

Supplement 1.

TRANSMEMBRANE PREDICTIONS* IN HUMAN LBR

| TMHMM | SOSUI | PSORT | PROT SCALE | TMAP | TM pred | TOP pred |
|---------|---------|---------|---------------|---------|---------|----------|
| 209-231 | 211-232 | 215-231 | 212-232 | 207-235 | 214-230 | 213-233 |
| 253-275 | 258-280 | 261-277 | 258-278 | 255-283 | 258-276 | 258-278 |
| 296-318 | 295-317 | 298-314 | 299-319 | 294-314 | 296-314 | 297-317 |
| 322-344 | 326-348 | 326-342 | 326-346 | 323-343 | 326-346 | 326-346 |
| | 388-410 | 392-408 | 386-406 | 387-407 | 391-411 | 389-409 |
| 414-436 | 413-435 | 418-434 | | 415-435 | 414-432 | 414-434 |
| 451-470 | 449-471 | 451-467 | 447-467 | 445-473 | 451-476 | 451-471 |
| 482-504 | 483-505 | 485-501 | 481-501 | 483-511 | 481-501 | 481-501 |
| 554-576 | | | 561-581 | 552-580 | 549-570 | 562-582 |

*<http://ca.expasy.org/tools/#pattern>

Supplement 2.

SIMILARITY OF LBR HOMOLOGS TO HUMAN LBR

| Gene / Species | Accession | Match to human LBR ¹ | | | Match to Pfam ² | |
|-----------------|--------------|---------------------------------|----------|---------|----------------------------|-----------|
| | | E value | Identity | Range | LBR_tudor | ERG4_ERG2 |
| LBR | | | | | | |
| Human | NP_919424 | | | | 6e-41 | 5e-221 |
| Mouse | NP_598576 | 0.0 | 79% | 1-615 | 8e-41 | 6e-213 |
| Platypus | XP_001514211 | 0.0 | 77% | 1-615 | 2e-40 | 9e-233 |
| Chicken | NP_990673 | 0.0 | 66% | 1-608 | 2e-41 | 0.0 |
| Frog | NP_001079301 | 2e-159 | 49% | 5-615 | 7e-41 | 1e-151 |
| Fish | CAJ15494 | 6e-170 | 50% | 1-615 | 9e-42 | 7e-170 |
| Sea urchin | XP_786536 | 3e-118 | 41% | 1-615 | 1e-15 | 8e-157 |
| Sea squirt | XP_002126360 | 1e-84 | 32% | 5-615 | 2e-12 | 3e-86 |
| TM7SF2 | | | | | | |
| Human | NP_003264 | 1e-136 | 59% | 207-615 | 0.12 | 3e-175 |
| Mouse | NP_082730 | 5e-136 | 59% | 207-615 | 0.13 | 6e-168 |
| Frog | NP_001079837 | 3e-145 | 61% | 203-615 | 0.64 | 3e-194 |
| Fish | NP_001008597 | 3e-138 | 58% | 203-615 | 0.69 | 2e-188 |
| DHCR7 | | | | | | |
| Human | NP_001351 | 3e-65 | 37% | 262-615 | 0.61 | 2e-85 |
| Mouse | NP_031882 | 3e-66 | 34% | 203-615 | 0.61 | 1e-85 |
| Platypus | XP_001506255 | 3e-73 | 36% | 215-615 | 0.61 | 6e-86 |
| Chicken | XP_420914 | 5e-72 | 33% | 178-612 | 0.61 | 1e-86 |
| Frog | NP_001079586 | 4e-68 | 34% | 203-612 | 0.61 | 3e-89 |
| Fish | NP_958487 | 1e-69 | 34% | 203-615 | 0.55 | 1e-88 |
| Sea urchin | XP_781710 | 3e-70 | 34% | 203-615 | 0.72 | 1e-92 |
| Sea squirt | XP_002127572 | 7e-72 | 36% | 203-615 | 0.44 | 3e-97 |
| Sea | XP_001630468 | 8e-76 | 40% | 260-615 | 0.35 | 2e-107 |
| anemone | | | | | | |
| Fungus | XP_001819932 | 8e-56 | 38% | 262-615 | 0.38 | 1e-62 |
| Plant | AF257178 | 2e-68 | 41% | 247-615 | 0.91 | 3e-72 |
| Drosophila dLBR | CAE54809 | 4e-26 | 24% | 110-615 | 0.44 | 2e-9 |

¹ E value of the match to human LBR, with percent identity to human LBR over the specified range of human LBR, using blastp to the NCBI nr database

² E value of the match to Pfam Hidden Markov Models LBR_tudor (PF09465) and ERG4_ERG24 (PF01222), using hmmpfam