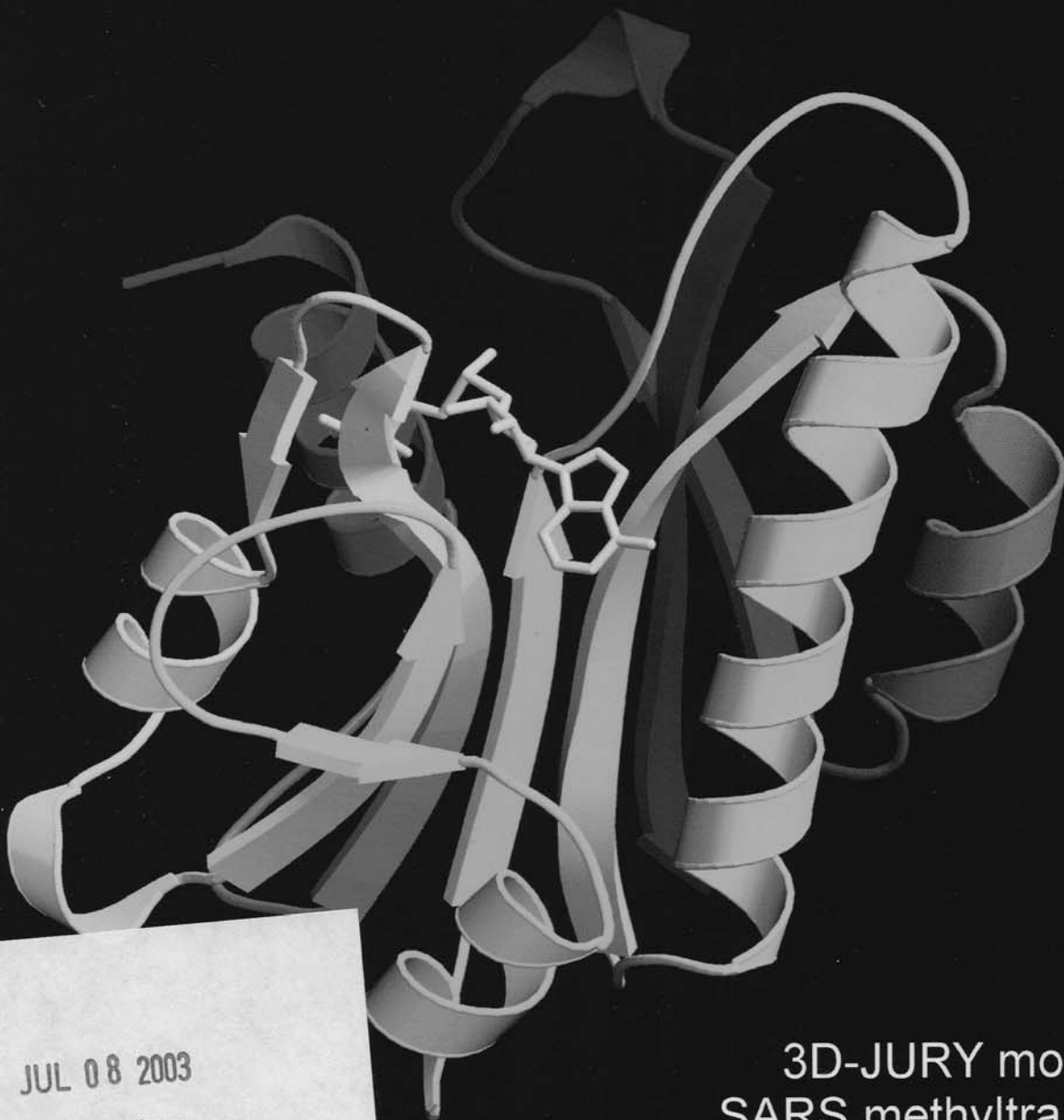


Nucleic Acids Research



JUL 08 2003

Science Library
University of California
Riverside

3D-JURY model of
SARS methyltransferase

OXFORD UNIVERSITY PRESS

DOCKET
ALARM

Find authenticated court documents without watermarks at docketalarm.com.

Subscriptions

Nucleic Acids Research is published twice monthly (24 issues per year). Subscriptions are entered on a calendar year basis only and are available as a printed version (including online access) or as online access only at a discount of 10% (+VAT in UK). Prices include postage by surface mail or, for subscribers in the USA and Canada by air freight, or in India, Japan, Australia and New Zealand, by Air Speeded Post. Airmail rates are available on request.

Annual subscription rate (Volume 31, 2003):

Institutional

Print and Online site licence: UK and Europe £1365, Rest of World \$2360.

Personal

Print and Online: UK and Europe £365, Rest of World \$621.

Back volume prices are available on request. Please add sales tax to the prices quoted.

Orders. Orders and payments from, or on behalf of, subscribers in the various geographical areas shown below should be sent to the Press office indicated.

The Americas: Oxford University Press Inc., 2001 Evans Road, Cary, NC 27513, USA.

Rest of the World: Journals Subscriptions Department, Oxford University Press, Great Clarendon Street, Oxford OX2 6DP, UK.

Tel: (+441865 or 01865) 353907; Fax: (+441865) 353485;

Email: jnl.orders@oup.co.uk

Advertising. To advertise in *Nucleic Acids Research* contact Oxford University Press (US office) in the Americas or Oxford University Press (UK office) in the Rest of the World (see addresses above).

© Oxford University Press 2003. All rights reserved; no part of this publication may be reproduced, stored in a retrieval system, or transmitted in any form or by any means, electronic, mechanical, photocopying, recording, or otherwise without either prior written permission of the Publishers, or a licence permitting restricted copying issued in the UK by the Copyright Licensing Agency Ltd, 90 Tottenham Court Road, London W1P 9HE, or in the USA by the Copyright Clearance Center, 222 Rosewood Drive, Danvers, MA 01923, USA.

Back volumes of this journal are available in 16 mm microfilm, 35 mm microfilm and 105 microfiche from University Microfilms International, 300 North Zeeb Road, Ann Arbor, MI 48106-1346, USA. Copies of articles published are also available from UMI.

Nucleic Acids Research (ISSN 0305-1048) is published twice monthly by Oxford University Press, Oxford, UK. Annual subscription price is US\$2360. *Nucleic Acids Research* is distributed by Mercury International, 365 Blair Road, Avenel, NJ 07001, USA. Periodicals Postage Paid at Rahway, NJ, USA and additional entry points.

US POSTMASTER: send address corrections to *Nucleic Acids Research*, c/o Mercury Airfreight International Ltd, 365 Blair Road, Avenel, NJ 07001, USA.

Typeset and printed by Information Press Ltd, Oxford, UK on acid-free paper.

Nucleic Acids Research

Contents

Volume 31 number 13, July 1, 2003

EDITORIAL		3289
Detection of reliable and unexpected protein fold predictions using 3D-Jury	K.Ginalski and L.Rychlewski	3291–3292
DSSPcont: continuous secondary structure assignments for proteins	P.Carter, C.A.F.Andersen and B.Rost	3293–3295
PROTINFO: secondary and tertiary protein structure prediction	L.-H.Hung and R.Samudrala	3296–3299
The PredictProtein server	B.Rost and J.Liu	3300–3304
GeneSilico protein structure prediction meta-server	M.A.Kurowski and J.M.Bujnicki	3305–3307
META-PP: single interface to crucial prediction servers	V.A.Eyrich and B.Rost	3308–3310
EVA: evaluation of protein structure prediction servers	I.Y.Y.Koh, V.A.Eyrich, M.A.Marti-Renom, D.Przybylski, M.S.Madhusudhan, N.Eswar, O.Graña, F.Pazos, A.Valencia, A.Sali and B.Rost	3311–3315
VADAR: a web server for quantitative evaluation of protein structure quality	L.Willard, A.Ranjan, H.Zhang, H.Monzavi, R.F.Boyko, B.D.Sykes and D.S.Wishart	3316–3319
ESPrint/ENDscript: extracting and rendering sequence and 3D information from atomic structures of proteins	P.Gouet, X.Robert and E.Courcelle	3320–3323
WebFEATURE: an interactive web tool for identifying and visualizing functional sites on macromolecular structures	M.P.Liang, D.R.Banatao, T.E.Klein, D.L.Brutlag and R.B.Altman	3324–3327
3MATRIX and 3MOTIF: a protein structure visualization system for conserved sequence motifs	S.P.Bennett, L.Lu and D.L.Brutlag	3328–3332
Motif3D: relating protein sequence motifs to 3D structure	A.Gaulton and T.K.Attwood	3333–3336
LOC3D: annotate sub-cellular localization for protein structures	R.Nair and B.Rost	3337–3340
Annotation in three dimensions. PINTS: Patterns in Non-homologous Tertiary Structures	A.Stark and R.B.Russell	3341–3344
NCI: a server to identify non-canonical interactions in protein structures	M.M.Babu	3345–3348
MolSurfer: a macromolecular interface navigator	R.R.Gabdoulline, R.C.Wade and D.Walther	3349–3351
CASTp: Computed Atlas of Surface Topography of	T.A.Binkowski, S.Naghizadeh and J.Liang	3352–3355

SEM (Symmetry Equivalent Molecules): a web-based GUI to generate and visualize the macromolecules	A.S.Z.Hussain, Ch.K.Kumar, C.K.Rajesh, S.S.Sheik and K.Sekar	3356–3358
Servers for sequence–structure relationship analysis and prediction	Z.Dosztányi, C.Magyar, G.E.Tusnády, M.Cserző, A.Fiser and I.Simon	3359–3363
POPS: a fast algorithm for solvent accessible surface areas at atomic and residue level	L.Cavallo, J.Kleinjung and F.Fraternali	3364–3366
MATRAS: a program for protein 3D structure comparison	T.Kawabata	3367–3369
LGA: a method for finding 3D similarities in protein structures	A.Zemla	3370–3374
Tools for comparative protein structure modeling and analysis	N.Eswar, B.John, N.Mirkovic, A.Fiser, V.A.Ilyin, U.Pieper, A.C.Stuart, M.A.Marti-Renom, M.S.Madhusudhan, B.Yerkovich and A.Sali	3375–3380
SWISS-MODEL: an automated protein homology-modeling server	T.Schwede, J.Kopp, N.Guex and M.C.Peitsch	3381–3385
STING Millennium: a web-based suite of programs for comprehensive and simultaneous analysis of protein structure and sequence	G.Neshich, R.C.Togawa, A.L.Mancini, P.R.Kuser, M.E.B.Yamagishi, G.Pappas Jr, W.V.Torres, T.F.eCampos, L.L.Ferreira, F.M.Luna, A.G.Oliveira, R.T.Miura, M.K.Inoue, L.G.Horita, D.F.de Souza, F.Dominiquini, A.Álvaro, C.S.Lima, F.O.Ogawa, G.B.Gomes, J.F.Palandrani, G.F.dos Santos, E.M.de Freitas, A.R.Mattiuz, I.C.Costa, C.L.de Almeida, S.Souza, C.Baudet and R.H.Higa	3386–3392
Integrated databanks access and sequence/structure analysis services at the PBIL	G.Perrière, C.Combet, S.Penel, C.Blanchet, J.Thioulouse, C.Geourjon, J.Grassot, C.Charavay, M.Gouy, L.Duret and G.Deléage	3393–3399
NRSAS: Nuclear Receptor Structure Analysis Servers	E.Bettler, R.Krause, F.Horn and G.Vriend	3400–3403
SSEP: secondary structural elements of proteins	V.Shanthi, P.Selvarani, Ch.K.Kumar, C.S.Mohire and K.Sekar	3404–3405
S Mfold web server for nucleic acid folding and hybridization prediction	M.Zuker	3406–3415
RNAsoft: a suite of RNA secondary structure prediction and design software tools	M.Andronescu, R.Aguirre-Hernández, A.Condon and H.H.Hoos	3416–3422
S Pfold: RNA secondary structure prediction using stochastic context-free grammars	B.Knudsen and J.Hein	3423–3428
Vienna RNA secondary structure server	I.L.Hofacker	3429–3431
PSEUDOVIEWER2: visualization of RNA pseudoknots of any type	K.Han and Y.Byun	3432–3440
A software tool-box for analysis of regulatory RNA elements	P.Bengert and T.Dandekar	3441–3445

Tools for the automatic identification and classification of RNA base pairs	H.Yang, F.Jossinet, N.Leontis, L.Chen, J.Westbrook, H.Berman and E.Westhof	3450–3460
GEPAS: a web-based resource for microarray gene expression data analysis	J.Herrero, F.Al-Shahrour, R.Díaz-Uriarte, A.Mateos, J.M.Vaquerizas, J.Santoyo and J.Dopazo	3461–3467
INCLUSive: a web portal and service registry for microarray and regulatory sequence analysis	B.Coessens, G.Thijs, S.Aerts, K.Marchal, F.De Smet, K.Engelen, P.Glenisson, Y.Moreau, J.Mathys and B.De Moor	3468–3470
GenePublisher: automated analysis of DNA microarray data	S.Knudsen, C.Workman, T.Sicheritz-Ponten and C.Friis	3471–3476
ExpressYourself: a modular platform for processing and visualizing microarray data	N.M.Luscombe, T.E.Royce, P.Bertone, N.Echols, C.E.Horak, J.T.Chang, M.Snyder and M.Gerstein	3477–3482
ChipInfo: software for extracting gene annotation and gene ontology information for microarray analysis	S.Zhong, C.Li and W.H.Wong	3483–3486
REDUCE: an online tool for inferring <i>cis</i>-regulatory elements and transcriptional module activities from microarray data	C.Roven and H.J.Bussemaker	3487–3490
Design of oligonucleotides for microarrays and perspectives for design of multi-transcriptome arrays	H.B.Nielsen, R.Wernersson and S.Knudsen	3491–3496
Multiple sequence alignment with the Clustal series of programs	R.Chenna, H.Sugawara, T.Koike, R.Lopez, T.J.Gibson, D.G.Higgins and J.D.Thompson	3497–3500
CLOURE: Clustal Output Reformatter, a program for reformatting ClustalX/ClustalW outputs for SNP analysis and molecular systematics	D.K.Kohli and A.K.Bachhawat	3501–3502
Tcoffee@igs: a web server for computing, evaluating and combining multiple sequence alignments	O.Poirot, E.O'Toole and C.Notredame	3503–3506
SLAM web server for comparative gene finding and alignment	S.Cawley, L.Pachter and M.Alexandersson	3507–3509
Theatre: a software tool for detailed comparative analysis and visualization of genomic sequence	Y.J.K.Edwards, T.J.Carver, T.Vavouri, M.Frith, M.J.Bishop and G.Elgar	3510–3517
MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences	S.Schwartz, L.Elnitski, M.Li, M.Weirauch, C.Riemer, A.Smit, NISC Comparative Sequencing Program, E.D.Green, R.C.Hardison and W.Miller	3518–3524
MAVID multiple alignment server	N.Bray and L.Pachter	3525–3526
EnteriX 2003: visualization tools for genome alignments of Enterobacteriaceae	L.Florea, M.McClelland, C.Riemer, S.Schwartz and W.Miller	3527–3532
MGAlignIt: a web service for the alignment of mRNA/EST and genomic sequences	B.T.K.Lee, T.W.Tan and S.Ranganathan	3533–3536
RevTrans: multiple alignment of coding DNA from aligned amino acid sequences	R.Wernersson and A.G.Pedersen	3537–3539
PromH: promoters identification using orthologous	V.V.Solovvev and I.A.Shahmuradov	3540–3545

Explore Litigation Insights

Docket Alarm provides insights to develop a more informed litigation strategy and the peace of mind of knowing you're on top of things.

Real-Time Litigation Alerts



Keep your litigation team up-to-date with **real-time alerts** and advanced team management tools built for the enterprise, all while greatly reducing PACER spend.

Our comprehensive service means we can handle Federal, State, and Administrative courts across the country.

Advanced Docket Research



With over 230 million records, Docket Alarm's cloud-native docket research platform finds what other services can't. Coverage includes Federal, State, plus PTAB, TTAB, ITC and NLRB decisions, all in one place.

Identify arguments that have been successful in the past with full text, pinpoint searching. Link to case law cited within any court document via Fastcase.

Analytics At Your Fingertips



Learn what happened the last time a particular judge, opposing counsel or company faced cases similar to yours.

Advanced out-of-the-box PTAB and TTAB analytics are always at your fingertips.

API

Docket Alarm offers a powerful API (application programming interface) to developers that want to integrate case filings into their apps.

LAW FIRMS

Build custom dashboards for your attorneys and clients with live data direct from the court.

Automate many repetitive legal tasks like conflict checks, document management, and marketing.

FINANCIAL INSTITUTIONS

Litigation and bankruptcy checks for companies and debtors.

E-DISCOVERY AND LEGAL VENDORS

Sync your system to PACER to automate legal marketing.