## Curriculum vitae (June 2017)

## 1. Personal information

Name: Adrian Egli, PD Dr. med. Dr. phil. (MD PhD)

Date/Place of birth: 26.09.1978 in Basel

Nationality: Swiss

Titles: Dr. med./MD (11/2004), Dr. phil./PhD (12/2008, summa cum laude), Clinical

Microbiology, FAMH (April 2015) and Privatdozent/PD (05/2015)

Contact: Phone: +41 61 556 5749, Mobile: +41 79 173 6229, Email: adrian.egli@usb.ch

Website: <a href="https://biomedizin.unibas.ch/research/research-group-leaders/">https://biomedizin.unibas.ch/research/research-group-leaders/</a>

http://appliedmicrobiologyresearch.net

#### 2. Education

2006 - 2008: PhD thesis (summa cum laude), "Cellular and humoral immunity against Polyomavirus

BK and human Cytomegalovirus in kidney transplanted patients". University of Basel

2004: MD thesis "Suicide and depression: suicides in the family and social environment",

University of Basel

**1998 - 2004:** Medicine at the University Basel, Switzerland

## 3. Employment History including Current Position

09/2015 - to date: Head of Division, Clinical Microbiology, University Hospital Basel

11/2014 - to date: Research Group Leader, "Applied Microbiology Research" Laboratory, Department of

Biomedicine

2012 - 2015: Fellow in Clinical Microbiology (FAMH), University Hospital Basel

2010 - 2011: Clinical Fellowship "Transplant Infectious Disease", University of Alberta (Canada), as

well as Post-doctoral fellowship, Li Ka Shing Institute for Virology, University of Alberta

2008 - 2009: Resident Internal Medicine, University Hospital Basel. Focusing: Haematology and

Infectious Diseases

**2005:** Resident Internal Medicine, Spital Dornach, Switzerland)

## 4. Institutional Responsibilities

01/2017 - to date: Secretary of the Personalized Health Cluster on Infectiology, University of Basel

12/2016 - to date: Swiss Biobanking Platform, Head of Working Group on Microbiology

## 5. Approved Research Projects

(i) microRNA profiling to assess the risk of infectious diseases (2010 - 2011): Role: Post doctoral fellowship – design and execution of experiments, data analysis, fundraising

(ii) Interferon lambda and vaccine response (2014 – 2017): Role: PI – design of studies, planning and supervising of experiments, data analysis, fundraising

(iii) Influenza Transmission in the City of Basel (2016 – 2019): Role: Partner status – due to restrictions of the Ambizione program on grants - major contributions to the whole project including study design, recruitment organisation, whole genome sequencing, data analysis, fundraising.

(iv) Campylobacter spp. in Basel – the impact of Fondue Chinoise (2016 - 2017). Role: PI – study design, sample collection, whole genome sequencing, data analysis, fundraising

(v) Understanding transmission of ESBL plasmids (2016 - 2019). Role: Co-applicant and partner - sample collection, whole genome sequencing, data analysis, fundraising

(vi) In vivo evolutions of bacteria during sepsis and antibiotic treatment (2016 – 2018): Role: PI – study design, sample collection, whole genome sequencing, data analysis, fundraising

(vii) Biobanking at the University Hospital and beyond (2016 – 2018). Role: Co-applicant - coordination of microbiological samples, fundraising.

(viii) Successful application in collaboration with the ETH Zurich for a NRP72 grant to develop a microfluid-based device, which will allow to rapidly assess minimal inhibitory concentrations. Role: Co-applicant – gold standard comparison against diagnostic performance, routine assessment of handling and performance, fundraising.

## 6. Supervision of Junior Researchers at Graduate and Postgraduate Level

**2013-2014**: Master thesis: Yvonne Hollenstein, B.Sc., Medical faculty, University of Basel, Project: "Travel medicine after allogeneic stem cell transplantation".

since 2014: PhD thesis: Mohamedyaseen Syedbasha, M.Sc., Department Biomedicine, University of Basel, Project: "Interferon lambda blocking molecules"

since 2015: PhD thesis: Janina Linnik, M.Sc., Department Biomedicine, University of Basel, Project:

"Computational Modelling of IFN lambda in vaccination".

2015-2016: MD thesis: Yvonne Hollenstein, pract. med., Medical faculty, University of Basel, Project:

"Influencing clinical factors on vaccine response"

## 7. Teaching Activities

Undergraduate Teaching (University of Basel):

November 2014: "Leukozyten im peripheren Blut" and "Infections in the immunosuppressed host"

**Fall Semesters 2015 and 2016:** Normalflora, Grampositive Kokken I and II, Gramnegative Stäbchen, Gramnegative Kokken, Sporenbildner und Anaerobier, Tutoriat A-PoT - Mikrobiologie 1 (TB Blut/Infektion/Abwehr), Aspekte der mikrobiologischen Diagnostik I and II, Tutoriat B-PoT - Mikrobiologie 1 and 2, Herd immunity and Transmission of pathogens

Spring Semesters 2016 and 2017: Repetitorium Mikrobiologie, gram positive / gram negative Bakterien.

· Postgraduate Teaching:

**Immunomeeting**: University of Basel (2014 - to date)

Advising on dissertations: University of Alberta (2010 - 2011) and University of Basel (2012 - to date)

**Supervising postgraduates**: University of Basel (2006 - 2008 and 2012 - to date), and University of Alberta (2010 - 2011)

## 8. Memberships in Panels, Boards / Individual Scientific Reviewing Activities

**Grants**: ESCMID scientific grants

Conferences: Poster Judge Swiss Society of Microbiology (Bern 2016), Abstract for ECCMID (Vienna, 2017)

Journals: American Journal of Transplantation, BMC Infectious Diseases, Clinical Transplantation, Journal

of Clinical Virology, Journal for Leucocyte Biology, Journal of Medical Virology, Journal for Microbiological Methods, Plos one, Swiss Medical Weekly, Transplantation, Transplant Infectious

Diseases

## 9. Active Memberships in Scientific Societies, Fellowships in Renowned Academies

2015 - to date Anresis, Swiss Surveillance for Antibiotic Resistance, Member of the Steering Committee and American Society of Microbiology (ASM)

2014 - to date Federatio Analyticorum Medicinalium Helveticorum (FAMH), European Society for Infectious Diseases and Microbiology (ESCMID), Board members of the Study Group: Genomics and molecular diagnostics (ESGMD) and of the Study Group: Epidemiological Markers (ESGEM)

2013 - to date Infectious Disease Working Group of the Swiss Transplant Cohort Study (STCS)

2013 - 2014 Post Doc Career Seminar Organisation Committee as Board Member, Department of Biomedicine, University of Basel

2006 - 2015 American Society of Transplantation (AST) - Infectious Diseases Community of Practice (ID COP), Fellow Representative ID COP 2013/2014, Basic Research COP and Trainee and Young Faculty COP

2005 - to date Alumni Medical Faculty, University of Basel and of University of Basel

1998 - 2004 Fachgesellschaft Medizin, University of Basel, Student representative medical faculty

## 10. Organisation of Conferences

**09/2017**, Full-day, international symposia: Translation of Next Generation Sequencing into routine application for Clinical Microbiology. Basel, Switzerland, Main organizer

**03/2017**, 1<sup>st</sup> ESCMID capacity forming workshop (3 day with 18 European faculty members) on MALDI-TOF based diagnostics, Basel, Switzerland, Main organizer with a total of 80 participants

**11/2015**, MALDI-TOF MS based typing: capacity forming workshop. Basel, Switzerland, Main organizer with a total of 25 participants

## 11. Prizes, Awards, Fellowships

2015	Alumni Awards of the Medical Faculty of the University of Basel for research activities
2014	Young Investigator Award American Society of Transplantation (San Francisco, USA) "Effect of
	Mycophenolate mofetil on Th2 and B cell response after influenza vaccination"

Young Investigator Award American Society of Transplantation (Seattle, USA) "H1N1-specific IL4 and IFN-gamma producing T-cells, T-follicular helper cells, and B-cell responses correlate to

seroconversion after transplantation"

## Major Scientific Achievements in the last 5 Years

The **rapid detection** of pathogens is an important first step in the epidemiological work-up of a fast evolving transmission chain. Pathogen **transmission is dependent on a series of complex factors** such as population densities, age structures, education and hygiene concepts, social and cultural behaviours, and individual and herd immunity including vaccine rates. The **recent technological advances allow sequencing of the whole genome** of pathogens, and **reconstruction of phylogenetic trees at the highest resolution allows us to explore this fascinating complexity**.

My main aims are: (i) to develop new diagnostic and screening assays for rapid detection of multidrug resistant and virulent pathogens; (ii) to explore novel typing technologies such as whole genome sequencing (including long reads e.g. Pacbio, Minion, Roche Genia) and MALDI-TOF mass spectrometry for clinical applications; (iii) to combine phylogenetic tree structures with the impact of individual and herd immunity at various scales using computational models; (iv) to understand geographical distributions of pathogens and herd immunity (e.g. vaccine rates); (v) to understand pathogen evolution in the context of the host/pathogen/environment interaction. This could lead to the identification of the most critical factors for transmission in dynamic environments. Such information will allow the generation of novel intervention strategies within hospitals and public health institutions, to reduce the transmission and overall burden of infections.

#### Development of new tools for pathogen transmission:

A crucial first step is the rapid assessment of patient specimens for potentially contagious pathogens. The use of MALDI-TOF mass spectrometry and isothermal amplification technologies are in my main focus of research (see publication list). Next, the combination of collected clinically meaningful pathogen isolates with clinical and epidemiological data is of importance. Such information may allow us to assess pathogen evolution at various stages of disease e.g. during evolutionary bottlenecks such as antibiotic selection pressure. The required key infrastructure includes a state-of-the-art biobanking, a clinical data warehouse, and an -omics core facility to describe in detail the pathogen pheno- and genotypes.

The **construction of a biobank** is already a personal focus. Using the recently received SNF Biolink grant, I am currently constructing the microbial part of a **biobank management software** for the University Hospital Basel. This will allow the linking of whole genome sequenced data of pathogens with respective phenotypical information such as resistance profiles. Interfaces to the Biozentrum and D-BSSE will allow broader collaborations using multiple –omics technologies. In addition, the **clinical data warehouse** will complement clinical and epidemiological data e.g. clinical course, movement in between wards. In various initiatives, I am coordinating this exchange of whole genome sequencing data and samples on a Swiss wide level.

Whole genome sequencing data routinely generated e.g. during an outbreak investigation, can be further used. Data mining of already existing information will further improve the efficacy of my research. The additional implementation of cutting edge technologies such as long read sequencing is crucial. Initial testing in research laboratory is followed by a translational phase into clinical applications. In collaboration with clinics, we can develop new diagnostics to detect transmission events with even greater precision, more cost effectively and faster than ever before.

## Understanding pathogen transmission with an environment:

Through various research projects, I am trying to improve the diagnostic process of e.g. antibiotic resistance. In addition, multiple projects help to shape my understanding of the complexity of transmission chains within environments.

- (A) **New diagnostics**: Recently, I started to collaborate within a NRP72 funding project together with the ETH Zurich (Dittrich Group). We aim to develop a **novel** microfluidic device, which will allow the **rapid determination of minimal inhibitory concentrations** for microbes. Similar to this, a subproject within the Personalized Health *Infectiology* cluster (multiple research groups) uses **sepsis** as a disease model to describe the most common evolving antibiotic resistant pathogens. First the **genomes of bacteria will be screened for evolving resistance** during an infection, using whole genome sequencing. Next, these resistance mechanisms will be integrated into an **ultra-rapid isothermal amplification panel assay** which allows us to genetically screen within minutes for resistance directly from patient material.
- (B) **Transmission of infectious disease:** In various projects I try to understand pathogen transmission at various scales, reaching from plasmid transmission between bacteria within hosts towards larger geographic areas.
- (i) Towards quantification of the contribution of plasmids to the spread of antibiotic resistance (two NRP72 grants). In a subproject, we aim to understand the within-host rate of plasmid exchange by using mouse models (collaboration with various ETH groups). In a second subproject (Tschudin Group), we will whole genome sequence ESBL-producing Enterobacteriaceae of the Clinical Microbiology strain collection and add prospectively collected isolates from the University Hospital and environment. In both subprojects we will need to

develop novel sequencing strategies in order to technically and analytically manage the requirements of plasmid genomics e.g. by using long read sequencing or mate pairing. Both projects will allow understanding of the factors influencing, and rates of, plasmid transmission within a host and the environment.

- (ii) Influenza transmission in the City of Basel (SNF interdisciplinary grant, ETH Zurich and Human Geography, University of Basel): In this project, we link the influenza cases of the flu season 2016/2017 with available metadata on place of living and working, usage of public transport and vaccine rates. The phylogenetic tree generated by whole genome sequencing will include geographical and immunological information. This project allows understanding of the complex factors modulating disease transmission within a city.
- (iii) Swiss-wide surveillance database a proof of concept with methicillin resistant Staphylococcus aureus (MRSA): For the preparation of potential large scale outbreaks, I currently coordinate the generation of a public health surveillance platform including multiple clinical and veterinary sites. We will adapt the nextstrain tool (www.nextstrain.org) to model infectious diseases using whole genome sequenced data throughout Switzerland. As a proof of concept this will start with MRSA, however, clearly aiming to expand this to multiple additional pathogens.

#### Vision for the future:

Clearly, the rapid dynamics and complexity of outbreaks are important challenges for hospitals and public health. These **challenges can best be addressed with state-of-the-art diagnostic workflows** considering the whole analytic process from sample collection to reporting of results, **cutting edge typing technologies**, **and the integration of local metadata** from patients also with **public health surveillance**. A dedicated research in infection epidemiology and clinical microbiology allows the transition of new technological developments, data integration and modelling to address the most urgent epidemiological questions now and in the future.

# Research Output List of the Last Five Years

# 1. Publications in International Peer-Reviewed Scientific Journals

https://www.ncbi.nlm.nih.gov/pubmed/?term=Egli+A

Total impact factor: 251.829, Personal H-index: 16, Sum of citations w/o self-citations: 1032

Original papers	Impact Factor
Evaluation of two novel chemiluminescence immunoassays for the detection of Clostridium difficile glutamate dehydrogenase and toxin A&B.	1.857
Blaich A, Frei R, Castellano C, Kiessling C, Geschke A, Rentsch KM, <b>Egli A.</b>	
J Microbiol Methods. 2017 Apr;135:63-65. doi: 10.1016/j.mimet.2017.02.004. Epub 2017 Feb 10.	
Comparison of two rapid biochemical tests and four chromogenic selective media for detection of	1.857
carbapenemase-producing Gram-negative bacteria.	
Hinić V, Amrein I, Stammler S, Heckendorn J, Meinel D, Frei R, <b>Egli A</b> .	
J Microbiol Methods. 2017 Jan 25. pii: S0167-7012(17)30022-2. doi: 10.1016/j.mimet.2017.01.012.	
A novel method for detection of IFN-lambda 3 binding to cells for quantifying IFN-lambda receptor	1.858
expression.	
Santer DM, Minty GE, Mohamed A, Baldwin L, Bhat R, Joyce M, <b>Egli A</b> , Tyrrell DL, Houghton M.	
J Immunol Methods. 2017 Mar 6. pii: S0022-1759(17)30004-2. doi: 10.1016/j.jim.2017.03.001.	
A Cross-Sectional Study of Colonization Rates with Methicillin-Resistant Staphylococcus aureus	3.057
(MRSA) and Extended-Spectrum Beta-Lactamase (ESBL) and Carbapenemase-Producing	
Enterobacteriaceae in Four Swiss Refugee Centres.	
Piso RJ, Käch R, Pop R, Zillig D, Schibli U, Bassetti S, Meinel DM, <b>Egli A.</b>	
PLoS One. 2017 Jan 13;12(1):e0170251. doi: 10.1371/journal.pone.0170251.  Outbreak investigation for toxigenic Corynebacterium diphtheriae wound infections in refugees from	4.575
Northeast Africa and Syria in Switzerland and Germany by whole genome sequencing.	4.575
Meinel DM, Kuehl R, Zbinden R, Boskova V, Garzoni C, Fadini D, Dolina M, Blümel B, Weibel T,	
Tschudin-Sutter S, Widmer AF, Bielicki JA, Dierig A, Heininger U, Konrad R, Berger A, Hinic V,	
Goldenberger D, Blaich A, Stadler T, Battegay M, Sing A, <b>Egli A</b> .	
Clin Microbiol Infect. 2016 Dec;22(12):1003.e1-1003.e8. doi: 10.1016/j.cmi.2016.08.010.	
Human microRNA responses predict cytomegalovirus replication following solid organ	6.344
transplantation.	0.011
Han SH, Kumar D, Ferreira VH, <b>Egli A</b> , Hirsch HH, Weisser M, Garzoni C, van Delden C, Bochud	
PY, Manuel O, Meylan P, Boggian K, Husain S, Mueller NJ, Humar A; Swiss Transplant Cohort	
Study	
J Infect Dis. 2016 Dec 21. pii: jiw596. doi: 10.1093/infdis/jiw596. [Epub ahead of print]	
The Technical and Biological Reproducibility of Matrix-Assisted Laser Desorption Ionization-Time of	3.057
Flight Mass Spectrometry (MALDI-TOF MS) Based Typing: Employment of Bioinformatics in a	
Multicenter Study.	
Oberle M, Wohlwend N, Jonas D, Maurer FP, Jost G, Tschudin-Sutter S, Vranckx K, <b>Egli A</b> .	
PLoS One. 2016 Oct 31;11(10):e0164260. doi: 10.1371/journal.pone.0164260.	
Association of daptomycin use with resistance development in Enterococcus faecium bacteraemia-a	4.575
7-year individual and population-based analysis.	
Egli A, Schmid H, Kuenzli E, Widmer AF, Battegay M, Plagge H, Frei R, Achermann R, Weisser M.	
Clin Microbiol Infect. 2016 Oct 13. pii: S1198-743X(16)30462-1. doi: 10.1016/j.cmi.2016.10.003. [Epub ahead of print]	
Impact of MALDI-TOF-MS-based identification directly from positive blood cultures on patient	4.575
management: a controlled clinical trial.	4.575
Osthoff M, Gürtler N, Bassetti S, Balestra G, Marsch S, Pargger H, Weisser M, <b>Egli A</b> .	
Clin Microbiol Infect. 2016 Aug 26. pii: S1198-743X(16)30329-9. doi: 10.1016/j.cmi.2016.08.009.	
[Epub ahead of print]	
An ELISA Based Binding and Competition Method to Rapidly Determine Ligand-receptor Interactions.	1.113
Syedbasha M, Linnik J, Santer D, O'Shea D, Barakat K, Joyce M, Khanna N, Tyrrell DL, Houghton M,	
Egli A.	
J Vis Exp. 2016 Mar 14;(109). doi: 10.3791/53575.	
Prevention of hepatitis C virus infection using a broad cross-neutralizing monoclonal antibody (AR4A)	3.951
and epigallocatechin gallate.	
O'Shea D, Law J, <b>Egli A</b> , Douglas D, Lund G, Forester S, Lambert J, Law M, Burton DR, Tyrrell DL,	
Houghton M, Humar A, Kneteman N.	
Liver Transpl. 2016 Mar;22(3):324-32. doi: 10.1002/lt.24344. Epub 2016 Jan 29.	
Complexity of Host Micro-RNA Response to Cytomegalovirus Reactivation After Organ	5.669

Original papers	Impact Factor
Transplantation.	
<b>Egli A</b> , Lisboa LF, O'Shea D, Asberg A, Mueller T, Emery V, Kumar D, Humar A. Am J Transplant. 2016 Feb;16(2):650-60. doi: 10.1111/ajt.13464. Epub 2015 Oct 13.	
Mannose-binding lectin protein and its association to clinical outcomes in COPD: a longitudinal study.	3.751
Mandal J, Malla B, Steffensen R, Costa L, <b>Egli A</b> , Trendelenburg M, Blasi F, Kostikas K, Welte T, Tarrog A, Louis B, Boardan W, Milankovia B, Aorta L, Bahda CC, Lagoma A, Boardan K, Both M	
Torres A, Louis R, Boersma W, Milenkovic B, Aerts J, Rohde GG, Lacoma A, Rentsch K, Roth M, Tamm M, Stolz D.	
Respir Res. 2015 Dec 18;16:150. doi: 10.1186/s12931-015-0306-3.	
Hcmv-miR-UL22A-5p: A Biomarker in Transplantation With Broad Impact on Host Gene Expression	5.669
and Potential Immunological Implications.  Lisboa LF, <b>Egli A</b> , O'Shea D, Åsberg A, Hartmann A, Rollag H, Pang XL, Tyrrell DL, Kumar D, Humar	
A.	
Am J Transplant. 2015 Jul;15(7):1893-902. doi: 10.1111/ajt.13222. Epub 2015 Apr 1.	F 000
CCL8 and the Immune Control of Cytomegalovirus in Organ Transplant Recipients. Lisboa LF, <b>Egli A</b> , Fairbanks J, O'Shea D, Manuel O, Husain S, Kumar D, Humar A.	5.669
Am J Transplant. 2015 Jul;15(7):1882-92. doi: 10.1111/ajt.13207. Epub 2015 Mar 12.	
T cells specific for different latent and lytic viral proteins efficiently control Epstein-Barr virus-	3.625
transformed B cells.  Nowakowska J, Stuehler C, <b>Egli A</b> , Battegay M, Rauser G, Bantug GR, Brander C, Hess C, Khanna	
N.	
Cytotherapy. 2015 Sep;17(9):1280-91. doi: 10.1016/j.jcyt.2015.06.003.	
Effect of Immunosuppression on T-Helper 2 and B-Cell Responses to Influenza Vaccination.	6.344
<b>Egli A</b> , Humar A, Widmer LA, Lisboa LF, Santer DM, Mueller T, Stelling J, Baluch A, O'Shea D, Houghton M, Kumar D.	
J Infect Dis. 2015 Jul 1;212(1):137-46. doi: 10.1093/infdis/jiv015. Epub 2015 Jan 14.	
The swiss transplant cohort study: lessons from the first 6 years.	1.493
Berger C, Bochud PY, Boggian K, Cusini A, <b>Egli A</b> , Garzoni C, Hirsch HH, Hoffmann M, Khanna N, Manuel O, Meylan P, Nadal D, van Delden C, Weisser M, Mueller NJ; Transplant Infectious Diseases	
Working Group, Swiss Transplant Cohort Study.	
Curr Infect Dis Rep. 2015 Jun;17(6):486. doi: 10.1007/s11908-015-0486-5.	
Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF) directly from positive blood culture flasks allows rapid identification of bloodstream infections in	1.459
immunosuppressed hosts.	
Egli A, Osthoff M, Goldenberger D, Halter J, Schaub S, Steiger J, Weisser M, Frei R.	
Transpl Infect Dis. 2015 Jun;17(3):481-7. doi: 10.1111/tid.12373. Epub 2015 May 19.	1 5 4 0
Travelling activity and travel-related risks after allogeneic haematopoietic stem cell transplantation - a single centre survey.	1.549
Hollenstein Y, Elzi L, Hatz C, Passweg J, Weisser M, Stöckle M, Halter JP, <b>Egli A</b> .	
Swiss Med Wkly. 2015 May 29;145:w14136. doi: 10.4414/smw.2015.14136. eCollection 2015. 2 / 3	0.057
Matrix-assisted laser desorption/ionization time of flight mass-spectrometry (MALDI-TOF MS) based typing of extended-spectrum β-lactamase producing E. colia novel tool for real-time outbreak	3.057
investigation.	
Egli A, Tschudin-Sutter S, Oberle M, Goldenberger D, Frei R, Widmer AF.	
PLoS One. 2015 Apr 10;10(4):e0120624. doi: 10.1371/journal.pone.0120624. eCollection 2015.  Influence of IFNL3/4 polymorphisms on the incidence of cytomegalovirus infection after solid-organ	8.736
transplantation.	0.730
Manuel O, Wójtowicz A, Bibert S, Mueller NJ, van Delden C, Hirsch HH, Steiger J, Stern M, <b>Egli A</b> ,	
Garzoni C, Binet I, Weisser M, Berger C, Cusini A, Meylan P, Pascual M, Bochud PY; Swiss	
Transplant Cohort Study.  J Infect Dis. 2015 Mar 15;211(6):906-14. doi: 10.1093/infdis/jiu557. Epub 2014 Oct 9.	
IL-28B is a key regulator of B- and T-cell vaccine responses against influenza.	7.003
Egli A, Santer DM, O'Shea D, Barakat K, Syedbasha M, Vollmer M, Baluch A, Bhat R, Groenendyk J,	
Joyce MA, Lisboa LF, Thomas BS, Battegay M, Khanna N, Mueller T, Tyrrell DL, Houghton M, Humar A, Kumar D.	
PLoS Pathog. 2014 Dec 11;10(12):e1004556. doi: 10.1371/journal.ppat.1004556. eCollection 2014	
Dec.	
Immunomodulatory Function of Interleukin 28B during primary infection with cytomegalovirus.	6.344
<b>Egli A</b> , Levin A, Santer DM, Joyce M, O'Shea D, Thomas BS, Lisboa LF, Barakat K, Bhat R, Fischer KP, Houghton M, Tyrrell DL, Kumar D, Humar A.	
KP, HOUGHIOH W, TYHEII DE, KUIHAI D. HUHIAI A.	
J Infect Dis. 2014 Sep 1;210(5):717-27. doi: 10.1093/infdis/jiu144. Epub 2014 Mar 11.  Seven hours to adequate antimicrobial therapy in urosepsis using isothermal microcalorimetry.	3.993

Original papers	Impact Factor
Wagenlehner F, Bonkat G. J Clin Microbiol. 2014 Feb;52(2):624-6. doi: 10.1128/JCM.02374-13. Epub 2013 Nov 13.	
Low Levels of Mannan-Binding Lectin or Ficolins Are Not Associated with an Increased Risk of Cytomegalovirus Disease in HIV-Infected Patients.  Egli A, Schäfer J, Osthoff M, Thiel S, Mikkelsen C, Rauch A, Hirsch HH, Bucher HC, Young J, Jensenius JC, Battegay M, Trendelenburg M; Swiss HIV Cohort Study.	3.730
PLoS One. 2013;8(1):e51983. doi: 10.1371/journal.pone.0051983. Epub 2013 Jan 4.  Comparison of the Effect of Standard and Novel Immunosuppressive Drugs on CMV-Specific T-Cell Cytokine Profiling.  Egli A, Kumar D, Broscheit C, O'Shea D, Humar A.	3.781
Transplantation. 2013 Feb 15;95(3):448-55. doi: 10.1097/TP.0b013e318276a19f.  Blockade of programmed death receptor-1 signaling restores expression of mostly proinflammatory cytokines in anergic cytomegalovirus-specific T cells.  Dirks J, <b>Egli A</b> (shared first co-author), Sester U, Sester M, Hirsch HH.  Transpl Infect Dis. 2013 Feb;15(1):79-89. doi: 10.1111/tid.12025. Epub 2012 Nov 26.	1.984
JC and BK polyomavirus-specific immunoglobulin G responses in patients thymectomized in early childhood.  Prelog M, <b>Egli A</b> , Zlamy M, Hirsch HH	3.287
J Clin Virol. 2013 Nov;58(3):553-8. doi: 10.1016/j.jcv.2013.08.035. Epub 2013 Sep 5.  Randomized Controlled Trial of High-Dose Intradermal Versus Standard-Dose Intramuscular	6.192
Influenza Vaccine in Organ Transplant Recipients. Baluch A, Humar A, Eurich D, <b>Egli A</b> , Liacini A, Hoschler K, Campbell P, Berka N, Urschel S, Wilson L, Kumar D. Am J Transplant. 2013 Feb 13. doi: 10.1111/ajt.12149. [Epub ahead of print]	
Late presentation of HIV despite earlier opportunities for detection, experience from an Irish Tertiary Referral Institution.  O'Shea D, Ebrahim M, <b>Egli A</b> , Redmond D, McConkey S.  Ir J Med Sci. 2013 Jan 16. [Epub ahead of print]	0.506
An Analysis of Regulatory T-cell and Th-17 Cell Dynamics during Cytomegalovirus Replication in Solid Organ Transplant Recipients. <b>Egli A</b> , Silva M Jr., O'Shea D, Wilson EL, Kumar D, Humar A	3.730
PLoS One. 2012;7(11):e43937. doi: 10.1371/journal.pone.0043937. Epub 2012 Oct 11  Emergence of Aspergillus ustus infection during azole therapy in transplantation – case series and review of the literature. <b>Egli A</b> , Fuller J, Humar A, Lien D, Weinkauf J, Nador R, Kapasi A, Kumar D	3.781
Transplantation, 2012, 94 (4) 1-8.  Clinical management of eight cases with human metapneumovirus infection after allogeneic hematopoietic stem cell transplantation.  Egli A, Bucher Ch, Dumoulin A, Stern M, Buser A, Bubendorf L, Gregor, M. Servida P. Sommer G, Bremerich J, Gratwohl A, Khanna N, Widmer AF, Battegay M, Tamm M, Hirsch HH, Halter J Infection, 2012, DOI 10.1007/s15010-012-0279-9	2.440
Case reports and letters	Impact Factor
Concern regarding the alleged spread of the hypervirulent lymphogranuloma venereum chlamydia trachomatis strain in Europe.  Seth-Smith HM, Galán JC, Goldenberger D, Lewis DA, Peuchant O, Bébéar C, de Barbeyrac B, Bénard A, Carter I, Kok J, Bruisten SM, Versteeg B, Morré SA, Thomson NR, <b>Egli A</b> , de Vries HJ.  Euro Surveill. 2017;22(15):pii=30511. DOI: http://dx.doi.org/10.2807/1560-7917.ES.2017.22.15.30511	5.983
When two and ½ men go camping von Rotz M, Dierig A, Heininger U, Chrobak C, Baettig V, <b>Egli A</b> . BMC Infect Dis. 2017 Jan 30;17(1):102. doi: 10.1186/s12879-017-2213-3.	2.69
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Fasel D., Mellmann, A., Cernela, N. Hächler H. Fruth A., Khanna N., <b>Egli A.</b> , Beckmann Ch., Hirsch	
H., Goldenberger D., Stephan R.	
JCM03459-13R1, J Clin Microbiology, accepted.	

Review article	Impact Factor	
Die nächste Revolution in der klinischen Mikrobiologie: Whole Genome Sequencing.	-	
Meinel D, Seth-Smith HMB, <b>Egli A</b> .		
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Egli A		
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Tyrrell L., Houghton M., Battegay M., O'Shea D.		
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Egli A., Humar, A., Kumar D.		
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Viral impact on long-term kidney graft function,	3.000	
Helanterä I., <b>Egli A.</b> (shared first co-author), Koskinen P., Lautenschlager I., Hirsch, H. J Inf Dis NA 2010, 24(2) 339-371		
Cytomegalovirus and polyomavirus BK posttransplant.	3.167	
<b>Egli A.,</b> Binggeli S., Bodaghi S., Dumoulin A., Funk G. A., Khanna N., Leuenberger D., Gosert R.,	3.107	
Hirsch H. H.		
Nephrol Dialysis Transpl 2007 22:(Supl8) 72-82.		
Polyomavirus BK after Kidney Transplantation – Role of Molecular and Immunologic Markers.		
<b>Egli A.,</b> Dumoulin A., Köhli S., and Hirsch H.H.	_	
Trends in Transplantation. 2009; 3(2):85-102		
Neue Diagnostik in der Transplantationsmedizin: Cytomegalovirus (CMV)-spezifische T-Zellfrequenz		
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Letter to the Editor: BKV replication and cellular immune responses in renal transplant recipients.	NA	
Binggeli S., <b>Egli A.,</b> Dickenmann M., Binet I., Steiger J., Hirsch H.H.	13/3	
Am J. Transpl. 2006; 6: 2218-2219		
7 iii 6. Transpi. 2000, 0. 22 to 22 to	1	

## 2. Peer-Reviewed Books / Monographs

None

## 3. Peer-Reviewed Conference Proceedings

None

## 4. Contribution to Books

**Egli A**, Kumar D, Humar A Immunodiagnostics of CMV Infection After Transplantation 2012, Nova publisher, Editor: Lautenschlager I

Helanterä I, **Egli A\***, Koskinen P, Hirsch HH and Lautenschlager I Impact of Polyomavirus BK and Cytomegalovirus on the Kidney Allograft In: *Kidney Transplantation: Challenging the Future,* 2012, 273-288; Massimiliano Veroux and Pierfrancesco Veroux (Eds); 2012; Bentham Science Publishers \*shared first co-author

## 5. Patents and Licences

2013 PCT/IB2013/060289 for "Immunomodulatory Peptides and Methods of Use Thereof" First Named Inventor: Egli, Adrian.

## 6. Oral Contributions to International Conferences

Very regular contribution to national and international conferences. E.g. 27th ECCMID, the European Congress of Clinical Microbiology and Infectious Diseases, which took place in Vienna, Austria, 22 – 25 April, 2017. Title: A multi-centre prospective evaluation of the new FilmArray meningitis/encephalitis panel for rapid PCR-based diagnostics

#### 7. Outreach Activities

University Night with Science Booth on Immunology and Pathogens
 Day of Lunginfection with Science Booth on Pathogens in pulmonary infections

#### 8. General Contribution to Science

Clinical Microbiology at the University Hospital Basel: Since 2015, I am the head of division and main responsible person for supervising the production of diagnostic results, technical and medical validation of results in the division of clinical microbiology. This mainly includes the identification of bacterial, viral and fungal pathogens, the antibiotic resistance testing, and typing of pathogens for epidemiological questions. The results are discussed with clinical colleagues and in particular infectious disease specialists on a daily basis. In addition, I am responsible for the research and development of novel diagnostic techniques for clinical microbiology. A major achievement was the implementation of whole genome sequencing as the first ISO accredited center in Switzerland. The key priority is the routine performance of the diagnostic laboratory with efficient, cost effective and rapid performance of assays.

Research group leader at the Department of Biomedicine: Since 2014, I am an independent research group leader. My main responsibility is to acquire grants and supervise undergraduate and graduate students and postgraduate fellows. A key priority since 2015 is the stronger translation of research activities into the routine diagnostics and further building the bioinformatics expertise to do infection epidemiology research.

11/2015 MALDI-TOF MS based typing for outbreak monitoring – 1d Workshop main organizer

University Hospital Basel

03/2017 ESCMID Capacity Forming Workshop on MALDI-TOF MS – 3d Workshop main organizer with 20

international faculty members and international post graduate students

University Hospital Basel

08/2017 Next Generation Sequencing Translation into clinical routine diagnostics – 1d symposium main

organizer. www.advances-in-microbiology.ch

## 9. Other Artefacts with Documented Use

None