

---

# Nucleic Acids Research

---

## Contents

Volume 35 number 18

---

### SURVEY AND SUMMARY

- DNA sequencing: bench to bedside and beyond C.A.Hutchison III 6227–6237

### GENOMICS

- S* Differentiation of core promoter architecture between plants and mammals revealed by LDSS analysis Y.Y.Yamamoto, H.Ichida, T.Abe, Y.Suzuki, S.Sugano and J.Obokata 6219–6226
- S* High-affinity DNA binding sites for H-NS provide a molecular basis for selective silencing within proteobacterial genomes B.Lang, N.Blot, E.Bouffartigues, M.Buckle, M.Geertz, C.O.Gualerzi, R.Mavathur, G.Muskhelishvili, C.L.Pon, S.Rimsky, S.Stella, M.M.Babu and A.Travers 6330–6337

### MOLECULAR BIOLOGY

- siRNA-dependent and -independent post-transcriptional cosuppression of the LTR-retrotransposon MAGGY in the phytopathogenic fungus *Magnaporthe oryzae* T.Murata, N.Kadotani, M.Yamaguchi, Y.Tosa, S.Mayama and H.Nakayashiki 5987–5994
- S* Tip60 functions as a potential corepressor of KLF4 in regulation of HDC promoter activity W.Ai, H.Zheng, X.Yang, Y.Liu and T.C.Wang 6137–6149
- The Mediator subunit MED1/TRAP220 is required for optimal glucocorticoid receptor-mediated transcription activation W.Chen and R.G.Roeder 6161–6169
- Tryptophane-205 of human topoisomerase I is essential for camptothecin inhibition of negative but not positive supercoil removal R.F.Fröhlich, C.Veigaard, F.F.Andersen, A.K.McClendon, A.C.Gentry, A.H.Andersen, N.Osheroff, T.Stevnsner and B.R.Knudsen 6170–6180
- Dynamic interactions within sub-complexes of the H/ACA pseudouridylation guide RNP O.A.Youssef, R.M.Terns and M.P.Terns 6196–6206
- S* The *Arabidopsis* homologs of trithorax (ATX1) and enhancer of zeste (CLF) establish ‘bivalent chromatin marks’ at the silent *AGAMOUS* locus A.Saleh, A.Al-Abdallat, I.Ndamukong, R.Alvarez-Venegas and Z.Avrarova 6290–6296
- S* Acetylation increases access of remodelling complexes to their nucleosome targets to enhance initiation of V(D)J recombination K.P.Nightingale, M.Baumann, A.Eberharter, A.Mamais, P.B.Becker and J.Boyes 6311–6321

### NUCLEIC ACID ENZYMES

- An archaeal orthologue of the universal protein Kae1 is an iron metalloprotein which exhibits atypical DNA-binding properties and apurinic-endonuclease activity *in vitro* A.Hecker, N.Leulliot, D.Gadelle, M.Graille, A.Justome, P.Dorlet, C.Brochier, S.Quevillon-Cheruel, E.Le Cam, H.van Tilbeurgh and P.Forterre 6042–6051

*Continued*

<i>S</i>	Fluorescence of 2-aminopurine reveals rapid conformational changes in the RB69 DNA polymerase-primer/template complexes upon binding and incorporation of matched deoxynucleoside triphosphates	H.Zhang, W.Cao, E.Zakharova, W.Konigsberg and E.M.De La Cruz	6052–6062
	Hot-spot consensus of fluoroquinolone-mediated DNA cleavage by Gram-negative and Gram-positive type II DNA topoisomerases	S.N.Richter, G.Giaretta, V.Comuzzi, E.Leo, L.A.Mitchenall, L.M.Fisher, A.Maxwell and M.Palumbo	6075–6085
	An aminoacyl-tRNA synthetase:elongation factor complex for substrate channeling in archaeal translation	C.D.Hausmann, M.Prætorius-Ibba and M.Ibba	6094–6102
	The hSNM1 protein is a DNA 5'-exonuclease	J.Hejna, S.Philip, J.Ott, C.Faulkner and R.Moses	6115–6123
<i>S</i>	Chaperone activation of the hepadnaviral reverse transcriptase for template RNA binding is established by the Hsp70 and stimulated by the Hsp90 system	M.Stahl, M.Retzlaff, M.Nassal and J.Beck	6124–6136
<i>S</i>	The human checkpoint sensor Rad9–Rad1–Hus1 interacts with and stimulates DNA repair enzyme TDG glycosylase	X.Guan, A.Madabushi, D.-Y.Chang, M.E.Fitzgerald, G.Shi, A.C.Drohatsky and A.-L.Lu	6207–6218
	Catalytic domain of restriction endonuclease BmrI as a cleavage module for engineering endonucleases with novel substrate specificities	S.-h.Chan, Y.Bao, E.Ciszak, S.Laget and S.-y.Xu	6238–6248
<i>S</i>	Structure-function study of maize ribosome-inactivating protein: implications for the internal inactivation region and the sole glutamate in the active site	A.N.-S.Mak, Y.-T.Wong, Y.-J.An, S.-S.Cha, K.-H.Sze, S.W.-N.Au, K.-B.Wong and P.-C.Shaw	6259–6267
	Structural and functional analyses of disease-causing missense mutations in Bloom syndrome protein	R.-B.Guo, P.Rigolet, H.Ren, B.Zhang, X.-D.Zhang, S.-X.Dou, P.-Y.Wang, M.Amor-Gueret and X.G.Xi	6297–6310
<b>RNA</b>			
<i>S</i>	<i>In vitro</i> and <i>in silico</i> analysis reveals an efficient algorithm to predict the splicing consequences of mutations at the 5' splice sites	K.Sahashi, A.Masuda, T.Matsuura, J.Shinmi, Z.Zhang, Y.Takeshima, M.Matsuo, G.Sobue and K.Ohno	5995–6003
<i>S</i>	Stabilization of SMAR1 mRNA by PGA2 involves a stem-loop structure in the 5' UTR	L.Pavithra, S.Rampalli, S.Sinha, K.Sreenath, R.G.Pestell and S.Chattopadhyay	6004–6016
<i>S</i>	A specific role for the C-terminal region of the Poly(A)-binding protein in mRNA decay	E.Simón and B.Séraphin	6017–6028
<i>S</i>	Engineering the rRNA decoding site of eukaryotic cytosolic ribosomes in bacteria	S.N.Hobbie, S.K.Kalapala, S.Akshay, C.Bruell, S.Schmidt, S.Dabow, A.Vasella, P.Sander and E.C.Böttger	6086–6093
<i>S</i>	Pseudoknot structures with conserved base triples in telomerase RNAs of ciliates	N.B.Ulyanov, K.Shefer, T.L.James and Y.Tzfati	6150–6160
<i>S</i>	Novel rapidly evolving hominid RNAs bind nuclear factor 90 and display tissue-restricted distribution	A.M.Parrott and M.B.Mathews	6249–6258
	Deletion of the nuclear exosome component RRP6 leads to continued accumulation of the histone mRNA HTB1 in S-phase of the cell cycle in <i>Saccharomyces cerevisiae</i>	R.Canavan and U.Bond	6268–6279
<i>S</i>	A critical three-way junction is conserved in budding yeast and vertebrate telomerase RNAs	Y.Brown, M.Abraham, S.Pearl, M.M.Kabaha, E.Elboher and Y.Tzfati	6280–6289

*Continued*

<i>S, M</i>	Identification of recognition residues for ligation-based detection and quantitation of pseudouridine and <i>N</i> <sup>6</sup> -methyladenosine	Q.Dai, R.Fong, M.Saikia, D.Stephenson, Y.-t.Yu, T.Pan and J.A.Piccirilli	6322–6329
<b>STRUCTURAL BIOLOGY</b>			
	The arginine finger of the Bloom syndrome protein: its structural organization and its role in energy coupling	H.Ren, S.-X.Dou, P.Rigolet, Y.Yang, P.-Y.Wang, M.Amor-Gueret and X.G.Xi	6029–6041
<i>S</i>	Sequence-dependent DNA deformability studied using molecular dynamics simulations	S.Fujii, H.Kono, S.Takenaka, N.Go and A.Sarai	6063–6074
<i>S</i>	NMR structure of a kissing complex formed between the TAR RNA element of HIV-1 and a LNA-modified aptamer	I.Lebars, T.Richard, C.Di Primo and J.-J.Toulmé	6103–6114
<i>S</i>	A study of 7-deaza-2'-deoxyguanosine-2'-deoxycytidine base pairing in DNA	M.Ganguly, F.Wang, M.Kaushik, M.P.Stone, L.A.Marky and B.Gold	6181–6195
<b>CORRIGENDUM</b>			6338
<b>METHODS ONLINE</b>			
	Sequence specific detection of DNA using nicking endonuclease signal amplification (NESA)	T.Kiesling, K.Cox, E.A.Davidson, K.Dretchen, G.Grater, S.Hibbard, R.S.Lasken, J.Leshin, E.Skowronski and M.Danielsen	e117 (9 pp.)
<i>S</i>	A <i>UTF1</i> -based selection system for stable homogeneously pluripotent human embryonic stem cell cultures	S.M.Tan, S.T.Wang, H.Hentze and P.Dröge	e118 (9 pp.)
<i>S</i>	Genomic profiling of CpG methylation and allelic specificity using quantitative high-throughput mass spectrometry: critical evaluation and improvements	M.W.Coolen, A.L.Statham, M.Gardiner-Garden and S.J.Clark	e119 (14 pp.)
	Short pyrosequencing reads suffice for accurate microbial community analysis	Z.Liu, C.Lozone, M.Hamady, F.D.Bushman and R.Knight	e120 (10 pp.)
	Back to basics: the untreated rabbit reticulocyte lysate as a competitive system to recapitulate cap/poly(A) synergy and the selective advantage of IRES-driven translation	R.S.Rifo, E.P.Ricci, D.Décimo, O.Moncorgé and T.Ohlmann	e121 (9 pp.)
	SAGETTARIUS: a program to reduce the number of tags mapped to multiple transcripts and to plan SAGE sequencing stages	L.Bianchetti, Y.Wu, E.Guerin, F.Plewniak and O.Poch	e122 (12 pp.)
<i>S</i>	Thermodynamic instability of siRNA duplex is a prerequisite for dependable prediction of siRNA activities	M.Ichihara, Y.Murakumo, A.Masuda, T.Matsuura, N.Asai, M.Jijiwa, M.Ishida, J.Shinmi, H.Yatsuya, S.Qiao, M.Takahashi and K.Ohno	e123 (10 pp.)
<i>S</i>	Surveillance of siRNA integrity by FRET imaging	A.Järve, J.Müller, I.-H.Kim, K.Rohr, C.MacLean, G.Fricker, U.Massing, F.Eberle, A.Dalpke, R.Fischer, M.F.Trendelenburg and M.Helm	e124 (13 pp.)

*M*, contains a novel method

*S*, Supplementary Material available at NAR Online