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SPIOL MTSSCLLSSTRNTT----ATTTAAAASYLPKHHYHHHLPLFKLQLPPLKS    46
ARATH MTLPYRFSSVRNHSLLLKTSHLCTPRSALGCCFSPKESPFFRKNTAQFLS    50
                      ⇓
SPIOL SHPILRLRNNSRFTYPLASLSSFADADGQE-HEEDVINADDHR-------    88
ARATH PQKHTSLP--LKLVCPLASFSSYADSEGEEQHHADQPIQNPHESSTVSNE    98

SPIOL -DDEGGA-----KSGMAQAFNISSKTAVAISVCIACAALTFPFFMKSIGQ   132
ARATH SDGKGNAEATGDFSGMAQAFHISSTTARAISIVIAFSALTLPIFMKSLGQ   148

SPIOL GMPFKTRVLSYVTLLFGFYMAWNIGANDVANAMGTSVGSGALTIRQAVLT   182
ARATH GLALKTKLLSYATLLFGFYMAWNIGANDVANAMGTSVGSGALTIRQAVMT   198

SPIOL AAVLEFSGALLMGTHVTSTMQKGILVANVFQGKDSLLFAGLLSSLAAAGT   232
ARATH AAVLEFSGALLMGTHVTSTMQKGILMANVFQGKDMLLFAGLLSSLAAAGT   248

SPIOL WLQVASYYGWPVSTTHCIVGSMVGFGLVYGGVNAVFWSSLAKVASSWIFS   282
ARATH WLQVASYYGWPVSTTHCIVGSMVGFGLVYGGAGAVFWSSLAKVASSWVIS   298

SPIOL PVLGAAMSFLVYKGIRRFVYSAENPGQAAAAAAPVAVFMGVTAISFAAFP   332
ARATH PILGALVSFLVYKCIRRFVYSAPNPGQAAAAAAPVAVFVGVASISSAALP   348

SPIOL LSKTLPLAIVQALACGAIGAVIVYRVINIQLGHLLAKSKTQHKDEPNPDN   382
ARATH LSKIFPIALSQALACGVAGAIVFDRIIRKQLGHLLAKTKSPETSQNQP--   396

SPIOL PEQKNIGLLSDIAGPKGTQLEIVYGVFGYMQVLSACFMSFAHGGNDVSNA   432
ARATH ---KTIGFLSDIAGPTGTQLEIVYGIFGYMQVLSACFMSFAHGGNDVSNA   443

SPIOL IGPLAAALSLLQVGAGSGAA-IQIPIDVLAWGGFGIVAGLMMWGYRVIST   481
ARATH IGPLAAALSILQNGAAAGGAEIVIPMDVLAWGGFGIVAGLTMWGYRVIAT   493

SPIOL IGKKITELTPTRGFAAEFAAASVVLFASKLGLPISATHTLVGAVMGVGFA   531
ARATH IGKKITELTPTRGFAAEFAAASVVLFASKLGLPISATHTLVGAVMGVGFA   543

SPIOL RGLNSVRAETVREIVTSWAVTIPVGGVLAVLYTAILTKGLSYVL         575
ARATH RGLNSVRAETVREIVASWLVTIPVGATLAVIYTWIFTKILSFVL         587
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