Keith Ballard:

Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase

Verba KA1, Wang RY1, Arakawa A2, Liu Y1, Shirouzu M2, Yokoyama S2, Agard DA3

1Howard Hughes Medical Institute (HHMI) and the Department of Biochemistry and Biophysics, University of California San Francisco, San Francisco, CA 94158, USA.

2RIKEN Systems and Structural Biology Center, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan.
3Howard Hughes Medical Institute (HHMI) and the Department of Biochemistry and Biophysics, University of California San Francisco, San Francisco, CA 94158, USA.

The Hsp90 molecular chaperone and its Cdc37 cochaperone help stabilize and activate more than half of the human kinome. However, both the mechanism by which these chaperones assist their "client" kinases and the reason why some kinases are addicted to Hsp90 while closely related family members are independent are unknown. Our structural understanding of these interactions is lacking, as no full-length structures of human Hsp90, Cdc37, or either of these proteins with a kinase have been elucidated. Here we report a 3.9 angstrom cryo-electron microscopy structure of the Hsp90-Cdc37-Cdk4 kinase complex. Surprisingly, the two lobes of Cdk4 are completely separated with the β4-β5 sheet unfolded. Cdc37 mimics part of the kinase N lobe, stabilizing an open kinase conformation by wedging itself between the two lobes. Finally, Hsp90 clamps around the unfolded kinase β5 strand and interacts with exposed N- and C-lobe interfaces, protecting the kinase in a trapped unfolded state. On the basis of this structure and an extensive amount of previously collected data, we propose unifying conceptual and mechanistic models of chaperone-kinase interactions.

In Vivo Conformational Dynamics of Hsp90 and Its Interactors

Cell Chem Biol. 2016 Jun 23;23(6):716-26.

Chavez JD1, Schweppe DK1, Eng JK1, Bruce JE2.

1Department of Genome Sciences, University of Washington School of Medicine, Seattle, WA 98195, USA.
2Department of Genome Sciences, University of Washington School of Medicine, Seattle, WA 98195, USA.

Hsp90 belongs to a family of some of the most highly expressed heat shock proteins that function as molecular chaperones to protect the proteome not only from the heat shock but also from other misfolding events. As many client proteins of Hsp90 are involved in oncogenesis, this chaperone has been the focus of intense research efforts. Yet, we lack structural information for how Hsp90 interacts with co-chaperones and client proteins. Here, we developed a mass-spectrometry-based approach that allowed quantitative measurements of in vitro and in vivo effects of small-molecule inhibitors on Hsp90 conformation, and interaction with co-

chaperones and client proteins. From this analysis, we were able to derive structural models for how Hsp90 engages its interaction partners in vivo, and how different drugs affect these structures. In addition, the methodology described here offers a new approach to probe the effects of virtually any inhibitor treatment on the proteome level.

Intracellular formation of α-synuclein oligomers and the effect of heat shock protein 70 characterized by confocal single particle spectroscopy

Biochem Biophys Res Commun. 2016 Jun 7.

Levin J1, Hillmer AS2, Högen T3, McLean PJ4, Giese A5.

1Department of Neurology, Ludwig-Maximilians-University, Marchioninistr. 15, 81377 Munich, Germany; German Center for Neurodegenerative Diseases - DZNE, Site Munich, Feodor-Lynen-Str. 17, 81377 Munich, Germany.
2Center for Neuropathology and Prion Research, Ludwig-Maximilians-University, Feodor-Lynen-Str. 23, 81377 Munich, Germany.
3Department of Neurology, Ludwig-Maximilians-University, Marchioninistr. 15, 81377 Munich, Germany.
4Department of Neuroscience, Mayo Clinic, Jacksonville, FL 32224, USA.
5Center for Neuropathology and Prion Research, Ludwig-Maximilians-University, Feodor-Lynen-Str. 23, 81377 Munich, Germany.

Synucleinopathies such as dementia with Lewy bodies or Parkinson's disease are characterized by intracellular deposition of pathologically aggregated α-synuclein. The details of the molecular pathogenesis of PD and especially the conditions that lead to intracellular aggregation of α-synuclein and the role of these aggregates in cell death remain unknown. In cell free in vitro systems considerable knowledge about the aggregation processes has been gathered. In comparison, the knowledge about these aggregation processes in cells is far behind. In cells α-synuclein aggregates can be toxic. However, the crucial particle species responsible for decisive steps in pathogenesis such as seeding a continuing aggregation process and triggering cell death remain to be identified. In order to understand the complex nature of intracellular α-synuclein aggregate formation, we analyzed fluorescent particles formed by venus and α-synuclein-venus fusion proteins and α-synuclein-hemi-venus fusion proteins derived from gently lyzed cells. With these techniques we were able to identify and characterize α-synuclein oligomers formed in cells. Especially the use of α-synuclein-hemi-venus fusion proteins enabled us to identify very small α-synuclein oligomers with high sensitivity. Furthermore, we were able to study the molecular effect of heat shock protein 70, which is known to inhibit α-synuclein aggregation in cells. Heat shock protein 70 does not only influence the size of α-synuclein oligomers, but also their quantity. In summary, this approach based on fluorescence single particle spectroscopy, that is suited for high throughput measurements, can be used to detect and characterize intracellularly formed α-synuclein aggregates and characterize the effect of molecules that interfere with α-synuclein aggregate formation.

Anti-aggregation activity of small heat shock proteins under crowded conditions

Int J Biol Macromol. 2016 May 24

Roman SG1, Chebotareva NA2, Kurganov BI2

1&2Bach Institute of Biochemistry, Research Center of Biotechnology of the Russian Academy of Sciences, Leninsky pr. 33, Moscow 119071, Russia.

It is becoming evident that small heat shock proteins (sHsps) are important players of protein homeostasis system. Their ability to bind misfolded proteins may play a crucial role in preventing protein aggregation in cells. The remarkable structural plasticity of sHsps is considered to underlie the mechanism of their activity. However, all our knowledge of the anti-aggregation functioning of sHsps is based on data obtained in vitro in media greatly different from the cellular highly crowded milieu. The present review highlights available data on the effect of crowding on the anti-aggregation activity of sHsps. There is some evidence that crowding affects conformation and dynamics of sHsps oligomers as well as their anti-aggregation properties. Crowding stimulates association of sHsp-client protein complexes into large-sized aggregates thus diminishing the apparent anti-aggregation activity of sHsps. Nevertheless, it is also shown that complexes between suboligomers (dissociated forms) of sHsps and client proteins may be stabilized and exist for longer period of time under crowded conditions. Moreover, crowding may retard the initial stages of aggregation which correspond to the formation of sHsp-containing nuclei and their clusters. Thus, dissociation of sHsps into suboligomers appears to be an important feature for the anti-aggregation activity of sHsps in crowded media.

sHSPdb: a database for the analysis of small Heat Shock Proteins

BMC Plant Biol. 2016 Jun 13;16(1):135.

Jaspard E1,2,3, Hunault G4

1Université d'Angers, UMR 1345 IRHS, SFR 4207 QUASAV, Angers, France. emmanuel.jaspard@univ-angers.fr.
2INRA, UMR 1345 IRHS, Beaucouzé, France. emmanuel.jaspard@univ-angers.fr.
3Agrocampus-Ouest, UMR 1345 IRHS, Angers, France. emmanuel.jaspard@univ-angers.fr.
4Université d'Angers, Laboratoire d'Hémodynamique, Interaction Fibrose et Invasivité tumorale hépatique, UPRES 3859, IFR 132, F-49045, Angers, France.

BACKGROUND:

small Heat Shock Proteins (sHSP) is a wide proteins family. SHSP are found in all kingdoms and they play critical roles in plant stress tolerance mechanisms (as well as in pathogenic microorganisms and are implicated in human diseases).

RESULTS:

sHSPdb (small Heat Shock Proteins database) is an integrated resource containing non-redundant, full-length and curated sequences of sHSP, classified on the basis of amino acids motifs and physico-chemical

properties. sHSPdb gathers data about sHSP defined by various databases (Uniprot, PFAM, CDD, InterPro). It provides a browser interface for retrieving information from the whole database and a search interface using various criteria for retrieving a refined subset of entries. Physicochemical properties, amino acid composition and combinations are calculated for each entry. sHSPdb provides automatic statistical analysis of all sHSP properties. Among various possibilities, sHSPdb allows BLAST searches, alignment of selected sequences and submission of sequences.

CONCLUSIONS:

sHSPdb is a new database containing information about sHSP from all kingdoms. sHSPdb provides a classification of sHSP, as well as tools and data for the analysis of the structure - function relationships of sHSP. Data are mainly related to various physico-chemical properties of the amino acids sequences of sHSP. sHSPdb is accessible at http://forge.info.univ-angers.fr/~gh/Shspdb/index.php .

Damian Guerra:

Kuruthukulangarakoola GT, Zhang J, Albert A, Winkler B, Lang H, Buegger F, Gaupels F, Heller W, Michalke B, Sarioglu H, Schnitzler JP, Hebelstrup KH, Durner J, Lindermayr C.

Nitric oxide-fixation by non-symbiotic hemoglobin proteins in Arabidopsis thaliana under N-limited conditions.

Plant Cell Environ. 2016 May 31;. [Epub ahead of print]PMID: 27245884 [PubMed - as supplied by publisher]

Wang H, Huang J, Li Y, Li C, Hou J, Liang W.
Involvement of nitric oxide-mediated alternative pathway in tolerance of wheat to drought stress by optimizing photosynthesis.
Plant Cell Rep. 2016 Jun 13;. [PMID: 27294277 [PubMed - as supplied by publisher]

Expression of alcohol dehydrogenase 5 in ovarian carcinoma: Effect on prognosis and therapeutic potential S. Sakra , S. Girib , R. Rattanb , E. Abdulfataha , V. Pardeshic , R.T. Morrisa , A.R. Munkarahb , R. Ali-Fehmia . a Wayne State University School of Medicine, Detroit, MI, USA, b Henry Ford Health System, Detroit, MI, USA, c Karmanos Cancer Center, Wayne State University, Detroit, MI, USA

Featured Poster Session

He W, Frost MC. Direct measurement of actual levels of nitric oxide (NO) in cell culture conditions using soluble NO donors. Redox Biology. 2016;9:1-14.

Prof. Vierling:

O'Meara TR, Veri AO, Polvi EJ, Li X, Valaei SF, Diezmann S, Cowen LE.
Mapping the Hsp90 Genetic Network Reveals Ergosterol Biosynthesis and Phosphatidylinositol-4-Kinase Signaling as Core Circuitry Governing Cellular Stress.
PLoS Genet. 2016 Jun;12(6):e1006142. PMID: 27341673 [PubMed - as supplied by publisher]

Chavez JD, Schweppe DK, Eng JK, Bruce JE.
InÂ Vivo Conformational Dynamics of Hsp90 and Its Interactors.
Cell Chem Biol. 2016 Jun 23;23(6):716-726. PMID: 27341434 [PubMed - as supplied by publisher]

Verba KA, Wang RY, Arakawa A, Liu Y, Shirouzu M, Yokoyama S, Agard DA.
Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase.
Science. 2016 Jun 24;352(6293):1542-7. PMID: 27339980 [PubMed - in process]

Sinha D, Srivastava S, D'Silva P.
Functional diversity of human mitochondrial J-proteins is independent of their association with the inner membrane presequence translocase.
J Biol Chem. 2016 Jun 21;. [Epub ahead of print] PMID: 27330077 [PubMed - as supplied by publisher]

Schulze A, Beliu G, Helmerich DA, Schubert J, Pearl LH, Prodromou C, Neuweiler H.
Cooperation of local motions in the Hsp90 molecular chaperone ATPase mechanism.
Nat Chem Biol. 2016 Jun 20;. [Epub ahead of print] PMID: 27322067 [PubMed - as supplied by publisher]

Deeng J, Chan KY, van der Sluis EO, Berninghausen O, Han W, Gumbart J, Schulten K, Beatrix B, Beckmann R.
Dynamic behavior of trigger factor on the ribosome.
J Mol Biol. 2016 Jun 16;. [Epub ahead of print] PMID: 27320387 [PubMed - as supplied by publisher]

SolÃs EJ, Pandey JP, Zheng X, Jin DX, Gupta PB, Airoldi EM, Pincus D, Denic V.
Defining the Essential Function of Yeast Hsf1 Reveals a Compact Transcriptional Program for Maintaining Eukaryotic Proteostasis.
Mol Cell. 2016 Jun 15;. [Epub ahead of print] PMID: 27320198 [PubMed - as supplied by publisher]

Aksu M, Trakhanov S, GÃ¶rlich D.
Structure of the exportin Xpo4 in complex with RanGTP and the hypusine-containing translation factor eIF5A.
Nat Commun. 2016 Jun 16;7:11952. PMID: 27306458 [PubMed - in process]

Adamczyk J, Deregowska A, Skoneczny M, Skoneczna A, Natkanska U, Kwiatkowska A, Rawska E, Potocki L, Kuna E, Panek A, Lewinska A, Wnuk M.
Copy number variations of genes involved in stress responses reflect the redox state and DNA damage in brewing yeasts.
Cell Stress Chaperones. 2016 Jun 14;. [Epub ahead of print] PMID: 27299603 [PubMed - as supplied by publisher]

Shu Q, Krezel AM, Cusumano ZT, Pinkner JS, Klein R, Hultgren SJ, Frieden C.
Solution NMR structure of CsgE: Structural insights into a chaperone and regulator protein important for functional amyloid formation.
Proc Natl Acad Sci U S A. 2016 Jun 13;. [Epub ahead of print] PMID: 27298344 [PubMed - as supplied by publisher]

Keshavarz-Tohid V, Taheri P, Taghavi SM, Tarighi S.
The role of nitric oxide in basal and induced resistance in relation with hydrogen peroxide and antioxidant enzymes.
J Plant Physiol. 2016 May 13;199:29-38. [Epub ahead of print] PMID: 27302004 [PubMed - as supplied by publisher]

Krasuska U, Ciacka K, Orzechowski S, Fettke J, Bogatek R, Gniazdowska A.
Modification of the endogenous NO level influences apple embryos dormancy by alterations of nitrated and biotinylated protein patterns.
Planta. 2016 Jun 14;. [Epub ahead of print] PMID: 27299743 [PubMed - as supplied by publisher]

Wang H, Huang J, Li Y, Li C, Hou J, Liang W.
Involvement of nitric oxide-mediated alternative pathway in tolerance of wheat to drought stress by optimizing photosynthesis.
Plant Cell Rep. 2016 Jun 13;. [PMID: 27294277 [PubMed - as supplied by publisher]

Liu B, Qian SB.
Characterizing inactive ribosomes in translational profiling.
Translation (Austin). 2016 Jan-Jun;4(1):e1138018. PMID: 27335722 [PubMed]

Chen C, Cui X, Beausang JF, Zhang H, Farrell I, Cooperman BS, Goldman YE.
Elongation factor G initiates translocation through a power stroke.

Proc Natl Acad Sci U S A. 2016 Jun 16;. [Epub ahead of print] PMID: 27313204 [PubMed - as supplied by publisher]

Physiologia Plantarum
Volume 157, Issue 3 Pages 255 - 399, July 2016

Special Issue: Plant Mitochondria

The roles of mitochondrial transcription termination factors (MTERFs) in plants (pages 389–399)
Víctor Quesada
Version of Record online: 14 MAR 2016 | DOI: 10.1111/ppl.12416

Cellular Signalling: Alert 15 June-21 June

Bridges between mitochondrial oxidative stress, ER stress and mTOR signaling in pancreatic β cells Review Article
Pages 1099-1104
Jing Wang, Xin Yang, Jingjing Zhang

Phosphorylated heat shock protein 27 promotes lipid clearance in hepatic cells through interacting with STAT3 and activating autophagy Original Research Article
Pages 1086-1098
Lei Shen, Zhilin Qi, Yanyan Zhu, Xiaomeng Song, Chunxia Xuan, Peiling Ben, Lei Lan, Lan Luo, Zhimin Yin

Nature Microbiology - Table of Contents alert, Volume 1, July 2016
Review Article | 24 June 2016

Drug resistance in eukaryotic microorganisms

Alan H. Fairlamb, Neil A. R. Gow, Keith R. Matthews & Andrew P. Waters
Nature Microbiology **1**, Article number: 16092 | doi:10.1038/nmicrobiol.2016.92

Making error-free DNA from RNA
DNA polymerase enzymes copy DNA into new strands of identical DNA. Reverse transcriptase (RT) enzymes copy RNA into DNA. Unlike many DNA polymerases, RT enzymes do not have a proofreading function that checks for errors in the newly synthesized DNA. Ellefson *et al.* use in vitro directed evolution and protein engineering to build an error-correcting RT from a prokaryotic DNA polymerase. The RT “xenopolymerase” shows increased fidelity as compared to natural RTs and should streamline and increase the precision of transcriptomics methods.
Science, this issue p. 1590

Plant Journal
IRE1, a component of the Unfolded Protein Response signaling pathway, protects pollen development in Arabidopsis from heat stress
Yan Deng, Renu Srivastava, Teagen D. Quilichini, Haili Dong, Yan Bao, Harry T. Horner and Stephen H. Howell
Accepted manuscript online: 15 JUN 2016 10:21AM EST | DOI: 10.1111/tpj.13239

Wu X, Jiang L, Yu M, An X, Ma R, Yu Z.
Proteomic analysis of changes in mitochondrial protein expression during peach fruit ripening and senescence.
J Proteomics. 2016 Jun 8;. [Epub ahead of print]PMID: 27288903 [PubMed - as supplied by publisher]

Schneider M, Rosam M, Glaser M, Patronov A, Shah H, Back KC, Daake MA, Buchner J, Antes I.
BiPPred: Combined sequence- and structure-based prediction of peptide binding to the Hsp70 chaperone BiP.
Proteins. 2016 Jun 10;. [Epub ahead of print]PMID: 27287023 [PubMed - as supplied by publisher]

Ansari MY, Haqqi TM.
Interleukin-1Î² induced Stress Granules Sequester COX-2 mRNA and Regulates its Stability and Translation in Human OA Chondrocytes.
Sci Rep. 2016 Jun 8;6:27611.PMID: 27271770 [PubMed - in process]

HanzÃ©n S, Vielfort K, Yang J, Roger F, Andersson V, Zamarbide-ForÃ©s S, Andersson R, Malm L, Palais G, Biteau B, Liu B, Toledano MB, Molin M, NystrÃ¶m T.
Lifespan Control by Redox-Dependent Recruitment of Chaperones to Misfolded Proteins.
Cell. 2016 May 31;. [Epub ahead of print]
PMID: 27264606 [PubMed - as supplied by publisher]

Shukla S, Parker R.
Hypo- and Hyper-Assembly Diseases of RNA-Protein Complexes.
Trends Mol Med. 2016 Jun 2;. [Epub ahead of print]PMID: 27263464 [PubMed - as supplied by publisher]

Kashani MR, Yousefi R, Akbarian M, Alavianmehr MM, Ghasemi Y.
Structure, Chaperone Activity, and Aggregation of Wild-Type and R12C Mutant Î±B-Crystallins in the Presence of Thermal Stress and Calcium Ion - Implications for Role of Calcium in Cataract Pathogenesis.
Biochemistry (Mosc). 2016 Feb;81(2):122-34.PMID: 27260392 [PubMed - in process]

Rivera-Contreras IK, Zamora-HernÃ¡ndez T, Huerta-Heredia AA, Capataz-Tafur J, Barrera-Figueroa BE, Juntawong P, PeÃ±a-Castro JM.
Transcriptomic analysis of submergence-tolerant and sensitive Brachypodium distachyon ecotypes reveals oxidative stress as a major tolerance factor.
Sci Rep. 2016 Jun 10;6:27686.PMID: 27282694 [PubMed - in process]

Tian S, Das R.
RNA structure through multidimensional chemical mapping.
Q Rev Biophys. 2016 Jan;49:e7.PMID: 27266715 [PubMed - in process]

Baranov PV, Michel AM.
Illuminating translation with ribosome profiling spectra.
Nat Methods. 2016 Feb;13(2):123-4.PMID: 26820545 [PubMed - indexed for MEDLINE]

tRNA-related sequences trigger systemic mRNA transport in plants
Wenna Zhang, Christoph Thieme, Gregor Kollwig, Federico Apelt, Lei Yang, Winter Winter, Nadine Andresen, Dirk Walther, and Friedrich Kragler
Plant Cell 2016 tpc.15.01056; Advance Publication June 7, 2016; doi:10.1105/tpc.15.01056 **OPEN**
http://www.plantcell.org/content/early/2016/06/07/tpc.15.01056.abstract
In plants, protein-coding messenger RNAs (mRNAs) can move via the phloem vasculature to distant tissues, where they may act as non-cell-autonomous signals. Emerging work has identified many phloem-mobile mRNAs, but little is known regarding RNA motifs triggering mobility, the extent of mRNA transport, and the potential of transported mRNAs to be translated into functional proteins after transport. To address these aspects, we produced reporter transcripts harboring transfer RNA (tRNA) - like structures (TLS) that were found to be enriched in the phloem stream and in mRNAs moving over chimeric graft junctions. Phenotypic and enzymatic assays on grafted plants indicated that mRNAs harboring a distinctive TLS can move from transgenic roots into wild-type leaves and from transgenic leaves into wild-type flowers or roots; these mRNAs can also be translated into proteins after transport. In addition, we provide evidence that di-cistronic mRNA:tRNA transcripts are frequently produced in Arabidopsis thaliana and are enriched in the population of graft-mobile mRNAs. Our results suggest that tRNA-derived sequences with predicted stem-bulge-stem-loop structures are sufficient to mediate mRNA transport and seem to be necessary for the mobility of a large number of endogenous transcripts that can move through graft junctions.

Imaging Reactive Oxygen Species-Induced Modifications in Living Systems

Giuseppe Maulucci, Goran Bačić, Lori Bridal, Harald HHW Schmidt, Bertrand Tavitian, Thomas Viel, Hideo Utsumi, A. Süha Yalçın, and Marco De Spirito

Antioxidants & Redox Signaling, Vol. 24, No. 16, June 2016: 939-958.

Abstract | Full Text HTML | Full Text PDF (1424 KB) | Full Text PDF with Links (736 KB)

Lighting the way to protein-protein interactions: recommendations on best practices for bimolecular fluorescence complementation (BiFC) analyses
Ralph Bock and Joerg Kudla
Plant Cell 2016 tpc.16.00043; Advance Publication April 20, 2016; doi:10.1105/tpc.16.00043 **OPEN**
http://www.plantcell.org/content/early/2016/04/20/tpc.16.00043

Shorter J.
Engineering therapeutic protein disaggregases.
Mol Biol Cell. 2016 May 15;27(10):1556-60.PMID: 27255695 [PubMed - in process]

Cheregi O, Wagner R, Funk C.
Insights into the Cyanobacterial Deg/HtrA Proteases.

Front Plant Sci. 2016;7:694.PMID: 27252714 [PubMed]

Eshleman N, Liu G, McGrath K, Parker R, Buchan JR.
Defects in THO/TREX-2 function cause accumulation of novel cytoplasmic mRNP granules that can be cleared by autophagy.
RNA. 2016 Jun 1;. [Epub ahead of print]PMID: 27251550 [PubMed - as supplied by publisher]

Garcia VM, Rowlett VW, Margolin W, Morano KA.
Semi-automated microplate monitoring of protein polymerization and aggregation.
Anal Biochem. 2016 May 29;. [Epub ahead of print]PMID: 27251433 [PubMed - as supplied by publisher]

Bracher A, Sharma A, Starling-Windhof A, Hartl FU, Hayer-Hartl M.
Degradation of potent Rubisco inhibitor by selective sugar phosphatase.
Nat Plants. 2015 Jan 8;1:14002.PMID: 27246049 [PubMed]

Fan D, Liu C, Liu L, Zhu L, Peng F, Zhou Q.
Large-scale gene expression profiling reveals physiological response to deletion of chaperone dnaKJ in Escherichia coli.
Microbiol Res. 2016 May-Jun;186-187:27-36.PMID: 27242140 [PubMed - in process]

Horowitz S, Salmon L, Koldewey P, Ahlstrom LS, Martin R, Quan S, Afonine PV, van den Bedem H, Wang L, Xu Q, Trievel RC, Brooks CL 3rd, Bardwell JC.
Visualizing chaperone-assisted protein folding.
Nat Struct Mol Biol. 2016 May 30;. [Epub ahead of print]PMID: 27239796 [PubMed - as supplied by publisher]

Kuruthukulangarakoola GT, Zhang J, Albert A, Winkler B, Lang H, Buegger F, Gaupels F, Heller W, Michalke B, Sarioglu H, Schnitzler JP, Hebelstrup KH, Durner J, Lindermayr C.
Nitric oxide-fixation by non-symbiotic hemoglobin proteins in Arabidopsis thaliana under N-limited conditions.
Plant Cell Environ. 2016 May 31;. [Epub ahead of print]PMID: 27245884 [PubMed - as supplied by publisher]

Zhang H, Ng MY, Chen Y, Cooperman BS.
Kinetics of initiating polypeptide elongation in an IRES-dependent system.
Elife. 2016 Jun 2;5. [Epub ahead of print]PMID: 27253065 [PubMed - as supplied by publisher]

Uchida S, Sato H, Yoneda M, Kai C.
Eukaryotic elongation factor 1-beta interacts with the 5' untranslated region of the M gene of Nipah virus to promote mRNA translation.
Arch Virol. 2016 May 28;. [Epub ahead of print]PMID: 27236461 [PubMed - as supplied by publisher]