

GENOM

Matt Ridley

The Epigenome Stephan Beck,Alexander Olek,2006-03-06 This is the first book that describes the role of the Epigenome (cytosine methylation) in the interplay between nature and nurture. It focuses and stimulates interest in what will be one of the most exciting areas of post-sequencing genome science: the relationship between genetics and the environment. Written by the most reputable authors in the field, this book is essential reading for researchers interested in the science arising from the human genome sequence and its implications on health care, industry and society.

Genome Matt Ridley,2006-05-30 The genome's been mapped. But what does it mean? Arguably the most significant scientific discovery of the new century, the mapping of the twenty-three pairs of chromosomes that make up the human genome raises almost as many questions as it answers. Questions that will profoundly impact the way we think about disease, about longevity, and about free will. Questions that will affect the rest of your life. Genome offers extraordinary insight into the ramifications of this incredible breakthrough. By picking one newly discovered gene from each pair of chromosomes and telling its story, Matt Ridley recounts the history of our species and its ancestors from the dawn of life to the brink of future medicine. From Huntington's disease to cancer, from the applications of gene therapy to the horrors of eugenics, Matt Ridley probes the scientific, philosophical, and moral issues arising as a result of the mapping of the genome. It will help you understand what this scientific milestone means for you, for your children, and for humankind.

Essentials of Genomics and Bioinformatics Christoph W. Sensen,2008-09-26 Provides an overview of

the rapidly evolving field of genomics with coverage of nucleic acid technologies, proteomics and bioinformatics. It includes chapters on applications in human health, agriculture and comparative genomics and also contains two chapters on the legal and ethical issues of genomics, a topic that is becoming increasingly important as genomics moves out of the laboratory into practical applications.

Adam and the Genome Scot McKnight, Dennis R. Venema, 2017-01-31 Genomic science indicates that humans descend not from an individual pair but from a large population. What does this mean for the basic claim of many Christians: that humans descend from Adam and Eve? Leading evangelical geneticist Dennis Venema and popular New Testament scholar Scot McKnight combine their expertise to offer informed guidance and answers to questions pertaining to evolution, genomic science, and the historical Adam. Some of the questions they explore include: - Is there credible evidence for evolution? - Do we descend from a population or are we the offspring of Adam and Eve? - Does taking the Bible seriously mean rejecting recent genomic science? - How do Genesis's creation stories reflect their ancient Near Eastern context, and how did Judaism understand the Adam and Eve of Genesis? - Doesn't Paul's use of Adam in the New Testament prove that Adam was a historical individual? The authors address up-to-date genomics data with expert commentary from both genetic and theological perspectives, showing that genome research and Scripture are not irreconcilable. Foreword by Tremper Longman III and afterword by Daniel Harrell.

Genetics Daniel L. Hartl, Elizabeth W. Jones, 2009 This handbook covers all dimensions of breast cancer prevention, diagnosis, and treatment for the non-oncologist. A special emphasis is placed on the long term survivor.

Genom - Die Extinction-Serie 2 A. G. Riddle, 2020-02-10 Der Kampf um die Zukunft der Menschheit geht in die zweite Runde Im Jahr 2003 wurde das erste menschliche Genom zerlegt und analysiert: Ein historischer Moment. Aber nur ein Wissenschaftler kennt die Wahrheit, die in unserer DNA verschlüsselt ist. Dieses Geheimnis kann alles ändern: Unsere Vergangenheit - und unsere Zukunft! Wer es besitzt, hat Macht über die gesamte Menschheit. Dr. Peyton Shaw, die das Vermächtnis des legendären Wissenschaftlers Paul Kraus erforscht, kommt einer globalen Verschwörung auf die Spur ...

Genom Alan Dean Foster, 2012-11-16 Whispr und Jiminy sind Gauner - und Melds: Menschen, die körperlich oder genetisch verbessert wurden. Sie überfallen einen Mann, um an seine künstliche Hand zu kommen und stehlen dabei eine Silberkette. Diese scheint wertvoller zu sein, als sie dachten, denn bald werden sie erbarmungslos gejagt...

Understanding our genetic inheritance ,1990

Humn Bio& Bio Cancer Bklt& Undstdg Hum Genom ANONIMO, 2005-07-01

The Gnomes of Genom Tony Curtis, 2009-02-26 His children always looked forward to their bedtime story every evening, and when his daughter died of cancer at the early age of 27, he remembered the good times, especially those few moments he spent reading her favourite stories, to her every night. Those times are special to every parent. A small sleepy village is surprised when garden gnomes are brought to life by a remote star, changing their dull little lives forever. Strange things begin to happen in the village. The gnomes decide they are going to do everything they can to help the villagers. There's Mustafa the leader of the clan, Sam and Ella the tiny twins, Lofty, with his wheelbarrow, Willy the Scottish gnome,

Raymond the rabbit, Timmy the tortoise, Dwain the train and many more; Although they work hard, nothing stops them from having fun. Eventually, the gnomes find that they can speak to their owners and the other villagers, and confess their part in all the mysterious happenings. The village of Genom will never be the same.

Resa genom Umeå Lappmarker i Vesterbottens län, förrättad år 1832 Johan Wilhelm Zetterstedt, 1833 Sveriges Kyrkolag af år 1686; jemte ännu gällande stadganden, genom hvilka den blifvit ändrad eller tillökt, utgifven af A. J. Rydén. Tredje öfversedda upplagan, med tillägg af de Ecklesiastika föreskrifter som tillkommit på grund af sednaste Riksdag, till början af år 1856 Sweden, 1856

Das Genom-Puzzle Claudia Eberhard-Metzger, Ingrid Glomp, Barbara Hobom, 2013-07-01 Etwa 3 Milliarden Genbausteine umfaßt das Erbgut des Menschen, an dessen Entschlüsselung Forscher in aller Welt arbeiten. Verständlich und aktuell informiert dieses Buch über die wichtigsten Forschungsprojekte und ihre Ergebnisse. Es zeigt, welche Hoffnungen in die medizinische Anwendung der Genforschung sich bislang erfüllt haben, wo Gentests und Gentherapien heute möglich sind oder wo sie in naher Zukunft entwickelt werden können. Eine kritische Diskussion gilt der Frage nach der Patentierung von Genen und der möglichen Diskriminierung von Personen und Volksgruppen durch Gentests. An ausgewählten Beispielen wird schließlich gezeigt, wie sich mit Hilfe der Gene ein Blick zurück in die Evolution tun läßt. Ein ausführliches Glossar mit der Erklärung wichtiger Fachbegriffe schließt das Buch ab.

Das Genom Ernst Peter Fischer, 2015-06-15 FISCHER KOMPAKT. Verlässliches Wissen kompetent, übersichtlich und bündig dargestellt. - Chromosom - Genkarte - Genom - Sequenz - Genprodukt - Basispaar

- Craig Venter - Protein - Doppelhelix - Gentechnik - Erbanlage - Genomsequenz - Allel - Eric Lander - Francis Collins - Genetik - Genregulation - Genomprojekt - Organismus - Genomforschung (Dieser Text bezieht sich auf eine frühere Ausgabe.)

Mit smukke genom Lone Frank, 2015-12-11 Hvem er jeg? En dna-kode oversat til kød og blod er det hurtige svar, men hvad betyder det? Bestemmer den nedarvede kode alt fra min hårfarve over partnervalg til jobsituation eller har ”jeg” noget at skulle have sagt her? Er der i det hele taget et frit og ubundet ”jeg”, eller gennemspiller ”jeg” bare et computerprogram i dna-kode, der dikterer mit liv og min død? Lone Frank har i Mit smukke genom sat sig for at finde ud af så meget om sine egne gener som muligt: Hvad er hendes prognose for brystkræft og er hun i familie med Dronning Victoria? Hvad er hendes livsudsigter? Hvad har formet hendes personlighed? Har hun den rigtige kæreste eller skal hun prøve sig frem på et genbaseret dating site? Hvor meget kan vi i det hele taget få at vide om os selv ved at kigge dybt i generne? Vil vi vide det, og hvad kan vi bruge vores viden til? Bliver vi mere eller mindre frie af at vide, hvem vi er genetisk set? Mit smukke genom er en fantastisk, humoristisk – og indimellem smertefuld – rejse gennem den nyeste genetiske videnskab og et felt, der gennem de sidste par år er blevet et supermarked med alt fra dating sites til slægtsforskning.

Genome-driven Search of Natural Products from Gram-negative Bacteria Andri Frediansyah, 2020
Gram-negative Bakterien stellen eine wertvolle Quelle für neuartige und biologisch aktive Naturstoffe dar. Einige Naturstoffe wurden bereits translational zu einem zugelassenen Medikament weiterentwickelt. Als erfolgreiche Beispiele sind hier die Krebsmedikamente Etoposid und Trabectedin oder das topische

Antibiotikum Mupirocin anzuführen. Die zahlreichen Genom-Sequenzierungen der letzten zwei Dekaden unterstützen den bisherigen Eindruck und legen den Schluss nahe, dass Gram-negative Bakterien ein noch viel größeres Potential aufweisen, Naturstoffe zu produzieren, als bisher angenommen wurde. Basierend auf diesem Wissen wurden bereits zahlreiche neue und diverse Naturstoffe aus weitverbreiteten und bekannten Gram-negativen Bakterien isoliert, z.B. der Gattung *Pseudomonas* und *Burkholderia* oder Myxobakterien. Angesichts des gegebenen Potentials fokussierte sich diese Doktorarbeit daher auf die chemische Erforschung von Sekundärmetaboliten von Gram-negativen Bakterien aus seltenen bzw. weniger bekannten Gattungen, die bislang nur unzureichend chemisch untersucht wurden. Die Genom-Analyse, unterstützt von einem chemischen Screening von sechs *Massilia* spp. ergab, dass eine der untersuchten Spezies, *Massilia albidiflava*, höchstwahrscheinlich einen neuen Sekundärmetaboliten produziert. Nach Hochskalierung des Fermentationsansatzes und chromatographischer Aufreinigung konnte der neue Naturstoff Massiliamide - ein zyklisches Peptid - gewonnen werden. Die planare Struktur wurde mittels NMR gelöst, wohingegen die absolute Konfiguration der Aminosäuren mittels der Marfey-LC-MS-Methode bestimmt wurde. Hinsichtlich der Bioaktivität, zeigte Massiliamide keine Zytotoxizität, jedoch eine starke Tyrosinase-Hemmung (IC₅₀: 1.15). Des Weiteren fiel während der komparativen Genom-Analysen auf, dass nahezu alle untersuchten Bakterien der Gattungen *Massilia* und *Telluria* ein Acyl-Homoserin-Lacton (AHL)-Biosynthesegencluster aufwiesen, welches nahelegte, dass Prozesse Quorum- Sensing-geregelt vonstatten gehen. Daher wurde, erstmals in diesen Gattungen, systematisch die Konzentration von AHLs zeit-aufgelöst bestimmt. Anschließend wurde in zahlreichen Bioassays die

physiologische Rolle der AHLs aufgespürt. Diese ergaben, dass AHLs die Motilität und die Biofilmbildung beeinflussen. Zusätzlich zeigte sich, dass die AHL-Produktion hingegen mit Gattungs-fremden Fettsäuren gehemmt werden kann.

Merungkai Genom Kevin Davies, 2001

Brave New Brain Nancy C. Andreasen, 2013-07-02 Nancy Andreasen, führende Neurowissenschaftlerin, Herausgeberin des angesehenen American Journal of Psychiatry und ausgezeichnet mit der National Medal of Science, zeigt uns in ihrem neuen Buch die Zusammenhänge zwischen Gehirn und Genom. Dank modernster Methoden und Entdeckungen in Neurowissenschaften und Molekularbiologie wissen Forscher mehr denn je über die Funktionen des Gehirns. Die Autorin beschreibt auf faszinierende und verständliche Weise, wie alles zusammenhängt - von Milliarden kleinster Neuronen im Thalamus bis hin zur moralischen Kontrollinstanz im präfrontalen Kortex. Sie erklärt die Entschlüsselung des Genoms, dessen 30000-40000 Gene fast alle in irgendeiner Form in unserem Gehirn aktiv sind. In fesselnden Geschichten beleuchtet sie aber auch, wie sich psychische Störungen entwickeln und welche Auswirkungen sie auf Patienten und Angehörige haben. Nancy Andreasen gelingt der Brückenschlag zwischen hochkomplexen Inhalten und spannender Lektüre.

Gametogenese og humant genom Milos Pawlowski, Det biologiske DNA indeholdt i sædcellen dannes ved processen kaldet gametogenese. Det består af forskellige faser, hvorefter mandlige og kvindelige kønsceller dannes. Strukturen af DNA tilvejebringer en mekanisme til arv. Konformationen, der er vedtaget af DNA, afhænger af hydratiseringsniveauet, DNA-sekvensen, mængden og retningen af

superviklingen, de kemiske modifikationer af baserne, typen og koncentrationen af metalioner og tilstedeværelsen af polyaminer i opløsning.

Performance of MCrAlX coatings Pimin Zhang, 2019-11-04 MCrAlY coatings (M=Ni and/or Co) are widely used for the protection of superalloy components against oxidation and hot corrosion in the hot sections of gas turbines. The drive for coating systems to bestow adequate oxidation and corrosion resistance upon the components becomes urgent as an inevitable result of the necessary improvement in engine combustion efficiency and service lifetime. Through the careful design of the composition, MCrAlY coating performance can be optimized to meet the needs under different service conditions and component materials, therefore, “MCrAlX”, with “X” stands for the minor alloying elements, is used to highlight the effect. In the present thesis, the performance of new MCrAlX coatings is investigated with respect to oxidation, hot corrosion and interactions between coating-superalloy substrates. Oxidation of MCrAlX coatings can be generally categorized into initial, steady and close-to-end stages. Coating performance can be affected by various factors at different stages, therefore, experiments were designed by targeting the oxidation stages. Investigation on the initial stage oxidation behavior of MCrAlY coatings with post-deposition surface treatments reveals the different growth mechanisms of alumina scales. Surface treatments significantly reduce the alumina growth rate by suppressing transient alumina development and aiding the early formation of γ -Al₂O₃, which improves the long-term oxidation performance of the coating. Similarly, the modification of minor alloy elements in MCrAlX coatings also serves the purpose. The oxidation behavior of new MCrAlX coatings was investigated at the steady oxidation stage, followed

by the microstructure observation, thermodynamic and kinetic simulations. As an alternative reactive element addition of Y, Ce shows a negative effect on the formation of columnar alumina scales of high strain tolerance. In comparison, Fe or Ru addition shows no influence on alumina growth, rather than strengthening the phase stability in the coating and reducing the interdiffusion between coating-substrate through different mechanisms. As the oxidation proceeds to the close-to-end stage, a reliable criterion to estimate the capability of coating to form γ -Al₂O₃ is of great importance to accurately evaluate coating lifetime. A temperature-dependent critical Al-activity criterion was proposed to better predict the formation of a continuous γ -Al₂O₃ scale based on correction of elemental activity using thermodynamic database to replace the empirical Al-concentration based criterion. Severe interdiffusion occurs between coating-substrate during high temperature oxidation, accelerating the degradation of the system. Interdiffusion behavior of diffusion couples of superalloys-MCrAlX coatings were examined. It is highlighted that the recrystallization of superficial layer of the substrate contributes to the secondary reaction zone formation and element interdiffusion controls subsequent zone thickening. Study on Type I hot corrosion behavior of new MCrAlX coatings shows that the addition of Fe has no influence on basic fluxing reactions before severe Al depletion from the coating occurs. Instead, it boosts the “effective” Al supply of coating by shifting the equilibrium concentration of Al in the γ phase to a low Al level. Besides, the pre-mature coating degradation at the coating-substrate interface was due to the fast growth of corrosion products from substrate induced large local volume expansions, resulting in early coating spallation. MCrAlY ytbeläggningar (M=Ni och/eller Co) används ofta för att skydda komponenter tillverkade av

superlegeringar mot oxidation samt högttemperaturskorrosion i de heta gasturbindelarna. Förbättrad förbränningseffektivitet och livslängd hos gasturbiner, gör att ytbeläggningssystemen måste besitta adekvata oxidations- och korrosionsmotstånd. Genom att omsorgsfullt utforma den kemiska sammansättningen hos MCrAlY ytbeläggningar kan deras prestanda optimeras för att möta kraven från olika driftförhållanden samt olika substratmaterial, därför används beteckningen MCrAlX för att belysa förändringar av den kemiska kompositionen, där X står för reaktiva legeringsämnen som tillsätts i mindre mängder. I denna avhandling undersöks prestandan hos en ny MCrAlX ytbeläggning med hänsyn till oxidation, högttemperaturskorrosion och interaktionen mellan ytbeläggningen och superlegeringssubstratet. Oxidation av MCrAlX ytbeläggningar kan generellt kategoriseras i tre faser; initiala, stabila och nära-slutet fasen. Ytbeläggningens prestanda kan påverkas av olika faktorer vid de olika faserna, därför utformades olika experiment för att undersöka de olika oxidationsfaserna. Undersökningen av den initiala fasen av oxidationsbeteendet hos MCrAlX ytbeläggningar som genomgått ytbehandlingar efter ytbeläggningsdeponeringen avslöjade olika tillväxtmekanismer hos aluminiumoxidskikten. Aluminiumoxidens tillväxthastighet reducerades signifikant av ytbehandlingarna, detta genom att undertrycka utvecklingen av övergående aluminiumoxid och bistå den tidiga tillväxten av γ -Al₂O₃, vilket förbättrar ytbeläggningens oxidationsprestanda långsiktigt. De reaktiva legeringsämnena som tillsätts i mindre mängder påverkar ytbeläggningens oxidationsprestanda på liknande sätt. Oxidationsbeteendet hos de nya MCrAlX ytbeläggningarna i den stabila fasen följdes av mikrostrukturundersökning, termodynamiska och kinetiska simuleringar. Det framkom att Ce visar en negativ effekt på bildandet av kolumnära

aluminiumoxidskikt med hög töjningstolerans som alternativt reaktivt legeringsämne till Y. Jämförelsevis ger Fe- eller Ru-tillsatser ingen påverkan på aluminiumoxidtillväxten, förutom att det förstärker fasstabiliteten i ytbeläggningen samt genom olika mekanismer reducerar interdiffusionen mellan ytbeläggningen och substratet. När oxidationsprocessen kommit till nära-slutet fasen, är det viktigt att uppskatta kapaciteten hos en ytbeläggning att bilda γ -Al₂O₃, detta då det är ett tillförlitligt kriterium för att noggrant kunna utvärdera ytbeläggningens livslängd. Därför föreslogs ett temperaturberoende kriterium för kritisk Al-aktivitet för att bättre kunna förutsäga bildandet av ett kontinuerligt γ -Al₂O₃-skikt. Kriteriet baserades på korrigering av legeringsämnens aktivitet genom att använda en termodynamisk databas, detta för att ersätta det empiriska Al-koncentrations baserade kriteriet. Vid högtemperaturoxidation sker en omfattande interdiffusion mellan ytbeläggningen och substratet, vilket accelererar degraderingen av ytbeläggningssystemet. Därför har interdiffusionsbeteendet mellan superlegeringssubstratet och MCrAlX ytbeläggningen undersökts i denna avhandling. Det framkom att rekristallisationen av ytliga skikt av substratet bidrar till formationen av den sekundära reaktionszonen och att interdiffusion kontrollerar zonens efterföljande tjocklekstillväxt. Undersökningen av Typ I högtemperaturskorrosionsbeteendet hos en ny MCrAlX ytbeläggning visar att legeringstillägg av Fe inte påverkar de grundläggande flödesreaktionerna innan en kritisk Al utarmning sker i ytbeläggningen. Istället stimulerar det tillförseln av Al genom att skifta jämviktskoncentrationen av Al i γ fasen till en låg nivå av Al. Det framkom också att den tidiga degraderingen av ytbeläggningen vid gränsskiktet mellan ytbeläggningen och substratet kommer av att den snabba tillväxten av korrosionsprodukter från substratet inducerade en stor lokal volymsutvidgning,

vilket ledde till tidig ytbeläggningsspallation.

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