

ADD-ON FELLOWSHIPS FOR INTERDISCIPLINARY SCIENCE – APPLICATION FORM –

The completed application form and all additional documents listed below should be returned to add-on@joachim-herz-stiftung.de. Application deadline is September 1 2015.

All application documents will only be reviewed by the selection committee.

PERSONAL DATA	
Surname, first name(s):	
Academic title:	
Date of birth:	
Gender:	
Research area:	
Institution / University:	
email:	

EDUCATION	
Field of study (including specialization and subsidiary subjects):	
Degrees:	
Further information:	

RESEARCH	
Research project:	
Supervisor / group leader:	
Start and duration of the project (PhD studies / postdoc position):	
Type and scheduled duration of basic funding (appointment at university / research institute, scholarship, etc.). Please indicate the name of the funding organization.	

INFORMATION ON USE OF FUNDING	
Plans for using the funds provided for interdisciplinary research and qualification (attending conferences, research visits, training, etc.):	
Further plans:	

The following documents need to be attached:

- Letter of motivation (max. one page)
- CV
- Short description of your research project (max. one page)
- Supporting letter of supervisor / group leader (stating her / his support and the need for fostering the applicant's interdisciplinary skills)
- Transcript of records

The following information is voluntary and aimed at identifying the needs of additional funds provided for the reconcilability of family and job.

RECONCILABILITY OF FAMILY AND JOB	
Children's birth dates:	
Please indicate your plans for using the funds provided for the reconcilability of family and job.	

Aaron Brooks | Postdoc@EMBL

Meyerhofstrasse 1 – 69117 Heidelberg – Germany

☎ +49 6221 387-8630 • ✉ aaron.brooks@embl.de • 🌐 aaronbrooks.info

Joachim Herz Stiftung

August 28, 2015

Dear Evaluating Committee,

I am applying for a Joachim Herz Stiftung Add-on Fellowship to supplement an ambitious systems genetics project I have proposed. The project combines longitudinal multiomic molecular profiles with genetics to better understand how Baker's yeast ages. While I have expertise in both bioinformatics and high-throughput transcriptomics methods, I would like to receive additional training in several emerging technologies to complement this skill set. More specifically, I would use Joachim Herz Stiftung funding to travel to several collaborating labs across the world where I will receive hands-on training in microfluidics, metabolomics, proteomics, and statistical machine learning methods.

I am currently a postdoctoral fellow with Lars Steinmetz at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany. The group is internationally recognized for its forward-looking approach to emerging technologies in systems genetics, pioneering a number of technologies widely used in the field. I joined the group to expand my interdisciplinary training, taking on a more complex model system (yeast) and learning how to measure cells at multiple molecular scales. Previously in my PhD, I studied the structure and function of gene regulatory networks (GRNs) in microorganisms. I developed machine learning algorithms to infer GRNs directly from high-throughput gene expression data for two phylogenetically diverse organisms. These genome-scale models were able to predict (accurately and quantitatively) mechanisms responsible for regulation of each gene in the genome (Brooks et al. 2014. Mol Syst Biol). With this project I gained valuable expertise in computational approaches (ensemble learning and graph theory) and several high-throughput experimental methods related to transcription. By the conclusion of my PhD, however, it was clear to me that comprehensive understanding of a biological system would require integrating across multiple scales of biological complexity.

The project I describe in my application emerged from an interest in how technology is reshaping healthcare. I have been fascinated by a new approach to preventative medicine that attempts to quantify and maintain "wellness" by combining longitudinal profiling with genetics. Here, I saw an opportunity to create a project that would have implications for data integration within the basic sciences as well as personalized medicine. I have therefore designed a project to study a phenotype related to wellness (aging) by combining genetics with longitudinal molecular profiling. My hope is that the project will contribute a data integration paradigm for holistic modeling approaches.

This project will be enriched by the training I will receive through Joachim Herz Stiftung funding. I will use these Add-on funds to conduct extended research stays in laboratories at Stanford, EMBL-EBI, and the University of Luxembourg. Each of these labs has expertise in a technology that will supplement my project. My bigger ambition is to carry some of these collaborations forward to take on other challenging problems in the future.

Thank you for the opportunity to apply for your prestigious award.

Sincerely,

Aaron Brooks

Currently
Postdoc @ EMBL

Aaron Brooks/PhD

Science of complex biological systems

Mail
aaron.brooks@
embl.de

Steinmetz Lab
Genome Biology Unit
EMBL,
Meyerhofstrasse 1
69117 Heidelberg,
Germany

Web
aaronbrooks.info
linkedin/aaron-brooks
github/scalefreegan

Twitter
@scalefreegan

Publications

DM Salvanha, N Jiang, **AN Brooks**, RZN Vêncio, NS Baliga. **GGB_{web}: a Gagggle-enabled, interactive genome browser for the web.** *In preparation.*

S Imam, S. Schaeuble, **AN Brooks**, NS Baliga, ND Price. (2015) **Data-driven integration of genome-scale regulatory and metabolic network models.** *Front. Microbiol.* 6:409

CL Plaisier, FY Lo, J Ashworth, **AN Brooks**, KD Beer, A Kaur, M Pan, DJ Reiss, FT Facciotti, NS Baliga. (2014) **Evolution of Context Dependent Regulation by Expansion of Feast/Famine Regulatory Proteins.** *BMC Systems Biology* 8(1):122.

H Westerhoff*, **AN Brooks***, E Simeonidis*, R García-Contreras*, F Boogerd, F He, VJ Jackson, V Goncharuk, A Kolodkin. (2014) **Macromolecular networks and intelligence in microorganisms.** *Front. Microbiol.* 5:379.

AN Brooks*, DJ Reiss*, A Allard, W Wu, DM Salvanha, CL Plaisier, S Chandrasekaran, M Pan, A Kaur, NS Baliga. **A system-level model for the microbial regulatory genome.** *Mol Syst Biol.* (2014) 10: 740.

AN Brooks, S Turkarslan, KD Beer, FY Lo, NS Baliga. (2011) **Adaptation of cells to new environments.** *Wiley Interdiscip Rev Syst Biol Med.* 3(5): 544–561.

* Denotes equal contribution

Research

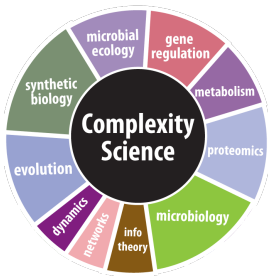
2015 - now **Postdoc** [EMBL | Genome Biology Unit](#)
Project: "Multiomics characterization of genetic variation in yeast."
Advisor: Prof. Lars Steinmetz, Associate Head of Unit and Senior Scientist

Education

2008 - 2014 **PhD Molecular and Cellular Biology** [University of Washington](#)
Dissertation: "Data-driven inference of dynamic transcriptional regulatory mechanisms in prokaryotes: a systems perspective."
Advisor: Prof. Nitin Baliga, SVP and Director, Institute for Systems Biology

2002 - 2007 **BS Biochemistry & BA Political Science** [University of New Mexico](#)
Thesis: "Characterization of the dynamic interactions of cytoplasmic poly(A) binding protein with poly(A) RNA."
Thesis Honors: Robert B. Loftfield Award
Advisor: Prof. David G. Bear
Summa Cum Laude
General University Honors
Minor: Philosophy

Research Interests



Wetlab

MolBio	★★★★★
Cytometry	★★★★★
Expression	★★★★★
Bioreactor	★★★★★
Sequencing	★★★★★
Microscopy	★★★★★

Programming

R	★★★★★
Python	★★★★★
Bash	★★★★★
SQL	★★★★★
Malab	★★★★★
HTML/JS	★★★★★
C++	★★★★★

Research Summary



In the news

05/2014	Knowing Networks <i>Outreach at USA Science and Engineering Festival</i>	NIH NIGMS Inside Life Science
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Awards

2010-2013	Office of Science Graduate Fellowship	Department of Energy
2009	Graduate Research Fellowship Honorable Mention	National Science Foundation
2006	Goldwater Scholarship	Barry M. Goldwater Foundation

Teaching & Outreach

2014	USA Science and Engineering Festival <i>Designed and facilitated a hands-on activity and web-based game to understand the structure and function of networks. Over 300 students have played the online game.</i>	Washington, D.C
2011	Introduction to Systems Biology <i>Co-organizer, lecturer</i>	Institute for Systems Biology
2009-now	Science Communication Fellow	Pacific Science Center, Seattle WA
2010	Graduate Teaching Assistant <i>MICRO 411: Gene Action</i>	Microbiology, University of Washington

Students mentored

08-12/2012	Robin Green Currently at Fred Hutchinson Cancer Research Center	PhD student at University of Washington, WA
05-08/2011	Darach Miller Currently PhD student at NYU	Undergraduate at UC Davis, CA
05-08/2010	Alexis Valauri-Orton Currently Ocean Acidification Intern at Ocean Conservancy	Undergraduate at Davidson College, NC

Other

2011	Complex Systems Summer School	Santa Fe Institute
2010	MCB Student Symposium <i>Co-organizer, Bioplasticity: flexibility within and beyond the code</i>	Fred Hutchinson Cancer Research Center

References

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MULTIOMIC FINGERPRINTS OF AGING IN A GENETICALLY TRACTABLE YEAST POPULATION

Aaron Brooks, EMBL

28.08.2015

New technologies are providing increasingly detailed measurement of biological systems. It remains a challenge, however, to integrate across these data to construct comprehensive representations of biological systems. A major goal in systems biology is to leverage heterogeneous molecular information and genetics to identify personalized intervention points that will predictively alter biological processes, such as disease. My postdoctoral project attempts to combine longitudinal multiomic profiles in a genetically diverse population with integrative computational methods to quantify genetic factors that contribute to lifespan regulation in Baker's yeast.

Aging is a complex biological process with both genetic and non-genetic components, some of which are conserved from yeast to humans. I use multiple recently developed high-throughput technologies to image physical properties related to lifespan and quantify the molecular composition of cells at several stages of aging across two growth conditions in a genetically diverse yeast population. This large collection of longitudinal, heterogeneous data are going to be integrated using data fusion techniques and combined with genetic information using statistical machine learning methods to identify genetic loci and molecular fingerprints that are diagnostic of aging and characterize their environmental (in)dependence.

My project leverages several emerging technologies to construct a multifaceted and longitudinal survey of the aging process. Microfluidics is used to measure multiple aging phenotypes in mother cells. In parallel, high-throughput omic technologies (epigenomics, transcriptomics, metabolomics, and proteomics) are applied to quantify the molecular composition of cells at several stages of the aging process. Integration of these large heterogeneous datasets will be performed using statistical machine learning algorithms that will derive multiomic fingerprints predictive of aging state. Each of these methods will be performed in a genetically diverse yeast population of 140 haploid segregants in two growth conditions to characterize the environmental (in)dependence for each of the genetic markers and their age-specific molecular fingerprints.

Given the complexity of the aging process, I expect to observe differences in aging not only between strains with different genetic backgrounds but also within isogenic strains at different stages in their lifetimes. By combining molecular fingerprints with genetics, I will be able to identify single and combinations of genetic loci that either predict or influence lifespan. The model will make predictions about the molecular scale at which particular genetic variations manifest, from immediate consequences on transcription to downstream effects on metabolism, and will distinguish genetic factors with environmental (in)dependence. Deconstruction of this complex phenotype will help determine whether molecular profiles and genetics are sufficient to diagnose a complex biological process and provide proof-of-principle approaches for integrating large heterogeneous datasets with genetic information to drive longitudinal, data-driven evaluation of complex phenotypes, including health in humans.

I am applying to the Joachim Herz Stiftung foundation to receive funding that will allow me to gain additional training in microfluidics, metabolomics, proteomics, and machine learning methods - each of which are central components of this project.

August 25th, 2015

Joachim Herz Stiftung Reference for Aaron Brooks

Dear Evaluating Committee,

I would like to provide the strongest recommendation for my postdoctoral student, Dr. Aaron Brooks, to be selected for the Joachim Herz Stiftung Add-on fellowship. Aaron is a talented and creative young scientist with exceptional skills in both bioinformatics and experimental molecular biology. The Joachim Herz Stiftung fellowship would enrich a systems genetics project he has crafted by providing an opportunity for Aaron to participate in extended research stays at several international collaborating institutions. In particular, the fellowship will allow Aaron to gain additional experimental training in metabolomics, proteomics and microfluidics, as well as computational training in statistical machine learning methods. These visits will not only allow Aaron to deepen his interdisciplinary training, but they will also give him an opportunity to forge his own collaborations as he moves towards an independent career.

I am an expert in genomics research and technology development with many years of experience managing interdisciplinary projects and international collaborations. I am Professor of Genetics at Stanford University and Co-Director of the Stanford Genome Technology Center. In addition, I have been leading a research group at the European Molecular Biology Laboratory (EMBL) and served as founding chairman of its Genome Biology Unit. My laboratory develops and applies cutting-edge technologies to investigate the genetic basis of diseases, with the ultimate goal of developing personalized, preventative medicine. We designed the first tiling microarray for yeast, which was a technological breakthrough that changed the view of how genomes are expressed. We also performed the first high-resolution, genome-wide map of yeast meiotic recombination outcomes, which has been described as a landmark in the field. These seminal approaches have become gold standard in transcriptomics and our technologies are now widely applied by others.

From my working experience with Aaron, I have learned that he has the background, technical expertise, and work ethic to guide complex projects to their completion. His deep biological knowledge is complemented by technical proficiency and creativity. Aaron can perform computation as well as design and perform experiments – a powerful combination for a 21st century biologist. This is a major reason I selected Aaron from among many talented applicants. He has previously developed sophisticated computational pipelines, managed large bioinformatic databases, created web applications, and performed as well as analyzed high-throughput experiments. He is

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fluent in several programming languages, including R, Python, JavaScript, and SQL and has technical proficiency in experimental biology, including molecular biology methods, microarray- and sequencing-based transcriptomics, and fluorescence-based methods (microscopy and cell sorting). After only a few months in my lab he has already established a new computational method for QTL detection and built an interactive web application, which he is preparing for publication.

Aaron started in my lab in April 2015. He joined my group to investigate the effects of genetic variation at several biological scales. Specifically, he aims to dissect the consequences of genetic variation in a segregating yeast population by combining multiple omic measurements, including quantification of the genome, transcriptome, proteome and metabolome. Integrating these high-throughput data sets remains a significant challenge in the field, in part because of the diversity of expertise required to produce, analyze, and interpret these many facets simultaneously. I hired Aaron because he has the interdisciplinary background to do exactly this. He is applying to the Joachim Herz Stiftung to help fund an ambitious new direction for this project. This new research direction will require Aaron to develop several technical proficiencies, which is the primary reason he is applying for Add-on funding.

Aaron has proposed to use this multitomic platform to combine genetics with longitudinal molecular profiles to understand how yeast age. In particular, he aims to: (1) decipher how genetic-factors contribute to quantitative measures of aging in a genetically diverse yeast population, (2) predict aging by combining genotype information with longitudinal assessment of molecular “fingerprints” and (3) understand how the environment modulates these genetic effects.

Yeast has been used previously as a model system to study conserved molecular processes associated with aging. Aaron will measure how aging varies across a genetically diverse population of hundreds of genotyped yeast segregants using a microfluidics platform to quantify lifespan and other optical properties related to aging (e.g. cell shape and size). In parallel, Aaron will measure longitudinal molecular of the epigenome, transcriptome, proteome, and metabolome across the aging process for hundreds of yeast segregants. Finally, he will combine this information using machine learning approaches to generate predictive models of the aging process that distinguish genetic and environmental effects.

The Joachim Herz Stiftung fellowship will be an excellent opportunity for Aaron to gain important research training in metabolomics, proteomics, microfluidics and new computational methods to enhance his project. The fellowship will also provide Aaron with funding to travel to international research conferences, where he will be able to present his work to leading researchers in several disciplines.

Aaron’s career has already undergone a major transition. Shortly after his university studies, Aaron gained computational proficiencies to complement his experimental training. He is now trying to take this interdisciplinary skillset and apply it on a large scale. The project Aaron

has proposed is ambitious. I have established collaborating partners throughout the world (e.g., EMBL Heidelberg, EMBL-EBI, Stanford, University of Luxembourg, Institute for Systems Biology) to support the project. Aaron is working with several of these groups currently to develop data collection and analysis pipelines. I would like Aaron to have an opportunity to conduct extended research stays at several of these institutions (EMBL-EBI, Stanford, and University of Luxembourg in particular) so that he can receive hands-on training in metabolomics, proteomics, microfluidics, and machine learning methods. The Joachim Herz Stiftung fellowship will provide this opportunity.

I fully endorse Aaron and his application for your fellowship given his personal merits, the scientific significance of the project, and the potential of the fellowship to enrich his career. Joachim Herz Stiftung funding will help Aaron establish exciting new methodologies, gain additional expertise, and – importantly – form international collaborations that will propel him forward towards a successful future career. I am confident that Aaron will take full advantage of the opportunity.

Please do not hesitate to contact me if you require further information.

Sincerely,

Lars Steinmetz



Lars Steinmetz, Ph.D.

Associate Head of Genome Biology Unit, EMBL
Professor of Genetics, Stanford University
Co-Director, Stanford Genome Technology Center

UNIVERSITY OF WASHINGTON

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Prepared on 7/23/2015

Aaron N Brooks

0826929

GRADUATE

05/16/XX

NO LONGER ENROLLED (LAST QTR SUMMER 2014)

Interdisc Graduate Progr MOLECULAR & CELLULAR BIO

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 * AND/OR LEAD TO STUDENT DISCIPLINARY SANCTIONS. *

GRE SCORES : VERBAL:650 QUANT:780 ANAL/WRITE:050

UNIVERSITY OF WASHINGTON DEGREES EARNED:
 DOCTOR OF PHILOSOPHY (MOLECULAR & CELLULAR BIOLOGY)
 SUMMER 2014 (08/22/14)
 UW:222.0 TRANSFER: 0.0 EXTENSION: 0.0 GPA: 3.87

Data-driven inference of dynamic transcriptional
 regulatory mechanisms in prokaryotes: a systems
 perspective

UNIVERSITY OF WASHINGTON AWARDS AND CERTIFICATES:
 CANDIDATE IN PHILOSOPHY 03/18/11

DETAIL OF TRANSFER CREDIT:
 UNIV OF NEW MEXICO, NM (4 YEAR SCHOOL)
 ATTENDED 2002-2007 DEGREE: BA 2007
 TOTAL CREDITS EARNED: 0.0

SUMMARY OF TRANSFER CREDIT:	LD	UD	TOTAL
TOTAL CREDITS EARNED:	0.0	0.0	0.0
TOTAL TOWARD DEGREE:	0.0	0.0	0.0

AUTUMN 2008		MCB	8
CONJ	533 DYNAMIC CHROMOSOME	1.5	3.8
CONJ	537 TRANSCRIPTIONAL REG	1.5	3.9
MCB	514 MOL CEL BIO LIT REV	2.0	CR
MCB	599 INT RES MOL CEL BIO	8.0	CR
QTR ATTEMPTED: 13.0 EARNED: 13.0 GPA: 3.85			
QTR GRADED AT: 3.0 GRADE POINTS: 11.5			
CUM ATTEMPTED: 13.0 UW EARNED: 13.0 TTL EARNED: 13.0			
CUM GRADED AT: 3.0 GRADE PTS: 11.6 CUM GPA: 3.87			

WINTER 2009		MCB	8
CONJ	526 INTRO TO SYS BIO	1.5	4.0
CONJ	534 NERVOUS SYSTEM DEV	1.5	3.6
GENOME	540 COMP MOL BIOL I	4.0	W3
MCB	515 MOL CEL BIO LIT REV	2.0	CR
MCB	599 INT RES MOL CEL BIO	8.0	CR
QTR ATTEMPTED: 13.0 EARNED: 13.0 GPA: 3.80			
QTR GRADED AT: 3.0 GRADE POINTS: 11.4			
CUM ATTEMPTED: 26.0 UW EARNED: 26.0 TTL EARNED: 26.0			
CUM GRADED AT: 6.0 GRADE PTS: 23.0 CUM GPA: 3.83			

SPRING 2009		MCB	8
BIOEN	555 CELL BIOMECH FUNCTN	3.0	4.0
CONJ	549 POP BIOL MICROORG	1.5	3.8
MCB	516 MOL CEL BIO LIT REV	2.0	CR
MCB	599 INT RES MOL CEL BIO	8.0	CR
QTR ATTEMPTED: 14.5 EARNED: 14.5 GPA: 3.93			
QTR GRADED AT: 4.5 GRADE POINTS: 17.7			
CUM ATTEMPTED: 40.5 UW EARNED: 40.5 TTL EARNED: 40.5			
CUM GRADED AT: 10.5 GRADE PTS: 40.7 CUM GPA: 3.88			

SUMMER 2009		MCB	8
MCB	600 INDEPNNT STDY/RSCH	2.0	CR
QTR ATTEMPTED: 2.0 EARNED: 2.0 GPA: 0.00			
QTR GRADED AT: 0.0 GRADE POINTS: 0.0			

CUM ATTEMPTED: 42.5 UW EARNED: 42.5 TTL EARNED: 42.5
 CUM GRADED AT: 10.5 GRADE PTS: 40.7 CUM GPA: 3.88

AUTUMN 2009		MCB	8
BIOEN	599 SPEC TOPICS BIOENG	3.0	3.8
MCB	533 EVOLUT GEN & GENOM	3.0	4.0
MCB	600 INDEPNNT STDY/RSCH	10.0	CR
QTR ATTEMPTED: 16.0 EARNED: 16.0 GPA: 3.90			
QTR GRADED AT: 6.0 GRADE POINTS: 23.4			
CUM ATTEMPTED: 58.5 UW EARNED: 58.5 TTL EARNED: 58.5			
CUM GRADED AT: 16.5 GRADE PTS: 64.1 CUM GPA: 3.88			

WINTER 2010		MCB	8
MCB	580 TEACHING PRACTICUM	2.0	CR
MCB	600 INDEPNNT STDY/RSCH	10.0	CR
QTR ATTEMPTED: 12.0 EARNED: 12.0 GPA: 0.00			
QTR GRADED AT: 0.0 GRADE POINTS: 0.0			
CUM ATTEMPTED: 70.5 UW EARNED: 70.5 TTL EARNED: 70.5			
CUM GRADED AT: 16.5 GRADE PTS: 64.1 CUM GPA: 3.88			

SPRING 2010		MCB	8
MCB	600 INDEPNNT STDY/RSCH	10.0	4.0
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00			
QTR GRADED AT: 0.0 GRADE POINTS: 0.0			
CUM ATTEMPTED: 80.5 UW EARNED: 80.5 TTL EARNED: 80.5			
CUM GRADED AT: 16.5 GRADE PTS: 64.1 CUM GPA: 3.88			

SUMMER 2010		MCB	8
MCB	600 INDEPNNT STDY/RSCH	2.0	4.0
QTR ATTEMPTED: 2.0 EARNED: 2.0 GPA: 0.00			
QTR GRADED AT: 0.0 GRADE POINTS: 0.0			
CUM ATTEMPTED: 82.5 UW EARNED: 82.5 TTL EARNED: 82.5			
CUM GRADED AT: 16.5 GRADE PTS: 64.1 CUM GPA: 3.88			

AUTUMN 2010		MCB	8
MCB	600 INDEPNNT STDY/RSCH	10.0	CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00			
QTR GRADED AT: 0.0 GRADE POINTS: 0.0			
CUM ATTEMPTED: 92.5 UW EARNED: 92.5 TTL EARNED: 92.5			
CUM GRADED AT: 16.5 GRADE PTS: 64.1 CUM GPA: 3.88			

WINTER 2011		MCB	8
CONJ	558 PROKARYOTIC BIOLOGY	1.5	3.7
MCB	600 INDEPNNT STDY/RSCH	10.0	CR
QTR ATTEMPTED: 11.5 EARNED: 11.5 GPA: 3.70			
QTR GRADED AT: 1.5 GRADE POINTS: 5.5			
CUM ATTEMPTED: 104.0 UW EARNED: 104.0 TTL EARNED: 104.0			
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87			

SPRING 2011		MCB	8
MCB	800 DOCTORAL DISSERTATN	10.0	4.0
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00			
QTR GRADED AT: 0.0 GRADE POINTS: 0.0			
CUM ATTEMPTED: 114.0 UW EARNED: 114.0 TTL EARNED: 114.0			
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87			

SUMMER 2011		MCB	8
MCB	800 DOCTORAL DISSERTATN	2.0	CR
QTR ATTEMPTED: 2.0 EARNED: 2.0 GPA: 0.00			
QTR GRADED AT: 0.0 GRADE POINTS: 0.0			
CUM ATTEMPTED: 116.0 UW EARNED: 116.0 TTL EARNED: 116.0			
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87			

UNIVERSITY OF WASHINGTON
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Page 2 of 2

Prepared on 7/23/2015

Aaron N Brooks

Interdisc Graduate Progr MOLECULAR & CELLULAR BIO

0826929

05/16/XX

GRADUATE

NO LONGER ENROLLED (LAST QTR SUMMER 2014)

AUTUMN 2011 MCB 8
MCB 580 TEACHING PRACTICUM 2.0 CR
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 12.0 EARNED: 12.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:128.0 UW EARNED:128.0 TTL EARNED:128.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

WINTER 2012 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:138.0 UW EARNED:138.0 TTL EARNED:138.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

SPRING 2012 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:148.0 UW EARNED:148.0 TTL EARNED:148.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

SUMMER 2012 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:158.0 UW EARNED:158.0 TTL EARNED:158.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

AUTUMN 2012 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:168.0 UW EARNED:168.0 TTL EARNED:168.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

WINTER 2013 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:178.0 UW EARNED:178.0 TTL EARNED:178.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

SPRING 2013 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:188.0 UW EARNED:188.0 TTL EARNED:188.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

SUMMER 2013 MCB 8
MCB 800 DOCTORAL DISSERTATN 2.0 CR
QTR ATTEMPTED: 2.0 EARNED: 2.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:190.0 UW EARNED:190.0 TTL EARNED:190.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

AUTUMN 2013 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:200.0 UW EARNED:200.0 TTL EARNED:200.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

WINTER 2014 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:210.0 UW EARNED:210.0 TTL EARNED:210.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

SPRING 2014 MCB 8
MCB 800 DOCTORAL DISSERTATN 10.0 CR
QTR ATTEMPTED: 10.0 EARNED: 10.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:220.0 UW EARNED:220.0 TTL EARNED:220.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

SUMMER 2014 MCB 8
MCB 800 DOCTORAL DISSERTATN 2.0 CR
QTR ATTEMPTED: 2.0 EARNED: 2.0 GPA: 0.00
QTR GRADED AT: 0.0 GRADE POINTS: 0.0
CUM ATTEMPTED:222.0 UW EARNED:222.0 TTL EARNED:222.0
CUM GRADED AT: 18.0 GRADE PTS: 69.7 CUM GPA: 3.87

----- DEGREE EARNED 08/22/14 -----
DOCTOR OF PHILOSOPHY (MOLECULAR & CELLULAR BIOLOGY)
UW:222.0 TRANSFER: 0.0 EXTENSION: 0.0 GPA: 3.87

CUMULATIVE CREDIT SUMMARY:
UW CREDITS ATTEMPTED 222.0 UW CREDITS EARNED 222.0
UW GRADED ATTEMPTED 18.0 EXTENSION CREDITS 0.0
UW GRADED EARNED 18.0 TRANSFER CREDITS 0.0
UW GRADE POINTS 69.6 -----
UW GRADE POINT AVG. 3.87 CREDITS EARNED 222.0

***** END OF RECORD *****

Aaron N Brooks
UNM ID: 525-51-7537
DATE OF BIRTH: 16-MAY-1984

THE UNIVERSITY OF NEW MEXICO
OFFICE OF THE REGISTRAR
ALBUQUERQUE, NEW MEXICO 87131-0001

PAGE: 1
DATE ISSUED: 26-SEP-2007

Course Level: Non Degree Graduate

Current Program

Non-Degree Program

Program : Non-Degree Graduate

College : Non-Degree Status

Campus : Albuquerque/Main

Major : Non-Degree

SUBJ	NO.	C	COURSE TITLE	CRED	GRD	R	PTS
------	-----	---	--------------	------	-----	---	-----

INSTITUTION CREDIT:

Fall 2007

IN PROGRESS WORK

CS	530		ABQGeometric & Prob Methods in CS	3.000		IN PROGRESS	
			In Progress Credits	3.000			

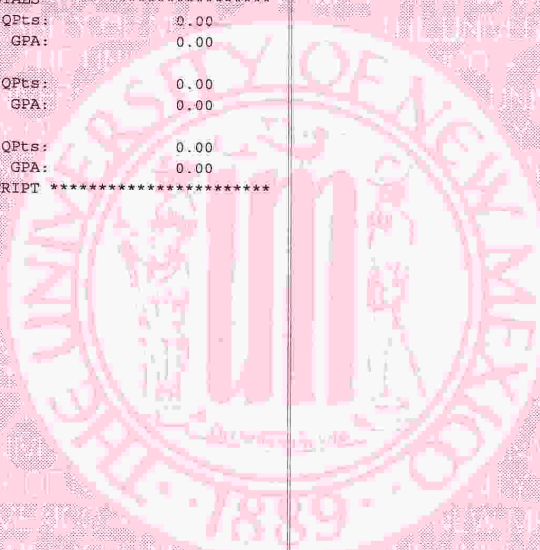
***** TRANSCRIPT TOTALS *****

INSTITUTION	Ehrs:	0.000	Qpts:	0.00
	GPA-Hrs:	0.000	GPA:	0.00

TRANSFER	Ehrs:	0.000	Qpts:	0.00
	GPA-Hrs:	0.000	GPA:	0.00

OVERALL	Ehrs:	0.000	Qpts:	0.00
	GPA-Hrs:	0.000	GPA:	0.00

***** END OF TRANSCRIPT *****



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BROOKS, AARON N
UNM ID# 100-02-2569

Kathleen F. Sena, Registrar

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PAGE: 1
DATE ISSUED: 26-SEP-2007

Course Level: Undergraduate				SUBJ	NO.	C	COURSE TITLE	CRED	GRD	R
								PTS		
Current Program				Institution Information continued:						
Bachelor of Science				CHEM	301	01	ORGANIC CHEMISTRY	3.000	A	12.00
Program : BS Biochemistry				CHEM	303L	01	ORGANIC CHEM LAB	1.000	A-	3.67
College : College of Arts and Sciences				CJ	130	01	PUBLIC SPEAKING	3.000	B+	9.99
Campus : Albuquerque/Main				MATH	163	01	CALCULUS II	4.000	A	16.00
Major : Biochemistry				PHIL	201	01	GREEK PHILOSOPHY	3.000	A	12.00
Degree Awarded Bachelor of Science 12-MAY-2007				UHON	121	01	SEM/ANCIENT LEGACY	3.000	A	12.00
Primary Degree				USP	235	01	S/KEYS TO THE FUTURE	1.000	A	4.00
College : College of Arts and Sciences				Ehrs: 18.000 QPts: 69.66						
Campus : Albuquerque/Main				GPA-Hrs: 18.000 GPA: 3.87						
Major : Biochemistry				Dean's List						
Dept. Honors: SUMMA CUM LAUDE IN BIOCHEMISTRY				Spring 2003						
Inst. Honors: SUMMA CUM LAUDE				University College						
Degree Awarded Bachelor of Arts 12-MAY-2007				CHEM	302	01	ORGANIC CHEMISTRY	3.000	B	9.00
Primary Degree				CHEM	304L	01	ORGANIC CHEM LAB	1.000	A	4.00
Program : BA Political Science				PHIL	442	01	INDIV PHILOSOPHERS	3.000	B+	9.99
College : College of Arts and Sciences				SPAN	276	01	ACCEL INTERMED SPAN	6.000	A	24.00
Campus : Albuquerque/Main				UHON	222	01	SEM/JRNY THRU GENIUS	3.000	A	12.00
Major : Political Science				Ehrs: 16.000 QPts: 58.99						
Minor : Philosophy				GPA-Hrs: 16.000 GPA: 3.68						
Dept. Honors: SUMMA CUM LAUDE IN UNIVERSITY HONORS PROGRAM				Dean's List						
Inst. Honors: SUMMA CUM LAUDE				Fall 2003						
SUBJ	NO.	C	COURSE TITLE	CRED	GRD	R				
				PTS						
TRANSFER CREDIT ACCEPTED BY THE INSTITUTION:										
2000:S		AP EXAMS								
Ehrs:		8.000 QPts:		0.00						
GPA-Hrs:		0.000 GPA:		0.00						
2001:S		AP EXAMS								
Ehrs:		14.000 QPts:		0.00						
GPA-Hrs:		0.000 GPA:		0.00						
2002:S		AP EXAMS								
Ehrs:		21.000 QPts:		0.00						
GPA-Hrs:		0.000 GPA:		0.00						
INSTITUTION CREDIT:										
Fall 2002										
University College		***** CONTINUED ON PAGE 2 *****								
***** CONTINUED ON NEXT COLUMN *****										

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PAGE: 2
DATE ISSUED: 26-SEP-2007

SUBJ NO. C	COURSE TITLE	CRED GRD PTS	R	SUBJ NO. C	COURSE TITLE	CRED GRD PTS	R
Institution Information continued:				Institution Information continued:			
UHON 301	01 SEM/GLOBALIZATION	3.000 A	12.00	ARTH 202	01 HISTORY OF ART II	3.000 A	12.00
Ehrs:	15.000 QPts:	57.99		BIOC 498	01 SENIOR HONORS RESRCH	2.000 A	8.00
GPA-Hrs:	15.000 GPA:	3.86		BIOL 456	01 IMMUNOLOGY	3.000 A	12.00
Dean's List				CHEM 312	01 PHYSICAL CHEMISTRY	4.000 A	16.00
Spring 2004				CHEM 546	01 T/BIOANALYTICAL CHEM	3.000 A	12.00
Arts & Sciences				POLS 240	01 INTERNATL POLITICS	3.000 A	12.00
BIOC 446	01 INTENSIVE BIOCHEM II	4.000 A	16.00	Ehrs:	18.000 QPts:	72.00	
BIOC 448	01 BIOCHEMICAL METHODS	3.000 A	12.00	GPA-Hrs:	18.000 GPA:	4.00	
BIOC 499	01 UNDERGRAD RESEARCH	1.000 A	4.00	Dean's List			
PENP 160	01 WGHTRNG & PHY COND	1.000 A+	4.33	Fall 2005			
PHIL 354	01 METAPHYSICS	3.000 A+	12.99	Arts & Sciences			
POLS 200	01 AMERICAN POLITICS	3.000 A	12.00	BIOC 497	01 SENIOR HONORS RESRCH	3.000 A	12.00
SPAN 302	01 T/DVLP SP WRITNG SKLS	3.000 A	12.00	BIOM 508	01 ADV CELL BIOLOGY	4.000 A+	17.32
Ehrs:	18.000 QPts:	73.32		PHIL 202	01 MODERN PHILOSOPHY	3.000 A	12.00
GPA-Hrs:	18.000 GPA:	4.07		POLS 280	01 INTRO POLIT ANALYS	3.000 A+	12.99
Dean's List				POLS 322	01 HUMAN RTS & POL VIOL	3.000 A+	12.99
Fall 2004				Ehrs:	16.000 QPts:	67.30	
Arts & Sciences				GPA-Hrs:	16.000 GPA:	4.20	
BIOL 581	01 ADV MOLECULAR BIOL	4.000 A	16.00	Dean's List			
CHEM 311	01 PHYSICAL CHEMISTRY	4.000 A+	17.32	Spring 2006			
PENP 124	01 BALLROOM DANCE	1.000 A	4.00	Arts & Sciences			
PHIL 356	01 SYMBOLIC LOGIC	4.000 A	16.00	BIOC 498	01 SENIOR HONORS RESRCH	1.000 A	4.00
POLS 300	01 T/MEDIA AND POLITICS	3.000 A	12.00	CHEM 454	01 INSTRUMNTL ANLYS/LAB	4.000 A+	17.32
POLS 342	01 AMER FOREIGN POLICY	3.000 A	12.00	PHIL 442	01 INDIV PH/EMERSON	3.000 A	12.00
Ehrs:	19.000 QPts:	77.32		POLS 307	01 POL OF ETHNIC GROUPS	3.000 A	12.00
GPA-Hrs:	19.000 GPA:	4.06		POLS 442	01 INTNL PEACEKEEPING	3.000 A	12.00
Dean's List				***** CONTINUED ON PAGE 3 *****			
Spring 2005				***** CONTINUED ON NEXT COLUMN *****			
Arts & Sciences							

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PAGE: 3
DATE ISSUED: 26-SEP-2007

SUBJ NO. C	COURSE TITLE	CRED GRD PTS	R	SUBJ NO. C	COURSE TITLE	CRED GRD PTS	R
Institution Information continued:				Fall 2007			
UHON 302	01 SEM/WITH LIT&JUSTICE	3.000 A	12.00	IN PROGRESS WORK			
Ehrs:	17.000 QPts:	69.32		BIOL 402AH ABQT: Intro Mathematical Biology	3.000 IN PROGRESS		
GPA-Hrs:	17.000 GPA:	4.07		In Progress Credits	3.000		
Dean's List				***** TRANSCRIPT TOTALS *****			
Summer 2006				INSTITUTION	Ehrs:	165.000 QPts:	657.90
Arts & Sciences					GPA-Hrs:	165.000 GPA:	3.98
UHON 301	01 SEM/BIODVRSTY IN AUS	3.000 A	12.00	TRANSFER	Ehrs:	43.000 QPts:	0.00
UHON 301	01 SEM/RSCH MTHD IN AUS	3.000 A	12.00		GPA-Hrs:	0.000 GPA:	0.00
Ehrs:	6.000 QPts:	24.00		OVERALL	Ehrs:	208.000 QPts:	657.90
GPA-Hrs:	6.000 GPA:	4.00			GPA-Hrs:	165.000 GPA:	3.98
Fall 2006				***** END OF TRANSCRIPT *****			
College of Arts and Sciences							
BIOC 463	ABQ Biochemistry of Disease I	3.000 A-	11.01				
BIOC 465	ABQ Biochemistry Education	3.000 A	12.00				
MUS 139	ABQ Music Appreciation	3.000 A	12.00				
POLS 376	ABQ Health Policy and Politics	3.000 A	12.00				
Ehrs:	12.000 QPts:	47.01					
GPA-Hrs:	12.000 GPA:	3.91					
Dean's List							
Spring 2007							
College of Arts and Sciences							
BIOC 499	ABQ Undergraduate Research	3.000 CR	A .00				
BIOL 402E	ABQ T: Biomedical Research II	1.000 A	4.00				
MATH 316	ABQ Applied Ordinary Diff Equas	3.000 A	12.00				
POLS 260	ABQ Political Ideas	3.000 A+	12.99				
POLS 362	ABQ Modern Political Theory	3.000 A	12.00				
Ehrs:	10.000 QPts:	40.99					
GPA-Hrs:	10.000 GPA:	4.09					
***** CONTINUED ON NEXT COLUMN *****							

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