```
> grl = exonsBy(TxDb.Hsapiens.UCSC.hg19.knownGene, "tx", use.names=TRUE); grl
GRangesList of length 82960:
$uc001aaa.3
GRanges with 3 ranges and 3 metadata columns:
      seqnames             ranges strand |   exon_id   exon_name exon_rank
         <Rle>          <IRanges>  <Rle> | <integer> <character> <integer>
  [1]     chr1 [11874, 12227]        + |         1        <NA>         1
  [2]     chr1 [12613, 12721]        + |         3        <NA>         2
  [3]     chr1 [13221, 14409]        + |         5        <NA>         3

$uc010nxq.1
GRanges with 3 ranges and 3 metadata columns:
      seqnames             ranges strand | exon_id exon_name exon_rank
  [1]     chr1 [11874, 12227]        + |       1      <NA>         1
  [2]     chr1 [12595, 12721]        + |       2      <NA>         2
  [3]     chr1 [13403, 14409]        + |       6      <NA>         3

$uc010nxr.1
GRanges with 3 ranges and 3 metadata columns:
      seqnames             ranges strand | exon_id exon_name exon_rank
  [1]     chr1 [11874, 12227]        + |       1      <NA>         1
  [2]     chr1 [12646, 12697]        + |       4      <NA>         2
  [3]     chr1 [13221, 14409]        + |       5      <NA>         3

...
<82957 more elements>
---
 seqinfo: 93 sequences (1 circular) from hg19 genome
```

GRangesList
  (list of GRanges)
  length(grl)
  grl[1:3]
  shift(grl, 1)
  range(grl)

GRanges
  grl[[2]]
  grl[["uc010nxq.1"]]

Two kinds of fun!
  introns =
    psetdiff(range(grl), grl)

  grr = unlist(grl)
  ## transform grr, then...
  grl = relist(grr, grl)

'flesh'   'skeleton'