 16.95 10% 13.25 0% | S 82% S 80% 100% | 46% 200% 80% 90% 200% | 75.9% 83.3% | 9% 13% 9% 19% 9% | 0% 7.2% 0% 3.3% 0% | 64% 17% 22% 0% 0% 0% | 27% 29.55 9% 7.45 9% 0.05 | 22% 821 67% 1001 100% 1001 | 45% 54.0% 100% 88.9% 100% 100.0% | 22% 0% 11% 0% 0% 0% | 27% 16. 0% 3. 0% 0. | 5% 0.7045 7% 0% 6% 0.4132 | 0.4582 0.5223 | 0.0513 0.1 0.0572 0.4 | 431 0.7843 226 0.2467 | 0.3754 0.5 0.6728 0.0 | 1441 0.3912 9512 0.4353 0606 0.3105 | 0.4302 0.39 0.2487 0.94 | 0.7 644 0.5 |
| ISO 3A13 Cyp3x13 Isoprotein comple Gar1 I chain Tubbüb | CPSAD_MOUSE GAR1_MOUSE TBB2B_MOUSE | ST KDa 23 KDa 50 KDa | 0% 0% 0% 25% | 0% 0.0% 20% 15.0% | N 100% N 80% | 100% 10 50% 6 | 00% 100.0% 60% 63.3% | 0% 15 0% 11 0% 15 15% 17 0% 0 20% 25 11% 28 | ns on 0.0 | 100% 0% 0% 7% 25% | 200% 2007 0% 07 0% 07 | 100.0% 0.0% 10 0.0% 10 | 0% 0% 0% 100% 5% 50% | 0% 0.0 100% 100.0 50% 41.7 | % 0% % 0% % 50% | 0% 0% 0% 0% 50% 50% | 0.0% 0.0% 50.0% 3 | 0% 0% 28% 29% | 0% 0.05 29% 35.25 | S 100% S 52% | 100% 100% 64% 50% | 100.0% 48.9% 1 | 0% 0% 0% 17% | 0% 0.0% 21% 15.9% | 20% 86% 20% 0% 52% 50% | 90% 92.05 0% 5.75 55% 52.65 | 90% 01 80% 1001 40% 441 | 0% 0.0% 100% 93.3% 27% 37.2% | 9% 14% 9% 9% 7% 6% | 20% B. 0% D. 18% 10. | 0% 0% 1% 0.5873 | 0.4225 | 0.1 0.4 0.1024 0.0 | 982 226 308 0.1489 | 0.4226 0.1389 0.2 | 0.3055 0.3055 0.4422 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.4226 0.3235 0.3651 0.3236 0.3651 0.3236 0.3651 | 0.0034 0.34 | A24 0. |
| subfamily C ment Drajc11 roleoglycan Prg2 sen inhibitor heavy 19h1 | PRG2 MOUSE ITIHI MOUSE | 53 kDa 1 54 kDa 101 kDa | 1% 25% 0% 100% | 6% 14.1% 0% | N 78% | 28% S | 81% 65.5% 0% | 11% 28 200% 0 | % 12% 20.4 100% | 4% 60% 0% | 0% 225 0% 05 | 0.0% | 0% 50% 0% 50% | 23% 41.T 50% 33.3 | % 20% % 100% | 50% 33% 50% 50% | 34.4% 65.7% | 0% 0% 4% 0% 68% 90% | 0% 0.09 0% 1.49 41% 63.09 | % 0% % 57% % 11% | 0% 0% 50% 60% 0% 12% | 0.0% 10 55.5% 3 7.5% 3 | 0% 100% 9% 50% 1% 20% | 100% 100.0% 40% 43.0% 47% 29.5% | 0% 0% 19% 0% 67% 62% | 0% 0.09 0% 6.59 1 100% 76.49 | 22% 601 0% 01 | 0% 0.0% 64% 52.0% 0% 0.0% | 200% 100% 48% 40% 22% 28% | 100% 100. 36% 41. 0% 23. | 0% 0.5064 6% 6% | 0.5220 0.4631 0.0518 | 0.1285 0.1 0.4226 0.4 0.4226 0.0 | 869 0.2181 226 0.1835 | 0.7801 0.6 0.1844 0.4225 0.4 | 0433 0.0136 0025 0.4224 | 0.1835 0.78 0.1835 0.78 | 941 0.0 123 |
| omain protein 1 Lasp1 Histitric e non-ATPase nec Pand12 | LASP1_MOUSE H12_MOUSE PSD12_MOUSE | 50 kDa 50 20 kDa 5 21 kDa 10 53 kDa 8 | ON SON ON SON ON SON | 100% 55.7% 100% 55.7% 100% 100.0% | N 50% N 0% N 17% | 50% 0% 15% | 0% 33.3% 0% 0.0% 8% 13.2% | 0% 0 0% 0 | N | 0% 60% 0% 100% | 80% 1009 100% 1009 92% 1009 | 80.0% 100.0% 100.0% | 0% 0% 0% 0% 0% 0% | 0% 20.0 0% 0.0 0% 6.1 | % 0% % 0% | 0% 0% 0% 0% 0% 0% | 0.0% 9 | 92% 100% 90% 92% 92% 100% 82% 90% | 82% 88.35 100% 97.45 80% 83.95 | % 20% % 8% | 9% 17% 9% 0% 0% 0% 10% 10% | 11.7% 2.6% 9.7% | 0% 0% 0% 0% 9% 0% | 0% 0.0% 0% 0.0% 10% 5.4% | 100% SSN 100% 100% 100% 100% | 96% 93.69 1 20% 100.09 1 20% 100.09 | 0% 151 0% 01 0% 01 | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0. 0% 0. 0% 0. | 0% 0.5509 0% 0.1632 | 0.3803 0.4226 0.0348 | 0.3226 0.3 0.4226 0.5364 0.1 | 851 0.5509 869 0.1632 | 0.3803 0.3 0.4226 0.4 0.0010 0.3 | 3226 0.3651 4226 3324 0.1869 | 0.18 | 84 0 |
| se-crotein kinase C DcR1 sembly protein 1-1 Nap14 Lgalc3 | DCLK1_MOUSE NP1L4_MOUSE LEG3_MOUSE | M kDa K3 kDa 8 27 kDa | 2% 91% | 82N 86.7N | N 13% | 9% 1 | 18% 13.3% | 0% 0 | ns on o.c | 0% 100% | 100% 1009 | 100.0% | ON ON | 0% 0.0 | % 0% | 0% 0% | 0.0% 10 | 17% 32% 00% 94% 30% 26% | 0% 16.75 100% 98.15 9% 21.75 | % SO% % O% % 20% | 50% 500% 6% 0% 70% 95% | 55.7% 3 1.9% 75.8% | 2% 17% 0% 0% 0% 4% | 0% 95.7% 0% 0.0% 0% 1.4% | 47% 59% 100% 100% 37% 11% | 69% 57.09 1 100% 100.09 1 0% 15.79 | 60% 321 0% 01 57% 891 | 26% 33.1% 0% 0.0% 100% 82.0% | 12% 7% 0% 0% 7% 0% | 9% 9. 9% 0. 9% 2. | 8% 0% 0.0377 2% | 0.0324 0.4225 0.6572 | 0.0292 | 0.0377 | 0.1763 0.4225 0.7481 | 0292 | 0.55 | 275 |
| e C1 inhibitor Serping1 dair and debute Alad Calu | HEM2 MOUSE CALU MOUSE | 55 kDa 10 55 kDa 10 57 kDa 6 | 0% 100% 7% 100% | 100% 100% 100.0% 40% 58.9% | N 0% N 22% | 9% 9% 6 | 0% 0.0% 60% 31.1% | 9% 0 9% 0 | 0% 0% 0.0 % 0% 0.0 | 0% 100% 0% | 100% 1009 100% 509 | 100.0% | 0% 0% 0% | 0% 0.0 50% | % 0% | 0% 0% 0% 0% | 0.0% 10 6 | 00% 100% 00% 100% 61% 53% | 100% 100.05 100% 100.05 78% 63.85 | S 0% S 0% S 26% | 9% 9% 9% 9% 47% 22% | 0.0% 0.0% 36.2% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 85% 83% | 200% 100.05 200% 100.05 90% 86.75 | 0% 01 0% 01 15% 171 | 0% 0.0% 0% 0.0% 10% 13.9% | 9% 9% 9% 9% | 0% 0. 0% 0. 0% 0. | | | | 338 0.8597 | | | | # |
| pain 2 MCBI2 pain Pth1 pping protein Capg Airam | FRH MOUSE CAPG MOUSE | 21 kDs 10 29 kDs 10 | 0% 100% 0% 100% | 100% 100.0% | 9% N 9% | 9% 9% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | N 0N 0.0 | 0% 0% 100% | 100% 679 100% 1009 | 55.6% 10 100.0% | 00% 00% 00% 00% | 22% 44.4 0% 0.0 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 2 0.0% 2 0.0% 10 | 72% 70% 00% 100% 00% 100% | 69% 70.75 94% 98.05 | S 27% | 30% 21% 0% 6% | 29.3% 2.0% | 2% 2% 2% 2% | 0% 0.0% 0% 0.0% | 88% 86% 90% 96% | 200% 91.17 88% 91.47 | 12% 141 12% 41 | 0% 8.9% 12% 8.6% | 9% 9% 9% 9% | 0% 0. 0% 0. | 0% 0.2697 0% | 0.0391 | | 501 0.2697 768 | | | | = |
| in-trans isomeras Fktp2 odifier 1 Ufm1 dase 1 reculators Ppp1r12a | PREP2 MOUSE UPM1 MOUSE MYPT1 MOUSE | 15 kDa 9 2 kDa 6 115 kDa 2 | 5% 100% 4% 57% 5% 50% | 100% 98.5% 63% 61.1% 0% 25.0% | S 5% S 26% S 75% | 9% 43% 3 50% 10 | 0% 1.5% 28% 38.9% 00% 75.0% | 9% 0 9% 0 | ns 200 0.0 | 0% 100% 0% 44% 0% 50% | 100% 1009 64% 899 0% 09 | 100.0% 65.7% 16.7% | 0% 0% M% 18% 6% 100% | 0% 0.0 11% 24.0 100% 83.7 | % 0% % 11% % 0% | 0% 0% 18% 0% 0% 0% | 0.0% 10 9.8% 10 0.0% 4 | 00% 100% 00% 75% 44% 58% | 100% 100.05 60% 78.35 50% 50.95 | 5 0% 5 0% 5 56% | 0% 0% 25% 40% 42% 50% | 0.0% 21.7% 49.1% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 75% 75% 42% | 200% 100.09 80% 55.79 | 0% 01 0% 251 25% 581 | 0% 0.0% 20% 34.3% | 9% 9% 9% 9% | 0% 0. 0% 0. | 0% 0.4226 0.7581 0% 0.7250 | 0.6352 0.3405 | 0.4226 0.2760 0.3 0.2087 0.0 | 0.4226 1185 0.2916 616 0.7250 | 0.6352 0.2 0.3406 0.2 | 4225 2760 0.5233 2087 0.0816 | 0.2063 | |
| ein 1 Free!1 bining protein 4 Ehd4 | FMNL1 MOUSE EHD4 MOUSE | 15 kDa 122 kDa 51 kDa 10 | 0% 100% | 100% 100.0% | S 08 | 9% | 0% 0.0% | 9% 0 | n on o. | 2% 100% | 100% 1009 | 100.0% | os os | 0% 0.0 | % 0% | 0% 0% | 0.0% 10 | 80% 100% 0% 10% 100% | 100% 93.35 100% 900.05 90% 88.75 100% 98.25 | S 20% | 0% 0% 0% 0% | 6.7% 0.0% 11.3% 1.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 20% 29% 0% 100% 93% | 50% 32.95 100% 97.65 | 90% 711 01 0% 71 | 50% 67.1% 0% 2.4% | 9% 9% 100% 9% 9% | 0% 0. | 9% 9% 0% | 0.4225 | 0.4 | 226 | 0.4225 | 0.4226 | | |
| Ctab Cat stol 4-kinase alol PHka | CATE MOUSE CATA MOUSE PHICA MOUSE | 37 KDs 8 50 KDs 10 237 KDs | 0% 100% 0% 100% 0% | 99% 89.0% 100% 100.0% | S 20S S 0S | 9% 9% | 0% 0.0% 0% | 9% 0 9% 0 | m 0% 0.0 m 0% 0.0 m 100% | 0% 100% 0% 100% 0% | 200% 2009 200% 2009 0% 09 | 100.0% | 0% 0% 0% 0% | 0% 0.0 0% 0.0 | % 0% % 0% | 0% 0% 0% 0% 100% 100% | 0.0% 9 0.0% 9 100.0% 10 | 92% 94% 95% 100% 10% | 90% 88.75 100% 98.25 100% | S 5% 5% | 16% 10% 0% 0% 0% | 1.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 95% 100% 100% 100% 100% | 100% 98.29 100% 100.09 | 9% 91 9% 91 | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0. 0% 0. | 9% | 0.4226 | 0.4225 | | 0.4225 0.4 | 4225 | | |
| essing factor 19 Ptpf19 protein 1 Cdc42sp1 myosin-ld Myo1d | PRP19_MOUSE : BORGS_MOUSE - MYO10_MOUSE | 55 kOs 3 K3 kOs 116 kOs 10 | 8% SON 0% 0% 0% | 45% 44.3% 0% 0.0% | N 63% N 100% OK | 50% S | SSN 55.7% DON 100.0% | 0% 0 0% 0 | ns on 0.0 | 0% S0% 0% 0% | 25% 1009 0% 09 | 58.3% 1 0.0% st | 20% 75% 20% 100% | 0% 41.7 100% 100.0 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 5 | 20% 20% 20% 20% 200% | 58% 63.75 6% 0.05 50% | % 42% % 100% | 20% 42% 100% 100% 0% 0% | 34.6% 100.0% | 5% 0% 0% 0% | 0% 1.8% 0% 0.0% 50% | 84% 81% 0% 0% 100% 100% | 1 200% 88.49 0% 0.09 1 200% 100.09 | 11% 291 100% 1001 0% 01 | 0% 9.9% 100% 100.0% 0% 0.0% | 5% 0% 0% 0% 0% 0% | 0% 1. 0% 0. 0% 0. | | 0.0796 0.5000 0.1885 | 0.1322 0.3 | 044 0.5917 | 0.0582 0.0 | 0.2836 | 0.50 | 1000 |
| th factor-regulat Higs ad polypeolide 2 Tropo ng protein 1 Citip 1 | LAP2B_MOUSE : CTBP1_MOUSE : | 95 kOs 2 50 kOs 2 16 kOs 1 | 0% 0% 5% 50% 1% 0% | 0% 0.0% 20% 31.7% 0% 3.7% | N 100N N 12N N 89N | 200% 10 0% 4 200% 10 | 00% 100.0% 40% 17.5% 00% 95.3% | 0% 0 62% S0 0% 0 | ns des 0.0 ns den 50.8 ns des 0.0 | 0% 0% 8% 17% 0% 0% | 0% 09 20% 409 0% 09 | 0.0% st 25.6% 0.0% st | 00% 100% 0% 0% 00% 100% | 100% 100.0 20% 6.7 100% 100.0 | % 0% % 83% | 0% 0% 80% 40% 0% 0% | 0.0% 67.8% 4 0.0% 1 | 0% 0% 60% 50% 12% 25% | 0% 0.05 40% 43.35 12% 18.15 | % 100% % 27% % 81% | 100% 100% 0% 0% 75% 82% | 100.0% 8.9% 3 79.9% | 0% 0% 3% 50% 6% 0% | 0% 0.0% 60% 47.8% 0% 2.1% | 25% 20% 36% 38% 18% 64% | 0% 15.09 59% 43.19 29% 30.49 | 75% 801 9% 151 72% 441 | 0% 85.0% 0% 8.2% 57% 58.1% | 9% 0% 9% 11% | 0% 0. 45% 48. 14% 11. | 0% 7% 0.6333 5% 0.4226 | 0.1885 0.9767 0.3449 | 0.3367 0.1 0.0513 0.0 | 885 351 0.4803 877 0.4226 | 0.1885 0.5462 0.5 0.1065 0.6 | 0.1885 5038 0.8628 0.057 0.0361 | 0.3549 0.91 | |
| laining protein 1 Sh3d19 few res. rethin Rgrd2 olein ADE2 Paics | RPRD2_MOUSE PURE_MOUSE | 55 kDs 157 kDs 17 kDs 8 | 0% 2% 80% | 9% 80.1% | N 18% | 200% 10 20% 2 | 21% 19.9% | 9% 0 | N 9N 9.5 | 0% 0% 100% | 9% 09 199% 1999 | 0.0% si 100.0% | 0% 100% 0% 0% | 100% 100.0 0% 0.0 | % 0% % 0% | 0% 0% 0% 0% | 0.0% | 0% 0% 10% 100% | 9% 91% 97.05 | 100% 100% % 0% | 100% 100% 0% 9% | 3.0% | 0% 0% 0% 0% | 0% 0% 0.0% | 0% 0% 100% 100% | 0% 0.09 100% 100.09 | 100% 1001 100% 1001 0% 01 | 100% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0. 0% 0. | 0% 0% 0.0022 | 0.4226 | 0.0229 | 0.0022 | 0.4225 0.0 | 0229 | | # |
| Assist too see 5002 Assist reculate Ccar2 and TDR recent Total | ASAHI MOUSE - | 15 kDs 10 103 kDs 5 | 25 805 0% 100% 0% 20% | 100% 100.0% 0% 23.3% 0% 27.8% | N 9% | 9% 90% 10 | 0% 0.0% 0% 70.0% | 9% 0 9% 20 | m on 0.0 m on 5.7 | 2% 100% 7% 50% | 100% 1009 100% 1009 50% 1009 | 93.3% 100.0% 66.7% | 0% 0% 0% 50% | 9% 0.0 9% 16.7 | % 0% % 0% % 50% | 9% 9% 9% 9% 75% 100% | 0.0% 10 9.7% 2 98.7% 2 | 25% 23% 25% 23% | 100% 100.05 100% 100.05 50% 36.15 | S 0% | 9% 9% 9% 99% | 0.0% 33.3% 2 | 9% 9% 5% 67% | 0% 0.0% 0% 0.0% 0% 30.6% | 100% 96% 75% 75% | 100% 98.75 100% 98.75 | 9% 91 9% 251 | 0% 0.0% 0% 0.0% | 9% 4% 25% 9% | 9% 1 67% 30 | 2% 5% 0.1229 0% 0.7067 | 0.4225 0.2087 | 0.4905 0.8 0.1994 0.2 | 025 H09 0.0782 | 0.2739 0.1 | 1027 0.8287 1027 0.6856 | 0.42 0.6214 1.00 0.7067 | 225 |
| lein SAR1b Sar1b Papin H domain-contai Zc3h4 | PPN_MOUSE ZC3H4_MOUSE | 22 kDa 9 139 kDa 141 kDa | 4% 80% 0% 0% | 90% 84.7% 9% 9.0% 90% 87.5% | N 9% | 9% 100% 10 | 0% 0.0% 00% 100.0% | 6% 20 0% 0 | ns 20% 15.3 | 2% 86% 2% 0% | 75% 925 05 05 | 84.1% | 0% 0% 0% | 0% 0.0 100% 100% | % 14% 0% | 25% 8% 9% 9% | 15.9% 16 | 00% 100% 0% 0% 0% | 86N 95.25 | S 200% | 0% 0% 100% 100% 80% | 93.3% | 0% 0% 0% 0% 0% | 165 4.8% 205 6.7% | 100% 100% 0% 0% 0% 0% | 200% 100.05 0% 0.05 0% 0.05 | 0% 01 100% 1001 100% 1001 | 0% 0.0% 100% 100.0% 100% 100.0% | 9% 9% 9% 9% | 0% 0. 0% 0. 0% 0. | 0% 0.9360 0% 0.6863 0% 0.6863 0% 0.2842 | 0.4226 | 0.1908 0.0 | 828 | 0.4225 0.4 | 4226 | 0.9350 0.42 | 226 |
| eductase SCR Dhrs1 Nucb1 nit alpha troe-6 ParreS | NUCBI_MOUSE PSA6_MOUSE | 54 kDs 8 53 kDs 10 27 kDs 8 | 2% 100% 0% 100% 9% 92% | 90% 87.5% 100% 100.0% 96% 91.8% | S 12% S 0% S 11% | 9% 2 9% 7% | 00% 100.0% 20% 11.0% 0% 0.0% 6% 8.2% | 4% 0 9% 0 9% 0 | ns 0% 0.0 ns 0% 0.0 ns 0% 0.0 | 4% 88% 2% 100% 2% 90% | 85% 1009 100% 1009 100% 1009 | 91.0% 100.0% 95.7% | 0% 15% 0% 0% 0% 0% | 0% 5.7 0% 0.0 0% 3.7 | % 12% % 0% | 0% 0% 0% 0% | 3.9% 10 0.0% 10 0.0% 10 | 00% 100% 00% 90% 00% 100% | 100% 100.05 87% 92.45 100% 100.05 | S 0% | 0% 0% 10% 13% 0% 0% | 0.0% 7.6% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 81% 80% 100% 100% | 200% 100.05 26% 79.05 200% 100.05 | 2% 01 19% 201 0% 01 | 0% 0.0% 26% 21.0% 0% 0.0% | 9% 9% 9% 9% | 0% 0. 0% 0. | 0% 0.6863 0% 0.2842 | 0.0628 | 0.1855 0.1 0.1945 0.0 0.0319 0.4 | 907 0.4925 052 225 0.2842 | 0.0628 0.1 0.0628 0.6 | 4225 2010 0.4226 1945 0.0052 0319 0.4226 | 0.6028 | |
| protess Tata3 persons class-3 Adh5 I death protein 5 Pdcd5 | ADHOL MOUSE POCOS MOUSE | 22 (22 (23 (23 (23 (23 (23 (23 (23 (23 (| 0% 100% 0% 100% 7% 22% | 100% 100.0% 100% 100.0% 33% 31.3% | S 05 S 455 | 9% 22% 3 | 0% 0.0% 23% 77.4% | 9% 0 27% 22 | m 0% 0.0 m 28 21.2 | 2% 100% 2% 100% 2% 45% | 200% 2009 200% 2009 45% 509 | 100.0% 100.0% 47.0% | 0% 0% 0% 0% | 0% 0.0 0% 0.0 13% 22.7 | % 0% % 0% | 0% 0% 0% 0% 27% 28% | 0.0% 10 0.0% 10 30.7% 6 | 10% 100% 10% 100% 62% 57% | 100% 900.05 100% 900.05 44% 54.45 | S 0% | 0% 0% 0% 11% | 0.0% 0.0% 8.8% 2 | 0% 0% 0% 0% 2% 42% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 60% 50% | 100% 100.05 100% 100.05 64% 57.95 | 0% 01 0% 01 10% 17 | 0% 0.0% 0% 0.0% 0% 8.9% | 0% 0% 0% 0% 30% 33% | 0% 0. 26% 33. | 0% 0% 2% 0.0044 | 0.6224 | | | | 0.009 0.1232 3513 0.6012 | | _ |
| Pro2b non-ATPasse rec Parnd11 B Abhd14b | PROSE MOUSE PSD11 MOUSE ABHER MOUSE | 161 KDs 17 KDs 7 22 KDs 10 | 0% 0% 5% 77% 0% 100% | 9% 7.2% 0% 0.0% 29% 76.8% 200% 100.0% 200% 100.0% 0% 0.0% | N 100% N 25% N 0% | 20% 10 23% 3 | 00% 100.0% 21% 23.2% 0% 0.0% | 0% 0 0% 0 | 75 | 0% 100% 0% 100% | 0% 09 100% 1009 100% 1009 | 100.0% 100.0% 100.0% 100.0% | 100% 0% 0% 0% 0% | 100% 0% 0.0 0% 0.0 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 10 | 0% 0% 00% 100% 00% 100% | 0% 0.05 100% 100.05 100% 100.05 | N 100% N 0% | 100% 100% 0% 0% 0% 0% | 100.0% 0.0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 100% 100% | 0% 0.09 100% 100.09 | 100% 1001 0% 01 | 100% 100.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 9% 0. 9% 0. 9% 0. | 0% 0% 0% 0% | | 0.0020 | 0.0020 | 0.0 | 0020 | | |
| 6 dehydratase Greds protease serine Trepras13 and apoptosis Ccar1 | GMDS_MOUSE TMPSD_MOUSE CGAR1_MOUSE | 12 kDa 10 50 kDa 132 kDa | 0% 100% 0% 0% 0% | 100% 100.0% 100% 0% 0.0% | N 0% 100% N 100% | 9% 199% 10 | 0% 0.0% 0% 00% 100.0% | 0% 0 0% 0 | 0% 0.0 0% 0% 0.0 | 0% 100% 100% 0% 0% | 100% 1009 100% 509 0% | 100.0% 8 83.3% | 0% 0% 0% 0% 0% 100% | 0% 0.0 50% 16.7 | % 0% % 0% 0% | 0% 0% 0% 0% | 0.0% 10 0.0% 5 | 00% 100% 50% 50% 10% | 100% 100.05 22% 44.45 13% | % 0% % 50% 70% | 0% 0% 0% 32% 62% | 0.0% 27.8% | 0% 0% 0% S0% 0% | 0% 0.0% 32% 27.8% 25% | 100% 100% 50% 32% 0% 20% | 1 100% 100.09 1 50% 44.49 1 0% 5.79 | 0% 01 0% 321 22% 401 | 0% 0.0% 50% 27.8% 22% 35.6% | 0% 0% 50% 23% 67% 40% | 0% 0. 0% 27. 67% 57. | 0% 8% 0.6244 8% | 1.0000 0.5549 | 0.9296 0.1 0.0704 0.4 | 341 0.6244 226 | 10000 0.7 00000 0.0 | 7347 0.6437 0.0012 | 1.00 | .000 496 |
| 1 Thbs 1 2 Tpd52 factor GTPsse- Artgsp2 | TSP1_MOUSE TPD52_MOUSE AFFG2_MOUSE | 130 kDa 34 kDa 9 57 kDa | 2% 89% 0% 7% | 100N 93.9N 0N 2.2N | N 9% N 99% | 11% 99% 10 | 0% 6.1% 00% 95.4% | 0% 0 7% 0 | ns on 0.0 | 0% 86% 4% 6% | 200% 881 0% 01 | 91.3% | 00% 00% 00% 1000% | 12% 8.7 100% 97.9 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 10 0.0% | 64% 61% 00% 89% 0% 0% | 43% 49.55 86% 91.55 0% 0.05 | % 23% % 0% % 100% | 28% 32% 11% 14% 100% 100% | 31.1% 2 8.5% 100.0% | 2% 11% 0% 0% 0% 0% | 25% 19.4% 0% 0.0% 0% 0.0% | 90% 100% 92% 100% 0% 0% | 1 200% 93.39 1 87% 93.09 1 0% 0.09 | 8% 01 100% 1001 | 0% 3.3% 12% 7.0% 100% 100.0% | 20% ON 0% ON 0% ON | 0% 3. 0% 0. | 3% 0.6571 0% 0.9558 0% 0.9000 7% 0.8000 | 0.0081 | 0.6801 0.7 0.4226 0.4 | 963 0.6571 226 0.4634 | 0.8143 0.8 0.8143 0.8 | 5801 0.7893 1540 0.4226 | 0.4226 0.4056 0.57 0.8038 0.55 0.6247 0.79 | D4 |
| ier homolog 2 Mich2 | MTCHE MOUSE NUTSE MOUSE NUTSE MOUSE | 109 KDs 13 KDs 4 129 KDs | 95 95 95 755 95 95 | 21% 63.6% 0% 0.0% | S 100% S 0% S 62% | 25% 6 20% 8 | 0% 0.0% 0% 0.0% 83% 83.2% | 9% 25 56% 25 33% 0 | N 28% 18.4 N 28% 36.4 N 17% 16.7 | 4% 25% 4% 67% 7% 0% | 235 601 235 601 | 66.5% | 0% 0% 0% 100% | 0% 0.0 | 5 33% 100% | 27% 40% 0% | 33.5% 1 | 22% 0% 12% 18% 0% 0% | 11% 13.95 0% 0.05 | S 05 S 05 | 25% 62% 25% 25% 25% 17% | 0.0% s 5.0% s | 25 255 85 825 05 2005 | 225 99.45 895 86.15 825 96.45 | 22% 12% 25% 0% | 0% 46.79 0% 11.69 0% 5.29 | 0% 401 0% 01 | 0% 13.3% 14% 4.8% 0% 0.0% | 28% 88% 78% 100% | 200% 40. 86% 83. 200% 91. | 7% 0.8038 7% 0.8038 | 0.7560 0.4226 | 0.0306 0.0 0.4 | 341 0.6344 226 863 0.6571 226 0.4634 861 0.003 842 226 0.6247 | 0.4225 0.4225 0.4225 | 0.4225 0.4225 0.5000 | 0.8038 0.55 0.6247 0.79 | 532 972 |
| oribosvitansfe Naprt Seotide-binding Hint1 sin 2/3 complex Arpo4 | PNCB MOUSE HINTI MOUSE ARPCA MOUSE | 50 kDa 10 14 kDa 8 20 kDa 10 | 0% 100% 3% 89% 0% 100% | 100% 100.0% 100% 90.7% 100% 100.0% | % 0% % 17% % 0% | 0% 11% 0% | 0% 0.0% 0% 9.3% 0% 0.0% | 9% 0 9% 0 | ns 200 0.0 | 2% 100% 2% 91% 2% 100% | 100% 1009 100% 939 100% 1009 | 100.0% 94.6% 100.0% | 9% 0% 9% 0% | 9% 0.0 7% 5.4 9% 0.0 | % 0% % 0% | 0% 0% 0% 0% 0% 0% | 0.0% 10 0.0% 10 0.0% 10 | 00% 100% 00% 100% 00% 100% | 100% 100.0% 100% 100.0% 100% 100.0% | S 0% | 0% 0% 0% 0% | 0.0% 0.0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% | 200% 100.05 200% 100.05 200% 100.05 | 0% 01 0% 01 | 0% 0.0% 0% 0.0% 0% 0.0% | 9% 9% 9% 9% | 0% 0. 0% 0. 0% 0. | 0% 0.5408 0% 0.5408 | | 0.1994 0.1 | 893 0.5408 | 0.1 | 1994 0.1893 | | Ξ |
| 1 PSI 3-kinase adacé Piklap1 se 1 reculators Ppp1r12c | JANES ANDERS JANES ANDERS JANES ANDERS JAN | 21 kDs 4 21 kDs 25 kDs | 0% 17% 0% 0% | 25% 27.2% 0% 0.0% | N 60% N 71% | 62% 2 68% 6 | 75% 67.2% 67% 66.9% | 9% 17 29% 38 | % 0% 5.5 % 22% 23.5 | 8% 23% 1% 0% | 0% 285 0% 05 | 0.0% | 77% 100% 80% 42% | 63% 79.8 22% 34.6 | % 0% % 60% | 0% 0% 58% 78% | 0.0% 4 65.4% | 62% 42% 0% 0% | 50% 46.75 0% 0.05 | S 678 S 678 | 57% 50% 50% 100% | 51.5% 72.2% 3 | 5% 0% 3% 50% | 0% 1.8% 0% 27.8% | 44% 67% 0% 100% 100% | 62% 59.29 | 9% 281 9% 91 | 295 35.4% | 9% 6% 200% 0% 0% | 5% 5. | 3% 0.6194 | | | | | 0471 0.0344 7522 0.0308 | | 700 347 |
| Catb hate dehidroos Gpd1 sunit alpha-1 Ap2a1 | GPDA_MOUSE AP2A1_MOUSE | 11 kDa 10 35 kDa 10 105 kDa | 0% 100% 0% 100% 0% 100% | 100% 100.0% 100% 100.0% 0% 23.3% | N 98 N 98 N 98 | 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 9% 0 9% 0 200% 0 | N 0N 0.0 N 0N 0.0 N 100N 66.7 | 0% 100% 0% 100% 7% 0% | 100% 1009 100% 1009 50% 509 | 100.0% 100.0% 33.3% | 0% 0% 0% 0% 0% 0% | 9% 0.0 9% 0.0 | % 0% % 0% | 0% 0% 0% 0% 50% 50% | 0.0% 10 0.0% 10 66.7% 2 | 00% 100% 00% 100% 78% 50% | 91% 97.05 100% 100.05 20% 49.35 | S 0% | 9% 9% 9% 9% 9% 9% | 3.0% 0.0% 0.0% 2 | 0% 0% 0% 0% 2% 50% | 0% 0.0% 0% 0.0% 80% 50.7% | 100% 90% 100% 100% 63% 60% | 89% 90.09 100% 100.09 42% 55.19 | 0% 901 0% 01 0% 201 | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 28% 20% | 0% 0. 0% 0. 57% 38. | 0% 0% 2% 1.0000 | 0.7671 | 0.6985 0.3 | 218 | 0.4225 | 0.1846 0.4226 | 1.0000 0.50 | 675 |
| Lbr cer-binding fact IE3 | LER MOUSE ILF3 MOUSE ENTRY MOUSE | F1 KDs 10 65 KDs | 0% 57% 0% 50% | 25% 60.7% 0% 15.7% | N 9% N 100% | 9% 50% 10 | 0% 0.0% 00% 83.3% | 0% 42 0% 0 | 75 75 39.3 N 0N 0.0 | 2% 67% 0% 0% | 50% 753 17% 01 | 63.9% 5.6% 10 | 0% 0% 0% 83% | 0% 0.0 100% 94.4 | % 23% % 0% | 50% 25% 0% 0% | 36.1% 3 0.0% 4 | 26% 67% 40% 40% | 28% 46.85 67% 48.95 | S 0% | 9% 9% 9% 9% 60% 33% | 0.0% 6 51.1% | 4N 33N 6N 0N | 63% 53.2% 0% 0.0% | 20% 50% 88% 100% | 80% 50.07 100% 95.87 | 0% 01 12% 01 | 0% 0.0% 0% 4.2% | 90% 50% 0% 0% | 20% 50. 0% 0. 2% 4 | 0% 0.9005 0% 0.5813 | 0.8838 0.0197 0.0526 | 0.8048 0.5 0.1850 0.0 | 193 003 0.5813 | 0.0197 0.1 | 1850 0.0003 | 0.9005 0.88 | 1838 |
| Mpo dicular 87 Kn87 se (NADPH) 3 Cbr3 | PERM_MOUSE KRTS7_MOUSE CBR3_MOUSE | 51 kDa 55 kDa 51 kDa | 0% 100% | | on. | 0% | | 200% O | ns. | | | | | | | | 20 | 100% 100% 100% | 100% 100.09 | s os | 0% 0% 0% | 0.0% | 0% 0% 0% | 0% 0.0% | 100% 100% 100% 95% | 96% 97.09 | 0% 01 | 4% 30% | 0% 0% 0% 0% | 0% 0. | 0% | 0.1897 | | | 0.1897 | | | Ξ |
| fein complex si Emc1 -GAP domain Arap1 -amplified segu Bcas1 | ARAPI_MOUSE BCASI_MOUSE BCASI_MOUSE | 112 kDs 3 162 kDs 57 kDs | 2% 40% | 50% 41.1% | N 17% | 40% 3 | 20% 25.6% | 50% 20 | ns 30% 33.3 | 2% 67% | 75% 809 | 73.9% | ON ON | 0% 0.0 | % 22% | 25% 20% | 26.1% 5 | 50% 50% 29% 100% 0% | 50% 50.05 0% 42.95 0% | % 0% % 43% | 0% 0% 0% 75% 100% 100% | 0.0% S 39.3% 3 | 0% 50% 9% 0% 0% | 50% 50.0% 25% 17.9% 0% | 32% 0% 50% 100% 75% 14% | 1 32% 22.25 1 88% 79.25 1 56% 48.25 | 0% 01 12% 01 25% 861 | 0% 0.0% 0% 4.2% 66% 51.7% | 67% 100% 28% 0% 0% 0% | 67% 77. 12% 16. 0% 0. | 8% 0.0070 7% 0% | 0.1296 0.3565 0.1144 | 0.2079 0.0 | 0.0728 085 039 0.6277 635 0.4228 | 0.0 0.2449 0.1144 | 0726 | 0.5126 0.12 | 375 |
| tivatino protein i Rap Igap Coro Is | RPGP1_MOUSE CORIC_MOUSE | 73 kDs 10 53 kDs 10 | 9% 17% 9% 10% | 6% 13.8% 100% 100.0% | N 71% N 0% | 72% S | 93% 75.7% 0% 0.0% | 10% 11 0% 0 | % 11% 10.6 % 0% 0.0 | 5% 6% 5% 100% | 7% 01 200% 821 | 43% (| 0% 97% 0% 0% | 56% 70.3 17% 5.0 | N 25% | 7% 44% 0% 0% | 25.4% | 12% 72% | 92% 83.75 | 5 85 | 22% 20% 22% 12% | 14.4% | 0% 6% 0% 6% | 0% 0.0% 0% 1.9% | 92% 98% 92% 88% | 0% 0.09 92% 90.09 | 100% S01 | 0% 500% 0% 500% | 0% 50% 0% 4% | 100% 50. 5% 2. | 0% 0.1368 8% 0.4226 | 0.3706 | 0.1128 0.5 | 839 0.6277 835 0.4226 | 0.1994 0.0 | 0.5508 0.553 0.8740 | 0.3078 | 1936 |
| medit rendered Lipper on render faring Lipp2 aining family or Ythoff3 | LPPRC_MOUSE LTBP2_MOUSE YTHD0_MOUSE | 157 KDa 10 195 KDa 54 KDa | 0% 100% 0% 0% | 100% 100.0% 0% 0.0% | N 0% | 9% 100% 10 | 0% 0.0% 00% 100.0% | 9% 0 | 55 05 05 05 05 05 05 05 05 05 05 05 05 0 | 0% 100% 0% 0% | 200% 0% 07 | 0.0% 10 | 0% 0% 0% 100% | 100% 100.0 | 0% % 0% | 0% 0% | 0.0% | 00% 100% 0% 0% | 100% 100.05 0% 0.05 | N 90% | 9% 9% 82% 199% 199% 199% | 0.0% 90.6% 1 | 0% 0% 0% 18% 0% 0% | 0% 0.0% 0% 9.4% 0% 0.0% | 100% 100% 0% 0% | 01 0.09 | 0% 01 75% 1001 | 100% 91.7% 100% 100.0% | 25% 0% 25% 0% | 0% B. | 2% | | | | | | 0.92 | 204 |
| dehydrogenase Bickdha cort receptor aut Torren70 containing links Clig1 | TOM/O MOUSE (CUP1 MOUSE | 50 kDs 8 56 kDs 2 156 kDs 10 | 1% 84% 5% 22% 0% 100% | 88% 84.3% 25% 27.8% 100% 100.0% | S 19% S 62% S 0% | 26% 2 62% 2 | 12% 15.8% 75% 68.1% 0% 0.0% | 9% 0 13% 0 9% 0 | N 0% 0.0 N 0% 4.2 N 0% 0.0 | 2% 67% 2% 67% 2% 100% | 200% 1009 0% 1009 | 88.9% | 12% 0% 12% 100% | 9% 11.1 9% | % 0% 0% | 0% 0% 0% | 0.0% 10 | 00% 100% 18% 0% | 100% 100.05 0% 6.15 | S 0% S 55% | 9% 9% 50% 75% | 0.0% 59.8% 2 | 0% 0% 2% 50% | 05 0.0% 25% 38.1% | 20% 20% 100% | 200% 14% 18.17 | 0% 60% 201 0% | 0% 57% 62.4% | 2% 10% 2% 10% | 29% 19. | 0.7185 5% 0.8949 | 0.1774 | 0.0129 0.4 0.0520 0.7 | 225 0.7185 270 0.9735 | 0.7883 0.4 | 0.4226 4095 0.9187 | | 943 |
| 5 Rabi5 sion-enhancing Resp5 noncos/cenase Fmc2 | REEPS MOUSE FMO2 MOUSE | 50 kDs 1 21 kDs 9 51 kDs 10 | 0% 7% 5% 79% 0% | 25% 27.8% 200% 100.0% 0% 5.7% 200% 91.3% 200% 0.0% 0% 0.0% | S 90% S 0% | 99% 10 9% | 00% 94.3% 0% 0.0% | 9% 0 5% 21 9% | N 9% 8.7 | 7% 8% 7% 86% 100% | 29% 105 94% 865 | 15.0% | 9% 71% 9% 9% 9% | 90% B4.4 0% 0.0 | % 0% % 14% 0% | 0% 0% 6% 14% | 0.0% S 11.5% S | 50% 0% 50% 100% 100% | 33% 27.85 100% 100.05 | S 50% | 100% 67% 0% 0% | 72.2% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% | 100% 100% 100.09 | 2001 01 0% 01 | 0% 0% 0.0% | 0% 0% 0% | 0% 0% 0. | 0.2545 0.7255 | | 0.2700 | 0.2645 | 0.2 | 2700 | 0.7255 | |
| toskeletal 23 Kr23 arbonylate carri Sic25a10 Pof1b | DIC MOUSE POF18 MOUSE | 12 kOs 5 52 kOs 5 | 0% 0% 0% 50% | 29% 42.9% | S 100% S 25% | 25% d | 425 21.05 | 25% 25 | N 281 25.3 | 2% 0% 2% 50% | 9% 00 59% 753 00 | 58.2% | 0% 100% 5% 0% | 0% 8.7 100% | % 0% % 25% | 9% 9% 59% 25% 9% | 23.2% 3 | 0% 0% 0% 2% | 20% 0.05 22% 21.75 0% 0.05 | S 100% S 100% | 100% 200% 14% 22% 100% 200% | 15.9% 6 100.0% | 2% 52% 2% 52% | 0% 0.0% 22% 52.4% 0% 0.0% | 0% 0% 12% 29% 0% 0% | 201 20.47 | 9% 161 9% 161 82% 961 | 0% 4.8% 94% 92.3% | 98 578 128 48 | 9% 74 6% 7 | 9% 0.2329 7% 0.4225 | 0.1220 | 0.2573 0.0 | 0.0989 | 0.3799 0.2 0.1054 | 2675 0.7332 | 0.4825 0.17 | 708 054 |
| in Rab-2A Rab2a C5 Rab11 | RABZA MOUSE COS MOUSE RUVEI MOUSE | 24 kDs 10 189 kDs | 0% 100% 2% 22% | 100% 100.0% 40% 35.6% | N ON | 9% 62% 6 | 0% 0.0% 60% 64.4% | 9% 0 | % 0% 0.0 | 0% 100% 0% 25% | 93% 1009 25% 09 | 97.6% | 0% 0% 5% 75% | 0% 0.0 100% 83.7 | % 0% % 0% | 2% 0% 0% 0% | 2.4% 10 0.0% 3 16.7% | 00% 100% 00% 100% 22% 22% | 100% 100.09 100% 100.09 | S 0% S 0% | 0% 0% 0% 0% 72% 57% | 0.0% | 0% 0% 0% 0% 5% 6% | 0% 0.0% 0% 0.0% | 100% 100% 100% 59% 60% | 100% 100.09 | 0% 01 01 41% 401 | 0% 0.0% | 0% 0% 0% | 9% 0. 9% 0. 9% 0. | 7% 0.4226 0% 0.4226 0% 0.4226 | | 0.4603 0.0 0.2254 | 0.1440 | | 0.0157 0.077 0.4226 | | 628 |
| toskeletal 17 Krt17 anosensitive ion Piezo2 vadenvistion so Nud21 | PIEZZ MOUSE CPSFS MOUSE | NS KOs 126 KOs 26 KOs | 0% 25% 0% 0% | 50% 25.0% 0% 0.0% | N 50% | 75% S | 50% 58.3% 86% 82.0% | 50% 0 | ns on 15.7 | 7% 0% 0% 0% | 0% 09 1009 0% 09 | 0.0% | 20% 100% 10% 67% | 100% 83.3 0% 67% 71.1 | % 50% % 20% | 0% 0% 0% 23% 23% | 15.7% 28.9% 1 | 0% 0% 15% 29% | 288 31.79 0% 0.00 100% 100.07 100% 100.07 100% 100.07 100% 100.07 100% 100.07 100% 100.07 100% 0.00 0% 0.00 0% 0.00 0% 0.00 0% 0.00 0% 0.00 | % 100% % 60% | 100% 100% 57% 82% | 100.0% | 0% 0% 5% 14% | 0% 0.0% 9% 12.9% | 20% ON | 0% 0.09 i 57% 40.29 | 100% 1001 42% 501 | 100% 100.0% | 0% 0% 25% 20% | 0% 0. 0% 15. | 0% 0.2254 0% 0.4226 0% 0.4226 | 0.1041 | 0.0912 0.0 | 0.2739 HDN 0.1954 | 0.0010 0.2 | 0377 0.4226 2354 0.0122 0505 0.1057 2090 0.7503 | 0.1954 0.81 | 540 |
| dino orolein Luc Luc7Q substory subunit - Parec 1 inhibitor Ppp Ir138 | PRS4_MOUSE 4 IASPP_MOUSE 1 | 17 kDs 19 kDs 6 19 kDs | 0% 0% 9% 79% 0% | 8% 2.8% 82% 76.3% 0% | N 32% 100% | 94% 5 22% 1 | 92% 91.0% 18% 23.7% | 13% 6 0% 0 0% | N ON 6.3 | 3% 0% 0% 88% 0% | 71% 1000 | 0.0% st | 20% 85% 12% 25% 20% | 100% 95.3 0% 13.7 | % 0% % 0% | 11% 0% 0% 0% | 0.0% 2 | 29% 25% 77% 92% 0% 0% | 9% 20.95 86% 85.05 0% 0.05 | % 56% % 23% % 100% | 67% 82% 8% 14% 100% 100% | 70.9% 15.0% 100.0% | 7% 8% 0% 0% 0% 0% | 9% 8.2% 0% 0.0% 0% 0.0% | 11% 25N 82% 75N 0% 0N | 40% 25.49 90% 82.89 0% 0.09 | 17% 251 100% 1001 | 60% 74.8% 10% 17.2% 100% 100.0% | 0% 0% 0% 0% | 0% 0. 0% 0. | .0% 0.4226 .0% 0.3549 | 0.6871 | 0.0761 0.0 | 902 0.2902 303 0.3849 | 0.7321 0.0 | 0555 0.1057 2099 0.7303 | 0.6482 0.00 | на |
| Colec 12 15 Service TERRO Trim25 | COL12 MOUSE TR25 MOUSE | 11 kOs 72 kOs 2 | 2% 20% | 22% 21.5% | S 22S | 20% | 225 25.25 | 56% 60 | % 44% 53.3 | 25 95 | 11% 209 | 13.4% | 6% 22% | 20% 25.2 | % 55% | 62% 62% | 00.4% | 005 75% 32% 32% | 0% 0.05 0% 0.05 0% 58.35 25% 30.65 | S 0% | 0% 0% 12% 25% | 0.0% 25.0% | 0% 25% 2% 50% | 100% 41.7% 50% 44.4% | 60% 100% | 100% B5.75 | 0% 01 | 0% 0.0% 0% | 40% 0% 40% 0% | 9% 13 9% 0 | 2% 0.1315 | 0.4571 | 0.0736 | 0.8857 | 0.4226 0.6 | 9391 9391 9319 0.1835 | 0.45 0.2945 0.6934 | 1571 |
| see if commit Aboc3 Seotide exchano Arhgef1 se 1 Ephx1 | NUPS MOUSE COL12 MOUSE TRUS MOUSE ACOUSE ACOUSE ACOUSE ACOUSE ACOUSE ACOUSE ASHED MOUSE FRAPI MOUSE ERAPI MOUSE ITHE MOUSE ITHE MOUSE 41 MOUSE AND MOUSE GAPPA MOUSE | 160 kDa 103 kDa 53 kDa 10 | 0% 0% 100% | 100% 100.0% | N 05 | 200% 9% | 0% 0.0% | 9% 0 | 05 05 0.0 | 0% 100% | 75% 1001 | 91.7% | 0% 0% | 0% 0.0 | 5 05 | 25% 0% | 5.2% | 100% 100% 88% 100% 67% 100% | 100% 95.85 100% 85.95 | S 12% | 9% 9% 9% 9% | 4.2% 0.0% 3 | 9% 9% 9% 9% | 0% 0.0% 0% 11.1% | 100% 80% 100% 100% 78% 87% | 88% 89.25 100% 100.05 85% 83.75 | 9% 91 9% 91 | 0% 0.0% 0% 0.0% | 9% 20% 9% 0% 22% 12% | 12% 10. 0% 0. 15% 16. | 25 | | _ | | | | _ | _ |
| culum aminopeo Erap1 lation initiation fa E/69h vitransferase 1-5 Ugitla6 | ERAPT MOUSE IF4H MOUSE UD16 MOUSE | 107 kDa 27 kDa 8 50 kDa | 2% 82% | 100% 88.4% | N 18% | 17% | 0% 11.6% | 9% 0 | N 0% 0.0 | 2% 86% | 57% 1009 | 81.0% | MX 42% | 0% 19.0 | % 0% | os os | 0.0% 9 | 00% 100% 92% 100% 92% 100% | 100% 100.05 100% 97.25 92% 94.25 | S 0% S 8% S 0% | 9% 9% 9% 9% | 0.0% 2.8% 0.0% | 0% 0% 0% 0% 9% 0% | 0% 0.0% 0% 0.0% 8% 5.8% | 100% 100% 100% 100% 89% 90% | 100% 100.09 100% 100.09 88% 88.99 | 0% 01 0% 01 | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 11% 10% | 0% 0. 0% 0. 12% 11. | 0% 0.6317 1% | 0.4226 0.2105 | 0.2683 0.2 | 0.6317 | 0.4225 0.2 | 2683 0.2697 1573 5000 | 0.21 | 105 |
| Epb41 yosin-VI Myo5 hala ouanviltar Greppa | MYOS MOUSE GMPPA MOUSE | 65 KDs 145 KDs 15 KDs 10 | 9% 8% 9% 100% 9% 100% | 0% 4.9% 100% 100.0% | N 94% 100% N 9% | 82% 10 9% 9% | 0% 92.4% 0% 9.0% | 9% 8 9% 0 9% 0 | % 0% 2.5 % 0% 0.0 | 8% 0% 100% 0% 100% | 200 1000 1000 1000 | 100.0% | 0% 100% 0% 0% | 9% 0.0 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 25 0.0% 25 | 0% 20% 00% 100% 00% 100% | 0% 6.79 100% 100.09 100% 100.09 | S 25% S 0% S 0% | 9% 9% 9% 9% 9% 9% | 74.6% 2 0.0% 0.0% | 5% 20% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 93% 71% 100% 100% | 96% 83.29 200% 100.09 | 0% 01 0% 01 | 0% 0.0% 0% 0.0% | 7% 29% 9% 0% | 100% 14% 15. 0% 0. | 7% 0% | 0.5584 | 0.5000 | 000 0.2567 | 0.0123 0.1 | 1573 | 0.4226 0.38 | 101 |
| ochore protein ; Zerlü ein, mitochondris Nidufab I mentary homolo Erh | ACPM MOUSE ERH MOUSE INACH MOUSE | 17 kDa 2 17 kDa 8 12 kDa 6 | 5% 67% 6% 86% 7% 32% | 57% 66.3% 69% 75.1% 69% 46.7% | N 9% N 9% N 9% | 9% 1 67% 6 | 0% 0.0% 13% 4.2% 60% 42.2% | 25% 22 20% 14 22% 0 | ns 42% 23.7 ns 25% 19.8 ns 20% 11.1 | 7% 80% 8% 83% 7% 67% | 40% 530 100% 1000 75% 1000 | 94.4% 90.6% | 9% 9% 9% 9% 19% 25% | 0% 0.0 0% 0.0 0% 19.4 | % 20% % 17% % 0% | 9% 9% 9% 9% | 39.2% 3 5.0% 3 0.0% 5 | 22% 0% 75% 100% 57% 50% | 9% 11.15 99% 75.05 99% 52.45 | S 0% | 0% 0% 0% 25% 50% 50% | 8.3% 2 47.6% | 2% 200% 5% 0% 0% 0% | 25% 16.7% 0% 0.0% | 0% 0% 50% 32% 72% 66% | 200% 51.17 200% 73.07 | 2% 67 12% 50 18% 50 | 0% 0.0% 0% 27.8% 0% 24.0% | 22% 0% 22% 0% | 9% 11. 9% 3 | 0% 0.0862 1% 0.1121 0% 0.0766 | | | | | 5855 0.2999 8234 0.8214 | | 111 226 |
| non-ATPase ne: Pamd5 s-trans isomeras Fkbp4 osamine ovroot Uap III | PSMOS MOUSE FREIPS MOUSE UAPIL MOUSE | 55 kDa 10 52 kDa 8 57 kDa 9 | 0% 100% 6% 100% 2% 100% | 100% 100.0% 100% 95.2% 100% 97.2% | N 0% N 0% N 8% | 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 2.8% | 0% 0 14% 0 | ns ons 0.0 ns ons 4.3 ns ons 0.0 | 0% 100% 8% 100% 0% 81% | 100% 1009 100% 1009 94% 1009 | 90.0% 900.0% 90.0% 91.6% 100.0% | 0% 0% 0% 0% | 0% 0.0 0% 0.0 0% 6.0 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 10 0.0% 10 1.0% 10 | 00% 100% 00% 100% 00% 100% | 100% 100.05 100% 100.05 100% 100.05 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% | 200% 100.09 200% 100.09 200% 100.09 | 0% 01 0% 01 0% 01 | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0. 0% 0. 0% 0. | 0% 0.4226 0% 0.4342 | | 0.4226 0.4226 0.2 | 714 0.4661 | 0.4 | 4226 0.2336 | 0.4226 0.4226 | |
| ASS rbrane divcoor: Nup210 sin of 170 kDs Cep170 | PO210_MOUSE : CE170_MOUSE : | 51 kDs 10 204 kDs 175 kDs | 0% 100% 0% | 100% 100.0% 0% | N ON | 0% 0% | 0% 0.0% | 0% 0 100 | ns 200% | 0% 100% 32% | 200% 2009 0% 09 | 100.0% | ON ON | 0% 0.0 0% 0.0 | % 0% % 67% | 0% 0% 100% 100% | 0.0% 10 88.9% | 00% 100% 0% 0% 0% 0% | 100% 100.05 0% 0.05 0% 0.05 | % 0% % 0% % 100% | 0% 0% 0% 0% 100% 100% | 0.0% 10 0.0% 10 | 0% 0% 0% 200% 0% 0% | 0% 0.0% 100% 100.0% 0% 0.0% | 92% 86% 0% 0% 0% | 100% 92.79 | 0% 01 0% 01 100% | 0% 0.0% | 8% 14% 200% 200% 0% | 0% 7. | 0.4226 | 0.2179 | 0.4 | 1179 026 | | | 0.4226 | .79 |
| elessing enzym Apeh Actrib | APEH MOUSE I ACTY_MOUSE I | 27 kDs 10 12 kDs 10 12 kDs 6 | 0% 100% 0% 100% 7% 78% | 100% 100.0% 100% 100.0% 86% 76.7% | N 0% N 0% N 22% | 0% 0% 22% 1 | 0% 0.0% 0% 0.0% 14% 23.3% | 0% 0 0% 0 | mi 0% 0.0 mi 0% 0.0 | 0% 100% 0% 100% 0% 75% | 100% 1009 100% 1009 88% 829 | 100.0% 100.0% 8 81.9% | 0% 0% 0% 0% | 0% 0.0 0% 0.0 17% 18.1 | % 0% % 0% | 0% 0% 0% 0% | 0.0% 10 0.0% 10 0.0% 8 | 00% 100% 00% 100% 82% 62% | 100% 100.05 100% 100.05 86% 77.25 | % 0% % 0% % 17% | 0% 0% 0% 0% 25% 34% | 0.0% 0.0% 18.7% | 0% 0% 0% 0% 0% 12% | 0% 0.0% 0% 0.0% 0% 4.2% | 100% 100% 100% 100% 82% 75% | 1 200% 100.09 1 200% 100.09 1 75% 77.89 | 0% 01 0% 01 | 0% 0.0% 0% 0.0% 12% 8.3% | 0% 0% 0% 0% 17% 13% | 0% 0. 12% 13. | 0% 0% 9% 0.4811 | 0.9453 | 0.9625 0.4 | 204 0.4811 | 0.1268 0.5 | 5187 0.1561 | 0.13 | 341 |
| protein 1 Shc1 renkein BATO Rad23b dum_Gold into Entir1 | SHC1 MOUSE R023B MOUSE | 53 kDs 10 53 kDs 8 53 kDs 8 | 0% 0% 9% 100% | 91% 93.3% 91% 93.3% | S 0% | 100% 10 0% | 00% 65.7% 9% 6.7% | 9% 0 9% 0 | m 0% 0.0 m 0% 0.0 m 50% 29.2 m 17% 15.1 m 0% 1.2 | 0% 100% 0% 88% 2% 01% | 100% 887 62% 724 | 91.7% | 0% 0% 0% 0% 0% | 12% 8.7 | 0% % 0% | 0% 0% 12% 27% | 0.0% 10 | 0% 0% 00% 80% | 0% 0.05 100% 93.35 | S 100% | 100% 100% 20% 0% | 100.0% 6.7% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 67% 100% 100% | 200% 500.75 200% 100.05 | 22% 22% 0% 01 | 0% 0.0% 0% 0.0% | 9% 9% 9% 9% 9% 9% | 0% 0 0% 0 | 0% 0.7819 0% 0.7466 | 0.1257 0.4226 0.5382 | 0.4226 0.9934 0.1 0.6075 0.6 | 835 0.7819 | 0.1257 0.4 0.4225 0.9 | 4225 9934 0.1835 | 0.7466 0.53 | 382 |
| ranscription for Biclaff milate reductors Pyor 1 rotein 1 Gig1 | PSCR1_MOUSE PSCR1_MOUSE GSLG1_MOUSE | 105 kDa 12 kDa 10 134 kDa | 0% 0% 0% 88% | 0% 0.0% 83% 90.4% | % 100% % 0% | 71% S 8% 3 | 82% 84.9% 17% 8.2% | 0% 29 0% 4 | % 17% 15.1 % 0% 1.2 | 7% 0% 2% 96% | 995 953 995 953 | 95.8% | 0% 67% 0% 4% | 100% BS.9 0% 1.3 0% | % 0% % 4% | 22% 0% 0% 5% 200% | 11.1% 2 2.9% 16 0.0% 16 | 20% 0% 00% 100% 00% 100% | 0% 6.75 100% 100.05 90% 96.75 | S 90% | 100% 100% 0% 0% 0% 0% | 93.3% 0.0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 10% 3.3% | 0% 0% 100% 100% 100% 100% | 20% 100.05 200% 100.05 | 100% 1001 0% 01 0% 01 | 100% 100.0% 0% 0.0% 0% 0.0% | 9% 9% 9% 9% | 0% 0. 0% 0. 0% 0. | 0% 0.3925 0% 0.3925 | 0.4226 | 0.4225 | 0.7900 023 0.2836 | 0.4225 0.4 | 4225 9834 0.1835 4751 0.4226 2297 0.4226 | 0.7900 0.4712 0.42 | 1226 |
| coll domain-cor Gcc2 tein GCP60 Acbd3 | GCC2 MOUSE GCP60 MOUSE ELAVI_MOUSE | 194 KDa 50 KDa 3 56 KDa 8 | 0% 0% 8% 27% 2% 62% | 0% 0.0% 27% 30.8% 25% 73.6% | N 100% N 62% N 12% | 200% 10 72% 2 28% 2 | 00% 100.0% 72% 69.2% 25% 25.4% | 9% 0 9% 0 | N 0% 0.0 N 0% 0.0 N 0% 0.0 | 0% 0% 0% 26% 0% 71% | 20% 00 20% 443 80% 863 | 0.0% 10 33.4% 0 79.0% | 00% 100% 60% 90% 90% 20% | 100% 100.0 56% 66.0 14% 21.0 | % 0% % 0% % 0% | 0% 0% 0% 0% 0% 0% | 0.0% 0.0% 3 0.0% 6 | 0% 0% 36% 17% 68% 100% | 36% 29.85 77% 81.85 | 100% % 64% % 32% | 100% 83% 64% 0% 23% | 70.2% 18.2% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 50% 93% 93% | 60% 56.79 100% 96.49 | 100% 40% 501 2% 21 | 60% 43.2% 0% 4.6% | 0% 0% 0% 0% | 0% 0. 0% 0. | 0% 0.7705 0% 0.5050 | 0.0362 0.2035 | 0.9029 0.0 0.5130 0.0 | 645 0.7705 0.5050 | 0.0062 0.5 0.2835 0.5 | 9029 0.0545 5130 0.0386 | 0.42 | |
| ne calcium-trans Abūb1 dino protein 1-lik Filip11 el polymerane 1 Parp1 | PARPI MOUSE PARPI MOUSE MECH MOUSE | 130 KDa 130 KDa 113 KDa 10 | 0% 82% | 100% 94.4% | N ON | 17% | 0% 5.6% | 9% 0 | n 0x 0.0 | 9% | 100% 1000 100% | 919" | 0% 0% | 9% | | 0% 0% 0% | 20 | 955 985 95 95 995 1995 | 0% 0.09 100% 100.09 | 05 5 1005 5 05 | 0% 0% 100% 100% 0% 0% | 0.0% 100.0% 0.0% | 9% 9% 9% 9% 9% 9% | 0% 4.2% 0% 0.0% 0% 0.0% | 100% 100% 0% 20% 100% 100% | 200% 100.05 0% 5.75 200% 100.05 | 2% 01 100% 801 0% 01 | 0% 0.0% 100% 93.3% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0. 0% 0. 0% 0. | 9% 9% 9% | 0.4226 | 0.4226 0.2063 ^ * | 226 0.8709 0.4226 | 0.4225 0.4 0.2 | 4226 2063 0.4226 4226 | 0.42 | uo |
| Faltachment or Napa F2 protein, solder Fabo5 | SNAA MOUSE THRE MOUSE FABPS MOUSE | MH MOR | 0% 100% 0% 100% | 92% 97.0% 92% 97.0% 100% 100.0% | N 0% 0% N 0% | 9% 9% | 0% 4.9% 9% 3.0% 0% 0.0% | 9% 0 9% 0 | 76 0% 0.0 76 0% 0.0 76 0% 0.0 | 0% 100% 0% 100% | 100% 1009 100% 1009 100% 1009 | 93.9% 100.0% 100.0% 100.0% 85.5% 37.3% 100.0% | 0% 0% 0% 0% | 0% 0.0 0% 0.0 | S 05 S 05 | 0% 0% 0% 0% 0% 0% | 0.0% 20 0.0% 20 0.0% 40 | 20% 100% 20% 100% 20% 100% | 100% 100.09 100% 100.09 100% 100.09 | N 0% | 9% 9% 9% 9% 9% 9% | 0.0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% | 200% 100.05 200% 100.05 200% 100.05 | 9% 91 9% 91 9% 91 | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 9% 0. 9% 0. 9% 0. | 0% 0.4226 0% 0% | | 0.4226 | | | | | # |
| containing and Kotd12 neceytransfers Alg2 factor receptor Epatit2 | ALG2 MOUSE - ESSL2 MOUSE - | 95 kDa 17 kDa 7 12 kDa | 100% SN 82% ON 0% | 62% 73.1% 0% 0.0% | N 13% N 100% | 9% 1 100% 10 | 13% 11.4% 00% 100.0% | 13% 9 0% 0 | % 25% 15.5 % 0% 0.0 | 5% 89% 5% 29% | 100% 1009 80% 889 32% 509 | 6 85.5% 6 37.3% | 6% 10% 12% 67% | 0% 5.2 50% 52.7 | % 6% % 0% | 0% 0% 10% 13% 0% 0% | 9.4% s 0.0% | 00% 92% 82% 50% 0% | 100% 97.65 75% 69.45 0% | % 0% % 0% 100% | 0% 0% 0% 0% 100% | 0.0% | 0% 7% 7% 50% 0% | 0% 2.4% 25% 30.6% 0% | 100% 91% 75% 50% 50% 50% | 72% 87.49 1 100% 75.09 1 42% 47.69 | 0% 91 0% 01 30% S01 | 7% 5.4% 0% 0.0% 29% 35.2% | 25% 50% 25% 50% | 21% 7. 0% 25. 29% 16. | .1% .0% 0.1475 .2% 0.0290 | 0.3510 0.7695 0.0025 | 0.7701 0.5 0.2 | 1748 1459 0.1548 1468 0.0090 | 0.1860 0.0115 | 0.1993 0.2149 0.0494 | 0.58 0.3326 0.76 0.19 | 1813 1895 1859 |
| Same-like prote TB12 Cygb te mannosvitran Dpm1 | TTL12 MOUSE CYGB MOUSE DPM1 MOUSE | 74 kDa 10 21 kDa 29 kDa 6 | 0% 100% 2% 67% | 100% 100.0% 60% 63.1% | N 0% | 9% 3 | 20% 17.8% | 0% 0 13% 25 | N 20% 19.3 | 2% 67% | | 62.2% | 0% 0% 13% 13% | 9% 10.9 | % 22% | 33% 25% | 0.0% 10 10 25.9% 2 | 00% 100% 00% 100% 75% 67% | 100% 100.05 100% 100.05 67% 69.45 | % 0% % 0% | 0% 0% 0% 0% 0% 33% | 0.0% 0.0% 19.4% | 0% 0% 0% 0% 0% 33% | 0% 0.0% 0% 0.0% 0% 11.1% | 100% 100% 100% 100% 50% 67% | 1 200% 100.09 1 200% 100.09 1 62% 61.19 | 0% 01 0% 01 50% 331 | 0% 0.0% 0% 0.0% 0% 27.8% | 0% 0% 0% 0% 0% 0% | 0% 0. 0% 0. 22% 11. | 0% 0% 1% 0.8755 | 0.2739 | 0.1409 0.8 | | | BRH 0.3702 | | |
| sets sub-family Abod3 194A helicase DC Ddd54 Gphn | ABCD3_MOUSE 1 DOXS4_MOUSE 1 GEPH_MOUSE | PS kDa 88 kDa 83 kDa 6 | 0% 0% 0% 2% 67% | 0% 0.0% 0% 25% 69.4% | N 0% 100% N 22% | 0% 10 33% 1 | 0% 0.0% 00% 25% 30.6% | 900 100 9% 0 | ns sons 100.0 | 0% 0% 0% 100% | 0% 100% 1009 | 100.0% | 0% 100% 0% 0% | 0% 0.0 | 0% % 0% | 0% 0% 0% | 0.0% 10 | SON SON | 100% | 0% | 0% 0% 0% | 0.0% S | 0% 50% 0% | 50% 50.0% 0% | 50% 67% | 67% 61.19 | 0% 01 | 0% 0.0% | 50N 23N | 22% 38. | 0.0002 | 0.1835 | 0.0002 | 0.0082 | 0.6 | 0002 | 0.18 | 100 |
| n protein nudC Nudc nutree 2 Prem2 | NUC MOUSE PARC MOUSE PARC MOUSE | 100 KDa 10 35 KDa 10 | 9% 9% 9% 100% 9% 100% | 0% 0.0% 82% 94.4% 100% 100.0% | N 100% N 0% N 0% | 200% 10 0% 1 | 05 0.0% | 9% 0 9% 0 9% 0 | m 0% 0.0 % 0% 0.0 % 0% 0.0 | 0% 0% 0% 100% 0% 100% | 100% 1009 100% 1009 | 100.0% 100.0% 100.0% 44.0% | 0% 0% 0% 0% | 9% 0.0 9% 0.0 | 5 0% % 0% | 0% 0% 0% 0% | 0.0% 10 0.0% 10 | 176 0% 10% 100% 10% 100% | 0% 5.65 100% 500.05 100% 500.05 | 5 0% 5 0% | 100% 100% 0% 0% 0% 0% | 94.4% 0.0% 0.0% | 9% 9% 9% 9% 9% 9% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 100% 100% | 0% 0.05 200% 100.05 200% 100.05 | 100% 1001 0% 01 0% 01 | 100% 100.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0. 0% 0. 0% 0. | 0% 0.4226 0% 0.4226 | | 0.4226 | 0.4226 | 0.4 | 4226 | | # |
| in V Centy tein SEC62 Sec62 Tru2 | CENPY MOUSE SECRE MOUSE - | 25 kDa 1 15 kDa 7 152 kDa | 2% 40% 2% 76% | 25% 25.0% 71% 73.4% | | 60% 9% | 75% 75.0% 0% 0.0% | 9% 0 27% 26 | % 0% 0.5 % 28% 25.5 | 0% 64% 6% 79% 100% | 50% 400 85% 700 | 44.0% 91.0% | 6% 46% 5% 0% | 50% 50.2 5% 3.2 | % 0% % 16% 0% | 6% 10% 15% 16% | 5.2% 6 15.5% 10 | 67% 67% 00% 100% 00% 100% | 78% 70.45 100% 100.05 | 5 23% 5 0% | 20% 22% 0% 0% 0% | 29.6% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 50% 50% 50% 50% | 62% 50.75 | 26% S01 | 28% 41.2% 0% 0.0% | 9% 9% 9% 9% 59% 33% | 9% 0. 50% 44 | 0% 0.1416 0.0440 | 0.1134 | 0.0215 0.0 | 633 0.0886 0.1835 | 0.1134 0.0 | 0.2223 0.1960 4226 | 0.0139 | 153 |
| on factor elF-22 Elf2b4 se family 1 mer Akr1c13 Cse fil luctase 1 Pigr1 | AKICD MOUSE XPOZ MOUSE | 58 kDa 10 57 kDa 10 110 kDa 10 | 0% 100% 0% 100% 0% 100% | 82% 94.4% 100% 100.0% 100% 100.0% | N 0% N 0% N 0% | 9% 1 9% 9% | 17% 5.6% 0% 0.0% 0% 0.0% | 9% 0 9% 0 | ns 0% 0.0 ns 0% 0.0 ns 0% 0.0 | 0% 100% 0% 100% 0% 100% | 100% 1009 100% 1009 100% 1009 | 100.0% 100.0% 100.0% | 0% 0% 0% 0% | 50% 50.2 5% 3.5 6% 0.0 6% 0.0 6% 0.0 | % 0% % 0% | 0% 0% 0% 0% 0% 0% | 0.0% 10 0.0% 10 0.0% 10 | 100% 100% 100% 100% | 100% 100.05 100% 100.05 | S 0% | 0% 0% 0% 0% 0% 0% | 0.0% | 9% 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% | 200% 100.09 200% 100.09 | 9% 91 9% 91 | 0% 0.0% 0% 0.0% | 9% 9% 9% 9% | 0% O. | 4% 0.4226 0% 0.4226 | | 0.4226 | 0.4226 | 0.4 | 4226 | | Ξ |
| ctase 1 Ptgr1 oles protein No Nap93 sining protein 1 Sun1 | PTGRI_MOUSE NLP90_MOUSE SUN1_MOUSE | 95 KDa 10 83 KDa 102 KDa | 0% 100% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% N 9% N 9% | 9% 9% | 0% 0.0% 0% 0.0% | 0% 0 200% 100 200% 100 | ns 200% 100.0 ns 200% 100.0 | 0% 0% 0% 0% | 0% 07 0% 07 | 9.0% | on on | 0% 0.0 0% 0.0 | % 100% % 100% | 100% 200% 100% 200% | 100.0% 100.0% | 0% 100% 0% 0% 0% 0% | 100% 100.05 0% 0.05 0% 0.05 | S 0% | 0% 0% 0% 0% | 0.0% 10 0.0% 10 | 0% 0% 0% 200% 0% 200% | 0% 0.0% 100% 100.0% 100% 100.0% | 100% 100% 0% 0% 0% 0% | 200% 100.05 0% 0.05 0% 0.05 | 0% 01 0% 01 | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 200% 200% 200% 200% | 2% 0, 100% 100, 100% 100. | 9% 9% 9% | 0.2161 | | | | | | 1161 |
| Rin4 Focad | FOCAD_MOUSE | 199 KDa 5 | 0% 67% | 62% 61.1% | 0% % 0% | 9% 9% | 0% 0.0% | 9% 0 59% 22 | % 12% 38.5 | 9% SON | 50% 1009 | 66.7% | 0% 0% | 0% 0.0 | % Son | 50% 0% | 33.3% | med 75% | 80.25 | m 0% | 9% 9% 6% 9% | 0.0% | xn 25% | ACS 19.8% | X/5 885 | 2005 89.85 | 9% 01 | US 0.0% | 188 128 | 9% 10 | 0.7769 | | | | | 1575 0.4753 | 0.7769 | |

| 1329 Z.4-denovi-GoA reductors miles Descri DECR MOUSE 36 KDs 1009 | N 100% 1000 100,0% 0% 0% 0% 0.0% | ON ON ON 0.075 100% 100% 100% 990.075 ON O | . ON 0.0% ON ON ON 0.0% 100% 100% | 100N 100.07N 0N 0N 0N 0.07N | 0N 0N 0N 0.5% 100N 100N 10 | N 100.0% ON ON ON 0.0% ON ON | 0% 0.0% 0% 0.0% 0% 0.0% | M 0.20M 0.42M |
|---|--|---|--|--|--|---|--|--|
| 1331 Ubicultir-like modifier-activating Uba5 UBA5 MOUSE 45 kDs 96% 1332 Beta-2-syntophin 5mb2 ShT02 MOUSE 55 kDs 07 1333 Nine-like protein Famt-S2b NiNE-1, MOUSE 55 kDs 1007 1330 Nine-like protein Famt-S2b NiNE-1, MOUSE 55 kDs 1007 1330 Nine-like protein Famt-S2b NiNE-1, MOUSE 55 kDs 1007 1330 Nine-like protein 1330 Nine-like | N 100% 100% 58,57% 4% 0% 0% 1,4% N 0% 0% 0.0% 50,0% N 0% 50,0% 50,0% N 0% N 0% 50,0% N 0% N 0% 50,0% N 0% | 0% 0% 0% 0.0% 100% 100% 100% 100.0% 0% 0% 0% 0% 0% 0% 0% 0% 0.0% 0% 0% 0.0% | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 50% 33.3% 100% 50% 50% 06.7% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 100% 100% | 100% 100.0% 0% 0% 0% 0.0% 0% 0.0% 25% 25% 32% 27.8% 100% 100.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 100% 100% 15% 75% 67% 72.2% 25% 20% 0 0% 0% 0% 0.0% 100% 100% 100 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 62% 67.2% 0.1000 0% 0.0% | 0.4226 0.4226 0.4226 0.4226 0.4226 0.0153 0.0759 0.4226 0.3266 0.0153 0.9759 |
| 1336 (Sentin-conting protein) (Sept. 1531 (Sept. 155.6) (15.6) (| 85 295 205 29.5% 08 295 205 15.2% 85 505 507 28.2% 08 09 08 0.0% 85 395 08 12.2% 08 08 08 08 0.0% 8 08 08 0.0% 20.0% 08 08 0.0% 08 8 08 08 0.0% 20% 08 08 08 0.0% | 60% 42% 50% 54.7% 50% 50% 25% 41.7% 0% 10% 55% 20% 56% 41.7% 60% 45% 50% 51.8% 0% 0% 120% 62% 100% 87.7% 0% 0% 22% 11.1% 0% 0% | 0% 3.3% 50% 40% 75% 55.0% 06% 20% 12% 5.0% 60% 20% 12% 5.0% 50.0 20% 12% 5.0% 50% 20% 12% 5.0% 50% 20% 12% 50% 10% 100% 100% 57% 88.9% 12% 50% | 08 6.7% 128 208 208 17.5% 08 23.2% 08 08 08 0.0% 28 23.2% 08 08 08 0.0% | 500 000 000 0000 10000 10000 200 1800 6000 8000 75.075 250 220 1 1500 8000 1000 75.775 200 00 1 1700 5000 679 01.175 500 500 2 | 10 10.000 00 00 00 00 00 00 00 00 00 00 00 0 | 20% 50.6% 0.3049 0.356 200% 93.3% 0.6128 0.376 20% 43.3% 0.9379 0.112 | 33 0.0000 0.1056 0.2552 0.0158 0.8503 0.4226 0.0557 0.7345 0.1007 0.1517 0.1507 0.4226 0.0345 0.17345 0.1007 0.1517 0.1507 0.1507 0.1507 0.0507 0.1507 0.0507 0.1507 0.0507 0.1507 0.050 |
| 1338 Golgin subhanly A member 5 Golgaf GODAS, MUSEE 62 KDs 0% 1330 Thy I membrane glooproblein Thy I Thrift MUSEE 18 KDs 19 KDs 1340 Naceshitakidosamininkhanderasi Gelet 7 GALT, MUSEE 75 KDs 1341 Luculari-rich research-containing a Lury LURY LURY 64 KDs 85 | 100% 100% 0% 0% | 80% 100% 100% 93.3% 0% 0% 17% 5.8% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 100% 100% 82% 94.4% 0% 82% 00% 00% 00% 00% 00% 00% 00% 00% 100% | 71% 77.2% 0% 0% 0% 0 0.0% 1 0% 0% 0% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 200% ON 22.8% 92% 75% 8: 200 200% 22.8% 92% 75% 8: 200 00 00 00 00 0.0% 100% 200 200 00 00 00 00 0.0% 100% 100% 100% | 0% 00.0% 100% 1% 00.0% 0% 0% 0.0% 90% 25% 1% 22.0% 0% 0% 0% 0.0% 90% 70% 1% 100.0% 0% 0% 0% 0.0% 0.0% 0.0% | 16% 16.4% 0.335 | 56 0.0187 0.0768 0.3356 0.0187 0.0768 |
| 1342 Macrochase micration inhibitory MF MF MOUSE 12 kDs 90% 1341 Actin-related orderio 23 consiles App 23 APP 23 APP 23 AVDUSE 21 kDs 100 1344 Farmylacetoscotase Fah FAAA, MUXEE 46 kDs 100 | 100% | 08 | 0% 0.0% 0% 0% 0% 0.0% 89% 100% 0% 0.0% 0% 0% 0% 0.0% 100% 100% 0% 0.0% 0% 0% 0% 0.0% 100% 100% | 100% 96.3% 11% 0% 0% 3.7% 82% 94.4% 0% 0% 17% 5.6% 100% 900.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.055 100% 89% 100 0% 0% 0% 0.050 89% 89% 100 0% 0% 0% 0.050 100% 100% 100 | 00 98.7% 0% 11% 0% 3.7% 0% 0% 0% 0% 0% 0% 0% 100.0% 0% 0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0.1969 1.000 0% 0.0% 0.797 0% 0.0% | 55 C.2590 C.1046 G.7592 G.2520 G.2525 G.1946 G.2525 G.1946 G.2525 G.1650 G.2644 G.4236 G.2526 G.1955 |
| 136 Seriral/Invariance ordein chosels PppDas PPDAA_MCUSE 35 Gbs 100% 136 Nuclear factor Pri-Racca-B 1030 NRb2 MPGB_MCUSE 37 Gbs 100% 1347 Pulmonary surfactori-associated 57pd 57FTPD_MCUSE 33 Gbs 1340 Subdress/sto-brists-is-delutores 18bs/db 34 Gbs 15 Gbs 100% | 1 1000 1000 100.0% 0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 100% 100% 100% 100% 100.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100% 100 | 100K 100.0% 0% 0% 0% 0.0% 0% 5.8% 67% 100% 100% 88.9% 1 100K 000 0% 0% 0 100K 000 0% 0 0% 0 0% | 0% 0% 0% 0.05 100% 100% 100% 100% 100% 100% 100% 10 | 06 100.0% 06 06 06 06 06 06 06 06 06 06 06 06 06 | 0% 0.0% 0.2% 0% 0.0% 0.2% | 95 02185 02185 03185 |
| 1340 Naclear core corrolles problem No. Nap54 NLP54_ACUSE 55 kDs 0% 1350 CP1A_6 dessinaturante inclination mobiles Colosid2 COACO_MOUSE 17 kDs 0% 1351 CP10500 brows with charminary only Coligit COST_MOUSE 12 kDs 241 | K ON ON O.DN 100N 100N 100N 100N 100.0% N ON ON O.DN 67N 75N 80N 73.9% N 29N 42N 34.2% 66N 71N 57N 65.8% | 0% 0% 0% 0.0% 0.0% 0% 0% 0% 0 0 0 0 0 0 | 100 100.0% ON ON ON 0.0% ON | 0% 0.0% 100% 100% 100% 100.0% 9% 6.7% 26% 86% 26% 26.7% 78.7% 0% 11.1% 67% 100% 100% 88.9% | 0% 0% 0% 0.0% 0% 0% 0% 0 11% 14% 18% 14.5% 0% 4% 0 0% 0% 0% 0.0% 1.0% 20% | N 0.0% 100% 100% 100% 100% 00 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0.8417 0.8971 | 44 0.1676 0.1981 0.3662 0.2013 0.4277 0.0553 0.5552 0.3306 0.0771 0.46971 0.1012 0.0404 0.1012 0.0404 0.1012 0.0404 0.1012 0.0404 0.1012 0.0404 0.1012 0.0404 0.1012 0.0404 0.1012 0.0404 0.1012 0.0404 0.1012 0.101 |
| 33S2 ATTO-deconsided RNA half-ress PT [Cdd82 DOME2 MOUSE 100 kDs 33S3 Frank-NVC-Reinsteinstein Artenit Mage MENP MOUSE 31 8Cs 100% 13S4 Millschendrid finion 1 proble Fist Fist Fist Fist AVX 20 kDs 12 kDs 120 kDs | 5 08 17N 5.57N 100N 100N 83N 94.4% 8 100N 100N 100.7% 08 08 08 0.0% 0.0% 8 71N 71N 74.7% 20N 29N 29N 257N 10 430 29N 25.7% 38N 29N 57N 44.1% | .0% | 2005 100.075 0% 0% 0% 0.075 0% 0% 0% 0.075 0% 0% 0% 0% 0.075 120% 120% 120% 120% 120% 120% 120% 120% | 0% 0.0% 100% 100% 100% 100.0% 100% 900.0% 0% 0% 0% 0.0% 28% 40.2% 27% 28% 21% 28.7% 0% 16.7% 0% 0% 0% 0.0% | 0% 0% 0% 0.05 0.0% 0% 0% 0 0% 0% 0% 0.05 95% 94% 10 12% 36% 21% 21.1% 20% 20% 4 20% 200% 100% 83.35% 0% 0% | 08 0.0% 100% 100% 100% 90.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 9% 0.0% 0.4226 9% 0.0% 0.195 22% 32.8% 0.1955 0.457 100% 80.0% 0.3023 0.422 | 0.0225 0.0226 0 |
| 1996. Calcium/calmedulin-decender (a. Careldál. KCCZO MXISEE. 55 KDa. 25K 1957. TBC1 domini family member 4. Tbc164. TBCD4 MXISEE. 147 KDa. 1350 Cmal horendos subfamily Ameril. Draight. DNIA5_MXISEE. 52 KDa. 69 | 6 50% 0% 25.0% 50% 50% 100% 55.7% 0% 0% 0% 0.0% 100% 100% 100% 100.0% | 25% 0% 0% 8.2% 0% 0% 100% 33.2% 50% 100% 100% 100% 100% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 50.0% 50% 0% 0% 95.7% 64% 67% 100% 100% 0% 0% 0.0% 0% 0% | 78% 69.4% 27% 12% 11% 18.4% 0% 0% 0.0% 100% 100% 100.0% | 9% 17% 11% 12.3% 90% 72% 90 100% 0% 0% 0.0% 0% 0% 0% 0 | N 0.0% 10% 10% 8% 12.2% 0% 0% N 0.0% 100% 100% 100% 100.0% 0% 0% | 0% 0.0% 0.4226 | |
| 1302 ARTINI-N-REMINISTRATION 1005 10 | 5 75N 100N 50.07N 0N 0N 0N 0N 0.5N N 100N 100N 100.07N 0N 0N 0N 0N 0.7N | 0% 0% 0% 0.0% 100% 100% 100% 100% 100% 0% 0% 0% 0% 0% 0% 0.0% 100% 10 | ON 0.075 ON ON ON 0.075 100% 100% 100% 100% 100% 100% 100% 100 | 1005 00.0% 05 05 05 05 1006 0.0% 1006 1006 868 95.2% 908 93.0% 05 05 08 00 005 | 0% 0% 0% 0.05% 100% 100% 20 0% 0% 10% 148 4.87% 0% 0% 1 11% 0% 10% 7.07% 95% 100% 100 | 05 05 05 05 05 05 05 05 05 05 05 05 05 0 | 9% 11.1% 9% 1.2% 0.2740 | 0.1917 0.1917 0.1917 0.1917 0.1917 0.1917 0.1919 0. |
| 15D. Advocate sistem membranes Apmap. APMAP MICES. 46 Kib. 215 15M. Vivosin. 5 chall. VINX, MOUSE. 28 Kib. 25 15E PDZ and LIM formin protein.3. PBIm3. PDLI3. MOUSE. 24 Kib. 28 | 6 828 71N 75.4% 14N 17N 29N 19.8% 8 0N 0N 0.0% 100N 100N 100N 100N 100N 500.0% 8 500.0% 500.0% 500.0% 500.0% | 14% 0% 0% 4.8% 75% 86% 100% 95.2% 25% 14% 0% 0% 0% 0.0% 0.0% 0.0% 0.0 0% 0.0 0.0 10.0% 0% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 10.0 1 | 0% 13.1% 0% 0% 0% 0.0% 100% 100% 100% 100% 10 | 100% 900.0% 0% 0% 0% 0.0% 0% 0.0% 100% 100% 100% 100.0% 0% 10.1% 100% 60% 100% 88.4% | 0% 0% 0% 0.0% 1.0% 100% 100% 0 0% 0% 0% 0.0% 1.7% 0% 1 0% 4% 0% 1.4% 0% 46% 3 | N 94-PS ON ON ON 0.055 ON | 0% 0.0% 0.2549 0.4226 0% 0.0% 0.5701 0% 0.0% 0.5701 0% 0.0% 0.5701 | C 144 C C C C C C C C C |
| 1357 Choline delivolroserase, mitodro Choli. CHDH_MDUSE 66 kDs 100% 1308 Castroline-3 Ged.3 GROS_MOUSE 21 kDs 1309 Florenoutulin Frood FMDO_MOUSE 43 kDs | K 86N 100N 95.2% ON 14N ON 48% | ON ON ON 0.0% 100% 100% 100% 100 ON | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100% 100 | 100% 100.0% 0% 0% 0% 0.0% 100% 97.9% 6% 0% 0% 0 2.1% 22% 17.1% 82% 88% 78% 82.9% | 0% 0% 0% 0.055 100% 100% 50 0% 0% 0% 0.055 92% 82% 8 0% 0% 0% 0.050 48% 50% 6 | 00 100.0% 0% 0% 0% 0.0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0.4226 4% 2.7% 0.066 0% 0.0% 0.0586 0.300 42% 41.0% 0.8586 0.300 | 54 0-2726 0-4226 0-4226 0-4226 0-4226 0-1527 |
| 1370 Carbohydrale sulfotransferase 1 Charl CHETI, MOUSE 47 KCs 201. 1371 Uses subsection with collect-coll Uses UKA, MOUSE 101 KDs 01. 1372 Tearsporter 1 Tep 01 ThP 01, MOUSE 102 KDs 100 KDs 1372 Tearsporter 1 Tep 01 ThP 01, MOUSE 102 KDs 100 KDs 1373 LEFTM and EF-bard domain-coll celeft LEFTM MOUSE 80 KDs 869 KDs 100 | \$ 20% 25% 21.7% 20% 40% 25% 28.2% \$ 0% 0% 0.0% 100% 100% 100% 100% 100 % \$ 100% 100% 100.0% 0% 0% 0% 0.0% \$ 100% 100% 100.0% 0% 0% 0.0% 0.0% | 60% 60% 50% 50.0% 10.0% 146% 296% 20% 21.0% 42% 42% 42% 42% 42% 42% 42% 42% 42% 42 | 40% 41.9% 43% 29% 60% 37.1% 32% 20% 100 100.0% 0% 0 0% 0 0% 0 0% 0 0 0 0 0 0 0 0 | 0% 17.8% 23% 40% 40% 37.8% 1 100% 100% 100% 0% 0.0% 100% 900.0% 0% 0% 0.0% 1 | 23% 60% 60% 44.4% 20% 60% 21 0% 0% 0% 0 0.00 00 100 100 0% 0% 0 0.00 0.00 100 100 0% 0% 0 0.00 0.00 100 100 0% 0 0% 0 0 0.00 100 100 0% 0 0 0 0 0 0.00 100 100 0% 0 0 0 0 0 0 0.00 100 0% 0 0 0 0 0 0 0 0 0.00 100 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 29.5% 40% 20% 25% 29.5% 40% | 0.0 0.04 | 00 07.289 0.3017 0.1494 0.2889 0.2250 0.1526 0.1526 0.1526 0.0003 0.0000 0.4768 54 0.4226 0.1894 0.4226 0.1894 0.4226 0.1894 |
| 1374 Tyrosine-prosinis Krassa JAK1 Jak1 JAK1_MCUSE 133 kDs 1375 Colorbrowns hard receive valves Ugoth GCPE_MCUSE 10 kDs 5.79 1376 Adeq/psusccinals Iyana Adel PLPEL_MCUSE 55 kDs 1007 | 6 28% 56% 50.1% 42% 28% 22% 37.9% N 100% 200% 100.0% 0% 0% 0% 0% 0.0% | 0% 25% 11% 12.0% 46% 60% 61% 55.0% 56% 30% 08 08 08 0.05% 100% 100% 100% 100.0% 00 00 | 28% 41.0% 0% 10% 0% 3.2% 20% 20% 20% 20% 20% 20% 20% 20% 20% 2 | 100K 100.0% 0% 0% 0% 0.0% 1.0% 20% 20% 53.2% 100K 100.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.6 0.5% 100% 100% 100 10% 10% 0% 6.7% 22% 20% 2 0% 0% 0% 0.6 0.5% 100% 100% 100 | 0% 100.0% 0% 0% 0% 0.0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0.0% 0.0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | | TO 0.0000 00951 0.7752 0.5462 0.0057 0.0050 0.3591 0.7502 0.5513 0.4162 0.0077 0.0050 0.3775 0.27751 0.0050 |
| 1277 Unconvenion in position is Min 128 | S 05 05 005 1005 1005 1005 1005 1005 100 | 05 | 100 | 203 97.75 203 5% 203 1075 1000 90.0% 0% 0% 0% 0.0% 0% 3.7% 89% 100% 100% 96.7% 1000 900.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 100% 100% 100% 100% 100% 1 | 10 10.0% 0% 0% 0% 0% 10.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0.422 0% 0.0% 0.422 0% 0.0% 0.6404 0.422 | 5 0.4226 0.5013 0.6464 0.4226 0.4236 0.5913 |
| 1381 Pieddo-F998 Indrolome 2, milec Pith 2 PITR2, MILUSE 20 Kills 45 Kills 1382 Sprainte-5 505 | 1 60% 25% 36.89% 65% 50% 50% 48.59% 8 20% 0% 5.7% 0% 0% 0% 0.0% 0.0% 3.5% 3 8 0% 9% 6.7% 56% 50% 66% 55.4% 55.4% 10 20% 20% 13.39% 100% 80% 60% 80.7% 55.4% 10 20% 20% 13.39% 100% 80% 60% 80.7% | 9% 10% 25% 14.7% 22% 28% 28% 22.4% 57% 50% 200% 80% 100% 93.7% 20% 17% 20% 15.9% 00% 00 23% 50% 27% 30.7% 25% 00% 22% 15.5% 62% 62% 00% 00% 00% 0.0% 00% 22% 00% 11.1% 100% 52% | 50% 55.6% 11% 12% 12% 12.0% 20% 0% 0% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 | 0% 5.7% 60% 50% 40% 45.7% 60% 00% 0.5% 0 0 0.5% 10 0 0.5% 10 0 0 0.5% 10 0 0 0.5% 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 10% 60% 60% 46.7% 25% 11% 1 10% 200% 100% 100.0% 0% 0% 0% 0 0% 0% 0% 0.0% 0% 0% 0 0% 0% 0% 0.0% 0 | 75 17.0% 25% 46% 23% 34.2% 50% 44% 35 0.0% 0% 0% 0% 0.0% 20% 200% 100% 30 0.0% 100% 100% 100% 1000% 00 0% 30 0.0% 100% 100% 100% 100% 00 0% | 50% 48.1% 0.6098 0.247 200% 100.0% 0.2055 0% 0.0% 0.3759 0.0059 | 0.4226 0.0004 0.2001 0.2011 0.0540 0.0579 0.5479 0.0015 0.0016 0.4226 0.0016 0.0025 0.0004 0.0005 0. |
| 1365 Pho quarine nucleoide suchano Arbat7 APRIG7 MOUSE 97 kDa 0% 1365 Early endocros artigen 1 East EEAL MOUSE 161 kDa 1367 EMILIN-12 Emilin2 EMIL2 MOUSE 117 kDa | 6 0% 0% 0.0% 100% 100% 100% 100.0% | ON ON ON 0.00 ON 00 ON 00 ON 000 ON 0 | 100% 100,0% 0% 0% 0% 0,0% 0% 0% | 08 0.0% 82% 88% 79% 53.1% 100% 93.2% 20% 08 08 67% 50% 16.7% 75% 75% 40% 53.2% | 77% 12% 21% 95.9% 0% 0% 0 9% 0% 0% 0.0% 100% 100% 10 5% 25% 10% 20.0% 0% 0% | 06 0.0% 100% 100% 100% 000.0% 0% 0% 06 100.0% 0% 0% 0% 0.0% 0% 0% | 9% 0.0% 9% 0.0% 0.422 | 5 - 4455 |
| 1380 Juscone-servanded PNA-binding on Statut STAUL MCUSE 54 kCa 0% 1380 Microse-schanded cerein known Might MCUSE 41 kCa 100% 1390 54-53 prolein betainlights Yahab 14330 MCUSE 28 kCa 25% 1391 Proleinsome subunit beta lype-I Pemb1 PSB1 MCUSE 26 kCa 22% | cm | 0% 0% 0% 0.075 0% 0% 0% 0% 0.075 100% 100% 0% 0% 0% 0.075 100% 100% 100% 100.075 0% 0% 0% 0% 0% 0.075 100% 100% 100% 50.7% 20% 0% 0% 0% 0% 0.075 100% 100% 100% 100.075 00.075 0% | 2000 100,000 000 000 0,000 000 000 000 000 000 000 000 000 1000 | 000 U.05% 100% 100% 100% 100.0% 100% 500.0% 0% 0% 0% 0.00% 100% 500.0% 0% 5% 5% 0% 4.0% 100% 500.0% 0% 0% 0% 0.00% | 976 976 976 0.075 976 976 976 976 976 976 976 976 976 976 | 708 JULY 100% 100% 100% 100.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 9% 0.0% 9% 0.0% 9% 0.0% 0.6214 0.189 9% 0.0% 0.4226 | 71 68572 6-522 6-516 6-186 6-8672 0-622 72 6-526 6-886 6-92 73 6-526 6-886 6-92 74 6-92 6-886 6-92 75 6-92 6-92 75 75 75 7 |
| 1932_DDRDX domain-containine prole Ddrgk1_DDRDX_MDLSE 36 kDa 36 kDa 1930_Dgrain-2 Cm2 CN2_MMUSE 33 kDa 36 kDa 1934_More histocomostibility actions 1 Hert3_MDLSE 42 kDa 699 | 4 27% 21% 31.9% 27% 22% 21% 30.5% 8 0% 0% 0.0% 100% 100% 100% 100% 90.0% % 91% 82% 80.5% 0% 0% 0% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0 | 36% 40% 38% 38.7% 22% 30% 36% 29.5% 44% 20% 0% 0% 0% 0.0% 0.0% 0.0% 0.0% 0.0% | 27% 30.0% 22% 50% 26% 38.9% 40% 22% 0% 0.0% 17% 26% 22% 25.1% 100% 100% 100% 100% 100% 100% 100% 1 | 29% 34.0% 0% 0% 14% 4.8% 1 38% 29.0% 62% 75% 62% 65.3% 1006 90.0% 0% 0% 0% 0.0% | 10% 67% 57% 61.3% 22% 0% 27 4% 10% 0% 4.6% 25% 40% 40 0% 0% 0% 0.0% 100% 100% | N 22.2% ON ON ON 0.0% 67% 100% N 30.8% 55% 52% 22% 47.2% 10% 7% ON | 67% 77.8% 0.7459 0.403 22% 13.0% 0.5568 0.203 | / 0.5056 0.5061 0.5091 0.4205 0.0201 0.5190 0.7305 0.2770 0.00001 0.0002 / 0.0004 0.0005 0.0000 0.0000 0.0000 0.0000 0.2710 0.2000 0.2011 0.2000 0.0007 0.0005 0.0005 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 |
| 1395 GTGGGGB protein 2 Alg512 ARG32 ARG32 ARG32 BD BB S S S S S S S S S S S S S S S S S | 000 000 000 000 000 000 000 000 000 0 | 000 000 0000 0000 0000 0000 0000 0000 0000 | . 20% 10.6% Cox 25% 30% 38.3% 80% Cox Ox Ox Ox Ox Ox Ox | 67% 65.8% 0% 0% 0% 0.0% 0% 0.0% 50% 100% 100% 83.3% | 000 000 000 000 000 000 000 000 000 00 | 0% 33.3% 0% 100% 0% 33.3% 100% 0% 0% 00% 0% 00% 0% 0% 0% 0% 0% 0% 0 | 9% 33.3% 100% 0.7109 0.017 | 11 0.1550 0.000 0.4100 0.0000 0.000 0.000 0.000 0.000 0.0000 0.0000 |
| 1999 Transcription actinator BRGI Serancia SMCA4_MOUSE 161 MOs 160 Mos 161 MOs 162 Mos 161 MOs 162 Mos 162 Mos 161 MOs 162 Mos 163 MOS 1 | 0% 0% 0% 4.2% 88% 88% 86% 95.9% % 10% 100% 83.2% 50% 0% 0% 15.7% | 00% 12% 14% 5.9% 17% 0% 0% 5.6% 52% 100% 0% 0% 0.0% | 80% 82.2% 17% 0% 20% 12.2% 0% 100% 100% | 100% 33.3% 0% 0% 0% 0% 0.0% 10 100% 00.0% 0% 0% 0.0% 100% 00.0% 0% 0% 0.0% | 000 000 00 00 000 1000 1000 1000 1000 | 0% 500% 8% 100.0% 0% 0% 0.0% 0% 0% 8% 100.0% 0% 0% 0% 0.0% 0% | | 0.4226 0.4226 0.4226 |
| 1403 Terrestruccerisis ribrombratus no PippS PIMS MCUSE 65 kGs 1404 Ethnicional sposide hydrolana 2 Ephs2 HYES MCUSE 62 kGs 1405 Parcel PSCNI_MCUSE 54 kGs | 100% 100% 0% 0% 0% 100% | 0% 0% 100% 100% 100% 100.0% 0% 0% 0% | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100% 100 | 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 1.00% 94% 10 0% 0% 100% 100% 10 0% 0% 0% 0.0% 100% 100% 10 | 05 97.9% 0% 6% 0% 2.1% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% | 36 0.4226 0.4226 0.4226 |
| 1407 Shanararan Southern (1907 | 8 08 08 6.7% 508 718 89% 70.1% 8 08 08 0.075 608 50% 100% 70.0% 6 678 08 22.2% 100% 22% 100% 77.8% | 20% 20% 13% 22.2% 0% 0% 0% 0.55 20% 63% 64% 64% 64% 64% 64% 64% 64% 64% 64% 64 | 60% 67.2% 20% 28% 60% 32.5% 12% 0% 0% 0% 0% 0% 0.0% 22% 22% 20% | 08 4.2% 50% 50% 30% 55.7% 0% 50% 50% 34.4% 77% 20% 50% 50% 65.6% | 18N 50N 20N 20.2% 14N 22N 21 10N 200N 0N 0N 0N 0.0% 2.0% 22N 29N 5: | % 24.2% 43% 50% 25% 39.3% 43% 17% % 39.7% 62% 71% 42% 50.3% 0% 0% | 50% 36.5% 0.4226 0.048 0% 0.0% 0.7972 0.679 | 95 0.7920 0.0462 0.8221 0.1575 0.3743 0.0462 0.3330 0.1514 0.7926 0.0465 0.0460 0.0000 0.1714 0.7926 0.0465 0.0460 0.0000 0.7972 0.0792 0.0463 0.0000 0.0000 0.0000 0.1153 |
| H4D ATP-bindox cannote sub-facilir. Abct2. ABCE2. MCMSE. 72 Mm. 285 H4D ERBAR, RhoGEF and electricirs. Erapt. FARPL MCMSE. 119 Mm. 119 Mm. H4D. Monothrollomic CI-introduction. MMMI. CTIM. MCMSE. 100 Mm. 100 Mm. H4D. Revealed crossing. Rev. Sci. Rev. Sci. 200 Mm. 100 Mm. 100 Mm. | \$ 62% 42% 50.7% 22% 28% 57% 29.2% 100% 0% \$ 100% 91% 97.0% 0% 0% 9% 1.0% \$ 100% 100% 90.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.07% 100% 82% 100% 85.1% 22% 12% 0% 0% 0% 0% 0.07% 100% 100% 100% 100% 100.07% 0% 0% 0% 0% 0% 0.07% 100% 100% 100% 100% 100.07% 0% 0% | 0% 13,9% 0% 0% 0% 0.0% 100% 100% 100% 0.0% 0.0% | 100N 100.0% 0% 0% 0% 0.0% 100N 00.0% 0% 0% 0% 0.0% 100N 100.0% 0% 0% 0.0% 0.0% | 0N 0N 0N 0.07% 100% 100% 100% 100 0N 0N 0N 0.07% 100% 100% 100% 100% 100% 100% 100% 1 | 0% 0% 0% 0% 0% 0.0 0% 0.0 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 05 0.0% 0.4226 06 0.0% 0.4226 | 0.0001 0.1183 0.0001 0.4226 0.4226 0.4226 |
| 1414 N-sicha-scahdramaterase 15. Nil Nas 15 | 6 100% 100% 100,0% 0% 0% 0% 0.0% 0.0% N 0% 0% 0.0% 93% 100% 100% 97.5% | 0% 0% 0% 0.0% 100% 100% 100% 100.0% 0% 0% 7% 0% 0% 2.4% 0% 0% 0% 0.0% 0.0% 100% 100% | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100% 100 | 100% 100.0% 0% 0% 0% 0.0% 0% 0.0% 100% 100% 80% 93.3% 0% 0.0% 100% 100% 100% 100.0% | 0% 0% 0% 0.0% 1.00% 0% 0% 20% 6.7% 20% 0% 0% 0% 0.00% 0.00% | 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9 | 0.000 | 85 G-1107 G00164 G-1207 |
| 1417 Nouri carriordomass (sciounido finanzio / NAUSO / NAUSO / 20 Kib. 20 Kib. 1418 Veri-hos-chain enovi-CoA redo / Tecr | 5 50% 481 50.7% 50% 60% 50% 40.7% 5 80% 28% 50.3% 50% 0% 0% 0% 0.0% 5 80% 28% 79.4% 20% 11% 22% 20.0% 6 100% 100% 100.0% 0% 0% 0% 0% 0.0% | 20% 17% 12% 17.2% 50% 50% 50% 50% 50% 27% 27% 20% 20% 20% 20% 17% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50 | 228 20.7% 1286 27% 286 28.25% 275 276 176 06 0.0% 27% 506 29% 35.3% 406 06 1 23% 14.6% 06 06 06 0.0% 0.0% 506 06 0.0% 06 06 06 0.0% 1000 1000 | 10% 17.7% 56% 50% 57% 542% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50 | 276 | 08 22.00% 60% 57% 25% 41.7% 29% 29% 30% 100% 0% 0% 0.00% 100% 100% 100% 0% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% 0% 0.00% | 0% 56.7% 0.1606 0.203 0% 0.0% 0.4054 0.6328 0% 0.0% | 28 0.9881 0.6565 0.4054 0.6328 0.9881 0.6925 |
| M21 Turnor prolisin CD4 | 6 576 50% 57.9% 22% 42% 50% 42.1% 6 100% 100% 100.0% 0% 0% 0% 0.0% m 100% 100% 100.0% 0% 0% 0% 0.0% | ON ON ON ON 0.07% 100% 100% 100% 100% 100% 152.27% 127% 407% ON ON ON 0.07% 1000% 1000% 1000% 1000% 100.07% ON ON | 40% 47.5% 0% 0% 0% 0% 0.0% 72% 67% 0% 0.0% 0% 0% 0 0.0% 100% 100% 100% 10 | 56% 64.6% 26% 32% 46% 35.4% 100% 90.0% 0% 0% 0% 0.0% 100% 97.2% 0% 8% 0% 2.8% | 0% 0% 0% 0.07% 78% 67% 100 0% 0% 0% 0.07% 100% 100% 100 0% 0% 0% 0.07% 100% 100% | 0% 81.5% 22% 22% 0% 0% 18.5% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | | 05 0.0050 0.0051 0.5804 0.2290 0.3805 0.0051 85 0.4296 0.4296 0.4296 0.4295 0.4296 0.4296 0.4296 94 0.1050 0.4296 0.4296 0.4296 0.4296 0.4296 |
| 1425 Protein 5100-A9 \$19000 \$1924, MCUSE 13 KDs 100% 1425 1444 | K 100K 00K 0K 0K 0K 0.5K K 100K 100K 100K 00K 0K | _9% | 0% 0% 0% 0% 0% 0.0% 100% 100% 100% 0% 0.0% 100% 10 | 92% 94.1% 10% 0% 8% 5.9% 100% 900.0% 0% 0% 0% 0.0% 100% 900.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 7.9% 89% 100 0% 0% 0% 0.0% 1.0% 100% 100 0% 0% 0% 0.0% 1.0% 100% 100 | N 89.2% 21% 9N 0% 19.0% 0N 2% N 100.0% 0N 0N 0N 0 00 0.0% 0N 0N N 100.0% 0N 0N 0N 0 0.0% 0N 0N | | |
| 5420. Deverable of networkship Annexes Registr. RBD3_MCUSE 25 McG 60 McG 1420. Scring passin-9 SmS SNSQ MCUSE 67 McG 60 McG 1420. Scring passin-9 SmS Pon3 PON3 MCUSE 29 McG 80 McG 1430. Scring passin-9 Pon3 PON3 PON3 MCUSE 29 McG 82 McG 1431. Collabor musicia collosifordio prof. Colp. CNSP MCUSE 20 McG 64 McG | \$ 295 278 284% 505 278 678 57.95 \$ 05 08 0.0% 5075 828 1008 1008 94.45 \$ 1008 1008 94.4% 08 08 08 0.0% 0.05 \$ 718 556 70.2% 88 208 208 2285 | 10% 14% 17% 13.7% 13.7% 10% 0% 0% 4.2% 50% 50% 12% 12% 12% 10% 0% 0% 5.2% 50% 100% 100% 12% 0% 5.0% 5.0% 5.0% 5.0% 5.0% 5.0% 5.0% | 100% 02.7% 25% 14% 0% 13.1% 0% 05 100% 100.0% 0% 0% 0% 0.0% 2.2% 0% 0% 3.0% 9% 0% 0% 3.0% 100% 86% 12% 16.9% 0% 0% 0.0% 0.0% 0.0% 0.0% | 08 0.0% 718 608 808 75.0% 258 15.7% 678 828 758 75.0% 868 90.5% 08 08 08 08 0.0% 1008 95.2% 148 08 08 4476 | 195 60% 20% 20.5% 0% 0% 1: 11% 17% 0% 9.3% 29% 56% 1 0% 14% 14% 9.5% 100% 100% 10 0% 0% 0% 0.0% 100% 100% 8 | 10 4.25 576 528 528 525 428 528 10 28.05 578 448 808 50.255 148 08 10 100.05 08 08 08 0.055 08 08 10 50.25 08 08 148 485 08 08 | 28% 32.3% 0.5478 0.252 28% 11.47% 0.542 9% 0.0% 0.9940 0.103 9% 0.0% 0.0940 1.000 | 00 6,0719 1,0000 0,177 0,174 0,174 0,177 0,946 0,220 0,0072 0,077 0,174 0,077 |
| EliZa Mouse Consistential on Initiation fig. EliZa ELIZA MOUSE 64 Kiba. 1005 H333 [Proteosome acchoire consistents of Parmia"] PSREZ MOUSE 27 Kiba. 1005 H344 [Entir-specific anciconomisis inhit. Balas(21) B(Z),1_MOUSE 57 Kiba. 509 | 6 898 100% 96.2% 0% 11% 0% 1.7% 8 100% 100.0% 0% 0% 0% 0% 0% 0.0% 0.0% 0. | 0% 0% 0% 0% 0.0% 100% 100% 100% 100% 100 | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 0% 0.0% 0% 0% 0% 0.0% 100% 100% 1 67% 66.7% 0% 0% 0.0% 0.0% | 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 1.0% 100% 100% 100 0% 0% 0% 0.0% 1.0% 100% 100 32% 100% 50 | 06 100.0% 06 06 06 0.0% 0.0% 06 06 06 06 06 06 06 06 06 06 06 06 06 | 6W 0.0W 1.0000 | 0.3033 0.0000 0.3033 |
| 1436 Nacionale sensitiva siement-bindi Ybc1 YBCX1_MCXES 26 MOs 218 1437 Perceidosini hornolog Parin PXEN_MCXES 166 MGs 218 1438 Nexestini-2 Ppp156b MESQ_MCXES 20 MCX | S 82S 90S 81,0% 29S 12S 10S 18,4% | 0% 0% 0% 0.0% 58% 51% 89% 09.1% 12% 5% | 11N 10.9% 0% 0% 0% 0.0% 100% 100% 100% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 86% 95.2% 0% 0% 14% 4.8% 0% 0.0% 25% 0% 40% 21.7% 100% 100% | 0% 0% 0% 0.0% 100% 80% 100 5% 200% 60% 78.3% 0% 0% 0% | 06 93.7% 06 20% 06 5.7% 08 06 100% 50% 08 08 08 | 0% 0.0% 0.2995 0.828 0.500 | 0.0009 0.25517 0.2506 0.8267 0.1333 0.5517 0.0009 0.00009 0.0009 0.0009 0.0009 0.0009 0.0009 0.00000000 |
| 1400 Dissolitoli profession 2 DSP DSP2_MCUSE 56 kGs 100% 1440 Accolonia-stravistics of cSI crist TSSD2p2 ASPP2_MCUSE 105 kGs 1441 Transmenterane protein 97 Treesf87 TMMST_MCUSE 21 kGs 100% 1442 Professiones subunit bins hys-4 Premb PSB4_MCUSE 20 kGs 90% 1442 Professiones subunit bins hys-4 Premb PSB4_MCUSE 20 kGs 90% 1442 PSB4_MCUSE 20 | 100% 200% 00.0% 0% 0% 0% 0.0% 0.0% | 9% 9% 9% 9.0% 9.0% 9.0% 9.0% 9.0% 97.7% 8% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 2,8% 0% 0% 0% 0.0% 100% 100% 0% 0.0% 8% 12% 0% 6,7% 100% 100% 0% 0.0% 0% 0% 0% 0.0% 100% 100% | 100% 100,0% 0% 0% 0% 0.0% 100% 100,0% 0% 0% 0% 0.0% 100% 100,0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 100% 100% 100 0% 0% 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100 | 00, 100,0% | 0% 0.0% 0.4226 0.1951 0% 0.0% 0.1984 | 0 100 000 1500 1500 1500 1500 1500 1500 |
| 1440 Ultri -specific prolesse 2 Utsp2 UFSP2_MOUSE \$2 KDs 100% 1444 Cytochrome b-c1 cornelex subari Upr 10 CDR MOUSE 7 KDs 80% 1445 AB1 interactor 1 Ab1 AB1 MOUSE \$2 KDs 0% 1445 AB1 MOUSE \$2 KDs 0% 144 | 4 100% 91% 97.0% 0% 0% 0% 0.0% 0.0% 5 71% 80% 77.1% 30% 29% 20% 22.5% 6 0% 0% 0.0% 100% 100% 100% 100 100 100 100 100 10 | 0% 0% 9% 3.0% 100% 100% 100% 100% 100.0% 00 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100% 100 | 67% 37.2% 40% 25% 0% 21.7% / 27% 42.4% 50% 50% 72% 57.6% | 0% 0% 100% 100% 100% 100% 100% 100% 100 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 29% 26.5% 0.9292 0.944 0% 0.0% 0.415 | 6-4026 6-4026 85 C-1020 6-8470 6-2022 6-3446 6-2022 0-3446 6-2026 6-4226 6-2026 12 6-2024 8-2012 6-2024 8-2012 6-2024 8-2012 6-2024 8-2 |
| 5447 Protein-9 Oct. OSS_ACUSE 76 kOs int. 5448 Calpain-2 catalytic subunit Capa ² CARQ_MCUSE 80 kOs int. 5449 Related dehydrogenase 2 Add 1s2 ALVA_MDUSE 57 kOs 5449 Related dehydrogenase 2 Add 1s2 ALVA_MDUSE 57 kOs | K 0% 7% 4.8% 92% 200% 92% 95.2% K 100% 100% 100.0% 0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 0.0% 0% 0% 0% 0% 0.0% 100% 10 | 300K 100.0% 0K 0K 0K 0.0% 0K 0K 0K 00K 0 0K 0 | 06 0.0% 100% 100% 100% 100.0% 1006 100.0% 0% 0% 0% 0.0% 1006 100.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% 0.0% 0% 0% 0 0% 0% 0% 0.0% 0. | 00 0.0% 100% 100% 100% 100% 000 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0.9856 0% 0.0% 0.9856 0% 0.0% | G 1917 G 2025 G 1927 G 1925 G 1926 G 1927 |
| HSD Ubliquille-2 Ubliquille-2 Ubliquille-2 UBLIQUIMUSE 67 KGs 295 1451 Mishi-Copi-binding position 2 Miscopi MISCOPI MISSOR 25 KGs 1005 1452 Probin SCAPS ScaRS SCAPS MUSSE 140 KGs | \$ 17% 50% 31.7% 71% 80% 50% 58.2% \$ 100% 100% 100.0% 00 00 00 00 0.25% \$ 00 00 0.0% 100% 100% 100% 1000% \$ 100% 100% 100.0% 00 00 00 00 0.25% | 0% 0% 0% 0.07% 25% 56% 40% 38.25% 55% 56% 0% 0% 0% 0.07% 0.07% 0.07% 50% 41.7% 100% 50% 0% 0% 0% 0.07% 100% 100% 100% 100% 100% 0.00% 0.00% | 6 60% 01.7% 0% 0% 0% 0.0% 60% 100% 50% 50% 50% 50% 0% 0% 0.0% 50% 50% 50% 50% 50% 50% 50% 50% 50% 5 | 60% 73.3% 60% 0% 62% 25.7% 50% 40.0% 80% 50% 50% 50% 60.0% 0% 0.0% 75% 100% 100% 91.7% 100% 900.0% 0% 0% 0.0% | 0% 0% 0% 0.07% 100% 44% 100 0% 0% 0% 0.07% 100% 56% 80 15% 0% 0% 8.2% 0% 0% 0% 0% 0% 0.07% 100% 100% 100 | 06 81.0% 0% 56% 0% 18.5% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 9% 0.0% 0.0990 0.740 9% 0.0% 0.1181 0.067 | 00 0.0712 0.1322 0.6190 0.7460 0.0712 0.1322 73 0.0000 0.2209 0.1161 0.0273 0.0007 0.2209 0.4226 0.4226 0.4226 |
| 1454 Risconnation Intel-derived contint Ring20: RECCES MCUSE 19 K/Ds 1455 Chrosof multimosticals body seed Chropid: Christian California Ca | N 25% 14% 12.1% 100% 75% 86% 85.9% N 100% 71% 90.7% 0% 0% 29% 9.5% N 0% 0% 0.0% 100% 100% 100% 100.0% | 0% 0% 0% 0.0% 100% 100% 100% 100.0% 0% 57% 32% 43% 27.0% 93% 57% 0% 0% 0% 0% 0.0% 100% 100% 100% 100.0% 0% 0% 0% | 0% 0% 0% 0.0% 50% 50% 50% 50% 50% 50% 50% 50% 50% 5 | 628 53.8% 418 228 578 43.7% 1008 900.0% 08 08 08 0.0% 868 87.7% 88 148 148 12% | 9% 0% 0% 2,9% 100% 0 0% 0% 0% 0.0% 1,0% 100% 88% 88 0% 0% 0% 0.0% 100% 92% 10 | 86 91.75 98 128 148 8.95 98 98 98 97.75 98 98 98 98 98 2.25 98 98 | 9% 0.0% 0.3358 0.955 9% 0.0% 0.4226 0.043 | N C C C C C C C C C C C C C C C C C C C |
| 1445 STASSMAN AND AND AND AND AND AND AND AND AND A | K 86N 89N 84.9N 20N 14N 11N 15.1N | 9% 9% 90% 9.0% 100% 100% 100% 100% 9% 0% 0% | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100% 100 | 91N 97.0% 0% 0% 9% 3.0% 98 100% 100% 100% 0% 100% 100% | 0% 0% 0% 0.0% 100% 100% 100 0% 0% 0% | 08 100.0% 08 08 08 08 08 08 | 9% 0.0% 0.0283 0.422 | 0.0000 0.0000 0.4225 0.0000 |
| 1451 LDP-glacose 4-spirerane Gale GALE MULES 20 kGs 100% 1450 1 | 1 100% 100% 100.0% 0% 0% 0% 0.0% 8 91% 91% 94.7% 0% 0% 0% 0.0% 0.0% 10 100% 0% 0% 0% | 9% 9% 9% 1,00% 100% 100% 100% 100.00% 9% 0% 0% 0% 9% 100% 100% 100% 100% 1 | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 0% 6.5% 6% 11% 0% 6.5% 100% 100% 0% 0% | 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0% 0.0% 0% 0% 0% | 2% 0% 0% 0.2% 100% 100% 20 2% 0% 0% 0.0% 100% 100% 100 200% 100% 0% 0% 0% | 50 100.0% 0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 9% 0.0% 9% 0.0% 100.0% | 0.1930 0.1917 0.1917 0.1917 0.7900 0.1930 0.1930 |
| 1465 Saccini-FoA-3-Intensit construi Detti SCOTI MUSE SI Kiba 100% 1466 Bakavolit transition initation to EISp ETSG MUSE SI Kiba 28% 1467 Toniin-14-Intensiting protein 1 Torialp1 TCP1_MUSE GT Kiba | 6 100% 100% 100.0% 0% 0% 0% 0.0% 0.0% 8 25% 40% 34.2% 62% 62% 50% 50% 58.2% 20% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 9% 0% 9% 0.0% 100% 100% 100% 100.0% 0% 0% 0% 0% 0% 12% 12% 10% 100% 100% | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 100% 100 | 1008 500.0% 0% 0% 0% 0.0% 75% 47.2% 67% 22% 25% 41.7% 22% 44.4% 0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 1.00% 100% 100 0% 26% 0% 11.1% 0% 25% 1 0% 50% 67% 55.0% 50% 100% 51 | 00 100.0% 00 00 00 00 000 00 00 00 00 00 00 00 | 9% 0.0% 0.9885 0.088 50% 33.3% 0.9885 0.313 | 56 0-6517 0-2206 0-8869 0-8237 0-3202 0-6000 0-8279 0-4226 0-7026 0-4226 0-3103 0-1026 0-4226 0-3103 0-1026 0-4226 0-3103 0-1026 0-4226 |
| 1940 1941 1940 | K 14N ON 10.3% 83N 86N 100N 89.7% | ON ON ON ON CON ON ON ON ON ON ON ON ON SOUN SOUN SOU | 6 100% 100.0% ON ON ON 0.0% 40% 25% 4 100% 95.2% ON ON ON 0.0 0.0% 44% 44% ON ON O | 17% 35.2% 56% 56% 82% 64.8% 6% 0.0% 100% 100% 100% 100.0% | 0% 0% 0% 0.0% 42% 55% 50 0% 0% 0% 0.0% 0.0% 0% 0% | 00 40.7% 57% 45% 50% 50.5% 0% 0% 0% 0% 0% 00% 100% 100% 100% 100 | 9% 0.0% 0.4753 0.2671 9% 0.0% | \$ C.0070 C.0004 C.4753 C.2075 C.0070 C.0004 |
| M72 Angiclerisis-converting enzyme Ace ACE MCUSE 191 MDs 1971 Angiclerisis-converting enzyme Ace ACE MCUSE 191 MDs 1972 Angiclerisis Statistical engagement AFT APPC APPC ADDISE 41 KDs 1978 1978 Profess Internal Confession Mrs. APPC APPC ADDISE 55 KDs 80 MS 42 KDs 42 | 100% ON | ON ON ON ON O.OPS 1000K | 0% 0% 0% 0% 0% 0% 000 100% 100% 100% 10 | 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0.0% 100% 100.0% 0% 0% 0.0% | 0% 0% 0% 0.05% 100% 100% 100 0% 0% 0% 0.05% 100% 100% 100 0% 0% 0.05% 100% 100% 100 0% 0% 0.05% 100% 100% 100% | 0% 100.0% 0% 0% 0% 0% 0.05 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0.8896 | 0.4226 |
| 1476 Tepomyosin alpha-1 chain Tem1 TEM1 MOUSE 23 50s 1477 TEM-4 memberiary resentance of 0g 0671 MOUSE 117 50s 07 1470 | 100% 100% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 08 08 08 1008 09 00 008 008 008 008 008 008 008 00 | 0% 0% 100% 58% 100% 100% 0% 0% 0% 0% 4.2% 17% 0% 0% 5.0% 100% 100% | 100% 56.1% 0% 42% 0% 13.9% 0% 0.0% 0% 0% 0% 0% 0.0% 1 100% 500.0% 0% 0% 0% 0.0% 1 | 0% 0% 0% 0.0% 1.0% 1.00% | 06 100.0% 06 06 06 0.0% 0.0% 06 06 06 06 06 06 06 06 06 06 06 06 06 | 0% 0.0% 0.7339 0% 0.0% 0.7339 | 86 0-0226 0-0239 0-0239 0-0155 |
| HEAD Secure of the Common Secure 44-41, Lensel IFAA JACUSE 47 KGs 100% 1480 Centrose of territation fractor subset Celf 5 CESTS JACUSE 63 KGs 0% 1481 Serum amylaid P-component April April SAMP JACUSE 25 KGs 1482 Heteroceneous nuclear ribercule) (Hompso ISAA JACUSE 31 KGs 26) | 5 0% 0% 0.0% 100 0% 100 100 100 100 100 100 100 10 | 0% 0% 0% 0.0% 100% 100% 100% 100.0% 0% 0% 0% 0% 0% 0.0% 0.0% 0% 0% 0.0% 0. | 000 000 000 000 000 000 220 1000 220 000 1000 10000 00 00 00 0.00 200 200 200 000 00 00 00 00 00 00 00 00 00 00 00 | 98 90 505 275 90 75 11,5% 90 8 25 10,5% 90 90 90 90 90 90 90 90 90 90 90 90 90 | Sen UN US USS 100% 100% 100% 100% 100% 100% 100% 10 | 00 100.000 000 000 000 000 000 000 000 0 | | 20 0.500 0.5 |
| 1463 Unconventional register by Myo16 MYO16 MOUSE 129 KDs 47% 1454 Pischarin homoloxy-like domain Phi662 PHI.02 MOUSE 141 KDs 1455 1454 KDs 1455 1454 KDs 1455 1455 KDs 1455 | 1 100% 0% 55.0% 22% 0% 100% 44.4% N 100% 100% 100.0% 0% 0% 0% 0.0% N 0% 0% 0.0% 100.0% 0.0% 0.0% | 0% 0% 0% 0.075 50% 100% 100% 83.275 50% 0% 0% 0% 0% 0.075 100% 100% 000% 0 0% 0% 0% 0% 0.075 100% 100% 0 0% 0 0% | 06 16.7% 06 06 06 0.0% 2.0% 200 06 06 06 06 06 06 06 06 06 06 06 06 0 | 985 90.7% 0% 0% 11% 3.7% 0% 0.0% 100% 100.0% 100.0% 100.0% 100% 10 | 7% 0% 0% 5.6% 100% 100% 10 0% 0% 0% 0.5% 0% 0% 0% 100% 100% 10 0% 0% 0% 0.7% | 00 100.0% 00 00 00 00 000 00 00 00 100.0% 00 00 00 00 000 00 00 0.0% 1000 1000 00 00 00 00 | 0% 0.0% 0.4684 0.199- 0% 0.0% 0% 0.0% | 0.30337 0.4226 0.4684 0.4226 0.2994 0.4226 0.4226 0.4226 0.4226 |
| 1467 Pyridosel kinsse Pdok PDIAK MCLISE 35 kGs 100% 1468 Picklise 1 47 kGs 100% 1468 Picklise 47 kGs 1469 Microsin resultatory light chain 128 Myl 25 Mil 25 MCLISE 20 kGs 579 1469 Mil 26 MCLISE 20 kGs 579 1469 MCLISE 20 kGs 579 1469 MCLISE 20 kGs 579 MCLISE 20 kGs | 6 100N 100N 100.07% 0% 0% 0% 0.07% 0% 0% 0% 50N 100.07% 100N % 40N 50N 49.07% 43N 60N 50N 51.07% | 0% 0% 0% 0.0% 100% 100% 100% 100.0% 0% 0% 0% 00 0% 00 0% 00 0% 00 0% 00 00 | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 12% 44.4% 0% 100% 57% 25.5% 20% 10% 1.2% 32.2% 0% 0% 0% 0.0% 40% 2.7% | 1005 900,0% 0% 0% 0% 0.0% 0% 10,0% 00% 50% 67% 52.2% 38% 34.7% 47% 66% 50% 52.2% | 0% 0% 0% 0.0% 100% 100% 10 10% 42% 22% 37.8% 29% 11% 50 12% 12% 13.1% 53.1% 64% 50% 4 | 00 100.0% 00 00 00 00 00% 00 00 00 00 00 00 00 | 9% 0.0% 59% 37.2% 0.214 12% 5.5% 0.200 0.000 | 00 0.2254 0.1172 0.4881 0.3375 0.5273 0.7325 0.4881 0.3490 0.0002 0.0071 0.0000 0.3084 0.3190 0.1540 0.0825 0.5480 0.1300 0.3084 0.3190 0.1540 0.0825 0.5480 0.1300 0.1300 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.000 |
| Head Journal - Section person person Printer la KAPO_MOUSE 43 KDa 52 KDa 12 KDa | 200 200 78.2% 40% 25% 0% 20.8% | Sec. | | SC 75 | 906 006 005 0.075 5076 5896 88 006 006 006 0.075 2076 228 22 006 006 006 0.075 8876 9076 88 006 006 006 0.075 006 006 006 | N 32.25 70% 47% 12% 34.7% 0% 0% 0% 0% 0% 0% 0% | 9% 0.0% 0.7503 0.171- 9% 0.0% 0.7503 0.7503 9% 0.0% 0.005 9% 0.0% 0.1885 0.1946 | 86 0.8842 0.6434 0.7503 0.7385 0.8842 0.6434 10 0.6426 0.0051 0.0065 0.0065 0.0040 0.6425 0.0051 10 0.7390 0.0051 |
| 1494 Inter-alcha-invosin Inhibitor hears ISEC | K 100N 100N 100.0% 0% 0% 0% 0.5 N 90N 100N 90.0% 18N 50N 0% 24% | ON ON ON 0.05% 100% 100% 100% 900.0% ON ON ON ON 100% 100% 100% 100% 100% 100% 100% 100 | 0% 0.0% 0% 0% 0% 0.0% 0.0% 120% 120% 0.0% 0% 0% 0.0% 120% 120% 0.0% 0.0% 0.0% 120% 120% 120% | 95% 85.1% 5% 4N 0% 3.1% 95% 95% 96% 0% 8N 5.8% 100% 96% 00% 0% 00% 0.0% | \$60 120 50 90.9% 1000 560 100 00 00 00 00 0.0% 920 1000 10 00 00 00 00 0.0% 920 920 1000 10 | 00 95.2% 00 00 00 00 00 05% 00 140 00 97.0% 70 00 00 2.4% 00 00 00 91.7% 120 96 06 7.0% 64 06 | | 55 G 1993 G 2591 G 2505 G 1197 G 2591 G 2597 G 2591 G 2597 G 2591 |
| 1400 Tripopticipi-poptidase 2 Tpp2 TPP2 MOUSE Mo IDs 100% 1400 Acvi-CoA synthetise family ment Acxi2 ACSF2 MOUSE 60 kCs 100% 1500 Acyticamitine hydrolase Ces2c EST2C_MOUSE 62 kDs | N 100N 100N 100.0% ON ON ON O.0% N 100N 100N 100.0% ON ON ON O.0% N 50N 20N 20N 20 N 100 N | ON ON ON O.ON 100N 100N 100N 100N 100 ON ON ON ON | 0% 0.0% 0% 0% 0% 0.0% 100% 100% 0% 0% 100% 100% 100% 100% 100% | 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0% 0.0% | 0% 0% 0% 0.0% 0.0% 100% 100% 000 00 00 0.0% 0.0% | 00 100.0% 016 016 016 0.0% 016 016 016 016 016 016 016 016 016 016 | 0% 0.0% 0% 2.4% 0.422 | 0.4226 |
| 1301 Linex large homolog 1 Dig1 DLG1_MDUSE 100 kDs 09 | NS 25% 38% 20.07% 100% 75% 63% 79.27% ON ON 200% 100% 100% NS 88% 90% 85.07% 20% 12% 10% 14.27% NS ON ON O.77% 100% 100% 100% 1000 75 | UN | 8-78 57.2% 0% 0% 0% 0.0% 50% 50% 57% 100% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 808 05.0% 50% 32% 20% 34.4% 0% 0.0% 100% 100% 100% 100.0% | 2% 0% 0% 0.0% 100% 100% 100% 200 0% 0% 0% 0.0% 0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0 | 781 1081/076 0/6 0/6 0/6 0/6 0/75 0/6 0/6 0/6 0/6 0/6 0/6 0/6 0/6 0/6 0/6 | | 00 6.0006 6.0006 0.1602 0.0000 0.0006 0.0000 |
| 1932 1 CCDS simulatures control act 1 of 100 (100 (100 (100 (100 (100 (100 (100 | s 100% 100% 100.0% 0% 0% 0% 0.0% | ON ON ON D.ON 100N 100N 100N 100 ON ON | 0% 0.0% 0% 0% 0.0% 100% 100% 100% | 100% 100.0% 0% 0% 0% 0.0% 100% 100.0% 0% 0% 0% 0.0% | 9% 9% 9% 9.0% 109% 109% 20 9% 9% 9% 10.0% 109% 109% 10 | 05 100.075 05 05 05 05 05 05 05 05 05 05 05 05 05 | 0% 0.0% | 0.0235 0.0229 |
| 1500 11 Control American Service 15 15 15 15 15 15 15 1 | % 100% 100% 100.0% 0% 0% 0% 0.0% 6 22% 20% 28.9% 0% 0% 0% 0% 0.0% | 67% 67% 80% 71.1% 29% 0% 25% 17.9% 0% 0% | ON 0.0% 71% 100% 75% 82.1% ON | 0% 0% 0% 1 50% 85.7% 0% 00 00 00 1 | 0% 100% 13 W 7W 7W | N 51 75 364 624 05 34 76 | 0% 0.3535 0% 3.8% 0.3535 | |
| 1973 1974 | 1008 1008 100.075 08 08 08 0.075 08 08 0.075 08 08 08 0.075 08 08 0.075 08 08 0.075 08 0.075 08 0.075 08 0.075 08 0.075 08 0.075 08 0.075 0. | \$78, \$678, \$880, \$77.75\$, \$298, \$08, \$258, \$17.578, \$09, \$0 08, \$08, \$08, \$0.078, \$1008, \$2008, \$09, \$09, \$09, \$09, \$00, \$00, \$00, \$0, \$00, \$0 | 6 0N 0.0% 73% 300% 25% 52.1% 0% 50% 50% 50% 100% 50% 100% 50% 100% 50% 50% 50% 50% 50% 50% 50% 50% 50% | 9% 0% 0% 0% 0% 0% 0 50% 65.7% 0% 9% 0% 0.0% 9% 0% 0 9% 6.7% 80% 100% 100% 50.2% 0% 0.0% 100% 100% 1000% | 00% | 05 51.75 28 67 05 34.75 25 85 06 0.75 100 100 100 100 00 05 07 0.75 100 100 100 100 00 05 | 0% 3.8% 0.1917 0.2254 | 0.2137 0.2187 0.5138 0.2254 0.5139 |
| 2002 Per-SPRING - Control Cont | 100 | \$75, \$70, \$80, \$71,75, \$205, \$00, \$205, \$17,95, \$05, \$0. 205, \$205, \$205, \$205, \$1005, \$1005, \$0. 205, \$205, \$205, \$205, \$1005, \$1005, \$205, \$1005, \$205, \$1005, | \$ 060 0.07% 22% 1260% 276% 52.1% 060 50% 50% 50% 50% 50% 50% 50% 50% 50% 50 | 00% 05.7% 00% 00% 00% 0.07% 0.00% 0. | 100% 100% 120% | No. 05.7% 28% 57% 0% 34.7% 2% 6% 6% 6% 6% 6% 6% 6% 6% 6% 6% 6% 6% 6% | 9% 3.8% 0.858 | |

| complex subunit SPT16 Supt16h St subosin-containing proteit NM NV SF-related matrix-associal Smarcd2 ST | PTGH_MOUSE 120 M_MOUSE 94 k MPD2_MOUSE 59 k | KDs 0% 0 Ds Ds | % 32% 11.1 % 0% % 0% | % 100% 10 20 20 | 0% 67% 88.9° 0% 100% 0% 100% | 7% 9% 0 0 | 0% 0% 0.07 0% 0% 0% 0% | N ON | 9%. | 100% 100% | 100% | ons ons | 6% 6% | 250 | N 100% 1/ 0% N 100% | 00% 91.7% 3 0% 33.3% 10 | 5% 0% 0 100% 0% 0% 100 | 8 557% 8 55.7% | 0% 0% 0% 0% 0% | S 0.0% 67% S 0.0% 0% | 100% 100% BB. | 2% 0% 01 50% 3001 | 0% 0.0% | 22% 0% 50% 0% | 0% 11.1% 0.4 | 226 0.8520 0.4226 | 0.0055 0.015 | 0.4226 0.4 | 0.0055 943 0.4225 | | 0.4225 | Ē |
|--|--|---|---|---|--|--|--|-------------------------------------|--------------------------------|---|----------------------------------|--|--------------------------|-------------------------------------|-------------------------------------|--|---------------------------------------|----------------------------------|------------------------------|--|--|--------------------------------------|---|-------------------------------|---|------------------------------------|--|-----------------------------------|--------------------------------|-----------------------------------|--------------------------------|------|
| d beta A4 precursor profes Apbb tip All in-associated protein 2 Ubag2 Uli se profesion Vill | BHP MOUSE 74 k | Ca KCa OS O | % 0% 0.0 | % 100% 10 | 0% 100% 100.0° | % 0% 0 | 0% 0% 0.09 | s os | os os | 0.0% 100% | 100% 100% | 100.0% 0% | 25 25 | 0.0% 0 | S 0% 1 | 50% 25.0% 3 0% 0.0% 10 | 5% 100% 50 0% 100% 100 | 5 75.0% 5 100.0% | 0% 0% 0% 0% | 6 0.0% 06 6 0.0% 06 | 0% 0% 0.1 | 75 100% 100° | 0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | = | _ |
| rich syndrome protein Wast2 W 3 Pkp3 Pk | ILL_MOUSE | Da 40% 61 Da 0% 0 | N 0N 23.3 N 0N 0.0 | % 60% 4 % 100% 8 | 0% 100% 55.7° 2% 100% 94.4° 0% 0% 0.0° | % 0% 0 % 0% 17 | 0% 0% 0.07 7% 0% 5.07 | S 50% 4 S 0% 1 | 0% 25% 0% 0% | 38.3% SON 0.0% SON | 60% 75% 67% 100% | 51.7% 0% 72.2% 50% | 255 05 225 05 | 0.0% 49 27.8% 01 | S 56% / S 0% | 62% 47.6% 5 0% 0.0% 10 | 5% 32% 50 0% 100% 100 | 5 46.0% 5 100.0% | 0% 11% 0% 0% | 6 6.5% 50% 6 0.0% 0% | 31% 52% 46. | 7% S0% 631 50% | 6 695 51.8% 6 0% 0.0% | 98 68 598 | | | 0.5074 0.503 | | | | 0.3374 | 0.11 |
| Tes Till dent zinc metalloonde Yme III Y | ES_MOUSE 46 k | Da 0% 1 | % 9% 9.0 % 9% 9.0 | % 100% 10 | 0% 100% 100.0° | | 0% 0% 0.07 0% | N 14% 2 | SN ON | 13.1% 86% | 75% 100% | 86.9% 0% | 9% 9% 9% | 0.0% 20 | N 0% | 0% 6.7% s 0% 10 | 0% 100% 100 0% 100% 100 | N 93.3% | DN DN | N 0.0% SON | ON ON | 50% 1001 0% 1001 | | 0% 0% 200% 0% | 0.2 | 123 0.5950 | 0.4226 0.717 | 0.2123 0.5 | 0.4225 000 | 0.7178 | 0.5000 | = |
| -1 Ppflip1 LI le-associated protein R Mapre1 M | IPB1_MOUSE 109 MARE1_MOUSE 30 k | KDa Da Son Si | N 67% 55.6 | | 0% 23% 44.4° | % 0% 0 | 0% 0% 0.09 | N 100N 10 | ON 100% 1 | 100.0% ON | 0% 0% | 0.0% 0% | 0% 0% | 0.0% 1001 | N 0% | 0% 0.0% 10 67% 88.9% | 0% 80% 100 0% 0% 23 | S 93.3% S 11.1% | 0% 20% 0% 0% | 6 5.7% 20% 6 0.0% 100% | 25% 0% 15.1 100% 100% 100.1 | 7% 60% 751 7% 0% 01 | 100% 78.3% 0% 0.0% | 20% 0% 0% 0% | 0% 6.7% 0% 0.0% 0.0 | 0.1885 0.4226 | 0.0765 | 0.0153 0.4 | 115 126 0.0765 | | 1.0000 | |
| dissociation inhibitor 2 Arhgdib Gi ceptor coactivator 5 Noos5 Ni | DIRZ MOUSE 23 k | Da 100% 100 Da 0% 0 | % 100% 100.0 % 0% 0.0 | % 0% 1 | 0% 0% 0.0° 0% 100% 100.0° 0% 0% 0.0° | % 0% 0 % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% | 200% 0% | 0% 500% | 0% 100% | One One | 0% 0% | 1001 | N 100% 11 N 0% | 00% 0.0% 10 | 0% 0% 0 0% 0% 0 0% 100% 100 | N 0.0% | 1% 10% 2 0% 0% 0% 0% | 66 0.0% 96% 66 0.0% 96% | 94N 300N 93. 0N 0N 0. | 2% 16% 61 2% 10% 500 | 6 0% 6.8% 6 100% 900.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.2396 | 0.239 | 6 02 | 106 | 0.2396 | | |
| obset masc enzyme. It Me2 Mi obses C11ort54 homok 1 5V CI id hydroxeroxide olute Gpe4 Gi | NOS4_MOUSE 35 k PX41_MOUSE 22 k | Da 100% 100 Da 50% Si | N 100% 100.0 N 100% | % SON S | 0% 0% 0% 0% 22% 44.4° | % 0% 0 | 0% 0% 0.09 0% 0% 0.09 0% 0% 0.09 | 100% 10 100% 10 N 60% 6 | 0% 100% 1 0% 100% 1 | 100.0% 0% 100.0% 0% 65.5% 40% | 0% 0% 23% 27% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 1000 0.0% 1000 | N 100% 1 | 00% 100.0% 00% 100.0% 67% 58.9% 4 | 0% 0% 0 0% 0% 0 0% S0% 22 | N 0.0% N 41.1% | 0% 0% 0% 0% | N 0.0% 100% N 0.0% 100% N 0.0% 67% | 100% 100% 100.1 100% 100% 100.1 67% 75% 69. | 7% 0% 01 7% 0% 01 6% 22% 221 | 6 0% 0.0% 6 25% 30.5% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 876 0.1496 | 0.6749 0.555 | 5 0.1876 0.1 | 156 0.8749 | 0.5555 | _ | |
| se nucleotide eschano Arhget2 Al snesvieni manonasult- (gC): M nkii risulmana isomeras (Rbp3 (R) | PRI_MOUSE 274 KEP3_MOUSE 25 k | KDs 0% 0 KDs Ds 100% 10 | % 200% % 200% 100.0 | 100% 10 % 9% | 0% 0% 0.0° | 0% 0 % 0% 0 | 0% 0% 0.07 | 100% 10 % 100% 10 | ON 100% 1 | 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 0.0% 100 | 1925 1 1925 1 | 676 58.9% 4 00% 100.0% | 0% S0% 22 0% 0 0% 0% 0 | K 41.1% K 0.0% | 0% 0% 0% 0% | % 0.0% 100% % 100% % 0.0% 100% | 100% 100% 100% 100% 100. | 0% 01 0% 01 2% 0% 01 | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 0.0136 | 0.0067 | 90 | 0.0067 | | _ | |
| min alpha-3 chain Tpm3 TF ma subunit alpha bosa-7 Parra7 Pf fold modifier-conjugatin Ufc1 Uf | PMS_MOUSE 33 k SA7_MOUSE 28 k FC1_MOUSE 19 k | Da 100% 10 Da 100% 10 Da 100% 8 | N 100% 100.0 N 100% 100.0 N 90% 92.7 | N 98 1 | 0% 0% 0.0° 0% 0% 0.0° 2% 10% 7.3° | 75 05 0 75 05 0 | 0% 0% 0.09 0% 0% 0.09 0% 0% 0.09 | N 100% 10 N 100% 10 N 86% 10 | 0% 100% 1 0% 100% 1 | 100.0% 0% 100.0% 0% 95.2% 14% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% 4.8% 0% | 0% 0% 0% 0% | 0.0% 100 0.0% 89 0.0% 100 | N 93% 1 N 93% 1 N 100% 1 | 00% 97.6% 88% 86.6% 1 00% 100.0% | 0% 7% 0 1% 17% 13 0% 0% 0 | 5 2.4% 5 13.4% 5 0.0% | 0% 0% 0% 0% | 6 0.0% 95% 6 0.0% 100% 6 0.0% 100% | 95% 89% 92.1 100% 100% 100.1 100% 100% 100. | 2% 5% 51 2% 6% 61 2% 6% 61 | 6 11% 7.1% 6 0% 0.0% 6 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0.7 | 0.2035 0.0151 | 0.4225 0.070 0.0151 0.1862 0.422 | 2 0.2 0.0 0.7006 | 0.4225 151 0.0151 0.1852 | 0.0702 | \pm | |
| a-derived growth factor 1985 198 a-3 chain C region 1 59/ 10 2 Lgala2 LB | DGF_MOUSE 25 k 24G3_MOUSE 44 k EG2_MOUSE 15 k | Da 100% 100 Da Da | N 100% 100.0 | N 98 | 0% 0% 0.0° | 7% 9% 0 | 0% 0% 0.05 | N 100% 10 100% 10 | 0% 100% 1 0% | 100.0% 0% 0% | 0% 0% 0% | 0.0% 0% | 0% 0% 0% | 0.0% 100 | N 100% 1/ N 100% 1/ 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% 6 100% | 100% 100% 100/ 100% 100% 100/ 49% 70% 72 | 2% 0% 01 2% 0% 01 7% 0% 511 | 0% 0.0% 0% 0.0% 0 27.3% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.2090 | | | 190 | | \pm | |
| B Lgale9 LE se 1 Dpsp1 Di graminate cylidylyfransi Cmas Ni | EGS MOUSE 40 k PEP1 MOUSE 46 k EUA MOUSE 48 k | Da 0% 1 Da 100% 10 Da 25% | % 0% 5.6 % 62% 88.9 % 25% 16.7 | % 100% 8 % 0% % 75% 10 | 2% 100% 94.4° 0% 0% 0.0° 0% 75% 83.3° | % 9% 0 % 9% 0 | 0% 0% 0.09 0% 22% 11.79 0% 0% 0.09 | N 50N 10 N 89N 10 N 6 | 0% 100% 2% 100% | 95.3% 0% | 0% 0% 33% 0% | 0.0% 11% | 0% 0% 0% 0% | 3.7% 50 | N 42% | 18% 28.5% S G% 38.9% | 8% 17% 71 0% 0% 0 | N 48.4% 1 | 6N 42N 1 0N 200N 2 | % 23.1% 78% % 61.1% 79% 100% | 64% 67% 63.0 72% 78% 75. 100% 75% 91. | 7% 11% 441 7% 0% 41 7% 0% 0 | 17% 24.1% 0% 1.2% 0% 0.0% | 11% 11% 21% 24% 2 | 2% 13.0% 0.5 2% 22.6% 0.5 5% 8.3% 0.9 | 770 0.0518 813 0.2031 036 | 0.0654 0.348 0.1135 0.015 0.710 0.1939 0.2863 | 4 0.5770 0.2 9 0.4 3 0.1036 | 126 0.0930 | 0.2575 0.4226 0.5813 0.5000 | 0.3936 | 0. |
| main family member 15 Tbc1d15 TE maintenance of chrom Smc1a St tase homolog 1 Lost1 LC | BC15 MOUSE 77 k MC14 MOUSE 143 CNL1 MOUSE 65 k | Da 100% 81 KDa 101 Da | N 85% 91.2 N 100% | % ex | 0% 0% 0.0° 0% 0% | % 9% 11 0 | 1% 15% 8.85 0% 0% | N 89% 8 | 2N 100% | 90.7% 0% | 0% 0% | 0.0% 11% | 17% 0% | 9.3% 100 501 | N 100% 1/ N 100% / | 00% 100.0% 86% 78.6% 1 0% 0.0% 10 | 0% 0% 0 0% 0% 14 | N 0.0% N 21.4% N 86.7% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% 6 13.3% 0% | 67% 100% 88.1 0% 0% 0. | 2% 2% 331 2% 2% 521 | 6 0% 11.1% 6 50% 68.1% | 0% 0% 12% 22% 1 | 0.9 0% 0.0% 0% 31.9% | 0.6102 | 0.1939 | 0.5 | 102 0.2863 122 | 0.9523 | 0.3422 | 0. |
| like modifier-activating Alg7 Algorithms Guab Bit Algorithms Guab Bit Algorithms Algorithms | TGT_MOUSE 78 k GLR_MOUSE 74 k MANAY MOUSE 123 | Da 100% 100 Da | N 100% 100.0 | % ex | 0% 0% 0.0* | 5 05 0 | 0% 0% 0.09 | N 100% 10 | ON 100% 1 | 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% | 0.0% 100 100 100 | N 100% 1/ N 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | S 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% | 100% 100% 100.) 100% 100% 100.) 50% 100% | 2% 0% 01 2% 0% 01 | 0% 0.0% 6 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.8109 | | 9.8 | 109 | | = | |
| sein-3 Snd S1 lightless-1 homolog Fili Fil second prop. ATD see per Danni M. Dr | NK3_MOUSE 19 k | Da 100% 2: KDa 100 Da 100% 100 | % 100% 77.8 % 100% 100.0 | % 0% 6 | 7% 0% 22.2° 0% 0% 0.0° | % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% 7 | SN 100% | 91.7% 0% | 25% 0% 0% 0% | 8.3% 0% | 0% 0% 0% 0% | 0.0% 1000 1000 0.0% 1000 | N 100% 11 N 100% 11 | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% N 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% | 100% 100% 100. 100% 100% 100. | 2% 0% 01 2% 0% 01 | 6 0% 0.0% 6 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0.6 0% 0.0% | 061 | 0.4226 0.422 | 0.6061 | 0.4226 | 0.4226 | - | |
| stion factor p65 Rela TF (Losidase 1 Qsox1 Q | FES_MOUSE 60 k | Da ON O | % 0% 0.0 | % 100% 10 | 0% 100% 100.0° | % 0% 0 | ON ON 0.09 | N ON 1 | 0% 0% | 0.0% 100% 0% | 100% 100% 0% | 100.0% 0% | 0% 0% 0% | 0.0% 01 | N 0% | 0% 0.0% 10 00% 100.0% | 0% 100% 100 0% 0% 0 | K 100.0% K 0.0% | 0% 0% 0% 0% | 6 0.0% 0% 6 0.0% 100% | 0% 0% 0.1 100% 100% 100.1 | 7% 100% 1001 7% 0% 01 | 6 200% 900.0% 6 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | = | |
| oisomerase 1 Top1 To mino crowth factor beta- Tgfb1i1 To | OP1_MOUSE 91 k | Ds 0% 0 Ds 0% 0 | % 100% 33.3 % 0% 0.0 | % 100% 10 % 100% 10 | 0% 0% 66.7° 0% 100% 100.0° | % 0% 0 % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 0N 10 | 0% 0% 0% 0% | 33.3% 100% 0.0% 100% | 0% 100% 100% 100% | 55.7% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% soon 0.0% or | N 75% I | 67% 80.6% 0% 0.0% s | 0% 25% 23 2% 92% 83 | N 19.4% N 88.6% | 0% 0% 8% 9% 1 | % 0.0% 100% % 11.4% 0% | 100% 0% 0% 0) | 0% 0% 01 2% 83% 811 | 6 71% 78.7% | 0% 0% 17% 19% 2 | 9% 21.3% | 000 0.1917 | 0.2901 0.183 | 5 1,0000 0.1 0.0 | 917 0.2901 964 0.0507 | 0.1835 | 0.0994 | 0.0 |
| is anhannan-hinding rand Agip Aj rituation armuma school Ubs2 Si murlander Shill, searcrish Ubp14s U | EBP1_MOUSE 128 AE2_MOUSE 71 k T14A_MOUSE 87 k | KDs 100% Ds 0% 0 | 100% % 0% 0.0 | 0% % 100% 10 | 0% 0% 100% 100.0* | 9% 9% 0 | 0% 0% 0% 0.07 | N ON | 0% | 200% | 100% | 0% | 96 | 200 200 01 | N 72% I N 192% II N 2% | 62% 62,7% 5 00% 500,0% 0% 0,0% 10 | 0% 14% 23 0% 0% 0 0% 100% 100 | N 32.5% N 0.0% N 100.0% | 0% 14% 0% 0% 0% 0% | 6 4.8% 100% 6 0.0% 100% 6 0.0% | 100% 100% 100.) 100% 100% 100.) 0% | 2% 0% 01 2% 0% 01 2001 | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.0290 | | 0.0 | 175 | | 0.4226 | |
| aminopeptidase 1 Xpnpep1 XI aminopeptidase 1 Xpnpep1 XI ated protein 2/3 complex Arpc5 AI | DNI_MOUSE 38 k PP1_MOUSE 70 k RPCS_MOUSE 16 k | Da 100% 10 Da 100% 10 | N 100% 100.0 N 100% 100.0 | N 98 | 0% 0% 0.0° | 5 0% 0 5 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% 10 N 100% 10 | ON 100% 1 | 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 100 0.0% 100 | N 50% 1 N 100% 1 N 100% 1 | 76% 59,8% 4 00% 100,0% 00% 100,0% | SN SSN 26 SN SN S SN SN S | 5 40.4% 5 0.0% | 0% 0% 0% 0% | 6 0.0% 92% 6 0.0% 100% 6 0.0% 100% | 100% 80% 90. 100% 100% 100. 100% 100% 100. | 2% 8% 01 2% 0% 01 2% 0% 01 | 0% 9,4% 0% 9,0% 0% 9,0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0.0306 | | 0.0 | 106 | | = | |
| a-25 chain C region Igh-3 IG al-binding protein 2 Cttp2 C actor recestor-bound pri Grb10 G | TEP2 MOUSE 44 k TEP2 MOUSE 49 k PB10 MOUSE 71 k | Da 10 Da 0% 2 Da 25% | 65 95 995 6.7 95 20% 15.0 | N 88N 8 | 0% 100% 89.2° 3% 70% 71.9° | % 13% 0 % 13% 17 | 0% 0% 4.25 7% 10% 13.17 | N 0% | 0% 0% 0% 0% | 0.0% 100% 10.8% 62% | 0% 100% 100% 100% 60% 100% | 100.0% 0% 74.2% 25% | 0% 0% 0% 0% | 0.0% 121 15.0% 01 | N 100% 1/ N 13% | 00% 100.0% 12% 14.2% 5 0% 0.0% 10 | 0% 0% 0 3% 75% 73 0% 100% 100 | N 0.0% N 77.2% N 100.0% | 0% 0% 0% 13% 1 | 6 0.0% 100% 6 8.6% 29% 6 0.0% | 100% 94% 98.1 14% 38% 25.1 | 2% 0% 01 8% 50% 711 | 2% 1.0% 38% 53.0% | 0% 0% 21% 14% 3 | 3% 1.0% 5% 20.2% 0.4 0.6 | 0.4225 225 0.1995 884 | 0.3776 0.058 0.1885 0.2254 0.802 0.964 | 2 0.2044 0.1 0.8869 | 125 129 0.1659 0.0441 | 0.0416 0.4220 0.0250 | 0.4226 5 0.1013 8 | 0.4 |
| Non N mbrane protein 43 Treen 43 Th from I recessor NE-X1 NHs N | CLN MOUSE 63 k | Da 100% 100 Da 100% 100 | N 200N 100.0 N 0N 0.0 N 0N 0.0 N 82N 88.9 | % 0% 1 | 0% 0% 0.0° 0% 100% 100.0° | % 0% 0 100 | 0% 0% 0.05 0% 0% 0.05 0% 0% 0.05 | S 90% 7 | 5% 100% | 88.2% 0% 0% 0.0% 100% | 0% 0% 0% | 0.0% 10% 100% | 25% 0% 0% | 11.7% 200 501 | N 0% 1 | 50% 50.0% 0% 29.5% | 0% 0% 0 0% 0% 0 | S 0.0% S | 0% 200% S 0% 62% 10 | 6 50.0% 50% 6 70.5% 47% | 100% 100% 83. 55% 57% 52 | 2% 0% 01 2% 0% 01 | 0% 0.0% 0% 0.0% | 50% 0% 53% 45% | 0% 16.7% 0.2 3% 47.2% | 495 0.3858 0.2507 | 0.2254 0.802 0.964 | 0.0000 6 0 0.3 | | 0.2495 | 0.3868 | 0.2 |
| ckle component 1 Papc 1 Pr me subunit beta type-5 Pamb5 Pr all domain-containing pri Codc47 | SPC1 MOUSE 59 k SBS MOUSE 25 k CD47 MOUSE 70 k | Da 0% 1 Da 82% 10 Da 72% 7 | % 0% 0.0 % 82% 88.9 % 38% 60.0 | % 100% 10 % 17% % 18% | 0% 100% 100.0° 0% 17% 11.1° 4% 54% 28.8° | % 0% 0 % 0% 0 | 0% 0% 0.07 0% 0% 0.07 4% 8% 10.49 | N 100% 10 N 80% 4 | 0% 100% 1 7% 100% | 100 N 100 ON ON 82 2% 20% | 100% 0% 0% 0% 0% | 0.0% 0% 6.7% 0% | 0% 0% 0% 0% | 0.0% 1000 11.1% AN | N 100% 1 | 0% 6.1% 5 00% 100.0% | 2% 90% 100 0% 0% 0 0% 20% 0 | S 93.9% S 95.7% | 0% 0% 0% 0% | 6 0.0% 18% 6 0.0% 100% 6 20.0% 324 | 7% 8% 11. 100% 100% 100. 0% | 2% 92% 931 2% 9% 91 23% 9% | 92% 89.0% 6 0% 0.0% | 0% 0% 0% 0% 22% 50% | 0% 0.0% 0% 0.0% 0.5 0.2 | 0.3613 835 245 0.3477 | 0.1859 0.092 0.1835 0.2543 0.095 0.0572 0.184 | 0.1835 2 0.2173 0.7 | 0.1809 0.1835 101 0.6375 | 0.0920 | A 0.2255 | 0.4 |
| in beta-like protein 2 TbG TB laketh-Addrich syndrome Wast W protes subunit FAMC* Few-21 | BL2 MOUSE 50 k ASL MOUSE 54 k AM21 MOUSE **** | Da 82% 9. Da 0% 0 | % 95% 88.9 % 0% 0.0 | % 0% 100% 10 | 8% 9% 5.6° 0% 100% 100.0° | % 17% 0 % 0% 0 | 0% 0% 5.69 0% 0% 0.09 | N 100% 9 N 0% | 2% 92% 0% 0% | 94.7% 0% 100% | 0% 0% 100% 40*** | 0.0% 0% 0% 100.0% ^~ | 85 85 95 | 5.3% 100 0.0% ~ | N 100% 1 | 00% 0.0% 10 22% 11.4% | 0% 0% 0 0% 100% 100 0% 100% | N 0.0% N 100.0% | 2% 2% 2% 2% | 6 0.0% 100% 6 0.0% 0% | 100% 100% 100. 0% 0% 0. | 2% 0% 01 2% 100% 1001 | 0% 0.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0.2 0% 0.0% | 0.0745 | 0.1835 0.2543 0.006 0.0572 0.184 0.4026 0.152 0.8671 0.422 | 2 0.1863 | 0.1853 | 0.9740 | | 0. |
| me-activating protein-bi G3bp2 Gi -CoA dehidroomaan Acad8 Al | CADE MOUSE 54 k | Da 0% 1 | % 11% 6.7 % 100% 100.0 | % 100% 9 % 0% 1 | 5% 89% 93.3° 0% 0% 0.0° | % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 17% N 86N 10 | 0% 0% 0% 100% | 5.6% 82% 95.2% 54% | 100% 100% 0% 0% | 94.4% 0% 4.8% 0% | 0% 0% 0% 0% | 0.0% 121 | N 0% | 0% 5.6% s 00% 100.0% | 2% 100% 100 0% 0% 0 | N 94.4% N 0.0% | 0% 0% 0% 0% | N 0.0% 0N N 0.0% 100% | 0% 0% 0.0 100% 100% 100.0 | 7% 100% 1001 7% 0% 01 | 100% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0.8 0% 0.0% 0.4 | 871 0.4226 226 | 0.8671 0.422 0.422 | 6 0.8671 0.4 6 0.4226 | 25 0.8671 | 0.4226 0.4226 | _ | |
| rold cis-trans isomeras Pidorta Pr celvicia-cosamine muta Pgm3 Al | KETA MOUSE 12 k GM1_MOUSE 59 k | Da 100% 100 Da 100% 100 Da 100% 100 | N. 200% 100.0 N. 200% 100.0 N. 200% 100.0 | % 0% 1 | 0% 0% 0.0* 0% 0% 0.0* | 76 0% 0 76 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% 10 N 100% 10 N 100% 10 | ON 100% 1 ON 100% 1 | 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 1000 0.0% 1000 | N 100% 11 N 100% 11 | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% | 0% 0% 0% 0% | 66 0.0% 100% 66 0.0% 100% | 100% 100% 100. 100% 100% 100. | 2% 0% 01 2% 0% 01 | 6 0% 0.0% 6 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | A 100% | | | _ | |
| a biosynthesia-like dom Pbid2 Pl r straknistir system 3.16 Skt/20 St | BLD2 MOUSE 32 k KGL2 MOUSE 118 | Da 100% 100 KDa 0% 1 | % 20% 100.0 % 200% 100.0 | % 0% 10 9% 0% | 0% 85% 88.2° 0% 0% 0.0° | % 0% 0 200% 100 | 0% 0% 0.09 0% 0% 0.09 | N 100% 10 | ON 93% | 97.6% 0% 98 | 90% 50% 0% 7% 0% | 2.4% 0% 100% | 0% 0% 0% 0% | 0.0% 1000 | N 100% 1 | 00% 100.0% 40% 13.2% | 0% 0% 0 0% 0% 0 | N 0.0% | 0% 0% 0 0% 200% 6 | n 0.0% n 86.7% | 100% 0% | 91 | | 0% 500% | 0.0% 0.5 | | 0.4226 | 0.4226 | | | = | 0. |
| ing protein 1 Globp1 G miles broads in restain in Club CI Cpne3 CI | TPB1_MOUSE 72.6 LU_MOUSE 146 PNE3_MOUSE 60.6 | Da 100% 10 KDa 100% 10 Da 100% 10 | N 200% 100.0 N 200% 100.0 N 200% 100.0 | N 98 | 0% 0% 0.0° 0% 0% 0.0° | 75 05 0 75 05 0 | 0% 0% 0.09 0% 0% 0.09 0% 0% 0.09 | N 100% 10 N 100% 10 N 100% 10 | 0% 100% 1 0% 100% 1 | 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 100 | N 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0 | S 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 100% 6 0.0% 100% | 100% 100% 100.1 | 2% 0% 01 2% 0% 01 | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | | | | | | \pm | |
| s protein 1 Treem63a CI tion factor BTF3 B#3 B* deriged protein FLJ4521 1 5V Y. | SCL1 MOUSE 92 k TF3 MOUSE 22 k J005 MOUSE 38 k | Da 100% 100 Da 0% 0 | N 200% 100.0 | N 98 8 | 0% 0% 0.0° 2% 91% 83.1° | % 0% 0 % 25% 17 | 0% 0% 0.09 7% 9% 15.99 | 100% N 100% 10 N 0% | 200% 20% 200% 1 | 0% 100.0% 0% 0.0% 60% | 0% 0% 50% 71% | 0.0% 0% 60.5% 40% | 9% 9% 50% 29% | 0.0% 100 39.5% 141 | N 100% 1 | 00% 100.0% 0% 4.8% 7 | 0% 0% 0 1% 50% 80 | N 0.0% | on on en son a | 5 0.0% 100% N 28.1% 0% | 100% 100% 100.0 100% 100% 100.0 0% 0% 0.0 | 2% 0% 01 2% 0% 01 2% 50% 1001 | 0% 0.0% 0% 0.0% 5 0% 05.7% | 0% 0% 0% 0% 50% 0% 1 | 0% 0.0% 0% 0.0% 0% 33.3% | 0.4226 | 0.4226 | 0.0472 0.9 0.4226 | 115 0.2107 | 0.7545 0.0472 | 2 0.8083 | 0. |
| Interchi symbose, max Gys.1 Graturation factor 1 Lmf1 LB | PARCI, MOUSE 0928 TETA MOUSE 0928 TETA MOUSE 2928 TETA MOUSE 2938 TETA MOUSE 1938 TETA MOUSE 2938 TETA MOUSE 2 | Da 100% Si Da 100% 10 | N 25% 75.0 N 50% 83.3 | % 0% 1 % 0% 1 | 0% 25% 8.3° 0% 0% 0.0° 4% 20% 17.0° | 75 0% 50 75 0% 0 | 0% 0% 15.79 0% 50% 15.79 | N SON S N 80N S | 2% 100% 2% 80% | 65.7% 0% 72.4% 0% | 0% 0% 0% 0% | 0.0% SON 0.0% 20% | 50% 0% 43% 20% | 23.3% 27.6% | 200% | 50% 50% 50% 70 8% 1 | 9% 0 9% 0 | S 12.2% 1 | 200% S 0% S | S 17.0% 100% | 50% 100% 100% | 01 01 00 00 00 | 5 0% 6 0% 0.0% | 50% 0% | 0.7 0% 0.5 0% 0.0% 0.0 | 250 949 0.5000 256 0.0531 | 0.4225 0.2482 0.8085 0.008 0.6478 0.4225 | 0.4226 4 0.0094 0.1 | | | A 0.5000 | 0. |
| bioceresis regulatory Rxd Ri nain-containing protein Brd4 Bi | PE1_MOUSE 42 k | Da 0% 0 | N 9N 0.0 | % 100% 10 100% | 0% 100% 100.0° 100% | % 9% 0 9% | 0% 0% 0.07 0% | N 0% | 0% 0% | 0.0% 100% | 100% 100% | 100.0% 0% | 0% 0% 0% | 0.0% 0 | S 0% | 25% 8.2% 10 0% 0.0% 10 | 0% 100% 75 0% 100% 100 | N 91.7% N 100.0% | DN ON DN ON | N 0.0% ON N 0.0% ON | 0% 0% 0/ | 7% 100% 100° 100% | 100% 100.0% | 0% 0% 0% | 0% 0.0% | 0.4226 0.4226 0.2588 | | 0.4 | 25 0.4225 | | 0.4226 | Ξ |
| ich glycoprotein Hrg Hill binding protein-related Osbpilla O | PIG_MOUSE 59 k | Da KDa | | | | | | 0% 10 10 | 0% 100% 0% 100% | 65.7% 100% | 0% 0% 0% 0% | 33.3% 0% | 9% 9% 9% 9% | 0.0% 631 | S 568 | GN 60.6% 3 | 7% 64% 38 | N 39.4% | 0% 0% | N 0.0% 57% | SON 60N 55 | PN 49% 501 | 40% 44.2% | on on | 0% 0.0% | | | 1 02 | | 0.7741 | = | - 10 |
| embrane-associated or Smap2 St din F2 receptor negati Pigfm FF | MAP2_MOUSE 47 k PRP_MOUSE 99 k | On On O | % 0% 0.0 | % 100% 10 | 0% 100% 100.0° | % 0% 0 | 0% 0% 0.09 | s os | on on | 0.0% 100% | 100% 100% | 100.0% 0% | 0% 0% | 0.0% 01 | N 20% N 100% | 0% 6.7% 10 | 0% 80% 100 0% 0% | S 93.3% | 0% 0% 0% 0% | % 0.0% 0% 100% | 17% 0% 5.1 100% 100% 100.1 | 7% 100% 821 7% 0% 01 | 5 100% 94.4% 5 0% 0.0% | on on | 0% 0.0% 0% 0.0% | 0.9045 | 0.5000 0.4226 0.422 | 0.9 | 0.2929 945 0.4225 | 0.4226 | = | Ξ |
| sein-1 Srx1 SI YPBC Mildh L1 | NK1_MOUSE 59 k YFSC_MOUSE 64 k | Da 101 Da 67% Si | n 90% 65.6 | % 0% 2 | 0% 0% 0.0° 0% 5% 20% 15.0° 2% 0% 9.3° | % 33% 25 | 0% 5% 0% 19.49 | N SON 7 | 2% 50% | 57.1% 25% | 0% 25% | 16.7% 25% | 29% 25% | 25.2% 1001 | N 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | K 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 88% | 100% 100% 100. 100% 100% 95. | 7% 0% 01 9% 0% 01 | 6 0% 0.0% 6 0% 0.0% | 0% 0% 12% 0% | 0% 0.0% 0% 4.2% 0.4 | 972 0.4226 | 0.0500 0.015 | 0.8600 | 0.1885 | 0.1835 0.5708 | 6 0.4226 | 0. |
| nily protein 3 Artisp5 Pf br-stimulated chosohoor Vasp Vi | PAFS_MOUSE 22 k PAFS_MOUSE 22 k PASP_MOUSE 40 k | Da 100% 100 Da 100% 100 | N 100% 100.0 | % 0% 1 | 0% 0% 0.0* 0% 0% 0.0* | % 0% 12 % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% 10 | 0% 100% 1 | 74.0% SIN 100.0% ON | 0% 0% | 0.0% 0% | 9% 11% 9% 9% | 0.0% 1000 401 | N 100% 11 N 22% 1 | 00% 100.0% 64% 35.6% 6 | 0% 0% 0 0% 78% 56 | N 0.0% N 64.4% | 0% 0% - | N 0.0% 100% N 0.0% 64% | 100% 100% 100. 100% 100% 100. 78% 55% 65. | 2% 0% 01 2% 0% 01 2% 36% 221 | 6 0% 0.0% 6 6% 34.7% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.0360 | | 0.000 | 160 | 0.450 | = | |
| peptidase D Cpd Cl eminotransferase 1 Gpt Al les remain ferire-hinden (gftp7 IB | BPO_MOUSE 152 LAT1_MOUSE 55 k BP7_MOUSE 29 k | KDs 100% Ds 100% 100 Ds 0% | 100% N. 100% 100.0 | 0% % 0% 100% | 0% 0% 0.0* 100% | 9% 9% 0 9% 9% | 0% 0% 0.09 0% 0% | N 100% 10 | ON 100% 1 | 100.0% OX | 0% 0% | 0.0% 0% | os os | 0.0% 100 | N 100% 1/ N 21% | 00% 500.0% 29% 27.2% 7 | 0% 0% 0 9% 69% 71 | N 0.0% N 72.8% | DN DN | N 0.0% 100% N 0.0% 47% | 100% 100% 100. 100% 100% 100. 50% 29% 41. | 7% 0% 01 7% 53% 501 | 6 0% 0.0% 6 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.1482 | 0.0130 | 0.1 | 182 0.0130 | | \pm | |
| intransister channel not CBQ6 CI Finà debutorounness not Gqqb Gi acetate-hydrolyzing este (ah1 IA | LICA MOUSE 29 k CDH MOUSE 49 k NH MOUSE 28 k | Da 100% 10 Da 100% 10 Da 100% 10 | N 200% 100.0 N 200% 100.0 N 200% 100.0 | N 98 | 0% 0% 0.0° 0% 0% 0.0° | 75 05 0 75 05 0 | 0% 0% 0.09 0% 0% 0.09 0% 0% 0.09 | N 100% 10 N 100% 10 N 100% 10 | 0% 100% 1 0% 100% 1 | 100.0% 0% 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 100 0.0% 100 0.0% 100 | N 100% 1/ N 100% 1/ N 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% N 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% 6 0.0% 100% | 100% 100% 100.1 | 2% 0% 01 2% 0% 01 | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | | | | | | \pm | |
| racting protein Tolip TO Passe activating protein 11 Arhgap 17 RV n-1 Dom1 D | OLIP_MOUSE 30 k HG17_MOUSE 92 k YN1_MOUSE 98 k | Da 17% 1/ Da 25% 2/ Da | N 22N 16.3 | % 62% 2 75% 6 | 0% 67% 67.8° 2% | 76 176 20 96 0 | 0% 11% 15.99 0% | S 0% 2 | DN DN | 3.3% 100% | 90% 100% 50% | 96.7% 0% | 0% 0% 0% | 0.0% 01 291 01 | 5 175 5 675 5 05 | 17% 11.1% 5 50% 63.9% 2 0% 0.0% 10 | 6% 67% 83 5% 32% 50 0% 100% 100 | 5 78.6% 1 5 36.1% 5 100.0% | 6% 17% 0% 0% 0% 0% | N 0.3% ON N 0.0% SON | 17% 0% 5/ 100% 100% | 2% 100% 671 01 50% | 5 100% 88.9% 5 0% | 0% 17% 0% | 0% 5.6% 0.0 0% | 0.0390 | 0.4823 0.752 0.0279 | 0.0078 0.4 | 123 0.2104 100 0.0279 | 0.5623 0.0250 | 0.5657 | 0.4 |
| o-chaperone Gdc37 Cdc37 Cl skdvknoskol 3.4.5-ktacho Inppl1 St solide N-lektadecanovkra Nmt1 Nf | DC37_MOUSE 45 k HP2_MOUSE 139 MT1_MOUSE 57 k | Da 100% 100 KDa 100% 100 | N 200% 100.0 0% N 200% 100.0 | N 98 | 0% 0% 0.0° | % 9% 0 | 0% 0% 0.07 0% 0% 0.07 | N 100% 10 | 0% 100% 1 | 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% 100 | N 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0 | S 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% | 100% 100% 100.1 | 25 05 01 25 05 01 | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | | | | | | \pm | |
| e protein 3 Luc70 LC e 2 Rueb2 Ri sal growth factor receptor Eight El | C7L3 MOUSE 51 k LVEZ MOUSE 51 k GFR MOUSE 135 | Da 14% 1/ Da 67% 6/ KDa 10/ | N 12N 12.3 N 50N 61.1 N 100N | N 86N 8 | 0% 88% 84.4° 2% 50% 38.9° 0% 0% | % 9% 10 % 9% 0 | 0% 0% 3.25 0% 0% 0.05 0% 0% | N 12% N 67% 10 100% 10 | 0% 20% 0% | 10.8% 75% 32% 0% | 100% 80% 0% 0% | 85.0% 13% 0% 0% | 0% 0% 0% | 4.2% 121 221 981 | 5 205 5 195 5 1005 | 29% 20.4% 5 24% 25.4% 6 86% 93.2% | 8% 80% 71 3% 81% 76 0% 0% 0 | N 79.6% N 73.6% N 0.0% | 0% 0% 0% 0% 6% 0% 1 | N 0.0% 20% N 0.0% 82% N 6.8% | 12% 32% 21. 86% 60% 75. 100% 100% | 2% 80% 881 2% 18% 141 01 | 67% 78.1% 6 60% 24.2% | 0% 0% 0% 0% | 0% 0.0% 0.8 0% 0.0% 0.3 | 314 0.8466 250 0.0097 0.2396 | 0.2184 0.258 0.0110 0.736 0.2396 | | | 0.5183 0.8838 0.7364 | 0.2396 | 0.4 |
| ome subunit bets type-3 Pemb3 Pt methylolutaryi-CoA Ivase Hingol Hill | SE3_MOUSE 23 k MGCL_MOUSE 34 k | Da 67% Si Da 100% 10 | N 90% 80.8 N 100% 100.0 | % 22% 5 % 0% | 4% 10% 19.2° 0% 0% 0.0° | 5 0% 0 5 0% 0 | 0% 0% 0.07 0% 0% 0.07 | N 100% 10 N 100% 10 | 0% 100% 1 | 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 1001 0.0% 1001 | N 100% 1/ N 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 | N 0.0% N 0.0% | 0% 0% 0% 0% | N 0.0% 100% N 0.0% 100% | 100% 100% 100. 100% 100% 100. | 7% 0% 01 7% 0% 01 | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 9% 0.0% 0.1 9% 0.0% | 157 | 0.1157 | 0.1157 | 0.1157 | | === | = |
| Hosiscton/i-O-alvcon/i-a GcmD G NDRGI NdrgI M | CNTS MOUSE 51 k | Da 100% 6 | % 100% 97.4 | % 0% | 9% 0% 2.6° | % 0% 0 | ON ON 0.07 | N 100% 10 | ON 100% 1 | 100.0% ON | 0% 0% | 0.0% 0% | 0% 0% | 0.0% 1001 | N 100% 1 | 00% 100.0% | 0% 0% 0 | N 0.0% | 0% 0% 0% | SON 100% | 50% 45% 48. 100% 100% 100. | 7% 23% 441 7% 0% 01 | 25% 37.6% 0% 0.0% | 17% 6% ; 0% 0% | 0% 14.1% 0% 0.0% 0.4 | 226 | 0.4226 | 0.4226 | 0.4226 | 0.3317 | 0.2077 | - 00 |
| imbrane emp24 domain-i Treed3 TR milv domain-containing p Schd2 St | MED3_MOUSE 25 k OFD2_MOUSE 75 k | Da 29% 2: Da 82% 9: | % 100% 97.4 % 32% 53.3 % 29% 26.5 % 50% 75.4 % 42% 34.5 | % 0% : % 22% 4 % 50% 6 % 17% : | 8% 0% 2.67 0% 67% 46.77 7% 71% 62.77 0% 33% 56.77 | % 21% 11 % 0% 7 | 1% 0% 10.89 7% 12% 7.99 | N 29% 3 N 92% 8 | 2% 25% 8% 88% | 30.2% 71% 88.9% 0% | 67% 57% 0% 0% | 65.1% 0% 0.0% 8% | 0% 14% 13% 13% | 4.8% OI | N 22% | 0% 11.1% 10 | 0% 22% 80 0% 0 | K 71.1% | 0% 32% 2 0% | % 17.8% 100% % 100% | UK UK U | 0% | 20.10 | ON ON | 0.2 | 394 882 | 0.4225 0.0881 0.225 0.3000 0.7010 0.3146 0.304 | 0.7760 0.2254 | 0.7187 | 0.4820 0.5830 | 4 | 0.5 |
| Nogau Paminian N Fibri Fi argonade-2 Ago2 Ai | BLN1_MOUSE 78 k GC2_MOUSE 97 k | Da Zin Zi Da | 100% | N 72% 6 | ON 58% 65.5° | n 0% 0 | 0% 0.09 | 100% | 100% | 03.3% k0% | 50% 0% | 30.7% 0% | 0% 0% | 0.0% S01 S61 5001 | N 82% 1 | 45% 61.4% 1 65% 61.4% 1 | 0% 0% 67 1% 17% 18 0% 0% 0 | N 15.3% 3 N 0.0% | 2% 0% 2 2% 0% 2 | N 23.2% S6N N 0.0% 100% | 57% 75% 62: 100% 100% 100. | 7% 27% 2007 8% 6% 01 2% 0% 01 | 6 0% 2.1% 6 0% 0.0% | 28% 42% 2 0% 0% | 2% 11.1% 0.2 5% 35.1% 0% 0.0% | | | 0200 | IIS USAG | 0.202 | 0.4260 | |
| ried protein Rab-SA RabSa Ri a I historomouthilite anti (Q-D1 15 one synthetisse Ges Gi | ABSA MOUSE 24 k A11_MOUSE 41 k SHB_MOUSE 52 k | Da 100% 10 Da 100% 8 Da 100% 10 | N 100% 100.0 N 100% 100.0 | % 9% 9% | 0% 0% 0.0° 0% 0% 0.0° | 75 0% 0 0% 16 75 0% 0 | 0% 0% 0.07 6% 0% 0.07 | S 100% 10 100% N 10 | 0% 100% 1 | 900.0% ON ON | 0% 0% 0% 0% | 0.0% 0% | 9% 9% 9% 9% | 9.0% 1001 601 1001 | 5 100% 1/ 5 78% 1 5 100% 1/ | 00% 100.0% 88% 75.1% 2 00% 100.0% | 0% 0% 0 0% 22% 13 0% 0% 0 | N 216% 1 N 20% | 0% 0% 0% 0% | % 0.0% 100% % 3.3% 100% % 0.0% 100% | 100% 100% 100. 100% 100% 100. 100% 100% 100. | 2% 0% 01 2% 0% 01 2% 0% 01 | 0% 00% 0% 00% 0% 00% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.0905 | 0.2021 | 0.0 | 0.0509 | | 0.4226 | |
| rene r reintene entrenit 77 CosTc Co led protein Rab-278 Rab27b Ri el leukemia transcription Philip1 P1 | OK7C_MOUSE 7 AC BIZ7S_MOUSE 25 A BIP1_MOUSE 81 A | Da 60% 21 Da 75% 81 Da | N 40% 35.0 N 33% 62.6 | N 20N 9 | 0% 40% 35.7° 0% 0% 0.0° | % 60% 25 % 25% 20 | SN 20% 28.39 SN 67% 37.29 | S 29% 3 S 100% 3 | 25 755 25 675 | 45.0% 43% 66.7% 0% | 23% 25% 0% 0% | 33.7% 29% 0.0% 0% | 22% 0% 67% 22% | 20.6% 01 23.3% 1001 171 | N 100% 1 N 100% 1 | 50% 50.0% 00% 500.0% 22% 16.3% 6 | 0% 0% 0 0% 0% 0 7% 40% 22 | N 0.0% 10 N 0.0% N 43.0% 1 | 0% 0% S 0% 0% 2% 50% S | ns 50.0% on ns 0.0% sess ns 40.7% on | 0% 0% 0/ 90% 93% 92 0% | 7% 75% 1001 7% 0% 01 0% 0 | 0% 91.7% 0% 9.0% | 25% 0% 6% 10% 200% 100% | 0% 8.3% 0.5 2% 7.9% 0.8 | 534 0.2254 810 0.0192 0.0439 | 0.6570 0.090 0.1283 0.316 | 9 0.7913 0.0 | 97 | 0.0071 0.5540 | 0 0.2832 0 0.0992 0.0395 | 0.1 |
| otional activator protein F Purb PI Ind-like protein 1 Mbn/1 M In-1 receptor accessory III rap III. | URB_MOUSE 34 k IBNL1_MOUSE 37 k .1AP_MOUSE 66 k | Da 100% 71 Da 0% 1 | N 100% 91.7 N 0% 0.0 | % 0% 2 % 100% 10 | 5% 0% 8.3° 0% 100% 100.0° | 75 05 0 75 05 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% 8 | 2% 100% 2% 0% | 94.4% 0% 0.0% 100% | 17% 0% 100% 100% | 5.6% 0% 100.0% 0% | 9% 9% 9% 9% | 0.0% 821 0.0% 221 | N 25% N 12% N 100% 1 | 90% 79.4% 1 0% 11.6% 7 00% 100.0% | 7% 25% 20 8% 88% 100 0% 0% 0 | 5 20.6% 5 86.4% 5 0.0% | 0% 0% 0% 0% | 6 0.0% 80% 6 0.0% 25% 6 0.0% | 100% 80% 85 17% 25% 22 | 7% 20% 01 2% 75% 821 | 20% 13.2% 5 25% 77.8% | 0% 0% 0% 0% | 0% 0.0% 0.7 0% 0.0% | 972 0.3952 0.2348 | 0.1283 0.316 0.2774 0.422 0.2137 0.015 | 0.7972 0.3 | 652 0.2774 648 0.2137 | 0.4223 | \pm | |
| Stored activate scales I. Floor. In Control activate scales I. Floor. In Control activate scales III See III | PSMI MOUSE 74 k PT MOUSE 20 k CAMI MOUSE 110 | Da 100% 10 Da 100% 10 KDa | ns 200% 100.0 | 9% % 9% | 9% 9% 9.5° | 9% 0 9% 0 | 0% 0% 0.09 | 100% 10 % 100% 10 | 0% 100% 1 0% 100% 1 | 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 9% 9% 9% 9% | 0.0% 1000 0.0% 1000 1000 | N 100% 1/ N 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% N 0.0% | 0% 0% 0% 0% | n 0.0% 100% n 0.0% 100% | 100% 100% 100.) 100% | 2% 0% 01 0% | 0% 0.0% | 9% 9% 9% | 0% 0.0% 0% | | | | | | $\pm \pm$ | Ē |
| ried protein Rab-15 Rab 15 Ro rolline-rich protein BAGS BagS Bag Pan Do | AGI MOUSE 23 k AGS MOUSE 121 AXI MOUSE 74 k | Da 100% 10 8Da 0% 0 | % 200% 100.0 % 0% 0.0 % 0% 0.0 | % 0% 1 % 32% 3 % 100% 10 | 0% 0% 0.0° 2% 25% 30.0° 0% 100% 900.0° | % 0% 0 % 62% 62 | 0% 0% 0.07 7% 25% 69.47 0% 0% 0.07 | N 100% 10 N 0% | 0% 100% 1 0% 0% 0% | 900.0% 0% 50% 0.0% 100% | 0% 0% 50% 100% 100% | 0.0% 0% 50% 100.0% 0% | 0% 0% 50% | 0.0% 100 251 0.0% 101 | N 100% 1 | 00% 100.0% 50% 41.7% 10% 12.3% | 0% 0% 0 0% 0% 0 | S 0.0% S 0.0% 2 | 0% 0% 5% 100% 5 | 6 0.0% 100% 6 58.3% 100% 6 8.8% 20% | 100% 100% 100. | 2% 0% 01 0% 2% 20% 394 | 0% 0.0% 6 88% 77.0% | 9% 9% 9% 19% 11% | 0% 0.0% 0% 7.0% | 0.3204 | 0.1994 0.0202 0.025 0.422 | 0.0156 | 0.0082 | 0.0120 | 0.6882 | 0. |
| med cell death protein 4 Pdcd4 P1 transcription factor II-I GdGI G | DCD4 MOUSE 52 k TF21 MOUSE 112 ASI MOUSE 112 | Da 100% 101 KDa 100% ^ | % 100% 100.0 0% | % 0% | 0% 0% 0.0° | % 0% 0 | 0% 0% 0.07 0% 0% | N 75N 10 | 0% 100% 100% 2% 700% | 91.7% 0% 97.2% 0V | 0% 0% 0% | 0.0% 25% | 0% 0% 0% | 8.3% 100 621 | N 100% 1/ N 100% 1/ N 100% | 00% 100.0% 00% 88.9% 3 | 0% 0% 0 2% 0% 0 | N 0.0% N 11.1% N 0.0% | 2% 2% 2% 2% | 6 0.0% 100% 6 0.0% 100% | 100% 100% 100.75% 100% 100% 100. | 2% 0% 01 0% 251 2% 0% 251 | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0.4 | 0.9401 045 0.4226 | 0.422 0.7525 0.422 | 0.9 | | 0.4220 | IS 0.4226 | 0. |
| main-binding protein 1 Sh3bp1 36 -7 Core7 Ci | BP1_MOUSE 65 k | Da KDa 100% 100 | N 100% 100.0 | % 0% | 0% 0% 0.0° | % 0% 0 | 0% 0% 0.09 | N 100N 10 | OK DOS | on on | 0% | 0% | ON ON | 2001 2001 | N 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | K 0.0% | 0% 0% 0% 0% | 6 0.0% 100% | 200% 200% 100. | 2% 0% 01 | 0% 0.0% | on on | 0% 0.0% | | | | | | | |
| tic translation initiation for EITSk EI in carbony-terminal hydro Usp15 US | IF3K_MOUSE 25 k BP15_MOUSE 112 | Da 70% 6/ KDa 10 | N 57% 63.8 | % 30% 2 | 0% 100% 1% 29% 23.3° | % 10% 14 0 | 0% 0% 4% 14% 12.99 0% | N 92% S | 6% 83% | 73.6% 0% 0% | 23% O% | 11.1% 18% 0% | 11% 17% | 15.3% 621 | N 100% 11 | 00% 88.9% | 0% 0% 0 0% 0% | N 0.0% 3 | 2% 0% 2% 0% | % 11.1% 100% 10.0% | 100% 100% 100. | 7% 100% 1007 7% 0% 01 | 6 0% 0.0% 0% | 0% 0% 0% | 0% | 992 0.4226 0.1835 | | 4 0.3868 | 0.0127 | 0.4226 0.4015 | 0.4226 | |
| in Map7 M communication on Spain 5 51 | TAB1_MOUSE 276 MP7_MOUSE 82 k PATS_MOUSE 97 k | KDs Ds 0% 0 | % 0% 0.0 % | % 100% 10 | 0% 100% 100.0° | % 0% 0 | ON ON 0.09 | N ON | on on | 0.0% 100% | 100% 100% | 100.0% 0% | on on | 0.0% 00 | N 17% | 0% 0.0% 10 | 2% 0% 29 0% 100% 100 | N 20.0% S | 0% 82% 7 0% 0% | n 68.3% on n 0.0% on | 0% 0% 0) | 0% 01 0% 100% 1001 | 6 100% 900.0% | 0% 0% | 0% 0.0% | | | 0.1 | 109 | | 0.0828 | |
| rental risutrana iaronaras Pgid Pi al rentain RS binasa airò RgaSka3 K3 al alpha-mannosidase Man2b1 M. | PID_MOUSE 41 k SSA3_MOUSE 84 k 94281_MOUSE 115 | Da 100% 10 Da 100% 10 KDa 100% 10 | N 200% 100.0 N 200% 100.0 | % 9% % 9% | 0% 0% 0.0° 0% 0% 0.0° | 75 0% 0 75 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% 10 N 100% 10 100% | 0% 50% 0% 100% 1 | 83.3% ON 100.0% ON | 0% 50% 0% 0% | 16.7% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 100 0.0% 100 100 | N 100% 1/ N 100% 1/ N 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% N 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% 6 0.0% 100% | 100% 100% 100/ 100% 100% 100/ 100% 100% 100/ | 2% 0% 01 2% 0% 01 2% 0% 01 | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0.4 0% 0.0% 0% 0.0% | 226 | 0.422 | 0.4226 | | 0.4226 | \pm | |
| ne 5-transferase thela-2 Get2 G chain specific acul-GoA Acadm Al a reductase Doar Pi | CADM MOUSE 46 k CAR MOUSE 46 k | Da 100% 100 Da 100% 100 Da 100% 100 | 66 200% 100.0 66 200% 100.0 66 200% 100.0 | % 0% % 0% | 0% 0% 0.0° 0% 0% 0.0° 0% 0% 0.0° | 75 9% 0 75 9% 0 | 0% 0% 0.07 0% 0% 0.07 0% 0% 0.07 | N 100% 10 N 100% 10 N 100% 40 | 0% 100% 1 0% 100% 1 | 100.0% 0% 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 9% 9% 9% 9% | 0.0% 1000 0.0% 1000 0.0% 1000 | N 100% 1/ N 100% 1/ N 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% N 0.0% N 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 100% 6 0.0% 100% | 100% 100% 100. 100% 100% 100. 100% 100% 100. | 2% 0% 01 2% 0% 01 2% 0% 01 | 6 0% 0.0% 6 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | | | | | | $\pm \mp$ | Ē |
| echain 3-seasch CoA+ Hed 17b12 Di type II cyloskeletal 71 Kd71 Kd biouthous protein 1 Aurol Av | 0612 MOUSE 35 k 2C71 MOUSE 57 k LP1 MOUSE | Da 100% 10 Da 23% 2 Da CW | % 100% 100.0 % 0% 19.4 % 62% #** | % 0% % 22% 5 | 0% 0% 0.0° 0% 50% 44.4° | % 0% 0 % 33% 25 % 50% | 0% 0% 0.07 5% 50% 35.17 2% 22% | N 100% 10 N 40% 2 | 0% 100% 1 9% 17% 0% 100% | 20.0% 0% 20.4% 40% | 0% 0% 63% 50% | 0.0% 0% 44.3% 20% 0.0% 1000 | 29% 23% 29% 23% | 0.0% 100 27.3% 0 50.0% | 5 100% 1/ 5 22% | 00% 100.0% 33% 22.2% 1 | 0% 0% 0 0% 22% 23 | S 28.9% S | 25 25 2 25 225 2 | S 20.9% 100% S 20.9% 40% | 100% 100% 100. 0% 0% 13. | 2% 0% 01 2% 40% 251 | 0% 0.0% 67% 43.9% | 0% 0% 20% 75% 2 | 0% 0.0% 2% 42.8% 0.5 | 042 0.6364 | 0.8618 0.368 | 1 0.9815 0.7 | 0.5105 | 0.9774 0.3954 0.7792 | 6 0.8411 | 0. |
| reconine-crolein kinase i PrpHib PI roinine-rich solicina fact Sraf5 St Lebrardate sonibase i Israra* | FP4B MOUSE 117 FBF5 MOUSE 31 k | 8Da 0% 0 | % 0% 0.0 % 0% 0.0 | % 100% 10 % 100% 10 | 0% 100% 100.0° 0% 100% 100.0° | 75 0% 0 75 0% 0 | 0% 0% 0.07 0% 0% 0.07 | N 0% | 0% 0% 5% 1000 | 0.0% 100% 91.7% | 100% 67% 100% | 88.9% ON | 20% 22% 0% | 11.1% 101 | 0% N 0% | 0% 3.2% 5 | 100% 100 0% 100% 100 | N 96.7% | 9% 9% 9% | ns 0.0% on | 0% 0% 0.1 | 7% 100% 100° | 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.4226 | 0.4226 | 0.4226 0.4 | 25 0.4225 | 0.4226 0.4226 | 3 | Ξ |
| Tyrn TF succinate synthetises iso Adias PI | PRN MOUSE 80 k | Da 100% 10 | N 100% 100.0 | 5 05 | 9% 9% 9.0° | 75 9% 0 | 05 05 0.00 | N 100% 10 | 0% 100% 1 | 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% | 0.0% 100 | 0% N 100% 1 | 00% 100.0% | 100% 0% 0% 0 | S 0.0% | 0% 0% | 05 0.0% 100% | 0% 0% 0. 100% 100% 100. | 75 100% 1001 75 0% 01 | 100% 100.0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0.4226 | 0.422 | | 26 | 0.4226 | = | = |
| etoscetate isomerane Getz1 M moloo subfamily C ment Dnajc1 Dt | NUC1_MOUSE 54 k | Da 100% 100 Da 100% 100 Da 67% 7 | % 100% 100.0 % 100% 100.0 % 100% 100.0 % 56% 64.1 | N 0% | | % 0% 0 % 0% 0 % 0% 0 % 25% 20 | 0% 0% 0.07 0% 0% 0.07 0% 44% 33.17 | N 100% 10 N 100% 10 N 56% 6 | 0% 100% 1 7% 82% | 50.0% 0% 68.5% 11% | 0% 0% 0% 17% | 0.0% 0% 0.0% 0% 9.3% 22% | 0% 0% 0% 0% 22% 0% | 0.0% 1000 0.0% 1000 22.2% | N 100% 1/ | 100.0% 00% 100.0% | 0% 0% 0 | N 0.0% | ON ON | S 0.0% 100% | 100% 200% 99. | 2% 2% 21 2% 2% 01 | 0% 0.7% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 0.4226 | | 0.3093 | | 0.4226 | 5 | |
| staining fibulin-like extrac Etempt F0 rv-associated protein of Rptor R0 carbosvi-terminal hydro Usp14 Ut | BLN3 MOUSE 55 k PTOR MOUSE 149 BP14 MOUSE 56 k | Da 100% 100 | ns 200% 100.0 | % ox | 0% 0% 0.0° 0% 0% 100.0° | % 0% 0 | ons ons 0.09 | 0% N 100% 10 | ON 100% 1 | 0% 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% | 0.0% 1001 | N 100% 1 | 0% 0.0% | 0% 0% 0 0% 0% 0 | N 0.0% 10 | 0% 200% 10 0% 0% | N 0.0% 100N | 50% 83% 58. 100% 100% 100. | 2% 12% 171 2% 0% 01 | 0% 9.5% | 47% 23% : 0% 0% | 2% 32.4% 0% 0.0% | | | 0.1 | 04 | | 0.0105 | |
| er CCOH domain-contal Zc3h11s Zc meonine-crotein shouch: Ppp3cs Pi mily-interacting protein: Rub11ffo* Rt | CHIA MOUSE 85 k P2SA MOUSE 59 k FIPS MOUSE 70 k | Da 0% 0 Da 100% 100 Da | % 0% 0.0 % 100% 100.0 | % 100% 10 % 0% | 0% 0% 0.0* | % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 0% 100% 10 | 0% 0% 0% 100% 1 | 0.0% 100% 100.0% 0% | 100% 100% 0% 0% | 100.0% one 0.0% one | 0% 0% 0% 0% | 0.0% 01 0.0% 1001 | N 100% 11 | 0% 0.0% 10 00% 100.0% | 0% 100% 100 0% 0% 0 2% 92% 99 | N 0.0% N 0.0% | 0% 0% 0% 0% | 66 0.0% 100% 66 0.0% 100% | 50% 0% 100% 100% 100.0 | 9% 0% 01 100% 5000 | 6 200% 6 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 0.5000 | 0.500 | 0.5 | 132 | 0.5000 | = | Ξ |
| ucine zipper and W2 dor Bzwl B3 cohombale hallands count AlgS All factor 35 subunit 3 SSTs7 | ZW1_MOUSE 46 k LGS_MOUSE 37 k | Da 100% 100 Da 100% 100 Da 20% | N 100% 100.0 N 100% 100.0 | % 0% 1 | 0% 0% 0.0° 0% 0% 0.0° | % 0% 0 % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 100% 10 N 100% 10 | ON 100% 1 | 100.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 1000 0.0% 1000 | N 100% 11 N 20% | 00% 500.0% 00% 10% 31.0% | 0% 0% 0 0% 0 9% 23% 0 | N 0.0% | 0% 0% 0% | N 0.0% 100% N 100% | 100% 100% 100. 100% 20% | 2% 0% 01 0% | 0% 0.0% 0% | 0% 0% 0% | 0% 0.0% 0% 0% 27.8% 0.1 | 105 0,9404 | 0.5442 0.775 | 4 0.1573 0.8 | IBI 0.3175 | 0.6796 0.0584 | 0.8529 | |
| Eh El El adhesion molecule Boam Bi | LN MOUSE 72 k | Da 0% | 0% d2.1 | 0% | 0% 0% 0%3° | 200% | 200% 100% | | 0% | - N. S. | 95 | A1 A | 87.8 100% 200% | 01 1001 | 5 0% 5 75% 1 | 25% 8.3% 1 00% 91.7% | 7% 10% 0 | 5 8.9% s | 25 925 7 25 255 | N 82.8% 0% N 8.3% 100% | 0% 0% 00 80% 75% 85 | 7% 0% 01 2% 0% 01 | 0% 0.0% 0% 0.0% | 200% 200% 21 0% 20% | 0% 100.0% 5% 15.0% | 0.4226 0.5873 | 0.5442 0.225 0.4226 0.0155 0.504 0.4283 0.588 | 0.2 | 0.2079 | 0.5045 | 0.0580 0.5873 | 0. |
| >-a Cnn3 Cl nucleolide-binding prote Gnb1 Gl 8-Sep SI | NEU MOUSE 35 k EDTE MOUSE 50 k | Da 90% 7 | N 100% 83.8 | 100N 10 % 20N 2 | 9% 0% 15.2 | 5 98 0 | 0% 0% 0.09 | N 78% 10 | 2% 50% 0% 100% | 19.7% 100% 92.6% 22% | 100% S0% 0% 0% | 83.3% 0% 7.4% 0% | 9% 9% 9% 9% | 0.0% 311 0.0% 1001 601 | N 26% N 86% N 50% | 25.8% 6 92% 92.5% 75% 61.7% 4 | 976 74% 80 0% 14% 8 0% 50% 25 | 5 74.2% 5 7.5% 5 38.3% | 25 25 25 25 25 25 | 6 0.0% 92% 6 0.0% 92% 6 0.0% 100% | 20% 20% 27 100% 100% 97 70% 83% 84 | PS 20% 67 PS 20% 01 PS 05 301 | 100% 62.2% 0% 2.6% 17% 15.6% | 0% 0% 0% 0% | 0% 0.0% 0.4 0% 0.0% 0.4 | 792 0.3754 0.1166 | 0.0158 0.504 0.4283 0.588 0.9190 0.666 | 8 0.4792 0.3 0.1 | 154 0.4283 165 | 0.5888 | = | |
| -contacting stayms \$2 Ubs20 Us despitions Pepd Pi or regulatory factor 2-bin Int2bpl 12 | EDL3 MOUSE 18 k EPD MOUSE 55 k EPL MOUSE 81 k | Da 86% 10 Da 100% 10 Da | N 100N 95.2 N 100N 100.0 | % 16% % 0% | 0% 0% 4.8° 0% 0% 0.0° | % 0% 0 % 0% 0 | 0% 0% 0.09 0% 0% 0.09 | N 88% 10 N 100% 10 | 0% 100% 0% 100% 1 | 95.8% 13% 100.0% 0% | 0% 0% 0% 0% | 4.2% ON 0.0% ON | 0% 0% 0% 0% | 0.0% 1001 0.0% 1001 | N 93% 11 N 100% 11 N 0% | 00% 94.4% 00% 100.0% 0% 0.0% 10 | 0% 17% 0 0% 0% 0 0% 100% 100 | S 5.0% S 0.0% S 100.0% | 0% 0% 0% 0% 0% 0% | 65 0.0% 94% 65 0.0% 100% 65 0.0% 0% | 100% 100% 98.1 100% 100% 100. 0% 0% 0 | 2% 6% 01 2% 0% 01 2% 100% 1001 | 6 0% 2.0% 6 0% 0.0% 6 100% 100.0% | 9% 9% 9% 9% | 0% 0.0% 0.9 0% 0.0% 0% 0.0% | uni 0.5928 | 0.9190 0.666 | 0.9297 0.5 | um 0.9190 | 0.6663 | = | |
| oin domain-containing p Tendc17 To ptional activator protein F Pura Pi A dehydrogenase family Acad10 Ar | XD17 MOUSE 14 k URA MOUSE 35 k CD10 MOUSE 110 | Da 100% 10 Da 83% 7 KDa 100% | % 100% 100.0 % 80% 79.4 100% | % 0% 2 % 17% 2 | 0% 0% 0.0° 5% 20% 20.6° 0% | % 9% 0 % 9% 0 | 0% 0% 0.07 0% 0% 0.07 | N 100% 10 N 70% 10 | ON 100% 1 | 900.0% 0% 84.9% 30% | 0% 0% 0% 15% | 0.0% 0% 15.1% 0% | 9% 9% 9% 9% | 0.0% 100 0.0% 71 | N 100% 1/ N 86% 1/ | 00% 85.7% | 0% 0% 0 9% 14% 0 | N 0.0% N 14.3% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 71% | 100% 100% 100. 89% 83% 81. | 2% 0% 01 2% 29% 111 | 0% 0.0% 5 17% 18.8% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% 0.6 | 002 0.6721 | 0.5318 0.739 | 1 0.6002 0.6 | 21 0.5318 | 0.7391 | $\pm \mp$ | Ē |
| acyldutathione hydrolase Hagh Gi ic immunodobulin recest Pigr Pi | LO2 MOUSE 34 k | Da 100% 100 | ns 100% 100.0 | % 0% | 0% 0% 0.0° | % 0% 0 | 0% 0% 0.09 | N 100% 10 | 0% 100% T | 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% 0% | 0.0% 1001 1001 | N 100% 1/ N 100% 1/ | 00% 100.0% 00% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% | 0% 0% 0% 0% | 6 0.0% 100% 6 0.0% 80% | 100% 100% 100. 72% 89% 80. | 25 05 01 25 205 241 | 0% 0.0% 11% 18.4% | 0% 0% 0% 4% | 0% 0.0% 0% 1.3% | 0.0562 | | 0.0 | 104 | | 0.4226 | |
| | | 100 | W 00 00 | % S04 6 | 2% CO% 55.67 | N 50% 22 | 2% SON 44.49 | S 0% | 0% 0% | 0.0% 60% | 50% A0% | 50.0% 40% | 50% 60% | 50.00V 00 | 1000 | 6% 6.3% 3 | OW COW 74 | FE ON 3 | DN 19% 2 | 20 EE 200 | 14% 17% 17 | 7% 20% 421 | 226 22.48 | CON 4200 1 | 0% 51.0% | 0.2233 | 0.4225 0.000 | 4 0.5263 0.0 | 0.1412 | 0.1122 0.5263 | 0.0179 | 0.1 |

| hase co-transcribed Prosc PROSC troe III domain-conta Endc3b END38 I | MOUSE 30 KDs 1 MOUSE 133 KDs | 100% 100% 80 0% 0 | N 93.3% 0N | N 9% | 20% 6.7% 0% | 0% 0% 100% 1 | 0% 0.0% 100% 100% | 100% 100% | 100.0% 0% | 0% 0% 0 | 0% 0% | os os o | 0% 100% 1 0% | 20% 100% 500.0% 0% 0% 0.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 100% 200% | 0% 0.0% 100% 100.0% | 100% 100% 1 0% | 0% 100.0% 0% 0% | 0% 0% | 0.0% 0% 200% | 0% 0% 0.0% | 0.4226 | 0.4225 | 0. | 1226 | 0.4226 | | |
|--|---|--|---|--|---|---------------------|---|---|--|--|---------------------|----------------------------------|--|---|--|-----------------------------|-----------------------------------|--|--|------------------------------|---------------------------------|--|--------|---|---|--------------------------------|--|--|------------------|
| countries-5-sulfatase Gre GNS_MC actor and substrate o Map MISP_M | OUSE 61 kOs MOUSE 72 kOs | | v 200.000 au | | | | av 0.00 | | | | | | 200% 1 0% | 20% 100% 100.0% 0% 0% 0.0% 1/ | 0% 0% 0% 0.0% 0% 100% 100% 100.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 0% 0% | 0% 0.0% 100% | 9% 199% 199% | 100.0% 0% | 0% 0% 0.0% | | 0.8596 0.4226 | 0.4226 | 0.8506 | 0.4226 0.4 | 236 | |
| drosenase lubicuinos Ndufb3 NDUB3 aled factor 2 Fal2 FAF2_M | DAMES 23 Mg 24 M | 50% 20% 20 50% 29 | N 30.0% S0N | N 60% | 60% 55.7% 29% | 0% 20% 2 50% | 20% 13.2% 50% 42% 50% | 50% 67% 32% 80% | 55.6% SON 54.4% ON | 25% 33% 36 0% 0% 0 | 7% 0% 2 0% 50% 6 | 15% 0% 8 2% 20% 45 | 2% 0% 5% 100% | 0% 0% 0.0% P 75% 75% 83.2% | 0% 75% 60% 71.7% 0% 0% 0% 0.0% | 20% 25% 0% 25% | 40% 28.3% 25% 16.7% | 0% 0% 100% 75% | 0% 0.0% 60% 0% 78.2% 0% | 50% 75% 0% 0% | 61.7% 40% 0.0% 0% | 50% 25% 38.3% 25% 40% 21.7% | 0.1080 | 0.0955 0.7466 0.0743 | 0.0099 0.0 0.2558 0.5 | 904 0.3505 9000 | 0.4225 0.4 0.1135 0.0 0.5000 | 687 0.6549 0. 0.9557 0. | 0.3505 0.7466 |
| translation initiation for EVS UPS MOX. CulD CULD M | 3.55 25 kDs MOUSE 59 kDs | 23% 57% 63 100% 100% 100 | N 51.0% 67N N 100.0% 0N | N 42% N 0% | 28% 49.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 50% 0% 0.0% 67Y | 67% 100% 100% 100% | 72.2% SON 88.9% 33% | 33% 0% 27 0% 0% 11 | 8% 0% 1 1% 0% | 0% 0% 0 0% 0% 0 | 0% 82% 0% 100% 1 | 28% 86% 81.8% 1 00% 100% 100.0% | 8% 22% 24% 18.2% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 82% 90% 2 100% 100% 2 | 0% 90.0% 18% 0% 100.0% 0% | 22% 0% 2% 0% | 9.4% 0% 0.0% 0% | 25% 40% 21.7% 50% 50% 46.7% 0% 0% 0.0% 0% 0% 0.0% | 0.2279 | 0.2296 0.0673 | 0.3387 0.1 0.4226 0.4 | 2979 0.2296 1226 | 0.1135 0.6 0.5000 0.0673 0.3 | 387 226 | |
| translation initiation fs ERS | NOUSE 103 KDs | 100% 100% 90% 100% 100 76% 92% 69 | 00 6 96.7% 100 6 79.2% 160 | 0% N | | 0% | 100% | | 0% | | 0% | | 100% 1 0% | 20% 100% 100.0% 0% 1/ | 0% 0% 0% 0.0% 0% 200% | 0% 0% 0% | 0% 0.0% 0% | 100% 0% 50% | 100% | 9% 50% | 9% | ON ON | 0.0046 | 0.5000 | 0.3338 0.0 | 0.5000 | 0.7525 0.3 | 236 | |
| produterate dehicho Dréid1 DréiK1_1 histolitan/i-CoA sinth Hingoi2 HMC52 | MOUSE 103 kDa 2 MOUSE 57 kDa | | | N 0% N 0% | 21% 15.8% | 8% 7% | 0% 5.0% 0% | 100% 100% | 29% | 0% 0% | 71% | 0% 0% 0 | 200% 1 200% 1 | 00% | 0% 0% 17% 5.6% 0% 0% | 0% 0% 0% 0% | 08 0.0% | 100% 100% 1 | 0% 00.0% 0% 0% 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% 0.0% | 0.6632 | 0.303 | 01 | 2065 | 0,22 | 0.5479 | |
| fic andiosenesis inhit Balap2 BAIP2 N e II cytoskaletal 79 Kr579 K2C79 N | MOUSE 50 kDs MOUSE 50 kDs | 25% 40% 23 | N 0.0% 100N N 32.8% 25N N 4.8% 40N N 31.0% 58N N 100.0% 0N N 96.3% 0N | N 100% 1 | 100% 100.0% 17% 27.2% | 0% 0% 50% 20% F | 0% 0.0% 0% 50% 40.0% 14% | i 0% 0% | 0.0% 100% 11.4% 52% | 100% 100% 100 40% 25% 40 | 7% 29% 4 | 0% 0% 0 10% 75% 47 | 9% 0% | 0% 0% 0.0% 10 67% 50% 38.9% | 0% 100% 100% 100.0% 0% 17% 0% 5.6% | 0% 0% 100% 17% | 0% 0.0% 50% 55.6% | 0% 25% 0% | 100% 0% 8.3% 25% | 0% 22% | 98 994% SON | 100% 67% 72.2% | | 0.2641 0.7915 | 0.7790 0. | 9120 0.3089 | 0.0722 0.1 | 940 0.6734 0: 719 0.6555 0: 263 0.5074 0 | 0.5942 |
| o coldane subunit 6/ Costar! CXSA1_5 protective protein Class PPGS M | MOUSE 12 kDs MOUSE 54 kDs | 25% 25% 43 100% 100% 100 | N 31.0% SEN N 100.0% ON | N SON | 57% 55.2% 0% 0.0% | 17% 25% 0% 0% | 0% 13.9% 14% 0% 0.0% 100Y | 90% 38% 1 20% 100% | 43.9% 86% 100.0% 0% | 0% 62% 45 0% 0% 0 | 4% 0% 2 | 10% 0% 50 0% 0% 0 | 7% 22% 0% 80% | 67% 25% 41.7% 4 86% 82% 83.0% | 7% 22% 75% 58.3% 0% 14% 17% 17.0% | 0% 0% 0% 0% | 0% 0.0% | 10% 17% 82% 82% | 2% 14.4% 80% 2% 77.8% 12% | 82% 82% 17% 32% | 82.2% 10% 22.2% 0% | 0% 0% 3.3% 0% 0% 0.0% | 0.5760 | 0.2641 0.7915 0.4226 0.1624 0.5042 0.4490 0.0094 0.4226 | 0.2642 0.0 | 9434 0.2006 0.4490 | 0.8282 0.1 0.0094 0.1 | | 0.4226 |
| zorne A transporter 1 Sic33a1 ACATN Re protein 2 Actb2 ACTSL | MOUSE 61 kDs MOUSE 42 kDs | 89% 100% 100 | N 96.3% ON | N ON | 0% 0.0% | 11% 0% | 0% 3.7% 82% | 1 100% SON | 87.8% OK | ON ON C | 0% 17% | 0% 20% 12 | 2% 100% 100% | 100% S0% | 0% 0% 0% 0% | 0% 50% | ONL | 100% S | os. | 0% 0% 25% | | ON ON | 0.3162 | 0.4225 | 0.1869 | | | 0.3162 | |
| ne protein 1 Epb411 E41L1, h andn-like protein 2 MKZ MKL2, M | MOUSE 22 CO | os. | 100% | N. | | -9% | - 0% | 98 | 100% | 100% | 0% | 9% | 9% | 9% V | 0% 20% 20% | 9% | 0% | 0% 0% | 0% 0.0% 100% | 100% 100% | 100.0% ON | 0% 0% 0.0% | | | | | | | _ |
| t component C9 C9 C09 MC M domain protein 4 Pdirek PDLH N | ACUSE 52 KCm MOUSE 36 KCm | 100% 100 | N. | 9% | ox | ON. | 98 | | | | | | 94% | 20% 94% 92.6% 0% 9% 0.0% 1 | 6% 11% 6% 7.4% 0% 100% 100% 100.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 9% 0% | 0% 3.0% 90% | 0% 100% 100% | 97.0% ON | 0% 0% 0% 0.0% | | 0.0572 | | 0.4225 | 0.0572 | | |
| otide recest protein 2 Tic36 TTC36 A r-2 protein homolog a Tra2a TRA2A I | MOUSE 52 kDs MOUSE 32 kDs | 50% 46% 0 0% 0% 0 | 5 32.1% S0N N 0.0% 89N | N 46N N 86N | 83% 59.8% 90% 88.2% | 0% 8% I | 276 8.7% 696 206 11.8% 08 | S8% 85% 0% 0% | 70.6% 22% 0.0% 80% | 37% 8% 23 75% 100% 80 | 5% 8% 5% 20% 2 | 5% 8% 6 15% 0% 15 | 9% 9% 9% 20% | 0% 100% 50.0% 10 0% 0% 6.7% | 0% 50% 0% 50.0% 0% 100% 100% 93.3% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 2 0% 0% | 0% 100.0% 0% 0% 0.0% 88% | 0% 0% 100% 100% | 95.8% 13% | 0% 0% 0.0% 0% 0% 4.2% | 0.1232 | 0.2254 0.6232 0.4226 0.4226 | 0.0628 0.0 | 0.2254 1176 0.7663 | 0.7758 0.1 0.5238 0.2 | | 0.4226 |
| couth factor receptor Epsil EPSil M seor protein 1 Rau1 RSU1 M | MOUSE 92 kDs MOUSE 32 kDs | 100% 100% 50 | N 83.3% ON | N ON | 50% 15.7% | 9% 9% | 0% 0.0% 500 | 2% 100% 100% | 83.3% 50% | 100% 0% 0% 16 | 7% 0% | 0% 0% 0 | 60% 60% 88% 1 | 25% 0% 28.3% / 00% 78% 88.4% | 0% 75% 100% 71.7% 2% 0% 22% 11.6% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 20% 17% 100% 100% 1 | 0% 28.9% 80% 0% 100.0% 0% | 83% 50% 0% 0% | 71.1% 9% 9.0% 9% | 0% 0% 0.0% 0% 0% 0.0% | 1.0000 | 0.9798 0.2137 0.7969 | 0.4226 1.1 | 0.9798 | 0.7909 0.4 | 226 | 0.1107 |
| erma Syring SYNPIG pendent-interacting p Bin1 BIN1_MC | MOUSE 140 KDs MOUSE 64 KDs | 0% 0% 0 100% 100% 100 | N 0.0% 100N N 100.0% 0N | N 200% 1 | 100% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% | 100% 100% | 100% | 0% 0% | 0% | 0% 0% | 200% 1 | 0% 00% 100% 100.0% | 0% 0% 0% 0.0% | 9% 9% | 0% 0.0% | 0% 100% 100% 2 | os 100.0% os | 200% 2% 0% | 0.0% OX | 0% 0% 0.0% | | | | | | | |
| associated quary/site Mag/1 MAG/1 M rocessing protein FT2 Fts[3 SPS1_M c linit/branefer protein Scn2 NATD M | MOUSE 162 KDs MOUSE 95 KDs MOUSE 59 kDs | 0% 0% 0 0% 0% 0 | N 0.0% 90% | N 200% N 80% 1 | 100% 85.7% | 20% 20% | 0% 13.2% 0% 0% 1000 | 9% 0% 1 0% 0% | 0.0% 100% 100.0% 0% | 100% 100% 100 | 0% 0% 0% 0% | 0% 0% 0 | 0% 0% 0% 100% 1 | 9% 1/ | ON 100N | 0% 0% 0% | 0% 0.0% | 100% 100% 1 | 0% 100.0% 0% | 200% | 0.0% 0% | 0% 0% 0.0% | | | 0. | 1835 | 0.1835 | 0.1835 | |
| Plerb2 PLX82 I carbonic anhydrase Ica ICA_MOI | MOUSE 205 KDs XOUSE 77 KDs | 100% 100% 100% 100% 100 | 010 | N ON | - | on on | | 100% | - | 0% | | 0% | 100% 1 100% 1 | 0% 100% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | | |
| hydrolase Blinh BLMH_M schalase 1 reculators Ppp Ir12b MYPT2_1 | MOUSE 52 kDs MOUSE 109 kDs | 100% 100% 100 | N 100.0% ON | N ON | 0% 0.0% | ON ON | 0% 0.0% 100% | 100% 100% | 100.0% OK | 0% 0% 0 | 0% 0% | 0% 0% 0 | O% 100% 1 | JON 100N 100.0% | 0% 0% 0% 0.0% | 0% 0% | 0% 0.0% | 100% 100% 1 0% 100% | 0% 100.0% 0% 0% | 0% 0% 0% | 0.0% ON 900% | 0% 0% 0.0% 0% | | | | | | | |
| expression K1 Fook1 FCBK1 sier dikinase 2 Sephs2 SP52 M | MOUSE 75 kDs MOUSE 46 kDs | 92% SON 100 | N 87.3% 18N | 900% N 20% | 0% 12.7% | ON ON | 0% 0.0% 639 | 93% 90% | 75.3% 28% | 17% 20% 24 | 7% 0% | 0% 0% 0 | 0% 0% 1 | 0% 0% 0.0% 10 00% 100% 100.0% | ON 100N 100N 100.0% ON 0N ON 0.0% | 0% 0% 0% 0% | 0% 0.0% | 0% 0% 100% 100% 1 | 0% 0.0% 100% 0% 100.0% 0% | 100% 100% 0% 0% | 100.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.2572 | 0.1844 | 0.0620 0. | 872 | 0.1544 0.1 0.0330 0.1 0.1994 0.4 | 620 | _ |
| utointegration factor Banf1 BAF_MD methionine synthase i Mat2s METR2_I | DUSE 10 kDs / MOUSE 44 kDs | 100% 100% 100 100% 89% 83 | N 100.0% ON N 90.7% ON | N 0% | 0% 0.0% 17% 9.3% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 1 200% 100% 1 80% 100% | 100.0% 0% 193.3% 0% | 20% 0% 0 | 7% 0% 1 | 0% 0% 0 | 0% 50% 0% 100% 1 | /5% 67% 63.9% 5 00% 100% 100.0% | 0% 25% 22% 35.1% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 100% 71% 100% 100% 1 | 5% 82.1% 0% 0% 100.0% 0% | 29% 25% 0% 0% | 17.9% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.7710 | 0.1938 0.0390 | 0.1853 0.4226 0.3 | 0.1938 | 0.0090 0.4 | 853 226 | |
| dent glucokinase Adpgk ADPGK n nordain with multinia Ritgans REPAS use C delta hone Priord KECD M | MOUSE SHICK S MOUSE 22 KDs | 0% 0% 100 0% 0% | 100.0% 0% | N 200% | 05 0.05 | 0% 0% 0% 0% | 0% 0.0% 100% 0% | 100% 100% | 100.0% 0% | 100% | 0% 0% | 9% | 0% 100% 1 0% | 20% 100% 100.0% 0% 0% 0.0% 1/ | 0% 0% 0% 0.0% 0% 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 2 13% 0% | 0% 100.0% 0% 0% 4.2% 88% | 0% 0% 100% 100% | 95.8% ON | 0% 0% 0.0% 0% 0% 0.0% | | 0.4226 | 0.4226 | 0.4225 0.4225 | 0.4 | 226 | |
| dent 5-choschofructol Pfkp PFKAP | MOUSE 80 kDs | 100% 100% 100 100% 100% 100 100% 100% 10 | N 100.0% 0% | N ON | 0% 0.0% 0% | 0% 0% 0% | 0% 0.0% 100% 0% | | 100.0% 0% | 0% 0% C | 0% 0% | 0% 0% 0 0% | 0% 100% 1 100% 1 | 30% 100% 100.0% 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 | os 100.0% os | 9% 9% | 0.0% 0% | 0% 0% 0.0% | | | | | | | |
| rephosphate synthes Fdgs FPPS_M sesociated protein as Ser3 SSRG_M | MOUSE 21 KDs | 100% 100% 100 54% 67% 67 | N 100,0% ON N 52,4% RN | N 9% N 11% | 0% 0.0% 17% 11.8% | 9% 9% 28% 22% 7 | 0% 0.0% 100% 17% 25.8% 75% | 57% 23% | 57.9% 0% 67.9% 13% | 0% 0% 0 0% 14% 8 | 9% 0% 9% 13% 4 | 0% 0% 0 12% 14% 23 | 2% 100% 1 2% 50% | 30% 100% 100.0% 50% 57% 52.4% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 9% 9% 50% 50% | 6% 0.0% 42% 47.6% | 100% 100% 1 50% 67% | 0% 100.0% 0% 2% 61.1% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 50% | 0% 0% 0.0% 22% 22% 38.9% | 0.4769 | 0.2535 0.1293 | 0.4352 0.0 | 5141 | 0.0456 0.1 | 853 0.8399 0. | 0.2535 |
| Metal Meta | MOUSE 15 KDs | 100% 100% 100 100% 100% 100 54% 67% 67 100% 100% 100 100% 100% 100 50% 50% 80 0% 0% 0 | N 100.0% ON N 60.0% ON | N ON | 0% 0.0% 17% 11.8% 0% 0.0% 0% 0.0% | 0% 0% 50% 50% | 0% 0.0% 100% 20% 40.0% 80% | 100% 100% 100% 152% 71% 100% 100% 100% 100% 100% 75% | 100.0% 0% 67.9% 12% 100.0% 0% 70.4% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 0% 20% 1 | 9% 9% 9 9% 9% 9 17% 25% 29 | 0% 100% 1 5% 86% 1 | 20% 100% 100.0% 00% 80% 80.6% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 14% 0% | 0% 0.0% 20% 11.4% | 100% 100% 1 88% 75% 1 | 0% 100.0% 0% 0% 87.5% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 13% | 0% 0% 0.0% 25% 0% 12.5% | 0.1859 | 0.9145 0.0845 | 0.3832 | | 0.4226 0.4 | 0.1859 0.1 | 0.9145 |
| schor protein 2 Akap2 AKAP2 histocorresibility and Cd74 HG2A M | MOUSE 99 kDs MOUSE 32 kDs | 0% 0% 0 | N 0.0% 100N | N 100N 1 | 100% 100.0% | 0% 0% | 0N 0.0% 0N | SON ON | 16.7% 100% | 20% 100% 83 | 2% 0% | 0% 0% 0 | 0% 32% 22% | 0% 0% 11.1% 6 60% 20% 27.4% | 7% 100% 100% 88.9% 6% 60% 80% 85.2% | 0% 0% 22% 0% | 0% 0.0% 0% 7.4% | 0% 0% 0% 50% | 0% 0.0% 100% 3% 27.8% 100% | 100% 100% 50% 67% | 100.0% 0% 72.2% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.4226 | 0.4225 0.4225 0.9831 | 0.4226 0.4 | 0.4225 | 0.4225 0.4 | 226 | |
| Set SET MO shoughale isomerase Mpi MPI MD | OLSE 33 KOs OLSE 47 KOs | 100% 100% 100 100% 100% 100 | N 100.0% 0N N 100.0% 0N | N ON | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 1009 | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% C | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 100% 1 | 20% 100% 100.0% 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | | _ |
| 3 Ansat2 ANX12 I enhancer-binding fact IE2 ILF2_MC | MOUSE 35 KDs ADUSE 43 KDs | 100% 100% 100 | N 100.0% 0N N 100.0% 0N N 0.0% 100N N 91.7% 0N N 100.0% 0N N 66.7% 0N N 0.0% 100N | N ON | 0% 0.0% | 0% 0% | 0% 0.0% 100% | 100% 100% | 100.0% 0% | 0% 9% 0 100% 0% 0 0% 0% 0 0% 0% 0 | 0% 0% | 0% 0% 0 | 200% 1 0% 83% | 20% 100% 100.0% 82% 86% 84.1% | 0% 0% 0% 0.0% 0% 0% 0.0% | 0% 0% 17% 17% | 0% 0.0% 14% 15.9% | 100% 100% 1 78% 100% 1 | 0% 100.0% 0% 0% 92.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 22% | 0% 0% 0.0% 0% 0% 7.4% | | 0.3714 0.0025 | 0.4226 | 0.0011 | 0.4274 | 0. | 0.3714 |
| Epn3 EPN0 M al import inner memb Timm44 TIMM4_M cycleine linese calabi. Gdr. GSRI M | MOUSE 51 kDs MOUSE 71 kDs | 200% 75% 100 100% 100% 100 | N 91.7% 00 N 91.7% 00 N 100.0% 00 | N 0N 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 0% 8.3% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 0% 1 100% 100% 6 2% 100% | 100.0% ON | 0% 0% 0 | 0% 0% 3 | 0% 0% 0 12% 0% 11 | 0% 1 1% 100% 1 | 0% 0% 0.0% 10 00% 100% 00% 100% | 0% 25% 100% 91.7% 0% 0% 0% 0% 0.0% | 0% 25% 0% | 0% 8.3% 0% 0.0% | 2% 2% 100% 100% 1 | 0% 0.0% 60% 0% 100.0% 0% | 9% S0% 9% 0% | 01.7% 40% 0.0% 0% | 25% 50% 38.3% 0% 0% 0.0% | 0.4226 | 0.4226 | 0.4226 0.4226 | 026 | 0.4226 | 0.4226 | 0.0544 |
| eferase and sulfurns Mocs3 MOCS3 in-containing protein TdreS TDRDS I | MOUSE 49 kDs MOUSE 82 kDs | 200% S0% S0 0% 0% 0 | N 66.7% ON N 0.0% 100N | N 50% | 50% 33.3% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 09 | ON ON | 0% 0.0% 100% | 100% 100% 100 | 0% 0% | 0% 0% 0 | 60% 0% 0% | 64% 64% 49.6% 6 0% 0% 0.0% 9 | 0% S6% S6% 50.4% 0% 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 60% 32% 0% | 5% 32.8% 60% 100% | 67% 75% | 67.2% 0% 0% | 0% 0% 0.0% | | 0.0692 0.4174 | | 0.0662 | 0.4174 | | |
| in cnoschodiesteras Smpd4 NSMA3, of cis-trans isomeras Pidp10 PKB10_3 c lineage cell-specif (MM) 1977 F1 | MOUSE 55 kDs MOUSE 55 kDs | | | | | 766 | | | | | | + + - | 200% 1 200% 1 | 0% 0% 0.0% 30% 60% 85.7% 00% 100% 900 8% | 0% 0% 0% 0.0% 0% 0% 20% 6.7% 0% 0% 0% 0% | 100% 100% 0% 0% | 20% 6.7% 0% 0.0° | 0% 0% 100% 100% 100% * | 0% 0% 0% 0% | 0% 0~ | 900% 0% | 0% AK 0 AK | | | | | | | - |
| dunit zeta-1 Copz1 COPZ1 profesio 3 Rbm3 Rbm3 Rbm3 N | 0.0000 0 | 100% 100% 100 100% 100% 100 100% 100% 10 | N 100.0% ON N 100.0% ON | N ON | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 1000 | 100% 100% 100% 100% | 100.0% ON 100.0% ON | 0% 0% 0 0% 0% 0 | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 100% 1 | 20% 100% 500.0% 00% 100% 500.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.74% | 0.5738 | | 5004 | 0.9195 | | _ |
| D KDs protein 13 Heps 13 HSP 13 J | MOUSE SENDS | 50% 63% 46 100% 86% 67 | 55,6% 20% | N 12% | 56% 29.4% | 20% 25% | 0% 15.0% 60% | SON SON | 53.2% 20% | 10% 25% 18 | 2% 20% 4 | 10% 25% 20 | 2% 100% 71% | 0% 0% 33.3% 62% 62% 66.9% | 0% 0% 100% 33.3% 0% 0% 0% 0.0% | 29% 200% 29% 28% | 0% 33.3% 22% 33.1% | 89% 75% | 25 84.95 25 | 0% 0% | 0.0% 11% | 25% 9% 15.1% | | | | | | 0.2457 | |
| Migeli MFGM_A protein Pvb PYB MC | MOUSE 51 kOs MOUSE 90 kOs | | 5 98.1% 98 | 8 208 | 405 12305 | 05 05 | 25 2.25 1005 | 2005 1005 | 100.0% 0% | 05 05 0 | 25 25 | 25 05 0 | 725 | 225 675 57.1% ; | 95 605 325 40.0% | 95 75 95 75 | 05 2.25 | 75% 80% 2 | 25 52.85 25 5 05 | 20% 62% | 35.6% ON | 0% 5% 1.0% 0% | 0.2413 | 0.7826 | 0.4226 | 0.7774 | 0.2412 | 0. | |
| mary amine celdas Acc3 ACC3 M hale cyrophosobok Prps2 PRPS2 | MOUSE 85 KDs 2 MOUSE 35 KDs | 100% 100% 100 100% 100% 100 100% 100% 10 | K 100.0% 0% | 9% % 9% | 0% 0.0% | 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% 100.0% 0% | 0% 0% 0 | 2% 0% | 0% 0% 0 | 200% 0% 200% 1 | 87% 100% 95.6% 00% 100% 500.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 13% 0% 0% | 0% 4.4% 0% 0.0% | 100% 100% 1 | 95 97.0% 95 96 100.0% 96 | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 7% 2.4% 0% 0% 0.0% | | 0.7093 | 0.4226 | | | 0. | 0.7093 |
| transferans M. 5 Germ GSTMC, is A tricesterans 1; Accit 3 ACCit 3, all cirk Cirk Cirk CRV, Mr. 11e-like protein 2 Ctg2 C1G2 2, 1 cession protein 13; Tart TSR1 M cusmine chosohori Hptt Mr. MPCIA, if myosin-la Myoria MPCIA, | MOUSE 27 KDs J MOUSE 15 KDs | 100% 100% 100 100% 100% 100 | N 100.0% ON N 100.0% ON N 100.0% ON N 100.0% ON | N 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 100% 1 | 20% 100% 100.0% 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | 0.4226 0.4226 | | 0.4226 | 0.4226 | | |
| C1g-like protein 2 C1gD C1QL2 II consino protein TS Tar1 TSR1_M | MOUSE 29 kDs MOUSE 92 kDs | 0% 100% 0 | N 33.3% 100N | N 9N 1 | 100% 65.7% | 9% 9% | 0% 0.0% 1009 | | 95 | | 0% | | 100% 1 | 005 | 0% 0% | 0% 0% | 100% | os. | 2% 2% | 0% | 200% | 100% | | 0.1835 | | | 0.1835 | | |
| ouanine phosphori Hiprit HPRT_M al myosin-la Myota MYOTA | MOUSE 25 KDs MOUSE 119 KDs | 2005 2005 200 | n 100.00 x 1 | N ON | 0% 0.0% | 0% 0% | 0N 0.0% 100N | 100% 100% | 100.0% 0% | 0% 0% 0 | 0% 0% | 0% 0% 0 | 0% 100% 1 | 20% 100% 500.0% | 0% 0% 0.0% | 0% 0% 0% | 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | | - |
| export factor 1 Nef1 NOF1_M 1-choschate (vase 1 Sgill SGPL1_1 | MOUSE 70 kDs MOUSE 64 kDs | | N 0.0% 100N | N 100% 1 | 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 1007 | 0% 0% 100% 100% | 0.0% 100% 100.0% 0% | 100% 100% 100 0% 0% 0 | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 1 | 0% 0% 0.0% 5 00% 100% 100.0% | 2% 100% 90% 91.1% 0% 0% 0% 0.0% | 17% 0% 0% 0% | 10% 8.9% 0% 0.0% | 0% 0% 100% 100% 1 | 0% 100.0% 0% | 75% 0% 0% | 22% 22% 0.0% 0% | 25% 0% 0.0% | | | | 0.0530 | 0.2079 0.0 | 903 0/ | 0.0530 |
| arbowlate reductas Pycri PSCR3 I nine-crotein chosphs Ppp2H PTPA M | MOUSE 29 KDs MOUSE 37 KDs | 100% 100% 100 100% 100% 100 | N 100.0% ON N 100.0% | N ON | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0N 0.0% 100N 0N 0.0% 100N | 1 200% 100% 1 200% 100% 1 200% 100% 1 200% 100% | 100.0% ON 100.0% ON | 0% 0% 0 | 0% 0% 1 | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 100% 1 | 20% 100% 100.0% 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | | |
| n E synthase 3 Piges3 TESP_M loA thickese A perce Acasts THIKA N | MOUSE 19 kDs MOUSE 44 kDs | 100% 80% 100 100% 100% 100 | N 93.3% ON N 100.0% ON | N 20% | 0% 6.7% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% | 200% 100% 100% 100% | 100.0% OK | 0% 0% 0 0% | 0% 0% | 0% 0% 0 0% | .0% 100% 1 100% 1 | 30% 100% 100.0% 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 5 100% 100% 5 85% 100% 5 | 0% 100.0% 0% 0% 94.9% 15% | 0% 0% 0% 0% | 0.0% 0% 5.1% 0% | 0% 0% 0.0% 0% 0% 0.0% | | 0.4226 0.4226 | | | 0.4226 | | _ |
| daamin Serpinf2 A2AP_M ing protein RBBP4 RBBP4 | MOUSE 55 kDs MOUSE 46 kDs | 100% 80% 100 | N 93.3% 0N N 4.2% 100N | N 20N | 0% 6.7% 0% 6.7% | on on | 0% 0.0% 100% 0% 0.0% 0% | 100% 100% | 100.0% 0% | 0% 0% 0 | 0% 0% | 0% 0% 0 | 200% 0% 90% | 45% 100% 98.3% 88% 86% 87.7% | 0% 0% 0% 0.0% 0% 12% 14% 12.3% | 0% 5% 0% 0% | 0% 1.7% 0% 0.0% | 100% 100% 1 88% 91% | 0% 100.0% 0% 8% 88.6% 12% | 9% 0% 9% 13% | 0.0% 0% 11.4% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.4226 | 0.4225 0.6222 0.4912 | 0.0099 0.4 | 1226 0.6222 | 0.4912 0.8 0.3800 0.4 | 099 | 0.4225 |
| anama americales Sett SNUT SNUT | MOUSE 142 KDs 2 MOUSE 47 KP- | 100% 80% 100 0% 12% 0 100% 0 50% 0 50% 0 50% 0 100% 100% 100% 100% 100% 100% 100 100% 100% | 8 4.2% 100% 8 0.0% 100% | | | 9% 9% 9% 9% | 9% 0.0% 0% 0% 0.0% ~~ | 98 09 | 9.0% 100% | 100% 100% 100 | 975 ON | 9% ON O | 105 165 675 1 | 0% 20% 11.4% 8 30% 80% 82.2% 7 0% 0% 0.0% | 65 100% 80% 88.6% 2% 0% 20% 17.8% 0% 100% 100% 900.000 | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0% 0% 1 100% 80% 1 0% 0% | 0% 93.7% 100% 0% 93.7% 0% 0% 0.0% 100% | 20% 50% 20% 0% | 67% 0% 100.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | | - |
| ranslation initiation fs E/G/2 E13/6 M ried protein 1 Nokap1 NCKP1 | MOUSE 29 KDs LMOUSE 129 KDs | 62% 79% 93 100% 100% | N 0.0% 100% N 78.0% 28% | N 21% N 0% | 100% 100.0% 7% 22.0% | 0% 0% 0% 0% | 0% 0.0% 80% 1009 | 92% 89% 200% | 85.9% 20% 0% | 8% 11% 12 0% | 1% 0% 0% | 0% 0% 0 0% | 0% 100% 100% 1 | 100% 00% 100% 500.0% | 0% 0% 0% 0.0% | 9% 9% 9% | 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | 0.1285 0.0 | | |
| mm-10 IIIS IL.15_MD in-18 Smx18 SNX18_II billion factor G Anti Antica A | MOUSE 50 KOs MOUSE 70 KC- | 0% 0% 0 100% 100% 100 | N 0.0% 100% N 100.0% 0% N 100.0% 0% | 0% N 100% 1 | 100% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0N 0.0% 0N 0N 0.0% 1000 | 0% 0% 100% (*********************************** | 0.0% 100% 100.0% | 100% 100% 100 0% 0% | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 0% 1000 | 0% 25% 8.3% 1/ 00% 100% 900 PM. | 0% 100% 25% 91.7% 0% 0% 0% 0% 0.00 | 9% 9% 9% 0% | 0% 0.0% 0% 0.0% | 100% 0% | 0% 100.0% 0% | 100% 0% 0~ | 90% 0% | 0% AN 0.00 | | 0.5560 0.4225 | 0.5000 | 0.5580 | 0.4226 0.5 | 000 | _ |
| decide-binding profe Graq GNAQ N shosphale synthase I Cps 1 CPSM N | MOUSE 42 KDs MOUSE 165 KDs | 100% 100% 100 100% | N 100.0% 0% | N ON | 0% 0.0% | 9% 0% 9% | 0% 0.0% 100% | 100% 100% | 100.0% 0% | 0% 0% 0 | 0% 0% | 0% 0% 0 | 0% 100% 1 100% 1 | 20% 100% 100.0% 00% | 0% 0% 0% 0.0% 0% 0% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 2 | 0% 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% 0.0% | | | | | | | - |
| Eatherion molecule Epcam EPCAM Bassociated progester: Pormc2 PCAM Brown | March Marc | 75% 83% 86 100% 67% 50 | N 81.3% ON 72.2% ON 38.9% ON 0.0% ON | N ON | 0% 0.0% 0% 0.0% 0% 0.0% 100% 88.9% | 25% 17% 7 0% 32% | 14% 18.7% 80% 50% 27.8% 1000 | 100% 100% 67% 90% | 93.3% ON 82.2% ON | 0% 0% 0 0% 0% 0 | 0% 20% 0% 0% 2 | 0% 0% 6 | 7% 82% 8% 32% | 825 1005 100.0% 805 505 71.1% 675 525 52.4% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 17% 20% 67% 33% | 0% 0.0% 50% 20.9% 63% 47,5% | 100% 100% 1 67% 44% 43% 50% | on 100.0% on on 53.7% sax | 0% 0% 32% 25% 0% 0% | 00% 0% 23.1% 22% 00% 57% | 0% 0% 0.0% 22% 25% 23.1% 50% 22% 46.8% | 0.2076 | 0.2494 0.4398 0.9514 0.3338 0.1035 0.1074 0.5096 0.4226 0.0574 0.5000 0.1734 | 0.0137 0.0705 0.7791 0.4226 0: | 0.0702 | 0.0 | 702 0.2076 0.0 0.6046 0.0 | 0.6428 |
| bosense lubiculor Ndub5 NDUB5 crolein with serine - Rops 1 RNPS1 | MOUSE 22 KDs MOUSE 34 KDs | 67% 25% 25 0% 0% 0 | N 38.9% 0% N 0.0% 100% | N 9N N 62N 1 | 0% 0.0% 100% 88.9% | 32% 75% 7 0% 32% | 75% 61.7% 23% 0% 11.7% 09 | 9% S0% 9% | 27.8% 0% 67% | 0% 0% 0 50% | 0% 67% 10 23% 5 | 90% 50% 72 90% | 2% 0% 0% | 0% 0% 6.7% | 0% 0% 0% 75.0% 60% 70.0% | 100% 25% 25% | 100% 20% 23.3% | 22% 22% 0% 0% 2 | 0% 22.2% 0% 0% 33.2% 100% | 0% 0% 100% 0% | 0.0% 67% 66.7% 0% | 67% 100% 77.8% 0% 0% 0.0% | 0.6120 | 0.1835 0.1074 0.5095 0.4225 | 0.7791 0.4226 0. | 1155 0.9299 | 0.2259 0.8 | 0.6120 0. 255 0.1155 0. | 0.1835 |
| containing kinase-bi Shikitp1 SHIKI J T-chosphoadenosin Perset DARKE | MOUSE 75 KDs MOUSE 75 KDs | 100% 0% | N 100.0% ~~ | N 0% | | 0% 0% | 0N 0,7%L 100% | 1000 | 100.0% ~~ | 0% 0% | 0% 0% | 9% ON 7 | 67% 67% | 0% 0% 0.0% 47% 50% 61.1% | 0% 25% 25% 16.7% 2% 22% 50% 38.9% 0% 0% | 200% 75% 0% 0% 0% 0~ | 75% 83.3% 0% 0.0% | 2% 12% 75% 67% 100% 100% * | 28 12.2% 0% 5% 72.2% 25% 0% 100.0% 0% | 28% 25% 25% 25% | 9.8% 92% 27.8% 0% | 965 785 77.9% 96 96 0.0% 96 96 0.0% | | | | 0.1734 | | | u-J081 |
| Chosphosdenosis | MOUSE 43 KDs MOUSE 119 KDs | 100% 100% 200 89% 62% 100 100% 100% 50 80% 50% 50 80% 100% 100 100% 100% 50 | N 82.7% 14N N 100.0% 0N | N 0% N 28% N 0% N 11% N 0% | 0% 0.0% 0% 17.3% 0% 0.0% 50% 27.0% 0% 6.7% 100% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 50% 0% 0.0% 100% 0% 0.0% 100% 0% 0.0% 100% | 1 200% 200% 1 200% 200% 1 200% 200% 1 200% 200% | 6 100.0% 0% 6 83.3% 50% 0% | | | 0% 0% 0 0% 0% 0 | | 30% 100% 100.0% 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 67% 1 100% | 0% 88.9% 0% 0% | 22% O% | 11.1% OK | on on 0.0% | | | | | 0.2549 0.3 | | |
| tein Hbs11 HBS1L I Tuf1 TWF1 N | MOUSE 75 kDs MOUSE 40 kDs | 90% 99% 50 90% 100% 100 | N 73.0% 20N N 93.3% 20N | N 11% N 0% | 50% 27.0% 0% 6.7% | 0% 0% 0% 0% | | | 100.0% 0% 100.0% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | | 30% 100% 100.0% 00% 100% 95.8% | 0% 0% 0% 0.0% 2% 0% 0% 4.2% | 0% 0% 0% 0% | 0% 0.0% | | 0% 0% 100.0% 0% | 0% 0% 0% | | 0% 0% 0.0% | 0.1483 | 0.1483 0.4226 0.7693 0.8109 | 0. | 0.4226 0.4226 | 0.1483 0.7893 0.1844 0.4 | | |
| na prolein subunit a Capast CAZA1_1 volument revision AV Wd-45 WTRAK | MOUSE 33 KDs | 100% 100% 100 | N 100.0% ON | N 0% | 0% 0.0% 100% | 0% 0% 0% | 0% 0.0% 100% 0% | 1 100% 100W | 100.0% ON | ON ON C | .0% on | 0% 0% 0 | .0% 80% 1 | 30% 82% 87.3% 3 | 0% 0% 18% 12.7% 0% | 0% 0% 0% | 0% 0.0% | 100% 89% 1 | 0% 98.3% 0% | 11% 0% | 3.7% ON | 0% 0% 0.0% | | 0.3037 0.1844 | 0.4226 | 0.3037 | 0.1844 0.4 | 226 | _ |
| and Kurboursholmorks Pfil PFKAL In or securioristicis all Apex1 APEX1 | MOUSE SS KON | 08 0 100% 100% 100 100% 100% 100 | N 100.0% 0N N 100.0% 0N | N ON | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 1009 | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 100% 1 | 20% 100% 500.0% 00% 100% 500.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | | - |
| nee incenzyme 1 Ak1 KAD1_M hicesterase 1 Lvols1 LVDs1 i | MOUSE 22 KDs MOUSE 25 KDs | 100% 100% 100% 100% | N 100.0% 0% | N ON | 0% 0.0% | 0% 0% 0% 0% | 95 0,0% 1005 | 200% 100% 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 86% 1 0% 100% 1 | 20% 100% 95.2% 100% 100% 100% | 6% 9% 9% 9.0% 6% 9% 9% 4.8% 9% 9% 9% 9% 9.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 2 100% 100% 2 100% 100% 4 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 90% 0% 90% 0% | 0% 0% 0.0% 0% 0% 0.0% | | 0.4226 0.4226 | | 0.4226 | 0.4226 | | |
| atid cohesion protein PdsSa PDSSA conf-terminal hydro UchiD UCHIS I | MOUSE 150 KDs MOUSE 25 KDs | 100% 100% 100% 100 | N 100.0% ON | 9% N 9% | 0% 0.0% | 0% 0% 0% | 0% 0.0% 100% | 100% 100% 100% | 100.0% ON | 0% 0% C | 0% 0% | 0% 0% 0 | 200% 0% 200% 1 | 100% 90% 100% 100.0% | 0% 0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% | 100% 100% 100% 1 | 0% 100.0% 0% | on on | 9% 9% 9.0% 9% | 0% 0% 0.0% | | | | | | | - |
| ny mesoan-activate: Map244 MP2K4_ hydrolase Bphi BPHs_M oxeolularate transar KusiG KATS M | MOUSE 33 KDs MOUSE 51 KDs | 100% 100% 100 100% 100% 100 | N 100.0% ON N 100.0% AV | 98 8 98 8 98 | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 100% 100% 100% 100% | 9% 100.0% 9% 100.0% 9% | 0% 0% 0 0% 0% 0 | 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 100% 1 | 925 1005 100.0% 905 1005 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 2 100% 100% 2 | 9% 100.0% 0% | 0% 0% | 0.0% ox | 0% 0% 0.0% | | | | _ | | | |
| e Iflavin-containing Maca ADFA M | MOUSE 60 kDs MOUSE 87 kDs | 08 0 0 0 0 1 0 0 0 1 0 0 0 0 1 0 | N 100,075 0N N 100,075 0N N 80,775 0N N 30,975 50N N 100,075 0N N 100,075 0N | N 0N N 100N | 0% 0.0% 22% 01.1% | 17% 14% 0% 0% | 0% 10.2% 80% 0% 0.0% 07 | 80% 100% 25% 0% | 85.7% 0% 8.2% 100% | 0% 0% 0 50% 0% 50 | 0% 20% 2 0% 0% 2 | 10% 0% 13 15% 100% 41 | 2% 32% 7% 100% 1 | 65% 25% 34.6% 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 67% 55% 9% 9% | 75% 65.4% 0% 0.0% | 0% 100% 100% | 9% 9% | 9% | 200% 0% | os. | 0.7404 | 0.0024 0.0927 | 0.0082 0. | 1005 | 0.0927 0.2 | 0.7404 254 0.2999 | |
| some complex subs Gps1 CSN1_M Ipo7 IPO7_MC containing protein Serve | ACUSE 119 KDs. 2 MOUSE 51 KC- | 100% 100% 100 100% 100% 100 | N 100.0% ON N 100.0% ON | N 98 | 0% 0.0% 0% 0.0% | 9% 9% 9% 9% | 9% 0.0% 100% 9% 0.0% 100% | 100% 100% 100% 100% | 100.0% ON 100.0% ON | 0% 0% 0 0% 0% 0 | 9% 9% 9% 9% | 9% 9% 9 9% 9% 9 | 0% 100% 1 0% 100% | 225 100% 100.0% 100% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0% 0% 0% 0.0% 0% 0% 0% | 9% 9% 9% 11% **** | 0% 0.0% 0% 14% 93.5** | 100% 100% 2 100% 100% 2 0% 0% | 0% 100.0% 0% 0% 100.0% 0% 0% 0.0% 7*** | 0% 0% 2% 21F | 0.0% 0% 0.0% 0% 73.8% 29% | 0% 0% 0.0% 0% 0% 0.0% | | | | 0.0190 | | - | 0.0190 |
| obein 148 Zrf146 ZN146 N min and FG recest+ Agig1 AGFG1 | MOUSE 50 KOs | 0% 0% 0 | N 0.0% 100N | 200% N 200% 1 | 100% 100.0% | 0% 0% | ox 0.0% or | ON ON | 100% | 100% | Ons. | 0% 0% | 0% 0% | 0% 0% 0.0% 10 0% 0% 0.0% 1 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | | | | | | |
| y homolog 2 Fermi2 FERM2 nvi-CoA hydratase. Auh ALHM N | MOUSE 78 KOs MOUSE 33 KOs | 100% 100% 100 100% 100% 100 | N 0.0% 100N N 100.0% 0N N 100.0% 0N | N ON | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 1 100% 100% 1 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% 0 0% 0% 0 | 0% 0% 1 | 0% 0% 0 0% 0% 0 | 0% 100% 1 | 94% 100% 95.5% | ON ON ON 0.0% | 0% 0% 9% 0% | 0% 0.0% | 100% 100% 2 | 0% 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% 0.0% | | 0.1907 | | | | | 0.1907 |
| protein 3 CNIS CHLS N ein-retaining recet Kdeir1 EFID21 1 | MOUSE 44 kDs | 22% ON 50 | N 27.8% ON | N ON | on 0.0% | 67% 100% | 50% 72.2% 239 | 100% 67% 22% | 6 44.4% OK | 0% 0% 0 | 0% 67% 2 | 0% 12% 67% 55 | 5% 0% | 94% 100% 95.5% 0% 50% 16.7% | 0% 0% 0% 0.0% | 8% 6% 100% 100% | 50% 83.3% | 100% 100% 5 100% 100% 5 | 0% 100.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% 20% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.4264 | 0.4226 0.6437 | 0.0572 | | | | 0.4226 |
| drosenase crolein Pdhx CEPX_5 Sh3gl1 SH3G1_1 | MOUSE 54 kDs MOUSE 42 kDs | 32% ON 50 50% SON 100 | N 27.8% 67N N 66.7% SON | N 100% N 50% | 50% 72.2% 0% 33.3% | 0% 0% 0% 0% | 0% 0.0% 33% 0% 0.0% | 25% 40% 100% | 32.8% 67% | 75% 60% 63 0% | 2% 0% | 0% 0% 0 0% | .0% 100% 56% | 67% 62% 61.6% | 0% 200% 4% 22% 28% 38.4% | 0% 0% | 0% 0.0% | 0% 0% 75% 75% 5 | 0% 16.7% 100% 0% 83.3% 25% | 25% 50% | 83.3% OK 16.7% OK | 0% 0% 0.0% 0% 0% 0.0% | 0.7711 | 0.6244 0.7547 0.1065 0.7908 0.2254 | 0.0572 0.4360 G | 0.1065 | 0.7347 0.4 0.7908 | 380 | |
| Taphp TPSN_M ferunded IBM to Ddg27 DDX27 receptor 4 Entend Entend | 1 MOUSE 42 KGs MOUSE 50 KGs 7 MOUSE 65 KGs 4 MOUSE 109 KGs 1 MOUSE 51 KGs 1 MOUSE 51 KGs 1 MOUSE 51 KGs 2 MOUSE 51 KGs 1 MOUSE 51 KGs MOUSE 50 KGs 2 MOUSE 50 KGs 2 MOUSE 50 KGs 2 MOUSE 50 KGs 2 MOUSE 60 KGs | | N 11.1% 100N | N 100% | 67% 88.9% | on on | 0N 0.0% 0N | 0% ON | 0.0% 100% | 100% 100% 100 | 0% 0% 0% | 0% 0% 0 | 0% 0% 1 | 9% 9% 9.0% 1/ 9% 9% 9.0% 1/ | 0% 0% 0% 0.0% 0% 100% 100% 100.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 1006 2 | 9% 75.0% 9% 9% | 0% 0% | 0.0% 50% | 0% 0% 25.0% | 0.4226 | 0.2254 | 0. | 1226 | 0.4226 | 0. | PCLL |
| endodesmic retics Abbas ATAA M | MOUSE 55 KDs MOUSE 114 KDs | | N 100.0% ON | N ON | 0% 0.0% | 0% 0% | 0N 0.0% 100N | 100% 100% | 100.0% 0% | 0% 0% 0 | 0% 0% | 0% 0% 0 | .0% 100% 1 100% 1 | 30% 100% 100.0% 00% | 0% 0% 0% 0.0% 0% 0% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 1 67% 83% | 0% 100.0% 0% 5% 75.0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 33% | 0% 0% 0.0% 17% 25% 25.0% | 0.4226 | 0.0351 | 9. | | 0.4226 | 0. | 0.0351 |
| cno adapter mole: Stam STAMI rotein 27 Rbm27 RBM27 of MLC (Stamethal Neuro) | MOUSE 119 KDs | | N 4,8% 100% N 0,0% 100% | N 100% 1 | 86% 95.2% 100% 100.0% | 0% 0% 0% 0% | 9% 0.0% 0% 0% 0.0% | 95 05 | 0.0% 100% | 100% 100% 100 | 975 | 9% ON O | 95 95 100s 1 | 0% 0% 0.0% 10 0% 0% 0.0% 1/ | 75 100% 100% 100.0% 0% 100% 100% 100.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 20 0.0% 100% 0% 0.0% 100% | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.4226 | 0.4226 | | | | | _ |
| antiviral-signaling c Mavs MAVS N sident coproporchis Copes HEMS M | MOUSE 53 KDs | 20% 42% 12 100% 100% 100 | N 25.1% 80% N 100.0% 0% N 0.0% 100% N 92.5% 0% N 100.0% 0% | N 52N N 0N | 88% 74.9% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 40% 0% 0.0% 100Y | 23% S0% 100% 100% | 41.1% 60% 100.0% 0% | 50% 50% 53 0% 0% 0 | 2% 0% 1 0% 0% | 2% 0% 5 0% 0% 0 | 5% 0% 0% 100% 1 | 50% 100% 50.0% 10 00% 100% 100.0% | 0% 0% 0% 33.3% 0% 0% 0% 0.0% | 9% 50% 9% 9% | 0% 16.7% 0% 0.0% | 0% 0% 100% 100% 1 | 0% 100.0% 0% | 100% 0% 0% | 67% 62% 0.0% 0% | 0% 0% 0.0% | 0.2182 | | | | 0.3385 0.3 | 578 0.4226 0. | 0.7103 |
| of activated T-cell Matc2 NFAC2 h-reculated GTP-1 Drg1 DRG1 M | MOUSE 100 KDs MOUSE 40 KDs | 0% 0% 0 100% 100% 28 | N 0.0% 100% N 92.5% 0% | N 100% 1 | 22% 7.4% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 100% | 92% 100% | 97.0% 0% | 9% 9% 2 | 0% 0% 0% 0% | 9% 9% 9 | 0% 100% 1 | 0% 0% 0.0% 10 00% 100% 900.0% | 0% 100% 100% 100.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 2 | 0% 0.0% 100% 0% 100.0% 0% | 0% 0% 0% 0% | 900,0% ON 0,0% ON | 0% 0% 0.0% 0% 0% 0.0% | 0.6271 | | 0.4226 0.1 | 5271 | 0.4226 0.4 | 226 | - |
| Migh MILPH change regulatory Sicila2r1 NHFF1 I | MOUSE 55 KDs | | N 100.0% 0N | N ON | 0% 0.0% | 0% 0% | 0% 0.0% 100% | 190% 190% | 100.0% OK | 0% 0% 0 | 0% 0% | 0% 0% 0 | 2% 100% 1 | 0% 100.0% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% | 17% 40% 1 100% 100% 1 | 25 32.5% 67% 05 100.0% 05 | 52% 50% 0% 0% | 56.7% 17% 0.0% 0% | 7% 9% 10.8% 0% 0% 0.0% | | 0.0547 | | 0.0135 | | 0. | 0.0696 |
| orse-amplified sepa Bicas3 BCA53 sterage OTUB1 Otub1 OTUB1 I | MOUSE 101 KDs MOUSE 31 KDs | 0% 0 100% 100% 100 | N 100.0% ON | 200% I | 0% 0.0% | 0% 0% | 0% 0.0% 100% | 0% 100% 100% | 100.0% 0% | 100% 0% 0% 0 | 0% 0% | 0% 0% 0 | 0% 100% 1 | 00% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 57% 60% 55.7% | 0% 0% | 0% 0.0% | 100% 100% 1 | 0% 100.0% 0% | 0% 0% | 0.0% ON | 0% 0% 0.0% | 0.0000 | 0.0492 | 0.0000 | | | 0,000 | 0.0492 |
| coenase lubiculnor Nduhi2 NDUA2 coenase lubiculnor Nduhi2 NDUA2 coenase lubiculnor Nduhi5 NFI PSI | MOUSE 11 KOs 6 MOUSE 13 KOs | 22% 20% 25 12% 17% 29 | N 25.1% 67N N 19.2% 694 | N 80% | 75% 73.9% 71% 80.8% | 0% 0% 0% 0% | 0% 0.0% 17% 0% 0.0% 17% 0% 0.0% 70% | 67% 0% 22% 50% | 900.0% 0% 80.0% 0% 27.8% 82% 20.1% 80% 100.0% 0% | 23% 100% 72 67% 75% 75 | 2% 0% 5 | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 50% 0% 50% 0% 60% 0% 0% | 00% 100% 100.0% 50% 57% 55.0% 42% 40% 44.3% 5 0% 0% 0.0% 100% | 0% 57% 60% 55.7% 0% 100% 100% 100.7% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 975 80% 18% 29% 0% 0% | an 75.7% 0% 0% 32.3% 92% 0% 0.0% 100% | 71% SO% 100% 100% | 67.7% 0% 100.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.9419 | 0.0492 0.0918 0.3273 0.0232 0.0573 | 0.8850 0.8533 0.1 0.0215 0.1 | H19 0.3273 | 0.0032 0.0 | 533 215 | |
| nositol transfer croti Pitpna PIPNA, ti asse-like protein Scyll SCYLI I | MOUSE 32 kDs MOUSE 89 kDs | 100% 100% 100 0% 0% 0 | N 100.0% 0N N 0.0% 100N | N 200N 1 | 0% 0.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 09 | 1 200% 100% 0% | 100.0% 0% 100% | 0% 0% 0 100% | 0% 0% 0% | 0% 0% 0 0% | O% 100% 1 | 20% 100% 100.0% | 0% 0% 0% 0.0% | on on | 0% 0.0% | 100% 100% 5 | ON 100.0% ON | 0% 0% | 0.0% 0% | 0% 0% 0.0% | | | | | | | |
| es growth factor Mydgf MhTDGF e-binding protein 2 Pabpn1 PABP2 I cycle 5-like protein CA-51 CPCR | MOUSE 32 kDs MOUSE 92 kP- | 29% 20% 0 | n 100.0% 0N N 16.2% 71N N 100.0% | N 90% 1 | UN 0.0% 100% 83.8% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 20% 0% 0.0% | 100% 100% 25% 23% | 100.0% 0% 5 25.1% 80% | 0% 0% 0 75% 67% 72 | 9% 0% | 0% 0% 0 | 10% 50% 33% | 12% 80% 87.8% 22% 40% 43.5% / 40% 50% 41.1% | 0% 17% 20% 12.2% 2% 67% 60% 56.5% 7% 60% 00% 58.00 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 32% 22% - | on 100.0% on on 35.6% 67% 35 32.8% 75% | 0% 0% 67% 60% 60% 67** | 0.0% 0% 64.4% 0% 67.2% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.3898 | 0.1869 0.1869 0.3814 0.0707 0.2700 0.0067 | 0.1204 0. | 0.1889 958 0.3814 0.2300 | 0.1869 0.0707 0.1 | 254 | - |
| Ik RED MC | ACUSE 65 KCs MOUSE 82 KCs | 0% 0% 0 0% 0% 17 | S 0.0% 100% S 5.6% 100% | N 100% 1 | 100% 100.0% 83% 94.4% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% 0% | 05 | 100% 100% | 100% | Ons Ons | 9% | 2% 2% | 0% 0% 0.0% 1/ 0% 50% 27.8% | 0% 100% 100% 100.0% 7% 100% 50% 72.7% | 9% 9% 9% PK | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | | 0.1994 0.2667 | | 0.2700 | | | |
| Pm DIMM M | MOUSE 117 KDs MOUSE 25 KDs | 100% 100% 100% 100% 100 | 5 100.0% 0% | N 9% N 9% | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100Y | 200% 200% 200% 200% | 100.0% 0% 100.0% 0% | 0% 0% 0 0% 0% 0 | 9% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 0% 100% 1 | 20% 100% 500.0% 00% 100% 500.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 2 | 0% 100.0% 0% | 0% 0% | 0.0% 0% | 0% 0% 0.0% | | | | | | | |
| Pm PINN M Pitml PEP M thoesterass 2 Lypis2 LYPA2 I | MOUSE 41 KDs MOUSE 20 KDs | 100% 100% 88 | S 95.8% 0% | 9% N 9% | 125 425 | 0% 0% 0% 0% | 0% 0.0% 100N | 100% 100% | 100.0% ON 0.0% 100% | 0% 0% 0 100% 100% 100 | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 | 00% 100% 100.0% | 0% 0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% | 100% 100% 100% 100% | 9% 9% | 0% 0% | 9% 9% | 0% 0% | 0.4226 | 0.4225 | 0. | 1226 | 0.4226 | | _ |
| Pro PINN M Processor with the Pinn Pinn Pinn Pinn Pinn Pinn Pinn Pin | | 100% 100% 100 | N 100.0% 0N N 82.1% 0N | N 9% | 0% 0.0% 0% 0.0% | 0% 0% 0% 25% | 0% 0.0% 29% 17.9% 829 | 88% 100% | 90.3% 0% | 0% 0% 0 | | 0% 0% 0 12% 0% 9 | | 20% 100% 100.0% 67% 50% 50.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 9% 9% 67% 22% | 0% 0.0% 50% 50.0% | 100% 100% 2 100% 2 | 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% 0% | 0% 0% 0.0% 0% 0% | 0.4546 | 0.0351 0.0714 | 0.1917 | | | 0.4546 0. | 0.0351 |
| Pro PINN M provisions relevance Plant PREP M trionaferana 2 Lypha LYPA3 1 nel II subunit alphal carekaa 2 CSS2 1 rentation storastion Setfer MCA3 M fination requisitor 1 MF11 MFR11, declare INACPH 2 Cb2 CB2 M tansporter position 1 Mark 1 Marxiv | MOUSE 25 KDs MOUSE 35 KDs | | | v av | 0% 6.7% | 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 100% 100% | 100.0% 0% | 0% 0% C | 0% 0% 0% | 0% 0% 0 | 200% 1 0% 100% 1 | 20% 88% 95.8% 00% 90% 96.7% | 0% 0% 12% 4.2% 0% 0% 10% 3.3% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 90% 71% 100% 100% 2 | 25 74.7% 20% 06 100.0% 0% | 29% 27% 0% 0% | 25.3% 0% 0.0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0.4226 | 0.0351 0.0714 0.0182 0.7693 0.4226 0.1891 | 0.0109 0 | 1226 0.0182 1549 0.4226 | 0.7893 0.6 0.1891 | 630 | 1 |
| Prin | MOUSE 26 KDs MOUSE 36 KDs WOUSE 16 KDs MOUSE 37 KDs | 90% 75% 71 80% 100% 100 88% 88% 57 | N 93.3% 20% N 77.4% 12% | N 13% | 43% 22.6% | 95 95 | | | | | | | | | | | | | | | | | | | | | | | |
| Proc. Plant Plan | MOUSE 25 KDs 1 MOUSE 36 KDs MOUSE 16 KDs 7 MOUSE 37 KDs MOUSE 59 KDs GOUSE 59 KDs MOUSE 71 KD- | 100% 75% 73 80% 100% 100 88% 88% 57 100% 100% 100 100% 100% 100 | K 93.3% 20% K 77.4% 12% K 100.0% 0% K 100.0% 0% | N 12N N 0N N 0N | 63% 22.6% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% | 200% 200% 200% | 100.0% ON | ON ON C | 0% 0% | 0% 0% 0 | .0% 1 | 90% 100% 500.0% 30% 100% 500.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.00 | 9% 9% 9% ~~ | 0% 0.0% | 100% 100% 2 100% 100% 2 | 0% 100.0% 0% 0% 0% | 0% 0% 0% | 0.0% 0% 0% | 0% 0% 0.0% 0% | | | | | | | _ |
| yels 5-like prolein Got21 COCCE, Got22 G | MOUSE 50 500 MOUSE 50 500 MOUSE 50 500 MOUSE 50 50 MOUSE 50 50 MOUSE 50 50 MOUSE 50 | 100% 75% 71 80% 100% 100 88% 58% 57 100% 100% 100 100% 100% 200 | N 93.3% 20% N 77.4% 12% N 100.0% 0% N 100.0% 0% | N 22N N 2N N 2N N 2N | 63% 22.6% 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 100% 0% 0.0% 100% | 100% 100% 100% 100% | 100.0% 0% 100.0% 0% | 0% 0% C | 0% 0% 0% 0% | 0% 0% 0 0% 0% 0 | 0% 100% 1 100% 1 0% 100% 1 | 00% 100% 900.0% 90% 100% 900.0% 10% 100% 900.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 9% 9% 9% 9% 9% 9% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 2 100% 100% 100% 100% 2 100% 100% 2 | 05 05 05 05 05 06 100.05 05 | 0% 0% 0% 0% 0% 0% | 9.0% 9% 9% 9.0% 9% | 0% 0% 0.0% 0% 0% 0% 0.0% | | | | 0.1201 | | | |

| fusion decredation prob. URd11 of SRNA synthase comps. Airsp2 at-streaking factor 1 Oed1 emb-interacting protein. Rab1(fio1 | UFD1_MOUSE 34.6 AMP2_MOUSE 35.6 OSTF1_MOUSE 24.6 REIP1_MOUSE 71.6 | 20 50% 40% 29% 20 73% 86% 29% 20 100% 100% 100% 20 0% | 39.5% 50% 40 80.4% 22% 34 100.0% 0% 0 | 2% 71% 53.8% 8% 22% 19.6% 2% 0% 0.0% | 0% 20% 0% 0% 0% 0% | 0% 5.7% 0% 0.0% 0% 0.0% 0% 0.0% | 25% 50% 100% 100% 100% 100% 0% | 100% 58.3% 25 100% 100.0% 0 100% 100.0% 0 67% 20.0% 0 100% 94.4% 0 | 8 50% 0% 41.7% 8 0% 0% 0.055 8 0% 0% 0.055 8 12% 0% 55% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 4 0% 0.0% 10 0% 0.0% 10 | 0N 100N 100N 80.0% 0N 100N 100N 900.0% 0N 75N 89N 88.0% 0N 0N 0N 0N 0.0% | 60% 0% 0% 20 0% 0% 0% 0 0% 25% 11% 12 100% 100% 100% 100 | 7% 9% 9% 7% 9% 9% 7% 9% 9% 7% 9% 9% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 86% 92% 1 0% 0% | 100% 100.0% 100% 100.0% 100% 92.5% 1 | 0% 0% 0° 0% 0% 0° 4% 8% 0° | S 0.0% 0% N 0.0% 0% N 7.5% 0% ON | 0% 0 0% 0 0% 0 | 0.0% | 0.4975 0.4226 0.0178 0.6249 0.2739 | 0.1722 0.0178 0.2379 | 0.1994 0.6 0.2104 0.5000 0.4226 0.3 | 0.4225 C H78 C 6349 C | 1 2282 0.1994 1 0178 1 2379 0.2194 0.5000 1.1835 0.4226 | 0.4226 | 0.4 |
|--|--|--|--|--|-----------------------------|---|---|---|--|-----------------------------|--|---|---|---|--|--|---|---|---|---------------------------|------------------------------|--|----------------------------|--|--|---|--------------------------------------|----------------|
| reconine kinase recedior Strap carbon/-terminal hydro Usp7 selerate dehydrosenase Sciothb | CORTY MOUSE 2418 STRIPL MOUSE 2418 STRIPL MOUSE 318 STRIPL MOUSE 158 STRIP | Dec 100% CPK CPK | 77.8% 0% 33 96.7% 0% 0 | 25 | 0% 0% 0% 0% 0% | 0% 0.0% | 100% 82% 100% 100% | 100% 94.4% 0 100% 100.0% 0 100% 100.0% 0 | % 17% 0% 5.6% 0% 0% 0% 0.0% | 0% 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 900.0% 0% 100% 100% 900.0% 0% 100% 100% 900.0% | 0% 0% 0% 0 0% 0% 0% 0 0% 0% 0% 0 | 75 05 05 75 05 05 75 05 05 | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 | 100% 100.0% 100% 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% 0N N 0.0% 0N | | 0.0% | 0.4226 | 0.1835 | | | 14226 | | |
| tic initiation factor 4A-II E/Ma2 illin-protein licase RNF3 Rnf31 protein 2 Bole2 | FNF31_MOUSE 119 BOLA2_MOUSE 10.60 | Da 100% 100% 100% CDa 00% 100% 100% | 100.0% 0% 0 | 2% 0% 0.0% 200% 2% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% | S 05 05 0.05 S 05 05 0.05 | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 100 100 | 0% 0% 0% 0 100% 20% 0 0% 0% 0% 0 | 2% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% | 00% 100.0% 0% | 9% | × | 200 | 0.0% | 0.000 | 0.7845 | 0.000 | 432 0.4917 0 919 0.1994 0 0.8947 | 443 0000 | 0.007 0.30 | 200 |
| meonine-protein phosph; Ppp2/2s mbrane 9 superfamily m Tm9st2 shydrosenses lubiquinor Ndutb7 | ZABA_MOUSE 52 ki TM952_MOUSE 75 ki NDUB7_MOUSE 16 ki | De ON 50% 22% De 50% ON 57% De 82% 62% 29% | 27.8% 100% 25 35.7% 0% 0 58.1% 12% 26 | 0% 23% 52.8% 2% 0% 0.0% 8% 71% 41.9% | 0% 25% 50% 100% 0% 0% | 42% 54.2% 0% 0.0% | 50% 100% 100% 40% 50% 75% | 50% 86.7% Si 100% 80.0% G 50% 58.3% Si | % 0% 52% 33.3% 0% 0% 0% 0.0% % 25% 52% 41.7% % 0% 0% 0.0% % 0% 0% 0.0% | 0% 60% 0% 60% | 0% 0.0% 6 0% 20.0% 10 0% 0.0% | 7% 32% 50% 50.0% 0% 100% 100% 100.0% 0% 0% 0% 0.0% | 23% 23% 25% 30 0% 0% 0% 0 67% 50% 100% 72 | 7% 0% 22% 7% 0% 0% 7% 22% 52% | 25% 19.4% 0% 0.0% 0% 27.8% | 60% 40% 67% 0% 0% | 75% 58.3% 4 50% 0% 0.0% 10 | 0% 0% 0 0% 0 0% 100% 100 | 0% 35.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 20% S0 23% S0 0% 0 | 0.0% | 0.1757 0.1257 0.9919 | 0.0701 0.0578 | 0.4011 0.0198 0.5 | 932 0.4917 0 919 0.1994 0 | 12345 0.0195 | 0.1917 0.35 0.1757 0.12 0.19 | 257 C |
| chain C region 1 5V 3 protein MYG1, mitocho Myg1 | IGHA MOUSE 37 ki MYG1 MOUSE 43 ki | Da 200% 100% 100% | 100.0% 0% 0 | 5/5 ON 0.0% | 0% 0% | 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 50% 05.7% 0 100% 00.0% 0 50% 53.3% 0 100% 100.0% 0 100% 100.0% 0 | % 0% 0% 0.0% | ON ON | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 900.0% 0% 100% 100% 900.0% | 0% 0% 0% 0% 0. 0% 0% 0% 0% 0. | 7% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% | 78% 92% 100% 100% 1 | 75% 58.3% 6 50% 0% 0.0% 10 0% 30.6% 3 85% 81.4% 1 | 11% 9% 8° 0% 0% 0° | % 93% 11% % 9.0% 0% | 9% S 0% G | 0.0% 8.3% 9.3% 0.0% | 0.0112 | | 00/0 | 0.0112 | 0.002 | 0.01 | H2 |
| ding prolein 26 Rbm26 schwing factor acetyling Palahitbi | REMAS MOUSE 114 | CDs 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0.0% 100% 100 100.0% 0% 0 | 0% 100% 100.0% 0% 0% 0.0% 0% 100% 100.0% 0% 75% 91.7% 1% 50% 73.8% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 100% 100% | 0% 0.0% 100 100% 100.0% 0 | % 0% 100% 100.0% % 0% 0% 0% 0.0% % 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 0% 0% 0.0% 0% 100% 100% 90.0% | 100% 100% 100% 100. 0% 0% 0% 0. | 7% 0% 0% 7% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 1 | 100% 100.0% | 00 00 01 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0% 0 | 0.0% | | | | | | | # |
| sorral-associated profeir Snap29 sin TAR Tall | SNP29 MOUSE 30 K | De ON ON 25% De ON 29% 50% | | | | 0% 0.0% 0% 0.0% | 25N 0N 60N 50N | 25% 15.7% 25 100% 70.0% 40 | % SO% ON 30.0% | 0% 0% 0% 0% | 0% 0.0% 2 0% 0.0% 3 | 0% 20% 22% 24.4% 2% 50% 0% 27.8% | 80% 80% 67% 75. 67% 50% 100% 72. | 7% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% | 67% 67% 50% 32% | 20% 51.1% 3 50% 44.4% 5 | 23% 23% 80 20% 67% 50 | x 48.9% 0% x 55.6% 0% | 0% 0 0% 0 | 0.0% | 0.5185 0.2235 0.1061 0.3785 | 0.1850 0.9424 | 0.1442 0.5 0.2307 0.1 | 02235 0 061 0.3785 0 | 1.1850 0.1442 1.9424 0.2307 | | = |
| on initiation factor alE.21 EE252 Norman COVEA mitorion CopEs | EIZES MOUSE 39 KI COOSA MOUSE 72 KI | 0a 100% 100% 100% 0a 50% 60% 60% | 100.0% 0% 0 50.7% 50% 40 | 2% 0% 0.0% 2% 40% 43.2% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 75% 100% | 100% 100.0% 0 100% 91.7% 20 | % 0% 0% 0.0% % 0% 0% 8.3% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% | 0% 100% | 0% 0% | 9% | 0% | 100% 100% 1 | 100.0% | 0% 0% 0 | s 0.0% ox | 0% 0 | 0.0% | 0.0380 | | 0.0 | 080 | | | = |
| in-containing protein H light issuome non-ATPasse net Pamd4 | PSMD4 MOUSE 123 | Ga 100% 100% 100% | 100.0% 0% 0 | 2K 0K 0.0% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 | N ON ON 0.0% | 0% 0% | 0% 0.0% s | 98 100% 100% 95.3% 08 100% 100% 90.0% | 11% 0% 0% 3 0% 0% 0 | PS 0% 0% | 0% 0.0% | 100% 100% 1 | 100% 100.0% | 0% 0% 0° | s 0.0% 0% | 0% 0 | 0.0% | 0.4226 | 0.4225 | | 0.4226 0 | 1.4225 | | # |
| nent C1+B subcompone C1sb inary protein 2 Map2 AP recentor complex ms Gosr1 | CS18_MOUSE 77 ki MUP2_MOUSE 21 ki GOSR1_MOUSE 28 ki | De 100% 100% De 50% 40% 0% | 30.0% 0% 20 | 2% 0% 2% 60% 25.7% | 50% 40% | 0% 40% 43.2% | 295 225 | 100% 32% 31.7% 20 | 0 0 0 9.5% | 42% 62% | 0% 35.7% 67% 50.7% | 0% 100% 0% 100% 100% 100.0% | 0% 0% 0% 0 0% 0% 0% 0 | 2% 2% 2% 2% 20% 2% | 0% 0.0% 0% 0.0% | 100% 100% 100% | 100% 100% 100.0% | 0% 0% 0° | S 0.0% 0% | 0% 0 | 0.0% | 0.9197 | 0.7591 | 0.4 | 539 G | 12097 | 0.1823 | |
| somal protein L12 mito: Mrpi12 ded provinal Envirolismo 1 57 7 protein C14ort159 hom: 1 57 | RM12_MOUSE 22 ki ENV1_MOUSE 70 ki CN159_MOUSE 66 ki | Da 100% 100% 100% Da 100% 100% 100% | 100.0% 0% 0 | 26 0% 0.0% 26 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 200% 50% 200% 100% 200% | 100% 83.3% Si | 0% 0% % 0% 0% 15.7% % 0% | 0% 0% 0% 0% | 0% 0.0% F | ON 67% 75% 73.9% | 20% 23% 25% 25 | 1% 0% 0% | 0% 0.0% | 71% 67% 1 94% 100% 100% 100% | 100% 79.4% 3 56% 83.2% 100% 100.0% | 9% 22% 0° 9% 9% 21° 9% 9% 0° | 5 20.6% 0% 5 10.4% 6% 5 0.0% 0% | 0% 0 0% 13 | 0.0% 6.3% 0.0% | | | | | 0.1859 | | |
| ta-tryosin inhibitor heavi 19h2 persoline-5-carbosviste d Aldh-4s1 d colled-coil domain-cor Gcc1 | ITIHE MOUSE 106 I ALAA1 MOUSE 62 KI GCC1 MOUSE 88 KI | Cla 100% 100% 100% 100% 100% 100% 100% 100 | 100,0% 0% 0 0,0% 100% 100 | 20% 0% 0,0% 20% 100% 100,0% 20% 00% 0,0% 20% 0,0% 20% 2,0% 20% 0,0% 20% 0,0% 20 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 20% 15.0% 100.0% | 100% 100% 0% | 100% 100.0% 0 | N 0% 0% 0.0% N 100% | 0% 0% 0% | 0% 0.0% 10 0% | 75 885 805 74.95 05 1005 05 | 42% 12% 20% 25 0% 0% 100% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 1 | 100% 100.0% 100% 100.0% | 0% 0% 0 0% 0% 0 | S 0.0% 0% S 0.0% 0% | 0% 0 0% 0 | 0.0% | 0.1105 | | | 0.1106 | | | |
| insse II subunit alpha Cank2s1 sasome non-ATPase rec Pamd3 lein homolos, milochond D10Jhu81e | CSK21 MOUSE 45 ki PSMD8 MOUSE 40 ki ES1 MOUSE 28 ki | Da 100% 100% 100% Da 100% 100% 71% Da 100% 100% 100% | 100.0% 0% 0 90.5% 0% 0 100.0% 0% 0 | 20% ON 0.05% 20% 1000% 100.07% 20% ON 0.05% 20% ON 0.05% 20% ON 0.0% 20% ON 0.0% 20% ON 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% | 0% 200.0% 0 100% 930.0% 0 100% 930.0% 0 100% 930.0% 0 100% 77.8% 0 | % 0% 0% 0.0% % 0% 0% 0.0% % 0% 0% 0.0% % 0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 900.0% 0% 100% 100% 900.0% 0% 100% 100% 900.0% | ON ON ON O. ON ON ON O. | 7% 0% 0% 7% 0% 0% 7% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 80% 1 100% 100% 1 | 100% 93.3% 100% 100.0% | 0% 20% 0° 0% 0% 0° 0% 0% 0° | % 6.7% 0% % 0.0% 0% % 0.0% 0% | 0% 0 0% 0 | 0.0% | 0.4226 | 0.4226 | 0.4226 | 0.4226 0.225 0.5343 | 0.4226 | | - |
| bicuinone celdoreductes Mind4 vise band 7 intecral memi Stom imbrane protein 1 Golm1 | NUMM_MOUSE 52 KI STOM_MOUSE 31 KI GOLMI_MOUSE 44 KI | Da 100% 75% 80% Da 0% 0% 0% Da | 85.0% 0% 0 0.0% 0% 0 | 2% 0% 0.0% 3 | 0% 25% 100% 100% 1 | 30% 15.0% 100% 100.0% | 67% 67% 0% | 100% 77.8% 0 | % ON ON 0.0% | 22% 22% 100% | 0% 22.2% 10 | 0N 32N 50N 61.1% 25N 0N 0N 0.0% | 0% 0% 0% 0. 0% 0% 0% 50% 16. | 2% 0% 67% 75% P% 100% 100% | 50% 38.9% 100% 50% 83.3% | 67% 100% 1 50% 1 | 100% 88.9% 100% 67% 54.4% 3 | 0% 0% 07 0% 0 27% 39% 221 | % 0.0% 32% % 50% % 29.3% 27% | 0% 0 0 11% 11 | 10.3% | 0.6240 0.3089 0.1987 0.0127 | 0.5000 | 0.5185 | 0.5343 | | 0.6240 0.50 0.15 0.54 0.540 | 367 C |
| evin bets Dtrb fragile X mental retardati Nufip2 dwell GTDwar 1 homolog Lag1 | DTNE_MOUSE 74 ki NUFP2_MOUSE 76 ki LSG1_MOUSE 73 ki | Da 0% 0% 0% Da 0% 0% 0% | 0.0% 100% 100 0.0% 100% 100 | 2% 100% 100.0% 2% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 500 500 | % 0% % 100% 100% 100.0% % 100% | 100% 100% 0% 0% 0% 0% | 0% 0.0% | 0% 0% 0% 0.0% 0% 0% | 0% 100% 100% 100% 100 100% 100% | 7% 0% 0% 0% 0% | 0% 0.0% | 0% 0% 100% | 0% 0.0% 10 | 00% 500% 500° | s 100.0% os | 0% 0 | 0.0% | | | 0.5 | 200 | | 0.5000 | = |
| d protein 4B Larp4b makes over less selv Cops2 ption factor ETV5 EM5 | LARME MOUSE 82 KI CISN2 MOUSE 52 KI ETYS MOUSE 56 KI | Da 0% 0% 0% Da 100% 100% 100% Da 0% | 0.0% 100% 100 100.0% 0% 0 | 2% 100% 100.0% 2% 0% 0.0% 100% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 200 100% 100% 0% | 20% 100.0% 0 | 100% 100% % 0% 0% 0.0% | 0% 0% 0% | 0% 0.0% 10 | 0% 0% 0% 0.0% 0% 100% 100% 900.0% | 100% 100% 100% 100. 0% 0% 0% 0 100% 100% | 2% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 1 | 0% 0.0% 10 00% 100.0% 0% 0.0% 10 | 00% 100% 100 0% 0% 0 00% 100% 100 | 5 100.0% ON 5 0.0% ON 5 100.0% ON | 0% 0 0% 0 | 0.0% | | | | | | | = |
| se family protein SDRDD Sdr39u1 shosphatase 1 regulators Ppp1r7 ecapping enzyme 1A Dcp1a | DODUT MOUSE 33 KI PPTRZ MOUSE 41 KI DODYA MOUSE 65 KI | Da 0% 0% 0% Da 100% 89% 100% Da 0% 0% 0% 0% | 96.3% 0% 11 0.0% 100% 100 | 2% 100% 1% 0% 3.7% 2% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 50% 00.0% 0 0% 0.0% 100.0% | % 50% 00 0.0% % 0% 0% 0.0% % 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% | 0% 100% 100% 900.0% 0% 0% 0% 0.0% | ON ON ON O. | 7% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 1 | 00% 100.0% 0% 0.0% 10 | 0% 0% 0 0% 0% 0 0% 100% 100 | S 0.0% 0% S 100.0% 0% | 0% 0 0% 0 | 0.0% | 0.4226 | 0.4225 | 0.5000 0.4 | 048 026 (| 0.5000 | | # |
| nonophosphatase 1 Impa1 cyl-amino acid synthase Pm25d1 hatidylinositol 4.5-bisoho Picb3 | IMPA1_MOUSE 30 K P2001_MOUSE 56 K PLCB3_MOUSE 139 | Date ON | 100.0% 0% 0 97.2% 8% 0 | 2% 0% 0.0% 2% 0% 2.8% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 100% 100.0% 0 | S 05 05 0.05 S 05 05 0.05 | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 50 100 100 5.75 100 100 100 100 100 100 100 100 100 10 | 0% 0% 0% 0 0% 0% 0% 0 0% | 7% 9% 9% 7% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% : | 100.0% | 0% 0% 0 0% 0% | s 0.0% 08 | 0% 0 | | 0.4226 | 0.4225 | 0.4 | 026 0 | 14226 | | |
| envarogensse lubiquinor Ndufb6 protein localization protei Nploc4 I O-methyltransferase do Comtd1 | NPL4 MOUSE 68 KI CMTD1 MOUSE 29 KI | 28 100% 100% 67% Da 0% 20% 32% Da 100% 100% 75% | 86.9% 0% 0 17.8% 100% 80 91.7% 0% 0 | 25 | 9% 9% 9% 9% | 42% 11.1% 0% 0.0% 0% 0.0% | 100% 100% 0% 25% 75% 50% | 100% 41.7% 100 100% 75.0% | N 0% 0% 0.0% N 50% 0% 50.0% N 0% 0% 0.0 | 0% 25% 25% 50% | 0% 0.0% 10 0% 0.3% 6 0% 25.0% | 905 676 500 50.0% 005 1005 1000 66.7% | 20% 0% 25% 15. 50% 0% 0% 16. | 75 20% 32% PS 50% 0% | 25% 26.1% 0% 96.7% | 0% 32% 1 50% 42% | 00% 51.7% 50% 47.6% | 9% 67% 0 9% 48% 25 | 100% 5 22.2% 50% 5 22.6% 50% | 0% 0 14% 25 | 16.7% | 0.5162 0.9230 0.3868 0.6257 | 0.0332 | 0.6228 0.3 0.1956 0.4 | 832 0.7835 6 026 0.7900 0 647 0.6354 0 | 1,0054 0.4908 1,6856 0.2104 | 0.4226 0.63 0.2254 0.54 | .317 G |
| hase subunit delta, milo AlpSd mplex subunit mu-1 ApEm1 | ATPO MOUSE 18 KI APIMI MOUSE 49 KI | 20 50% 0% 20 82% 75% 82% 20 80% | 80.6% 17% 20 | 25 17% 19.4% 25 | 95 95 205 | 0% 0.0% | 88% R2% | 75% 80.8% 17 100% 0% 100% 97.0% 0 | N 20% 25% 19.2% 0% | os os | 0% 0.0% 10 0% 200% 0% 3.0% 10 | 20 425 05 19.4% 05 715 676 79.4% 55 505 05 41.7% | 0% 0% 0% 0 0% 29% 22% 20 0% 0% 0% 0 | 75 75% 67% 7% 0% 0% 7% 25% 50% | 0% 0.0% 0% 0.0% 100% 58.3% | 0% S0% 67% 67% 0% | 865 73.0% a 505 | 20 20 24 20 20 24 | 0.0% 200% 27.0% 0% | 50% 23 0% 0 100% 50 | 0.0% | 0.9547 0.6354 0.6588 | 0.9210 | 0.3595 0.5 | 647 0.6354 0 | 19210 0.3595 | 0.45 | |
| cholesterol ester hydrolas Noeh1 anaformino growth factor Libp1 | 200 MAN 190 MA | Da 88% 100% 100% CDs | 95.8% (% C | N 0% 0.0% | 12% 0% | 0% 4.2% | 100% 92% | 100% 97.0% 0 | N 0% 0% 0.0% | ON 9% | 0% 3.0% 10 | 88 1009 1000 1000 1000 1000 1000 1000 10 | 0% 0% 0% 0 0% 0% 0% 0 | 7% 0% 0% | 0% 0.0% | 100% 0% | 100% 100° W | 0% 00% 00% | % 05% 20% | 0% 0% | 0.00 | 0.8372 | 0.4226 | 0.4225 | | | 0.8372 | |
| recnine-crolein phosphs Ppp1cb e synthetase Gad | PP1B MOUSE 37 K | Da 100% 100% 100% Da 100% 100% 100% | 100.0% 0% 0 | 20% | 0% 0% 0% | 0% 0.0% | 100% 100% | 100% 100.0% 0 | N 0% 0% 0.0% N 0% 0% 11.1% | 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% 0% 100% 100% 100.0% | ON ON ON O. ON ON ON O. | 7% 0% 0% 7% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 92% 1 | 100% 100.0% 100% 97.4% | 0% 0% 07 0% 8% 07 | % 0.0% 0% % 2.6% 0% | 0% 0 0% 0 | 0.0% | 0.4226 | 0310* | 07525 07 | 0.4226 0765 0.3373 0 | 3105 0.75× | | = |
| O-colinitovitransferase Cpt1s strume A thioesterase 9. Acot9 | CPTIA MOUSE 88 KI ACOTS MOUSE 51 KI | Da 100% 100% 100% | 100.0% 0% 0 | 0% 0% 44.4% 0% 0% 0% 0% 0% 0% 0.0% 0.0% | 0% 0% | 0% 0.0% | 100% 100% | 00 000 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0% 0% | 20 20 20 | 0% 67% 0% 55.6% 0% 100% 100% 100.0% | ON ON ON O. | 9% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 100% 44.4% 0% 0.0% | 98% SON 100% 100% 1 | 71% 69.6% 100% 100.0% | 0% 0% 07 0% 0% 07 | N 0.0% 12% N 0.0% 0% | 50% 29 0% 0 | 30.4% | | | | | | 0.68 | 886 |
| h regulator Aven Aven serior variante housel no Grb2 dutamid hidrolase Grb | 97071. JOSEPH 1990. 1990 | De 0% 20% 0% De 100% 100% | | | | 0% 0.0% | 0% 0% 100% 40°* | 0% 0.0% 100 0% 0.0% 100 100% 100.0% 0 | N DN DN DDS | 0% 0% 0% 0% | 0% 0.0% 6 0% 0.0% 10 | 0% 100% 100% 000.0% 05 05 05 05 05 05 0.0% 0.0% 0 | 100% 100% 100% 100 38% 57% 42% 45 0% 0% 0% 0 | 75 95 95 75 95 95 | 0% 0.0% 0% 0.0% | 75% 58% 100% | 72% 00.0% 100% 100.0% 0% 0.0% 16 88% 73.0% 3 100% 100.0% | 5N 42N 12 | S 25.4% 0% | 0% 0 | 0.0% | 0.4226 | 0.4225 | 0.4 | 0.1339 | 14226 | | = |
| osto-1 Gira hype I cuticular Hart Kri21 ordical import parameters and Townstill | GLEXT MOUSE 12 KI KIHI MOUSE 47 KI TOMO MOUSE 30 KI | De 100% 100% De 0% 100% | 9% 0 9% 0 | 0% 2% 100% 23.7% | 0% 200% 0% | 0% 0.0% | 100% | 100% | 0% 0% | 9% | 0% 16 | 0N 100N 100N 100.0% | 0% 0% 0% 0 0% 0% 00 20 | 7% 9% 9% 9% 9% 50% 90% | 0% 0.0% 63% 70.8% | 100% 100% 3 | 00 0.0% | 0% 0% 0° | S 0.0% 0N | 0% 0 60% 100 | 0.0% | 0.4226 0.4226 | 0.7693 | 94 | 026 03373 6 | 10253 0.0051 | 0.27 | 2710 |
| maccialed membrane or Vapb shydrosenase lubiculnor Ndufa7 | VAPE MOUSE 27 KI NDUAT MOUSE 13 KI DRIVE MOUSE 10 KI | 20 08 208 08 208 08 208 208 208 208 208 | 77.8% 9% 0 50% 0 | 2% 0% 0.0% 2% | 17% 22% 0% 0% | 17% 22.2% | 100% 100% 22% 22% | 100% 100.0% 0 100% 55.6% 63 | N 0% 0% 0.0% N 67% 0% 44.4% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 3 | | 0% 0% 0% 0 67% 100% 0% 55 | 25 25 25 25 25 25 25 25 25 25 25 25 25 2 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 50% | 00% 100.0% 0% | 0% 0% 0 50% 100 | S 0.0% 0N | 0% 0 0% 0 | 0.0% | 0.0572 0.6102 0.6501 | 0.0572 | 0.4420 0.6 | 0.3373 6 1102 0.6501 0 | 1.4881 0.4420 | 0.0572 | - |
| ed olicomeric Goldi com: Cog5 led GTP-bindino protein: Rhog se membrane protein 2 Scarb2 | COGS MOUSE 91 KI RHOG MOUSE 21 KI SCREZ MOUSE 54 KI | Da 50% 100% CDa 0% Da 0% 0% 0% Da 100% 100% 100% | 400.0W 0W 0 | W 00 0.00 | ON ON | 50% 83.3% 0% 0.0% | 0% 0% 100% 100% | 100% 100.0% | S 05 05 0.05 | 100% 100% 0% 0% | 05 0.0% 8 | 8N 100N 100N 95.8N 0N 100N 67N 88.9N | 0% 0% 0% 0 0% 0% 0% 0 | 75 128 08 75 08 08 | 0% 4.2% 22% 11.1% | 50% 100% 100% 1 100% 83% 88% 75% | 95 100.0% 1005 100.0% 88% 90.7% 90% 94.2% | 0% 17% 0° 0% 0% 0° | N 0.0% 0% N 0.0% 0% N 5.6% 0% N 0.0% 12% | 0% 13 25% 10 | 0.0% 4.2% | 0.4433 0.7240 | 0.4225 | 0.1917 | 0.4225 0.4225 0.4225 | 0.4226 | 0.4226 1.00 0.72 | 0000 0 7240 |
| dein homolog 1, mitocho Grpel1 ime subunit beta type-7 Pamb7 conjugation factor E4 A Ube-fa | GRPE1 MOUSE 24 KI PSB7 MOUSE 30 KI UBE4A MOUSE 118 | Da 100% 100% 100% Da 100% 100% 100% CDa 100% 100% 100% | 100.0% 9% 0 100.0% 9% 0 100.0% 9% 0 100.0% 9% 0 | 26 0% 0.0% 26 0% 0.0% 26 0% 0.0% 26 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% C | N 0% 0% 0.0% 0% 0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 10 | 00 100% 67% 88.9% 00 100% 50% 83.3% 00 100% 100% 900.0% | 0% 0% 50% 15. 0% 0% 0% 0 | PS 98 98 25 98 98 | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 | 100% 100.0% 100% 100.0% | 0% 0% 0 0% 0% 0 | S 0.0% 0% S 0.0% 0% | 0% 0 0% 0 | 0.0% | 0.4226 | 0.4225 | | 0.4225 | 14226 | | |
| c purine 5'-nucleotidase N5C2 soulated transcription co: Crtc3 s-2A chain C region, ms (gh-1a | SNEC MOUSE 65 KI CRECS MOUSE 67 KI GCAM MOUSE 44 KI | Da 100% 100% 100% Da 100% 100% | 100.0% 0% 0 | 2% 0% 0.0% 2% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% | 100% 100.0% | % 0% 0% 0.0% | 0% 0% | 0% 0.0% 10 | 0N 100N 100N 900.0% 0N 0N 0N 0.0% 0N 100N 100N 900.0% | 0% 0% 0% 0 100% 100% 100% 100 0% 0% 0% 0 | 7% 0% 0% 7% 0% 0% 7% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 1 | 0% 10 100% 100.0% | 0% 100 0% 0% 0 | 0% % 0.0% 0% | 0% 0 | 0.0% | | | | | | | + |
| te-rich protein 5 Erich5 a-alucan-branchino enza Gbe 1 beta-2 ligb2 | ERICS MOUSE 39 KI GLGB MOUSE 80 KI ITEZ MOUSE 85 KI | Da 100% 100% 100% Da 100% | 100.0% 0% 0 | 2% 0% 0.0% 0% 0% | 0% 0% | 0% 0.0% 0% | 100% 100% | 100% 100.0% | % 0% 0% 0.0% % 0% 0% 0.0% | 0% 0% | 0% 0.0% 50 | 100% 100% 0% 100% 100% 900.0% | 0% 0% 0% 0% 0% 0 | 9% 9% 9% | 0% 0.0% | 100% 100% 100% 100% 1 | 100% 100.0% | 0% 0% 0% 0% 0 | 0 0% 0 00% 0% | 0% 0 | 0.0% | | | | | | | - |
| family homolog 3 Fermi3 southolissierol 7-abha-hs Cyp3lis1 oin-related transmembra Tms2 | CP39A_MOUSE 54 ki TMX2_MOUSE 34 ki | Da 100% 100% | 100.0% 0% 0 16.7% 0% 0 | 2% 2% 0.0% 0.0% 2 | 0% 0% 0% 0% 00% 50% 1 | 0% 0.0% 100% 83.3% | 100% 100% 33% 50% | 100% 100.0% 0 100% 61.1% 0 | % 0% 0% 0.0% % 0% 0% 0.0% | 0% 0% 67% 50% | 0% 0.0% 0% 38.9% | 0% 100% 100% 100.0% 0% 0% | 0% 0% 0% 0. 0% 0% | 2% 0% 0% 100% | 100% | 0% 0% | 100N 100.0% | 0% 0% 0° | % 0.0% 0% 100% | 200% | 0.0% | 0.1656 | 0.4225 | 0.0927 | | | 0.1656 | - |
| eranerosaai'arviasterasa Pgg2 olit-2 Dac2 ad olinometric Gold come Cog2 | PONZ MOUSE 40 M DSC2 MOUSE 100 COG2 MOUSE 82 M | Da 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0.0% 0% 0 0.0% 0% 0 0.0% 0% 0 93.3% 0% 0 90.7% 11% 0 | 2N 0% 0.0% 1 2N 0% 0.0% 1 2N 50% 16.7% 1 2N 0% 0.0% | 200% 200% 1 200% 200% 1 | 20% 100.0% 50% 83.2% 0% 5.7% 0% 0.0% | 0% 0% | 0% | 0% 0% 0% 0.0% % 0% 0% 0.0% | | 2005 05 4.25 10 05 0.05 10 | 2N 22N 25N 30.6N 6N 6N | 0% 17% 0% 5 0% 0% | 2% 62% 52% 200% | 75% 63.9% 100% | 22% 25% 0% 22% | 50% 36.1% 20% 17.8% | 0% 0% 0 0% 22% 80 | S 0.0% 67% S 37.8% 100% | 75% 50 23% 0 | 63.9% | 0.5384 | 0.4225 | 0.4 | 0.4226 0 0.2450 0.26 | 1.5365 | 0.4226 0.6525 | 0000 0 1204 |
| ore subunit beta type-5 Perib5 oreal protein of 135 kDs Cep135 | 538A3 MOUSE 56 KI P585 MOUSE 29 KI CP135 MOUSE 133 | Da 89% 91% 100% Da 89% 100% 83% EDa | 93.7% 0% 0 90.7% 11% 0 | 25 05 0.0% 25 175 9.2% | 0% 0% | 0% 6.7% 0% 0.0% | 98% 100% 100% 100% | 100% 95.8% 0 100% 100.0% 0 | % 0% 0% 0.0% % 0% 0% 0.0% | 13% 0% 0% 0% | 05 4.2% 10 05 0.0% 10 | 0% 100% 100% 100.0% | 0% 0% 0% 0 | 2% 2% 2% | 0% 0.0% | 100% 100% 1 | 100% 100.0% | 0% 0% 0 0% | s 0.0% 0% | 0% 0 | 0.0% | 0.1294 | 0.1876 | 0.1 | 994 6 | 11994 | 0.6995 | - |
| rmal membrane-associal Simap ally androsen-reculated Sang portibonucleotidase, cvb NSc | SIMAP_MOUSE 97 K SARG_MOUSE 65 K NTSC_MOUSE 23 K | Da 0% Da Da 100% 100% 100% | 100% | 26 06 0.0% 26 06 0.0% | 0% 0% | 0% 0.0% | 100% 100% | 100% 100.0% | s os os 0.0% | on on | 0% 0.0% 10 | 0% 0% 0% 100% 100% 100.0% | 93% 100% 0% 0% 0% 0 | 2% 0% 0% | 0% 0.0% | 50% 0% 100% 100% : | 0% 16.7% S 100% 100.0% | 85% 60% 100% 100° 0% 0% 0° | s 83.3% os s 9.0% os | 15% 0% 0 0% 0 | 0.0% | | | | | | | _ |
| r protein sorting-associal Vps29 onate 5-liposygenase Alos5 num cofactor biosynthes Mocs1 | VPS29_MOUSE 20.6 LOKS_MOUSE 78.6 MOCS1_MOUSE 70.6 | De 100% 100% 100% De 100% 100% | 100.0% 0% 0 | 26 06 0.0% | ox ox | 0% 0.0% | 100% 100% | 100% 100.0% | s os os 0.0% | 0% 0% | 0% 0.0% 10 | 0% 100% 100% 900.0% 0% | 0% 0% 0% 0 0% | 2% 0% 0% 0% | 0% 0.0% | 100% 100% 100% 89% | 00 10.75 100.05 | 0% 0% 0 0% 0% 0 | S 0.0% 0% S 0.0% 0% | 0% 0 11% 0 | 3.7% | | | | | | | - |
| of 90 kDs heat shock o Ahsart nolog (st) | ArSAI_MOUSE 30 K | Da 90% 100% 50% Da 0% 20% 30% | 75.7% 20% 0 15.7% 100% 80 | 26 50% 23.2% 26 70% 83.2% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 67% 100% 0% 40% | 50% 72.2% 33 100% 45.7% 100 | N 0% 50% 27.8% N 60% 0% 53.3% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 60% 67% 75.0% 0% 100% 50% 83.2% | 0% 20% 32% 17. 0% 0% 50% 16. | 75 05 05 75 05 205 75 05 05 | 0% 6.7% 0% 0.0% | 100% 100% 100% 100% | 100 100 0% 100% 100 0% | 0% 0% 0 0% 0% 0 | S 0.0% 0% | 0% 0 0% 0 | 0.0% | 0.8403 0.1869 0.4132 0.4226 | 0.9564 | 0.1994 0.8 0.2079 0.4 | H03 0.2079 0 H32 0.4226 0 | 1.7585 0.1994 1.0377 0.2079 | 0.42 | 4226 0 |
| Scation licensing factor Morn5 -1.5-bischoschatase iso Fbp2 | MCM5_MOUSE 82 ki F16P2_MOUSE 37 ki | Da 100% 100% | 100.0% 0% 0 | 2% 2% 2% 0.0% | 0% 0% 0% | 0% 0.0% | 100% 100% | 100% 100.0% | N ON ON 0.0% | 0% 0% | 0% 0.0% 10 | 0% 100% 100% 900.0% 0% 100% 100% 900.0% | 0% 0% 0% 0 0% 0% 0% 0 | 7% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 | 100 100.0% | 0% 0% 0 0% 0% 0 | N 0.0% 0% N 0.0% 0% N 0.0% 0% N 0.0% 0% | 0% 0 | 0.0% | | | | | | | = |
| dng cassets sub-family Abcatla storal represent 65-be GataSb | ABCBA MOUSE 1841 PRISS MOUSE 65 K | Oa 100% 100% 100% Da 100% 100% 100% | 100.0% 0% 0 | 76 ON GOS | OK OK | 00 0.0% | 100% 100% 0% | 100% 100.0% | 500% 0% 0.0% | 0% | OK 0.0% 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% 0% 0% 0.0% | 0% 0% 0% 0. 100% 100% 100% 100 | 7% 0% 0% 2% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% | 100.0% | 0% 0% 0 00 100% | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0% 0 | 0.0% | | | | | | | # |
| stion initation factor TFI Taffib icin-like protein 1 Hycall lease I EC154 Hycall | TAFSE MOUSE 27 KI HPCL1 MOUSE 22 KI | Da 100% 100% 100% | 100.0% 0% 0 | | 0% 0% 0% 0% | | 0% 100% 100% 100% 100% | 100% 100.0% 0 | % ON ON 0.0% | 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 000 1000 1000 1000 00 000 00 1000 1000 | 100% 100% 100% 100. 0% 0% 0% 0. | 7% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 | 100% 100.0% | 0% 0% 0 | % 0.0% 0% | 0% G | | | | | | | | = |
| abfamily Amember 1 Golga1 | GOGAL MOUSE 87 KI | Da 0% 0% 0% | 0.0% 100% 100 | 28 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0% | 0% 0.0% 100 | N 100% 100% 100.0% | 0% 0% | 0% 0.0% 25 | 0% 100% 100% 100.0% | 0% 0% 0% 0 | 2% 0% 0% | 0% 0.0% | 100% 100% | 100 100 0% | 0% 0% 0° | s 0.0% ox | 0% 0 | 0.0% | 0.0195 | | | | | 0.01 | 100 |
| asbin-2 Ron2 factor NF-kacca-B c/05 NRb1 onlucating enzyme UBC Ube2i | TMF2 MOUSE 508 50 50 50 50 50 50 50 50 50 50 50 50 50 | On | 100% | 200% 2% | 0% | 0% 0% | 0% 0% 100% | 0% 0.0% 100 100% | N 200 200 100.0% | ON ON | 0% 0.0% 6 0% 3 | 2% 42% 62% 58.7% 0% 0% 25% 8.2% 2% 100% 100% 94.4% | 22% 57% 22% 41, 100% 100% 75% 91, 17% 0% 0% * | 7% 9% 9% 7% 9% 9% 2% 9% 9% | 0% 0.0% 0% 0.0% | 60% 67% 32% 25% 100% 80% | 0% 42.2% 4 50% 36.1% 3 00% 93.3% | 0% 22% 100 12% 75% 50 0% 20% 7 | S 57.8% ON S 52.8% 33% S 6.7% ON | 0% 0 0% 0 | 0.0% 11.1% 0.0% | 0.5270 0.0677 0.9045 | 0.0178 | 0.1846 | 0.5270 0.0648 0.9045 | 0.1546 | 0.42 | 1226 |
| in, mitochondrial Nin arin p58/p45 Nup58 multivesicular body orol Chep3 | NEUL MOUSE 80 H NUPSE MOUSE 50 H CHMP3 MOUSE 25 H | 0s 0s 0s 0s 0s 0s 0s 0s | 0.0% 100% 100 0.0% 100% 67 | 2% 100% 100.0% 7% 100% 88.9% | 0% 0% 0% 22% | 0% 0.0% 0% 11.1% | 200% 0% 0% 0% 0% | 100% 100% 100 0% 0.0% 50 | 0% 0% % 100% % 100% 100% 83.3% | 0% 0% 50% 0% | 0% 16.7% | 0% 0% 25% 0.2% 2% 100% 100% 94.4% 0% 100% 00 0.0% 100% | 0% 0% 0% 100% 100% 100% 100% 100% 100% | 9% 9% 9% 9% 9% 9% | 0% 17% 5.6% | 100% 100% 1 0% 0% 100% | 00% 100.0% 0% 0.0% 10 | 0% 0% 0 0% 100% 100° | 5 0.0% 0% 5 100.0% 0% | 0% 0 0% 0 | 0.0% | | | 0.3 | 0.4225 C | 14225 | 0.7972 | 4226 0 |
| attachment factor B2 Safb2 asylation factor S ArtS se C-2 Lys2 | SAFEZ MOUSE 112 APPS MOUSE 21 M LYZZ MOUSE 17 M | Ca 0% 100% 100% 100% | 100.0% 0% 0 | os 00% | 0% 0% 0% | 0N 0.0% | 100% 100% | 0% 100% 100.0% (| N 0% 0% 0.0% | on on | 0% 0.0% 10 | 0% 100% 100% 100.0% 0% 60% 67% 75.5% | 0% 0% 0% 0 0% 40% 32% 24 | 9% 9% 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 1 | 100% 100.0% | 0% 100% 0% 0% 0 0% 0% | N 9.0% 0% 0% | 0% 0% 0 | 0.0% | 0.1869 | | | 0.1869 | | | Ξ |
| tic translation initiation fo Eliffax n phosphorylase, liver fo Pygl carbon/-terminal hydro Famtilla | IF1AX MOUSE 16 M PYGL MOUSE 97 M FA63A MOUSE 51 M | Da 100% 100% 100% Da 100% | 100.0% 0% 0 | 2% 0% 0.0% 2% | 0% 0% | 0% 0.0% | 100% 100% 100% | 100% 100.0% c | N 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | | 0% 0% 0% 0 0% 0% 0% 0 | 75 95 95 75 95 95 | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0 0% 0% 0 0% 0% 0 | S 0.0% 0% S 0.0% 0% S 0.0% 0% | 0% 0 0% 0 | 0.0% | | | | | | | |
| ipose A2 Plu2g1b eductase-related protein Akr1bil esin Siglec1 | POR ADDRESS | Da 100% 100% 100% Da CDa | 100.0% 0% 0 | 2N 0N 0.0% | 0% 0% | 06 0.0% | 100% 100% | 100% 100.0% 0 | N 0% 0% 0.0% | | 0% 0.0% 20 0% 0.0% 20 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% 0% 100% 100% 100.0% 0% 100% 100% 100.0% 0% 100% 100% 100.0% | 0% 0% 0% 0 0% 0% 0% 0 | 7% 0% 0% 7% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 | 100% 100.0% 100% 100.0% | 0% 0% 0 0% 0% 0 | s 0.0% 0% s 0.0% 0% | 0% 0 0% 0 | 0.0% | | | | | | | |
| 7 protein KIAA 1324 Kiss 1324 slog 3 protein SIC3 orold cis-trans isomeras (Robp9 | K1324 MOUSE 1111 SUT3 MOUSE 168 I FKEP9 MOUSE 63 K | Cm 100% 100% 100% Cm Da | 100.0% 0% 0 | 2% 0% 0.0% | 0% 0% | 0% 0.0% | 100% 100% | 100% 100.0% C | N 0% 0% 0.0% | 0% 0% | 0% 0.0% 10 10 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% 0% 100% 100% 100.0% | ON ON ON O. ON ON ON O. ON ON ON O. | 7% 0% 0% 2% 0% 0% 2% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% | 100% | 0% 0% 07 07 | 0% % 0% | | | | | | | | | |
| aductase-related creates Archible select Signed Sig | APEAT MOUSE 35 KI SPAIN MOUSE 47 KI FASSE MOUSE 45 KI | 26 26 26 26 26 26 26 26 26 26 26 26 26 2 | 0.0% 100% 80 | 2N 100N 93.3% | 0% 20% | 0% 6.7% | ON ON | 0% 0.0% 500 | % 100% 100% 100.0% | 0% 0% | 0% 0.0% 3 | 0% 100% 100% 100.0% 0% 100% 100% 100% 500.0% 2% 25% 0% 19.4% | UN 0% 0% 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. | 7% 0% 0% 7% 0% 0% 9% 17% 25% | 0% 0.0% 0% 0.0% 22% 25.0% | 100% 100% 1 | 20% 20.6% 6 | 0% 0% 0 57% 75% 80 50% 60% 40 | s 73.9% 0% | 0% 0 | 5.6% | 0.9230 | 0.1917 | 0.0136 0.4 | 226 0.0007 6 0.9126 0 | 0.0215 | 0.4226 0.05 | .554 0 |
| syncerificia Acidia SGT1 homolog Sugiti Lilian 130 kTin revision en Opp1 | SGT1 MOUSE 38 K | De ON | 69.4% 25% 0 | 2% 0% 2% 67% 30.6% | | 0% 0% 0.0% | 100% 100% 25% 67% | 100% 100.0% (100% 53.9% 2 | N 0N 0N 0.05 N 30N 0N 36.1% | 0% 0% 0% 0% | 0% 0.0% 3 0% 0.0% 3 0% 0.0% 10 0% 0.0% 10 0% 0.0% 10 | 08 1008 1008 50.0% 08 1008 08 33.2% | 0% 0% 0% 0 100% 0% 100% 05 100% 0% 100% 05 | 7% 9% 9% 7% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 1 0% 50% 1 | 00% 100.0% 100% 50.0% 10 | 9% 9% 00 0% 50% 0 | x 41.7% 0% x 0.0% 0% x 50.0% 0% | 0% 0 0% 0 | 0.0% | 0.8582 0.7250 | 0.4141 | 0.7215 0.8 | | 1.8980 1.4141 0.7215 | 0.86 | auf (|
| s. control of a section Pyc2 s. control of a section Lamp2 I solicing regulatory grob Exp1 | SOTT MOURE 384 (CREAT MOURE) 484 (CREAT MOURE) 4 | a 67% 63% 67% ba 100% 100% 100% ba 0% 0% 0% 0% | 100.0% 20% 20 100.0% 0% 0 0.0% 100% 100 | ES 23% 34.7% 2% 0% 0.0% 2% 100% 100.0% | 9% 9% 9% 9% 9% 9% | 0% 0.0% 0% 0.0% 0% 0.0% | 86N 78N 100N 100N | 75% 79.5% St 100% 100.0% C | n 22% 25% 20.5% N 0% 0% 0.00% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 500.0% 0% 100% 89% 95.2% | 0% 0% 0% 0 0% 0% 0% 0 | 75 95 95 75 95 95 | 0% 0.0% 11% 3.7% 0% | 0% 0% | 00% 93.7% | 9% 9% 0 9% 9% | N 0.0% 20% 20% | 0% 0 100% | 67% | 0.0322 | 0.4225 | 0.4225 | | | 0.72 | 7226 0 |
| cificity misoen-activates Map2k1 officity misoen-activates Map2k1 officin elementary factor A. Town1 | MP2K1 MOUSE 43 KI TCEA1 MOUSE 34 KI | 0% 0% 0% 0s 100% 100% 50% 0s 100% 100% 100% | 83.3% 0% 0 100.0% 0% 0 | 20 50% 15.7% 20 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 100% 100.0% 0 | N 0N 0N 0.0% N 0N 0N 0.0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% | 0% 0% 0% 0 0% 0% 0% 0 | 75 05 05 75 05 05 | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% 100% 100% | 100 100 0% 100 100 0% | 0% 0% 0° 0% 0% 0° | s 0.0% 0% 8 0.0% 0% | 0% 0 0% 0 | 0.0% | 0.4226 | 0.4225 | 0.4 | 225 0 | 14225 | | = |
| cose 1-chosohate unidu Ugp2 sperone MESO Mesdc2 | UGPA MOUSE 57 KI MESO MOUSE 25 KI | De 100% 100% 100% De 100% | 100.0% 0% 0 | 2% 0% 0.0% 2% | 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 100% 100.0% 0 | N 0% 0% 0.0% N 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% | 0% 0% 0% 0 0% 0% 0% 0 | 75 95 95 95 95 95 | | | 100 00 100 00 100 00 100 100 100 100 10 | 0% 0% 0 0% 0 | S 0.0% 0% | 0% G | 0.0% | | | | | | | # |
| thorail F and placeatin d. Faru2 Lad1 wat- and acid-stable sh; Pring1 of cylonol factor 1 Not1 a protein 1 Seu 13 shoglycarale mutase Bogm sled transcription factor (Russ) | LAD1 MOUSE 59 H HAP2E MOUSE 21 H | De 100% 100% 100% | 100.0% on o | os 0.0% | 0% 0% | 0% 0.0% | 100% 100% | 100% 100.0% | N 0N 0N 0.0% | 0% 0% | 0% 0.0% 10 | 0% 0% 000.005 0% 100% 100% 900.005 0% 100% 100% 900.005 0% 100% 100% 900.005 0% 0% 0% 0.005 | 100% 100% 0% 0% 0% 0 | 75 05 05 | 0% 0.0% 0% 0.0% 0% 0% 0.0% 0% 0.0% | 100% 100% 1 | 100% 100% 100.0% | 0% 0% 0° | S 02% 0% | 0% G | 0.0% | | | | | | | # |
| a protein 1 Snu13 phoglycerate mutuse Epgm sted transcription factor Every | NIGL I MOUSE 14 KI PMGE MOUSE 30 KI RUNKI MOUSE | De 100% 100% 100% De 100% 100% 100% | 100.0% 0% 0 100.0% 0% 0 | 2% 0% 0.0% 2% 0% 0.0% | on on | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 100% 100.0% 0 | N 0% 0% 0.0% N 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% | 0% 0% 0% 0 0% 0% 0% 0 100% 100% 100% | 9% 9% 9% 7% 9% 9% 9% 7% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0 0% 0% 0 | S 0.0% 0% S 0.0% 0% | 0% 0 0% 0 | 0.0% | | | | | | | = |
| shouthabase 1 regulators Ppp1r14a er protein 598 Zh1598 ed oligomeric Gold rows Conf. | PP14A MOUSE 17 M ZNESS MOUSE 99 M COGE MOUSE | Da ON ON ON | 0.0% Son 83 0.0% AN ** | 2% 100% 77.8% 2% 75% 38.9% | 50% 17% 100% 60% | 0% 22.2% 25% 81.79 | ON ON | 0% 0.0% 500 0% 0.0% | % 86% 67% 84.1% % 32% 32% 27.7% | 0% 14% 100% 47% | 22% 15.9% 67% 77.8% | 0% 0% 0% 0.0% | 100% 100% | ON ON | ON ON | 100% | | ON DO | | 0% | | | | 0.5 | 750 0 | 2697 | 0.7390 | - |
| -ike modifier-activating - Uba5 slatase, milochondrial Fech se protein Kawrish | UBAS MOUSE 118 HEMH MOUSE 47 KB | Cis 100% 100% 100% 100% 100% 100% 100% 100 | 100.0% 0% 0 | 2% 0% 0.0% 2% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% C | 0% 0% 0% 0.0% % 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% | 0% 0% 0% 0 0% 0% 0% 0 | 7% 0% 0% 7% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 | 100% 100.0% 100% 100.0% | 0% 0% 07 0% 0% 0 | % 0.0% 0% % 0.0% 0% | 0% 0 0% 0 | 0.0% | | | | | - | | # |
| cyte cytosolic protein 2 Lcp2 chain C region 1 5/ | ICP2 MOUSE 50 M | Da 100% | 100.0% | 26 06 0.0% | 0% 0% | 0% 0.0* | 100% 100% 100% 100% | 100% 100.0% C | N 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% s | 0% 50% 0% 16.7% 5% 100% 100% 94.9% 0% 100% 100% 900.0° | 100% 50% 100% 83. 15% 0% 0% 5 0% 0% 0% ^ | 7% 0% 0% 1% 0% 0% | 0% 0.0% 0% 0.0% | 100% 0% 100% 85% | 82% 89.2% 100% 100.0% | 0% 100% 0% 15% 17 0% 0% | 5 10.7% ON | 0% 0 0% 0 | 0.0% | 0.6244 0.4954 | | 0.1842 | 0.6344 0.4954 | 0.1542 | | = |
| C.Flate? diflamed.Fini Echil debutrosesse B. rhair Ldbb choschate cylidylybynal Drutty | ECHI MOUSE 35 KI LOHB MOUSE 37 KI POYIA MOUSE 37 KI | Da 100% 100% 100% | 100.0% 0% 0 | 26 05 9.0% | os os | 0% 0.0% | 100% 100% 0% | 100% 100.0% | S 05 05 0.05 | 0% 0% 0% | 0% 0.0% 10 | 0% 100% 100% 100.0% 0% 100% 100% 100.0% | 0% 0% 0% 0 0% 0% 0% 0 100% 100% 100% | 2% 2% 2% 2% 2% 2% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0 0% 0% 0 | S 0.0% 0% S 0.0% 0% | 0% 0 0% 0 | 0.0% | 0.4224 | | | 0.4225 | | | = |
| i a half LIM domains ono PhQ eductore STEAP3 Steep3 professe 2 Mcot2 | FHL2 MOUSE 32 M STEA3 MOUSE 55 M MCPT2 MOUSE 77 M | Da 100% | 98 | | 0% | | | | | | 26 | 0% 0% 11% 3.7% 0% 100% 100% 900.0% 0% 100% 100% 900.0% | 100% 100% 89% 95. 0% 0% 0% 0% 0. 0% 0% 0% 0% 0 | 7% 9% 9% 7% 9% 9% | 0% 0.0% 0% 0.0% | 17% 8% 100% 100% 1 | 0% 8.7% 8 100% 100.0% | 0% 92% 100 0% 9% 0 9% 9% 7 | S 91.9% 0% S 0.0% 0% S 0.0% 0% | 0% 0 0% 0 | 0.0% | 0.5101 | | | 0.5101 | | | Ŧ |
| meonine-crotein kinase ; 5924 enic reticulum metalione Emp1 5-monophosphate synths Umps | STICH MOUSE 40 KI ERMPI MOUSE 100 UMPS MOUSE 52 KI | On 100% 75% 100% Cla On 100% 100% 80% | 91.7% 0% 20 93.3% 0% 0 | 0% 0% 8.2% 2% 20% 6.7% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 67% 100% 100% 100% | 100% 100.0% | N 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 10 | 0% 67% 100% 88.9% 0% 0% 0% 0.0% 0% 100% 100% 100.0% | 0% 22% 0% 11. 0% 0% 0% 0% 0 0% 0% 0% 0 | 7% 6% 0% 0% 7% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 100% 100.0% 0% 0.0% | 100% 83% 3 33% 0% 100% | 00% 94.4% 0% 11.1% | 0% 17% 0/ 0% 0% 0/ 0% | 5 5.6% 0% 5 0.0% 67% 0% | 0% 0 100% 100 | 0.0% 80.9% | 0.7103 0.6856 0.4226 0.4226 | 0.8520 | 0.6244 0.3 0.4 0.4 | 103 0.6856 0 026 0 | 1.4226 | 0.42 | 1226 |
| ase subunit beta-like on: Clybi | CLYSL MOUSE 38 KI COSSC MOUSE 45 KI | De 86% 100% 100% De 0% 0% 0% 0% | 95.2% 14% 0 0.0% 100% 100 0.0% 100% 100 | 2N 20N 5.7% 2N 0N 4.8% 2N 100N 100.0% 2N 100N 100.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 0% 0% 0% 22% | 100% 100.0% 0 0% 0.0% 100 0% 11.1% 100 | % 0% 0% 0.0% % 100% 100% 100.0% % 67% 100% 88.9% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 06 06 06 0.05 | 100% 100% 100% 100 | 25 05 0N | 0% 0.0% | 100% 100% 1 0% 0% | 0% 0.0% 10 | 0% 0% 0 100 0% 100% 100 | S 0.0% 0% S 100.0% 0% | 0% 0 0% 0 | 0.0% | 0.4226 | | 0.4226 0.4 | | 0.4226 | | = |
| oil domain-containing on Codolido main-containing protein Ociad1 | OCAD1_MOUSE 28 ki | | | | 0% 0% | ms 0.0% | 100% 100% | 100% 100.0% 0 | % O% O% 0.0% | 0% 0% | 0% 0.0% 10 | OK 100% 100% 500.0% | 0% 0% 0% 0 | w I ov ov | 06 0.0% | 100% 100% 1 | 100.0% | 0% 0% 0 | s 0.0% 0% | 0% 0 | 0.0% | | | | | | | \rightarrow |

| MCMS C1806 MCMS 43 606 MCMS 79 806 MCMS 79 806 MCMS 23 806 MCMS 23 806 MCMS 24 806 MCMS 24 806 MCMS 23 806 MCMS 2 | 288 1008 10 1008 10 1008 1008 10 1008 1008 | 2N 94.4% 2N 100.0% 2N 100.0% | 2% 2% 2% 2% 2% 2% 2% 2% 2% 2% 2% 2% 2% 2 | 50% 0.0% 17% 5.0% 0.0% 0.0% 0.0% 0.0% | 9% 0 9% 0 9% 0 | 25 255 E | 50% 8.2% 86% | 200N 88N 2 | 00% 91.1% | 50% 01 0% 01 | 6 06 00 | 0% | | | | | | | | | | | | 0% 100.0% 0 | N 0N 0 | | % 0% | 0.0% | 1.0000 | 7059 0.030 0.422 0.500 | 0.5000 | 1.0000 | | 0.5000 | 0.5000 | | |
|--|--|--|---|--|--|--|--|--|--|--|-----------------------------------|--|--|--|--|--|--|--------------------------|-------------------------------------|---------------------------|---|-------------------------------------|---|---|---|---|---------------------------|--|---------------------------------------|--|-------------------------------------|----------------------------|------------------|----------------------------|---------------------------------|-------------------|----------------------------|
| MARIE MARI | 0% S0% 10 | 28. 100.0% 28. 100.0% 28. 100.0% 28. 100.0% 28. 27.8% 29. 58.9% 29. 58.9% 29. 100.0% 29. 100.0% 20. 0.0% | 2% 2% 202% 2% 2% 202% 2% 2% 202% | 0% 9.0% 100% 0% 9.0% | 9% 0 | 25 25 5 | | | | - | | 25 14% | 12% | 05 8.95 | 200% | 90% 100% 1 | 00.0% 0% | 9% | 0% 0.0% 0% | 100% | 100% | 0.0% 100% 50% | 29% 46 | 05 39.5% 0 | N 98 0 | n 00% so | % 71% 6 | DN 60.5% | 0.9537 | 0237 | w 0.477# | 0.798 | | 0.4774 | 0.4226 0.42 | 0.0237 | $\overline{}$ |
| XXE 2 2 450. COME 79 100. XXE 1 3 100. XXE 1 3 100. XXE 2 3 100. XXE 5 100. | 0% S0% 10 | 27.8% 27.8% 28. 27.8% 29. 58.9% 29. 55.6% 29. 100.0% 29. 0.0% 1 | 0N 0N | 0% 0.0% | | 05 05 | 0.0% 100% | 200% I | 100% 100.0% | 9% 01 | 0% 0.0 | 2% 0% 0% | 9% | 05 0.0% | 200% 50% | 88% 100% 100% 0% 0% | 95.8% 0% 50% 0.0% 100% | 100% | 0% 0.0% 0% 100% 100.0% | 9% 13 9% 0 | 0% 0% 0% | 4.2% 100% 100% | 100% 100 100% 100 0% | 0% 100.0% 0 0% 100.0% 0 | N 98 0 | N 00% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% | 0.4 | 4226 0.422 5000 | 8 | | 0.5000 | | | 0.4226 | 0.4226 |
| ACUSE 23 AGA MUSE 23 AGA MUSE 23 AGA MUSE 23 AGA MUSE 33 AGA MUSE 53 AGA MUSE 54 AGA MUSE | 0% S0% 10 | 27.8% 7% 58.9% 3% 55.6% 3% 100.0% 3% 0.0% 1 | 50% 100% | | 0% 0 | 2% 2% 0 | 0.0% 100% 0% | 200% 1/ 200% | 100% 100.0% | 0% 09 09 100% | 0% 0.0 | 2% O% O% | 0% 0% | 05 0.0% | 100% 1 100% 1 | 00% 100% 1 00% 100% 1 | 00.0% 0% 00.0% 0% | 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 1% 0% 1% 0% 0% | 0.0% 100% 0.0% 100% 50% | 100% 100 100% 100 100% 6 | 0% 100.0% 0 0% 100.0% 0 7% 72.2% 50 | N 0N 0 N 0N 0 | % 0.0% 0 % 0.0% 0 % 27.8% 0 | % 0% 1 % 0% 1 | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | | | |
| MUSE 37 65 MUSE 34 105 MUSE 34 105 MUSE 34 105 MUSE 32 105 MUSE 31 105 MUSE 31 105 MUSE 31 105 MUSE 51 | 0% S0% 10 | 2% 55.6% 2% 100.0% 2% 0.0% 1 | | 67% 72.2% 22% 41.1% | 0% 0 0% 0 | 0% 0% 0 0% 0% 0 | 0.0% 75% 0.0% 80% | 75% 50% | 0% 50.0% 50% 60.0% | 25% 25% 20% 50% | 100% 50.0 50% 40.0 | 1% 0% 1% 0% | 0% 0% | 0% 0.0% 0% 0.0% | 200% 1 50% 0% | 00% 100% 1 100% 0% 0% | 00.0% on Son 0.0% 100% | 6 0% 6 100% 1 | 0% 0.0% 0% 100% 100.0% | 0% 0 0% 0 | PN DN | 0.0% 100% 100% 0.0% 0% | 100% 100 75% 100 0% 0 | 0% 100.0% 0 0% 91.7% 0 0% 0.0% 100 | N 0% 0 N 25% 0 N 100% 100 | ns 0.0% 0 ns 0.3% 0 ns 100.0% 0 | % 0% : | 0% 0.0% 0% 0.0% 0% 0.0% | 0.4255 0.6 0.9259 0.0285 0.4 | 6244 0.265 0.006 | 94 0.2322 97 0.0267 | 0.4656 | 0.6344 | 0.2654 | 0.2322 | | |
| DESC | 0% S0% 10 | | 23% S0% 0% 0% 100% 100% | 50% 44.4% 0% 0.0% 100% 100.0% | 0% 0 0% 0 | 0% 0% 0 0% 0% 0 0% 0% 0 | 0.0% 100% 0.0% 100% 0.0% | 75% si | 100% 91.7% | 0% 255 0% 1009 | 6 0% 8.3 6 100% 100.0 | PN ON | 0% | 016 0.0% | 200% 1 75% 0% | 00% 100% 1 67% 75% 0% 0% | 00.0% 0% 72.2% 25% 0.0% 100% | 6 23% 6 100% 1 | 0% 0.0% 25% 27.8% 100% 100.0% | 0% C | PIG CING | 0.0% 100% 0.0% 80% 0.0% 0% | 100% 100 100% 100 0% 20 | 0% 100.0% 0 0% 93.3% 20 0% 6.7% 100 | N 0% 0 N 0% 0 N 100% 80 | ns 0.0% 0 ns 6.7% 0 ns 93.3% 0 | % 0% : | 0% 0.0% 0% 0.0% | 0.0206 | 0.015 0.009 4225 | 0.4226 | 0.0286 | 0.0708 0.4228 | 0.0099 | 0.4226 | | |
| 0.555 34.50s 0.055 43.50s 0.055 64.00s 0.055 40.00s 0.055 40.00s 0.055 30.00s 0.055 41.00s 0.055 41.00s 0.055 21.00s | | | 100% 100% | 100% 100.0% | 0% 0 | OK OK 0 | 0.0% 0% | OK | 0% 0.0% | 100% 1009 | 100% 100.0 | P% 0% | 0% | 0% 0.0% | 200% 1 0% | 0% 0% 0% 100% 1 | 0.0% 100% 00.0% 0% 0.0% 100% | 0% 0% 100% | 0% 0.0% 0% 100.0% | 9% C | PK 0% | 0.0% 0% 0.0% 100% 0.0% 0% | 0% 21 100% 100 0% | 5% 8.3% 100 5% 100.0% 0 100 | N 200% 75 N 20% 0 N 200% | N 917% 0 | % 0% | 0.0% | 0.4 | 4226 | 0.4226 | | 0.4225 | | 0.4226 | | |
| 00.55 41 KDs 00.55 39 KDs 00.55 51 KDs 00.55 41 KDs 00.55 28 KDs | | 28 50.0% I | 100% S0% | 0% 50.0% | 9% 0 | 26 26 5 | 0.0% | 0% | 100% | 1009 | 98 | | 9% | 05 | 100% 100% 62% | 0% 0% 00% 100% 100% 100% | 00.0% 0% 0% 88.9% 33% | 98 | 0% 0.0% 0% 11.1% | 9% C | IN ON | 0.0% 100% 100% 0.0% 50% | 100% 100 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 0% 83.2% 50 | N 98 0 N 98 0 | N 0.0% 0 N 0.0% 0 N 16.7% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% | | 7972 0.310 | | | 0.7972 | | | | |
| OUSE 41 kDs 40 kDs 40 kDs 71 kDs | 75% 100% 10 100% 100% 10 | 25 91.75 25 100.05 | 25% 0% 0% 0% | 0% 8.2% 0% 0.0% | 9% 0 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 100% 0.0% 100% | 200% 2/ 200% 2/ | 100% 100.0% 100% 100.0% | 9% 01 9% 01 | 0% 0.0 0% 0.0 | 7% 0% 7% 0% | 9% 9% | 0% 0.0% 0% 0.0% | 100% 1 100% 1 | 90% 100% 1 | 00.0% 0% 00.0% 0% | 9% | 0% 0.0% 0% 0.0% | 9% C | IN ON | 0.0% 100% 0.0% 100% | 100% 100 100% 100 | 05 100.0% 0 05 100.0% 0 | N 9N 0 | 6 00% 0 | 5 05 5 05 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 0.4226 | | 25 | 0.4226 | 0.8214 | 0.4225 | | | |
| | 0% 100% 100% 10 | 2% 100.0% | 0% 0% 0% 0% | 0% 0.0% | 900% 0% 0 | 2% 2% 5 | 0.0% 100% | 200% I/ | 100% 100.0% | 9% 01 | 9% 9.0 | n os | 9% | 06 0.0% | 85% 1 100% 1 | 00% 92% 00% 100% 1 | 92.4% 0% 00.0% 0% | 0% 0% | 0% 0.0% 0% 0.0% | 15% 0 0% 0 | IN SIN | 7.6% 100% 0.0% 100% | 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 | N 9N 0 | N 0.0% 0 | % 0% % 0% | 0.0% | 0.0 | | | | | | | 0.2228 | |
| OUSE 31 KOs ADUSE 41 KOs ADUSE 33 KOs | 0% 23% 2 0% 0% 100% 100% 10 | 25. 20.6% 25. 0.0% 26. 100.0% | 25% 22% 100% 100% 0% 0% | 0% 33.7% 100% 100.0% 0% 0.0% | 75% 22 9% 0 | 295 45 25 25 2 25 25 2 | 5.6% 17% 0.0% 0% 0.0% 100% | 25% 100% 1r | 25.0% 0% 100% 100.0% | 32% 255 200% 0% 05 | 17% 25.0 100% 0% 0.0 | 7% S0% 0% 7% 0% | | 50% 50.0% 0% 0.0% | | 75% 67% 60% 0% 00% 82% | 80.6% 0% 24.8% 71% 94.4% 0% | 25% 40% | 33% 19.4% 100% 70.5% 0% 0.0% | 0% 0 14% 0 | 1% 0% 1% 0% | 0.0% 80% 4.8% 32% 5.6% 86% | 100% 63 26% 0 100% 93 | 75 82.2% 20 05 23.0% 67 15 92.2% 0 | N 9N 33 N 50N 63 N 9N 6 | % 17.8% 0 % 61.1% 0 % 0.0% 14 | % 0% % 14% 3 | 0% 0.0% 0% 15.9% 0% 7.8% | 0.7303 0.9 0.9 0.1 | 9106 0.014 9397 0.304 7649 0.422 | 13 0.0140 15 0.1840 25 0.2029 | 0.2839 | 0.9105 | 0.2945 | 0.5531 0.79 0.0198 | 0.3799 | 0.0905 0.4226 0.4226 |
| OUSE 41 kDs OUSE 39 kDs OUSE 35 kDs | 100% 100% 0% 11% | 26 3.7% 1 | 0% 0% 100% 78% | 100% 92.5% | 0% 0 0% 11 | 2% 1% 0% 2 | 3.7% SON | 200% 0% | 50% 33.3% 500% 500% 100.0% 6% 0.0% | 50% 1009 | 50% 66.7 | | 0% | 0% 0.0% | 90% 1 90% | 92% 100% 92% 100% 0% 10% | 90.6% 0% 90.6% 20% 3.3% 100% | 9% 8% 100% | 0% 0.0% 0% 9.4% 90% 96.7% | 9% C | PN 0% PN 0% | 0.0% 100% 0.0% 17% 0.0% 0% | 100% 100 67% 43 0% 100 | 0% 100.0% 0 2% 42.1% 67 0% 33.2% 100 | N 0% 6 N 0% 43 N 100% 0 | % 0.0% 0 % 36.5% 17 % 66.7% 0 | % 0% 1 % 22% 1 | 0% 0.0% 6% 21.4% 0% 0.0% | 0.2134 0.4 | 0527 4534 0.944 | 1,0000 | 0.2577 | 0.2978 0.4634 | 0.6530 | 1.0000 0.42 | 0.0701 | 0.4226 |
| USE 61 kDs CUSE 53 kDs CUSE 85 kDs | 100% 100% 10 0% 1 | 2% 2% 100.0% 2% | 0% 0% 200% | 0% 0.0% 100% | 0% 0 | 0% 0% 0 0% 0% 0 | 0.0% 100% 0% | 200% 1/ 200% 1/ 0% | 00% 100.0% 0% 0.0% | 0% 09 100% 1009 | 50% 66.7 0% 0% 0% 0% 0.0 | 1% 0% 1% 0% | 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 | 50% 50% 00% 100% 1 0% 0% | 66.7% 0% 00.0% 0% 0.0% 100% | 50% 0% 100% | 50% 33.3% 0% 0.0% 100% 100.0% | 0% C | PN CN PN PN CN PN CN PN CN CN PN CN | 0.0% 100% 0.0% 100% 0.0% 0% | 100% 100 100% 100 0% 0 | 0% 100.0% 0 0% 100.0% 0 0% 0.0% 100 | N 0% 0 N 0% 0 N 100% 100 | ns 0.0% 0 ns 0.0% 0 ns 100.0% 0 | % 0% : | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | 0.1835 | | | | |
| OUSE 62 kDs OUSE 47 kDs OUSE 34 kDs | 0% 0% 100% 100% 100% 100% 100% 100% | 2% 66.7% 2% 66.7% | 0% 0% 0% 0% | 100% 100.0% 100% 33.3% 0% 0.0% | 0% 0 0% 0 | 2% | 0.0% 0% 0.0% 100% 0.0% 100% | 200% 2: | 0% 100% 100.0% 100% 100.0% | 9% 01 9% 01 | 100% 6 0% 0.0 6 0% 0.0 | 0% 0% 0% 0% | 0% 0% | 0% 0.0% 0% 0.0% | 0% - 100% 1 | 0% 0% 00% 100% 1 | 0.0% 100% 100.0% 0% 100.0% 0% | 6 100% : | 0% 0.0% 0% 0.0% | 0% C | PIG ONG | 0.0% 100% 0.0% 100% | 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 | 100% 100 N 0% 0 N 0% 0 | ns 0.0% 0 | 0% 0% 1 | | 0.4226 | 0.422 | × | | | | | | |
| USE 123 KDs MOUSE 42 KDs | 75% 100% 10 100% 100% 8 | N 95.8% | 0% 0% | 13% 42% | 9% 0 | 26 26 C | 0.0% 100k | 200% | 100% | 98 | 9% | 100% | OK. | 0% | 100% | 00% | 05 | 98 | 01 0.0% | 9% 0 | ns on | 0.0% 100% | 100% 100 | DK 100.0% 0 | N ON C | a 00% 0 | n on | 0.0% | 0.5271 | 0.422 | | 0.4226 | | 0.4226 | 0.50 | 100 | |
| OUSE 50 kOs OUSE 70 kOs | 100% 100% 10 | 2% 100.0% | 9% 9% | 0% 0.0% | 9% 0 | 28 28 5 | 0.0% 100% | 199% II | 100% 100.0% | 9% 01 | 9% 9.0 | 7% ON | 9% | 05 0.0% | 100% 1 100% 1 | 00% 100% 1 | 00.0% 0% 00.0% 0% | 9% | 0% 0.0% 0% 0.0% | 9% G | IN ON | 0.0% 0.0% 100% | 100% 100 | DN 100.0% 0 | N 98 6 | n 0.0% o | S 0% | 0.0% | | 0927 | | | | | | 0.0927 | |
| MOUSE SEKON OUSE SEKON | 100% 100% 10 82% 100% 10 | 2% 100.0% 2% 94.4% | 0% 0% 17% 0% | 0% 0.0% 0% 5.6% | 9% 0 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 100% 0.0% 100% | 200% 2/ 200% 2/ | 100% 100.0% 100% 100.0% | 9% 09 9% 09 | 0% 0.0 0% 0.0 | 7% 0% 7% 0% | 0% 0% | 0% 0.0% 0% 0.0% | 100% 1 100% 1 | 00% 100% 1 00% 100% 1 | 00.0% 0% 00.0% 0% | 0% 0% | 0% 0.0% 0% 0.0% | 9% G | PN ON | 0.0% 100% 0.0% 100% | 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 | N 9N 0 | N 0.0% 0 | % 0% : | | | | æ | 0.4226 | | 0.4225 | | | |
| ADUSE 121 KDs MDUSE 91 KDs USE 98 KDs | | | | | | | | | | | | | | | 100% 1 100% 1 | 00% 100% 1 00% 100% 1 | 00.0% 0% 00.0% 0% | 0% 0% | 0% 0.0% 0% 0.0% | 9% G | IN ON IN ON | 0.0% 100% 0.0% 100% | 100% 100 100% 100 | 0% 100.0% 0 0 0% | N 9N 0 | N 0.0% 0 | % 0% · | 0.0% | | | | | | | | | |
| OUSE 13 KDs OUSE 48 KDs OUSE 42 KDs | 100% 100% 10 100% 100% 10 | 2% 100.0% 2% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 100% 0.0% 100% | 200% St 200% St | 100% 100.0% 100% 100.0% | 0% 01 0% 01 | 9% 0.0 9% 0.0 | 7% 0% 7% 0% | 9% 9% | 0% 0.0% 0% 0.0% | 200% 1 200% | 100% | 00.0% 0% | - 88 | 0% 0.0% 0% | 9% C | 0% | 0.0% 100% | 100% 100 100% 100% | 0% 100.0% 0 | N 0% 0 0% | 0.0% 0 | % 0% 0% 0% | 0.0% | | | | | | | | | |
| DUSE 61 kDs MDUSE 55 kDs ADUSE 25 kDs | 0% 20% 100% 33% 10 | 26 6.7% 26 77.8% | 80% 60% 0% 32% | 75% 71.7% 0% 11.1% | 20% 20 0% 22 | 25 25% 21 25 25% 11 | 1.7% 0% | 25% | 20% 15.0% | 100% 753 | 9% B5.0 | PS 0% | 0% | 0% 0.0% | 92% | 00% 100% 0% 0% 00% 71% | 0.0% 100% 87.4% 0% | 0% 100% 0% | 0% 100% 100.0% 14% 4.8% | 9% C | PK 0% PK 0% PK 14% | 0.0% 0% 7.8% | 100% 100 0% 0 78% 100 | 0% 100.0% 0 0% 0.0% 100 0% | N 0% 0 N 100% 100 11% 0 | ns 0.0% 0 ns 100.0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% | 0.4580 | 0.422 9265 0.715 | 26 0.1885 57 | 0.2457 | 0.9221 | 0.0422 0.6393 | 0.1885 0.00 | 0.7767 | 0.0059 |
| 3USE 45 KDs DUSE 71 KDs | 75% 10 0% 0% 1 | on 0.0% 1 | 25% 100% 100% | 100% 100.0% | 0% 0 | 0% 0% 0 | 0.0% ON | 200% 1 | 0% 0.0% | 0% 09 100% 1009 | 100% 100.0 | 7% 0% | 0% | 0% 0.0% | 200% 1 200% 1 | 00% 100% 0% 0% | 00.0% 0% 0.0% 100% | 0% 0% 100% | 0% 0.0% 0% 100.0% | 0% 0 0% 0 | 1% 0% 1% 0% | 0.0% 100% 0.0% 100% | 100% 100 100% 100 0% 0 | 0% 100.0% 0 0% 100.0% 0 0% 0.0% 100 | N 0% 0 N 100% 100 N 100% 100 | ns 0.0% 0 ns 100.0% 0 | 16 0% | 006 0.0% 006 0.0% | J.M. 0.4 | 2.00 | | 5.5000 | V-120 | 0.000 | | | |
| DUSE 17 kDs MOUSE 72 kDs ADUSE 55 kDs | 100% 100% 10 | 9K 100.0% | 0% 0% 0% 17F | 0% 0.0% 11% 9.7% | 0% 0 | 2% 0% 0 | 0.0% 75% 100% 0.0% 100% | 200% 1: 200% 4: | 100% 91.7% 100% 100.0% | 25% 01 0% 01 | 0% 8.3 | 0% 0% 0% | 0% 0% | 0% 0.0% | 200% 1 200% 1 | 00% 100% 1 | 00.0% 0% 00.0% 0% | 6 0% 6 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | HS ON | 0.0% 100% 0.0% 100% | 100% 100 100% | DN 100.0% 0 | N 0% 0 | % 0.0% 0 | % O% | 0.0% | 0.4226 | 0 100 | 0.4226 | 0.4226 | | 0.1994 | 0.4226 | | |
| OUSE 5 KOs ADUSE 31 KOs SUSE 41 KOs | 100% 100% 10 100% 100% 10 | 25 100.0% 25 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 25 25 2 25 25 2 | 0.0% 100% 0.0% 100% | 200% 2/ 200% 2/ | 100% 100.0% 100% 100.0% | 9% 01 9% 01 | 0% 0.0 0% 0.0 | 7% 0% 7% 0% | 9% 9% | 05 0.0% 05 0.0% | 100% 1 100% 1 | 90% 100% 1 90% 100% 1 | 00.0% 0% 00.0% 0% | 0% 0% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | IN ON | 0.0% 100% 0.0% 100% 0.0% 100% | 100% 100 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 0% 100.0% 0 | N 9N 9 | N 0.0% 0 N 0.0% 0 | % 0% : | 0% 0.0% 0% 0.0% | | | | | | | | | |
| MOUSE 70 kDs DUSE 62 kDs DUSE 61 kDs | | | | | | | | | | | | | | | 100% 1 | 20% 100% 1 71% 20% | 00.0% 0% | 0% 0% 0% | 0% 0.0% | 9% 0 9% 0 | PS ON | 0.0% 100% 100% | 100% 100 95% 100 100% 100 | 0% 100.0% 0 0% 0 0% 100.0% 0 | N 9% 0 | ns 0.0% 0 | % 0% 5% | 0% 0.0% 0% 0.0% | | | | | | | | | |
| MOUSE SS KON MOUSE SS KON OUSE SS KON | 0% 100% 100% 10 | 25 25 100.0% | 202% 0% 0% | 100% 0% 0.0% | 9% 0 | 25 25 2 | 0% 0.0% 100% | 50% 200% 2 | 100% 100.0% | 200% S01 | 0% 0.0 | 0% 0% | 9% 9% | 05 0.0% | | | 00.0% on 61.1% Son | 6 67% | 0% 0.0% 0% 38.9% | 9% C | IN ON | 0.0% 100% 0.0% 80% | 57% 63 100 | 25 67.9% 20 25 | | | % 0% ; | 0.0% | 0.5000 0.7 | 7721 0.092 | 27 0.3215 | 0.5000 | 0.7721 | 0.0927 | 0.3215 | | |
| 0.5E 42 kDs 0.5E 51 kDs 0.0SE 41 kDs | 100% 100% 10 100% 100% 10 | 2% 100.0% 2% 2% 100.0% | on on | 0% 0.0% 0% 0.0% | 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 100% 100% 0.0% 100% | 200% St 200% St 200% St | 100% 100.0% 100% 100.0% 100% 100.0% | 9% 01 9% 01 | 9% 0.0 9% 0.0 9% 0.0 | 7% 0% 7% 0% 7% 0% | 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% | 00% 100% 100% 100% 100% | 00.0% 0% | 9% | 0% 0% 0% 0.0% | 9% 9 | 0% 0% 0% | 100% 0.0% 100% | 100% 100% 100 | 05 100.0% 0 | N 9N 9 | n 90% 0 | % 0% % 0% | 06 0.0% | | | | | | | | | |
| OUSE 40 KDs OUSE 29 KDs OUSE 30 KDs | 100% 100% 10 100% 100% 10 14% 22% 2 | 25 100.0% 25 100.0% 25 23.6% | 0% 0% 0% 0% 86% 67% | 0% 0.0% 0% 0.0% 77% 76.4% | 9% 0 9% 0 | 2% 2% 2 2% 2% 2 2% 2% 2 | 0.0% 100% 0.0% 100% 0.0% 67% | 200% 2: 200% 2: 50% 2: | 100% 100.0% 100% 100.0% 100% 72.2% | 0% 09 33% 509 | 9% 0.0 9% 0.0 9% 27.8 | PS 0% PS 0% | 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 0% | 00% 100% 00% 100% 0% 0% | 00.0% 0% 00.0% 0% 0.0% 100% | 0% 0% 100% | 0% 0.0% 0% 0.0% 25% 91.7% | 9% 0 9% 0 | N 0% | 0.0% 100% 0.0% 100% 8.3% 25% | 100% 100 100% 100 0% 0 | 0% 100.0% 0 0% 100.0% 0 0% 8.2% 29 | N 98 0 N 98 0 | n 0.0% 0 n 0.0% 0 n 0.2% so | % 0% % 0% % 100% 10 | 0% 0.0% 0% 0.0% 0% 83.3% | 0.0661 0.4 | 4226 0.050 | S 0.0295 | 0.0661 | 0.0021 | 0.2125 | 0.3293 | 0.0286 | 0.4226 |
| MOUSE 28 KDs OUSE 55 KDs | 100% 100% 10 100% 80% 10 | 2% 100.0% 2% 93.3% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 20 | 2% 2% C | 0.0% 80% 6.7% 80% | 86% 1/ 75% 1/ | 100% 85.0% 100% 85.0% | 0% 01 0% 01 | 0% 0.0 0% 0.0 | Ph 20% Ph 20% | 14% 25% | 0% 11.4% 0% 15.0% | 90% 100% 1 | 67% 100% 00% 100% 1 | 82.2% 0% 00.0% 0% | 0% | 0% 0.0% 0% 0.0% | 20% 23 0% 0 | PN ON | 17.8% 100% 0.0% 100% | 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 | N 0N 0 | ns 0.0% 0 | % 0% 1 | 0% 0.0% 0% 0.0% | 0.1946 0.3 0.4580 0.4 | 2079 0.207 0.422 4226 0.422 | 79 0.1946 26 0.1885 26 | | 0.4226 | 0.4226 | 0.15 | HS 0.2079 180 | 0.2079 0.4226 |
| 305E 34 kDs IDUSE 55 kDs OUSE 16 kDs | 100% 100% 10 100% 100% 10 100% 100% 10 | 0% 100.0% 0% 100.0% 0% 100.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 0% 0% 0 0% 0% 0 | 0.0% 100% 0.0% 100% 0.0% 100% | 75% 5/ 100% 1/ 100% 1/ | 100% 91.7% 100% 100.0% 100% 100.0% | 0% 255 0% 05 0% 05 | 0% 8.3 6 0% 0.0 6 0% 0.0 | PN 0% PN 0% PN 0% | 0% 0% 0% | 0% 0.0% 0% 0.0% | 93% 1 100% 1 | 00% 100% 100% 100% 1 | 94.4% 17% 100.0% 0% 100.0% 0% | 6 0% 6 0% | 0% 5.6% 0% 0.0% 0% 0.0% | 0% C | PIG CRG | 0.0% 100% 0.0% 0.0% | 100% 100 100% 100 100% 100 | 0% 100.0% 0 0% 0% | 0% C | ns 0.0% 0 ns | | | 0.4226 0.4 | 4226 0.422 | 0.4226 | 0.4226 | 0.4226 | 0.4226 | 0.4226 | | |
| OUSE 69 kDs OUSE 21 kDs OUSE 61 kDs | 100% 100% 10 100% 100% 10 | 0% 100.0% 0% 100.0% | ON ON | 0% 0.0% | 0% 0 0% 0 | ON ON C | 0.0% 100% 0.0% 100% 100% | 200% 1/ 200% 1/ 200% | 100% 100.0% 100% 100.0% | 0% 01 0% 01 0% 01 | 6 0% 0.0 6 0% 0.0 | 7% 0% 7% 0% 0% | 0% 0% 0% | 0% 0.0% 0% 0.0% | 200% 1 200% 1 200% 1 | 00% 100% 1 00% 100% 1 | 00.0% 0% 00.0% 0% 00.0% 0% | 6 0% 6 0% | 0% 0.0% 0% 0.0% | 0% C | PIG CING | 0.0% 100% 0.0% 100% 0.0% 100% | 100% 100 86% 100 | 0% 100.0% 0 0% 95.2% 0 | N 0% C | % 0.0% 0 % 4.8% 0 | 96 | | 0.4 | 4226 | 0.4226 | | 0.4225 | | 0.4226 | | |
| OUSE 55 kOs OUSE 35 kOs 60USE 57 kOs | 17% 20% 100% 100% 10 | 2% 12.2% 2% 100.0% | 93N 92N 9N 9N | 100% 87.8% 0% 0.0% | 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 25% 0.0% 100% | 200 I | 0% 8.3% 100% 100.0% | 75% 1009 9% 09 | 91.7 9% 9.0 | % 0% % 0% | 9% | 0% 0.0% 0% 0.0% | 100% | 0% 0% | 0.0% 100% | 100% | 100% 100.0% | 9% 9% 0 | n os | 0.0% 0% | 100% 0% 0 | DN 0.0% 71 | 0% N 100% 100 | % 90.5% 29 | 0% % 0% | DS 9.5% | 0.7284 | | | | 0.4225 | | | 0.4226 | |
| MOUSE 51 KDs MOUSE 54 KDs | | | | | | | | | 100% B0.5% | 25% 09 | 0% 8.3 | PS 0% | 22% | 05 11.1% | 200% 200% 200% | 00% 100% 00% 100% | 00.0% 0% 00.0% 0% | 9% | 0% 0.0% 0% 0.0% | 9% C | 05 05 05 | 0.0% 100% | 100% 100 | 28 100.0% 0 | S 08 0 | 0.005 | S 0S | 0.0% | 0.2901 | 0.808 | 95 94 0.0726 | 0.6856 | 0.3587 | 0.6344 | 0.31 | 105 | 0.2254 |
| CUSE 47 kDs CUSE 12 kDs | 67% 67% 5 25% 10% 2 | 2% 61.1% 5% 20.0% | 22N 22N 75N 82N | 50% 38.9% 75% 76.7% | 9% 0 9% 10 | 2% 2% 2 2% 2% 2 | 0.0% 67% 3.2% 20% | 82% 1/ 12% | 0% 10.8% 0% 10.8% | 33% 179 80% 889 | 9% 15.7 100% 89.2 | % 0% % 0% | 9% 9% | 0% 0.0% 0% 0.0% | 100% 1 0% | 00% S0% 0% 0% | 83.2% 0% 0.0% 100% | 0% 100% | 50% 16.7% 100% 100.0% | 9% G | PN ON | 0.0% 100% 0.0% 0% | 100% 100 0% | 0% 100.0% 0 100 0% 75.7% 40 | N 9N 0 | n 0.0% 0 | % 0% % 0% | 05 0.0% | 0.1336 0.4 0.3002 0.6856 0.3 | 4226 0.313 0.057 2044 0.422 | 0.2254 72 0.2044 85 0.8193 | 0.1336 0.1574 0.6856 | 0.4225 | 0.3133 0.0051 0.4225 | 0.2254 0.2044 0.42 0.8193 | 126 | 0.4225 |
| DUSE 43 KDs USE 35 KDs ADUSE 36 KDs | 0% 100% 100% 10 100% 100% 10 | 2% 100.0% 2% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 100% 0.0% | 100% 1/ 2/ | 100% 100.0% 100% | 9% 01 | 0% 0.0 0% | 7% O% | 9% | 0% 0.0% 0% | 88% 100% 1 | 50% 0% 00% 100% 1 | 45.8% 0% 00.0% 0% 00.0% 0% | 0% 0% 0% | 0% 0.0% 0% 0.0% | 12% S0 0% 0 | N 100% 1 N 0% N 0% | 54.2% 0% 0.0% 100% 0.0% 100% | 0% 0 100% 100 100% 100 | 0% 0.0% 0 0% 100.0% 0 0% 100.0% 0 | N 9N 0 N 9N 0 | N 0.0% 200 N 0.0% 0 N 0.0% 0 | % 100% 10 % 0% | 0% 100.0% 0% 0.0% 0% 0.0% | 0.3 | 2123 | | | | | | 0.2123 | |
| CUSE 133 KDs CUSE 59 kDs KDUSE 46 KDs | 100% 100% 10 100% 100% 10 100% | 2% 100.0% 2% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 100% 0.0% 100% | 200% 3/ 200% 3/ 200% | 100% 100.0% | 9% 01 9% 01 | 0% 0.0 | 0% 0% | 0% 0% 0% | 06 0.0% | 100% 100% | 100% 100% 100% 1 | 00.0% 0% | 9% | 0% 0.0% 0% 0.0% | 9% S | 0% 0% 0% | 0.0% 100% 100% | 100% 100 100% | 05 100.0% 0 0 0 | N 0% 0 | n 0.0% 0 | % 0% · | | | | | | | | | | |
| MOUSE 54 KOs SE 36 KOs ADUSE 19 KOs | 100% 100% 10 0% 100% | 25 100.05 | 0% 0% 0% 0% | 0% 0.0% | 0% 0 0% | 25 25 2 | 0.0% 100% | 100% 1/ 100% | 0% 100.0% | 0% 09 | 100% | PS 0% | 0% 0% | 0% 0.0% 0% | 200% 1 0% 200% 1 | 0% 0% 0% 0% 00% 100% | 0.0% 0% 0.0% 100% 00.0% 0% | 100% | 0% 0.0% 0% 0.0% | 9% C | PS 0% PS 0% | 0.0% 100% 0.0% 0% 0.0% 100% | 0% 100% 100 100% 100 | 0% 100.0% 0 100 0% 100.0% 0 | N 20% C | n 00% 0 | % 0% % 0% | 06 0.0% | | | | | | | | | |
| IOUSE 47 KOs IOUSE 51 KOs | 100% 100% 10 | 2K 100.0% | ON ON | on con | 0% 0 | on c | 100% | 100% D | 100% 100.0% | 0% 09 | 0% 0.0 | PN 0% | 0% | 0% 0.0% | 100% 1 | 00% 100% 1 | 016 | 0% | 01 0.0% | 0% 0 | ns on | 100% | 100% 100 | 0% 100.0% 0 | N 0% C | n 00% 0 | % O% | 00 0.0% | | | | | | | | | |
| OUSE 133 KDs 3USE 127 KDs | | | | | | | | | | | | | | | 200% 1 | 00% 100% 1 | 00.0% ons | 000 | 0% 0.0% 0% 0.0% | 0% C | PIG ON | 0.0% 100% 0.0% 100% | 100% 100 100% 100 | DN 100.0% 0 | 0% N 0% 0 | ns 0.0% 0 | 0% % 0% | | | | | | | | | | |
| CUSE 46 kDs CUSE 23 kDs CUSE 82 kDs | 83% 100% 10 | 25 94.4% | 0% 0% 0% | 0% 0.0% 0% | 17% 0 | 25 25 2 25 1005 | 100% 5.6% 100% | 200% 2/ 200% 2/ | 100% 100.0% 100% 100.0% | 9% 01 9% 01 | 0% 0.0 0% 0.0 | 7% 0% 7% 0% | 9% 9% | 05 0.0% 05 0.0% | 67% | 50% 80% 0% 0% | 65.6% 0% 0.0% 0% | 9% | 0% 0.0% 0% 0.0% | 33% S0 | N 20% 7 | 36.4% 100% 00.0% 0% | 100% 100 0% 0 | 0% 100.0% 0 0% 0.0% 0 | N 98 0 | ns 0.0% 0 | % 0% 1 | 05 0.0% | | | | | | | | | |
| ADUSE 45 kDs OUSE 73 kDs MOUSE 55 kDs | 0% 0% 100% 100% | 28 0.0% 1 | 100% 100% 0% 0% | 100% 100.0% | 9% 0 9% 0 | 2% 2% C | 0.0% ON 100% | 200 200% | | 200% 2009 0% 09 | | ON. ON. | 0% 0% | | 200 1 2000 1 | 0% 22% 00% 100% 1 | 11.1% 100% 00.0% 0% 22.2% 0% | 75% 6 0% | 67% 80.6% 0% 0.0% 0% 0.0% | 0% 23 0% 0 100% 100 | 05 05 15 05 16 225 | 8.3% S0% 0.0% 100% 77.8% S0% | 0% 0 100% 100 100% 100 | 0% 16.7% 50 0% 100.0% 0 0% 83.2% 0 | N 100% 100 N 0% 0 N 0% 0 | % 83.3% 0 % 0.0% 0 % 0.0% 50 | % 0% : | 0% 0.0% 0% 0.0% 0% 16.7% | | | 25 0.4225 | | 0.8947 | 0.1917 | 0.4226 | | |
| 0.05E 37 kDa 0.05E 37 kDa 0.05E 54 kDa | 100% 100% 10 100% 100% 10 100% 100% 10 | 2% 100.0% 2% 20.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 2% 2% 5 2% 2% 5 | 0.0% 100% 100% 0.0% 100% | 200% 2/ 200% 2/ | 100% 100% 100.0% | 9% 01 9% 01 | 9% 0.0 | 0% 0% 0% | 9% 9% | 05 0.05 | 100% 1 | 90% 100% 1 90% 100% 90% 100% 1 | 00.0% 0% | 9% 9% 6 9% | 0% 0.0% 0% 0.0% | 9% 0 | 1% 0% 1% 0% | 0.0% 100% 100% 0.0% | 100% 100 100% 100 100% 100 | 2% 100,0% 0 2% 100,0% 0 2% | N 9% 0 N 9% 0 | N 0.0% 0 N 0.0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% | | | | | | | | | |
| MOUSE 35 KOs MOUSE 35 KOs | 100% 100% 10 100% 100% 10 100% 100% 10 | 2% 100.0% 2% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 25 25 25 25 25 25 25 25 25 25 25 25 25 2 | 0.0% 100% 0.0% 100% | 200% 1/ 200% 1/ 200% 1/ | 100% 100.0% 100% 100.0% | 9% 01 9% 01 | 0% 0.0 0% 0.0 | 7% 0% 7% 0% | 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 100% | 00% 100% 00% 100% | 00.0% 0% 0% | 9% | 0% 0.0% | 9% 0 9% 0 | PS ON | 0.0% 100% | 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 | N 98 0 | n 0.0% 0 | S 0% | 0.0% | | | | | | | | | |
| ACUSE 35 KDs MOUSE 15 KDs | 60% 60% 3 20% 20% 3 | 25 37.8% 26 24.4% | 40% 60% 90% 90% | 67% 55.6% 67% 75.6% | 20% 0 | 2% 2% E | 5.7% SON | 75% 22% | 33% 52.8% 20% 27.8% | 25% 255 75% 679 | 22% 27.8 10% 72.2 | PS 25% | 9% | 22% 12.4% | 100% 1 100% 1 | 00% 100% 1 0% 20% | 00.0% 0% 6.7% 25% 20.0% 90% | 9% 9% 25% | 0% 0.0% 40% 30.0% | 9% 0 75% 71 | 05 005 05 40% | 0.0% 100% 0.0% 100% 0.0% 17% | 100% 100 100% 100 25% 0 | 0% 100.0% 0 0% 100.0% 0 0% 13.9% 12 | N 9N 9 N 90N 92 N 90N 92 | n 00% 0 | % 0% % 25% 5 | 0% 0.0% 0% 47.2% | 0.3405 0.5 0.5655 0.0 | 5074 0.032 0528 0.422 | 85 0.0639 85 0.5185 | 0.0612 | 0.5223 | 0.0651 | 0.4244 0.35 0.5185 | 0.2923 | 0.0217 |
| AUSE 53 kDs AUSE 52 kDs OUSE 54 kDs | 0% 0% 1 | 2% 25.6% | 100% 0% 50% 22% | 22% 0% 50% 44.4% | 0% 100 | 67% 2% 100% 2% 0% 0 | 0% 0% 0.0% 60% | ON SON | 0% 58.9% | 67% S01 0% 40% S01 | 50% 50% 41.1 | 22% 100% | 50% | 50% 0% 0.0% | 0% 0% 100% | 0% 67% 50% | 100% 67% 72.2% 0% | 22% | 50% 27.8% | 0% 22% | SON ON | 50% 0% 0.0% 100% | 0% 0 | 0% 0.0% 100 0% 0.0% 0 | N 50% 100 | ns 50 ns 83.3% 0 | % 10 % 50% | 0% 16.7% 0% 16.7% | 0.6749 0.1 | 5000 1994 0.378 | 0.5000 | 0.8450 0.5000 0.6749 | 0.1994 | 0.8612 | 0.0903 0.84 0.1984 0.50 | 150 0.2929 100 | 0.8612 |
| MOUSE 11 kDs OUSE 103 kDs MOUSE 52 kDs | 100% 100% 10 0% S | 2% 100.0% 2% 1 | 0% 0% 100% | 0% 0.0% 50% | 0% 0 0% | ON ON C | 0.0% 100% | 100% S | 0% | 0% 01 | 100% | PN ON | 0% | 0% 0.0% | 92% 1 50% 0% | 00% 75% 0% 0% 0% 0% | 85.1% 17% 15.7% 0% 0.0% 100% | 6 0% 6 0% 6 100% 1 | 25% 13.9% 0% 0.0% 100% 100.0% | 9% 0 50% 990 | PN DN PN PN DN PN DN PN DN DN PN DN | 0.0% 100% 83.3% 67% 0.0% 0% | 22% 0% 0 | 0% 100.0% 0 0 0% 0.0% 100 | N 0% 0 N 0% N 100% 100 | ns 0.0% 0 23 ns 100.0% 0 | % 67% % 67% | 0% 0.0% | 0.1 | 1994 0.199 2628 0.500 | я — | | | | | 0.2628 | |
| 2USE 32 KDs ADUSE 61 KDs ADUSE 43 KDs | | | | | | 2% 2% C | 0.0% 100% 0.0% 75% | 96N 1 | 100% 85.9% | 25% 149 | 06 13.1 | ON ON | 9% | 0% 0.0% | 200% 1 75% 200% 1 | 67% 100% 1 67% 100% 1 | 00.0% ons 80.6% ons 00.0% ons | 6 0% 6 0% | 0% 0.0% 0% 0.0% | 25% 33 25% 33 | PIG ONG | 0.0% 100% 19.4% 100% 0.0% | 100% 100 100% | DN 100.0% 0 | N 0% C | ns 0.0% 0 | % O% | 0.0% | 0.3344 | | | 0.3344 | | 0.0342 | | 0.1917 | |
| 3USE 11 kDs MOUSE 21 kDs OUSE 24 kDs | 100% 67% 9 100% 100% 10 100% 100% 10 | 25 72.25 25 100.05 25 100.05 | 0% 28% 0% 0% 0% 0% | 50% 27.8% 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 25 25 2 25 25 25 2 | 0.0% 100% 0.0% 100% 0.0% 100% | 67% 1/ 100% 1/ 100% 1/ | 100% 88.9% 100% 100.0% 100% 100.0% | 9% 225 9% 05 9% 05 | 9% 11.1 9% 0.0 9% 0.0 | 7% 0% 7% 0% 7% 0% | 9% 9% 9% | 05 0.0% 05 0.0% | 200% 200% 200% | 90% 100% 1 | 00.0% 0% 00.0% 0% | 9% | 0% 0.0% 0% 0.0% | 9% c | IN ON | 0.0% 100% 0.0% 100% | 0% 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 | 100% N 0% 0 N 0% 0 | n 0.0% 0 | 0% % 0% | 0% 0.0% 0% 0.0% | 0.4204 | | | 0.4204 | | | | | |
| OUSE 43 kDs USE 131 kDs WOUSE 93 kDs | 0% 0% | ٠, | 100% 100% | | 95 0 | 25 | cos. | | os. | 200% | 100% | os. | | 95 | 200% | 00% 78% 00% | 92.8% 0% | 98 | 225 7.4% | 9% 0 | es es | 0.0% 90% | 87% 83 100% 100 | 2% 87.8% 10 2% | S 125 7 | S 10.0% 0 | 0% | 25 225 | 0.5 | 5637 | | | 0.7636 | | | 0.4225 | |
| OUSE 46 kDs MOUSE 6 kDs | 57% 86% 6 | 2% 69.8% 2% 20.0% | 42N 14N | 22% 30.2% 20% 6.7% | 9% 0 90% 60 | 2% 2% 5 | 0.0% 71% 7.7% 22% | 80% S | 83% 78.2% 100% 44.4% | 29% 209 | 17% 21.7 | % 0% % 67% | 9% 75% | 0% 0.0% 0% 47.7% | 100% 1 50% | 00% 100% 1 83% | 00.0% 0% 50% | 98 | 17% | 0% 100% | 0% | 50% | 71% 8 | 25 55.25 28 | N 29% 17 | % 0.0% 0 % 27.6% 13 | % 0% % 0% | 0% 0.0% 0% 4.2% | 0.4312 0.9 | 9431 0.884 | 0.4183 94 | 0.4312 | 0.7908 | 0.8847 | 0.4617 | 0.4226 | 0.0572 |
| 005E 50 kOs 005E 50 kOs 005E 34 kOs | 100% 71% 67% 3 | 25 57.1% 26 | 29% 22% | 67% 42.9% 100% | 95 0 | 2% 2% 5 | 100% 0.0% 67% | 100% 1/ 67% 1/ | 100% 100.0% 100% 77.8% | 9% 01 17% 331 | 9% 0.0 9% 16.7 100% | 75 0% 75 17% | 9% 9% | 0% 0.0% 0% 5.0% | 200% | 00% 100% 1 | 00.0% 0% | 9% | 0% 0.0% | 9% 0 | 0% | 0.0% 100% 100% | 100% 100 | 0% 100.0% 0 | N 98 C | n 90% 0 | % 0% · | | | | | | | | | | |
| MOUSE 105 KDs MOUSE 12 KDs MOUSE 53 KDs | 100% 100% 10 | 2% 100.0% | ox ox | 0% 0.0% | 0% 0 | 2% 2% 5 | 0.0% 100% | 100% | 90% 95.7% | 0% 09 | 10% 3.3 | ns os | 9% | os 0.0% | 100% 1 100% 1 | 00% 100% 1 00% 100% 1 | 00.0% 0% 00.0% 0% 0.0% 100% | 0% 0% 100% | 0% 0.0% 0% 0.0% 100% 100.0% | 9% 0 9% 0 | N 0% N 0% | 0.0% 100% 0.0% 100% 0.0% 0% | 100% 100 100% 100 0% 0 | 0% 100.0% 0 0% 100.0% 0 0% 0.0% 100 | N 0% 0 N 0% 0 N 100% 100 | N 0.0% 0 N 0.0% 0 N 100.0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.4226 | | 0.4226 | 0.4226 | | | 0.4226 | | |
| DUSE 65 KDs ADUSE 77 KDs MOUSE 20 KDs | 100% 67% 100% 10 | on 88.9% | 0% 0% | 0% 0.0% | 22% 0 | 2% 2% 11 | 1.0% 67% | 67% | 80% 71.1% | 0% 09 | 0% 0.0 | 0% 23% | 22% | 20% 28.9% | 200% 0% | 100% 0% 0% | 0.0% 0% | 0% | 0% 0% 0.0% | 0% 100% 100 | 0% 1% 100% 5 | 100% 100% 00.0% 0% | 100% 100 | 0% 100.0% 0 0% 0 | N 0% 0 | ns 0.0% 0 | % 0% % 10 | 00.0% | 0.2465 | 0.015 | 23 0,0029 | | | 0.97 | 0.24 | 85 | 0.0153 |
| BUSE 51 KDs BUSE 47 KDs | 22% 50% 8 0% | 78 52.4% 8% 56.3% | ##N ON ON ON | 22.2% 0% 0.0% | 22% 42 67% 50 990% | m 0% 25 0% 14% 43 | 0.4% 100% 0.7% 50% | 67% 1/ 67% 1 | 86% 67.5% | 0% 00 0% 00 | 0% 11.1 0% 0.0 | PN SON | 22% 100% | uni 0.0% 14% 32.5% | 200% 0% | 100% 0% 0% 0% | 0.0% 0% | 50% 0% 6 0% | 0% 15.7% 0% 0.0% | 20% C | TR 0% 100% 100% 100% 100% | 00.0% 0% | 100% 100 0% 0 | 0% 100.0% 0 0% 0.0% 0 | N 0% 0 | m 0.0% 0 | % 100% 10 | 0% 100.0% | | | 0.4228 | 0.5185 | 0.6592 | 0.7972 | 0.50 | 184 | 0.9206 |
| MOUSE 34 KDs DUSE 33 KDs | | | 16N 16N | 25% 17.9% | 0% 0 | 0% 0% 0 0% 0% 0 | 0.0% 60% 0.0% 60% | 75% S | UN 0.0% | 40% 253 | 9% 100.0 0% 21.7 | 7% 0% | 0% | 05 0.0% 05 0.0% | 200% 1 0% | 0% 100% 0% 100% | 00.0% 0% 33.3% 0% | 100% 6 0% 6 0% | 0% 0.0% 0% 0.0% | 0% 0 100% 100 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0.0% 100% 0.0% 100% | 100% 50 100% 100 100% 100 | 0% 100.0% 0 0% 100.0% 0 | N 0% 0 | 10.7% 0 | % 0% 1 | 00 0.0% 00 33.2% | 0.7802 | 0.037 5185 | 77 0.2044 | 0.7802 | U 12/44 | 0.0377 | 0.2044 | 0.5185 | = |
| 0.05E 124 KDs 0.05E 124 KDs 0.05E 50 KDs | | | 0% 0% 0% 0% | 0% 33.3% | 9% 0 9% 0 | 25 25 5 25 25 | 0.0% 100% 100% 75% | 200% 2/ 100% 2/ 100% 2/ | 100% 100.0% 100% 91.7% | 9% 1909 9% 99 25% 99 | 0% 33.3 0% 0.0 0% 8.3 | 7% 0% 1% 0% | 0% 0% 0% | 05 0.0% 05 0.0% | 200% 3 200% 3 200% 3 | 00% 100% 1 00% 100% 1 | 00.0% 0% 00.0% 0% | 9% 9% 9% | 0% 0.0% 0% 0.0% | 9% 0 9% 0 | 05 05 05 05 05 05 05 05 05 05 05 05 05 0 | 0.0% 100% 0.0% 100% 0.0% 100% | 100% 100 100% 100 100% 100 | 25 100.0% 0 25 100.0% 0 25 100.0% 0 | N 98 0 | N 0.0% 0 | % 0% % 0% | | 0.4225 | 0.422 | db 0.422/b | 1.0000 | | | | | |
| #0.5E 44.0a 0.5E 15.0a | 100% 100% 10 100% 100% 10 | 25 100.0% | 0% 0% 0% 0% | 0% 0.0% | 9% 0 | 25 25 2 | 100% 100% 100% 100% | 200% 3/ 200% 3/ 200% 3/ | 100% 100.0% | 9% 01 9% 01 | 0% 0.0 | 0% 0% 0% | 9% 9% | 05 0.05 | 200% 1 | 90% 100% 1 | 00.0% 0% 00.0% 0% | 9% 9% | 0% 0.0% 0% 0.0% | 9% C | 1% 0% 1% 0% | 0.0% 100% 0.0% 100% | 100% 100 100% 71 | 0% 100.0% 0 0% 91.7% 0 | N 9N 0 | n 0.0% 0 n 0.0% 0 | % 0% % 0% | 05 0.0% 05 0.0% | 0.4 | 4225 | 0.4226 | | 0.4226 | | 0.4226 | | |
| MOUSE 105 KDs MOUSE 21 KDs OUSE 50 KDs | 100% 100% 100% 0% 0% | 26 0.0% | 0% 0% 100% 100% | 100% 100.0% | 9% 9% 0 | 26 26 2 | 100% 0.0% (W | 100% 1/ 0% | 100% 100.0% 0% 0.0% | 0% 09 100% 1000 | 0% 0.0 100% 100.0 | 7% 0% 2% 0% | 9% 9% | 0% 0.0% 0% 0.0% | 200% I | 00% 100% 0% | 00.0% 0% 0.0% 100* | 0% 100% | 0% 0.0% 100% 100.0% | 9% 9% | IN ON | 67% 0.0% 100% 0.0% 0% | 75% 81 100% 101 | 85 75.4% 0 85 100.0% 0 85 0.0% 100 | N 0% 0 N 0% 0 N 100% 100 | N 0.0% 23 | % 25% 1 % 0% | 2% 23.6% 2% 0.0% 2% 0.0% | | | | | | | | | |
| MOUSE 55 KDs MOUSE 64 KDs CUSE 73 KDs | 100% 100% 10 0% | 2N 100.0% | 0% 0% 100% | 0% 0.0% | 9% 0 9% | 25 25 5 | 0.0% 100% 0% | 100% D | 00% 100.0% 0% | 9% 01 199% | 100% | 2% 0% 0% | 9% | 0% 0.0% 0% | 200% 1 0% | 00% 100% 1 | 00.0% 0% 100% | 100% | 0% 0.0% | 9% 0 | ns on | 0.0% | 100% 100 0% | 100 | 9% C | | 0% % 0% | 25 | | | | | | | | | |
| DUSE 70 kDs MOUSE 102 kDs OUSE 63 kDs | | 26 | | 100% | | 9% | 0% | | | 100% | | 0% | | | 9% | 100% | 100% | 100% | 0% | 9% 0 | 0% | 0% 100* | 100% 40 | 0% 100.0% A | 100% 100 % 0% 0 | ns 0.0% A | 0% % % 0% | 0% 0.0% | | | | | | | | | |
| | March Marc | March Marc | 196 196 | March Marc | March Marc | March Marc | March Marc | March Marc | March Marc | March Marc | Martin | March Marc | March Marc | March Marc | March Marc | March Marc | March Marc | Martin | Martin | Martin | Martin | Martin | The Part No. 1981 1981 1981 1981 1981 1981 1981 198 | The Part No. 1989 1999 1999 1999 1999 1999 1999 199 | The color The | The Part No. 1961 1961 1961 1961 1961 1961 1961 196 | The Part No. 19 | | | Secondary Seco | | | | | | | |

| 24 homolog Vac 14 -decendent chosohat Mdp1 -desendent shosohat Mdp1 -desendent shosohat Mdp1 -desendent shosohat Mdp2 -gonula adherens prot Myzap | VAC14_MOUSE 88 MGDP1_MOUSE 19 SNRPA_MOUSE 32 MYZAP_MOUSE 54 | HOs 90% 10 HOs 60% 5 HOs 50% 6 HOs 0% | % 52% % 52% % 100% | 03.3% 0% 01.4% 60% 12.2% 50% 0.0% 100% | 0% 0 42% 42 22% 0 100% 100 | 0.0% 0.48.0% 0.27.8% 0.100.0% | 20% 0% 0% 0% 0% 0% | 0% 6.77 0% 0.07 0% 0.07 0% 0.07 | 6 0% 67 6 67% 50 6 100% 6 0% 0 | % 67% 44.45 % 67% 61.11 % 0% 0.00 | 22% 22% 2% 20% 2 | 0% 0% 0.0% 0% 32% 38.9% | 00% 23% 0% 0% 0% 0% | 33% 55.6% 0% 0.0% | 67% 80% 100% 0% | 100% 100% 93.3% 2 100% 75% 91.7% 0% 0% 0.0% 10 | 25 25 25 5.75 25 25 25 5.75 26 100 100 100 100,075 | 22% 2% 2% 2% 2% 2% 2% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 82% 1 100% 75% 0% 0% | 005 94.4% 05 0.0% 1 | 0% 17% 0% 25% 00% 100% 10 | x 50% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.1500 0.2913 0.904: 0.808 | 0.0093 | 0.0132 0.2913 0.5 0.2 | 0.0093 0.008 0.3293 | 0.0132 | 0 | |
|--|--|--|--|--|---|---|--|--|--|---|--|--|---|--|--|--|--|--|--|---|--|--|--|--|--|---|--------------------------------------|---|---|-------------------------------|----------------------|-------|
| translation initiation for Eiffer se-1 Acy1 sid-binding globulin SerpinaS | ACYL MOUSE 46 CBG MOUSE 45 DROW MOUSE 45 | KDa 100% 10 KDa 100% 10 KDa 100% 10 | N 100% N 100% | 00.0% 0% 00.0% 0% | 9% 0 9% 0 | N 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.05 0% 0.05 | 5 100% 100 5 100% 100 100% 100 | % 100% 100.05 % 100% 100.05 | 9% 9% | 0% 0% 0.0% 0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | os 0.0% os 0.0% | 100% 100% 100% | 100% 100% 100.0% 100% 100% 100.0% | 2% 2% 2% 2.0% 2% 2% 2% 2.0% 2% 2% 2% 2.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 1 100% 100% 1 | 00% 100.0% | 0% 0% 0% | 25 0.0% | 0% 0% 0% | 0% 0.0% | | | | | | | |
| sphatase 1 regulators Ppp1/21 Fetub ophosphatase 3 Imped1 | PPR21 MOUSE 88 FETUS MOUSE 43 IMPA3 MOUSE 39 | IKDs IKDs IKDs 100% 10 | N 100% | 0.0% 0% | 0% 0 | n 0.0% | 0% 0% | 0% 0.09 | | 100% | | 9% | | os. | 2% 100% 62% | 100% 100% 100.0% 50% 100% 72.2% 50% 100% 72.2% 100% 100.0% 100% 100.0% 100% 100.0% 00% 100% 100.0% | 250 | 0% 0% 0% 0% 22% 50% | 0% 0.0% 0% 27.8% | 100% 100% 100% 1 | 00% 100.0% | 0% 0% 0% 0% | x 0.0% | 0% 0% 0% 0% | 0% 0.0% | 0.199 | 0.1994 | | | | 0.1994 | 0.19 |
| ipo9 onition particle 9 kDa Srp9 hatino enzume E1 rei Nae1 | SPP09 MOUSE 10* ULA1_MOUSE 60 | 5 KDa 100% S 1 KDa 100% 10 1 KDa 100% 10 | N 50% N 100% N 100% | 95.7% 0% 90.0% 0% 90.0% 0% | 9% 0 9% 0 | n 0.0% n 0.0% n 0.0% | 0% 50% 0% 0% 0% 0% | 50% 33.39 0% 0.09 0% 0.09 | 6 100% 100 6 100% 100 6 100% 100 | % 100% 100.05 % 100% 100.05 | 0% 0% | 0% 0% 0.0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 200% 200% 200% | 100% 100% 500.0% 100% 100% 500.0% 100% 100% 500.0% | 50 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 06 0.0% 06 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0.422 | | | | | | 0.18 |
| ding LIM protein 1 Fblim1 I in initiation factor TFI Taf5 -binding protein 3 Lob3 I | FBL11_MOUSE 411 TAFS_MOUSE 87 LDB3_MOUSE 76 | KDs KDs KDs 0% | n 0% | 100% | 100% 100 | n . | 0% | ON. | | | | | | | 0% | 0% 0% 0.0% 10 0% | 0% 100% 100% 100.0% 0% 100% 0% 0% 50% 16.7% 0% 0% 60% 20.0% | 0% 0% 0% 0% 0% | 0% 0.0% | 24% 0% | 0% 4.8% 0% | 96% 100% 10 | 0% 95.2% 0% 0.0% 3 | 0% 0% | 0% 0.0% | 0.422 | | 0.4 | 4225 1798 A 1797 | | 5 200 | |
| cetylase 1 Hidac1 II ar ribonuciecorolein 1 Snrpf II protein ubi-64 Dpt2 II | REQUIMOUSE 55 REQUIMOUSE 44 | RDs 0% 5 | % 50% % 60% % 0% | 0.0% 100% 0.0% 100% | 50% 50 75% 40 100% 100 | ns 71.7% ns 71.7% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 6 25% 0 6 0% | % 67% 30.67 0% | 25% ti | 20% 33% 52.4% 100% 100% | 0% 0% 0% | 0% 0.0% 0% | 90% 100% 25% | 0% 50% 76.7% 100% 40% 80.0% 23.3% 7 | 0% 0% 50% 16.7% 0% 0% 60% 20.0% 0% 75% 80% 76.7% | 20% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 67% 100% 100% 100% 1 0% 22% | 60% 75.6% 00% 100.0% 0% 11.1% 1 | 0% 0% 0% 0% 00% 67% 10 | 0% 0.0% 2 0% 0.0% 0% 88.9% | 2% 0% 0% 0% 0% 0% | 90% 24.4% 0% 0.0% 0% 0.0% | 0.9363 0.423 0.386 | 0.1245 0.1245 0.0051 | 0.0702 0.9383 0.4 0.4228 0.3 | 4226 0.1012 4226 0.1245 5861 0.0051 | 0.0702 0.4226 | 0.2254 | 0.4 |
| In reductate 2 Plgr2 | PTGRS_MOUSE 36 SARNP_MOUSE 24 | RDs 100% 10 RDs 100% 10 | N 100% | 00.0% 0% 00.0% 0% | 9% 0 9% 0 | n 0.0% n 0.0% | 0% 0% 0% 0% | 9% 0.05 9% 0.05 | 5 100% 100 5 100% 100 | % 100% 100.07 | 9% 9% | 0% 0% 0% 0.0% | 0% 0% 0% 0% | os 0.0% | 200% 200% | 100% 100% 100% 100.0% | 25 25 25 25 25 25 25 25 25 25 25 25 25 2 | 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 00% 00% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0420 | 0.022 | 0.020 | 0.420 | | | |
| soluble protein 1 Basp1 septidate 1 Citic shall liMutomains non Dist | BASPI MOUSE 22 CATC MOUSE 52 EN 1 MOUSE 52 | KOs KOs | 100% | | | n . | | 96 | 100 | % 100% | | ox ox | 9% | os. | 200% 200% 200% | 100% 100% 100.0% 100% 100% 100.0% | 05 05 05 05 000 05 05 05 05 000 05 06 05 05 05 000 | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 00 00% 00 00% | 2% 0% 2% 0% | 9% 0.0% 9% 0.0% | 0.522 | | 0.5 | 5220 | | | |
| secretory protein E1 Npc2 area A synthetises AC Acam3 difactor I Cli | NPC2 MOUSE 16 ACSM0 MOUSE 66 CFAI MOUSE 67 | KDs 100% | | 9% | | | 9% | | | 100% | | 0% | | ON. | 200% 200% | 100% 100% 100.0% | N 0N 0N 0.00 N 0N 0N 0.00 | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 1 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 25 0.0% 25 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | |
| receptor complex me Gost2 plex subunit MC13 Mc13 help-colled-col-helps Chchd2 | GOSPO MOUSE 25 MIC13 MOUSE 13 CHCHO MOUSE 16 | KDs 67% 1 KDs 0% 2 KDs 0% 2 | N 52% N 2% N 22% | 0% 22% 22% 22% 22% 100% 22% 100% 22% 100% 22% 100% 22% 100% 20% 11.1% 100% 20% 100% 100% 100% 100% 100% 100 | 57% 50 75% 100 67% 67 | % 45.0% % 91.7% % 77.0% | 0% 29% 0% 0% 0% 0% | 0% 9.55 0% 0.05 0% 0.05 | 6 80% 100 6 0% 0 | % 100% 93.35 % 0% 0.05 % 50% 50.05 | 20% 1 200% 1 | ON ON 0.0% SON 67% 88.9% SON 50% 50.0% | 20% 0% 0% 0% 0% 0% | 0% 6.7% 22% 11.1% 0% 0.0% | 62% 0% 62% | 0% 0% 0.0% 10 100% 3 | 05 | 22% 0% 0% 0% 0% | 50% 0% 0.0% | 50% 0% 0% 0% 50% 75% | 00% 0% 0.0% 60% 61.7% | 9% 50% 100% 5 50% 25% 4 | 25 55.7% S 26 56.7% S | 9% 9% 9% 9% | 9% 50% 33.3% 9% 0.0% | 0.0576 0.624i 0.4226 0.1296 0.398i | 0.4672 0.4226 0.0988 0.4226 | 0.5950 0.0220 0.8520 0.1 0.2495 0.1296 0.3 0.4226 0.4226 | 0.0220 1835 0.4225 3980 0.0988 | 0.81 0.3379 0.42 0.2425 | 5 0.6245 6 0.1835 | 5 0.0 |
| otein sortino-associat Vpe4b ession factor 2 Myef2 I n-containing mTOR-in Deptor | VPS4B MOUSE 49 MYEF2 MOUSE 63 DPTOR MOUSE 46 | HOs 100% 6 HOs 0% 2 | % 100% % 0% | 18.9% 0% 11.1% 100% | 9% 0 67% 100 | n 0.0% | 0% 0% 0% 0% 0% 0% | 0% 11.17 0% 0.09 0% 0.09 | 6 0% 100 6 20% 33 | % 100% 55.75 % 100% 51.15 | 200% 80% | ON ON 33.3% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 200% 0% | 00% 100% 100.0% 0% 0% 0.0% 10 | 0% 0% 0% 0.0% 0% 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 0% 0% 100% | 00% 100.0% | 0% 0% 50% 100% 0% | N 0.0% | 2% 0% 2% 0% | 0% 0.0% | | | 0.4226 0.4226 0.5 0.2438 | 5000 4226 0.1140 0.7706 | 0.4226 0.42 | 0.5000 | 0.4 |
| line traci-binding grot Ptbp3 dent RNA helicase DC DdxDy in Cdc73 | DOXIV MOUSE 73 CDC73 MOUSE 61 | KDs 50% 6 KDs 0% | 65 0% 65 0% | 0.0% 100% | 89% 89 100% 100 | % 63.3% % 100.0% | 0% 0% 0% 0% 11% 0% 0% 0% 0% 0% 0% | 0% 0.09 11% 0% 0.09 | 6 100% 100 6 0% 0 | % O% | 200% S | 0% 100% 20% | 0% 0% 0% 0% | 0% 0% 0.0% 0% 0.0% | 56% | 00% 100% 85.2% 4 0% 0% 0.0% 10 0% 0% 10 | IN 0N 0N 14.8N ON 75N 100N 91.7N ON 100N | 0% 0% 0% 25% 0% | 0% 0.0% 0% 8.3% | 100% 100% 1 0% | 00% 100.0% 1 | 0% 0% 50% | 0.0% | 0% 0% 50% | 0% 0.0% | 0.0762 0.4228 | 0.1140 | 0.0762 0.4 | 4225 0.1140 0.7706 | | | 0. |
| ducino adapter molec Stan2 domain-interacting n Nifk 1 ociated membrane or Vamp2 | MKETI MOUSE 35 VAMP2 MOUSE 13 | KDa | % 0% % 0% % 100% | 0.0% 100% 0.0% 100% | 100% 100 100% 100 0% 0 | ns 100.0% ns 100.0% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 0% 0.09 | 6 0% 0 6 0% 0 | % 0% 0.07 % 0% 0.07 | 200% 1/ 200% 1/ | 20% 20% 100.0% 20% 20% 100.0% 20% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 20% 20% 20% | 0% 0% 0.0% 10 0% 0% 0.0% 10 0% 0% 6.7% 9 100% 100% 900.0% | 0% 100% 100% 100.0% 0% 100% 100% 93.3% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 100% 100% 1 | 0% 0.0% 1 00% 100.0% | 00% 100% 10 00% 0% | 0% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | | 0.4226 | | 0.4226 | | | |
| nelated 70 kDs protei Heps2 II clear ribonucleoprote Smps1 II Inyl aminopeptidase Linpep II | RLDA_MOUSE 25 LCAP_MOUSE 11 | I KDs 100% 10 7 KDs 100% 10 | 06 | 0% 00.0% 0% | 0% | | on on | | 100% | | on | ON ON 0.0% | ons | | 500% 500% | 22% 0% 44.4% 000% 82% 94.4% 000% | 0% 67% 200% 55.6% 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 17% 5.6% | 60% 100% 100% 100% 1 100% 100% 1 | 67% 68.9% 00% 100.0% 00% 100.0% | 60% 0% 3 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.522 0.423 | 0.4226 | 0.5 | 5221 | | 0.4226 | 5 0. |
| naseireductase SDR Dhrs7 I olein kinase Lyn Lyn lase Sts | LYN_MOUSE 59 STS_MOUSE 67 | KDs 100% 10 KDs | N 100% | 00.0% e% | 0% 0 | n 00% | 0% 0% | 0% 0.09 | 6 100% 100 | 100% 100.09 | ON | 9% | 0% 0% | 0% 0.0% | 100% 100% 100% | 0006 826 94.4% 0006 1006 100.0% 1006 1006 100.0% 1006 100.0% 1006 100.0% | 0% 0% 0% 0.05% 0.0 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 1 | 00% 100.0% | 0% 0% | x 0.0% | 2% 0% | 0% 0.0% | | | | | | | |
| Casp8 vinarodain kinasa 7 P9/7 70 kDa protein 12A Hepa12a | PTK7_MOUSE 118 HS12A_MOUSE 75 | KOs B KOs KOs | | | | | | | | | | | | | 200% 200% | 100% 100% 100.0% 100% 100% 100.0% | 26 06 06 0.05 26 06 06 0.05 | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 1 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 25 0.0% 25 0.0% 26 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | |
| sphosphale aldolase (Aldoc mase family cylosolic, Sulf (b) | ALDOC MOUSE 39 STIBL MOUSE 35 | KDs 100% | | 9% | | | os. | | 200 | N. | 98 | os. | 98 | | | | | | | 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 05 0.0% 05 0.0% | 2% 0% 2% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | |
| rane protein 109 Timerri 09 k homolog 2 Hook2 | TM109 MOUSE 25 HOOKS MOUSE 83 | KDs 82% 10 KDs 0% | 8 62% 8 98 | 0.0% 100% | 9% 0 199% 199 | N 0.0% | 17% 0% 0% 0% | 22% 15.79 0% 0.09 | 6 83% 100 6 | S 80% 87.85 | - 9% | 0% 0% 0.0% 6% 50% 53.2% 0% | 17% 0% | 20% 12.2% 0% 0.0% | 200% | 50% 67% 72.2% | 25 05 05 0.075 | 0% 50% | 225 27.8% | 100% 100% 1 | 00% 100.0% | 0% 0% | 25 0.0% | 9% 9% 9% | 0% 0.0% | | 0.5555 | 0.1809 | 0.0756 | | 5 0.1994 | 0. |
| e II cytoskeletal 75 Kr575 Gen | GRN MOUSE 60 GRN MOUSE 63 | IKDs 0% 100% 10 | % 0% % 50% % 32% % 200% % 82% % 0% | 8.1% S0% 11.1% 0% 30.0% 0% 19.4% 29% | 9% 0 9% 0 9% 0 17% 17 200% 100 | S 0.0% 2 S 0.0% | 00 0% 0% 0% | 67% 88.95 9% 0.05 | 6 0% 6 100% 100 | 0% % 100% 100.09 | 0% 0% | 0% 0% 0.0% 0% 0% 12.2% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 69% | 50% 67% 58.9% 4 | 2% S0% 32% 41.1% | 0% 0% 0% 0% | 0% 0.0% | 86% 60% 100% 100% 1 | 0% 67% 70.8% | 16N 42N 3 | 29.2% 29.2% | 0% 0% 0% 0% | 9% 0.9% 9% 0.9% | 0.4226 0.273 | | 0.0631 0.2 0.1869 0.3263 | | 0.42 0.0531 0.1559 | 6 | |
| nly AAA domain-cont Atad1 -fath-soid-CoA lisss Acal5 doreductase GLYR1 Glyr1 | ATAD1 MOUSE 41 ACSL5 MOUSE 76 GLYRI MOUSE 60 | KDs KDs KDs ON | % 0% % | 100% | 100% 100 100% | N. | 0% 0% 0% | 9% | | 8 | | 20% | 9% | | 2% 52% 100% | 9% 57% 61.1% 50% | 2% 2% 2% 0.0% 2% 0% 0% 0.0% | 50% 50% 33% 0% | 67% 22% 38.9% 0% | 0% 0% 100% 100% 1 | 0% 0.0% 00% 100.0% | 0% 0% 3 0% 0% | 05 11.1% 20 05 0.0% | 0% 100% 0% 0% 0% 0% | 67% 88.9% 0% 0.0% | 0.019 | 0.2048 | 0.1 | 1155 0.0903 5000 0.2048 | | 0.1155 | 0. |
| olisomeric Goldi com Cog3 in protein 20-3 Tg3 indent protein kinase Priaca | Colon Colo | KDs 0% KDs 100% 10 | % 0% % 0% % 100% | 0.0% 0% 0.0% 0% | 0% 0 200% 100 0% 0 | N 0.0% 3 | 200% 200% 0% 0% 0% | 200% 100.05 0% 0.05 0% 0.05 | 6 0% 0 6 100% 100 | % 0% % 0% % 100% 100.09 | 0% 1/2 0% | 0% 100% 0.0% 0.0% 100% | 100% 100% 0% 0% 0% | 0% 0% 0.0% 0% | 100% | 0% 100% 100.0% | 100% 0% 0% 0% 0.0% | on on | 0% 0% 0.0% | 0% 0% 100% 100% 1 | 0% 0.0% 1 00% 100.0% | 00% 100% 10 0% 0% | 0% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | |
| s protein 6 Sunt5 inne N-methyltransfer Prmt1 Cpme1 | ANM1 MOUSE 42 CPNE1 MOUSE 59 | KDs 0% 100% 10 KDs 10 | % 0% % % 100% | 0.0% 100% | 90% 500 0% 0 0% 0 | N 100.0% | 0% 0% 0% 0% | | 100% 100 100% 100 | 0% % 100% | 200% 0% | 0% 0% | 0% 0% | on. | 100% 100% | 0% 0% 0.0% 10 100% 100% 100.0% 100% 100% 100.0% | 0% 100% 100% 100.0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | os 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | E |
| ociated Ece domain-: Reps1 see I isoform alpha Cank1a1 sebusation rentein 1911 Sbds | KC1A MOUSE 39 SEDS MOUSE 29 | KDs 0% KDs 100% | % 0% 100% 100% | 0.0% 100% 9% 9% | 100% 100 0 | ni 100.0% | 0% 0% 0% | 0% 0.09 0% 0% | 100% 100 100% 100 6 0% 100% 100 100% 100 100% 100 5 100% 100 | 0% % 100% 100.07 | 9% 9% | 0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% | 100% 100% | 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% | 2% 0% 0% 0.07% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% 1 | 00% 100.0% | 9% 9% 9% 9% | os 0.0% | 2% 0% 2% 0% | 0% 0.0% | | | | | | | |
| PIGD 20A1 Cyp20a1 (see A-2-activating pro Plas | PLODI MOUSE 85 CP20A MOUSE 52 PLAP MOUSE 87 | KDs 100% 10 KDs 100% 10 | 100% N 100% | 00.0% 0% 0% | 9% 0 9% | S 0.0% | 0% 0% 0% 0% | 9% 0.09 | 100% 100 5 100% 100 | % 100% 100.05 % 100% 100.05 | 0% | 0% 0% 0.0% 0% 0% 0.0% 0% 0% 0.0% | 0% 0% 0% 0% | 05 0.0% | 200% 200% | 100% 100% 100.0% 100% | 25 | 0% 0% 0% | 0% 0.0% 0% | 100% 100% 1 100% 1 | 00% 100.0% 00% | 0% 0% 0% 0% | 25 0.05 | 0% 0% 0% 0% | 0% 0.0% 0% | | | | | | | |
| protein 512 Zn512 ein shosshodiesteras Smpd3 | 25612 MOUSE 64 NSMA2 MOUSE 71 | KDs KDs | | w.m. | | | | | | % 100% 100.07 | - | 0% 0% 0.0% | | ov 0.00 | 25 | 0% 0% 10 | 75 1005 05 05 0075 | 9% 9% 9% 9% | 100% | 0% 80% 86% | 0% 92% 87.4% | 200 200 200 200 | 25 0.0% 1 | 0% 0% 4% 14% | 9% 12.6% | | | | | | | |
| containing protein 2 NNrc2 I | NHLC2 MOUSE 78 PTMS MOUSE 11 | KDs 10 | 100% N 100% | 0.0% 100% | 0% 0 100% 100 | S 100.0% | 0% | 9% 9% 9% | 100% 100 6 0% 0 | % 100% 100.09 | 9% | ON ON 0.0% | 0% 0% 0% 0% | 0% 0.0% | 100% | 100% 100% 100.0% | N 98 98 9.00 | 0% 0% | 0% 0.0% | 100% 100% 100% 100% 1 | 00% 100.0% | 0% 0% 0% 0% | x 0.0% | 2% 0% 2% 0% | 0% 0.0% | | | | | | | |
| cell nuclear antigen Pons i bifunctional enzyme Ethadh | PONA MOUSE 29 ECHP MOUSE 76 KDYR MOUSE 62 | HDs 100% | 100% | 9% 9% | 0 | N. | 9% 9% | 9% | 1006 | | 2000 | | 00 | | 100% | 100% 100% 100.0% | 08 08 0.00 08 08 | 9% 9% 9% | 0% 0.0% | 100% 100% 100% 1 | 00% 00% 100.0% | 0% 0% 0% | 2% W 0.0% | 0% 0% 0% 0% | 0% 0% 0.0% | | | | | | | |
| in-7 Sm/7 egulator BAX Bax on ATPase 115 kDa a Abs640a1 | SNY MOUSE 45 BAX MOUSE 21 VPP1 MOUSE 96 | KDs 100% 10 | N 100% | 0.0% 0% | 0% 0 | n 0.0% | 0% 0% | 0% 0.09 | 5 100% 100 | % 100% % 100% 100.07 | - 0% | 0% 0% 0.0% | 0% 0% 0% | 0% 0.0% | 100% 100% | 100% 100% 67% 80% 82.2% 50% 0% 50.0% | 0% 0% 0% 0% 0% 0% 0.0% | 0% 33% 0% 50% | 0% 20% 17.8% 100% 50.0% | 71% 75% 50% 50% 1 | 75% 73.8% 00% 66.7% | 0% 0% 0% 0% | 00% 2 00 00% 5 | 9% 25% 0% 50% | 25% 26.2% 0% 33.3% | 0.477. 0.5492 0.5000 0.4226 | 0.2079 | 0.1835 | | | 0.4772 | 2 0. |
| olein choschatase no P(pn1 I coprolein 4 Cd35 I NA polymerase II tran Sub1 | PTN1_MOUSE 50 CD36_MOUSE 53 TCP4_MOUSE 14 | KDs 10 KDs 82% 10 KDs 100% 10 | 66 200% 66 200% | 94.4% ON 30.0% ON | 0% 0 0% 0 | ns 0.0% | 27% 0% 0% 0% | 100% 0% 5.69 0% 0.09 | 100% 100 6 100 6 75% 0 | % 100% % 0% 25.07 | 25% 1 | ONE ONE 75.0% | 0% 0% 0% 0% | 0% 0.0% | 75% 100% 100% | 0.00% 100% 57% 50% 00% 00% 00% 00% 00.0% 0 | 2% 0% 0% 0.0 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 71% 75% 50% 50% 5 100% 100% 1 100% 100% 1 100% 88% 1 100% 100% 1 | 00% 100.0% 00% 100.0% 00% 95.8% | 0% 0% 0% 0% | 06 0.0% 06 0.0% | 0% 0% 0% 0% 0% 0% | 25% 25.2% 0% 33.3% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 0.5000 0.422 0.4226 0.0955 0.422 0.422 | 0.5560 0.4226 5 0.4226 | 0.1015 0.0855 0.4 0.4 | 4226 0.4226 4226 0.4226 | 0.42 | 5 | 0. |
| e-5-choschate isome Grpda1 Midomain protein 2 Pdim2 Iso subfamily 8 ment Dnajb5 I | PDLI2 MOUSE 38 DNJBS MOUSE 40 | KDs 100% 10 KDs 0% | % 500% · | 0.0% 0% | 0% 0 100% 100 | ns 0.0% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 6 100% 100 100% 6 0% 0 | % 100% 900.09 % 0% 0.07 | 0% 0% 100% 1 | ON 016 0.0% 30% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 200% 0% 0% | 82% 100% 94.4% 0% 17% 5.6% 10 0% 0% 0.0% 10 | 0% 12% 0% 5.6% 0% 100% 82% 94.4% 0% 100% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 12% 0% 0% 0% | 00% 100.0% 0% 4.2% 0% 0.0% 1 | 0% 0% 75% 100% 10 | 0% 0.0% 0% 91.7% 1 0% 100.0% | 0% 0% 2% 0% 0% 0% | 0% 0.0% 0% 4.2% 0% 0.0% | 0.423 0.853 | 0.4226 | 0.4 0.7 | 4226 0.4226 7972 | | 0.4226 | 5 |
| Desirs (h namenal Elimbilians, into Lydfip1 whose drawnin, mechanic (800) | DEMA_MOUSE 451 LIBSF1_MOUSE 79 ISOC1_MOUSE 32 | KDs 0% 100% 10 | % 0% % 100% | 0.0% 100% 00.0% 0% | 90% 100 9% 0 | ns 0,0% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 6 0% 0 6 100% 100 | % 0% 0.05 | 900 D | 20% 20% 100.0% 0% 0% 0.0% | 0% 0% | 0% 0.0% | 200% 200% | 0% 0% 0.0% 10 100% 100% 100.0% 100% 100% 100.0% | 0% 100% 100% 100.0% 0% 0% 0% 0.00 0% 0% 0% 0.00 | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 9% 9% 9% 9% | 00% 00% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | |
| della aminormalarea Abat della della aminoria della amidatno Pam | ACSL4 MOUSE 79 AMD MOUSE 10 | KOs KOs P KOs | | | | | | | 100% | | 98 | | ons | | 200% | 100% 100% 100.0% | os os 0.05 | 9% 9% | 0% 0.0% | 100% 100% 1 100% 100% | 00% 100.0% 0% 66.7% | 0% 0% 0% 0% 10 | % 0.0% % 33.3% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | |
| e-binding effector pro Rabeg2 verting factor acetylhy Patah1b3 protein-like 1 ZIpi1 | PATRO MOUSE 251 ZFPL1 MOUSE 34 | KDs KDs ON | s 9s | 0.0% ex | 9% 0 | 0.005 2 | 200% 100% | 100% 100.05 | | n. | | os. | 100% | | 200 200% | 100% 100% 100.0% | 2% 0% 0% 0.0% 2% 0% 0% | 0% 0% 100% | 0% 0.0% 100% | 100% 100% 1 | 00% 100.0% | 0% 0% | x 0.0% | 0% 0% | 0% 0.0% | | | | | | | |
| dent protein descelul Sirt2 g protein 3 Rambp3 onine-protein phosphs PppSc | RANES MOUSE 53 PPPS MOUSE 35 | KDs 100% 10 KDs 100% 10 | N 100% | 0.0% 0% 0.0% 0% | 9% 0 | n 00% | 0% 0% | 0% 0.09 0% 0.09 | 5 100% 100 5 100% 100 | % 100% 100.09 | 98 | 0% 0% 0.0% | 0% 0% | 05 0.0% | 75% 100% | 100% 100.0% 00.0% 00.0% 00.0% 100% 100% | 0% 0% 0% 8.2% 0% 0% 0% 9.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 25 0.0% 25 0.0% 26 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.422 | 5 | 0.4 | 4225 | | | |
| phogenase 13 Rdh13 | DRES MOUSE 77 RDH13 MOUSE 36 | KDs 100% 10 | 5005 | 80% 98 | 08 0 | 8 995 | 0% 0% | 98 9.00 | 100% | 5 1005 100.05 | 9% | 05 05 05 | 0% 0% | 08 0.0% | 200 | 60% 50% 10 | 25 05 05 005 25 525 | 9% 9% | 0% | 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 25 0.0% 25 0.0% | 9% 9% 9% 100% | 9% 0.9% | 0.070 | | 0.0 | 0764 | | | |
| ng protein 1 Hebp1 olein kinsse HCK Hck in-containing protein Nudod1 | HEBPI_MOUSE 21 HCK_MOUSE 59 NUDC1_MOUSE 67 | KDs 100% 10 | 100% % 100% | 0.0% 0% | 95 0 | n 00% | 0% 0% | 0% 0.07 | 6 100 | % 100% | | 0% 0% | 0% | os. | 100% 100% 100% | 100% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 1 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 25 0.0% 25 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | | | | | | | |
| smidsse Gbs suppressor protein 1 Mbs/1 1 ain only protein 2 Fcho2 | GLCM MOUSE 581 MTSS1_MOUSE 82 FOHO2_MOUSE 89 | KOs KOs | n 0% | | 100% 100 | ns. | ON. | 0% 0.09 0% | 100% 0% | | 0% 100% | | ONS ONS | | 100N | 00% 100% 100.0% 0% 0% 0.0% 10 | 0% 0% 0% 0.0% 0% 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% | | 00% 100.0% 00% 100.0% | 0% 0% 100% | N 0.0% | 0% 0% | 0% 0.0% | | | | | | | |
| ed alanine-rich C-kina Marcks 1 L2 Ma2 1 rbosypeptidase A Cps3 | MARCS MOUSE 301 MAL2 MOUSE 19 CEPAS MOUSE 49 | I KDs I KDs | | | | | | | 100 | sc . | | ON. | 0% | | 200% 200% | 100% 100% 100.0% | 0% 0% 0% 0.0% 0% | 0% 0% 0% | 016 0.0% | 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | |
| nd polyadenylation sp. Cpsf2 falty sprid transport to St27a4 cmillion particle 12 kD Scpf9 | CPSF2 MOUSE 881 S27A4 MOUSE 72 SRP19 MOUSE 16 | kDa 0% kDa 100% kDa 75% 6 | % 0% % 62% | 0.0% 100% 0% 19.4% 25% | 100% 100 0% 22% 22 | n 100.0% | 0% 0% 0% 100% | 0% 0.09 0% 0.09 | 67% 6 75% 80 | % 82% 79.41 | 9% 25% | 20K 17K 20.6% | 22% | 0% 0.0% | 0% 0% 50% | ON DON 50.0% S | 0% 50% 50% 33.3% 0% 100% 0% 50.0% | 100% 50% 100% 0% 0% | 50% 85.7% 0% 0.0% | ON ON | 00% 100.0% 00% 100.0% 00% 100.0% 00% 17.0% 00% 17.0% | ox ox | 2% 0.0% 20 2% 20 2% 0.0% | 0% 100% | 98 | 0.0544 | 0.5705 | 0.0544 | 0.0572 | | 0.1835 | 5 0.1 |
| ome & thinesteness ? Acct2 is.commission numbris Propcb for weight phosphoton Acct1 | ACCT2 MOUSE 50 MPPB MOUSE 55 PPAC MOUSE 18 | KDs 100% 10 KDs 75% 10 | N 100% 100% N 100% | 0.0% 0% 0.7% 25% | 9% 0 9% 0 | N 0.0% | 0% 0% 0% 0% | 0% 0.07 0% 0.07 | | 100% | 9% 9% | 0% 0% 0.0% | 0% 0% 0% | 0% 0.0% | 100% 100% | 100% 100% 100.0% 100% 100% 100.0% | 0% 0% 0% 0.07% 0% 0% 0% 0.07% 0% 0% 100% 55.7% | 0% 0% 0% 0% 0% | 0% 0.0% | 100% 100% 1 100% 100% 1 100% 75% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% 0% 25% | 00% 00% 00% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.4226 0.422 | 0.4226 | 0.4226 0.4226 0.4 | 4225 0.4225 | 0.4226 | | |
| ctor protein 4 Cdc42ep4 sin-1 Ron1 cationic amino acid Sic7a1 | RONI_MOUSE 36 CTR1_MOUSE 67 | KDa KDa KDa 100% 10 | 0% N 100% | 0.0% 0% | 200 | N 0.0% | 0% 0% | 0% 0% 0.09 | 0% 5 100% 100 | s 100% 100.07 | 200% | 0% 0% 0.0% | 0% 0% | 0% 0.0% | 2% 2% | 100% 0% 33.3% 10 78% 91% 80.0% 2 100% | 0% 0% 100% 55.7% 0% 22% 9% 20.0% | | 0% 0.0% 0% 0.0% | 33% 20% 100% 100% 1 | 0% 17.8% 00% 100.0% | 67% 80% 10 0% 9% | 05 82.2% 05 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.073 | 5 | 0.0 | 8923 0736 | | | |
| roprotein 15-Sep rescent cell anticer-il Limit | SEP15 MOUSE 181 LIMS1 MOUSE 37 | KDa 925 7 KDa 925 7 KDa 95 2 | N 88% N 22% | 19.4% 100% | 25% 13 25% 67 | % 19.2% % 80.6% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 6 75% S0 6 0 | 100% % 100% 75.05 % | 25% | 0% 6% 0% 25.0% | 0% 0% 0% | 0% 0.0% | 2005 28% 25% | 100% 100% 100.0% 100% 40% 72.6% 2 42% 60% 42.6% 7 | 25. 25. 26. 20.05 26. 26. 26. 27.45 26. 27. 40.0 57.45 27. 40.0 57.45 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 67% 1 60% 80% 1 | 00% 88.9% 00% 80.0% | 0% 0% 0% 22% 40% 22% | 00% 00 11.1% 00 20.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.7291 0.483 0.072 0.9295 | 0.6870 0.1787 | 0.4906 0.7291 0.4 0.5000 0.9296 | 4833 0.6870 0726 0.1787 | 0.4905 | | |
| Ansati k homolog 3 Hook3 | ANNA MOUSE 37 HOOKS MOUSE 83 | KOs IKOs | 3 23 | 200 200 | 486 50 | 0 4445 | 0% 0% | 98 9.00 | 5 1005 0 | | 95 2 | | 05 05 | | 50% 60% | 0% 0% 0.0% 5 | 08 578 498 57.498 08 08 08 08 085 08 08 08 18.75 08 288 288 41.15 08 288 208 77.25 08 08 08 08.75 08 08 08 08 08 08 08 08 08 08 08 08 08 08 | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 100% 1 100% 67% 1 60% 80% 1 100% 100% 1 100% 100% 1 100% 100% 1 | 00% 95.8% 00% 100.0% | 0% 0% 0% 0% | 25 0.0% 1 25 0.0% | 2% 0% 2% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 4.2% 0% 0.0% | 0.535 | 1 | 0.4 | 4225 0136 | 0.000 | 0.4226 | 5 |
| dynein 1 light intern Dync 112 on ATPase subunit D Alpfiv1d Ni cle-trans isomeras Pol11 | VATO MOUSE 28 PPIL1 MOUSE 18 | KDs 10 | N 100% | 100% | 9% 0 | n. | os os | 9% | 100% 100% | 100% | 0% 0% | 0% | 0% 0% | 0% | 200% 200% 200% | 100% 100% 100.0% 100% 10 | 2% 2% 2% 0.0% 2% 2% 2% | 0% 0% 0% 0% | 0% 0.0% 0% | 100% 100% 1 0% 100% 83% 1 | 00% 100.0% 00% 94.4% | 0% 0% 100% 0% 17% | N 0.0% | 2% 0% 0% 0% | 0% 0.0% | 0.422 | 5 | 0.4 | 4226 | | | |
| FBVA polymerase II tr Med15 I microtubule-associa Emit I | MED 15 MOUSE 87 EMAL 1 MOUSE 90 GSDMD MOUSE 53 | KDs KDs | | | | | | | | | | | | | 9% 100% | 0% 10 100% 100% 100.0% | 0% 100% 0% 0% 0% 0% 0.0% | 0% 0% 0% 0% 0% | 0% 0.0% | 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 05 0.0% 05 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | |
| D Gadmdc1 (| AREGI_MOUSE 45 MEDI2 MOUSE 69 | kDs 20% 2 kDs 20% 2 | ni 29% ni 0% | 25.7% 80% | 71% 71 0% 0 | % 743% % | 0% 0% 100% | 0% 0.09 100% | 6 22% 25 0% 0 | % S0% 36.11 | 62% 0% | 75% 50% 63.9% 0% | 0% 0% 100% 100% | 0% 0.0% | SON | 100% 100% 83.3% S 0% 0% 100% 100% 100.0% | 0% 0% 0% 16.7% 0% 0% | 0% 0% 900% | 0% 0.0% 100% | 100% 0% 0% | 00% 100.0% | 90% 9% 9% | 90 | 0% 0% 100% | | 0.2918 | 0.0705 | 0.2918 | 0.0705 | | | |
| D Gadmdc1 associated phosphop Skap2 tation factor GTPase- Artgap1 at Rho GTPase 2 Rhot2 | | kDa 100% 10 | N 50% | 00.0% 0% 05.7% 20% 05.9% 22% | 0% 0 42% 40 52% 40 | ns 0.0% ns 33.3% ns 41.1% | 0% 0% 0% 0% | 0% 0.07 0% 0.07 0% 0.07 | 6 100% 100 6 100% 67 6 100 | % 100% 55.97 % 100% 55.97 | 0% 0% | 0% 0% 0.0% 23% 0% 11.1% 0% 0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% | 100% 100% 100.0% 100% 100% 100% 100.0% | 0% 0% 0% 0.0% 0% 0% 0% 0.00% | 0% 0% 0% 0% | 0% 0.0% 0% 0% 0.0% | | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 00% 00% | 0% 0% 0% 0% | 0% 0.0% | 0.1771 | 0.0377 0.0136 | 0.1771 | 0.0377 | | | |
| D Gadmid: 1 sasocialed phosphos Stap2 tation factor GIPrase Artipp1 al Rho GIPrase 2 Rho(2) open dearninase Hinbs 1 Artip2 sasocialed rante Stap1 | APP2_MOUSE 39 SKP1_MOUSE 19 | kDs 67% S | | 33.3% 0% | 0% S0 25% 20 | N 15.7% | 0% 0% 0% 0% | 0% 0.07 0% 0.07 | 4 AMOS AND | 67% N 100% 100.07 | 9% 9% | 22% | ons ons | os. | 200% 2% 200% | 00% 100% 100.0% 0% 0% 0.0% 10 100% | 0% 0% 0% 0.0% 0% 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 1 25% 14% 100% 75% 1 | 00% 100.0% 25% 21.4% 00% 91.7% | 0% 0% 50% 64% 4 0% 25% | 00 00% 0 52.0% 2 0 6.3% | 0% 0% 5% 21% 0% 0% | 0% 0.0% 33% 26.6% 0% 0.0% | 0.4226 0.9365 0.9385 | 0.4226 0.1885 | 0.4028 0.7103 0.9386 0.4 | 0.4225 0184 4225 0.1885 | 0.7103 | 0.0171 | |
| O Gadreit I associated ehosphee Skap2 billion factor GTPase- Artgap1 list on factor GTPase- Artgap1 list on factor GTPase Proc | HEMS MOUSE 39 AREP2 MOUSE 38 SKP1 MOUSE 19 ASSA1 MOUSE 85 NMES1 MOUSE 10 ELOB MOUSE 13 | KDs 57% S KDs 100% 10 KDs 100% 7 | N 50% | 5.0% 0% | | 0.0% | 0% 0% 0% 17% 0% | 205 12.25 | 5 100% 100 5 100% 100 | % 100% 100.07 % 100% 100.07 % 100% 100.07 | 9% | 23% 0% 0% 0.0% 0% 0.0 0.0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 200N 9N | 0% 25% 8.3% 10 | 2% 0% 0% 0.0% 2% 100% 25% 91.7% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 1 | 00% 100.0% 0% 0.0% 1 | 0% 0% 00% 100% 10 | 25 0.0% 25 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0.422 | | 0.4 | | 0.18 | 9 | |
| D Gadmict sanociale debackes Stap2 state factor GFPsae- Artgap1 at Pto GFPsae- Per Stap2 spending state factor GFPsae- Artgap2 spending state factor GFPsae- Artgap2 spending state factor state factor spending state factor spending state factor spending spending state factor spending state factor spending spe | PART LOUIS | HCBs 67% 5 HCBs 100% 10 HCBs 100% 7 HCBs 100% 7 HCBs 100% 10 HCBs 100% 10 HCBs 100% 10 | N 90% N 90% N 100% N 90% | 15.0% 0% 10.0% 0% | 200% 0% 0 | | 0% 0% | 95 0.07 95 | 100% 100 0% | S 100% 100.07 | 2% 100% | ON ON 0.0% | 0% 0% 0% | 05 0.0% | 200% 200% | 100% 100% 100.0% 100% 100% 100.0% | 25 | 0% 0% 0% 0% | 0% 0.0% | 100% 90% 1 | 00% 96.7% | 0% 20% | 25 3.25 25 3.25 | 2% 0% | 0% 0.0% | 0.422 | 5 | 0.4226 0.4 | 4225 | 0.4226 | | |
| CCHC domain-contai Zocholi pied neutral arrino se Sk:386 sesociated membrana Lamp1 lhypein 1-4 Serpina1d serotein licase TRMC TrimDS | HEMO_MOUSE 30 AFFEE_MOUSE 32 AFFEE_MOUSE 32 AFFEE_MOUSE 32 AFFEE_MOUSE 35 AFFEE_MOUSE 35 AFFEE_MOUSE 31 AFFEE_MOUSE 31 AFFEE_MOUSE 31 AFFEE_MOUSE 31 AFFEE_MOUSE 31 AFFEE_MOUSE 32 AFFEE_MOUSE | HADB | N 90% N 90% N 100% N 100% N 100% N 200% 200% | 15.0% 0% 10.0% 0% 17.8% 0% 10.0% 0% | 200% 0% 0 0% 0 100 | S 0.0% | 9% | | | | | | | w ar- | 2% 2% 20% | 0% 0% 0.0% 10 100% 100% 100.0% | 0% 100% 100% 100.0% 0% 0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 0% 0% 100% 100% 1 | 0% 0.0% 1 00% 100.0% | 00% 100% 10 0% 0% | 25 100.0% 25 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | |
| CCHC domain-contai Zocholi pied neutral arrino se Sk:386 sesociated membrana Lamp1 lhypein 1-4 Serpina1d serotein licase TRMC TrimDS | HEMA] MOUSE 30 APPER MOUSE 32 APPER MOUSE 32 ASSAT MOUSE 32 ASSAT MOUSE 32 ASSAT MOUSE 32 ASSAT MOUSE 32 ELOB MOUSE 32 ECHO MOUSE 32 ECHO MOUSE 32 ECHO MOUSE 32 ECHO MOUSE 33 ECHO MOUSE 33 ECHO MOUSE 34 ANATA MOUSE 34 ANATA MOUSE 32 ECHO MOUSE 33 ESTE MOUSE 34 E | HGB | S 52% N 82% N 102% N 102% N 102% N 102% N 102% N 102% | 15.0% 0% 10.0% 0% 17.0% 0% 10.0% 0% | 900% 9% 0 9% 0 100 | S 9.0% | 9% (w) | | 100% *** | s 100% 222.00 | . 0% | 0% 0% 00** | | | 6000 | 100% 50% 67% 47.2% 7 | 0% 5% 50% 32% 52.8% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% 1 | 00% 100.0% 0% 4 PM | 0% 0% 0% 0% | % 0.0% % 95.2% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0° | 0.048 0.6087 0.808 | 0.2187 | 0.3195 0.6087 0.8 0.4226 0.4 | 0.2187 | | | |
| CCHC domain-contai Zocholi pied neutral arrino se Sk:386 sesociated membrana Lamp1 lhypein 1-4 Serpina1d serotein licase TRMC TrimDS | HEMA MOUSE 10 | 150a 578 5 | N 90% N 100% N 100% N 100% N 100% N 100% OX | 15.0% 0% 00.00% 0% 00.00% 0% 00.00% 0% 00.00% 0% 00.00% 00 | 200% 0% 0 0% 0 100 200 0% 0% 0% 0% 0% 0% | S 0.0% | 9% 9% 9% 9% 9% | 0% 0.09 0% 0.00 | 100% 100 6 0% | N 100% 100.07 | 200 C | ON ON 0.0% | 0% 0% 0% 0% | gs 0.09 | 25% (%) | | | 9% 9% | 0% 0.0% | 100% 100% 1 100% 100% | 00% 100.0% | 0% 0% | 0.0% | - OW | | | | | | 0.3195 | | |
| CCHC domain-contai Zocholi pied neutral arrino se Sk:386 sesociated membrana Lamp1 lhypein 1-4 Serpina1d serotein licase TRMC TrimDS | HERD JACKSE 20 | 150a 57b 5 | N 90% N 100% N 100% N 100% N 100% N 100% OX | 15.0% 9% 15.0% 9% 17.8% 9% 100% 100% 100% 100% 11.1% 100% 11.1% 100% 11.1% 100% 10.0% 9% | 202% 2% 0 2% 0 100 2% 2% 2% 2% 2% 2% 2% 2% 2% 2% | S 92% S 92% S 93.2% S 93.2% S 93.2% S 94.2% S 92.2% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.09 0% 0.09 0% 0.09 0% 0.09 | 100% 200 6 0% 6 40% 0 6 100% 100 6 100% | % 20% 20.07 % 20% 20.07 % 100% 100.07 | 200 200 200 200 200 200 200 200 200 200 | 0% 0% 0.0% 0% 80% 00.0% 0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 25% 0% 50% 100% | 0% 20% 6.7% 10 100% 100% 83.3% S 100% 100% 900.0% | 0% 0% 0% 16.7% 0% 0% 0% 0.0% | 0% 0% 0% 0% | | | 00% 100 m. | 0% 0% | 06 0.0°C | 0% 0% 0% 0% | 0% 0.0% | 0.4226 0.4226 | 1,0000 | 0.4226 0.4 | 4225 1.0000 | 0.3195 | | - |
| CCHC domain-contai Zocholi pied neutral arrino se Sk:386 sesociated membrana Lamp1 lhypein 1-4 Serpina1d serotein licase TRMC TrimDS | HERD SAUGHE 20 | 150m 57% 5 | N. 92% N. 92% N. 92% N. 92% N. 100% N. | 15.0% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% | 200% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 65 9.0% 65 9.0% 65 9.0% 66 9.0% 66 9.0% 66 9.0% 67 9.0% 68 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 | 100% 100% 6 00% 6 40% 0 6 100% 100 6 100% 100 6 100% 100 6 100% 100 6 100% 100 | % 100% 100.07 % 20% 20.07 % 100% 100.07 % 100% 100.07 % 100% 100.07 % 100% 100.07 % 100% 100.07 | 200% 200% 21 00% 00% 00% 00% 00% 00% 00% 00% 00% 00 | 0% 0% 0.0% 0% 00% 0.0% 0% 0% 0.0% 0% 0% 0.0% 0% 0.0% 0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0% 0.0% 0% 0% 0.0% | 25% 2% 50% 50% 100% 100% 100% 100% | 0% 20% 6.7% 10 100% 100% 83.3% 5 100% 100% 100.0% 100% 100.0% 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 16.7% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 100% 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% 0% 0% | 06 0.0% 06 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.4226 0.422 | 1,0000 | 0.4226 0.4 | 1.0000 | 0.3995 | | |
| COFFS demissionated, Zochell seider neutral errors aus Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Textical demanischerotisterium in Textical demanischerotisterium in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Statistical senschlaringen in Statistica | HEMB_LOUSEE | 150m 57% 5 | N 90% N 100% N 100% N 100% N 100% N 100% OX | 15.0% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% | 200% 9% 0 9% 0 9% 0 9% 0 9% 0 9% 0 9% 0 | 6 9.0% 6 9.0% 6 9.0% 6 9.0% 6 9.0% 6 90.0% 6 90.0% 6 90.0% 6 90.0% 6 90.0% 6 90.0% 6 90.0% 6 90.0% 6 90.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 | 100% 200 5 0% 6 40% 5 6 100% 200 6 100% 500 6 100% 300 6 100% 300 6 100% 300 6 100% 300 6 00% 300 | % 20% 20.07 % 20% 20.07 % 100% 190.07 % 100% 190.07 % 100% 190.07 % 100% 190.07 | 200% 200% 60% 21 00% 00% 00% 00% 200% 200% 200% | 0% 0% 0.0% 0.0% 0.0% 0% 0% 0% 0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0% 0.0% 0% 0.0% | 25% 0% 50% 300% 300% 300% 300% 0% 300% | 0% 20% 6.7% 10 00% 100% 100.0% 50 100% 100% 100.0% 100% 100% 100.0% 100% 100.0% 100% 100.0% 100% 100.0% 100% 100.0% | 0% 0% 0% 18.7% 0% 0% 0% 0% 0.0% 0% 0% 0% 0% 0.0% 0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% 0% 0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 100% 100% 1 100% 100% | 00% 100.0% 00% 100.0% 00% 100.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | | | | 1.0000 | 0.3985 | | |
| COFFS demissionated, Zochell seider neutral errors aus Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Textical demanischerotisterium in Textical demanischerotisterium in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Statistical senschlaringen in Statistica | HEND LOUSE | 150m 57% 5.0 | N 90% N 100% N 100% N 100% N 100% N 100% OX | 15.0% 98: 000.00% | 9000 000 000 000 000 000 000 000 000 00 | S | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 0% 0.07 | 100% 206 6 0% 6 6 00% 0 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 00% 0 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 6 100% 500 | % 100% 100.09 % 200% 20.09 % 200% 20.09 100% 1000% % 100% 100.09 % 100% 100.09 % 100% 100.09 % 100% 100.09 % 100% 100.09 % 100% 100.09 % 100% 100.09 % 100% 100.09 % 100% 100.09 % 100% 100.09 | 200% 200% 200% 200% 200% 200% 200% 200% | 0% 0% 00% 00% 80% 800% 00% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 25% 0% 50% 100% 100% 100% 100% 0% 100% 0% 10 | 0% 20% 6.7% 10 00% 100% 13.3% 5. 100% 100% 100.0% 100.0% 100% 100% 100.0% 100% 100.0% 100.0% 100% 100.0% 100% 100.0% 100% 100.0% 100% 100.0% 100% 100.0% | 0% 0% 0% 16.7% 0% 0% 0.0 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 100% 100% 1 100% 100% | 00% 100.0% 00% 100.0% 00 00 00 00% 100.0% 00% 33.7% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 0.4226 0.4228 0.2229 0.5180 0.6244 | | | 1.0000 | 0.3985 | 9 0.5185 | 5 0 |
| COFFS demissionated, Zochell seider neutral errors aus Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Textical demanischerotisterium in Textical demanischerotisterium in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Statistical senschlaringen in Statistica | MARCHA M | 150m 57% 5.0 | N 90% N 100% N 100% N 100% N 100% N 100% OX | 15.0% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% | 900 00 00 00 00 00 00 00 00 00 00 00 00 | S. 93.2% S. 93.2% S. 93.2% S. 93.2% S. 93.2% S. 93.2% S. 93.2% S. 93.2% | 9% | 9% 0.07 9% 0.07 | 1000% 2006 5 00% 5 00% 5 1000% 200 6 1000% 300 6 1000% 500 6 1000% 500 6 1000% 500 6 1000% 500 6 1000% 500 6 1000% 500 6 1000% 500 6 000 0 | % 100% 900.07 % 20% 20 900.07 % 100% 900.07 | \$ 0% \$ 200% \$1 0% \$200% \$2 0% | 0% 0% 0.0% 00% 80.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | 25% 0% 50% 100% 100% 100% 100% 0% 100% 0% 100% 0% 100% 0% 100% 0% 100% 0% 100% | 0% 20% 6.7% 10 00% 100% 10.3% 5.2% 5.00% 100% 900.0% 5.00% 100% 900.0% 5.00% 100% 900.0% 5.00% 100% 900.0% 5.00% 100% 900.0% 5.00% 100% 900.0% 5.00% 100% 900.0% 5.00% 00% 0.0% 5.00% 00% 0.0% 5.00% 100% 100% 5.00% 100% 100% 5.00% 100% 100% 5.00% 100% 100% 5.00% 100% 100% 5.00% 100% 100% 5.00% | 20 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 1 100% 100% 1 100% 100% 1 100% 100% | 00% 100.0% 00% 100.0% 0% 00% 100.0% 00% 100.0% 00% 33.2% 75% 47.2% | 0% 0% 0% 00 00 00 00 00 00 00 00 00 00 0 | 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 2% 190% 56.7% 25% 19.4% | | | | 1,000 | 0.3925 | 9 0.5105 | 5 0. |
| COFFS demissionated, Zochell seider neutral errors aus Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Textical demanischerotisterium in Textical demanischerotisterium in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Statistical senschlaringen in Statistica | FERD, MAJOR 19 | 150m 572 5 150m 572 5 150m 500 10 150m | N 90% N 100% N 100% N 100% N 100% N 100% OX | 15.0% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% | 900% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 6. 3.0% 6. 3.0% 6. 3.3% 6. 33.3% 6. 35.5% 6. 35.5% | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0,000 0% 0,000 | 100% 100% 56 6 100% 100 100% 100% 100% 100% 100% 10 | M 1000% 700,070 M 200% 20,070 M 200% 100,070 M 1000% 1000% M 1000% 1000% | 00% 10 | 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | COS. GOS. GOS. GOS. GOS. GOS. GOS. GOS. G | 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | 25% ON 50% SON | 08 20% 6.7% 50 20% 50 2 | N | 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% | 100% 100% 1 100% 100% 1 100% 100% 1 100% 100% | 00% 100.0% 000.0% 00% 000.0% 0 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 2% 0.0% 2% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | | | | 1.0000 | 0.3925 | 9 0.5105 | 0.8 |
| COFFS demissionated, Zochell seider neutral errors aus Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Sichalde senschlaringen in Textical demanischerotisterium in Textical demanischerotisterium in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Textical senschlaringen in Textical demanischerotisterium in Textical senschlaringen in Statistical senschlaringen in Statistica | 20HCB_MOUSE 78 538A5_MOUSE 53 LAMP1_MOUSE 44 A1AT4_MOUSE 46 TRISS_MOUSE 79 | 100. 278 5 100. 100. 100. 100. 100. 100. 100. 10 | N 90% N 100% N 100% N 100% N 100% N 100% O 100% | 55.0% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% | 900% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | N. S. | 9% | 0% 0.070 0% 0.070 | \$ 100% \$ 100 \$ 5 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 | 50 100% 300.07 50 20% 20.07 50 20% 300.07 50 20% 300.07 50 20% 300.07 50 100% 300.07 50 | \$00% \$200% \$ | 5% 50% 50% 50% 50% 50% 50% 50% 50% 50% 5 | ON O | 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | 25% ON 50% SOM 500% S | 08 20% 6.7% 100 08 100% 100% 13.7% 15 000 100% 100% 100.0% 000% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100.0% 100% 100% 100% 100.0% 100% 100% 100% 100.0% 100% 100% 100% 100.0% 100% 100% 100% 100.0% 10 | 10 | 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | ON 0.0% ON 0.0 | 100% 100% 1 100% 100% 1 100% 100% 1 100% 100% | 00% 100.0% 000.0% 000 000.0% 00 | 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9% 9 | 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0 | 050 050 050 050 050 050 050 050 050 050 | 9% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0. | 0.2929 0.5180 0.6264 | | 0.3059 0.0044 | 1225 1.0000 11004 1200 0.2500 | 0.3985 | 9 0.5%5 | 5 0.0 |

| sociated membrane or Vernpill rolein phosphatese no Pipn 1 1 tase Iflavin-containing! Macb | VAMPE MOUSE 11 kOs PTN11 MOUSE 65 kOs AOFE MOUSE 59 kOs | 100% 100% 100 100% 100% 100 100% | 100,0% 0% 100,0% 0% | 6 0% 0 6 0% 0 | 0% 0.0% 09 0% 0.0% 09 | 5 0% 5 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% | 100% 100.0% | 98 | 0% 0% 0/ | 25 05 | 9% 9 9% 9 | n 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 9% 9 9% 9 9% 9 | 6 0% 0.0% 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% 100% | 100% 100.0% (100% 100.0% (100% | % 9% 0 % 9% 0 | S 0.0% 09 S 0.0% 09 | 0% 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | | |
|--|--|--|---|--------------------------------------|--|--------------------|--|--|---|------------------|------------------------------|--------------------------|---|---|------------------------|--|-------------------------|--|----------------------|--|---|--|--------------------------|---------------------------------|----------------|--|--------|------------------------|------------------|----------------------------|--|----------------------------|------------------|------|
| e IV collegenate Mmp2 ir cross-complementin Xrcr* | PATE 100.000 | 100% | - Au | | | | | 100% 100% | 100% 100.0% | 98 | MN 9% 0/ | C/M 0% | 978 O | 0.0% | 50% 100% | 100% 83.3% 100% 83.3% 100% 100% 9% 9% 9% 100% 900.0% | SON ON | 0% 16.7% 0% | 0% 0 | 0% 0.0% 0% | 100% 100% 100% | 100% | % UN | 09 09 | UN | 05 | | - | | _ | | | | |
| r 70 kDs protein 4L Hepsell no motif, single-strands (Rbms2 | REMSZ MOUSE 94 KDs REMSZ MOUSE 41 KDs | | | 100 | es. | | 9% | | | | | | | | 100% | 100% 0% | 2% 100% | 9% 200% | | 05 0.05 6 05 6 05 6 05 6 05 | 100% 100% | 1 200% 100.0% | % 0% 0 | S 0.0% 09 | 0% | 0% 0.0% | | | | | | | | |
| biosenesis protein BFL Brist of chromosome conde Roc1 | RCC1_MOUSE 45 kDs | 0% 0% 0 | 0.0% 100% | 5 100% 100 | 0% 100,0% 09 | 6 0% | 0% 0.0% | 0% 0% | | 100% 10 | ON. | 0% | 9% | | 100% 100% | 0% 100% 100.0% | ox ox | 0% 0.0% | 0% 0 | 0% 0.0% | 100% 100% | 100% 100.0% | % 0% C | x 0.0% 09 | 0% | 0% 0.0% 0% 16.7% | | | | | | | | |
| ry acidic protein Glap | GFAP MOUSE 50 KDs | 100% | | 9% | | 0% | | | | | | | | | 0% 0% | | 100% 100% | | 0% 0 | | 50% 86% 0% | 100% 78.0% | % 18% C | S 4.85 529 | | | | | | | | | | |
| ane protein complex is Emc7 | EMC7 MOUSE 25 KDs | 0% 25% 0 100% 100% 50 100% 100% 50 100% 100% 50 100% 100% 50 100% 100% 50 100% 100% 50 | 8.3% 100% | 6 50% 100 | 0% 83.3% 09 | 1 25% | 0% 8.2% | ON CON | 1000 METE | 100 | 0% | W 60 | 0% | | 22% | 0% 67% 55.8% | 22% | 62% 22% | 22% | 22% | 0% 0% | 0% 0.0% 50 | % 100% C | % 50.0% SON | 0% 1 | 0% 50.0% 0% 0.0% | 0.500 | 00 0.7103 | 0.3379 0.5 | 1,0000 | 0.2628 | 0.3329 | 0.6220 | 0.00 |
| Mod Mod | MTX1_MOUSE 35 kOs ATG3_MOUSE 35 kOs | 100% 100% 500 100% 100% 100 | 6 100.0% 0% | 0% SC | 0% 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | 0% 50% 50% 100% 100% 100% 100% 100% 100% | 100% 900.0% | 0% 0 | 0% 0% 0.0 0% 0% 0.0 | 2% 0% 2% 0% | 0% 0 0% 0 | ns 0.0% | 100K 100K | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 6 0% 0.0% | 0% S0% 100% 100% | 100% 88.9% | % 2/% C | % 11.1% 09 5009 % 0.0% 09 | Son | 0% 0.0% | 0.010 | 02.02 | 0.2048 | 180 05000 | 0222 | 0.2019 | | |
| v molecular chaperone Bag1 41-N-acety/-beta-duc Ndy1 | BAG1_MOUSE 40 kDs NGLY1_MOUSE 74 kDs | 100% 100% 100% 0% | 9% | 6 0% | 09 | 6 0% 6 100% | | 100% 100% 100% | 100% 100.0% | 0% 0 | 0% 0% 0. | 2% 0% | 0% 0 | 0.0% | 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% | 0% 0.0% | 0% 0 0% | 6 0% 0.0% | 100% 100% | 1 200% 100.0% 0 | % 0% C | % 0.0% OF | One | 0% 0.0% 0% 0.0% | | | | _ | | | | |
| no motif, sindle-strands (Rbms.1 II1 homolog 2 Dd2 | REMS1_MOUSE 44 kOs DOI2_MOUSE 45 kOs | 0% 0% 0 100% 100% 100 | 0.0% 100% 100.0% 0% | 6 100% 100 6 0% 0 | ON 100.0% ON | 6 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | ON ON | 0% 0.0% 100% | 100% 10 | 0% 100% 100.0 0% | 2% 0% | 0% O | N 0.0% | 0% 0% 100% 100% | 0% 0.0% 100% 100.0% | 100% 100% 0% 0% | 100% 100.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 0% 0% 100% 100% | 0% 0.0% 100 1 100% 100.0% 0 | % 100% 100 % 0% 0 | % 100.0% 09 % 0.0% 09 | 0% | 0% 0.0% | | | | | | | | |
| d protein R-Ras Ross | THEM MOUSE 24 KOs | 100% 100% 100 100% 100% 100 | 100.0% 0% 100.0% 0% | 6 0% 0 6 0% 0 | 0% 0.0% 09 0% 0.0% 09 | 5 0% | 0% 0.0% 0% 0.0% | 100% 100% | 100% | 9% | os os | 0% | 9% | N | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 100% 100.0% 0 | % 0% 0 | S 0.0% 09 S 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | 0.422 | | | | | | | |
| e protein KIF3B KIF3b signal cointegrator 1 Trip4 | KIF36_MOUSE 85 kDs TRP4_MOUSE 65 kDs | 0% 0% 0 | 6 0.0% 100% | 5 100% 100 | 0% 100.0% 09 | 5 0% | 0% 0.0% 0% 0.0% | | 05 0.05 | 100% 10 | 0% 100% 100. | 0% | 9% | | 9% | 0% 0.0% 100% 90.0% 100% 90.0% 100% 90.0% 0% 100% 90.0% 100% 100.0% 100% 91.7% 100% 91.7% | 100% | 200N | 0% | 0% | 23% 0% | 98 11.7% 6 | % 100% 100 | x 88.9% 09 | 0% | 0% 0.0% | 0.422 | 26 | | 0.4225 | | | | |
| sonine-protein phosphy Ppp2/5c | 2ASG MOUSE 61 kDs | 190% | 0.0% 100% 0% | 6 100% 100 6 | 05 500,0% 05 | 5 0% | 0% 0.0% | ON ON | 05 0.05 | 100% 10 | 0% 100% 100. | 2% 0% | 0% 0 | 0.0% | 0% 100% | 100% | 0% | 0% | 9% | ON. | 100% 100% | 100% 100.0% | % 0% C | s 0.0% on | 0% | 0% 0.0% | | | | | | | | |
| nt component C1o rec Cd93 | CTORT MOUSE 59 KOs | 06 | | 100% | | 0% | | | | | | | | | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 9% 0 | 0% 0.0% | 1005 | 2005 | 98 0 | - | OS. | SON . | | | | _ | | | | |
| otidase Nicatalytic chi Cpn1 saminidase subunit alb Hexa | CEPN MOUSE 52 kDs HEXA MOUSE 61 kDs | | | | | | | | | | | | | | 75% 100% 100% 100% | 100% 91.7% 100% 100.0% | 25% 0% 0% 0% | 0% 8.3% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% | 100% 1 100% 100.0% | % 0% C | N 0.0% 09 | 0% | 0% 0.0% | | | | | | | | |
| tidase complex subunit Spcs1 ntally-regulated GTP-1 Drg2 | SPCS1_MOUSE 18 kOs DRG2_MOUSE 41 kOs | 100% 100% 50 100% 100% 100 | 6 83.3% 0% 6 100.0% 0% | 6 0% S0 | 0% 15.7% 09 0% 0.0% 09 | 5 0% | 0% 0.0% 0% 0.0% | 100% 50% 60% 100% | 100% 83.3% 100% 85.7% | 20% | 0% 0% 0. 0% 0% 6. | 2% 0% 2% 20% | 50% O | N 15.7% | 50% 50% 100% 100% | 100% 55.7% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 50% S0 0% 0 | 6 0% 33.3% 6 0% 0.0% | 100% 100% 100% | 100% 100.0% | 9% % 9% 0 | s 0.0% on | 0% 0% | 0% 0.0% | 0.4226 | 0.5185 | 0.4225 0.4 | 226 226 | 0.4225 | 0.422 0.4226 0.422 | 15 | 0. |
| ovroehoschatase 2. mi Pps2 see 2 Ctps2 | PYRG2_MOUSE 55 kOs PYRG2_MOUSE 65 kOs | 100% 100% 100 100% 100% | 100.0% 0% | 6 9% C | 0% 0.0% 09 | 5 0% | 0% 0.0% | 100% 100% 100% | 100% 100.0% 100% | 9% | 0% 0% 0.1 0% | 2% 0% | 9% 0 | N 0.0% | 100% 100% 100% | 100% 100.0% | 0% 0% 0% | 0% 0.0% | 9% O | 6 0% 0.0% | 100% 100% 100% | 200% 100.0% (| % 9% C | S 0.0% 09 | 0% | 0% 0.0% 0% | | | | | | | | |
| continue crotein shoughs Ppp fcc | PPIG MOUSE 37 KOs TRACT MOUSE 50 KOs | 100% 100% 50 100% 100% 100 100% 100% 100 100% 100% 100% 100% | 100.0% 0% | 6 0% 0 | 0% 0.0% 09 0% 0.0% 09 | 6 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% | 100% 100.0% | 0% | 0% 0% D | 2% 0% | 0% 0 | 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 22% | 0% 0.0% 0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% 6 0% 33.2% 6 0% 0.0% 6 0% 0.0% 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% 100% 100% 100% 100% | 200% 100.0% 0 | % 0% 0 | % 0.0% 09 % 0.0% 09 | 0% | 9% 0.0% 9% 0.0% 9% 0.0% 9% 0.0% 90% 0.0% 90% 0.0% 90% 0.0% | 0.500 | 20 | | 0.5000 | | | | |
| Coroža emolog 1 Niti | CORDA MOUSE 60 kDs NT1 MOUSE 36 kDs | 100% 100% 100 | 100.0% 0% | 6 0% 0 | 0% 0.0% 09 | 6 0% | 0% 0.0% | 100% 100% | 100% 100.0% | 9% | on on o | 2% 0% | 0% 0 | n 0.0% : | 100% 100% 0% 0% | 100% 100.0% | on on | 0% 0.0% | 0% 0 | 016 016 0.07% 016 0.07% 016 0.07% 016 0.07% 016 0.07% | 20% 10% 100% 100% | 20% 15.7% 60 100% 100.0% | % 20% 40 % 0% 0 | % 56.7% 209 % 0.0% 09 | 20% | 0% 25.7% 0% 0.0% | | | | | | | | |
| n Nupl3 Nupl3 ation factor gamma Grefg | NLP43 MOUSE 42 kOs GMFG MOUSE 17 kOs | 0% 0% 0 100% 100% 100 | 0.0% 100% 100.0% 0% | 6 200% 100 6 2% 0 | ON 100.0% 09 | 6 0% | 0% 0.0% 0% 0.0% | ON ON 100% | 0% 0.0% 100% | 100% 10 | 0% 100% 100.0 0% 0% | 2% 0% | 0% 0° | ns 0.0% | 0% 0% 100% 100% | 0% 0.0% 100% 100.0% | 100% 100% 0% 0% | 100% 100.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 0% 0% 100% 100% | 0% 0.0% 100 1 200% 100.0% 0 | % 100% 100 % 0% 0 | % 100.0% 09 % 0.0% 09 | Oni Oni | 0% 0.0% | | | | | | | | |
| se-activatino protein 11 Arhgap18 al colvruciectide phosp Prikp | PNKP_MOUSE 57 kOs | 100% | | 0% | | CHL | | 100% | | 0% | | 0% | | | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% | 100% 100% | 1 200% 100.0% 0 | % 0% C | % 0.0% 09 | One | 0% 0.0% | | | | | | | | |
| nucleoide/iransferass Tret Corolla corolla corolla corolla nerelog 1 Net | AATF_MOUSE 59 kDs | 0% 0% 0 | 0.0% 100% | 5 100% 100 | ON 100.0% ON | 5 0% | 0% 0.0% | 0% | 0% | 100% | 100% | 0% | | ns. | 9% | | 100% | | 9% | | _ | 100% 100% 100,0% | | | | 0% 0.0% | | | | | | | | |
| entein sortino sessorial Vpp65 | VPS45_MOUSE 65 KDs | 0% 0% 0 | 0.0% 100% | 5 100% 100 | ON 100.0% OF | 5 0% | 0% 0.0% | - ON | | 100 | os . | | 9% | | 100% | ev 0.00 | 1000 | 100V 100 0V | | | 100% | 2005 100.05 | S 28 C | 09 | - 05 | 98 095 | | | | _ | | | | |
| din Gili synthase 1 Pigs 1 | POHI MOUSE 69 KOs | | | | | | | | | | | | | | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 0% 0.0% | 100% 100% | 100N 100.0% (| % 0% C | 09 W 0.0% 09 | 0% | 0% 0.0% | | | | _ | | | | |
| rotein kinase CSK Csk t and cell motility prote Elmo1 | CSK MOUSE 51 kDs ELMO1 MOUSE 84 kDs | | | | | | | | | | | | | | 100% 100% 100% | 100% 100.0% | 0% 0% 0% | 0% 0.0% | 0% 0 0% | 0% 0.0% | 100% 100% | 1 200% 100.0% (200% | % Q% C | S 0.0% 09 | 0% | 0% 0.0% | | | | | | | | |
| ral amino acida transo Sic7a5 2A chain C region sec 1 5V | GCAB MOUSE 37 KDs | 100% 100% 100 | 100.0% 0% | 98 6 | 0% 0.0% 09 | 0% | 0% 0.0% | 100% 100% | 100% 100.0% | 9% | 0% 0% 0. | 2% 0% | 0% 0 | 0.0% | + | | \perp | + | _ | \vdash | 100% | 100% | 9% 0 | | 0% | 0% | | | | | = | | _ | |
| pe is curroular Hb2 Krift2 mai-associated protein Snag23 | SNP23 MOUSE 23 KOs | 50% 50% 50 50% 1000 | 50.0% 50% | 50% SG | ON 50.0% OF | 5 0% | 0% 0.0% | 100% CN | 100% *** | 101 | 0% | 94. ~ | 9% | ns 11 *** | 20% 67% | 23% 40.0% | 60% 0% | 22% 31.1% | 20% 33 | 22% 28.9% | 60% S0% | 50N 53.7N 20 | N 9N 50 | S 23.3% 209 | son | 0% 23.3% | 0.440 | 0.5460 | 0.0745 | 0.7489 | 0.3901 | 0.000 | 0.7447 | 0.0 |
| d dutathione 5-bande Mgst1 | 1892, 1902, | 100% 100% 100 | 100.0% | 6 0% | ON 0.0% ON | 6 0% | 0% 0.0% | 2000 975 2006 | 100% | | 0% 0% | - 05 | 9% 0 | n | 50% 50% 100% 100% | 20% 40.0% 100% 100.0% | 0% 0% 0% 0% | 9% 9,0% 9% 9,0% | 50% 50 0% 0 | 80% 80.0% 6 0% 0.0% | 17% 67% 100% 100% | 50% 44.4% 1 | % 9% 6 | S 0.0% 839 | 22% | 0% 55.6% | 0.016 | 25 | | _ | - | U.Par. | 0.8165 | 5 |
| darobase Fuom | FUCM MOUSE 17 KDs LXN MOUSE 25 KDs | 100% 100% 100 100% 100% 100 | 100.0% 0% 100.0% 0% | 6 0% C | 0% 0.0% 09 0% 0.0% 09 | 6 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 9% | 0% 0% 0. 0% 0% 0 | 2% 0% 2% 0% | 0% 0 0% 0 | 0.0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% (100% 100.0% (| % 0% 0 | % 0.0% 09 % 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | | | | | | | | |
| ficity protein phosphat Dusp3 replex subunit Mc25 Chchd5 | DUS3 MOUSE 20 KDs MIC25_MOUSE 30 KDs | 100% 100% 200 100% 100% 200 100% 100% 200 100% 100% 100 0% 0% 0 0% 0 0 | 6 100.0% 0% 6 0.0% 100% | 6 0% 0 6 100% 100 | 0% 0.0% 09 0% 0.0% 09 0% 0.0% 09 0% 0.0% 09 0% 0.00% 09 | s ons | 0% 0.0% 0% 0.0% | 100% 100% 0% 0% | 100% 100.0% 0% 0.0% | 9% 1 | 0% 0% 0.0 0% 100% 100.0 | 2% 0% 2% 0% | 0% 0° | ns 0.0% : | 100% 100% 0% 0% | 100% 100.0% 0% 0.0% | 0% 0% 100% 100% | 0% 0.0% 100% 100.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 0% 0% | 100% 100.0% 0 | % 0% 0 % 100% 100 | % 0.0% 09 % 100.0% 09 | 0% | 0% 0.0% 0% 0.0% | | | | | | | | |
| reased matrix-associat Smarch1 s perceidase 2 Gps2 | GPK2 MOUSE 22 kOs | | 0.0% 100% 100.0% 0% | 100% 100 | 0% 100.0% 09 0% 0.0% 09 | 0% | 0% 0.0% | | 1000 | | | | | | 100% 100% | 0% 100% 100.0% | 0% 0% | 900% 0% 0.0% | 0% 0 | 0% 0% 0.0% | 100% 100% | 0% 1 200% 100.0% 0 | % 0% 0 | % 0.0% 09 | 0% | 0% 0.0% | | | | | | | _ | |
| in-containing protein 7 Sh2d7 | SHEDT MOUSE 51 KDs | 100% 100 | - AUUTN 0% | - O% C | UN UUN 09 | COS. | UA 0.0% | 400% S00% | 100% 100.0% | 0% | | P. 10% | 0% O | 0.0% | 100% 100% | 100% 900 0% | 0% 6% | 0% 0.0% | 0% ^ | CRL 0.00 | 0% 0% 100% 100% | 0% 0.0% 100 100% 100.0% | % 100% 100 % 0% | % 100.0% 09 % 0.0% *** | One One | 0% 0.0% 0% 0.0% | | | | _ | | | 1 | |
| mai protein 530, mitor Mrps30 sking Old | RT30_MOUSE 50 kOs ON MOUSE 36 kOs | 100% | 0% | 6 | 09 | | | | | | | \pm | | | 25 205 | 0% 6.7% | 100% 80% | 100% 93.3% | 98 0 | 05 0.0% | 100% 0% 0% | \$500 53.2% 2.6 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1) | 0% % 100% *** | 5 100.0% O | 0% | 0% 0.0% | 0.422 | 26 | | 0.4226 | | | | |
| nulusine Oursenhilarate Plod1 celdase Manba | RTDS MOUSE 50 kDs COS MOUSE 50 kDs COS MOUSE 50 kDs COS MOUSE 50 kDs COS MOUSE 50 kDs 50 | | | | | | | | | | | | | | 100% 100% 100% | 100% 100.0% | 0% 0% 0% | 0% 0.0% | 0% 0 0% | 0% 0.0% | 100% 100% 100% | 100% 100.0% | 9% % 9% 0 | S 0.0% 09 | 0% | 0% 0.0% | | | | | | | | |
| oniusaino erzyme E2 Ube2vi | STID1_MOUSE 35 KDs UB2V1_MOUSE 16 KDs | 75% 100% 67 | 50.6% 25% | 6 0% 22 | 25 12.45 01 | 5 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 50% 100% | 100% 83.2% 100% 0% 0.0% 100% 900.0% 100% 900.0% | 50% | os os 16. | 7% 0% | 9% 9 | n 0.0% | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 0% 0.0% | 100% 100% | 200% 100.0% (| % 9% C | % 0.0% on | 0% | 0% 0.0% | 0.0947 | 0.1917 | 0.4226 0.8 | 947 | 0.1917 | 0.4226 | | |
| in-containing family or Ythdf1 | YTHO MOUSE 61 KDs | 100% 100% 100 0% 0% 0 100% 100% 100% 100% 100% 100% | 0.0% 100% | 5 100% 100 | ON 100.0% OF | 5 0% | 0% 0.0% | 0% 0% | 0% 0.0% | 100% 10 | 0% 100% 100. | 2% 0% | 9% 9 | 0.0% | 0% 0% | 100% 500.0% 100% 500.0% 0% 0.0% 100% 500.0% 100% 500.0% | 100% 100% | 0% 0.0% | 0% 0 0% 0 | 05 0.05 | 0% 0% | 2005 0.0% 100 200 0.0% 100 2005 100.0% 5 2005 100.0% 5 1000 100.0% 5 | N 100N 100 | N 100.0% 09 | 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.422 | os. | 0.4226 | 0.4226 | | 0.4226 | | |
| vision factor-like prote Arilla protein 22 Znf22 | AFLINA MOUSE 21 kDs ZNF22 MOUSE 27 kDs | 100% 0% 0% 0 | 0.0% 100% | 6 100% 100 | 0% 100.0% 09 09 0% 100.0% 09 | 5 0% | 0% 0.0% | 100% 100% 0% | 100% 100.0% | 200% | 0% 0% 0/ 100% | 2% 0% | 9% 0 | N 0.0% : | 100% 100% 0% 0% | 100% 100.0% 0% 0.0% | 0% 0% 100% 100% | 9% 0.0% 9% 0.0% 100% 100.0% | 9% 9 9% 9 | 6 0% 0.0% | 100% 100% 0% 0% | 100% 100.0% 1 | % 9% 0 | % Q.0% Q9 | 0% | 0% 0.0% | | | | - | | | | |
| visition factor-like prote ArD inding protein 2 Step2 | AFL3 MOUSE 20 KDs STX82 MOUSE 65 KDs | 100% 100% 100 100% 100 | 100.0% 0% | 9% 0 | 0% 0.0% 09 0% | 0% | 0% 0.0% 0% | 100% 100% | 100% 100.0% | 9% 1 | 0% 0% 0. | 2% 0% | 9% 9 | 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 0 100% 100.0% 0 | % 0% 0 % 0% 0 | % 0.0% 09 % 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | | | | | | | | |
| ota homolog Pelo nosidase 2C1 Man2c1 | PELO MOUSE 43 kDs MAZCI_MOUSE 116 kDs | 100% 100% 100 100% 100 | 100.0% 0% 100.0% 100% | 9% 0 | 0% 0.0% 09 | 0% | 0% 0.0% 0% | 100% 75% 100% | 100% 91.7% | 9% 2 9% | SN ON B | 2% 0% | 0% 0 | 0.0% | 100% 100% | ON. | 0% 0% | 200% | 0% 0 | 0% | 100% | | 98 | | 0% | | 0.4226 | | 0.4 | 226 | | | | |
| Afgh no protein foe 1 homok Rbfox2 | RFOX2 MOUSE 47 KDs | 0% 0 | 100% | | DS 09 | | 05 | 1000 1000 | | 200% | | 0% | | | 0% 0% | 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% | 0% 0 0% 0 | 0% 0.0% | 176 06 | . no. 5.0% c | % 100% 100 | S 94.4% 09 | 0% | 0% 0.0% | 0.422 | | | 0.4225 | | | | |
| ate 15-liposygenase Alox15 | LOX15 MOUSE 75 KDs | 100% 100% 100 100% 100% 100 0% | 100.0% 0% | 6 0% 0 | OK 0.0% ON | 6 0% | 06 0.0% | 100% 100% | 100% 100.0% | - 0% | 0% 0% 01 | 25 0% | 0% 0 | ns 0.0% | 100% 100% 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 | 6 0% 0.0% | 94% 100% | \$ 200% \$80.0% 6 200% 6 200% 6 200% 60.37% 6 200% 60.37% 6 200% 60.07% 6 200% 100.07% 6 200% 100.07% 6 200% 100.07% 6 200% 100.07% 6 200% 100.07% | % 0% 0 % 0% 0 | K 0.0% 69 | 0% | 0% 2.0% 0% 0% 0.0% | 0.422 | | | | | | 0.4225 | 5 |
| in-binding dutamic aci Sh3bgrG mb homolog Numb | SHOLS MOUSE 10 KDs NUMB_MOUSE 71 KDs | 100% 100 0% | 4 | 9% C | ON. | 0% | ON | 200% ON: | 100% | 100% | 0% 0% | 0% | 0% 0 | P6 | 100% 100% 0% | 100% 100.0% | 0% 0% 100% | 0% 0.0% 100% | 0% 0 | 0% 0.0% | 100% 80% 0% | 100% 93.3% 0 | % 20% C | % 6.7% 09 09 | ON | 0% 0.0% | 0.422 | 26 | 0.4226 | 0.4226 | | 0.4226 | | |
| r adhesion molecule 1 Icam1 ociated protein 70 Swsp70 | SWP70_MOUSE 59 kDs | | | | | | | | | | | | | | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 1 200% 100.0% 0 | % 0% 0 | % 0.0% 09 % 0.0% 09 | Oni Oni | 0% 0.0% | | | | | | | | |
| hatidylcholine acyltrar Lpcat2 | MACC MOUSE 115 Kits AFTIN MOUSE 101 Kits AFTIN MOUSE 171 Kits BRICS MOUSE 47 Kits BRICS MOUSE 20 Kits BRICS MOUSE 20 Kits LMP2 MOUSE 100 Kits SPICES MOUSE 100 Kits SPICES MOUSE 100 Kits SPICES MOUSE 100 Kits SPICES MOUSE 20 KITS SPICES MOUS | 100% 100% | 100.0% | 6 0" | os 0.0" · | | 06 A.M. | 100% ***** | 100% *** | 0" | m ~ - | 94. ~ | | n 0.00 | 100% | 100% | 0% | 0% | 0% | ON. | 2,32% 100% | 2000 100.0% | - UN C | a uos 09 | ON. | 0.0% | | | | _ | | | 1 | |
| agrammer (600 d 1000)2 il municar differentiatio Medal will-containing revisio Trimid | MNDAL MOUSE 51 KDs | ADDRS 100 | | 98 6 | NA 9575 09 | - 05 | -A 0.0% | ASSN 100% | 1005 100.05 | 98 | 23 0 | CN 05 | 62 0 | 0.0% | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 0% 0.0% | 100% | 100% | 9% C | | ON. | 2% | | - | | _ | - | | - | |
| ent-resision revision Securi | SMUI MOUSE 50 KDs CMGA MOUSE 52 KDs | 100% | 9% | 5 | - 01 | 4 | | 100% 100% | 100% 100.0% | 98 | 0% 0% D | 2% 0% | 9% 9 | n 0.0% | 100% 100% | 100% 100.0% 22% 11.1% | 0% 0% | | 0% 0 | | 100% 100% 100% 100% | 100N 100.0N | % 9% 0 | 5 0.0% 09 | 0% 0% | ox 0.0% | | | | | | | | |
| nt component CB beta CBb se-activatino protein G GI2 | CORD MOUSE 65 KDs GTZ MOUSE 79 KDs | 0% 0% 0 | 0.0% 100% | 5 100% 100 | ON 100.0% ON | 6 0% | 0% 0.0% | | | | | $+ \mathbb{I}$ | | + + + - + - + - + - + - + - + - + - + - | 200% 200% 0% 0% | 20% 100.0% 23% 11.1% | 0% 0% 100% 100% | 0% 0.0% 67% 88.9% | 0% 0 0% 0 | 0% 0.0% 6 0% 0.0% | 0% 0% | 0% 0.0% 10 | % 100% 100 | x 100.0% 01 | 0% | 0% 0.0% | 0.422 | 25 0.4225 57 0.5000 | | 0.4226 | 0.4226 | | _ | |
| muceur ribonucleos: Prpf31 mplex subunit ZNF326 Znf326 prieme I ACTR2 | 2N25 MOUSE 55 KDs | 0% 0% 0 | 0.0% 100% 0.0% 100% | 5 100% 100 6 100% 100 | 0% 100.0% 09 | 5 0% | 0% 0.0% | 0% 0% 100% *** | 0% 0.0% | 100% 100% 100 | 0% 100% 100. | 2% 0% 3% 0% | 9% 9 | 0.0% | 9% 9% 10% 10% | 22% 0% 0.0% 100% 100.0% 100% 100.0% | 100% 100% 100% 0% 0% 0% | 67% 100% 100,0% 0% 0,0% 0% 0,0% | 0% 0 0% 0 | 00 0.00 | 200% 100% 0% 0% | 0% 0.0% 100 100% 100 00 | % 200% 100 % 200% 100 | N 100.0% 09 | 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0.925 | 0.5000 | | 0.1257 | 0.5000 | | 1 | |
| orier dikinase 1 Sepha1 | SPS1 MOUSE 43 KDs CC115 MOUSE 20 KP= | 100% 100% 100 0% 0% 22 | 100.0% 0% | 6 0% C | 0% 0.0% 09 7% 88.9% 09 | 6 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% 0% 100% 100.0% | 9% | 0% 0% 0/ 0% 100% | 2% 0% | 9% 0 9% 0 | 0.0% | 100% 100% 32% 100% | 100% 100.0% | 0% 0% 67% 0% | 0% 0.0% | 0% 0 0% 0 | 05 0.0% | 100% 100% | 100% 100.0% | % 9% C | S 0.0% 09 | | | 0.5770 | 0.3241 | 0.5 | 770 | 0.3241 | | - | |
| tein A-II Apox2 monochosphate deltys (mpdb2 | APOAZ MOUSE 11 KDs IMDHQ MOUSE 56 KDs | 100% 100% 100 100% 100% 100 | 100.0% 0% 100.0% 0% | 6 0% C | 0% 100.0% 09 0% 0.0% 09 0% 0.0% 09 0% 0.0% 09 0% 0.0% 09 0% 0.0% 09 0% 0.0% 09 | 5 0% 5 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 9% | 0% 0% 0. 0% 0% 0 | 2% 0% 2% 0% | 0% 0 0% 0 | N 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 200% 100.0% (200% 100.0% (200% 100.0% (200% 100.0% (| % 0% 0 % 0% 0 | S 0.0% 09 S 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | | | | | | | | |
| domain-containing on Cod-115 lein A-II lein A-II Aposiz enconclosabale delno: (impelio ed cel deeth acciein 9 Polodi II) selves accidic elonado, Estec control de control delno control delno control | NNSE, MASSE 54 SAN NNSEA, MASSE 51 SAN NNSEA, MASSE 51 SAN NNSEA, MASSE 51 SAN NNSEA, MASSE 54 SAN NNSEA, MAS | 0% 0% 0 0% 0% 0 100% 100% 10 100% 100% 10 0% 0% 33 100% 100% 10 100% 100% 10 100% 100% 10 100% 100% 10 100% 100% 10 100% 100% 10 100% 100% 10 | 100.0% 0% | 96 0 | 0% 0.0% 09 0% | 0% | 0% 0.0% 0% | | 100% | 9% | 9% | 0% | - 0 | rs. | 100% 100% | 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 2006 100.0% 20 | % 0% 0 | 5 0.0% 09 5 0.0% 09 | 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | | |
| teine-specific elongatic Eefsec Aber10 | ATX10 MOUSE 54 kDs | 100% 100 100 | | 9% 0 | ON ON | 0% | ON ON | 100% 100% 100% 100% | | 9% 9% | 0% | 0% | 0% 0% | 1 | 100% 100% | 100% 100.0% 0% 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% | % 0% 0 | S 0.0% 09 | 0% | 0% 0.0% | | | | | | | | |
| Cactin unaminate lyane Npi se kidney indirem min Cla | NPL MOUSE 35 KDs | 100% | | 0% | | ON | | | | | - | + | | 1 1 | 200% 200% | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0° | 0% 0.0% 0% 0.0% | 100% 100% | 100% 100.0% | 200% % 0% 0 | % 0.0% 09 | 0% | 0% 0.0% | | | | _ | | | _ | |
| Sehvdrosenase Isuanor Ngo1 | NGO1_MOUSE 31 kOs PLSI_MOUSE 70 kOs | | _ | \vdash | | - | | | | | - | + | _ | | 67% 100% 100% 100% | 100% 88.9% 100% 100.0% | 33% 0% 0% 0% | 0% 11.1% 0% 0.0% | 0% 0° | 6 0% 0.0% | 100% 100% 100% 100% | 1 200% 100.0% 0 1 200% 100.0% 0 | % 0% C | % 0.0% 09 % 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | 0.422 | 26 | | 0.4226 | | | - | |
| ral amino acids transp Sk7a8 ubunit 5 Pfdn5 | PFDS_MOUSE 17 kDs | 100% 100% 100 75% 67% 67 | 6 100.0% 0% 6 89.4% 25% | 6 0% C | 0% 0.0% 09 2% 30.6% 09 | 6 Ons | 0% 0.0% 0% 0.0% | 100% 100% 67% 100% | 100% 100.0% 100% 88.9% | 22% | ON ON D. | 2% 0% 1% 0% | 0% 0 0% 0 | N 0.0% | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 6 0% 0.0% | 100% 100% | 1 100% 100.0% (1 100% 83.2% (| % 0% C | % 0.0% on | One | 0% 0.0% | 0.2177 | 0.0082 | 0.4226 0.2 | 177 | 0.0002 | 0.4226 | | |
| Astronomessa rutori Sghg Inn ATDess school A Appliedd I | CSEO MOUSE 18 KOs VACD1 MOUSE 40 KOs | 100% 100% 100 100% 100% 100 | 100.0% 0% 100.0% 0% | 6 0% C | 0% 0.0% 09 0% 0.0% 09 | 5 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% 50% 0% | 100% 100.0% 100% 100.0% 0% 15.7% | 0% | 0% 0% 0. | 2% 0% 2% 0% | 9% 0° | ns 0.0% | 100% 100% 67% | 50% 72.2% | 0% 0% 0% | 9% 0.0% | 0% 33 | 50% 50% 27.8% | 50% 100% 100% 100% | 100% 83.7% | % 9% 0 % 9% | S 0.0% S09 | 0% 0% | 0% 16.7% | 0.808 | 98 0.5000 94 0.1994 | 0.4226 | _ | - | 0.689 | 0.8088 0.1294 | 0.1 |
| ne cendinase 1 lyd | SYVNI_MOUSE 57 kOs | 0% 0% 100 100% 100% 100 | \$ 100.0% 0% \$ 100.0% 0% \$ 33.3% 0% \$ 100.0% 0% \$ 100.0% 0% | 6 0N 0 6 0N 0 6 0N 0 6 0N 0 | 0% 0,0% 09 0% 0,0% 09 0% 0,0% 00 0% 0,0% 00 0% 0,0% 09 0% 0,0% 00 | 100% 5 0% | 0% 0.0% 0% 0.0% 0% 06.7% 0% 0.0% 0% 0.0% | 50% 0% 100% | 0% 15.7% 100% 100.0% | 98 | 0% 0% 0/ 0% 0% | 2% 50% 2% 0% 2% 0% | 100% 100 0% | 63.3% | | 1000 877 77 | | au | | | 1000 | 1000 100.0% | | | | ev 0.000 | u.3000 | | | _ | \vdash | 0.685 | ~ | |
| ass protein 6 Marip6 | ATPS MOUSE 0 KOs THAM! MOUSE 20 KP | 750 E76 E7 100% 100% 100 100% 100% 100 0% 0% 100 100% 100% 100 100% 100% 100 100% 100% 100 100% 100% 100 | 100.0% 0% | 6 0% | 0% 0.0% 09 | 6 0% | 0% 0.0% 0% | 100% 200% 50% 0% 100% 100% 100% 100% 100% 100% 100% 100% | 100% 100.0% | 98 | | | 0% 0 0% 0 100% 1007 0% 0 0% 0 0% 0 | 0.0% | 100% 100% | 100% | 0% 0% | 0% | 9% 9% | 06 | 67% 100% 100% | 200% 100.0% 4 | % 0% C | S 0.0% 00 | 0% | 0% 0.0% | | | 0.5000 | _ | - | | - | |
| etion factor beta Gmfb -containing, RNA-bind, Khdrbe3 | FPES, MULSE 17 KDs. CROS MULSE 18 KDs. 19 KDs. 18 KDs. 19 KDs. | 100% 100 | | 9% 0 | ON. | CHL | 0% | 400 | 100% | | 9% | | 9% 9 | S 0.0% 1 S 0 | 100% 100% | 100% 100.0% 0% | 0% 0% | 0% 0.0% 200% | 0% 0 | 0% 0.0% 0% | 100% 100% 0% | 9% 100.0% 0 | % 0% 0 % 100 | S 0.0% 09 | 0% | 0% 0.0% | | | | | | | | |
| ribosel alvoshudrobse Adprhi2 norme A synthetase 2 Acces1 | ARNL2 MOUSE 39 KOs ACS2L MOUSE 75 KOs | 100% | | 9% | | 0% | | 100% | | 9% | | 0% | _ | | | 100% | on | 9% | 0% | 0% | 100% 100% 100% 100% | 100% 100.0% 0 | % 9% 0 % 9% 0 | 5 0.0% 09 5 0.0% 09 | 0% 0% | 0% 0.0% 0% 0.0% | | | | _ | | | _ | |
| dehydrogense (acety Pdk3 | POKS MOUSE 46 KDs | 100% | | 9% | 0% | 0% | es l | 100% ***** | 100% *** | 0" | m ~ - | 94. ~ | | n 0.00 | 100% | \rightarrow | 9% | \rightarrow | | \Box | 100% 100% 100% 100% | 1000 100.0% | N 9% | w ws/5 09 | 0% | en 0.0% | | | | _ | \vdash | | - | |
| 1 protein Rab-27A Rab27a din E synthase 2 Ptoes2 | REIZYA MOLISE 25 KDs PGESZ MOLISE 43 KDs | 0% 75% 100 100% 100% 400 | 58.3% 0% 100.0% ^~ | 6 0% C | 0% 0.0% 1009 0% 0.0% 04 | 5 25% 5 0% | 0% 41.7% 0% 0.0% | 100% 80% 100% 100% | 100% 93.3% 100% 100 PK | 9% | 0% 0% 0. | 2% 0% 2% 0% | 20% O | S 6.7% | 100% 100% | 100% 100% 500.0% | 0% 0% | 0% 0.0% | 98. 0 | 0% 0.0% | 99% 100% 100% 75% | 88% 92.1% (| % 0% 0 % 25% | S 0.0% 119 S 0.2% 00 | Ons Ons | 2% 7.9% 0% 0.0% | 0.3542 | 26 PS 0.4226 | 0.8857 0.4225 | 0.4226 0.6075 | | 0.364 | 2 | |
| phosphoprotein PEA-1 Pea 15 M114A2 Fam114a2 | PEA15 MOUSE 15 KDs F1142 MOUSE 54 KDs | 100% 100 67% 57% 40 | 0% 54.5% 22% | 6 42% 60 | 0% 09 09 0% 45.4% 09 0% 0.0% 09 | 6 0% | 0% 0.0% | 50N 42N | 100% 54.3% | 50% S | 7% 0% 35 | 7% 0% | 0% 0 | n 0.0% | 100% 100% 100% | 67% 88.9% | 0% 0% 0% | 22% 11.1% | 0% 0° | 0% 0.0% | 75% 67% 0% | 100% 80.6% 2 | % 32% C | % 19.4% On | 0% 100% | 0% 0.0% | 0.6582 | 0.4226 | 0.0 | 0.6075 | 0.4225 | | | |
| al NI 11-acetyl-spermin Pack in-related protein 5. ml GlnS | PACK MOUSE 55 KDs GLENS MOUSE 16 KDs | 100% 200 0% 75% 200 100% 100% 200 100% 100% 200 67% 57% 40 100% 100% 200 100% 100% 200 100% 100% 200 100% 100% 200 100% 100% 200 | 100.0% 0% | 6 0% 0 6 0% 0 6 0% 0 | 0% 0.0% 09 | 6 0% | 0% 0.0% | \$00% \$00% \$00% \$2% \$00% \$00% \$100% \$00% \$100% \$00% | 100% 100% 100.0% | 0% | 0% 0% 0.1 | 0% 0% 0% | 0% 0 | 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% | 100% 100% | 100% 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 1 100% 100.0% 0 1 100% 100.0% 0 | % 0% 0 | % 0.0% 09 % 0.0% 09 | Ons Ons | 0% 0.0% 0% 0.0% | | | | | | | | |
| o-prosphate oddase Prpo vohosphate 1-phospha Inpp1 | INPP_MOUSE 43 kOs NECES MOUSE 43 kOs | 100% 100% 100 100% 100% 100 | 100.0% 0% 100.0% 0% | 6 0% 0 | 0% 0.0% 09 0% 0.0% 09 | 6 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 900.0% 100% 900.0% | 0% 1 | 0% 0% 0.0 | 2% 0% | 0% 0° | m 0.0% : | 200% 200% 200% 200% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 1 200% 100.0% 0 1 200% 100.0% 0 | % 0% 0 % 0% 0 | % 0.0% 09 % 0.0% 09 | One One | 0% 0.0% 0% 0.0% | | | | _ | | | - | |
| n-1 Palm nd histidine-rich doma Chordc1 | PALM MOUSE 42 KDs CHRD1 MOUSE 37 KDs | 100% 100% 100 | 100.0% 0% | 6 0% 0 | 0% 0.0% 09 | s 0% | 0N 0.0% | 100% 100% | 100% 100.0% | | 0% 0% 0. | 2% 0% | 0% 0 | n 0.0% | 0% 32% 100% | 100% 44.4% | 100% 67% 0% | 0% 55.6% | 0% 0 0% | 6 0% 0.0% | SON SON | \$2000 \$2.7% \$4 \$2000 \$91.7% \$4 \$2000 \$91.7% \$4 \$2000 \$91.7% \$4 \$2000 \$90.00% \$4 \$2000 \$100.00% \$4 \$2000 \$2000 \$4 \$2000 \$ | N 50N SC | % 50.0% OF | One | 0% 0.0% | 0.867 | is . | | 0.8875 | | | _ | |
| mai rentain I 75 miles MgG3 incontaining rentain F Ubgs5 | DEGRES COLOR COL | 100% 100% 100 100% 100% 100 0% 0% 0 100% 100% 100% 100 100% 100% 100 | 0.0% 100% | 5 100% 100 5 0% | ON 100.0% ON | 5 0% | 0% 0.0% | 100% | 100% 100 0% | 100% | 100% | 0% 0% | 0 | S. 5.7% S. 0.0% S. | 0% 0% 100% 100% | 0% 0.0% 100% 100.0% | 100% 100% 0% 0% | 100% 100.0% 0% 0.0% | 0% 0 0% 0 | \$ 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0. | 0% 0% 100% 100% | 0% 0.0% 100 100% 100.0% | % 100% 100 % 0% 0 | 5 100.0% 09 5 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | | | | | | | | |
| mily protein ABFRACL Abract sociated protein X Tanax | ABRAL MOUSE 9 KDs TSNAX MOUSE 33 KDs | 100% 100% 100 100% 100 | 100.0% 0% | 9% 0 | 0% 0.0% 09 0% | 0% | 0% 0.0% 0% | 100% 100% 100% 100% | 100% 100.0% | 9% | 0% 0% 0/ 0% | 2% 0% | 0% 0 0% | 0.0% | 100% 100% 100% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 100% 100,0% (100% 100,0% (| % 9% 0 | % 0.0% 09 % 0.0% 09 | 0% 0% | 0% 0.0% 0% 0.0% | | | | | | | 1 | |
| osa 11-beta-dehistroa Hedi 151 indo-beta-N-acetistus Engase | ENASE MOUSE 83 KOs | | | | | | | | 100% | | 98 | + | | 8 | 100% | 100% 100.0% 100% | 0% 0% 0% | 95 0.0% | 0% 0 0% | 0% 0.0% | 100% 100% 100% | 200% 100.0% 0 | % 9% c | 5 9.0% 09 5 09 | 0% | 00 0.0% | | | | _ | | | _ | |
| e b-245 heavy chain Cybb mai protein L15, mary Mouth | CY245 MOUSE 65 KDs | m. ^ | | 900% -~ | es. | 0% | ON. | 2005 | 100% | 100% | 23 | 106 | 62 0 | | 100% 100% 0% | 100% 100.0% | 0% 0% 100% | 0% 0.0% 50% | 0% 0 0% | 0% 0.0% 50% | 100% 100% 22% ~~ | | % 0% % 62% | 09 | 0% 22% | + | 0.500 | 20 | | 0.5038 | 0.5000 | | 0.7952 | 2 0 |
| aculation factor deficie Mcfd2 embrane-associated or Smap1 | MOFEE MOUSE 16 KDs SMAP1 MOUSE 46 KDs | 71% 60% 50 0% 0% 0 | 6 50.5% 29% 6 0.0% 100% | 6 40% 50 6 100% 100 | ON 39.5% OF | 5 0% 5 0% | 0% 0.0% 0% 0.0% | 50% 22% 0% 0% | 50% 44.4% 0% 0.0% | | 7% 50% 55.0 0% 100% 100.0 | 2% 0% 2% 0% | 0% 0 0% 0 | S 0.0% : | 200% 200% 22% 0% | 100% 100.0% 6% 11.1% | 0% 0% 67% 100% | 0% 0.0% 100% 88.9% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 0% 50% | 0% 55.7% 100.7% 20.0% 20 | 9% % 59% 100 | S 83.3% 01 | 0% | 0% 0.0% | 0.1270 | 0.0237 F2 0.4225 | 0.4225 | 220 | | 0.4226 | | |
| ckpoint protein BUB3 Bub3 ich protein 1 Crip1 | BUB3 MOUSE 37 kOs CRP1 MOUSE 9 kOs | 100% 100% 100% 100 | 9% | 9% 0 | 0% 09 | 0% | 0% | 100% 100% | 100% 100% 100% 0% 8.3% 0% 9.0% | | 0% 0% 0% 0% | $+ \exists$ | 0% 0 0% 0 | is : | 32% 100% 100% 60% | 80% 71.1% 80% 80.0% | 67% 0% 0% 40% | 20% 28.9% 20% 20.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 90% 60% 67% 67% | 100% 80.0% 20 100% 77.8% 20 | % 40% 0 % 33% 0 | 5 20.0% 09 5 22.2% 09 | 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 0.721 | 19 0.2011 54 0.2254 | 0.2254 0.1835 | 0.7972 0.7219 0.8964 | 0.0237 0.4225 0.2811 0.2254 0.4225 | 0.4226 0.2254 0.1835 | + | E |
| cipority probin (MAS) (MAS) cipority probin (MAS) (MAS) cipority (MAS) cipo | AKTS1 MOUSE 27 KOs | 95 1005 100 05 05 0 | 0% 83.3% 50% 50% 0.0% 100% 0.0% 100% 100% | 5 200% 100 | US 16.7% 09 0% 100.0% 09 | 5 0% | 0% 0.0% 0% 0.0% | 100% 25% 0% | 0% 8.2% | 25% 10 | 0% 100% 91. | 7% 0% | 9% 9 | 0.0% | 0% 0% | 110% 100.0% 0% 0.0% | 0% 0% 100% 100% | 0% 0.0% 100% 100.0% | 0% 0 0% 0 | 0% 0.0% | 100% 100% 0% 0% | 100% 100.0% 1 0% 0.0% 100 | % 9% 0 % 100% 100 | 5 100.0% 09 | 0% 0% | 0% 0.0% 0% 0.0% | 0.4226 | 0.4226 | 0.4225 0.4 | 226 | d.4225 | 0.4226 | _ | |
| domain-containing on Code5 nother protein 6 About | CCDOS MOUSE 53 KDs AKAPS MOUSE 75 kDs | 0% 0% 0 0% 0% | 0.0% 100% | 6 100% 100 6 100% 100 | ON 100.0% 09 | 6 0% | 05 0.0% | 0% 0% | 0% 0.0% | 100% 10 | 0% 10°% | 0% | 9% 0 | 0.05 | 95 m | 0% | 100% 100% | 100% 100.0% | 0% ^ | 0% 0.0% | 100% | 0% U.0% 10 | % 100% 100 % 100% | S 09 | Pric. | 0% | | | | _ | | | _ | |
| al scyl-coenzyme A or Acoxò pimerase Galm | ACCING MOUSE 78 KDs GALM MOUSE 38 KDs | 00 00 | 100% | | - 0 | | | 100% 10°% | 100% 100 PM | 0% | 0% 0% 0) 0% 0% 0) | 2% 0% | 9% 0 | n 0.0% | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 | 6 0% 0.0% | 100% 100% | 100N 100.0N 4 | % Q% r | x 0.0% 01 | 0% | 0% 0.0% | | | | | | | | |
| ng protein Rheb Rheb 2 Mmm2 | RHEB MOUSE 20 KDs MMFRQ_MOUSE 105 KDs | 100% 100% 100 | 100.0% 0% | 6 0% 0 | 0% 0.0% 09 | s ons | 0N 0.0% | 100% 100% 0% | 100% 100.0% 100% 100.0% | 9% I | 0% 0% 0. | 2% O% O% | 0% O | 0.0% | on on | 100% 0% 0.0% 100% 900.0% 100% 900.0% | 0% 100% | 0% | 0% | 0% | 100N 50% | 0% Si | 9% C | % 09 | Ons | 0% | 0.711 | 17 | | 6.7117 | | | | |
| comain-containing on Codc90b Immirization-cromoting Tppp3 | TPPP3 MOUSE 19 kOs | 100% 100% 100 | 100.0% 0% | 6 0% 0 | 0% 0.0% 09 | 6 0% | 0% 0.0% | 0% 100% 100% | 100% 900.0% 100% 900.0% | 90% | 0% 0% 0.0 0% 0% 0.0 | 2% 0% | 0% 0 | n 0.0% : | 0% 0% 100% 100% | 0% 0.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100 0% 0 | 100% 100.0% 0% 0.0% | 0% 0% 100% 100% | 0% 0.0% 0 1 100% 100.0% 0 | % 25% C | % 8.3% 9009 % 0.0% 09 | 75% 1 0% | 0% 91.7% 0% 0.0% | 0.500 | | | 0.4226 | | | 0.4226 | |
| subunit zeta-2 Copg2 | COPZZ MOUSE 23 KOs | 100% 100% 75 | 91.7% 0% | 6 0% 25 | SN 8.2% 09 | 5 0% | 05 0.0% | 100% 100% 100% 100% | 100% 100.0% | 9% | 0% 0% 0.0 | 2% 0% | 0% 0 0% 0 | 0.0% | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 0% 0 0% 0 | 6 0% 0.0% 6 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% | % 0% 0 | S 0.0% 09 | 0% | 0% 0.0% | 0.4226 | 0.5000 0.4225 | 0.4 | 0.5000 226 | 0.4225 0.4225 | | _ | |
| Average prominer and the Superstance of the Superst | RISC MOUSE 51 KDs | 2% 0% 20 100% 100% 100 | 5.7% 100% 100.0% 0% | 5 0% 0 | 0% 93.2% 09 0% 9.0% 09 | 0% | 0% 0.0% 0% 0.0% | 200% 200% | US. | 9% | 0% 0% 0/ 0% 100% 0% | 0% | 95 0 | | 100% 100% 100% 200% | 100% 100.0% | 0% 0% 9% 15° | 0% 0.0% | 9% 0 9% 0 | 00 0.0% 00 0.0% | 100% 100% | 100% 100,0% 0 | % 200% % 0% 0 | S 0.0% 09 | 0% 0% | 0% 0.0% | 0.4226 | 0.4228 | 0.4 | 0.5453 | 3.4225 | | 1 | |
| ine-rich nuclear phose Arp32e ir cross-complementin Xrcc5 | ANGE MOUSE 30 KDs XPCCE MOUSE 60 KDs | 100% 100% 100 | 100.0% 0% | 6 0% 0 | 0% 0.0% 09 | 5 0% | 0% 0.0% | 100% 100% | 100% 100.0% | 9% | 0% 0% 0. | 2% 0% | 0% O | 0.0% | 100% 100% 100% 100% | 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% | 9% 0 9% 0 | 0% 0.0% | 100% 100% 100% 100% | 100% 100.0% | % 0% 0 | S 0.0% 09 | 0% p% | 0% 0.0% | | | | | | | | |
| steine-rich domains o Lmcd1 Sehvdrosenase family Aldh (s2) | ALIAS MOUSE 55 KDs | | | | | | | | | | | | | | 100% 100% 100% | 100% 100.0% | 0% 0% 0% | 0% 0.0% | 0% 0 0% | 0% 0.0% | 100% 75% 100% 100% | 100% 91.7% 0 100% 100.0% 0 | % 25% C | S 8.2% 09 S 0.0% 09 | 0% | 0% 0.0% 0% 0.0% | 0.422 | | | 0.4226 | | | | |
| une turnalme-modeln of Dives | PTPRA MOUSE 94 KOs ECP2 MOUSE 18 KOs | | \perp | | _ | \vdash | | | | | | + | | | 100% 100% 100% | 100% 100.0% | 0% 0% 0% | 0% 0.0% | 0% 0 | 0% 0.0% | 85% 100% | 100% 94.9% 1 | N 9N 0 | K 5.1% 09 | 0% | 0% 0.0% | 0.422 | 26 | | 0.4225 | | | 1 | |
| cationic protein 2 Ear2 | | 0% | | 200% | | 0% | | 1000 1 | 1000 MT | - | | | | | 100% 100% | 100% 100.0% | 0% 0% | 0% 0.0% | 9% 9 9% 9 | 05 0.0% | 100% | 100% | 98 0 | | 0% | 95 | | | | _ | | | - | |
| cationic protein 2 Ear2 1-Sep ptidase Naubunit 2 Cpn2 | CPNQ MOUSE 60 KDs | | | | | | | | 100% 700.0% | 98 | on on 0 | CR 0% | 926 0 | 0.0% | coco 1925 | AND 100.076 | MA 9% | JB 93% | 975 0 | | | | | | | | | | | | | | _ | _ |
| cationic protein 2 Ear2 1-Sep ptidase Naubunit 2 Cps2 d protein Rab-Sib 1 CuLA-associated fac Doaf7 Franscription complex CncG | CORE MADE 2010-1-2011 M | 200% 200 0% 0% 0 0% 0% 0 | 0.0% 100% 0.0% 100% | 6 100% 100 6 100% 100 | 0% 100.0% 09 0% 100.0% 09 | 5 0% | 0% 0.0% 0% 0.0% | ON ON | 0% 0.0% | 100% 10 | 0% 100% 1000 | 25 05 | 9% 0 | 0.0% | ON. | 9% | 100% | 100% | 0% | ON ON | 0% 100% | 9% | 100% 100 % Q% | N | 0% 0% | 9% | 0.500 | 00 | | 0.5000 | | | | _ |

| Section 1 | DAPI MOUSE 5 DAPI MOUSE 1 DOXSO MOUSE 8 STOR MOUSE 5 | 0 KDs 100 1 KDs 100 2 KDs H KDs | 100% | 100% 100.0% 100% | 9% 0 | 0% 0.0 0% | N ON | 0% 0% 0. 0% | 0% 100% | 100% 100% | 100.0% 0 | s 0s | 08 0.0% | 0% 0% | 0% 0.09 | 100% 100 100% 9% | 9% | 01 1001 | 5 0% 5 100 | | N ON | 0% | 0% 100% | 100% 100.0% | 9% 9% 4000 · · | ons | 0.0% 0% | 0% 0 | 0.0% | | | | | | | | Ē |
|---|---|--|----------------------------|---|-----------------------------|--|-----------------------|---|----------------------------------|---|----------------------------------|------------------------|-------------------------------|--------------------------|-------------------------------|----------------------------------|----------------------------|-------------------------------------|------------------------------------|-------------------------------------|-------------------------|--|--------------------------------|--|-------------------------------------|--------------------|----------------------------------|------------------------|--|---------------------------------|------------------|--------------------------------|----------------------------|----------------------------|----------------------------|--------|----|
| onal coactivator YAP1 Yap1 sale D4 P164 mobility group box fami Tox4 sinine delminase type- Pad4 | PLD4 MOUSE 5 TOX4 MOUSE 6 PADH MOUSE 7 | 6 KDs 6 KDs 6 KDs | 0% | | 200 | IN. | | os. | | | | | | | | 200 0 200 100 20 0 | IN 100% IN 0% | 100.0% 01 0.0% 1001 | 5 0% 0 5 100% 100 | 0.0% 0 100.0% 0 | N 9% N 9% N 9% | 0% 0.0% 10 0% 0.0% 10 | 0% 0% 0% 100% | 100% 100.0% | 100% 100% 0% 0% 0% 0% | 0% | 95 95 95 | 0% 0 0% 0 | 0.0% | | | | | | | | Ħ |
| e-binding protein 1 Gbp1 drial-processing peolds Propos min-containing protein 4 Uben4 | GEP1 MOUSE 5 MPPA MOUSE 5 UEXNA MOUSE 5 | 8 kDs 71 6 kDs 71 6 kDs 80 | 50% 5 80% | 50% 58.3% 75% 78.3% | 25% SC 20% 20 | N 50% 41.7 N 25% 21.7 | S 98 S 98 | ON ON D. | 0% 50% 0% 75% | 50% 100% 100% 100% | 66.7% S0 91.7% 25 | % 50% % 0% | 0% 33.3% 0% 8.3% | 0% 0% 0% 0% | 0% 0.05 0% 0.05 | 100% 100 100% 100 100% 100 | N 67% | 88.9% OF | 6 0N 23 6 0N 0 | 11.1% 0 0.0% 0 | N ON | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% | \$7% 08.9% 100.0% | 0% 0% 0% 0% | 32% 0% | 11.1% 0% 0.0% 0% | 0% 0 0% 0 | 0% 0.0% 0.6 0% 0.0% 0.2 | 1,0000 1402 | 0.0980 | 0.3379 0.6856 0.4226 0.2482 | 1,0000 | 0.0000 | 0.3379 0.4226 0.3021 | | Ħ |
| hsine N-methyltransfera; Setd3 onalbsome complex sub; Cope8 sphatase-1 Acyp1 | SETD3 MOUSE 6 CSN6 MOUSE 2 ACYP1 MOUSE 1 | 7 kDs 100 7 kDs 100 1 kDs 100 | 5 100% 5 100% 5 100% | 100% 100.0% | 0% C 0% C | N ON GO | 0% 0% 0% | 0% 0% 0. 0% 0% 0. | 100% 100% 100% 0% 100% | 100% 100% 100% 100% 100% 100% | 100.0% 0 100.0% 0 100.0% 0 | % 0% % 0% % 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.09 0% 0.09 0% 0.09 | 100% 100 100% 100 100% 100 | % 100% % 100% % 100% | 100.0% on | 5 0% 0 5 0% 0 | 0.0% 0 | N 0% N 0% | 0% 0.0% 10 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% 0% 100% | 100% 100.0% 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0% 0% 0% | 0.0% 0% 0.0% 0% 0.0% 0% | 0% 0 0% 0 0% 0 | 0% 0.0% 0% 0.0% | | - | 2201 | 0.100 | | 0.221 | | |
| seholoid scytransferasi Lpcst3 rtvl oeolidase/L-ascarsoi Aerg/1 stdylinostoi transfer orot Pitpnb | MBDAS_MOUSE 5 ASGL1_MOUSE 3 PIPNB_MOUSE 3 | 6 kDa 100 H kDa 100 H kDa 100 | 5 100% 5 100% | 100% 100% 100.0% | 0% C | 0% 0% 0% 0% 0.0 | 0% 0% % 0% | 0% 0% 0. | 100% 0% | 100% 100% 100% 100% | 100.0% 0 | ns ons | 0% 0.0% | 0% 0% | 0% 0.0% | 100 100% | 100% 100% | 01 | 0% 0 | 6 | on N | 0% 10 10 0% 10 | 0% 0% 0% 100% | 100% | 0% 0% 0% 0% | Ons. | 0% 0% 0% | ons o | 0% | | | | | | | | |
| ment C1o tumor necrosis C1qtnf5 dependent calcium chan Cscna2d1 | C1QTS MOUSE 2 CA2D1 MOUSE 1 MFAP1 MOUSE 5 | 5 kDa 25 kDa 25 kDa | | | | | | | 2000 | | | | | UN | | 100N 100 | 100% | 100.0% 01 | 6 0% 0 | 0.0% 0 | N ON | 0% 0.0% | 100% 0% 100% | 200% 200% 100% 100.0% | 0% 0% | 0% | 0.0% 0% | 0% 0 0% 0 | 06 0.0% | | | | | | | | = |
| dehydrogenase 11 Rdh11 In-2 Prom2 amine-3-kinase Fn3k | PROME MOUSE 9 PROME MOUSE 9 FROK MOUSE 3 | 5 kDs 100 0 kDs 5 kDs | 100% | | 0% | IX. | 0% | OS. | 100% 100% 100% | 100% 100% 100% 100% 100% | 100,0% 0 100,0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | | | | | | | | | | | | | | | 0.4226 | | | 0.4226 | | | | |
| -acid glycoprotein 1 Orm1 FAM19081 Fam190b1 convision factor-related o Arthy1 lostoclosamine-6-suffatas Gains | FIRST MOUSE 8 ARESE MOUSE 2 GALNS MOUSE 5 | H KOs E KOs E KOs E KOs | | | | | | 500 | 100% 67% | 22% | 33 | N N 67N | | ON ON | | 100% 88 100% | 9% | 95.8% 01 | 5 12% 0 5 200 | 125 0 | N ON | 0% 0.0% 10 0% 10 | 0% 100% | 100% 100.0% | 0% 0% | 0% | 00% 0% | 98 3 | DN 0.0% | 0.4226 | | | 0.4226 | | | | Ħ |
| ntigen Cd44 Sependent protein Knase Prior2b utin-protein Igase KCMF Komf1 | CDH4 MOUSE 8 KAP3 MOUSE 4 KOMF1 MOUSE 4 | 6 kDs 25 6 kDs 25 2 kDs 0 | 5 0% | 22% 25% 8.2% | 75% 100% 100 | 67% % 75% 91.7 | 0% % 0% | 0% 0% 0% 0. | 2% 0% | 0% 0% | 0.0% 100 | s 100% | 100% 100.0% | os os | 0% 0.09 | 60% 67 80% 67 90% 0 | % 50% % 22% % 25% | 50.0% 00 60.0% 200 8.2% 1000 | 6 0% 25 6 22% 62 6 100% 25 | 6 8.3% 40 6 40.0% 0 6 91.7% 0 | N 22N 2 N 0N N 0N | SN 32.8% 7 SN 0.0% 10 SN 0.0% 5 | 5% 67% 0% 67% 0% 32% | 67% 69.4% 100% 88.9% 50% 44.4% | 0% 0% 0% 32% 50% 67% | 0% 0% 50% | 0.0% 25% 11.1% 0% 55.0% 0% | 22% 2 0% 0 | 25 30.5% 26 0.0% 26 0.0% | 0.1496 0.1829 1226 0.0286 | 0.1484 | 0.4226 | 0.4225 0.1829 0.0286 | 0.1484 | 0.0153 | 0.0921 | = |
| Sehvokosensee Subiouinor Nidurbi 1 nioribulose-1-phosphate d Apip ome P450 261 Cypile1 | MIND MOUSE 2 OPZET MOUSE 5 | 7 KDs 23 7 KDs 100 7 KDs 100 | 5 22% 5 100% | 50% 38.9% 100% 100.0% | 98 G | N 50% 55.6 N 0% 0.0 | % 17% % 0% | 0% 0% 5 0% 0% 0 | 8% 50% 9% 100% | 200 100% 100% 100% | 100.0% 0 | % 100% % 0% | 0% 0.0% | 0% 0% 0% 0% | 0% 0.09 | 0% 0 100 | N 0% N 100% | 0.0% 1009 | 5 100% 100 0% 0 0% | 100.0% 0 | N 9% 9% | 05 0.0% | 0% 100% 0% 0% | 100% 100.0% | 9% 9% 9% 9% | os | 0.0% 0% | 0% 0 100% | 0.0% | 1769 | 0.0198 | 0.5770 | | 0.0153 | 0.422 | 26 | = |
| s aminosectidase NPEPS Npepi1 freorine-crotein kinase) Vrk1 medin-6 and thrombosco Stepon | PEPL1_MOUSE 5 VRK1_MOUSE 5 SBSPO_MOUSE 2 | S KDs O KDs O KDs | | 100% 0% | 100% | 100% | 0% | 0% 0% | 100% | 0% | | × | 100% | ON. | 0% | 100% 100 100% 0% 0 | IN 100% 100% | 100.0% 01 01 1001 | 5 0% 0 5 0 6 100% | 0.0% 0 | N ON | 0% 0.0% 10 0% 10 | 0% 100% 0% 100% 0% 0% | 100% 100.0% 100% 100.0% 0% 0.0% | 0% 0% 0% 0% 100% 100% | 0% 0% 100% 9 | 0.0% 0% 0.0% 0% 00.0% 0% | 0% 0 0% 0 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | | |
| nteracting protein 4 Trip10 complex component 1 Exec 1 rtin-3 Tripc3 technology protein 1 GPs2 | EXOC1 MOUSE 1 TNPOS MOUSE 1 GREZ MOUSE 5 | 02 KDs 02 KDs 04 KDs | | | | | | | | | | | | | | 100% 100 100% 100 | N 100% | 01 01 | 5 0% 5 0% | | N ON N ON | 10 | 0% 100% 100% 100% | 100% 100.0% 100% 100% 100.0% | 0% 0% 0% 0% | 0% 0% 0% | 0.0% 0% | 0% 0 0% 0 0% 0 | 0% 0.0% 0% 0% 0% 0.0% | | | | | | | | |
| ADP-ribosulardinine1 hv Adprh sted protein Rab-45 Rab-45 nal protein SS kinase albt RpsSka1 | ADPRI MOUSE 4 RABAB MOUSE 2 KSSA1 MOUSE 8 | 0 kDs N kDs 2 kDs | | | | | | | | 100% | | ON. | | ON. | | 200 200N 200N | 100% 100% | 01 | 0% 6 0 | . 0 | ON N | 0% 20 0% 10 | 0% 100% 100% 0% 100% | 200% 100.0% | 0% 0% 0% 0% | One One | 0% 0% 0.0% 0% | 0% 0 0% 0 | 06 0.0% | | | | | | | | |
| hegein H Clah | CATH MOUSE 3 LGMN MOUSE 4 | 2 kDs 100 7 kDs 9 kDs 100 | 5 100% 5 100% | 100% 100.0% 100% 100.0% | 9% 0 | N 0% 0.0 | S 98 | 0% 0% 0. 0% 0% 0. | 0% 100% 0% | 100% 100% 100% | 100.0% 0 | % 0% 0% | 0% 0.0% | 0% 0% | 0% 0.05 | 100% 100 100% 100 86% 86 | % 100% % 75% | 100.0% 01 82.1% 141 | 5 0% 0 5 14% 25 | 0.0% 0 17.9% 0 | N ON N ON | 0% 0.0% 10 0% 0.0% 7 | 0% 100% 5% 22% | 100% 100.0% 100% 59.4% | 0% 0% 25% 67% | 0% 0% | 0.0% 0% 30.6% 0% | 0% 0 0% 0 | 05 0.0% 05 0.0% | 0.5828 | 0.0377 | 2000 | 0.5828 | 0.0377 | 0.7000 | | Ħ |
| ed C3 boblinum toen s. Rac2 oral membrane protein P. Pex14 lanabsome complex subs. Cops7s | PEX14 MOUSE 2 PEX14 MOUSE 4 CSN/A MOUSE 3 | 0 KUB 20 11 KUB 0 11 KUB 0 | 100% 5 50% 5 100% | 0% 16.7% 100% 100.0% | 100% Sc 0% C | % 86% 77.5 % 100% 83.2 % 0% 0.0 | 5 05 5 05 | 0% 0% 0. 0% 0% 0. | 0% 0% 0% 100% | 100% 100% | 100.0% | 5 05 | 05 0.05 | 05 05 | 05 0.05 | 67% 100 0 100% 100 | N 2005 N 205 N 1005 | 82.2% 01 100.0% 01 | 5 0% 0 100% 100 5 0% 0 | 0.0% 22 | N 9N 2 | 0% 17.8% 10 0% 0.0% 10 | 0% 75% 0% 0% | 200% 91.7% 200% 91.7% 200% 100.0% | 0% 0% 100% 0% 0% | 0% 0% 0% | 0.0% 0% 0.0% 0% | 25% 0 0% 0 | 05 8.3% 05 0.0% | 0.5017 | 0.4225 | 7300 | 0.5000 | | 0.288 | 0.5017 | = |
| iption factor GATA-4 Gata4 NDRG2 Ndrg2 systems (vans Scly | SCLY MOUSE 4 SCLY MOUSE 4 | 5 kDs 0 1 kDs 100 7 kDs 100 | 5 67% 5 67% | 0% 0.0% 100% 88.9% | 100% 100 0% 33 0% | N 100% 100.0 N 0% 11.1 | 5 0% 5 0% | 0% 0% 0. 0% 0% 0. | 0% 0% 0% 100% 100% | 0% 0% 200% | 0.0% 100 | % 100% % 0% | 100% 100.0% | 0% 0% 0% 0% | 0% 0.05 | 200 00 100% 100 100% 100 | % 0% % 100% % 100% | 0.0% 1001 100.0% 01 100.0% 01 | 5 100% 100 5 0% 0 5 0% 0 | 6 100.0% 0 6 0.0% 0 6 0.0% 0 | N 9N N 9N | 0% 0.0% 0% 0.0% 10 0% 0.0% 10 | 0% 0% 0% 100% 0% 100% | 0% 0.0% 100% 100.0% | 100% 100% 0% 0% 0% 0% | 100% 9 0% | 00.0% 0% 0.0% 0% | 0% 0 0% 0 | 0% 0.0% 0.4 | | 0.4225 | 0.4226 | | 0.4226 | | | Ħ |
| er/throcyte membrane or Mpp1 pic regulator 1 Pleg1 ne N-methyltransferase Homt | EMES MOUSE S PURGI_MOUSE S HINMT_MOUSE S | 2 kDs 100 7 kDs 0 | 0% | 100% 0% 0.0% | 0% 100% 100 | 0% 100% 100.0 | 9% 5 9% | 0% 0% 0. | 0% 0% 100% | 100% 100% | 100.0% | % % 0% | 0% 0.0% | 0% 0% | 0% 0.05 | 100% 100 100% 100 | IN SON | 93.3% 01 66.7% 01 | 5 0% 20 5 0% 200 | 6 5.7% 0 6 33.3% 0 | N 98 N 98 | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% | 100% 100.0% | 9% 9% 9% 9% | 0% | 9.0% 9% 9% | 0% 0 | 0.0% | 0.4226 | 0.4226 0.1835 | | 0.4225 | 0.4226 0.1835 | | | |
| de exchange factor SIL 1 SIII SPS1-related proline-alar SIGIS NpSnap homolog 1 Npsnap1 | SIL1 MOUSE S STKIN MOUSE 6 NPS1 MOUSE 3 | 2 kDs 100 0 kDs 50 0 kDs 100 | 5 100% 5 22% 5 100% | 100% 100.0% 100% 100.0% | 9% 0 50% 0 | N 0% 0.0 | % 0% % 0% | 0% 0% 0. 27% 0% 0% 0. | 0% 100% 0% 0% 100% | 100% 100% | 100.0% 0 | N ON | 0% 0.0% | ON ON | 0% 0.09 | 100% 100 | 100% | 100.0% 01 | 98 9 | 0.0% 0 | N 0% | 0% 0.0% 10 | 100% 0% 100% | 100% 100.0% | 0% 0% | 0% | 0.0% ox | 0% 0 | 0.0% | | | | | | | | |
| tigen Cd9 setyl-CoA synthetase Ascs seracconase/arvisidenase Pon1 | CD9 MOUSE 2 AACS MOUSE 7 PONI_MOUSE 4 | 5 kDa 100 5 kDa 100 6 kDa 100 | 5 100% | 100% 100.0% 100% | 0% 0 | 0% 0% 0.0 | % 0% | 0% 0% 0. 0% | 0% | 100% | | | 0% | | 0% | 100% 100 100% 100 100% 100 | % 100% % 100% | 100.0% 01 100.0% 01 | 6 0% 0 6 0% 0 | 0.0% 0 | N ON N ON | 0% 0.0% 10 0% 0.0% | 0% 100% 100% 100% | 100% 100.0% 100% 100% | 0% 0% 0% 0% | 0% 0% 0% | 0.0% 0% | 0% 0 0% 0 | 0% 0.0% 0% 0% | | | | | | | | = |
| reporter ZIPS Sk29aS ion protein A 70 kDs DN Rps1 cephoprotein 3 Golph3 | S39A5 MOUSE 5 RFA1 MOUSE 6 GOLP3 MOUSE 3 | 5 kDs 100 9 kDs 44 kDs 100 | 100% 100% | 100% 100.0% | 0% 0 | N 0% 0.0 | % 0% | ON ON O. | 0% 100% 0% 100% | 100% 100% 100% 100% | 100.0% 0 | % O% | 0% 0.0% | 0% 0% 0% 0% | 0% 0.09 | 100% 100% 100 | N 100% | 500.0% On | K 0% 0 | 0.0% 0 | N ON | ON 0.0% 10 | 0% 100% | 100% 100.0% | 0% 0% | ON. | 0.0% ON | ON O | 06 0.0% | | | | | | | | |
| n subunit 2 Prim2 sind-like protein 2 Min/2 desul-Coli decerbosciess Echdol | PFD2 MOUSE 1 MBN2 MOUSE 4 ECHO1 MOUSE 3 | 7 kDs 100 0 kDs 0 5 kDs | 5 100% 5 100% 5 0% | 100% 100.0% | 9% 0 100% 100 | N 0% 0.0 | 5 0% 5 0% | 0% 0% 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. | 0% 100% 0% 100% 0% 100% | 100% 100% 100% 100% 0% 100% 100% | 100.0% 0 100.0% 0 | % 0% % 0% | 0% 0.0% 100% 0% 0.0% | 0% 0% 0% 0% | 0% 0.05 0% 0.05 | 75% 100 25% 0 | % 100% % 100% % 0% | 91.7% 251 8.2% 751 100.0% 01 | 5 0% 0 5 100% 100 6 0% 0 | 8.3% 0 8.3% 0 91.7% 0 | N ON N ON N ON | 0% 0.0% 10 0% 0.0% 10 0% 0.0% 0% 0.0% 10 | 0% 100% 0% 100% 0% 0% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 100% 100% | 0% | 0.0% 0% 0.0% 0% | 0% 0 0% 0 | 05 0.0% 05 0.0% | 0.4226 0.4226 | 0.4226 0.4226 | | 0.4225 0.4225 | 0.4225 0.4225 | | | Ħ |
| regulated protein Denr NA-associated Sm-like or Lam3 sinding protein 3 Ybs3 | DENR MOUSE 2 LISKO MOUSE 1 YBOXO MOUSE 3 | 2 KDs 100 2 KDs 100 9 KDs 100 | 100% 100% 5 100% | 100% 100.0% 100% 100.0% | 9% 0 | N 0% 0.0 | 5 05 5 05 | 0% 0% 0. 0% 0% 0. | 0% 100% 100% 0% 100% | 100% 100% 100% 100% 100% 100% | 100.0% 0 100.0% 0 100.0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 100% 100 100% 100 100% | % 100% % 100% 100% | 100.0% 01 100.0% 01 | 5 0% 0 5 0% 0 | 0.0% 0 0.0% 0 | N 9N N 9N | 0% 0.0% 0% 0.0% 10 0% 10 | 100% 0% 100% 0% | 100% 100.0% | 9% 9% 9% | 0% | 0.0% 0% 0% | 0% 0% 0 | 0.0% | | | | | | | | |
| phosphatase 1A Ppm1a lement modulatory factor Tmf1 -hydroniase 1 P3h1 | PPMIA MOUSE 4 TMF1 MOUSE 1 P2H1 MOUSE 5 | 2 kDs 22 kDs 22 kDs 44 kDs | ON | 0% | 200 | N 100% | | os os | 100% 0% | 0% | 200 | N N | 100% | 0% 0% | 9% | 200% 200 200% 0 | N 40% | 21.7% 261 | 5 100% 60 | 0.00% 0 | N ON | 0% 0.0% 10 | 0% 100% 0% 100% | 200% 100.0% | 0% 0% 0% 0% | 0% | 90% 0% 90% 0% | 0% 0 0% 0 | 05 0.0% | | | | | | | | = |
| n Strm1 MP kinase 2. mitochondri Crepk2 in N-acelyticansferase Cit Creft | CMPK2 MOUSE 5 CMLOI MOUSE 2 | 7 KDs 100 0 KDs 5 KDs 100 | 5 100% | 100% 100.0% | 9% 0 | n on 00 | 98 | 0% 0% 0. | 100% 0% 100% | 100% 100% 100% | 100.0% | % 0% % 0% | 0% 0.0% | 0% 0% 0% 0% | 0% 0.09 | 100% 100 | 100% 100% | 100.0% 01 | 98 9 | 0.0% 0 | N ON | 0% 0.0% 10 0% 10 | 0% 100% 0% | 100% | 0% 0% 0% | 0% | 9% 9% | ON. | DS. | | | | | | | | |
| transporter Sk25s2 oddial import inner memb Draic 19 | CUL2 MOUSE 8 S2SA2 MOUSE 8 TIM14 MOUSE 1 | 7 kDa 100 17 kDa 100 12 kDa 2 kDa 0 | 5 100% 5 0% | 100% 100.0% 0% 0.0% | 0% 0 100% 100 | N 0% 0.0 | % 0% % 0% | 50 | 0% 0% | 0% 0% | 0.0% 100 | % 100% | 100% 100.0% | on on | 06 0.09 | 100% 25% 23 | n ox | 19.4% 253 | 6 67% 100 | 0 80.6% 0 | N ON | 05 0.0% | 0% 100% 0% 0% | 50% 0% 0.0% | 9% 9% 50% 100% | 0% | 83.3% SON | 0% Si | DN 16.7% | 0.1917 | 0.1917 | | 0.8947 | 0.1917 | 0.4226 | 0.4226 | 6 |
| ated protein R-Ras2 Rras2 mmed cell death protein 5 Pdcd5 ated protein Rap-15 Rap 15 | PDCDS_MOUSE 1 PAP1B_MOUSE 2 | 3 kDa 100 4 kDa 100 11 kDa 100 | 5 100% 5 100% | 100% 100% 100.0% 100% 100.0% | 0% C | 0% 0% 0.0 % 0% 0.0 | 0% % 0% % 0% | 0% 0% 0. 0% 0% 0. | 100% 0% 100% 0% 100% | 100% 100% 100% 100% | 100.0% 0 100.0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 100% 100 100% 100 100% 100 | PK 100% PK 100% | 100.0% 01 100.0% 01 | 6 0% 0 6 0% 0 | 0.0% 0 0.0% 0 | N 0% N 0% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% 0% 100% | 100% 100.0% 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 0% 0% | 0% 0% 0% | 0.0% 0% 0.0% 0% 0.0% 0% | 0% 0 0% 0 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | | |
| indino endothelial reculato Emper coll domain-containino on Codc 127 alad protein Rep-2c Rep2c in-2 Scm2 | EMPER MOUSE 7 CC127_MOUSE 3 RAP2C_MOUSE 2 SCRNQ_MOUSE 4 | 6 kDs 6 10 kDs 6 11 kDs 7 | 6 0% 6 100% | 17% 5.6% 100% 100.0% | 100% 100 | N 83N 944 | % 0% % 0% | ON ON O. | 0% 0% 0% 100% | 0% 100% 100% 100% | 33.3% 100 | % 100% 0% % 0% | 0% 66.7% | 0% 0% 0% 0% 0% | 0% 0.09 | 200 200 2000 200 2000 200 | N 100% | 0.0% 679 100.0% 01 | 6 S0% S0 6 0% 0 | 6 55.6% 22 6 0.0% 0 | N SON S N ON N ON | 0% 44.4% 0% 0.0% 10 | 50% 0% 100% 0% 100% | 100% 100.0% 100% 100.0% | 9% 9% 9% 9% | On. | 0.0% 0% 0.0% 0% | 0% 0 0% 0 | 0.4 0% 0.0% 0% 0.0% | 835 | | 0.4935 | | | | | Ħ |
| NOT transcription complex Cnot2 Pliculate family member Cot2 resolvinden rentein side Nobg1 | CNDT2_MOUSE 6 CELF2_MOUSE 5 NCEP1_MOUSE 9 | O KOs O H KOs IZ KOs | 0% | 0% 0.0% | 100% 100 | N 100% 100.0 | % 0% | 0% 0% 0. 0% | 0% ON | OK | 100 | % 100% | | 0% 0% | | 0% 40% 0 100% | 0% % 22% 100% | 24.4% 601 01 | 5 100% 67 5 0 | 1 75.6% 0 1 75.6% 0 | N ON | 0% 0.0% 10 0% 0.0% 10 | 0% 0% 50% 100% | 100% 83.2% 100% | 9% 50% 9% 50% | 0% | 15.7% OX | 0% 0 0% 0 | DN 0.0% | 0.0516 | | | 0.0516 | | | | |
| mani if is subcommonated Citys Strill 1-7 Strill | C1QA MOUSE 2 STRNO MOUSE 8 STX7 MOUSE 8 | 5 kDs 5 kDs 7 kDs (| s es | 0% 0.0% | 100% 100 | 0% 100% 100.0 | S 08 | 0% 0% 0. | os. | 100% | | 0% | 98 | 98 | 98 | 100% 100 100% 100 100% 100 | % 100% % 100% 0% | 100.0% on 100.0% on | 5 0% 0 5 0% 0 6 00 0 | 0.0% 0 0.0% 0 | N 9N N 9N N 9N | 0% 0.0% 10 0% 0.0% 5 0% 0.0% 8 | 0% 100% 0% 100% 0% 0% | 100% 100.0% 100% 83.2% 100% 95.8% | 9% 9% 59% 9% 199% 9% 9% | 0% 0% 0% | 0.0% 0% 16.7% 0% | 0% 0 0% 0 0% 0 | 06 0.0% 06 0.0% | 0.4226 1.0000 0.4226 | 0.5000 | | 0.4225 1.0000 | 0.5000 | | 0.4226 | 6 |
| e and olycine-rich protein Carp2 cylohogeni licese ABHD15 Abhd12 r of nuclear factor kapps-likbip | CSRP2 MOUSE 2 ABD12 MOUSE 4 IKP_MOUSE 4 | 1 kDs 5 kDs 3 kDs | | | | | | | | | | | | | | 100% 46 100% 100 0% 0 | 8 100% 8 100% | 82.1% 01 100.0% 01 1001 | 5 54% 0 5 0% 0 5 100% | 17.9% 0 6 0.0% 0 | N 9N N 9N N 9N | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% 0% 0% | 200% 100.0% 200% 100.0% | 0% 0% 0% 0% 80% 100% | 0% 0% | 0.0% 0% 0.0% 0% | 0% 0 0% 0 | 05 0.0% 05 0.0% | 0.4226 | | | 0.4225 | | | | |
| sted protein Rab-35 Rab35 lin-1 Ntp1 seen C-endoseptidase en Poolce succinate synthetase iso Adest1 | RABIS MOUSE 2 NEP1 MOUSE 1 PCOC1 MOUSE 5 PURAT MOUSE 5 | O KDa O KDa O KDa | | | | | | | | | | | | | | 100% 100 100% 100 100% | % 100% % 100% 100% | 100.0% OF | 5 9% 0 5 9% 0 | 0.0% 0 | N ON N ON | 08 0.0% 10 08 0.0% 08 10 08 10 | 0% 100% 0% | 100% 100.0% 100% | 0% 0% 0% | 0% | 00% 0% 0% | 98 3 | DS 0.0% | | | | | | | | Ħ |
| e kinase M-type Ckm in family homolog 1 Fermit! Z-dependent protease int Serpina (0. | FERMI MOUSE 7 ZPI MOUSE 5 | 3 kDs 7 kDs 2 kDs | | | | | | | | | | | | | | 100 100% 100 | N 100N | 100.0% 01 | 9% 0 | 0.0% 0 | on n on | 0% 0.0% | 100% 0% 100% | | 9% 9% 9% | | 9% | 0% | | | | | | | | | |
| se and poviadenvision so CpsN- selar transport protein 20 1820 e nucleotide-binding prote Gna11 nine adenceytransferase i Me2b | IFT20 MOUSE 1 GNA11 MOUSE 4 MAT28 MOUSE 3 | 5 kDa (2 kDa 100 7 kDa 100 | 5 20% 5 100% 5 100% | 0% 6.7% 100% 100.0% | 75% 60 0% 0 | N 67% 67.2 N 0% 0.0 | % 25% : 0% % 0% | 0% 23% 25. 0% 0% 0. | 7% 0% 100% 0% 100% | 0% 0% 100% 100% 100% 100% | 0.0% 86 100.0% 0 100.0% 0 | % 100% % 0% | 0% 95.2% 0% 0.0% | 14% 0% 0% 0% 0% 0% | 0% 4.89 0% 0.09 0% 0.09 | 0% 0 100% 100 100% 100 | 75 0% 76 100% | 0.0% 1001 100.0% 01 100.0% 01 | 6 100% 100 6 0% 0 6 0% 0 | 100.0% 0 0.0% 0 | N 0% N 0% | ON 0.0% 10 ON 0.0% 10 ON 0.0% 10 | 0% 100% 0% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% | 0.0% 0% 0.0% 0% | 0% 0 0% 0 | 0.4 0% 0.0% 0% 0.0% | 1226 | 0.4226 | 0.0124 | | 0.0171 | 0.023 | 721 | 0. |
| sociated death domain or Fadd 6+1 exchange regulatory Siciativ2 ription elongation factor B Toeb1 | FADD MOUSE 2 NHFF2 MOUSE 3 ELOC_MOUSE 1 | 3 kDa 100 7 kDa 2 kDa 100 | 100% | 100% 100% 100% | 0% | ONL ONL ONL | 0% | ON ON | 100% 100% 100% | 100% 100% 100% 100% 100% 100% | 100.0% 0 100.0% 0 100.0% 0 | % 0% % 0% % 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.09 0% 0.09 0% 0.09 | 100% 100 100% 100 100% 100 | % 100% % 100% | 100.0% 01 | 6 0% 0 6 0% 0 | 0.0% 0 | N ON ON | 0% 0.0% 10 10 0% 0.0% 10 | 0% 100% 0% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% | 0.0% 0% 0% 0.0% 0% | 0% 0 0% 0 | 0% 0.0% | | | | | | | | |
| ription factor A. mitochon; Them nase-interacting serine/th. Mink1 nine aminopeptidase 1. Metap1 rid smide hydrolase 1. Each | MONITARIAN MOUSE 4 MAPTI MOUSE 4 EAANT MOUSE 5 | 5 kDs 100 5 kDs 100 5 kDs 100 | 5 100% 5 100% 5 100% | 100% 100.0% 100% 100.0% | 0% C | N 0% 0.0 | 0% % 0% % 0% | 0% 0% 0. 0% 0% 0. | 0% 100% 0% 100% | 100% 100% 100% 100% 100% 100% | 100.0% 0 100.0% 0 100.0% 0 | % O% % O% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 100% 100 100% 100% | % 100% 100% % 100% | 100.0% 01 | 9% 0 | 6 0.0% 0 | N ON | 0% 0.0% 10 0% 10 | 0% 100% 0% | 100% 100% | 9% 9% | 0% | 9% | ON. | 200 | | | | | | | | Ħ |
| a intrarelisier channel ren Click antigen-like protein B Cd009b oblity group protein B3 Hingb3 | CLICS MOUSE 6 C2000 MOUSE 3 HMG83 MOUSE 2 | 3 kOs 7 kOs 5 kOs | Asses | | | | | | 1000 | | 66.04 | | | 25 25 | 08 00 | 100% 100 100% | N 100% | 100.0% 01 | 98 9 | 0.0% 0 | N ON | 0% 0.0% 0% 10 | 0% 100% 100% 0% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% 0% | 0% | 0.0% 0% 0.0% 0% | 0% 0 0% 0 | 0.0% | | | | | | | | |
| pagmal-associated protein Snap47 in family member 5 58h5 shanolamine-hydrolyzino Nasa | SNP47 MOUSE 4 SLFNS MOUSE 1 NAAA MOUSE 4 | 7 kDa 0 01 kDa 0 kDa | 6 6% | 0% 0.0% | 100% 100 | N 100% 100.0 | S ON | 0% 0% 0. | 25. | | | | | | | 100% 100% 100 | N 100% | 100.0% 01 | 5 05 0 | 0.0% 0 | N ON | 0% 0.0% 10 | 0% 100% | 100% 100.0% | 0% 0% | os. | 0.0% 0% | 0% 0 | 0.0% | | | | | | | | |
| in subunit 3 Dcin3 CoG-binding domain prob Mbd3 palobulin-binding probein 1 gbp1 | DCTNO MOUSE 2 MBD3 MOUSE 3 IGBP1 MOUSE 3 | 11 kDa 100 2 kDa 0 9 kDa 100 | 5 60% 5 0% 5 0% | 100% 85.7% 0% 0.0% 100% 55.7% | 0% 40 100% 100 0% 100 | N 0% 13.2 N 100% 100.0 N 0% 33.2 | 5 0% 5 0% 5 0% | 0% 0% 0. 0% 0% 0. 0% 0% 0. | 0% 67% 0% 0% 0% 100% | 200% 20% 20% 200% 100% | 0.0% 100 100.0% 0 | % 100% % 0% | 0% 100% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 67 0% 0 100% 100 | % 100% % 0% % 100% | 88.9% 01 0.0% 1001 100.0% 01 | 5 22% 0 5 100% 100 6 0% 0 | 11.1% 0 100.0% 0 0.0% 0 | N 9N N 9N N 9N | 0% 0.0% 10 0% 0.0% 0% 0.0% 10 | 0% 100% 0% 0% 0% 100% | 200% 100.0% 0% 0.0% 200% 100.0% | 0% 0% 100% 100% 0% 0% | 200% 1 200% 1 | 0.0% 0% 100.0% 0% 0.0% 0% | 0% 0 0% 0 0% 0 | 0% 0.0% 0.8 0% 0.0% 0.8 0% 0.0% 0.4 | 1226 | 0.9045 | 0.4226 | 0.4225 | 0.9045 | 0.5000 | | |
| 1-like protein 5 Epb415 in subunit 3 Vbp1 ale kinase Guk1 oversel protein 121 mino Mod21 | PFD3 MOUSE 2 KGUA MOUSE 2 RGUA MOUSE 2 | 2 kDa (0) 2 kDa (0) 2 kDa (0) | 100% | 200% 100.0% | 9% 0 9% 0 9% 1 | N 100% 100.0 | 5 05 5 05 05 | 0% 0% 0. 0% 0% 0. | 0% 0% 0% 100% 100% | 200 100% 100% 100% | 100.0% 0 100.0% 0 | % 100% % 0% % 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 100% 100 100% 100 | 0% 100% | 100.0% 01 01 | 5 0% 0 5 0% 0 | 0.0% 0 | N 9% N 9% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% | 20% 100.0% 200% 100.0% | 9% 9% 9% 9% 100% 100% | 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0 0% 0 | 0% 0.0% 0% 0.0% | | | | | | | | Ħ |
| n Tan proton ATPase subunit G Alpfiv1g1 ordrial peptide methionine Mara | TSN_MOUSE 2 VATG1_MOUSE 1 MSRA_MOUSE 2 | 5 kDa 100 4 kDa 100 5 kDa 100 | 5 100% 5 100% 5 100% | 100% 100.0% 100% 100.0% 100% 100.0% | 0% C 0% C | N 0% 0.0 N 0% 0.0 N 0% 0.0 | % 0% % 0% % 0% | 0% 0% 0. 0% 0% 0. 0% 0% 0. | 0% 100% 0% 100% 0% 100% | 100% 100% 100% 100% 100% 100% | 100.0% 0 100.0% 0 100.0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.09 0% 0.09 | 100% 100 100% 100 100% | % 100% % 100% 100% | 100.0% 01 100.0% 01 | 5 0% 0 5 0% 0 | 0.0% 0 0.0% 0 | N ON N ON | 0% 0.0% 10 0% 0.0% 10 0% 10 | 0% 100% 0% 100% 0% 100% | 1000 100.0% 1000 1 | 0% 0% 0% 0% 0% 0% | 0% 0% 0% | 0.0% 0% 0.0% 0% 0.0% 0% | 0% 0 0% 0 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | | |
| r core complex protein Nu Nup50 shill cytosol factor 4 NcM rin homobov domain-cont Plakhfil pendent RNA helicase DC DddSte | NUPSO MOUSE 3 NOF4_MOUSE 3 PROF1_MOUSE 3 DXXBA_MOUSE 4 | 9 kDs 0 9 kDs 11 kDs 0 9 kDs 100 | 6 0% 6 100% | 100N 100.0% | 100% 100 100% 0% 0 | ns on go | 0% 0% | 0% 0% 0. | 0% | 100% | 100 | % 0% | 100% | 0% | ON. | 200% 0 | 100% 100% 0% | 0.0% 1009 | 6 100% 100 6 0 100 6 0 | 6 100.0% 0 6 0 | N ON | 0% 0.0% 0% 10 0% 10 | 100% 0% | | 0% 0% | | 0% | ons ons | | | | | | | | | = |
| aband-break repair prote Rad21 lectin domain family 11 m Clec11a kalikrein KRb1 | RAD21 MOUSE 7 CLC11 MOUSE 3 KLKB1 MOUSE 7 | 2 KDs IS KDs 1 KDs | | | | | | | | | | | | | | 0% 0 0% 100% 100 | 0% 0% 15 100% | 0.0% 1009 100.0% 09 | 6 100% 100 6 100 6 0% 0 | (100.0% 0 (0.0% 0 | N ON | 0% 0.0% 10 0% 0.0% | 0% 100% 0% | 100% 100.0% 0% 100% | 0% 0% 100% | 200% 200% | 0.0% OK | 0% 0 | 0% 0.0% 0% | | | | | | | | |
| lysine 5-ceidase Los Los bissions and artennains in Coadr | LYCK MOUSE 4 CXAR MOUSE 4 | O KDa 7 KDa O KDa | | 200% | | 0% | | 98 | | | | | | | | 200% 100 0% 0 | N 100% | 0.0% 1009 | 5 0% 0 5 100% 100 | 0.0% 0 100.0% 0 | N 98 | 0% 0.0% 10 0% 0.0% | 0% 0% 0% 100% | 100% 100.0% | 0% 100% 0% 0% | 0% | 0% 0% 0% | 0% 0 | 05 0.0% | | | | | | | | = |
| type-5 receptor 2 Ephb2 osomal protein L7-like 1 Rp(7)1 of proteine 4 Mopt4 | EPHEZ MOUSE 1 RL7L MOUSE 2 MCPTH MOUSE 2 | 10 kDs 9 kDs 7 kDs | s 0% | 0% 0.0% | 100% 100 | N 100% 100.0 | S 08 | 0% 0% 0. | 0% | | | | | | | | | | | | | 10 | 0% 100% | 100% 100.0% | 0% 0% | 0% | 0% 0% | 0% 0 | 06 0.0% | | | | | | | | |
| orrol kinase, mitochondri: Agk 5100-A4 5100e4 sylsourate hydrolase Utah pendent G-phospholase Utah | AGK_MOUSE 4 S10A4_MOUSE 1 HUH_MOUSE 1 PEKAM_MOUSE 1 | 7 kDs 0 2 kDs 100 4 kDs 100 5 kDs | 5 205 5 1005 5 1005 | 100% 100.0% 50% 83.3% | 100% 100 0% 0 0% 0 | N 0% 0.0 N 50% 15.7 | 5 05 5 05 | 0% 0% 0. 0% 0% 0. | 0% 100% 0% 67% | 200 200% 200% 100% | 0.0% 100 0.0% 33 100.0% | % 100% % 0% % 0% | 0% 11.1% 0% 0.0% | 0% 0% 0% 0% | 0% 0.05 0% 0.05 | 200% 80 200% 200 | IS 25 IS 1005 IS 05 | 93.2% 01 66.7% 01 | 5 20% 75 5 20% 0 5 0% 200 | 58.3% 50 6.57% 0 6.33.3% 0 | N 50N 2 N 0N N 0N | SN 41.7% SN 0.0% 7 SN 0.0% 10 | 0% 0% 5% 80% 0% 50% | 0% 0.0% 25% 75.7% 100% 83.2% | 25% 0% 0% 50% | 25% 25% 0% | 77.8% 0% 16.7% 0% 16.7% 0% | 20% 6 20% 0 0% 0 | 7% 22.2% 2% 6.7% 2% 0.0% 0.7 | 0.1222 1972 0.6856 | 0.4226 0.6856 | 0.7972 0.7972 | 0.4042 0.6856 | 0.0377 0.4225 0.6856 | 0.7972 | 0.4226 | 15 |
| nucleotide-binding crots Gng5 ment component 1 Q sub C1gbp ise family domain-contains Nemal1 | GBGS MOUSE 7 C108P_MOUSE 3 MMRL1_MOUSE 3 | 'KDs 100 I1 kDs 100 I4 kDs 100 | 5 100% 5 100% | 100% 100% 100.0% 100% 100.0% | 9% 9% 0 | 0% 0% 0% 0.0 0% 0.0 | 98 8 98 8 98 | 0% 0% 0. 0% 0% 0. | 100% 0% 100% 0% 100% | 100% 100% 100% | 100.0% | % % % 0% | 0% 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0% 0% 0.09 | 200% 100 200% 100 200% 100 | N 100% N 100% N 100% | 100.0% 01 100.0% 01 100.0% 01 | 5 0% 0 5 0% 0 6 0% 0 | 0.0% 0 0.0% 0 0.0% 0 | N 9% N 9% N 9% | 0% 0.0% 10 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% | 25% 91.7% 100% 100.0% | 0% 0% 0% 0% | 25% | 0.2% 0% 0% 0.0% 0% | 0% d | 0% 0.0% 0% 0.0% | | 0.4226 | 0.4226 | | 0.4226 | 0.4226 | | E |
| otic translation initiation fs EIS4e2 NRss Ness convistion factor-like crote Artibo | RASN MOUSE 2 ARLES MOUSE 2 MEMO MOUSE 2 | 5 KDs (1 KDs) 11 KDs (2 KDs) 100 | 100% 100% 5 100% | 9% 11.1% 100% 100.0% | 100% 63 0% 0 100% 100 | 100% 88.9 1% 0% 0.0 | 5 05 5 05 | 50% 50% 20. 50% | 0% 0% 100% 0% 100% | 0% 0% 200% 200% 100% | 0.0% 100 100.0% 0 | % 100% % 0% % 0% | 0% 0.0% | 0% 0% 0% 0% 0% 0% | 0% 0.09 | 20% 00 100% 100 100% 100 | N 200 N 100% N 100% | 0.0% 1000 100.0% 00 100.0% 00 | 5 100% 100 6 0% 0 6 0% 0 | 6 100.0% 0 6 0.0% 0 6 0.0% 0 | N 9% N 9% N 9% | 0% 0.0% 10 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% | 100% 100.0% 100% 100.0% | 9% 9% 9% 9% 9% 9% | 0% 0% | 0.0% 0% 0.0% 0% | 0% 0 0% 0 | 0% 0.0% 7% 22.2% 8% 6.7% 8% 6.7% 9% 0.0% 9% 0.0% | uad . | 0.4226 | 0.4026 | | 0.4226 | | | E |
| Nedd5 seome subunit piCin Cine ta -13 Capn 13 | NEDOS MOUSE 9 ICLN_MOUSE 2 CAN13_MOUSE 7 | 1 kDa 100 15 kDa 100 15 kDa 100 | 5 100% 5 100% | 100N 100.0% | 0% 0 0% 0 | N 0% 0.0 | % 0% 0% | ON ON O. | 0% 100% 100% | 100% 100% | 0 0 | % | 0% 0% | ONL ONL | ON. | 100% 100 | 100% 100% | 100.0% 01 | 6 0% 0 | 0.0% 0 | N ON | 0% 0.0% 10 0% 10 | 0% 100% 0% 100% 0% 100% | 100% 100.0% 82% 94.4% | 0% 0% 0% 0% 0% 0% | 0% | 0.0% 0% 0.0% 0% | 0% 0 0% 0 0% 1 | 0% 0.0% 7% 5.6% | | | | | | | | E |
| dehvdrosenase lubiouinor Ndufbli me production factor 2 ho Rpt2 ienvi-dichoschale Delta-ia Idi1 | NDUBS_MOUSE 2 RPF2_MOUSE 3 IDH_MOUSE 2 | 2 kDs 100 5 kDs 0 5 kDs | K 100% K 23% | 900 100.0% 9% 11.1% | 0% C | N 0% 0.0 % 100% 85.9 | % 0% % 0% | 0% 0% 0. 0% 0% 0. | 0% 100% 0% | 100% 100% | 100.0% 0 | % 0% | 0% 0.0% | ons ons | 016 0.09 | 100K 100 | 0% 100% | 100.0% 01 | S 0% 0 | 0.0% 0 | N ON | 0% 0.0% 10 | 0% 100% | 100% 100.0% | ON ON | ons | 0.0% ON | Ons 0 | 06 0.0% | | | | | | | | E |
| non acidic protein 1 Prap1 flores him innes harbonal Cog7 hype I culicular Ha5 Kr05 overal distribution Subsensia Most3 | PARPL MOUSE 1 COOT MOUSE 2 KRTIS MOUSE 5 MGSTI MOUSE | 7 KDs 100 17 KDs 100 7 KDs | 100% 100% | 100N 100.0% | 9% 0 | N 0% 0.0 | % 0% | 0% 0% 0. 0% | 0% 100% | 100% 100% | 100.0% 0 | s 0s | 0% 0.0% | ox ox | 0% 0.09 | 100 | n ov | 0.0% | 98 | 0.0% 100 | 9% N 999% *0 | 0% 100.0% A | on 22% | 43% 60.2% 25% 32.P% | 20% 18% 0% 0% | 57% | 21.8% 0% 12.5% 60% | 67% 31 | 00 0.0% 85 54.7% | 0.0171 | | | 0.4226 | | | 0.0359 | |
| ni reductase family memb Cbr4 I nucleotide secialon recei Mms19 specific chaperone A Toca | CERA MOUSE 2 MMS19 MOUSE 1 TECA MOUSE 1 | 5 kDa 100 13 kDa 100 3 kDa 100 | 100% 100% K 100% | 100% 100.0% 100% 100.0% | 9% 0 | N 0% 0.0 N 0% 0.0 | S 08 | 0% 0% 0. 0% 0% 0. | 0% 100% 100% 0% 100% | 100% 100% 100% 100% 100% | 100.0% 0 100.0% 0 | % 0% % 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 0% | 0% 0.05 0% 0.05 | 100% 100 100% 100 | N 100% N 100% | 100.0% or | 0% 5 0% 0 5 0% 0 | 0.0% 0 | 9% N 9% N 9% | 0% 0.0% 10 0% 0.0% 10 | 0% 100% 0% 100% 0% 100% | 100% 100.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0% | 0% 0.0% 0% 0.0% 0% | 0% 0% 0 | 0% 0.0% 0% 0.0% 0% 0.0% | | | | | | | | Ε |
| osomal protein L41, miloc MrpH1 osomal protein L24, miloc MrpE4 , type II cytoskeletal 80 Kr80 Dr1 | RMP1_MOUSE 2 RADRA_MOUSE 2 R2CR0_MOUSE 5 NC2B_MOUSE 5 | 5 KDs (1 K)) K)) K))))))))))))))))))))))))))) | 0% 0% | 9% | 100% 100 100% | 100% | 98 | 0% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0% | 0% 0% 0% | 100 | 100% | 100% 100% 100% | 98 | 9% 9% | 9% 0 9% 0 | 05 05 05 05 | 0.0% 1009 0.0% 1009 | 5 100% 100 5 100% 100 5 0% ^ | 100.0% 0 100.0% 0 | N 9% | 0% 199,0% 4 100,0% 100 0% 0,0% 10 0% 0,0% 10 0% 0,0% 0,0% 0,0% 0,0% 0,0% 0,0% 0,0% | 9% 9% 9% 9% 9% 9% | 42% GB.2% 25% 32.8% 100% 100.0% 100% 100.0% 100% 100.0% 100% 100.0% 100.0% 100.0% | 100% 100% 100% 100% 100% 100% | 100% 9 | 0% 0% 0% | 0% 0 0% 0 0% 0 | 05 0.0% | | | | | | | | Ħ |
| connancheductane SCR: Dhra4 aled protein Rel-B Relb ear-binding cost-associa Necap! | DHRS4_MOUSE 2 RALD_MOUSE 2 NECP1_MOUSE 3 | 0 kOs 100 3 kOs 0 kOs 0 | 5 100% 5 0% | - | 0% C | IN. | 9% 9% | ON. | 100% 0% | 100% 100% 75% 0% | 25.0% 100 | % 0% % 25% | 0% 100% 75.0% | 0% 0% 0% | 0% 0% 0.09 | 100% 100 100% | 100% 100% | 100.0% 01 | 98 9 | 0.0% 0 | N ON | 0% 0.0% 0% 10 | 0% 100% | 200% 200% 100.0% | 98 98 | Ons Ons | 90% ON | 0% | 05 0.0% 05 0.0% | 1226 | | 0.4226 | | | | | H |
| many conserved signaline Ecsit | CORST MOUSE 5 | r KDs C | 5 0% | 0% 0.0% 0% 0.0% | 100% 100 | Th 100% 100.0 | 9 98 5 98 | 0% 0% 0. 0% 0% 0. | 57% C% | | 100 | % | | ON. | | 98 0 | D | 1009 | 100% | | 96 | | 25 05 | | 100% 100% | 4 | 9% | 0% | | _ | | | | | | | + |

| icase KH KH CH presidents protein cutC Cutc CU dutnositol 3-kinase reo PKGr1 PB res DAFO 4811 Conditi CD | HK MOUSE 2010 UTC MOUSE 2010 ISA MOUSE 0410 | Da 100% | LOON | | DN ON | | 0% 0% | | 100% 10 10 | ION ION | - 01 | 0% | | 0% 0 | N. | 200% 200% | 100% | 900.0% | | N 00% | 0% 0% | 0% 100% 1 | 2005 100.05 | 0% 0% | ons | 0.0% ON | 0% 0% | 0.0% | | | | | = | | | |
|---|---|------------------------------------|-------------------------------------|---|--|--|---------------------|---|--------------------------|--|---|------------------------|--------------------------------|--------------------|----------------------------------|--|---|--|---------------------------------------|-----------------------------------|--------------------------|--|---|---------------------------------|--------------------|----------------------------------|---------------------------|-------------------------------------|--------------------------------------|------------------------------------|-----------------|----------------------------|--------|------------------|------------------|------|
| ydroglase 3 P3h3 P3i rnesin Ina Alh II histocompatibility and PG-As PA | INC. MOUSE 82 H INC. MOUSE 55 H A2D MOUSE 28 H | Da Da OS | SON ON | 16.7% 100 | DN 50% | 100% 83.3% | 0% 0% | 00 0.00 | | | | | | | | 0% 0% 42% | 00% 100% 0% 0% 67% 40% | 1009 1009 49.4% 421 | 8 | 5 383% 1 | 0% 0% 0% 0% 2% 0% | 0% 12.2% | ON. | 100% | | | os. | | | 0.1790 | | | 0.1110 | | | 0.10 |
| nabsome complex sub, CopeS CS il domain-containing on CodoSI CO indige periodo Dick1 Dic | SNS MOUSE 36 H CD91 MOUSE 50 H CD61 MOUSE 47 H | Da 100% | 0% 0% 0% 0% | 100.0% 0 0.0% 100 0.0% 67 0.0% 100 100.0% 0 | 0% 0% 0% 200% 7% 200% 0% 200% 0% 0% 0% 0% 0% 0% | 0% 0.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 10 0% | 0% 100% 0% 0% | 900.0% 01 0.0% 1001 | % 0% % 100% | 0% 0.0% 100% 100.0% | 0% 0 0% 0 | % 0% 0.1 % 0% 0.1 | 75 1 75 05 | 00% 100% 0% 0% | 0.0% 1009 | 9% 0 5 100% 100 | N 100.0% | 9% 9% 9% | 0% 0.0% 0% | 00% 100% 100.05 0% 0% 0.05 | 0% 0% 100% 100% | 100% | 0.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% | | | 0.4226 | | | 0.4226 | 6 | |
| r protein 622 ZH622 ZH6 nydronicotinamide dehs Ngp2 ND 17-beta-debydrowness (feet TH6 Did | ME22_MOUSE 53 A QO2_MOUSE 26 A HER MOUSE 27 A | Da 0% | 0% 0% 100% 100% | 0.0% 100 0 100.0% 0 | 0% 100% 0% 0% | 100% 100.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 0% 100% | 2% 100% 100% | 100 ms 01 | % 100% % | 0% 0.0% | 0% 0 0% 0 | % O% O. | 9% 100% 1 | 0% 0% 00% 100% | 0.0% 1009 | 5 100% 100 0% 0 | S 100.0% | 0% 0% 0% | 0% 0.0% 0% 100% 1 | 0% 100% 100.09 00% 100% 100.09 | 200 000 000 000 | 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | | | | |
| cled RNA columerase II Poir2c RPI trial fission factor MW MFI grand transferase have. Enhances | PB3_MOUSE 31 P FF_MOUSE 33 P GTA_MOUSE 65 P | Da 0% | 0% 0% | 100 | 200% 0% | 100% 0% 0.0% | 0% | 0% 0% 0% 0% | 100% 10 | 0% 0% | 100.0% 01 | % 0% | 100% 100% | 0% 0 | 0% 0% | 60% 0% | 00% 100% 00% 50% 0% 0% 0% 0% | 0.0% 1000 | 6 100% 100 | N 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% | 00% 20% 100.09 0% 0% 0.09 | 0% 0% 100% 100% | 100% | 0.0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% | 0.0704 | | | 0.0704 | _ | | | |
| NA-binding protein Luc Luc71 LUC site-1 Arb1 Arb1 Arb1 | JC7L MOUSE 441 | Os Co | 0% 0% | 100.0W 0 | 200% | 100% | UN | 016 0.0% | | | 2001 | 76 | 0x 0.0x | 0% | | 0% 100% 1 | 0% 0% 00% 100% | 0.0% 1001 100.0% 01 | 6 100% 100 6 0% 0 | N 100.0% | 0% 0% 0% 0% | ON 0.0% ON 0 ON 0.0% 100% 1 | 0% 00% 100% 100.09 | 100% 100% 0% 0% | 0% | 0% 0.0% 0% | 0% 0% 0% | 0.0% | | | | | _ | | | |
| In Adpog AD omal protein L49, mitor MrgH9 RM | DIPO MOUSE 27 I | Da Da | ON JOH | | 0% | 0.00 | 100% | | 1000 21 | 2001 | | | 0.00 | | | 0K | 00% 0% | 1001 | 0% 6 100 | K . | 0% | on on | 500% 0% | 100% 100% | One | 0% | 0% | | | | | | === | | | |
| ASC ATI | TLAZ MOUSE 669 FC4A MOUSE 449 | Da 1005 Da | 100% 200% 100% 200% | 100.0% 0 | 25 25 | 05 005 | 0% 0% 0% | 0% 0.0% | 100% 10 | 100 100% 100 100% | 100.0% 01 | S 05 | 0% 0.0% | 0% 0 | S 05 0 | 75 2005 25 05 | 9% | 1009 | 5 100 | N | 25 | 0% 0% | 0% 0% 0.09 | 100% 100% | 100% | 100.0% 0% | on on | 0.0% | | | | | === | | | |
| int component CB albhy CBa CO oxformoususele learners Hyl HYI | ORA_MOUSE 669 YI_MOUSE 309 | Da Da | | | | | | | | | | | | | | 100% 1 100% 1 | 00% 100% | 100.0% 01 | 6 0% 0 | N 0.0% | 0% 0% | 0% 0.0% 0% 0.0% | | 03 03 | | - 05 | ON. | | | | | | === | | | |
| nic reticulum Gold inte Englic2 EPI nd palate transmembras Ciptum I CU | RGIZ MOUSE 429 LP1L MOUSE 629 | Da 05 | 0% 62% 100% | 22.2% 0 | 0% 0% 0% 0% | 0% 0.0% | 200% 100% 20% 0% | 32% 77.8% | 67% S | 0% 50% 0% 50% | 33.3% 01 38.9% 01 | % 0% % 0% | 0% 0.0% 0% 0.0% | 100% S0 23% 100 | N 50N 65 | PS 98 | 0% 100% 0% 0% | 33.3% 01 0.0% 01 | 5 0% 0 5 0% 0 | N 0.0% 10 N 0.0% 10 | 0% 200% 0% 200% 1/ | 0% 66.7% 0% 0% 100.0% | | 0% | 200 | 200% | | 0.711 | 17 | 0.7972 0.0704 | | | | 0.7111 | 7 | 0. |
| protein 2 Tom12 TM drocusteroid-Delbuilli D Ebp ED | MILZ MOUSE 569 BP_MOUSE 269 | Da 05 | 50% 200% 100% 200% | 50.0% 100 100.0% 0 | 0% 0% 50% 0% 0% | 0% 50.0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 50% 10 100% 10 | 0% 100% 0% 100% | 100.0% O | N 0% | 0% 0.0% | 0% 0 0% 0 | s os o | 25 100% 25 100% 1 | 92% | 01 01 100,0% 01 | 5 0% | N 0.0% | 0% 0% 0% | 100% 1 100% 1 | 00% 200% 100.09 00% 200% 100.09 | 9% 9% 9% 9% | 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | === | | | |
| clos subfamily C ment Draig 7 DN in SELD Seld Seld SE | NUCT MOUSE 56 H | Da 100% Da 0% | 0% 0% | 0.0% 100 | 0% 100% | 100% 100.0% | 9% 9% 9% | 0% 0.0% | 0% | 0% 0% | 0.0% 1001 | N 100% | 100% 100.0% | 0% 0 | s os o | 100% 25 32% | 100% 9% | 675 | 5 200 | N . | 2% 2% | 0% 100% 0% | | 9% | | 9% | 00 00 | | | 0.5000 | | | 0.5000 | | | |
| re subunit beta type-10 Parti 10 PSI I histocompatibility anti HS-D1 HA | SB10 MOUSE 299 A12 MOUSE 419 | On On | 100% | | | on con | | 0% | | | - | | | | | 70% 1 75% | 90% 100% 86% 100% | 90.0% 301 86.9% 131 | 6 0% 0 6 14% 0 | N 10.0% | 0% 0% 2% 0% | 0.0. 1900.0 1900 | 00% 100% 100.09 | 0% 0% | 0% | 0.0% 0% | 0% 0% | 0.0% | 0.4226 | | | 0.4225 | _ | | | |
| oldoreductase-like orol Crystl QC blease inhibitor A3G Serpina3g SP volvo rockin Mucho Mil | ORLI MOUSE 39 P PA3G MOUSE 49 P NORP MOUSE 12 P | Da Da | 67N 75N | 80.6% O | N. 32K | 10x 104% | 0% 0% | . m nm | 67% 6 | 2% 90% | 71.1% 331 | w 22% | 304 28 94 | 0% 0 | w 0% 0.1 | 0% 100% | 22% 6% | 1009 09 | 6 GN 100 | K 65.7% | 0% 0% 0% | 06 0.0% 626 | 00% 100% 50% 63% 61.59 | 22% 50% | 22% | 38.9% ON | 0% 0% | 0.0% 0.457 | 9 0.2832 | 0.1174 0.2 | 58 0.4571 | 0.2832 | 0.1174 | 0.2358 | | |
| nase subunit epsion. mi Alpõe ATI /WD repeal-containing Tota TBI Austicing factor 50572 Bras 2 50 | TPSE_MOUSE 6 KG BL1X_MOUSE 57 K DE27_MOUSE 26 K | Da 0% | 0% 0% 0% 0% | 100.0% 0 0.0% 100 | 0% 0% 0% 100% | 0% 0.0% 100% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% S 0% | 10% 100% 0% | 93.3% 01 | % 20% % | 0% 6.7% 100% | 0% 0 0% | % 0% 0.1 % 0% 0.1 | 7% S0% 0% | 22% 100% 0% 0% | 61.1% S01 0.0% 1001 22.2% 1001 | 67% 0 5 100% 100 5 100% 22 | N 38.9% N 100.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 32% | 22% 100% 77.89 50% 22% 38.99 67% 100% 88.99 | 0% 67% 67% 50% | 67% 67% | 22.2% 0% 61.1% 0% | 0% 0% 0% 0% | 0.0% 0.423 | | | 23 0.4226 56 | 0.6075 0.0198 0.0785 | 0.1917 | 0.5623 0.0636 | | |
| dinarhimmaina saduri Kdar KD din4 Olim4 CLI | DSR MOUSE 369 LFIM MOUSE 579 | Da 100% | | 0 | DN | w 0.00 | 98 | | 1000 10 | | 400 OF 01 | | ev 0.00 | | | 9% 9% | 95 95 | 0.0% 1000 | 5 100% 100 | N 100,0% | 0% 0% 0% 0% | 0% 72% 0% 0.0% 0% | 50% 0% 40.59 17% 0% 5.69 | 0% 0% 62% 62% | 0% 50% | 0.0% 29% 61.1% 33% | 50% 100% 17% 50% | 59.5% 33.2% | 0.0198 0.0765 0.6770 0.4226 | | | 0.0198 | | | 0.6770 | 2 |
| annina.rentain ritrants PppSc PPI ine zioner and W2 dor Bzs2 BZ | PPS MOUSE 579 ZW2 MOUSE 4619 | Da 100% | 100% 100% 100% 100% | 100.0% 0 100.0% 0 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% 0% 0.0% | 100% 10 100% 10 | 0% 100% 0% 100% 0% 100% | 100.0% or 100.0% or 100.0% or 100.0% or 100.0% or | % 0% % 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | % 0% 0.1 % 0% 0.1 | 75 100% 1 75 100% 1 | 90% 90% 100% | 100.0% 01 | 5 0% 5 0% 0 | S 0.0% | 0% 0% 0% 0% | 100% 1 0% 0.0% 100% 1 | 00% 100% 100.09 | 9% 9% 9% 9% | 0% | 0.0% 0% 0% | 0% 0% 0% | 0.0% | | | | | | | | |
| ase 4 Rhase4 RN 55e Ste ST help 10 Treeh10 TV | NASA MOUSE 17 A TX4 MOUSE 34 A (\$10 MOUSE 54) | Da 100% | 200% 100% 100% 100% | 100.0% | 0% 0% | 0% 0.0% | 0% 0% | 9% 0.0% | 100% 10 | 100% | 100.0% 01 | % 0% | 0% 0.0% | 0% 0 | % 0% 0.1 | 200 1000 1 2000 1 1000 1 1000 1 1000 1 1000 1 1000 1 | 00% 100% 00% 100% | 100.0% 01 | 0% 0 | S 0.0% | 0% 0% | 0% 0.0% 100% 1 100% | 200% 100.09 200% 100.09 | 0% 0% 0% 0% 0% | 0% 0% | 0.0% 0% 0% | 0% 0% 0% | 0.0% | | | | | === | | | |
| gen Cd81 CD RNA NE-adenosine the Cagep OS dulancial Schountaine Dinal 2s Did | DB1_MOUSE 26 H SGEP_MOUSE 36 H MOA_MOUSE 46 H | Da 100% Da 100% | 100% 100% 100% | 100.0% 0 | 0% 0% 0% 0% | 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% | 26 | 100 100% | | ons | 0% | - | % 0% | 100% 1 100% 1 | 00% 100% 00% 100% | 100.0% 01 100.0% 01 | 5 0% 0 5 0% 0 | S 0.0% | 2% 2% 2% 2% | 0% 0.0% 100% 1 0% 0.0% 100% | 00% 100% 100.09 | 0% 0% 0% 0% 0% | 0% | 0.0% 0% 0% | 0% 0% | 0.0% | | | | | === | | | |
| omal protein L26, mitor, MrgE30 RM S-glucosamine kinase Nagk NA penin-like protein 1 Suff SV | AGK MOUSE 30 H | Da Da | es. | 100 | DK 100% | | 0% 0% | | 0% | | 1001 | | | 0% | | 2% 100% 1 | 0% 00% 100% | 100.0% 01 | 5 25 0 | N 0.0% | 9% 9% 9% | 0% 0.0% 100% 1 | 0% 0% 0.09 00% 100% 100.09 | 67% 100% 0% 0% | 100% | 88.9% 23% 0.0% 0% | 0% 0% 0% 0% | 11.1% | | | | 0.4225 | === | | 0.4226 | 15 |
| sal tarceting signal 1 ne Psc5 PE okinin receptor type A Cicker CC nuclear ribonucleoprote Stroc RU | EXS MOUSE 719 CKAR MOUSE 489 UTC MOUSE 179 | Da 100% | 0% 100% 0% 0% | 100.0% 0 | 200% 0% 0% 0% 100% | 0% 0.0% 100% 100.0% | 0% 0% 0% 0% | 6 0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% | 100% 10 0% | 100% 22% | 100.0% 01 | % 0% % | 0% 0.0% 62% | 0% 0 | % 0% 0.1 | 25. | os os | 0.0% 1009 | 5 100% 100 | N 100.0% | os os | 0% 0.0% 100% 1 0% 0.0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0 | ON 22% 11.17 | 100% 100% | 67% | 88.9% ON | on on | 0.0% 0.500 | 0 0.4226 | 0.8 | 88 0.5000 | 0.4226 | == | 0.8088 | | |
| racting and GLEBS mt 2n207 2N6 chain V-II region 26-10 1 5V KV protein-sorting-associal Vps26 VP | V2A7_MOUSE 53 H V2A7_MOUSE 12 H P536_MOUSE 44 H | Da : | 0% 0% 100% 75% 100% | 91.7% 0 | 999% 9% 9% 25% | 100% 0% 8.3% | 0% 0% 0% | 016 0.076 | 100% 7 | 10% 100% FSW 100% | 91.7% 01 | 0% % 25% | 0% 0% 8.2% | 0% 0 | % 0% 0.1 | 40% 50% 7% 100% 1 | 22% 20% 67% 100% 00% | 31.1% 601 72.2% 501 | 6 67% 80 6 22% 0 | K 27.8% | 0% 0% 0% 0% 0% 0% | ON 0.0% SON ON 0.0% 82% | 32% 0% 27.85 75% 80% 79.45 00% | 50% 67% 17% 25% 0% 0% | 20% | 72.2% 0% 20.6% 0% | 0% 0% 0% 0% | 0.0% 0.500 0.0% 0.0% 1.000 | 0.8485 0.6735 | 0.0339 0.0339 0.4225 0.40 | 36 26 1.0000 | 0.8485 | 0.0339 | 0.0136 | | |
| asome non-ATPase rec Pand9 PS nalssome complex sub: Cops5 CS -associated speck-like Pycard AS | SMS MOUSE 25 A SNS MOUSE 36 A SC MOUSE 21 A | Da 100% Da 100% Da | 100% 100% 100% 100% 100% 100% | 100.0% 0 100.0% 0 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 6 0% 0.0% 6 0% 0.0% | 100% 10 100% 10 | 00% 200% 15% 200% 10% 200% 10% 200% 10% 200% | 100.0% 01 100.0% 01 | 0% % 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | % 0% 0.1 % 0% 0.1 | 9% 100% 1 9% 100% 1 | 00% 100% 100% 00% 100% | 100.0% 01 | 6 0% 0 6 0% 0 | N 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 1 0% 100% 0% 0.0% 100% 1 | 00% 500% 100.09 00% 500% 100.09 | 0% 0% 0% 0% | 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | | | | |
| In-crokein licase FBNG1 Ring1 RBN stoantigen Sp-100 Sp100 SP obsiln J chain Johan IGJ | NG1_MOUSE 43 H P100_MOUSE 55 H U_MOUSE 18 H | Da Os Da | 0% 0% 0% | 0.0% 100 | 202% | 100% 100.0% | 0% 0% | 010 0.0% | | | | | | | | 2% 17% 100% 1 | 0% 0% 00% 100% | 1001 675 100.0% 01 | 5 100% 5 100 5 0% 0 | N 0.0% | 0% 0% 2% 0% 0% | 0% 0.0% 100% 0% 100% 0% 100% 1 | 0% 67% 100% 88.95 | 100% 100% 0% 33% | 0% | 11.1% 0% | 0% 0% 0% 0% | 0.0% | 0.4226 | | | 0.4225 | | | | |
| ribrose 1. ribroribate in Mrif Mill dustrousness 1 miles Prodh PR NFMN cyclass Tide Tid | TNA MOUSE 39 A ROD MOUSE 68 A GFC MOUSE 60 A | Da SOS Da | 100% 100% | 50 | 0% 0% | os | 9% 9% | | 100% | 100% 100% 100% | - 01 | 0% | 0% 0% 0% | ON G | 0% 0% 0% | 100% | 100% 100% | 01 | | N. | 25 | 0% 100% 1 100% | 00% 100% 100.09 | 9% 9% 9% | 0% | 0.0% 0% 0% | ons ons | 0.0% | | | | | === | | | |
| me P450 251 Cyp2x1 CP eonine-crolein kinase / 594 579 a bicsynfhesis-like dom Pbid1 P58 | P2S1_MOUSE | Da Da LOOK | 100% 100% | 100.0% 0 | 0% 0% | | | | | | 100.0% 01 | s 0s | 0% 0.0% | 0% 0 | s os o | 75% 25 | 100% | 251 | s 08 0 | × | 9% | 0% 100% 1 | 00% 100% 100.09 00% | 9% 9% 9% | O%. | 0.0% 0% | ons ons | 0.0% | | | | | === | | | |
| ty immunosiobulin osmi Fogr2 FO tino islet-derived proteir Reg3g RD conucleoprotein comple Nhp2 NH | DGRQ_MOUSE 37 H BG3G_MOUSE 19 H P2_MOUSE 17 H | Da Son | 22% 200% | 61.1% 50 | 05 625 | 0% 38.9% | 0% 0% | 08 0.0% 08 0.0% | 50% 10 | 10% SON | 65.7% 901 | s 0s | 50% 33.2% | 0% 0 | s os o | 200% 1 79% 2% 62% | 90% 100% 90% 100% 50% 75% | 500.0% 09 59.5% 219 53.9% 229 | 6 0% 0 6 10% 0 6 50% 25 | N 10.5% N 36.1% | 0% 0% 0% 0% | 08. 100% 100% 100% 100% 100% 100% 100% 100 | 00% 100% 88.9 7 | 20% 0% 22% 0% | 0% | 11.1% 9% | ons on | 0.0% 0.8411 | 9 0.1447 | 0.9061 0.30 | 79 0.8419 | 0.1447 | 0.9061 | 0.3379 | | |
| - associated Sm-like or Lamb LSP sin-containing family or Ythdt2 YTh -82 Sh3gb2 SH | SME_MOUSE 10 A THD2_MOUSE 62 A HLB2_MOUSE 44 A | Da 05 | 0% 0% 0% 0% | 0.0% 100 0.0% 100 | 0% 0% 100% 0% 100% | | 0% 0% 0% 0% | 00 0.0% 00 0.0% 00 0.0% 00 0.0% 00 0.0% 00 0.0% | 100% 10 0% | 0% 100% 0% 0% 0% 0% | 930,0% 01 0,0% 2001 190,0% 01 100,0% 01 | % 0% 100% % 100% | 0% 0.0% 100% 100% 100.0% | 0% 0 0% 0 | % 0% 0.1 % 0% 0.1 | 75 1995 1 95 75 95 | 00% 100% 0% 0% 0% 0% | 0.0% 1001 0.0% 1001 | 5 0% 0 5 100% 100 5 100% 100 | S 0.0% S 100.0% | 0% 0% 0% 0% | 0% 0.0% 100% 1 0% 0.0% 0% 0% 0.0% 0% | 00% 100% 100.05 0% 0% 0.05 0% 50% 15.75 | 0% 0% 100% 100% 100% 100% | 20% 100% 50% | 0.0% 0% 100.0% 0% 83.3% 0% | 0% 0% 0% 0% | 0.0% 0.0% | 0.4226 | 0.40 | 26 | 0.4225 | _ | 0.4226 | | |
| oschohistidine shosoh Phpt1 PH C62 C0 re inhibitor PI31 subun Pamf1 PS | HP14 MOUSE 149 OF2 MOUSE 199 SMF1 MOUSE 309 | Da 100% Da 100% Da 0% | 100% 100% 100% 100% 22% 0% | 100.0% 0 100.0% 0 11.1% 100 | 0% 100% 0% 0% 0% 0% 0% 0% 0% 67% 0% 200% 000 100% 100% | 0% 0.0% 0% 0.0% 100% 88.9% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 10 100% 10 0% | 0% 100% 0% 100% | 100.0% 01 100.0% 01 | % 0% % 0% | 0% 0.0% 0% 0.0% | 0% 0 0% 0 | % 0% 0.1 % 0% 0.1 | 75 100% 1 75 100% 1 0% | 00% 100% 00% 100% 0% 0% | 100.0% 01 100.0% 01 0.0% 1001 | 6 0% 0 6 0% 0 6 100% 100 | N 0.0% N 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 1 0% 0.0% 100% 1 0% 0.0% 0% | 00% 100% 100.09 00% 100% 100.09 | 0% 0% 0% 0% | 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | 16 | 0.4226 | 0.4226 | | 0.4226 | | | |
| protein C forf123 home 1 5V CA soulatory dutamine/l/sii Srek1 SR lv molecular chaperone Bag4 BA | A123 MOUSE 18 H REKT MOUSE 57 H AG4 MOUSE 49 H | Da Da Os | 0% 0% 0% 0% | 0.0% 100 | 9% 999% 9% 199% | 0% 100% 100% 100.0% | 0% 0% 0% | 0% 0% 0% 0.0% | 0% | 0% 100% 0% 0% | 0.0% 1001 | 200% 100% | 100% 100.0% | 0% 0 | % 0% 0.1 | 100% 1 0% 2% | 00% 100% 0% 0% | 0.0% 1001 | 5 100% 100 | N 100.0% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0.0% 0% | 0% 0% 0.09 | 0% 100% 100% 100% | 200% | 100.0% 0% | 0% 0% 0% | 0.0% | | | | | _ | | | |
| n Fg2 FG bischoschate aldolase I Aldob ALI ne assembly chaperone Pang1 PS | IDOB_MOUSE 49 is SMGI_MOUSE 39 is | Da Da | 200% | | 500% | ON. | 0% | 016 0.0% | 100% 10 | 100% | 01 | % 0% | 0% | 0% | 0% % | 100% 1 100% 1 | 0% 00% 00% 100% | 100.0% 01 | 100% 6 0% 6 0% 0 | N 0.0% | 0% 0% 0% 0% | ON 0.0% 100% | SON 32K 27.89 | 100% S0% | 67% | 72.2% 0% 0% | 0% 0% | 0.0% | | | | | _ | | | |
| protein 10 Not10 NO nuclear ribonucleoprotei Snrnp40 SN francolonin mictorarbot Fdg AD | NRNO_MOUSE 39 H DRO_MOUSE 54 H | Ds 0% Ds 100% | 0% 0% | 0.0% 100 | DN 100% | 100% 100.0% | | | 100% | | 01 | × | | O% | | 50% 50% 100% 1 | 00% | 1001 501 | 5 9% | K . | 0% 0% 0% 0% | 0% 100% 1 100% | 00% 100% 100.09 | 0% 0% 0% | One | 0.0% 0% 0% | 0% 0% | | | | | | | | | |
| tase 1 Cips 1 PY ic granule protein Ngp NG winn withwrite it munt Draib1 DN | VRGI_MOUSE 67 A GP_MOUSE 19 A NUB1_MOUSE 38 A | Da OS Da | 0% | 100 | DN 100% | | 0% 0% | | | | | | | | | 200 1 200 1 | 100% 00% 100% | 100.0% 01 | 5 0% 0 | N 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 1 | 92% 100% 97.65 00% | 9% 7% 9% | 0% | 2.4% 0% | on on | 0.0% | 0.4226 | 0.2048 | | 0.4225 | 0.2048 | | | |
| differentiation antioen Cd14 CD ne subunit bets type-6 Pambil PS | ATL MOUSE 38 / D14 MOUSE 39 / S88 MOUSE 30 / | Da Da | | | | | | | | | | | | | | 100% 1 100% 1 100% 1 | 00% 100% 00% 100% 00% 100% | 100.0% on 100.0% on | 5 0% 0 5 0% 0 | N 0.0% | 2% 2% 2% 2% 2% 2% | 0% 0.0% 100% 1 0% 0.0% 100% 1 | 200% 200% 100.05 00% 200% 100.05 | 0% 0% 0% 0% | 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | _ | | | |
| Il histocomustibility ant IPG-As HAC sucleotide-binding prote Graso1 GN stimulated tocorrotein re Lar LSE | NAO MOUSE 40 H SR_MOUSE 66 H | Da Da | 100% | | - 0% | | ON | | | | | | | | | 100% 1 | 00% 100% 00% | 100.0% 01 | 9% 0 | s 0.0% | 9% 9% | 08 0.0% 100% 1 | 00% 100% 100.05 00% 100% 100% | 9% 9% | 0% 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% | 0.4226 | | | | _ | | 0.4226 | |
| for protein Tapo TSF swin homolog YKTS YMS YK ne activator complex su Pame3 PSF | SPO MOUSE 193 KT6_MOUSE 223 SME3_MOUSE 293 | Da 100% Da 100% | 200% 100% 200% | 100.0% 0 | 2% 2% 2% 2% | 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% | 100% 10 | 20% 100% | 100.0% 01 | % 0% | 0% 0.0% | 0% 0 | % 0% 0.1 | 7% 100% 1 | 00% 100% 00% 100% 00% 100% | 100.0% or 100.0% or | 0% 0% 0 6 0% 0 6 0% 0 8 0% 0 | S 0.0% | 0% 0% 0% 0% | 005 0.0% 10008 1 005 0.0% 10008 1 | 00% 67% 88.95 00% 100% 100.05 00% 100% 100.05 | 0% 0% 0% 0% | 0% 0% | 0.0% 0% 0.0% 0% | 0% 23% 0% 0% 0% 0% | 0.0% | 0.4226 | | | | == | | 0.4226 | |
| expenses 1 Sold SU executed protein 1 Symp1 SY, related developmental Iff41 IFF | YAPI MOUSE 419 TRD1 MOUSE 509 | Da 100% | 100% 100% 67% 0% | 100.0% 0 33.3% 62 | 2% 2% 2% 2% | 0% 0.0% 100% 55.6% | 0% 0% 0% 22% | 0% 0.0% 0% 11.7% | 100% 10 0% | 0% 100% 0% | 100.0% 01 | % 0% % 100% | 0% 0.0% | 0% 0 100% 0 | % 0% 0.1 % 0% 0.1 | 75 1005 | 05 05 | 0.25 | | 8 90% / | 25 225 D | 05 96.75 95 | | | | 2005 | | 0.225 | и | | 0.9037 | | _ | 0.5770 | 0 | |
| tro-D-tructose reductes Akr1e2 Akr acul coenzume A thice Acol7 BA | KCL2 MOUSE 349 ACH MOUSE 439 | Da OS | 100% | 100 | ON ON | 05 005 | 0% 0% 0% | | 100% 21 | 100% | 100.0% | s 0s | 08 008 | 0% 0 | 8 08 0 | 200 1 | 00% 100% | 100.0% 01 | 6 0% 0 | N 0.0% | 0% 0% | 100% 1 0% 0.0% 100% 2 0% 0.0% 2 | 00% 200% 100.09 00% 200% 100.09 | 0% 0% 0% 0% | 0% | 0.0% ON 0.0% ON | 0% 0% 0% 0% | 0.0% | | | | | == | | | |
| d CULA-associated fac Doaf13 DC Creat CN | CA13_MOUSE 51 A MA1_MOUSE 28 A | Da 0% | | 100 | 0% | | 0% | | | | | | | | | 100% 1 | 00% | 100.0% | 0% | 0.0% | 0% 0% | 100% 1 | 00% 500% 100.09 | 0% 0% | 0% | 0.0% 0% | 0% 0% | 0.0% 0.280 | | C 1798 . C 1 | | | _ | 0.2882 | | |
| ox prolein homolog 1 Cbs1 CB ular body subunit 12A Mib 12a MB | EX1_MOUSE 211 EX2_MOUSE 291 | Da 50% Da 0% | 50% 50% 50% 0% | 16.7% 100 | 0% 50% | 0% 0.0% 100% 83.3% | 0% 0% 0% 0% | 0% 0.0% | SON S | 0% 0% | 16.7% 501 | % 100% | 100% 83.3% | 0% 0 | % 0% 0.1 | 75% 200% 1 75% | 90% 100% 90% 50% | 61.7% 251 | 6 40% 50 500 | K 38.3% | on on | 0% 0.0% 100% 1 0% 0.0% 60% 0% 0% | 75N 200N 78.39 0N 200N 100.09 | 40% 25% 100% 100% | One | 21.7% OK | ons ons | 0.0% | | 0.6883 | 26 1.0000 | 0.3038 | 0.6883 | 0.4226 | | |
| overnolina ilso rivo Septila AS nel revisasire di ASIO Ball BS | SMIA MOUSE 50 A | Da Da | 100% 200% 100% 200% | 100.07% 0 | 25 | 0% 0.0% | 05 | 98 | 100% 10 | 100 100% 10% | 90.0% | S 05 | 08 0.0% | 0% 0 | 8 08 0 | 200% 1 200% 1 200% | 00% 100% 00% 100% | 50.0% Or 00.0% Or 00. | 5 0% 0 | N 0.0% N 0.0% | 2% 2% 2% 2% | 0% 0.0% 100% 1 0% 0.0% 100% 1 | 00% 200% 100.09 50% 100% | 9% 9% 9% 9% | 0% | 9.0% 0% 9.0% 0% | 0% 0% 50% | 0.0% | 0.1444 | | | | === | | 0.1444 | 4 |
| me profein 50 Wdr77 ME n Ciapin1 CP | EPSO MOUSE 37 PIN1_MOUSE 33 P | Da 05 Da 1005 | 0% 0% 100% 100% | 0.0% 100 100.0% 0 | 0% 100% 0% 0% | 100% 100.0% 0% 0.0% | 9% 9% 9% 9% | 6 0% 6.7% 0% 0% 0.0% 6 0% 0.0% 6 0% 0.0% 6 0% 0.0% 6 0% 0.0% 6 0% 0.0% 6 0% 0.0% | 22% | | 621 | N | 400V 400.0V | 0% | | 100% 1 100% 1 | 50% 50% 0% 0% 0% 00% 100% 100% 100% 00% 00% 0 | 100.0% 01 | 5 0% 5 0% 0 | s 0.0% | 0% 0% 0% 0% | 05 0.0% 100% | 50% 00% 100% | 9% 9% | 0% | 9% 9% | 98 | | | | | | | | | |
| hype intermediate filame Virsac VM pid transfer protein Plip PLT commitmental LAT miles MonAT DM | MAC_MOUSE 19 H | Da Da | | | | | | | | 0% | | | 100% | | 95 | 2% 100% 1 | 0% 0% 00% 100% | 0.0% 1009 100.0% 09 | 5 100% 100 5 0% 0 | N 100.0% | 2% 2% 2% 2% | 0% 0.0% 0% 0% 0.0% 100% 1 | 0% 0% 0.09 00% 100% 100.09 | 100% 100% 0% 0% | 100% 0% | 100,0% 0% 0,0% 0% | 0% 0% 0% 0% | 0.0% | | | | | === | | | |
| hospholipase B-like 2 PBd2 PLI Stated ordein Knase i Prisas1 AAI lector protein 2 Cdp43so2 BO | LBL2 MOUSE 66 A APK1 MOUSE 64 A ORG1 MOUSE 23 A | Da Da | | | | | | | 100% | | 91 | × | | on | | 100% 1 100% 1 | 00% 100% 00% 100% | 100.0% 01 100.0% 01 | 5 0% 0 5 0% 0 | S 0.0% | 0% 0% 0% 0% | 0% 0.0% 100% 1 0% 0.0% 100% 1 | 00% 100% 100.09 00% 0% 0.07 | 0% 0% 0% 0% | 100% | 0.0% 0% 0% 100.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | == | | | |
| nd cyclase/cyclic ADP Cd38 CD ding protein Stembp ST d hydrolase Ces2s Ces2s ES | D38 MOUSE 34 9 TABP MOUSE 48 9 ST2A MOUSE 62 9 | Da OS | | 100 | 2% | | 9% | | ON. | | 1001 | × . | | on | | 100N 1 | 90% 100% 100% | 100.0% 01 | 98 9 | N 0.0% | 0% 9% | 05 0.0% 100% | 200% 00% 200% | 9% 9% | 0% | 98 | 9% 9% 9% | | | | | | | | | |
| specific gene 8 protein Plac8 PU pendent mannose-6-ch MSpr MP requisitory factor 3 Int 3 IRF | PRD MOUSE 319 F3 MOUSE 479 | Da 100% : | 100% 100% 100% | 100.0% 0 | DN DN | 0% 0.0% | 0% 0% 0% | 0% 0.0% 0% 0% 0% 0% 0% | 100% 10 100% 10 | 10% 10% 100% | 83.3% OI | % 0% 0% | 0% | 0% 0 | % % 0% | 67% 100% | 75% 83% 50% 83% | 75.0% 01 77.8% 01 | 5 0% 0 5 0% 0 | N 0.0% 2 N 0.0% | 2N 25% 0N 50% | 7% 25.0% 80% 7% 22.2% 67% 1 | 67% 67% 71.15 00% 100% 88.95 00% 100% 100.05 | 0% 0% 0% 0% | 0% 0% | 0.0% 20% 0.0% 22% 0.0% 0% | 22% 22% 0% 0% 0% 0% | 28.9% 11.1% 0.0% | 0.5848 0.5813 | 0.2097 0.40 | 26 | | _ | | 0.5848 0.5813 | 3 0. |
| rier family 25 member Sk25a45 525 nic reticulum-Golal inte Engic 3 ER ing protein 3 Tauribp3 TXI | 2545 MOUSE 32 H RG23 MOUSE 43 H C183 MOUSE 14 H | Da 100% Da 100% | 50% 100% 100% | 100.0% 0 | 0% 0% | 50% 0.0% | 0% 0% | 0% 0.0% | 100% 5 | 0% 100% 0% 100% | 83.3% 01 | % O% | 0% 0.0% | 0% S0 | % ON 15. | P% 100% 1 | 00% 100% | 100.0% 01 | s 0% 0 | N 0.0% | on on | ON 0.0% 100% 1 | 00% 500% 100.09 | ON ON | 0% | 0.0% 0% | ons ons | 0.500 | 10 | | 0.5000 | | | 0.4226 | 0 | |
| Spanc SPI ornal protein L22. milor Mrpt22 RM associated protein Crisp CR | PRC_MOUSE 34 k MG2_MOUSE 24 k RTAP_MOUSE 46 k | Ds Ds Ds | | | | | | | | | | | | | | 90% 0% 0% | 43% SON 67% ON | 57.6% 201 1001 22.2% 1001 | 57% 50 6 22% 100 | K 42.4% | 0% 0% 0% 0% | 0% 0.0% 100% 0% 0% 0.0% | SDOW ON | 0% 100% 100% | 0% | 0% 0% | ON ON | | 0.9651 | | | 0.0651 | | | | |
| nlegator 2 Bin2 Bih elerane 1E Cestle ES controveren Notes (er3ip1 (R3 | INC MOUSE 53 H STIE MOUSE 62 H DIP MOUSE 9 KG | Da Da Da 100% | 100% 100% | 100.0% 0 | 0% 0% | 0% 0.0% | 0% 0% | 01 0.0% | 100% 100% 10 | 10% 100% | 100.0% 01 | N ON | 0% 0.0% | 0% 0% 0 | s os o | 100% 1 75 100% | 92% 100% 67% 100% | 100.0% O1 | 5 0% 0 | N 0.0% | 0% 0% 0% 33% | 0% 0.0% 0% 11.1% 100% 1 | 00% | 0% 0% | | 98 | ons | | 0.4226 | 0.4226 | | | === | | 0.4226 | 15 0 |
| in Novemberia (Lonetho Cog3 CO n of very long chain falt Elbell ELG sudeolide-binding prote GnatO GN | OQ3_MOUSE 419 LOV1_MOUSE 339 NA3_MOUSE 419 | Da 100% Da 100% | 100% 200% 100% 200% 100% 200% | 100.0% 0 100.0% 0 | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 10 100% 10 | 00% 100% 00% 100% | 100.0% 01 100.0% 01 | N 0% | 0% 0.0% | 0% 0 | % 0% 0.1 % 0% 0.1 % 0% 0.1 | 75 100% 1 | 00% 100% 100% 00% 100% | 100.0% 01 | 9% 9 6 9% 9 | S 0.0% | 9% 9% 9% | 0% 100% 1 0% 1,00% 1 | 00% 100% 00% 100% 100.09 00% 100% 100.09 | 0% 0% 0% 0% | 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | _ | | | |
| ificity mitosen-activates Map2k2 MP Il domain-containing pn Codc25 CC A-decapping enzyme Nud16 NU | P2K2_MOUSE | Da Da | 100% 100% 100% | | 9% 9% | ON. | 0% | 0% | 100% 10 100% | 10% 10% 100% | 100.0% 01 | 0% % 0% | 0% 0.0% | 0% 0 0% | % 0% 0.1 | 25 100% 1 | 00% 100% 100% 00% 100% | 100.0% 01 | 5 0% 0 5 0% 0 | N 0.0% | 9% 9% 9% 9% | 0% 0.0% 100% 1 0% 0.0% 1 | 00% 100% 100.09 | 0% 0% | 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | | | | |
| lity group projein HMG Hinga1 HM I-dimethylarginine dime Ddah1 DD I-1 receptor antaponist Illim IL1 | MGA1 MOUSE 123 DAHI MOUSE 313 IRA MOUSE 203 | Da Da | | | | | | | | | | H | | | | 100% 100% 1 | 00% 100% 100% | 100.0% 01 | 5 05 0 | S 0.0% | 0% 0% 0% 0% | 100 | 00% 100% 100.09 00% 100% 100.09 | 0% 0% 0% 0% | 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | | | | |
| antichenale - cysteine I Ppcs PP e 2-glycoprotein Augo1 ZAS II histocomusibility ant 3 5V HSS | PCS MOUSE 34 9 QG MOUSE 35 9 822 MOUSE 30 9 | Da Da | | | | | | | | | | H | | | | 100% 1 100% 1 | 00% 100% 00% 100% | 100.0% 01 100.0% 01 | 9% 5 9% 9 5 9% 9 | S 0.0% | 0% 0% 0% 0% | 0% 0.0% 1 0% 0.0% | 00% | 98 | | | os | | | | | | | | | |
| idase NiSe SN blease inhibitor A3M Serpina3m SP/ da-4A chain Tubb4s TSS | PAJM MOUSE 679 BBHA MOUSE 509 | Da 100% | 0% 100% 0% 100% | 100.0% 0 33.3% 100 | 0% 0% 0% 100% | 0% 0,0% 0% 66,7% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 10 100% | 100% | 100.0% 01 | % 0% % | 0% 0.0% | 0% d 0% | % 0% 0.1 | 2% 2% | 00% 0% 0% | 0.0% 1009 | 0% 5 75% 100 | s 917% | 0% 0% 25% | 000 0.05% 3 100% | 00% 50% 50% 66.75 0% | 0% 25% 0% 100% | 25% | 16.7% 0% 200% | 0% 25% 25% 0% | 16.7% | | 0.4226 | | 0.5560 | 0.5351 | 0.1835 | 0.5560 | 0 0 |
| k factor-binding protein Hstp1 HSS surface anticen CD47 Cd47 CD SM12 homolog Lam12 LSI | SBP1 MOUSE 9 kg D47 MOUSE 33 k SM12 MOUSE 22 k | Da 100% | 0% 0% | 100.0% 0 0.0% 100 | 0% 0% 0% 100% | 0% 0.0% 100% 100.0% | 0% 0% 0% 0% | 016 0.0% 6 016 0.0% | 22% 100% 10 0% | 0% 100% 0% 0% | 100.0% 01 0.0% 1001 | % 0% % 100% | 0% 0.0% 100% 100.0% | 0% 0 0% 0 | % 0% 0.1 % 0% 0.1 | 50% 1 7% 100% 1 7% 0% | 00% 67% 00% 100% 0% 0% | 72.2% S01 100.0% 01 0.0% 1001 | 6 0% 22 6 0% 0 6 100% 100 | N 27.8% I N 0.0% I N 100.0% | 0% 0% 0% 0% 0% 0% | 0% 0.0% 22% 0% 0.0% 100% 1 0% 0.0% 0% | 75N 67N 58.39 00N 75N 91.79 0N | 67% 25% 0% 0% 100% | 25% 25% 100% | 41.7% ON 8.3% ON ON | 0% 0% 0% 0% | 0.0% | 0.5153 0.4226 | 0.40 | 26 | 0.5153 | | 0.4226 | | |
| musuesicular body prof Chmp1b1 Cht formin and FG repeat-1 Agtg2 AG chated profein kinase i Prkeg1 AA | GFG2 MOUSE 49 A AKG1 MOUSE 38 A | Da Da | UN | | 900% 900% | 100% | 0% | 0% | ON. | ons | 2001 2001 | % | 100% | ons ons | ON. | 200% 1 0% 200% 1 | ons 0% 0% 0% 00% 100% | 100.0% 01 0.0% 1001 100.0% 01 | 6 0% 0 6 100% 100 6 0% 0 | N 100.0% | 0% 0% 0% 0% | on 0.0% 100% 1 on 0.0% 0% on 0.0% 100% 1 | 000 00 0.09 000 500 83.29 | 0% 0% 100% 100% 0% 0% | 100% | 0% 100.0% 0% 0.0% 0% | 0% 0% 0% 50% | 0.0% | 0.4226 | | | | | | 0.4226 | 8 |
| pid scramblase 1 Placr1 PLS REGI Creg1 CR sin family homolog 1 Wash1 WA | REGI MOUSE 24 P IASHI MOUSE 52 P | Da 100% Da 0% | 200% 0% 0% | 0.0% 100 | 0% 100% | 0% 100% 100.0% | 0% 0% 0% | 0% 0.0% | ON. | | 1001 | s . | | ON. | | 100% 100% 1 | 0% 100% 0% 0% | 100.0% 01 0.0% 1001 | 5 0% 0 5 100% 100 | S 0.0% S 100.0% | 0% 0% 0% 0% | 0% 0.0% 100% 1 0% 0.0% 100% 1 | 00% 57% 88.99 00% 100% 100.09 | 0% 0% 0% 0% | 0% | 0.0% ON | 0% 23% 0% 0% | 11.1% | 0.5770 | | | | | | 0.5770 | U |
| ago nashi homolog Magoh MG ht chain Tctes-type 1 Dynit1 DYI almodulin-dependent o Camik2g KD | GN_MOUSE 17 A YLT1_MOUSE 12 A DC2G_MOUSE 60 A | Ωs 100% Ωs 100% | 200% 100% 200% | 100.0% 0 | DN ON | 0% 0.0% | 9% 9% | 0% 0.0% | 100% 100% | 100% | 91 | % % | 0% | 0% 0% | ON. | 100% 1 100% 1 67% | 00% 100% 00% 100% 32% 25% | 100.0% 01 100.0% 01 41.7% 221 | 5 0% 0 5 0% 0 5 22% 75 | N 0.0% N 0.0% | 0% 0% 0% 0% 0% 32% | 0% 0.0% 100% 1 0% 0.0% 100% 1 0% 11.1% 1 | 00% 200% 100.09 00% 200% 100.09 | 0% 0% 0% 0% | 0% | 0.0% 0% 0.0% 0% | | 0.0% | 0.7117 | | | | | | | |
| en-like CdS CD | DSL_MOUSE 10 A MED_MOUSE 10 A GS 10_MOUSE 21 A | Da Os Da | 0% | 100 | 2% | 100% | 0% 0% | 9% | | | | H | | | | 200% 0% 200% 1 | 50% 100% | 100.0% 01 | 5 50% 5 0% 0 | 5 0.0% | 0% 0% 0% 0% | ON 0.0% 3 | 00% 0% 0% 00% 100% | 100% 100% 0% | 50% | 98 | 0% 50% 0% 0% 0% | | 0.7117 | | | 1.0000 | | | 0.5000 | N . |
| ornal protein LSO, mitoc MrpISO RM of G-protein signaling Rgs10 RG | | LO . | 100% | | | 67% | 0% | 2% 2% | | 25 | | 100% | | | 8 | 100N 1 | 100% | 01 | 98 | | os os | | | | 0% | 0.0% ox | on on | 0.0% | | | | | _ | | | |
| oreal protein LSO, mileo MtpSO RM of G-crotein signaling Rgs 10 RG s protein Rgs 10 RG chain V region ACISB 22 1 52 158 tital import inner memb Timm17b Tit | MS1_MOUSE 133 178_MOUSE 183 | Os OS | 33% | 100 | ea . | | | | | | | | | | TR.1 0% | 1 1 | 1 1 | | 1 1 | 1 1 | | | | | | | | | | | | | | | _ | - |
| 1995 1995 | MS1_MOUSE 13.9 178_MOUSE 18.9 446C_MOUSE 45.9 EF1_MOUSE 29.9 5MS_MOUSE 10.9 | Da 05 Da 05 Da 05 Da 1005 | 0% 0% 0% 20% 0% 20% | 5.7% 100 100.0% 0 | 200% DN 100% DN 0% | 100% 80% 93.3% 0% 0.0% | 9% 9% 9% 9% | 0% 0.0% 0% 0.0% | 100% 10 | 0% 100% 10% 100% | 100.0% 01 | % 0% | 0% 0.0% | 0% 0 | % 0% QJ | 2% 100% 1 | 67% 40% 00% 100% | 35.6% 01 100.0% 01 | 5 0% 40 5 0% 0 | N 13.3% 10 N 0.0% | 0% 33% 0% 0% | 0% 51.1% 0% 0% 0.0% 100% 1 | 60% 0% 13.25 00% 100% 100.05 | 0% 40% 0% 0% | 0% | 13.3% 200% 0.0% 0% | 20% 100% 0% 0% | 73.3% 0.0% | 0.4045 | 0.2714 | | 1,0000 | 0.0133 | 0.4226 | 0.5745 | 0 0. |

| Mills | ED4 MOUSE 30 H SB1 MOUSE 36 H SC1A MOUSE 42 H | KDs SOS | 100% 100 100% | % 83.3% % 100.0% | 9% 9% 9% | 0% 0.0% 0% 0.0% | | 0% 0% 16.7 0% 0% 16.7 | % 100% 100% % 100% | 200% 200% 200% 200% | 100.0% 01 100.0% 01 | N 0% N 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 2% 2% 100% | 0% 0 100% | 0% 100% 0% | 100% 100% 0% | 100.0% 00 | 9% 99 | 0.0% 0% | 0% 0% 0.0% 100% | 100% 100 9% | % 100% % | 98 | 0% 0% 0% | 0.0% | 5 | | | = | | 3.4226 | Ξ |
|---|--|----------------------------------|----------------------------------|----------------------|-----------------------------|--------------------------------|---------------------------------------|---|--------------------------|-------------------------------------|------------------------------------|------------------|-------------------------------|--------------------------|-------------------------------|---|---|---------------------------|-----------------------------|--|-------------------------|--|--|--------------------------|------------------|---------------------------------------|---|-------------------------------------|------------------|-------------------------|--------|---------------------|---------------|--------|--------------|
| erane 2 Hiros2 Hill arrinase Cds Cl | MOIO MOUSE 351 | KDs 100% KDs 100% KDs | 100% | n 100.0% | 9% 9% | US 0.05 | 98 | 0% 0.0 | 100% | 100% | nel IZh 01 | - 05 | 0% | NA 975 | 05 0.05 | 100% 100% 100% 100% | 100% 100 100% 100 | 0% 0% 0% 0% | 9% 9% 9% 9% | 0.0% 0% 0.0% 0% 0.0% 0% 0.0% 0% | 9% 09 9% 09 | 100% 0.0% 0.0% 100% 1100 | ON 200% 100.0% | 9% 0 | s 0s | 90% 0% | 0% 0% | 0.0% | | | | = | | | |
| protein C4bpa C- protein Signimi Si | BIPA MOUSE 529 25TM MOUSE 489 | KOs KOs | 0% 0 | % % 100.0% | 200% | 100% | | 0% 0% | W 1000 | 205 | 200 DE 01 | 80% | os 0.0% | 9% | ov 0.00 | 100% 100% | 100% 100 | 2% 0% | 9% 9% 9% | 0.0% 0% | 0% 09 | 0.0% 100% 1 | 0% | 9% 0 | N | 9% | 0% 700 | | 0.7952 | 0.5000 | | == | | 0.7 | 7957 |
| ning fibulin-like extrac Efemp2 FE all pyrusete carrier 2 Mpc2 M | LN4_MOUSE 49 H PC2_MOUSE 14 H | KDs 100% | 100% 100 | % 100.0% | 9% 9% 9% 9% | | | 0% 0% 0.0 | 75 100% | 100% 100% 100% 100% | 100.0% 01 | N 0% | 0% 0.0% | ON ON | 0% 0.0% | 0% 0% | 0% 0 | D% 100% | 50% 100% | 83.2% ON | 50% O | 95.7% ON 100% 1 | ON ON 0.0% ON 100% 100.0% | 22% £2 0% 0 | N 0% 3 | 0.0% 67% 0.0% 0% | 23% 200% E | 0.0% | 0.7800 | | | 0.1224 | | 0.1 | 1224 |
| rai methytransferase Trmt112 TF unal homolog 1 Jagn1 J/ i-protein ligase REX1 Rbx1 RB | R112_MOUSE 14 H HGN1_MOUSE 21 H EX1_MOUSE 12 H | KDs 100% KDs 100% KDs | 100% 100 | % 100.0% % | 0% 0% | 0% 0.0% 0% | 5 0% | 0% 0% 0.0 0% 0% 0.0 | 100% PN 100% | 100% 100% 100% 100% | 100.0% 01 | N 0% | 0% 0.0% 0% | ON ON | 0% 0.0% 0% | 100% 100% 100% 100% | 100% 500 100% 100% 500 | 0% 0% 0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 09 0% 09 | 0.0% 100% 1/ 0.0% 100% 1/ | ON 100% 100.0% ON 100% 100.0% | 0% 0 | % 0% | 0.0% 0% | 0% 0% | 0.0% | | | | _ | | | |
| Stated protein kinsse Mapk14 M il development protein CRIght CI au5 III-65 III | K14_MOUSE 41 s TOP1_MOUSE 33 s RS_MOUSE 88 s | kOs kOs | | | | | | | | | | | | | | 100% 100% 100% | 100% 100 | 0% 0% 0% | 0% 0% | 0.0% on | 0% 09 | 0.0% 100% 1/ 100% 1/ | ON 100% 100.0% ON | 0% 0 0% 0 | % 0% % | 0.0% 0% 0% | ons ons | 0.0% | | | | === | | | |
| Taku TS ceptor-like factor 3 Crif3 CI | RLF3 MOUSE 50 H | kDa kDa kDa 100% | | | | | | | | | | | 0% 0.0% | | | 100% | 100% | ons | 0% | ON | | 100% 1 | 0% 0% 0% 100% 100.0% | 9% 0 | % S0% % 0% | 0.0% ON | ons sons ons ons | 0.0% | | | | _ | | | |
| iport present SECUS Bright St inse dinamenase mili Trobe TR lad numbrasida, biolon Niggr Ni | ALH MOUSE 50 P PCR MOUSE 21 P | KDs 100% KDs | 100% 100% | | 99 | | Olk | ON. | 100% | 100% | 100.0% | is on | 0% 0.0% | ON ON | 0% 0.0% | | | | | | | 100% 1 | os. | 0% 0 | × | 98 | os | | | | | | | | |
| 6234A Fam234a F3 aport protein GDT1B Gobtlo Ga accident differentiation Mandre M | DHA MOUSE 619 OTIO MOUSE 159 | KOs KOs KOs KOs KOs | 100% | | 9% 9% | | 22% | ON. | 79% | 100% 100% 100% | 91.7% 01 | 0% N 0% | 0% 0.0% | 25% 9% | 05 8.25 | 50% 0% | 50% 33 50% 95 | 2% 0% 2% 0% | 0% 0% 0% 0% | 0.0% 50% | 200% 500 | 66.7% 83.7% 62% | 76 756 FD 496 | 9% 0% 0 | s 0s | 0% | 33% 35% 7 | 0.710 | 0.0831 | 0.1353 | | | | 0.7103 | 0831 |
| B homologous protei Chp1 Cl d protein 2/3 complex ArpcSl Al | P1_MOUSE 223 PSL_MOUSE 173 | kDa kDa 100% | 100% 100 | % 100.0% | 0% 0% | 0% 0.05 | s ox | os os oo | Ps 100% | 100% 100% | 100.0% 01 | N 0% | 0% 0.0% | 0% 0% | 0% 0.0% | 22% 22% 100% 100% | 22% 33 100% 100 | 2% 67% 0% 0% | 67% 67% 9% 9% | 66.7% 0% 0.0% 0% | 0% 09 0% 09 | 0.0% S0% 0.0% 100% 1 | SN 50% 41.7% ON 100% 100.0% | 50% 75 9% 0 | % 50% 5 % 0% | 8.3% ON 0.0% ON | 0% 0% 0% 0% | 0.0% | 0.4226 | | | 0.4225 | | | |
| ceat-containing prote Armo I All otein sortino-associat Vps25b VI | MC1_MOUSE 31 A | KDs 100% KDs | 100% 100 100% 100 | % 100.0% % | 9% 9% 9% | 0% 0.0% | 5 05 | 0% 0% 0.0 0% 0% 0.0 0% 0% 0.0 0% 0% | 7% 100% 100% | 100% 100% 100% 100% | 100.0% 01 100.0% 01 | N 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100 100% 100 | 0% 0% 0% 0% | 9% 9% 9% 9% | 0.0% 0% | 9% 09 9% 09 | 0.0% 100% 1 0.0% 100% 1 | ON 200% 100.0% ON 200% 100.0% | 9% 0 9% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | _ | | | |
| ibitor, milochondrial Alpiff A' olein kinase Yes Yes1 YI t chain 1. cytoolasmic Dynilf D' | IF I MOUSE 129 IS MOUSE 619 IS MOUSE 109 | KDs 100% KDs 100% | 100% 100 | 8 | 9% 9% | 0% | 9% | 0% 0% 0% 0% | 100% | 100% 100% | 91 | N 0% | | ON ON | | 100% 100% 100% 80% 100% | 100% 100 100% 86% 88 | DS 0% DS 20% | 0% 0% 0% 0% | 11.4% 99 | 0% 09 0% 09 0% 09 | 0.0% 100% 1/ 100% 0.0% 100% | 0% 100% 100.0% 100% 0% 100% 93.2% | 9% 0 9% 20 | % 0% % 0% | 6.7% 0% | 0% 0% 0% 0% | 0.0% | 0.6226 | 0.1946 | | 0.6226 0 | 0.1945 | | |
| reace avatem Hiprote Grah Gr halcoenase-like hidn Hdhd2 HS sport protein USE1 Use1 US | SH MOUSE 19 A SHOW MOUSE 29 A SE1 MOUSE 31 A | KDs 100% KDs | 100% 100 100% 100 100% 100 | % 100.0% % | 9% 9% 9% | 0% 0.0% 0% | 5 05 | 0% 0% 0% 0% 0.0 0% 0.0 0% 0.0 0% 0.0 0% 0.0 0.0 | 7% 100% 100% 75% | 100% 100% 100% 100% 100% 100% | 100.0% 01 100.0% 01 91.7% 01 | N 0% N 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% 25% 0% | 0% 0.0% 0% 0.0% 0% 8.3% | 100% 100% 100% | 100% | ON. | 0% 0% 0% | 98 | 0% 09 0% | 100% 11 55.75 100% 55.75 100% 55.75 67% 0.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% 10.05 100% | OK OK | 0% 0 0% 0 | % % | 9% | ON ON | 0.422 | 1 | | | _ | | 2.4226 | |
| sis factor receptor b Tradid TF spy homolog 4 Crep 4 CI spy homolog 3 Crep 3 CI | NPY4_MOUSE 28 A NPY4_MOUSE 28 A NPY3_MOUSE 31 A | kOs kOs | 100% | | 98 | | | ON. | 100% | 100% | 01 | s . | ox. | ON. | ON. | 100% 100% 100% 100% | 100% 100 | 0% 0% | 0% 0% 0% | 0.0% 0% | 0% 09 0% 09 | 100% 11 0.0% 100% 100% | 0% 100% 100.0% 100% | 0% 0 0% | 0% | 0.0% 0% 0% | 0% 0% 0% | 0.0% | | | | | | | _ |
| ase inhibitor Kazal-h. Spirik 1 15 component receptor Crill Cl | KI_MOUSE 8 KE RIL_MOUSE 54 K | Da 100% KDa | 100% 100 | % 100.0% | 0% 0% | 0% 0.09 | s os | ON ON 0.0 | PN 100% | 100% 100% | 100.0% 01 | N 0% | 0% 0.0% | ON ON | 016 0.0% | 100% 100% 100% | 100% 500 | 0% | 0% | 0.0% | 00 | 100% 100% 11 | ON 100% 100.0% | 0% 0 | % 0% % 0% | 0.0% ON | ons ons | 0.0% | | | | == | | | |
| rase-like protein 13 Mett/13 M | P_MOUSE 53 P ET13_MOUSE 79 P | kDs kDs 100% | 100% | | 0% 0% | | gn. | 0% | | | | | | | | 100% 100% | 100% 100 | DNs Ons | 0% 0% | 0.0% on | 0% 00 | 0.0% | | | | | on on | | | | | _ | | | |
| porter-like protein 1 Sio44s1 C | R.I. MOUSE 73 H | kDa kDa 100% | 100% 100 | % 100.0% | 0% 0% | 0% 0.09 | s 0% | 0% 0% 0.0 | 25. | 100% | | | es. | | os. | 100% 100% | 100% 100 | D% 0% | 9% 9% | 0.0% 0% | 0% 09 | 0.0% 50% 1 | 0% 200% 100.0% 0% 200% 53.2% 0% 200% 53.2% 0% 200% 100.0% 0% 200% 100.0% | 9% 0 | N 0% | 0.0% SON | | | 0.4226 | | | | | 0.4 | 4225 |
| nhorisatur obnanbro Gdpd1 G mhuhurir arid raran Gabarap G X1 Bik1 Bi | DPD1_MOUSE 36 H BRAP_MOUSE 14 H BK1_MOUSE 9 HC | kDa 100% kDa 100% Da 100% | 100% 100 100% 100 50% | % 100.0% % 100.0% | 0% 0% 0% 0% | 0% 0.05 0% 0.05 | 5 0% 5 0% | 0% 0% 0.0 0% 0% 0.0 | % 100% % 100% | 100% 100% 100% 100% | 100.0% 01 100.0% 01 | N 0% N 0% | 9% 0.9% 9% 0.9% 9% 0.9% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% 50% 0% | 100% 500 100% 500 | 0% 0% 0% 0% | 0% 0% 0% 0% 100% 0% | 0.0% 0% 0.0% 0% 50.0% 0% | 0% 09 0% 09 0% 09 | 0.0% 100% 1/ 0.0% 100% 1/ 0.0% 100% 1/ | ON 100% 100.0% ON 100% 100.0% ON 100% 100.0% | 0% 0 0% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | ON ON ON ON ON ON ON ON ON | 0.0% | 0.2254 | 0.5612 | | 0.2254 0. | 0.5612 | | |
| c helo-boo-helix pro Bhha 15 Bi mhase 2 Cers2 Cl | A15 MOUSE 22 A | KDs 50% KDs 100% | 0% 100 100% 100 | % 50.0% % 100.0% | 50% 200% 0% 0% | 0% 50.09 0% 0.09 | 5 0% 5 0% | 0% 0% 0.0 0% 0% 0.0 | 7% S0% 7% 100% | 100% 100% | 501 | N 0% | | 0% 0% 0% 0% | | 100% | 1000 | 0% | - | 98 | | 1000 | 0% 100% 0% 100% 100.0% | | s 0s | 0.00 OV | os os | 0.5612 | 2 | | 0.5612 | === | | | |
| operation potein NS New2 No errier-associated me Scamp3 Si | SA2 MOUSE 30 P | KDs OS | 9% 0 | s 0.0% | 100% 100% | 100% 100.05 | s os | 0% 0% 0.0 | 7% 0% | 200% 100% | 1001 | N 1 | 00% 0% | 0% | 0% 0% | 0% 0% 100% | 9% 0 100% | 0% 100% 0% | 100% 100% 0% | 100.0% 0% 0% | 9% 09 09 | 0.0% 100% 1/ 0.0% 100% 1/ | ON 100% 100.0% | 9% 0 | N 0% | 00% ON | on on | 0.0% | | | | _ | | | |
| in G-III Apoc3 Al N domain-containing Pythin1 IF | OCS_MOUSE 119 IX_MOUSE 479 | 100% kDs 100% kDs | 100% 100 | N 100.0% | 0% 0% | 0% 0.0% | 5 0% | 0% 0% 0.0 | 100% | 100% | | | es. | MA . | os. | 100% 100% | 100% 500 | D% O% | 0% 0% | 0.0% 0% | 0% 09 0% 09 | 0.0% | 200% 100.0% 200% | - | 0% 0% | 95 95 | 0% 0% | wash . | | 0.0170 | | | 0.5170 | | |
| Amount | TP_MOUSE 24 P M1A_MOUSE 22 P | KDs 0% | 75% 23 100% 100 0% 0 | 5 00.4% 5 0.0% | 0% 25% 0% 100% 100% | 67% 30.65 0% 100% 100.05 | 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 0% 0% 0.0 0% 0% 0.0 | 200 67% 100% 7% 0% | 100% 100% 0% 0% | 0.0% 1001 | N 0% N 100% 1 | 90 100.0% | 0% 0% 0% 0% | 0% 0.0% | 200% 100% 200% 100% 200% 100% | 50% 83 100% 100 100% 100 | 2% 0% 0% 0% 0% 0% | 0% 50% 0% 0% 0% 0% | 15.7% 0N 0.0% 0N 0.0% 0N | 0% 09 0% 09 | 0.0% 100% 1/ 0.0% 100% 1/ 0.0% 100% | 0% 200% 100.0% 0% 200% 100.0% | 9% 0 9% 0 | N 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | 0.4226 | Janu 0500 | U.EJEG | U-1/20 0. | 0.5000 | | |
| factor BTF3 homok B#3H B* Sbd6 S* DerQ DI | DL4 MOUSE 17 A DX16 MOUSE 37 A DRL2 MOUSE 28 A | KDs 100% KDs 100% KDs 100% | 100% 100 100% 100 | % 100.0% % 100.0% | 0% 0% 0% 0% | 0% 0.09 | 5 0% 0% 5 0% | 051, 055 0.0 051, 055 0.0 051, 052 0.0 051, 052 0.0 052, 053 0.0 053, 054 0.0 054 0.0 055 0.0 055 0.0 056 0.0 | 7% 100% 100% | 100% 100% 100% | 01 | N 0% | ON. | 0% 0% 0% 0% | ON. | 1000, | 100% 100% 100% | 0% 0% 0% | 0% 0% | 200 100N | 00 | 0.0% 100% 100% 1100% 100% 100% 100% 100% | 0% 200% 100.0% 200% | 0% 0 0% 0 | % 0% 0% | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0% 0% 0% | 0.0% | 0.5000 | 0.5000 | | | | 0.5 | 5000 |
| protein 11 Mup11 M protein 15 May18 M | MPS MOUSE 259 LP11 MOUSE 219 LP18 MOUSE 219 | KDs 100% KDs | 100% | | 0% 0% | | ON. | 0% | | 100% | | | 0% | | ON. | 100% 100% 100% 83% | 100% 100 100% 94 | 0% 0% 4% 0% 4% 0% | 0% 0% 17% 0% | 0.0% 0% 5.6% 0% | 0% 09 0% 09 | 0.0% 100% 11 0.0% 100% 1 0.0% 100% | ON 100% 100.0% ON 100% 100.0% ON 100% 100.0% | 0% 0 0% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | ONE | 0.0% | 0.4226 0.4226 | | | 0.4226 | | | - |
| protein 6 Mup6 M obsin Rab-21 Rab21 Ri | UP6 MOUSE 211 | kDs 100% | 100% | = | 0% 0% | | 0% | ON. | 100% | 100N | 01 | N 0% | | ON ON | | 100% 82% 100% 100% | 100% 94 100% 100 | 4% 0% 0% 0% | 17% 0% 0% 0% | 5.6% ON 0.0% ON | 0% 09 0% 09 | 0.0% 100% 10 0.0% 100% 1 | ON 100% 100.0% | 0% 0 0% 0 | % C% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | 0.4226 | | | 0.4226 | | | |
| in andrewskense (Lob) LC S Vinp Si | LTI MOUSE 443 LS MOUSE 213 | kDs 100% kDs 100% | 100% 100 | n 100.0% | 0% 0% 0% 0% | 0% 0.05 | 90% 9% | 0% 0% 0.0 | 100% 7% 100% | 100% 100% 100% 100% | 100.0% 01 | 0% 5 0% | 0% 0% 0.0% | 0% 0% 0% 0% | 0% 0% 0.0% | 100% | | | 9% | | 250% | | | | | | | 0.500 | | | | _ | | | # |
| rykansferans 5 Gg5 G rykansferans 5 Gg5 G rate dehydrosenas Bdh2 Bl | OTD 1 MOUSE 33 H GTS MOUSE 62 H GH2 MOUSE 27 H | KDs 100% KDs 100% | 100 | % | 0% | 0% | 0% | 0% 0% | 100% | 100% 100% 100% | 100.0% 01 | 0% | 0% 0.0% | ON ON | 0% 0.0% | 100% 100% 100% 100% | 100% 100 100% 100 | DN 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 100% 1 0.0% 1 0.0% 100% 1 0.0% 1 0.0% 100% 1 0.0% 1 0.0% 100% 1 0.0% 1 0. | ON 100% 100.0% | 9% 0 | % 0% | 0.0% 0% | os os | 0.0% | | | | | | | |
| fein 1 Tom III TI ed consonessor inte Morig2 M 4 Smel SI | MILI MOUSE 53 A DRIZ MOUSE 18 A OKA MOUSE 52 A | KDs 05 KDs 05 | 9% 0 9% 0 | % 0.0% % 0.0% | 100% 100% 100% 100% | 100% 100.09 100% 100.09 | 5 0% 5 0% | 0% 0% 0.0 0% 0% 0.0 | 7% 0% 7% 0% | 0% 0% 0% 0% | 0.0% 1001 0.0% 1001 | N 100% 1 | 00% 100.0% 00% 100.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 100% | C/W. | | AN CAN | | ON 00 | | 0% | | | | en. | | | | | == | | | |
| tein 705 27/705 27 ontaining protein 1 Pdod11 PS | 205 MOUSE 8 KG | Da 100% kDa 0% | 0% 0 | % 0.0% | 0% 100% 100% | 0% 100% 100.09 | 9% 5 9% | 0% 0% 0.0 | 100% PS 0% | 100% 100% 9% | 100.0% 01 | N 0% | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 05 05 | 0% 0 | D% 100% | 100% 100% | 100.0% on | 0% 09 | 0.0% 0% | SN 50% 25.0% | 100% 75 | N 50% 3 | 5.0% 0% | on on | 0.0% | 0.2254 | 0.225 | | 0.2254 | 0.2254 | | |
| import inner memb Timmila1 Ti reductase DMr D' | MEA MOUSE 119 REMOUSE 229 | KDs 1005 KDs 1005 | 100% 100 100% 100 | % 100.0% | 0% 0% 0% 0% | 0% 0.05 | 5 0% 0% | 0% 0% 0.0 0% | 7% 100% | 100% 100% | 100.0% 01 | N 0% | 0% 0.0% | 0% 0% | 05 0.05 | 100% 100% 100% 100% | 100% 100 100% 100 | 0% 0% 0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 09 0% 09 | 0.0% 100% 1 0.0% 100% 1 | ON 100% 100.0% ON 100% 100.0% | 9% 0 9% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | _ | | | |
| icair protein RADZ RadZ3a RS i subfamily C ment Drajc6 D1 5 homolog Mak15 M | SZSA MOUSE 40 H NUCE MOUSE 30 H AK16 MOUSE 35 H | KDs 100% KDs 100% KDs 0% | 100% 100% 0% 0 | s 0.0% | 9% 9% 9% 9% 100% 100% | 100% 100.05 | 9% 9% | 0% 0% 0% 0.0 | 100% 7% 0% | 200% 200% 200 0% | 0.0% 1001 | N 100% 1 | 0% 0.0% 0% 100.0% | 0% 0% | 0% 0.0% 0% 0.0% | 100% 100% 100% 100% | 100% 100 100% 100 | 2% 0% 2% 0% | 9% 9% 9% 9% | 0.0% 0% 0.0% 0% | 0% 09 0% 09 | 0.0% 100% 0.0% 100% 1 | ON 100% 100.0% | 0% 0 | % 0% | 0.0% 0% | os os | 0.0% | | | | | | | |
| oyrusate carrier 1 Mpc1 M in Snca 5' hosphate aldolase Dera DI | PC1 MOUSE 123 FUA MOUSE 143 BOC MOUSE 359 | kDa 100% kDa | 100% | | 0% | | 0% | ON. | 100% | 100% 100% | 100.0% 01 | N ON | 0% 0.0% | os os | 0% 0.0% | 100% | 50% 100% | 0% | 0% S0% 0% | 99 | 0% 09 | 100% 11 | ON 100% | 0% 0 | % 0% | 98 | ON ON | | 0.5000 | | | 0.5000 | | | _ |
| amine-6-ohosphat Amdhd2 Ni B- and B1-cell-sox Mxb1 Mi | AGA_MOUSE 43 P | KDs KDs | | | | | | | | | | | | | | 100% 100% 100% | | 0% 0% | 0% | 0 N | 0% | 100% | 200% ON 200% | 0% 0 | 0% % 0% | 0% | 0% 0% 0% | 170 | | | | === | | | |
| tactor jun-B Junb Ji. obde-binding prote Gni1 Gi | NB_MOUSE 36 P | kOs kOs | 100% 0 | % | 0% | 100% | | 0% 0% | | | | | | | | 0% 0% | 0% 0 | 0% 100% | 100% 100% | 100.0% on | 0% 09 | 0.0% | ON BOOK | 900 | % % | ON ON | ons ons | 214 | | | | _ | | | |
| tur cluster scaffold Mu1 N 27 Sm27 St 1 Tmem167a Ki | 01_MOUSE 29 k 0027_MOUSE 61 k 5HA_MOUSE 8 kC | KDs 100% KDs 25% | 100% 100 | s 91.7% | 0% 0% | 0% 0.07 | 0 N 5 25 N | 05 05 8.3 | Ph 100% | 67% 100% | 88.9% 01 | N 0% | 0% 0.0% | 0% 22% | 0% 11.1% | 100% 50% 0% | 50% 33 | 2% 0% | 0% 0% | 0.0% 50% | 200% 500 | 100% 10 100% 66.7% 100% | ON 100% 100.0% | 0% 0 0% | % 0% | 00% 0% 0% | ons ons | 0.0% | 2 | 0.0535 | | _ | | 0.8520 | |
| of RTR domain.com Zbb20 ZB | 082 MOUSE 30 H F20 MOUSE 81 H 51 MOUSE 12 H | kDa 100% kDa 0% | 100% 100 0% 0 | % 100.0% % 0.0% | 0% 0% 100% 100% | 0% 0.05 100% 100.05 | S ON | 0% 0% 0.0 0% 0% 0.0 | 7% 100% 7% 100% | 200% 100% 20% 100% | 100.0% 01 | 5 0% 500% | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 200% 200% 0% 0% 100% 100% | 100% 100 0% 0 100% 100 | 0% 0% 0% 100% 0% 0% | 0% 0% 100% 100% 0% 0% | 0.0% 0% 100.0% 0% | 0% 09 0% 09 0% 09 | 0.0% 100% 1/ 0.0% 0% 0.0% 1/ | ON 200% 100.0% ON 0% 0.0% ON 100% | 0% 0 100% 100 | % 0% % 100% % | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | === | | | |
| sting expires E1 ca Ubs3 UB siccensise-like hidn Hdhd3 Hd | MAS MOUSE 52 A SHOW MOUSE 20 A SECTION OF THE SECTION OF THE SECTI | KDs 100% KDs 100% | 50% 0 | % 50.0% | 0% 50% 0% 50% | 100% 50.07 | 9% 5 9% | 0% 0% 0.0 | ns os | 100% 100% | 1001 | N ON | 2% | 0% | 0% | 100% 100% 100% 100% | 100% 500 | 0% 0% 0% 0% | 0% 0% 0% 0% | 0.0% 0% | 0% 09 | 0.0% 100% 1 | ON 100% 100.0% | 0% 0 | % 0% | 0.0% 0% | 0% 0% | 0.0% | | | | == | | | |
| enia factor 2 M/2 M ZIP-bindino protein Roago RI | F2 MOUSE 28 P NAGC MOUSE 44 P | kDs 0% | | × | 100% | 100% | 9% | 98 | 0% 100% | | 2001 01 | K K | | ON ON | | 9% 199% 199% | 0% 100% 100 | 100% 0% 0% | 200% 9% 9% | 0.0% 0N | 0% 09 | 0.0% 100% 1 | ON 100% 100.0% | 9% 0 | % 0% | 0.0% ON | on on | 0.0% | | | | == | | | |
| Z Rp2 XI I-dehydrosensse m Tdh TI | P2_MOUSE 39 A | KDs KDs 100% | 100 | N. | 9% | os | 98 | - 05 | 100% | 100% 100% | 100.0% 01 | s 0% | 0% 0.0% | os os | 0% 0.0% | 100% 100% | 100% 100 | 0% 0% | 0% 0% | 0.0% 0% | 0% 09 | 0.0% 100% 1 | ON 100% 100.0% | 0% 0 | N 0% | 0.0% 0% | 0% 0% | 0.0% | | | | _ | | | |
| analation initiation to EPHebp2 45 Il cuticular Hb5 Kr85 KI | IBP2 MOUSE 13 H | kDa kDa | 100% | | 98 | | | ON. | | | | | | | | 100% 100% | 100% | 0% | 9% 9% | 98 | ON 00 | 100% 1/ | ON 200% 100.0% ON 200% 100.0% | 9% 0 | N 0% | 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | | | | |
| Cd97 C1 o-X carbon/peolida Prop P1 sied prolein kinase Mapk9 M | 007_MOUSE 90 H 3P_MOUSE 55 H 609_MOUSE 48 H | KDs KDs KDs 100% | 100 | % | 0% | on | on | 0% | | 100% 100% | | 0% | ox. | ON | on. | 9% 100% 100% | 100% 100 | 200% | 0% 0% | 0.0% 0% | 0% 09 | 100% 1/ 100% 1/ 0.0% 100% | 0% 0% 100% | 0% 0 0% 0 | % % 0% | 0% 0% | 0% 0% | | | | | _ | | | |
| fins protein-related Osbpi2 Of ine-protein phosphs Opped1 Of as marker phosphs March 18 | SBL2_MOUSE SS A PPED_MOUSE SS A MEDI_MOUSE SA A | kDs 100% kDs | 100% 100 | % 100.0% % | 0% 0% | 0% 0.0% 0% | s os | 0% 0% 0.0 0% | 100% | 100% 100% | | 0% | 0% | 0% | ON. | 100% 100% 100% 100% | 100% 100 100% 100 | 0% 0% 0% 0% | 0% 0% 0% 0% | 0.0% on | 0% 09 0% 09 | 0.0% 100% 10 0.0% 100% 1 | ON 200% 100.0% ON 200% 100.0% | 0% 0 0% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | === | | | |
| severthesis protein Cog9 C/ B Fam3b F/ | DOS MOUSE 35 N | kDa 100% kDa | 100% 100 | % 100.0% | 0% 0% | 0% 0.0% | s os | 0% 0% 0% 0% 0.0 | 7% 100% | 500% 500% | 100.0% 01 | N 0% | 0% 0.0% | ON ON | 0% 0.0% | | 1000 1000 | | | 0.000 | | 100% 11 | ON 88% 95.8% | 0% 0 | % 13% | 4.2% ON | on on | 0.0% | | | | == | | | |
| n consenior nell ent Cd34 Cl in Crisi Cl | 27 MOUSE 419 80, MOUSE 349 | kDs kDs | | | | | | | | | | | | | | 100% 100% 100% 100% 100% 100% | 100% 100 | 0% 0% 0% | 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 09 0% 09 | 0.0% 100% 1 0.0% 100% 1 100% 1 | ON 82% 94.4% ON | 9% 0 9% 0 | % 17% % | 55% 0% 0% | ons ons | 0.0% | 0.4226 | | | 0.4225 | | | |
| ina kinasa mitorbo Dguck Di ng kinasa Tp53rk P1 protein ISG15 Ing15 IS | SUCK MOUSE 32 N SPK MOUSE 27 N GIS MOUSE 18 N | KOs KOs | 100 | 8 | | on. | | - 05 | | | | | | | | 100% 100% 67% 71% | 100% 100 60% 55 | 0% 0% 0% 0% | 0% 0% 14% 20% | 0.0% 0% 11.4% 33% | 0% 09 14% 209 | 0.0% 100% 11 22.5% | ON 100% 100.0% ON 100% | 9% 0 | % 0% % 0% | 0.0% ON | 0% 0% 0% | 0.0% | | | | _ | | | |
| rotein Rab-SB RabSb Ri poteining protein 5 Wdr5 W ted obserborotein Arm 19 All | 955 MOUSE 24 9 DRS MOUSE 37 9 8210 MOUSE 12 9 | kDa 100% kDa | 100% 100 0% 0 | % 100.0% % | 9% 9% 200% | 0% 0.09 100% | 5 0% | 0% 0% 0.0 0% 0% | 7% 100% | 100% 100% | 100.0% 01 | 0% | 0% 0.0% | 0% 0% | 0% 0.0% | 200% 200% 0% 0% | 100% 100 0% 0 | 0% 0% 0% 100% | 0% 0% 100% 100% | 0.0% 0% 100.0% 0% | 0% 09 0% 09 | 0.0% 100% 1/ 0.0% 0% | 0% 100% 100.0% 0% | 0% 0 100% 100 | N 0% | 0.0% 0% 0% | ons ons | 0.0% | | | | | | | _ |
| hesion molecule A F11r JA ubunit beta type-9 Pamb9 P1 | M1_MOUSE 32 x 509_MOUSE 23 x | kOs kOs | 100% 100% | | 98 | | | ON ON | | 100% | | ON. | | 9% | | 100% 100% 100% 100% | 100% 100 100% 100 | 0% 0% 0% 0% | 0% 0% 0% 0% | 0.0% 0% 0.0% 0% | 0% 09 0% 09 | 100% July 100% J | ON 100% 100.0% ON 100% 100.0% | 9% 0 9% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | 0.5000 | | | 0.5000 | | | |
| tidic acid chosohat: Acp5 P1 redrobenzene-1.2-d Dhsh D1 | AS MOUSE 48 H | KDs KDs | | | | | | | | | 400 OW | | | | | 100% 100% 100% 100% | 100% 1000 60% 655 100% 1000 0% 0 100% 1000 100% 1000 100% 1000 100% 1000 | DN DN DN | 0% 0% 0% | 0.0% 0% 0.0% | 9% 09 9% | 0.0% 100% 1/ 100% 1/ | 0% 20% 100.0% 0% 20% 100.0% 0% 20% 100.0% 0% 20% 100.0% 0% 200% 100.0% | 0% 0 0% 0 | 0% % 0% | 005 0% | 0% 0% | 0.0% | | | | = | | | + |
| semetrate Mu / Gath7 Gi le triphosphate diph Entpd1 E1 led plant pathopene Glipr2 Gi | STP1_MOUSE 57 A | kDa kDa | ASST 100 | 100.0% | 93 95 | US 0.05 | 98 | N 05 0.0 | 100% | xx675 100% | -00.07h 01 | 0% | we 0.0% | MA 9% | US 0.0% | | | | 0% 0% 0% | 0.0% 0% | 0% 09 | | | | | | | | | | | _ | | | |
| 1-fucosidase Fuca1 Fi 1-3 Npm3 M protein 2 Praf2 P1 | NO MOUSE 52 PM3 MOUSE 19 PM3 MO | kDs 22% kDs 100% | 67% 100 100% | % 66.7% | 67% 32% 0% 0% | 0% 33.35 | 5 0% 0% | 0% 0% 0.0 0% 0% 0.0 0% 0% 0.0 0% 0% 0.0 | 7% 32% 100% | 100% 100% 100% 100% | 77.8% 621 100.0% 01 | N ON | 0% 22.2% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 50% 67% 100% 100% | 100% 72 100% 900 | 2% 50% 0% 0% | 22% O% | 27.8% 0% 0.0% 0% | 0% 09 0% 09 | 0.0% 100% 1/ 0.0% 100% 1/ 0.0% 100% 1/ | ON 200% 100.0% ON 200% 100.0% ON 200% 100.0% | 0% 0 0% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% 0% 0% | 0.0% 0.725 0.0% 0.725 | 0.1994 | 0.8305 0.4221 | 0.7250 | 0.1994 0 | 0.8305 0.4226 | | |
| main-containing on Code58 Ci Il subunit bets Cank2b Ci rotein Rei-A Reis | DSS MOUSE 17 I | kDa 100% kDa 100% | 100% 100 100% | % 100.0% | 0% 0% 0% 0% | 0% 0.0% | 5 0% 0% | 0% 0% 0.0 0% | 7% 100% 100% | 100% 100% 100% 100% | 100.0% 01 | N ON | 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% | 100% 500 | 0% 0% 0% 0% | 0% 0% 0% 0% | 0.0% 0N | 0% 09 0% 09 | 0.0% 100% 11 0.0% 100% 1 | ON 100% 100.0% ON 100% 100.0% | 0% 0 0% 0 | % 0% % 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% | | | | = | | | |
| is factor alcha-indu Trifaipă 17 - carbooviale 3-deh Nadhi Ni | PE MOUSE 239 SOIL MOUSE 419 | kDs 100% kDs 100% | 100% 100% 100 | % 100.0% | 0% 0% 0% 0% | 0% 0.0% | on N on | 0% 0% 0.0 | 100% PN 100% | 100% 100% | 100.0% 01 | N ON | 0% 0.0% | 0% 0% 0% | 0% 0.0% | 100% 100% 100% 100% | 100% 100 100% 100 | DN | 0% 0% 0% 0% | 0.0% 0N | 0% 09 0% 09 | 0.0% 100% 11 0.0% 100% 11 | | 0% 0% | | 0% 0% | | 0.00 | 0.5000 | | | 0.5000 | | | + |
| Contractors of Mose Mills Contractors | DEE MOUSE 193 BPQ MOUSE 523 | kDa 100% kDa | 100% | \vdash | 9% 9% | | 9% | ON. | 100% | 100% 100% | 100.0% 01 | N 0% | 0% 0.0% | on on | 0% 0.0% | 100% 100% 100% 100% | 100% 100 | 0% 0% | 0% 0% | 0.0% 0% | 0% 09 | 100% 10 100% 0.0% 100% 1 | 200% 100.0% 200% 100.0% | 9% 0 9% 0 | 0% 0% | 0% 0% 0.0% | 0% 0% 0% 0% | 0.0% | 0.5000 | | | 5,500 | | | # |
| M2 activator Gm2a Si nisminumbrandorim Capt1 CI component CB garn CBo Ci | P3 MOUSE 21 A PT1 MOUSE 46 A DBG MOUSE 22 A | KDs KDs | 100% | ± 1 | 98 | | | ON | | 100% | | | 0% | | os | 100% 100% 100% 100% | 100% 900 | 0% 0% 0% 0% | 0% 0% 0% 0% | 0.0% 00 | 0% 09 | 0.0% 100% 1 | 0% 100% 100.0% 100% | 9% 0 | 0% | 0.0% 0% | 0% 0% | 0.0% | | | | == | | | |
| entimicrobial sectide Comp Ci 5-Sep Si | MP MOUSE 193 | KDs KDs | | | | | | | | | | | | | | 100% | 100% | 0% 0W | 0% 0% | 0.0% *** | 0% 09 0% 09 | 100% 1/ 100% 1/ | ON 100% 100.0% | 9% 0 9% 0 | % % 0% | 0% 0% 0.0% 0% | 0% 0% | 0.0% | | | | = | | | Ξ |
| n superfamily cont lish 15 subunit sigma-1 Ap3s1 Ai | UR MOUSE 469 | KDs KDs 67% | 100% 100 | S 88.9% | 22% ON | 0% 11.15 | s 08 | os os oo | PS 100% | 50% 100% | 83.2% 01 | S 0% | 0% 0.0% | 0% 50% | 05 15.7% | 100% 100% | 100% 100 | 0% 0% | 0% 0% | 0.0% 0% | 0% 09 | 0.0% 100% 1 | ON 2001 100.0% ON 01 0.00 | 0% 0 0% 0 | s 0s | 9% 9% 9% | 0% 0% | 0.0% 0.797 | 2 | 0.4226 0.4226 0.5000 | 0.4226 | 0.5000 | 0.4225 | 3.4226 | + |
| hate pyrophosphok Prps1 P1 TP-binding protein Rhoc Ri | PS1 MOUSE 351 FOC MOUSE 221 | kDa 100% | 100% 100 | % 100.0% | 9% 9% | 0% 0.09 | 5 9% | 0% 0% 0.0 | 7% 100% 100% | 200 200% 200% 200% 200% 200% | 100.0% 01 100.0% 01 | N 0% N 0% | 0% 0.0% 0% 0.0% | 0% 0% 0% 0% | 0% 0.0% 0% 0.0% | 200% 200% 200% 200% | 100% 100% 100 | 67% 0% 0% | 4505 0% 0% 0% | 0.0% 0% | 9% 00 0% 00 | 0.0% 100% 1 0.0% 100% 1 0% 0% 100% 100% 1 0.0% 100% 1 0.0% 1 | 0% 20% 100.0% 0% 20% 100.0% | 100% 100 0% 0 0% 0 | 100% 90 % 0% | 0.0% 0% 0.0% 0% | 0% 0% 0% 0% | 0.0% 0.797. 0.0% 0.0% 0.0% | 25000 | | | | | | |
| susson factor subsr Catff Ci trabase-like Sdal Si n recognition protein Pglyrgt Pi | SI MOUSE 35 A | 60s 0% 60s 100% 60s | 100% | 1 | 0% 0% | 100% | 9% 9% | ON ON | | | | | | | | 2% 2% 100% 100% | 0% 0 | 200% 0% | 100% 100% 0% | 100.0% 0% | 0% 09 | 0.0% 1 100% 1 | 0% 0% 200% 100.0% | 9% 0 | % % 0% | 0.0% ON | 0% 0% 0% 0% | 0.0% | | | | = | | | |
| cerol lipsase ABHDK AbhdS All acetytransferase 2 Nat2 All chloride-dependent Kintus | NOS MOUSE 36 P NOS MOUSE 34 P | kOs kOs | 100% *** | | - | 016 | | 0% 0% | 100% | 100% 100% 100% 100° | 100.0% 01 | N 0% | 0% 0.0% 0% 0.0% | 0% 0% | 0% 0.0% | 100% | 100% | 0% | 0% | 99 | 00 | 100% 1 | ON 100% 100.0% | 0% 0 | % 0% | 0.0% ON | 0% 0% | 0.0% | | | | _ | | | |
| se HTATIP2 Htstp2 HT s dehvdrosensse-lik Scopth SI | DAIZ MOUSE 27 A | kOs kOs | | - | - 01 | | | - | | 100% | | | 0% | | os os | 100% 100% | | 0% | 0% | ON. | 0% | 100% | 004 2008 000 000 000 000 000 000 000 000 00 | 0% | % 0% | 0% | 0% 0% | | | | | == | | | |
| in C region 4 5V IG sohate 3-epimerase Rps RS | HE_MOUSE 471 | kOs kOs 100% | 100% 100 | % 100.0% | 0% 0% | 0% 0.0% | s os | 0% 0% 0.0 | % 100% | 100% 100% | 100.0% 01 | N ON | 0% 0.0% | on on | 0% 0.0% | 100% 100% | 100% 100 | 0% 0% | 0% 0% | 0.0% ox | 0% 00 | 100% 11 0.0% 100% 11 | 0% 0% 100% 100.0% | 0% 0 0% 0 | % 0% | 0% 0.0% 0% | ON ON | 0.0% | | | | _ | | | |
| complex subunit To Tprkb TF artists renkin EAMS Familitib F1 d and recorderinal a Not 18 | HOLEE 20 H | KDs KDs | 100% 100 | 76 | ON | ON | | DN DN | 100% | 100% 100% | 100.0% 01 | n 0% | oni 0.0% | UN 0% | 0% 0.0% | 25 25 25 25 20% | 9% 0 | D% 100% | 0% 100% 100% 100% | 100.0% ox | 0% 09 0% 09 | 0.0% 0% 100% | 0% 0% 0.0% 100% | 0% 0 100% 100 | % 0% % 100% % | 00% 0% 00% 0% | 0% 0% 0% 0% | 0.0% | | | | == | | | |
| nit alpha-5 Kpna1 (8) | N7 MOUSE 35 A N5 MOUSE 60 A JFL3 MOUSE 60 A | KDs 100% | Ŧ | \Box | 0% | | 0% | | + | 100% | | 0% | | 9% | | 100% | 100% 100% | 0% | 9% 9% | 93 | 09 00 | | ON 100% | | % 0% % | | 0% 0% | | $\vdash \neg$ | | | = | | | Ŧ |
| Lpan LF ng prolein 4 Rhp4 Ri | NN MOUSE 439 | KDs KDs | 100% 100 | S | 98 | 0% | | ON ON | | 100% | | | 0% | | os. | 2% 67% | 100% 80 | 100% DN 25% | 22% 0% | 19.4% 9% | 0% 09 | 0.0% | 0% 0% | 100 | % 100% | | 0% 0% 0% | | 0.2355 | 0.1917 | | 0.2355 0 | 0.1917 | | |
| stromelscleroderma Sascal St definate-associated Lcn2 N | SA27 MOUSE 21 P SAL MOUSE 23 P | kDa 0% | 0 | % 100.0% | 100% | 100% | 98 | 9% 0.0 | 100% | ON . | | 100% | | 9% | | 20% 100% | 0% 100% 500 | D% 0% | 100% 100% 0% 0% | 9.0% 00 | 0% 09 0% 09 | 0.0% 100% 1 | 0% 100% 0% 100% | 9% 0 | s 05 | 98 | 0% | | | | | = | | | |
| atir-binding protein (Rhob (R) protein NCK1 Nck1 Ni d RNA polymerases (Pol/2h (R) | 1908 MOUSE 201 1918 MARKE 239 1918 MARKE 239 1918 MARKE 169 187 MOUSE 16 | KCs KCs | 100% 0% 0 | 8 | 0% 200% | 100% | | 0% 0% | | ON. | | 100% | | 9% | | 100% 50% | 100% 62% | 0% 0% | 20% | 99 | 01 | 100% 100% 1/ 50% 1/ | 0% 200% 83.2% | 0% 0 0% 0 | % % 0% | 9% 9% 9.0% 59% | 0% 0% 1 | 16.7% | 0.2788 | 0.0903 | | 0.5000 0. 0.4225 | 0.1257 | 0.8 | 8088 4226 |
| 2-binding protein Syn(2bp 5' | CI2B MOUSE 169 | kDa 0% kDa 100% | 2% | 8 | 100% 100% 0% | on. | 9% 9% | ons ons | + | | | | $+$ \mp | | | 0% 0% 100% | 0% 0 100% | DN 100% | 100% 100% 0% 0% | 100.0% 00 | 9% 09 9% 09 | 0.0% 0% 1 | 0% 0% 0.0% 0% 100% | 40% 100 0 | % 100% I | 0.0% 60% | 0% 0% 2 0% 0% | 20.0% | | | | 0.4226 | | 0.4 | 4226 |
| 6-chosphate isome Greda? | VP12 MOUSE 11 V | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

| binding prolein 2 Rbp2 | RET2_MOUSE | 16 kOs | | | | | | | | | | | | | | | | | | | 100% | | 0% | | | N. | 10 | 0% 100% S | 6% 95.2% | 0% 0% | 14% 4.85 | 9% | 0% 0% | 0.0% | | | | | | | |
|--|---|--|--------------|----------|-----------|---------------|---------|------------|-----------------|-----------|--------------------|----------|-----------|--------------|----------------|--------------|---------|------|----------|--------------|-----------|---|----------|-------------|------------|-------|--|---|----------------|-------------|-------------|----------|----------|----------------------|---------|---|--------|---------------|---|--------|--------|
| binding prolein 2 Rbp2 face A33 antigen Gps33 YIPFS Yipf5 | GPA33_MOUSE | 36 kDa | | | | | - | | | | 33% 28.99 | | | | | | | | | | 100% | | 9% | - | | N . | 10 | 10% 100% 8 10% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.01 | 9% | 0% 0% | 0.0% | | | | | | 0.0000 | |
| | | | | | S 44.4% | | | 22% 55.6 | 25 225 25 25 | 22% 0% | 0% 0.09 | S 100% | 100% 100 | ns 100.0% | 0% 0% 0% 0% | 0% 0.0 | 200% | 62% | 0% 0.0% | 100% | 1001 | 0. | 0% | 9% | 0% | | | 10% 100% 10 | | | | | | | 7 | | 0. | 0377 | | 0.1090 | - |
| | | | 100% | 100% | | 9% | 9% | | 9% | 0% | | 100% | | | 0% | | 0% | | | 100% 100% | 1000 | 66. | 0% | 9% | 9% 9% 0 | 0% | 10 | 100% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.05 | 9% | 0% 0% | 0.0% | | | | | | | |
| glucosyltransferase 1 Pogluti keletal embryonic nucle (Mastri) | MSTNI MOUSE | 46 kDa | | 100% | | | 0% | _ | | 0% | | 0% | - | σ. | 100% | 6% | 0% | | 20% | 100% | 100% 1009 | 65 900.0% | 0% 0% | 0% 0.05 | 0% 0 | N 0% | 0.0% 1/ | 100% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.05 | 9% | 0% 0% | 0.0% | | | | | | | - |
| | | | | | | | | | | | | 500 | | | | | | | | 100% | 100% 1009 | ns 100.0% | 0% 0% | 0% 0.05 | 9% 0 | 5 0% | 0.0% 1 | 00% 160% 160% 160% 160% 160% 160% 160% 1 | | 0% 0% | | 9% | 0% | | | | | | | | |
| Agin Clec3b nogen Agi | ARPIN_MOUSE | 25 kDa | _ | _ | | | _ | | | | | | | | _ | | _ | | _ | 100% | 100 | 6. | O% | 9% | 9% | 0% | - 1 | 100% 100% 10 | 0% 100.0% | 9% 9% | 0% 0.01 | 9% | 0% 0% | 0.0% | | | _ | _ | | | - |
| Clec3b | TETN_MOUSE | 22 kDs | _ | _ | _ | | _ | _ | | _ | _ | | _ | | _ | | _ | | _ | 100% | 100% 1009 | 6. 500.0% | 0% 0% | 0% 0.05 | 98 9 | S 0% | 0.0% | 100% 10 | 98 | 99 | 0% | - 00 | 0% 0% | _ | | _ | _ | _ | _ | | - |
| osphatase 18 Ppm1b | ANGT_MOUSE PPM/IB_MOUSE | 43 kDa | | | | | | | | | | | | | | | | | | | 1000 | | | | - | | - 1 | 10% 20 | 0% | 9% | 0% | 9% | 0% | | | | | | | | |
| G Chig | CATG_MOUSE | 43 kDs 29 kDs 13 kDs 12 kDs 11 kDs 47 kDs 47 kDs 47 kDs | | | | | | | | | | | | | | | | | | | | | | | | | | 100% | | 0% | | | 0% | 0.0% 0.0% 0.0% | 0.4226 | | 0.4726 | 0.4226 | | 0.4226 | |
| ton ATPase subunit F Atp6v1f | VATF_MOUSE | 13 kDa | | 100% | | | 0% | _ | | 0% | | | | | 0% S0% | 0% 16.7 | % 0% | 0% | 016 0.0% | 100% | 100% 50 | 6 83.3% | 0% 0% | 50% 15.79 | 0% 0 | K 0% | 0.0% 1 | 10% 10 | ON. | 0% | 0% | 0% | 0% | | 0.4226 | | 0.4226 | 0.4225 | | 0.4226 | |
| Comparison Permits | 3 SINAD MOUSE | 12 KDs | | 0% O | | | 0% | _ | | 0% | _ | | 100 | 06 | _ | 0% | _ | | ON. | 100% | 100% 1000 | 6 900 0% U | 0% 0% | 0% 16.75 | 0% 0 | N 0% | 0.0% 1 | 10% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.00 | 0% | 0% 0% | 0.0% | 0.0000 | | _ | 0.0000 | _ | | - |
| protein 13 Bc(2113 | B2L13_MOUSE | 47 kDs | ON. | | | 100% | | | 0% | | | | 100% | | On | | | 0% | | 100% | | | 0% | | 0% | - | 1 | 10% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.01 | 0% | 0% 0% | 0.0% | | | | | | | |
| omal protein L14. mitoc Mrpi14 | RM14_MOUSE | 16 kDs | 0% | 0% 0 | % 0.0% | 100% | 100% 10 | 100% 100.0 | 2% 0% | 0% | 0% 0.09 | N. 0% | | | 100% | | 0% | | | | - 01 | % | | 100% | | 0% | | ON. | | 100% | | 0% | | | | | | | | | |
| Nationmentally and HOA's | HAVE MOUSE | 47 KDB | | _ | | | _ | _ | | _ | _ | | 100 | ns. | _ | 6% | _ | _ | ON. | 200% | 100% 1000 | 6. 100.0% I | DIE DIE | 0% 0.05 | 0% 0 | N UN | 0.0% | 100% 50 | 6% 95.7% | 0% 0% | 14% 4.87 | - 0% | 0% 0% | 0.0% | _ | _ | _ | _ | _ | | |
| histocompatibility anti HG-K1 yloid A-2 protein Sas2 | SAAZ MOUSE | 14 kDa | | | | | | | | | | | | | | | | | | 100% | 86% 100 | N 95.2% | 0% 14% | 0% 4.07 | 0% 0 | N 0% | 0.0% | 1000 | | | | | | | | | | | | | |
| nime of historian control of Appet inime of historian fact Staff in the staff of th | ASCC1_MOUSE | 41 kDa | 100% | 67% | | 9% | 33% | | 9% | 0% | | | | | | | | | | | | | | | | | | 0% 0% 0% 100% 10 100% 100% 100% 10 | | | | | | | | | | | | | |
| inimazirk infiritor fort 5mg | SRSF9_MOUSE | 26 kDa | | | | | _ | _ | | _ | _ | | _ | | _ | | _ | _ | _ | _ | - 0 | 6. | | 200% | | 0% | - 1 | 90% 0% 100W | ov son ov | 0% 100% | OV 0.00 | 9% | 0% | 0.09 | _ | _ | _ | _ | _ | | |
| | | | | | | | | | | | | | | | | | | | | 100% | | | O% | | 9% | | | 100% | - | 9% | 00 00 | | 0% | 0.00 | | | | | | | |
| omolex protein LAMTI Lamfor2 | LTOR2_MOUSE | 13 kDa | | | | | | | | | | 100% | 100% | | 0% 0% | | 0% | 9% | | 100% | 100% 1009 | % 100.0% I | 0% 0% | 0% 0.05 | 9% 0 | N 0% | 0.0% | 100% 10 | ON. | 9% | 0% | | 0% 0% | | | | | | | | |
| complex protein LAMTI Lambr2 ding cofactor B Tbcb coder ZIP11 Sic29x11 Man(7)GicNAc(2)-PP Aig12 | TROS MOUSE | 27 kDs | 100m | 100 | % 400.0W | - AW | aw. | 0% | w ov | - OW | 0% | 100% | 100 | | 9% 9% | 0% | 0% | | aw . | 100% | 100% | | 0% 0% | _ | 9% 0 | N. | _ | 100% | | 9% | | | 0% | _ | _ | _ | _ | | | | |
| Man(7)GcNAc(2)-PP Ale(2 | ALG12 NOUSE | 55 kDa | 10000 | 400 | 0.000 | | | 05 05 | 28 98 | | W 8.00 | ALCON . | 100% | | 011 | | | 0% | - | | | | | | | | | | | | | | | | | | | | | | |
| carolene 9'.10'-poyoen Bco2 nt C1s-A subcompone C1ss | BCDC2_MOUSE | 60 kDs | | | | | | | | | | | | | | | | | | | | | | | | | | 26 | 9% | | 0% | | 9% | | | | | | | | |
| nt C1s-A subcompone C1sa endert protein kinase Prkacb | CS1A_MOUSE | 77 kDa | | | | | | - | | | _ | 100% | | | | | - | - | _ | 100% | | | O% | | 9% | | | 100% 10 | | | | | | | | | _ | _ | | | - |
| encert prosen scrase: PTsaco see T2 Praset2 | RAPLE MOUSE | 30 kDs | 100% | 100% | | 0% | 9% | O'S. | | | | 100% | 100% | | 0% 0% | | 0% | 9% | | 100% | 100% 100 | 6 100.0% | 0% 0% | 0% 0.05 | 9% 0 | N 0% | 0.0% 1 | 10% 100% 10 | 0% 100.0% | 9% 9% | 0% 0.07 | 9% | 0% 0% | 0.0% | | | | | | | - |
| ng protein BA RbmBa | REMMA_MOUSE | 20 kDs | | 100 | % | | | 0% | - | | 0% | | | | | | | | | 100% | 100% 67 | % 88.9% | 0% 0% | 33% 11.15 | 0% 0 | N 0% | 0.0% 1 | 0% 100% 10 | 0% 100.0% | 9% 9% | 0% 0.05 | 9% | 0% 0% | 0.0% | 0.4225 | | | 0.4225 | | | |
| se T2 RraseQ ng protein BA RbmBs hain V-V region LS (F) 4 5V | KVSAS MOUSE | 13 kDs | - | _ | + | \rightarrow | _ | _ | + | - | _ | _ | _ | + | _ | _ | + | | _ | 100% | saw con | w 83.39 | 0% | ov sr= | 9% | | 0.00 | 100% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.07 | 9% | 0% 0% | 0.0% | + + + | _ | _ | _ | _ | | + |
| sephorylase 1 Upo 1 | UPP1_MOUSE | 34 kDs | | | | | | | | | | | | | | | | | | -205 | 100% 1000 | 6 | 9% | 0% | - VA 0 | N 0% | 1000 | 100% | | 0% 0% | | 0% | 0% | | | | | | | | |
| 2 chain C region Igk:2 | LAC2_MOUSE | 11 kDs | | | | | | | | | | | | | | | | | | | - | | | | | | - 1 | 10% 75% 10 | ON 91.7% | 0% 25% | 0% 8.35 | 0% | 0% 0% | 0.0% | | | | | | | |
| -splicing factor 38A PrpfS8a | PRIMA MOUSE | 37 kDa | 400W | 0 | % 400.00° | | 10 | 200% | | - 00 | 0% | V 400W | - now | ev 400 000 | aw | - AW | | | ov 0 | 0% | - O1 | 66 100 | ON ON | 200% | 0% | 0% | 0.00 | | \perp | _ | | _ | _ | | _ | | _ | _ | | | _ |
| -1 Gvo1 | GLYG MOUSE | 37 kDa | 100% 100% | 100% 100 | % 100.0% | 0% | 0% | 0% 0.0 | 7% 0% | 0% | 0% 0.09 0% 0.09 | % 100% S | 100% 100 | % 700.0% | J16 016 | 0% 0.0 | 0% | 0% | 0% 0.0% | 100% | 100% | 100.0% | 0% 0% | JR 0.09 | 0% 0 | m 0% | 0.0% | 100% | _ | 0% | | | 0% | | | | | | | | |
| n-crotein licase ARth1 Arth1 | ARI_MOUSE | 64 kDs | | 100% | | | 0% | | | 0% | - | | - | | | | | | | | 100% 1000 | 66 | 0% | 0% | 0 | K 0% | - 1 | 100% | | 0% 0% | | 0% | 0% | | | | | 0.5000 | | | 0.5000 |
| einase inhibitor 3 Timp3 | TIMP3_MOUSE | 24 kDs | $-\epsilon$ | | + | - | av | | + | | | 1000 | - ANN | w 400 00 | aw | - Au | | | ov 0 | 0% | 0% 01 | 66 0.0% 10 | 100% | 100% 100.09 | 0% 0 | N 0% | 0.0% | 0% 0% | + | 67% 100% | - | 33% | 0% | | \perp | | | 0.5500 | | | 0.5000 |
| velin phosphodiesteras Smpd2 | NSMA_MOUSE | 47 kDs | 100% | 100% | + | 0% | 0% | _ | 0% | 0% | | 100% | 100% 100 | % 100.0% | 0% 0% | 0% 0.0 | 7% 0% | 0% | 0% 0.0% | 300% | 1000 | 66 100.0% | UN 976 | 0% 0.09 | 9% 0 | 016 | 0.0% | | + | _ | | | _ | _ | | | _ | | | | |
| hain V-V resion (8-IF) 4- 5V persionae 7 Gps7 Gps7 sphorylase 1 Upp1 2 chain C region 1922 chain C region 1922 chain C region 1922 chain C region 2024 his residual 1922 chain C region 1922 chain c | PLP2_MOUSE | 17 kDa | | 100 | % | - 11 | | 0% | | | 0% | | 100 | S | | 9% | | | 0% | 100% | 100% 1009 | ns 100.0% | 0% 0% | 0% 0.05 | 0% O | 6 0% | 0.0% 1 | 100% 100% | 95 | 9% | 0% | 9% | 9% | | | | | | | | |
| restler, secretabel me Scamp2 nearly and ansalouse Frita yield A-1 protein Sea1 | SCAME_MOUSE | 36 kDa | - | 100 | % | - | | 0% | \perp | - | 9% | _ | - | $+$ \neg | | | _ | | | 100% | 100% 1009 | ns 100.0% | 0% 0% | 0% 0.05 | 0% 0 | K 0% | 0.0% 1 | 100% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.01 | 9% | 0% 0% | 0.0% | \perp | | | \perp | | | - |
| | | | | | | - | _ | _ | + | - | _ | 100% | _ | + | 4% | _ | 0% | _ | _ | 200% 93% | 21% 100 | S 54 9% | 7% 14% | 0% 107 | 9% 9 | n 0% | 4.5% | 100% | + | 4% 4% | | 95 | 25 | | | _ | _ | | _ | | + |
| acetylase 10 Hdac10 | HEATO MOUSE | 72 kDs | 100% | 100% | | 0% | 0% | | 9% | 0% | | 100% | 100% 100 | ns 100.0% | 0% 0% | 0% 0.0 | 25 0% | 0% | 0% 0.0% | 445 | ZAS ASSO | S 50.23 A | 78 488 | 98 022 | 20 20 | N 500 | 5.0.0 | | | | | | | | | | | | | | |
| acetylane 10 Hdac10 nt chain Tcten-type 3 Dyn83 hain V region 441 4 5V | DYLT3_MOUSE | 13 kDs | _ | _ | | | _ | | | | | 100% | 100% 100 | % 100.0% | Q% 0% | 9% 0.0 | 2% 0% | 9% | 0% 0.0% | | _ | | | _ | | | - 1 | 0% 100% 10 0% 86% 10 0% 100% 10 100% 10 | | 9% 9% | | 9% | 0% | | | | _ | _ | | | - |
| nain V region 441 4 5V olease 1 Mopt1 | MOPTI_MOUSE | 13 kDa | | _ | | | _ | _ | | _ | _ | | _ | | _ | | _ | _ | _ | 100% | 100% 1009 | 6, 500.0% | 0% 0% | 0% 0.05 | 98 9 | N 0% | 0.0% | 25 | 0% PF 791 | - AN - ANN | 0% | | 9% | 0.09 | _ | _ | _ | _ | _ | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | 1 | 0% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.07 | 0% | 0% 0% | 0.0% | | | | | | | |
| elastane Elane 1 cycle protein 123 hg Cdc 123 | ELNE_MOUSE | 29 kDa | _ | _ | | | _ | | | | | | | | _ | | _ | | _ | | _ | | | _ | | | _ | 100% | | 99 | | | 0% | | | | _ | _ | | | - |
| n cycle protein 123 ha Cdc123 | CD123_MOUSE | 39 kDa | 100% | 67% 62 | S 77.8% | 6% | 98 3 | 22% 11.1 | S 98 | 22% | 0% 11.15 | S 67% | 100 | _ | 9% | av | 22% | | aw . | | | | | | | | | | | | | | | | _ | _ | _ | _ | _ | | |
| -like domain-containin PhtSa | PHESA MOUSE | 12 kDa | | 100% | | | 0% | - | | 0% | *** | | 4000 400 | | | | | | - | 50% | 100% 100 | 6 83.2% 9 | 0% 0% | QN 15.79 | 9% 0 | N 0% | 0.0% 1 | 0% 100% 10 0% 0% | 0% 100.0% | 9% 9% | 0% 0.07 | 9% | 0% 0% | 0.0% | 0.4226 | | | 0.4225 | | | |
| ain-containing protein Nudod2 -like domain-containin PhSa n-protein ligase RINGS Ref2 | RING2_MOUSE | 35 kDs | 0% | 9% | | 100% | 100% | | 9% | 0% | | | | | | | | | | 9% | 0% 05 | % 0.0% 10 | 100% | 100% 100.05 | 9% 0 | N 0% | 0.0% | 0% 0% | | 100% 100% | | 9% | 0% | | | | | | | | |
| Ins2 | INS2_MOUSE | 12 kDa | 100% | 100% 100 | % 100.0% | 6% | 9% | 0% 0.0 | 25 25 | 0% | 0% 0.05 | 8 | 100% 100 | 8 | 09 | 9% | _ | 9% | 0% | 4000 | 100 | 6. | ov. | 0% | | 0% | - | 25 | 0% 100.0% | AV 00 | 0% | | 95 | 0.09 | | _ | _ | | _ | | |
| f RNA polymerase II tr Med 19 | MED 19 MOUSE | 25 kDs | | | | | | | | | | | | | | | | | | 4000 | 0% 01 | % | 100% | 100% | - 0 | K 0% | | | | | 00 00 | | VS VS | 000 | | | | | | | |
| hosohate mannosvitrar Dpm3 | DPNO_MOUSE | 10 kDs | 100% | 100% 100 | % 100.0% | 0% | 0% | 0% 0.0 | 2% 0% | 0% | 0% 0.09 | % 100% : | 100% 100 | ns 100.0% | 0% 0% | 0% 0.0 0% | 2% 0% | 0% | 0% 0.0% | 100% | 1000 | 06 1 | 0% | 0% | 0% | 0% | - 1 | 100% | ON 100.0% | 0% 0% | 0% 0.05 | 0% | | | | | | | | | |
| socialed membrane or Vamp3 | TORUS MOUSE | 11 kOs 35 kOs | 100% | 100% 100 | % 100.0% | 0% | 0% | 0% 0.0 | 2% 0% | 0% | 0% 0.09 | 100% | 100% 100 | N 100 0% | 0% 0% | 0% 0.0 | 106 006 | - 04 | 0% 0.0% | 100% | 100% 1000 | 55 0.055 100 55 05 05 05 05 05 05 05 05 05 05 05 05 0 | 0% 0% | 0% 0.09 | 0% 0 | 0% | 0.0% 1 | 10% 100% 10 | 0% 100.0% | 0% 0% | | | | 0.0% | _ | _ | _ | | _ | | |
| Inscendin Joseph GR PMZ (1974) | MED11_MOUSE | 13 kDs | 0% | 0% | | 100% | 100% | | 0% | 0% | | 0% | 20000 200 | 100.014 | 100% | 0.0 | 0% | - VA | 0.014 | 0% | 0% | 10 | 10% 100% | UN | 0% 0 | K COL | - | 0% 0% | 0% 0.0% | 100% 100% | 100% 100.01 | 0% | 0% 0% | 0.0% | | | | | | | |
| tein P Sepp1 | SEPPI_MOUSE | 43 kDs | | 100% | | | 0% | | | 016 | | | | | | | | | | 100% | 100% 1000 | ni 100.0% i | 0% 0% | 0% 0.09 | 0% 0 | K 0% | 0.0% | | | | 0% | | 0% 0% | | | | | | | | |
| C-1 Lyz1 | LYZI_MOUSE | 17 kDs | O% | - 0 | % | 0% | _ | 0% | 300% | | 100% | | - 0 | ns . | _ | 100% | _ | | 0% | _ | 100% | | | | | N. | - | 10% 100% 10 10% 100% 10 | ov ton ov | | OV 0.00 | - Av | | 0.09 | | | _ | | | | |
| ible RNA-binding grote Cirbo | CIPEP MOUSE | 19 kDs | | _ | | | | _ | | | | | _ | | _ | | _ | | _ | | 100 | 06 | _ | 9% | | 0% | 1 2 | 10% 100% 10 | ON 100.0% | 0% 0% | 0% 0.07 | 9% | 0% 0% | 0.0% | | | | | | | |
| a remails factor activate (rights) | HGFA MOUSE | 71 kDs | | | | | | | | | | | | | | | | | | 100% | - | - | O% | | 0% | - | | 100% 10 | 9% | 9% | 0% | - | 0% 0% | | | | | | | | |
| M1078 Fam107b | Th F107B_MOUSE | 16 kDa | | | | | | | | | | | | | | | | | | 100% | | | 0% | | 9% | | | 100% 10 100% | | 9% | | | 0% | | | | | | | | |
| k protein beta-5 Hapb5 | HEPES MOUSE | 15 kOs | 100m | _ | _ | - AW | _ | _ | - av | _ | _ | 4000 | _ | | aw . | | - AW | | _ | 100% | LOOK . | | | | 0% 0 | | | 25% 10% 100% 6 | | | | | 0% 336 | 44.00 | 0.4225 | _ | _ | | | | 0.4225 |
| recombine revision I AMTI Lander3 sentranse protein 1 Vmp1 se c codane subunit 77 Con7a01 factor 7s. misochondo Tafm in-binding protein 2 Whg2 trans protein 147 Transid-147 | VMP1 MOUSE | 46 kDa | 100% | 100% 100 | % 100.0% | 9% | 0% | 0% 0.0 | 2% 0% | 0% | 0% 0.09 | N 100% 1 | 100% | | 9% 9% | | 0% | 9% | | 100% | 100 | 06 | 0% | 0% | 9% | 0% | | 100% | 20 00.00 | 9% | 00 00 | | 0% | 16.1.8 | | | | | | | |
| e c coldane subunit 7/ Cos7s21 | COX7R_MOUSE | 12 kDs | | 0% 0 | % | | 200% 10 | 100% | | 0% | 0% | | | | | | | | | 9% | | 10 | 10% | | 9% | | | 100% 0% | 2% | 100% | 0% | | 0% 100% | | | | | | | | |
| factor Ts. mitochondri Tafm | EFTS_MOUSE | 35 kDs | | - | | - | | | _ | _ | aw . | - ov | _ | | 400V | | - AW | | _ | _ | 100% | | 9% | _ | | N. | | | | | | 9% | | 0.0% | | _ | _ | | | | |
| brane protein 147 Treem147 | 47 TM147 MOUSE | 25 kDs | 100% | - 0 | | 0% | - 16 | 200% | 9% | | 98 | OS. | 100% | | 200% | | 0% | 96 | | | | | | | | | | 0% | | 2005 | | | 0% | | | | | | | | _ |
| tase 2 Bace2 | BACE2_MOUSE | 56 kDa | - | | | - *** | | | | | | | | | | | | - | | | | | | | | | 10 | 0% 100% 10 0% 100% 10 | ON 100.0% | 98 98 | 0% 0.05 | 9% | 0% 0% | 0.0% | | | | | | | |
| in-binding protein 2 Wbp2 brane protein 147 Treent47 fase 2 Bace2 eta-2 Tpsb2 em cell antigen Paca | TRYB2 MOUSE | 31 kDa | - | _ | + | - | _ | _ | _ | | _ | _ | _ | _ | _ | | + | | _ | _ | _ | | | _ | | + | - 1 | 100% 10 | 0% 100.0% | 0% 0% | 0% 0.07 | 9% | 0% 0% | 0.0% | + + | _ | _ | | _ | | |
| em cerangen Paca dunitaloha-4 Kresi | IMAA MOUSE | 13.6Da | 100% | 100% 200 | % 100.0% | 9% | 9% | 0% 0.0 | 25 0× | 0% | 96 0.09 | N 100% | | _ | 9% | | Price. | | _ | 100% | 500 | os · | 0% | 9% | 9% | 095 | _ | ON 22% 6 | 25 25.2% 0% | 93 93 | 0% 0.05 | 2005 | 7th 33% | 56.73 | | | | | | | |
| bunit alpha-4 Kpns3 CU reculator, mitochi, Smdt1 | EMPE_MOUSE | 12 kDs | - | 100 | | | | - 45 | - 40 | | | - Common | | | | | _ | | | | Asso | | | | | | | | | | | | | | | | | | | | |
| ractor Neil ricoled-related protein Stp1 growth factor-binding lights CoA discoversase don Phythd1 complex protein LAMTI LamterS | NM_MOUSE | 35 kDs | | _ | + | - | | | + | | _ | | | + | | | _ | | _ | 100% | saw com | ev 200 000 | 0% | 0V F | 0% | - T | 0.00 | 100% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.05 | 9% | 0% 0% | 0.0% | - T | | | | | | - |
| growth factor-binding (gf=le | ALS MOUSE | 57 kDs | | | _ | _ | | | _ | | | | | _ | | | | | | 100% | 100% 1000 | 65 500,0% 1 65 500,0% 1 66 500,0% 1 66 500,0% 1 60 500,0% 1 60 500,0% 1 60 500,0% 1 | 0% 0% | Q% 0.05 | 9% 0 | N 0% | 0.0% | | _ | | | | _ | | | | | | _ | | |
| OA diceroenase don Phyhd1 | PHYD1_MOUSE | 32 kDs | | | | | | | | | | | | | | | | | | | 100% | | 0% | - 207 | - 0 | K | | 100% | | 0% | | | 0% | | | | | | | | |
| omplex protein LAMTI Lamter5 | LTORS MOUSE | 10 kDa | 100% | 100 | | | _ | ow. | 1 | | av | | _ | _ | | | _ | | _ | 50% | 0% 01 | 6 16.7% 9 | 20% 100% | 100% 83.35 | 0% 0 | N 0% | 0.0% | 0% 100% | 0% 33.3% | 100% 0% | 100% 65.75 | 0% | 0% 0% | 0.0% | 0.6856 | | _ | 0.6856 | | | _ |
| half LIM domains pro FhS | FHL3_MOUSE | 32 kDs | 100% | 100 | - | 0% | _ | - N | J. J. | | OW. | _ | _ | + | | | _ | | | 32% | 0% S01 | % 27.8% G | 7% 100% | 50% 72.25 | 0% 0 | N 0% | 0.0% 1 | 10% | _ | 0% | | 0% | | | | | | | | | |
| nal protein L43. mitoc MrpH3 | RMAS_MOUSE | 20 kDs | | | | | | | | | | | | | | | | | | 0% | 0% 01 | 0.0% 10 | 100% | 100% 100.05 | 0% 0 | K 0% | 0.0% 1/ 0.0% 1/ 0.0% 1/ 0.0% 1/ | 0% 0% | 0% 0.0% | 100% 100% | 100% 100.01 | 0% | 0% 0% | 0.0% | | | | | | | |
| LOS delegiorans del Prijetti combine rostian LASITI Lameter's name/reductane SCIR: Dhra11 half LIM domains one Phili mail crotain L43, mileo MgA3 coleodis-bindine prote Greg corression-enhancino; ReepS in domain family 10 m; Clac 10s | GBG2_MOUSE | 8 kDa | 1000 | | + | - T | av | | + - | | | 1000 | | + | aw . | - | +- | - | | 100% | 100% 1000 | 66 100.0% | 0% 0% | 0% 0.05 | 0% 0 | N 0% | 0.0% 1 | 100% 100% 10 | 0% 100.0% | 0% 0% | 0% 0.01 | 0% | 0% 0% | 0.0% | \perp | | | \rightarrow | | | - |
| n domain family 10 m Cler 10s | CLC10 MCV FOR | 22 KDB 35 KDB | 100% | and a | + | 9% | UN. | _ | UN. | UN. | _ | 100% | _ | + | Jik | _ | - 0% | | _ | 100% | 100% 100 | ns 100.0% | 0% 0% | 9% p.m | 9% 0 | N 095 | 0.0% | 4.0 | ON | _ | 0% | - | psc | | | _ | _ | | _ | | + |
| Addisonantina_dalid Dpagt1 | GPT_MOUSE | 46 kDa | | | | | | | | | | 100% | 100% | | 0% 0% | | 0% | 0% | | | 100 | | | 207 | | | | | | | | | 2/4 | | | | | | | | |
| historosamino, delle Dpagti I historosaia factor 15 Pgx19 oxprolein P1 Fosp1 | PEX19_MOUSE | 33 kDs | - | | - | | | _ | | | _ | | | - | | | | | _ | - | | | | | | - | 10 | 12% | - | 9% | | 9% | | | | | | | | | + |
| ox protein P1 Foxp1 | POKPI_MOUSE | | | | % 100.0° | | 200% | 0% 0.0 | 96 00 | 0% | 06 A 70 | N 100% | 1006 100 | ns 100 ms | 0% *** | 0% 0.0 | m / | 6% | os 0.00 | 1006 | 100% 1000 | N 100 0% | 0% 0% | 0% 0.00 | 0% | s ov | 0.0% | + | + | _ | - | - | + | _ | | _ | _ | _ | _ | | + |
| ein-1 M1 Indent-like kinase 5 Cds5 e II cuticular 1955 Kr85 | CDKS MOUSE | 33 kDs | 100% | 100 | 100.0% | 575 | 9% | | CR (2%) | 0% | cm 0.05 | 100% | 100% 100 | % 100.0% | 9% 0% | 9% 0.0 | 75 DN | 9% | 0% 0.0% | 200% 200% | 100% 1000 | N 100.0% | 0% 0% | 0% 0.05 | 9% 0 | 5 05 | 0.0% | | | | | | | | | | | | | | |
| Il cutcular Hb6 Kr86 | CDKS_MOUSE KRTBS_MOUSE | 33 kDs 53 kDs | 0% | 100% | \Box | 9% | 9% | _ | 100% | 0% | | - | | | | | | | | | 100% | | 9% | | | N | | | - | | | - | | | | | | | | | |
| osis factor receptor a Ngtr renuncebbulin domak Vsiq1 | TNR16_MOUSE VSIG1_MOUSE | | - | _ | + | \rightarrow | _ | _ | + | - | _ | _ | _ | _ | _ | _ | + | | _ | - | _ | | | _ | | + | _ | 25 | 0% 0% | _ | 0% | _ | 9% | _ | + | _ | _ | | _ | | + |
| maturation factor 2 Dynam? | DOXAZ MYRE | 35 kDa | - | _ | - | _ | | | \perp | | | | | - | | | _ | | _ | | | | | | | | | 100% | NO. | | 0% | | 0% | | | | | | | | |
| e maturation factor 2 Duces2 ded corecressor-inte Morip1 | MCRI1_MOUSE | 11.kDa | | | | | | | | | | | | | | | | | | 2% | | 10 | 0% | | 0% | | | | | | | | | | | | | | | | |
| ICI Phici | PEDC1 MOUSE | 22 kDs | 100% | 100% 100 | 100.0% | 9% | 9% | 0% 0.0 | 25 05 | 0% | 0% 0.05 | N 100% | 100% | _ | 0% 0% | | 0% | 9% | _ | 4000 | 100 | 66 | | 0% 0.00 | - au | 0% | 0.00 | 25 | 9% | _ | 0% | _ | 9% | _ | + + | _ | _ | | _ | | + |
| ini A-4 protein Swal | SAM MOUSE | 15 kDa | - | 100 | - | _ | | | \perp | | 98 | | | - | | | _ | | _ | 100% | 100% 1000 | N 100.0% | 0% 0% | 9% p.m | 9% 0 | N 095 | 0.0% | | + | | | | + | | | | | | | | |
| 2C1 Ptdc1 ein C-I Apoc1 loid A-4 protein Sas4 ein V19-17 Igk-V19-1 | -17 KVSA1_MOUSE | 16 kDs | | | | | | | | | | | 100 | N . | | 9% | | | 0% | 100% | 100% 100 | ns 100.0% | 0% 0% | 0% 0.05 | 9% 0 | N 0% | 0.0% 1 | 10% | | 9% | | 9% | \perp | | | | | | | | |
| | | | | | 400 OC | | av. | ow | w | - 00 | w | V 400V | - now | w 400.00 | av | - AV | | | av a= | | | | | | | | | | + | _ | | _ | _ | _ | + + | _ | _ | _ | _ | | + |
| cleolide-binding prote Grail 1 231 homolog Bud31 | SUDAY MOUSE | 40 kDs 12 kDs | 100% | 100% 100 | 100.0% | 6% | 9% | 0% 0.0 | 25 05 | 0% | 0% 0.09 | % 100% : | 100% 100 | m 100.0% | 0% 0% | 0% 0.0 | 0% | 0% | 0.0% | 100% | 100% | 66 | 0% | _ | 0% 0 | N | _ | os os | _ | 100% 1000 | | 0% | 0% | _ | | _ | _ | | _ | | + |
| famvlaminecyclotrans Goact | | | | 200 | | | | - | | | viii . | 100% | 100 | 100.01 | 0% | - Wa (0.0 | 0% | | | | 1000 | 06 | | 0% | | 0% | - 1 | 100% | | 0% 0% | | 0% 0% | 0% | | | | | | | | |
| tamvtaminecyclotrans Ggact protein A 32 kDs sub Rps2 | GGACT_MOUSE RFA2_MOUSE FABPL_MOUSE ECP1_MOUSE STARS_MOUSE | 30 kDa 14 kDa 17 kDa 24 kDa 53 kDa 23 kDa 24 kDa | | | | | | | | | | | | | | | | | | 100% | - | | 0% | | 0% | - | - 1 | 10% 100% 10% | | 0% 0% 0% | | 0% | | | | | | | | | |
| binding protein, liver Fabp1 cationic protein 1 Ear1 | FABPL MOUSE | 14 kDs | - | _ | + | | | _ | \perp | | | | _ | _ | | | _ | | _ | 100% | 100% | er 200 000 | 0% 0% | W 5 | 0% 0 | N OF | 0.00 | 100V - | ov 100 ov | au | Ow 1.55 | | ow C'' | 0.00 | | | _ | | | | _ |
| nd lipid transfer protein Sharif | STARS MOVER | 17 KDB 24 kDb | - | _ | + | - | _ | _ | \perp | - | | _ | _ | _ | _ | | _ | | _ | 200% | 100% 1000 | 100.0% | UN 076 | UN 0.09 | 0% 0 | 06 | U.076 D | 100% | um 100.0% | JN 0% | UN. 0.01 | UN. | 0% | 0.0% | | _ | _ | | _ | | |
| oylate transporter 1 Sic15a1 | MOTI_MOUSE SOSDI_MOUSE ERD22_MOUSE | 53 kDs | 100% | | | 0% | | | 0% | | | | | | | | | | | | 100% | | 0% | | | K . | | 10% | | 0% | | 0% | | | | | | | | | |
| domain-containing pro Souldc1 | SOSDI_MOUSE | 23 kDs | $-\epsilon$ | | + | - | | | + | - | | 100% | 100% | + | 0% 0% | - | 0% | 0% | | - | - | | | | | + | | \perp | + | | - | - | \perp | | \perp | | | \rightarrow | | | - |
| prosein-retaining reces Kdelr2 | ERD22_MOUSE | 24 kDs | 1000 | 100 | _ | | _ | ner l | 1 | - | av | _ | _ | _ | _ | _ | + | | _ | - | dis | | 0% | _ | 900 | | _ | + | + | _ | | - | _ | _ | + | _ | _ | | _ | | + |
| gittes Gal historomosthillo seti (G)_ | GALA_MOUSE HAIL_MOUSE | 41 kDs | 100% | 100% | | 0% | 9% | | 98 | 0% | 98 | | | - | | | _ | | _ | 100% | | | 0% | | 0% | + | _ | | + | | | | + | | | | | | | | |
| | | | | _ | \Box | | | _ | | | | _ | | - | | | - | | | 100% | 100% 1009 | ns 100.0% | 0% 0% | 9% 0.05 | 9% 0 | N 0% | 0.0% | | - | | | - | | | | | | | | | - |
| | DCTNS_MOUSE TRYB1_MOUSE | 21 kDs | - | _ | + - | \rightarrow | _ | _ | - | - | _ | | _ | _ | _ | | + | _ | _ | 100% | _ | - | 0% | _ | 9% | - | _ | | _ | | | | _ | _ | _ | | _ | | | | +- |
| ubunit 6 Dictri6 Tpsab1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |