

---

# Nucleic Acids Research

---

## Contents

Volume 35 number 16

---

### COMPUTATIONAL BIOLOGY

- M* A survey of bacterial insertion sequences using IScan A.Wagner, C.Lewis and M.Bichsel 5284–5293
- S, M* A systematic strategy for large-scale analysis of genotype–phenotype correlations: identification of candidate genes involved in African trypanosomiasis P.Fisher, C.Hedeler, K.Wolstencroft, H.Hulme, H.Noyes, S.Kemp, R.Stevens and A.Brass 5625–5633

### GENOMICS

- S* Does distance matter? Variations in alternative 3' splicing regulation M.Akerman and Y.Mandel-Gutfreund 5487–5498

### MOLECULAR BIOLOGY

- S* Correlation between binding rate constants and individual information of *E. coli* Fis binding sites R.K.Shultzaberger, L.R.Roberts, I.G.Lyakhov, I.A.Sidorov, A.G.Stephen, R.J.Fisher and T.D.Schneider 5275–5283
- S* Phospho-epitope binding by the BRCT domains of hPTIP controls multiple aspects of the cellular response to DNA damage I.M.Munoz, P.A.Jowsey, R.Toth and J.Rouse 5312–5322
- Cdc18/CDC6 activates the Rad3-dependent checkpoint in the fission yeast N.Fersht, D.Hermand, J.Hayles and P.Nurse 5323–5337
- S* Ubiquitylation-independent degradation of Xeroderma pigmentosum group C protein is required for efficient nucleotide excision repair Q.-E.Wang, M.Prætorius-Ibba, Q.Zhu, M.A.El-Mahdy, G.Wani, Q.Zhao, S.Qin, S.Patnaik and A.A.Wani 5338–5350
- A persistent RNA·DNA hybrid formed by transcription of the Friedreich ataxia triplet repeat in live bacteria, and by T7 RNAP *in vitro* E.Grabczyk, M.Mancuso and M.C.Sammarco 5351–5359
- Protein p56 from the *Bacillus subtilis* phage  $\phi$ 29 inhibits DNA-binding ability of uracil-DNA glycosylase G.Serrano-Heras, J.A.Ruiz-Masó, G.del Solar, M.Espinosa, A.Bravo and M.Salas 5393–5401
- S* MeCP2 interacts with HP1 and modulates its heterochromatin association during myogenic differentiation N.Agarwal, T.Hardt, A.Brero, D.Nowak, U.Rothbauer, A.Becker, H.Leonhardt and M.C.Cardoso 5402–5408
- S* Biochemical reconstitution of abasic DNA lesion replication in *Xenopus* extracts S.Liao, Y.Matsumoto and H.Yan 5422–5429
- S* Repeat-associated siRNAs cause chromatin silencing of retrotransposons in the *Drosophila melanogaster* germline M.S.Klenov, S.A.Lavrov, A.D.Stolyarenko, S.S.Ryazansky, A.A.Aravin, T.Tuschl and V.A.Gvozdev 5430–5438
- Protein/DNA arrays identify nitric oxide-regulated *cis*-element and *trans*-factor activities some of which govern neuroblastoma cell viability S.Dhakshinamoorthy, S.R.Sridharan, L.Li, P.Y.Ng, L.M.Boxer and A.G.Porter 5439–5451

*Continued*

|                             |  |   |           |
|-----------------------------|--|---|-----------|
|                             | Hairpin structure within the 3'UTR of DNA polymerase $\beta$ mRNA acts as a post-transcriptional regulatory element and interacts with Hax-1         | E.Sarnowska, E.A.Grzybowska, K.Sobczak, R.Konopiński, A.Wilczyńska, M.Szwarc, T.J.Sarnowski, W.J.Krzyżosiak and J.A.Siedlecki | 5499–5510 |
|                             | $\beta$ -Catenin binds to the downstream region and regulates the expression C-reactive protein gene   | Y.S.Choi, J.Hur and S.Jeong   | 5511–5519 |
| <i>S</i>                    | Tup1-Ssn6 and Swi-Snf remodelling activities influence long-range chromatin organization upstream of the yeast <i>SUC2</i> gene                      | A.B.Fleming and S.Pennings  | 5520–5531 |
| <i>S</i>                    | A facilitated tracking and transcription mechanism of long-range enhancer function   | X.Zhu, J.Ling, L.Zhang, W.Pi, M.Wu and D.Tuan   | 5532–5544 |
|                             | Defective DNA base excision repair in brain from individuals with Alzheimer's disease and amnesic mild cognitive impairment                          | L.Weissman, D.-G.Jo, M.M.Sørensen, N.C.de Souza-Pinto, W.R.Markesbery, M.P.Mattson and V.A.Bohr                               | 5545–5555 |
| <i>S</i>                    | The PMC2NT domain of the catalytic exosome subunit Rrp6p provides the interface for binding with its cofactor Rrp47p, a nucleic acid-binding protein | J.A.Stead, J.L.Costello, M.J.Livingstone and P.Mitchell   | 5556–5567 |
| <b>NUCLEIC ACID ENZYMES</b> |  |   |           |
| <i>S</i>                    | T4 DNA ligase is more than an effective trap of cyclized dsDNA   | C.Yuan, X.W.Lou, E.Rhoades, H.Chen and L.A.Archer   | 5294–5302 |
|                             | DNA polymerase proofreading: active site switching catalyzed by the bacteriophage T4 DNA polymerase  | E.Fidalgo da Silva and L.J.Reha-Krantz  | 5452–5463 |
| <i>S</i>                    | A randomized library approach to identifying functional <i>lox</i> site domains for the Cre recombinase  | J.Sheren, S.J.Langer and L.A.Leinwand   | 5464–5473 |
| <b>RNA</b>                  |  |   |           |
|                             | Tissue-specific splicing regulator Fox-1 induces exon skipping by interfering E complex formation on the downstream intron of human F1 $\gamma$ gene | K.Fukumura, A.Kato, Y.Jin, T.Ideue, T.Hirose, N.Kataoka, T.Fujiwara, H.Sakamoto and K.Inoue                                   | 5303–5311 |
| <i>S</i>                    | Fluorescent probing for RNA molecules by an unnatural base-pair system   | M.Kimoto, T.Mitsui, Y.Harada, A.Sato, S.Yokoyama and I.Hirao  | 5360–5369 |
| <i>S</i>                    | Ligand-induced folding of the <i>thiM</i> TPP riboswitch investigated by a structure-based fluorescence spectroscopic approach                       | K.Lang, R.Rieder and R.Micura   | 5370–5378 |
| <i>S</i>                    | Interactions of the G quartet forming semaphorin 3F RNA with the RGG box domain of the fragile X protein family                                      | L.Menon and M.-R.Mihailescu   | 5379–5392 |
|                             | Translational control of the interferon regulatory factor 2 mRNA by IRES element   | D.Dhar, S.Roy and S.Das   | 5409–5421 |
| <i>S</i>                    | Muscleblind-like 1 interacts with RNA hairpins in splicing target and pathogenic RNAs  | Y.Yuan, S.A.Compton, K.Sobczak, M.G.Stenberg, C.A.Thornton, J.D.Griffith and M.S.Swanson                                      | 5474–5486 |
| <i>S</i>                    | Ligand recognition determinants of guanine riboswitches  | J.Mulhbachter and D.A.Lafontaine  | 5568–5580 |
|                             | The three transfer RNAs occupying the A, P and E sites on the ribosome are involved in viral programmed -1 ribosomal frameshift                      | M.Léger, D.Dulude, S.V.Steinberg and L.Brakier-Gingras  | 5581–5592 |

*Continued*

|                       |  |   |               |
|-----------------------|--|---|---------------|
| <i>M</i>              | <b><i>In silico</i> detection of tRNA sequence features characteristic to aminoacyl-tRNA synthetase class membership</b>   | É.Jakó, P.Ittzés, Á.Szenes, Á.Kun, E.Szathmáry and G.Pál  | 5593–5609     |
| <i>S</i>              | <b>Identification of determinants in the protein partners aCBF5 and aNOP10 necessary for the tRNA:Ψ55-synthase and RNA-guided RNA:Ψ-synthase activities</b>                                      | S.Müller, J.-B.Fourmann, C.Loegler, B.Charpentier and C.Branlant  | 5610–5624     |
| <b>METHODS ONLINE</b> |  |   |               |
|                       | <b>Thermodynamically modulated partially double-stranded linear DNA probe design for homogeneous real-time PCR</b>   | S.Huang, J.Salituro, N.Tang, K.-C.Luk, J.Hackett Jr, P.Swanson, G.Cloherly, W.-B.Mak, J.Robinson and K.Abravaya | e101 (12 pp.) |
| <i>S</i>              | <b>Filtering genes to improve sensitivity in oligonucleotide microarray data analysis</b>  | S.Calza, W.Raffelsberger, A.Plöner, J.Sahel, T.Levellard and Y.Pawitan  | e102 (10 pp.) |
| <i>S</i>              | <b>High-precision mapping of protein–protein interfaces: an integrated genetic strategy combining <i>en masse</i> mutagenesis and DNA-level parallel analysis on a yeast two-hybrid platform</b> | M.Pajunen, H.Turakainen, E.Poussu, J.Peränen, M.Vihinen and H.Savilahti   | e103 (11 pp.) |
|                       | <b>One step construction of PCR mutagenized libraries for genetic analysis by recombination cloning</b>  | A.-M.Khalil, J.A.Julius and J.Bachant   | e104 (12 pp.) |
| <i>S</i>              | <b>Avoiding false-positive signals with nuclease-vulnerable molecular beacons in single living cells</b>   | A.K.Chen, M.A.Behlke and A.Tsourkas   | e105 (12 pp.) |
|                       | <b>Choreography for nucleosomes: the conformational freedom of the nucleosomal filament and its limitations</b>  | M.Engelhardt  | e106 (15 pp.) |
|                       | <b>Live cell imaging of repetitive DNA sequences via GFP-tagged polydactyl zinc finger proteins</b>  | B.I.Lindhout, P.Fransz, F.Tessadori, T.Meckel, P.J.J.Hooykaas and B.J.van der Zaal                              | e107 (9 pp.)  |

*M*, contains a novel method

*S*, Supplementary Material available at NAR Online