analytical chemistry

ACS Chemistry for Life®

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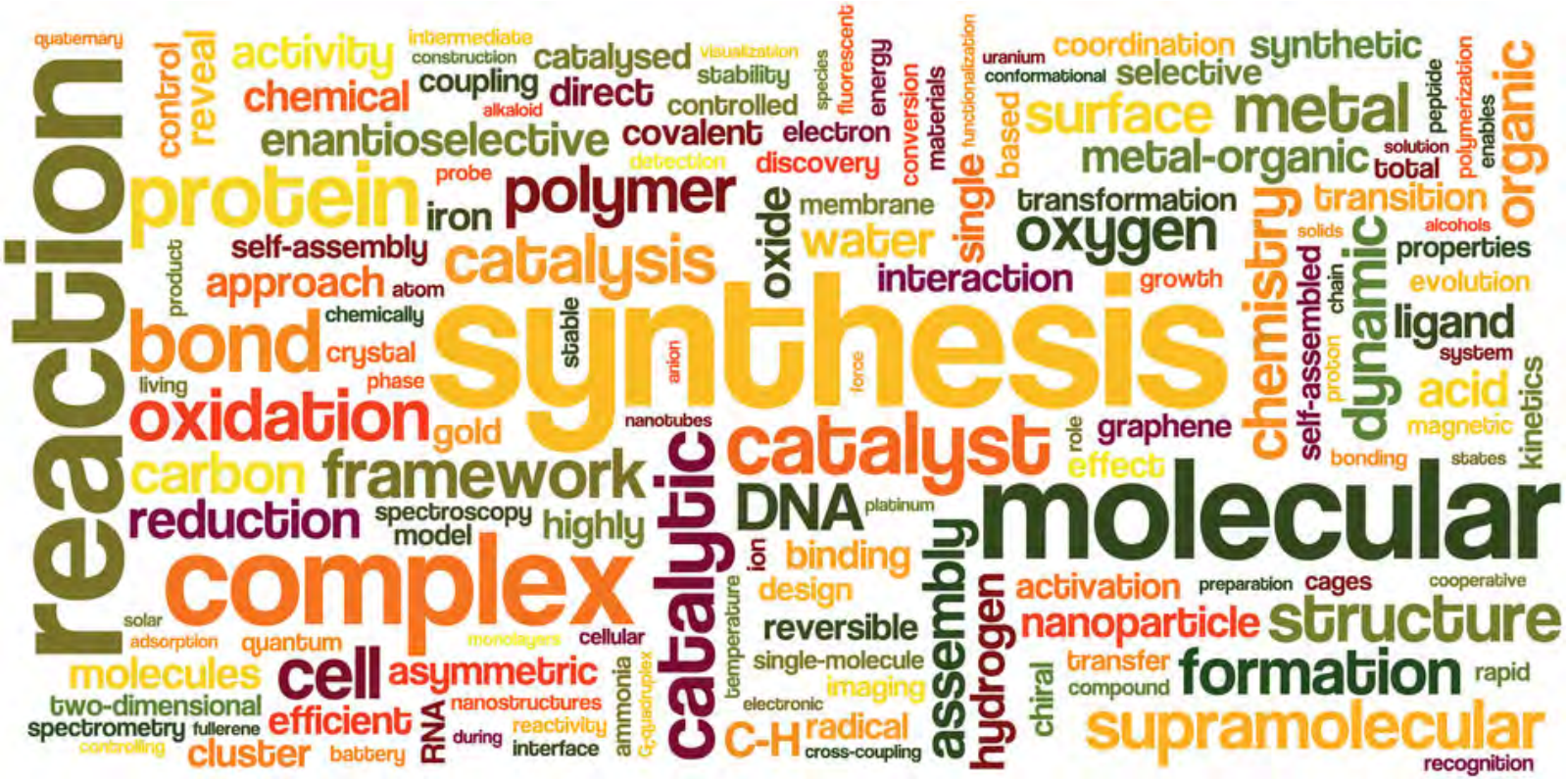
陳玉如
中研院化學所

Associate Editor
Analytical Chemistry

B
impact
G

At NTUCM, we strive for “high impact”
rather than”
~~high impact factor”~~.

Identify Mr. Right Journal



Common words

from the titles of first 60 papers published in Nature Chemistry

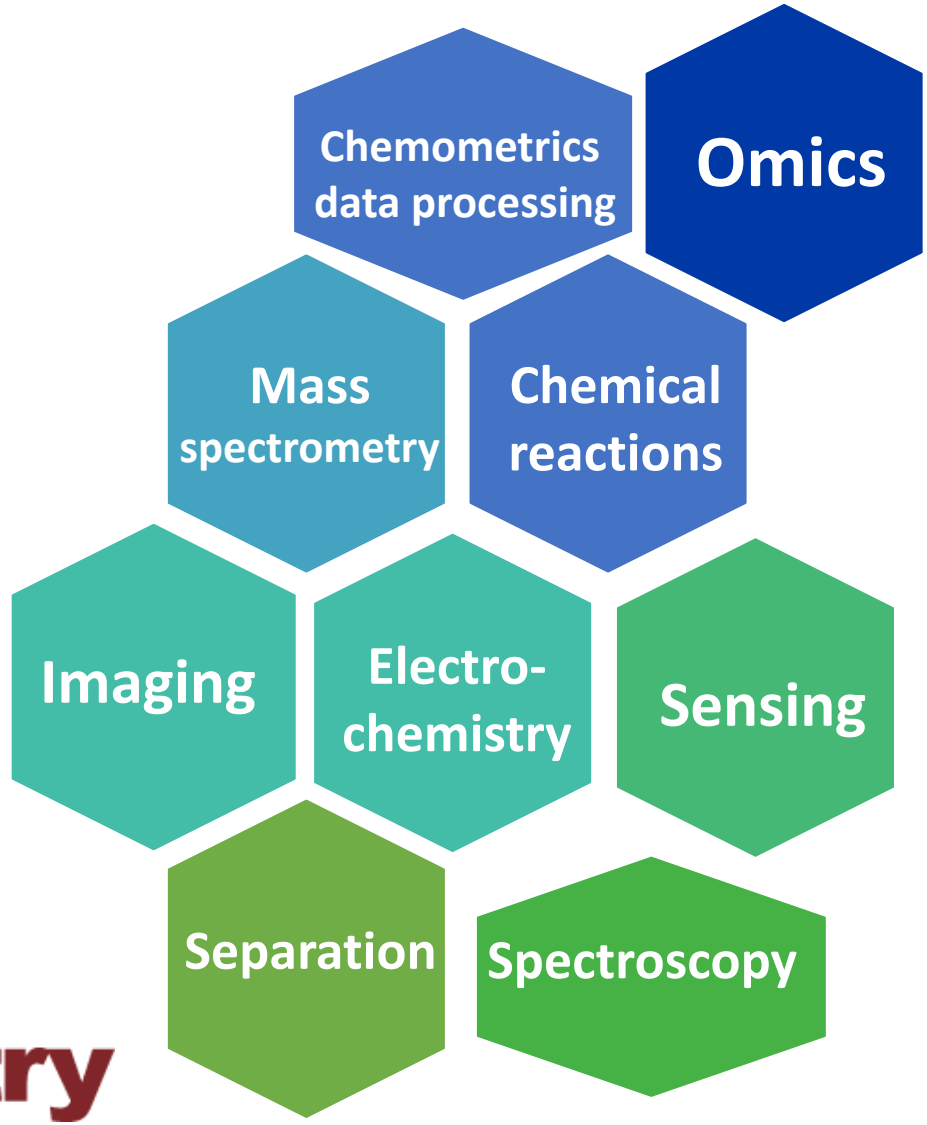
Nature Chemistry
6, 255–257, **2014**

ACS Editors' Handbook

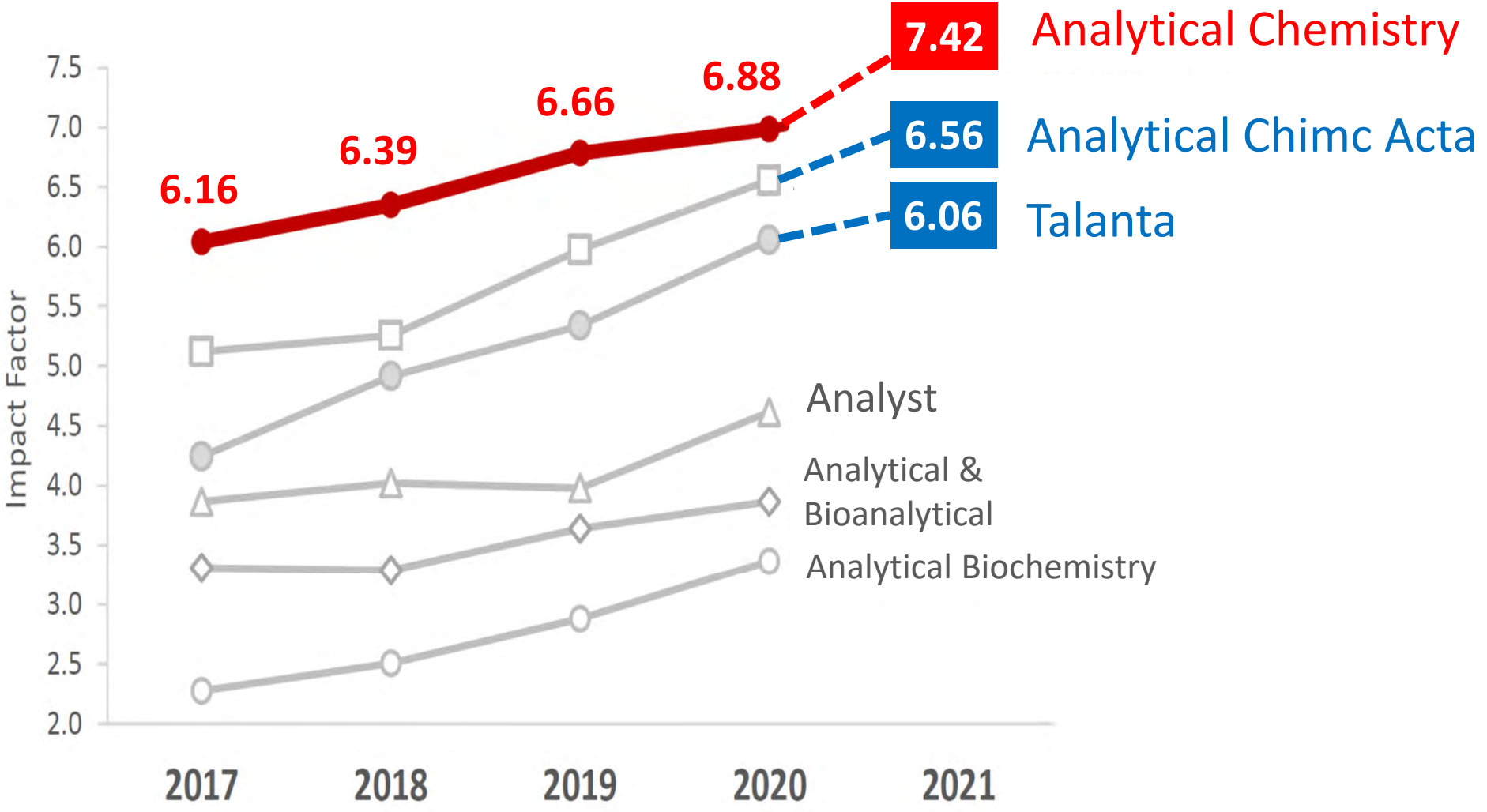
UPDATED APRIL 2022

Papers dealing with known analytical methods should offer a **significant**, **original** application of the method, a **noteworthy improvement**, or **results on an important analyte**.

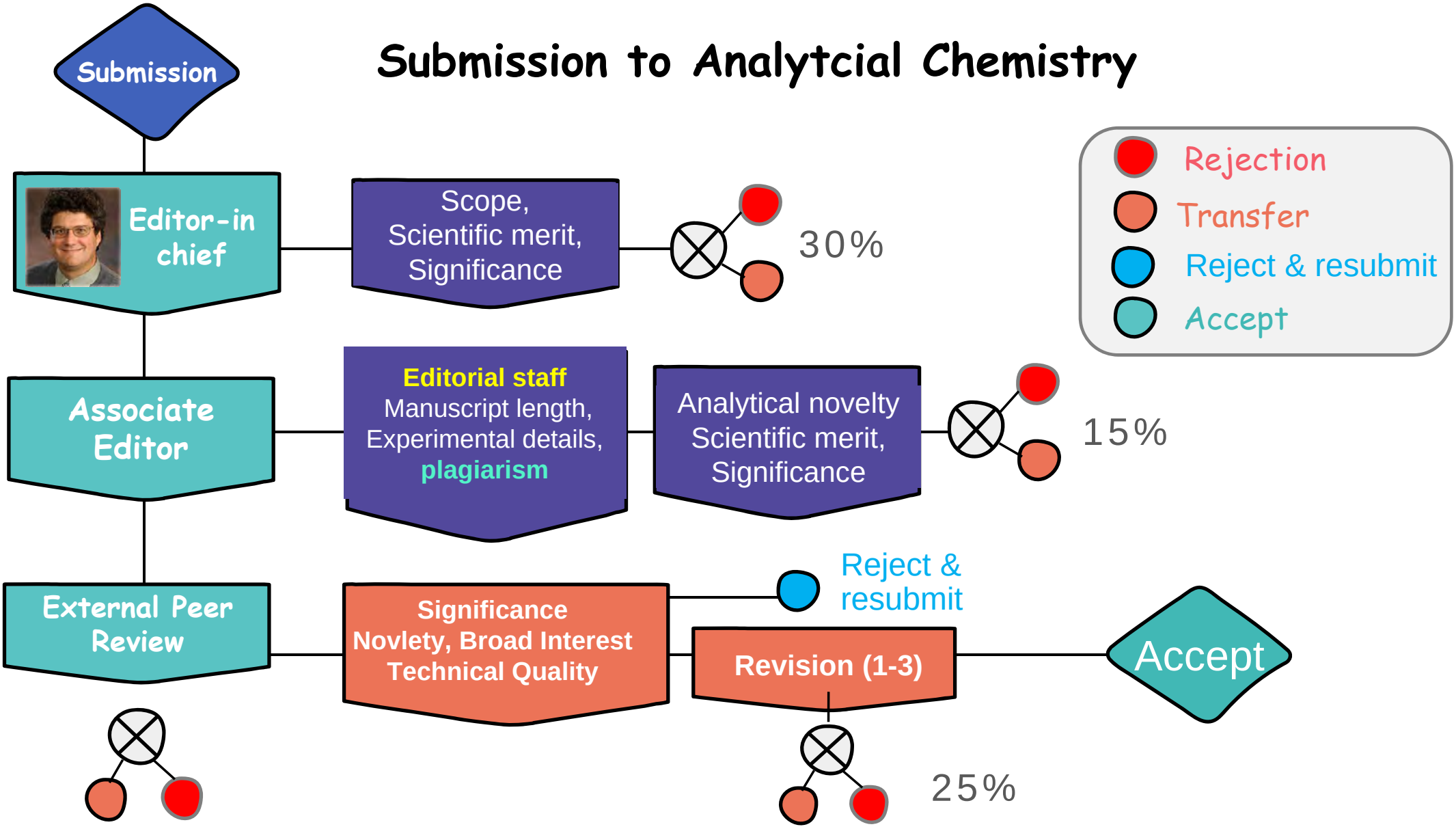
analytical chemistry



The Most Cited Journal in Analytical Chemistry*



Submission to Analytcial Chemistry



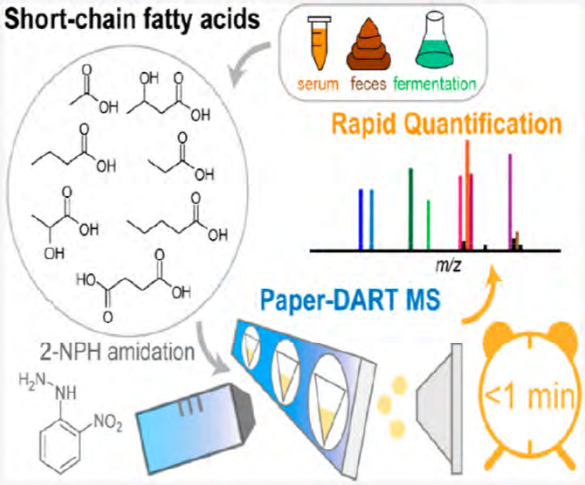
analytical chemistry

pubs.acs.org/ac Technical Note

Rapid Quantification of Gut Microbial Short-Chain Fatty Acids by pDART-MS

Cheng-Yu Weng,[⊥] Ting-Hao Kuo,[⊥] Laura Min Xuan Chai, Hsin-Bai Zou, Tzu-Hsuan Feng, Yun-Ju Huang, Jemmy C. Tsai, Ping-Hsun Wu, Yi-Wen Chiu, Ethan I. Lan, Lee-Yan Sheen, and Cheng-Chih Hsu*

ABSTRACT: Short-chain fatty acids (SCFAs) are small molecules ubiquitous in nature. In mammalian guts, SCFAs are mostly produced by anaerobic intestinal microbiota through the fermentation of dietary fiber. Levels of microbe-derived SCFAs are closely relevant to human health status and indicative to gut microbiota dysbiosis. However, the quantification of SCFA using conventional chromatographic approaches is often time consuming, thus limiting high-throughput screening tests. Herein, we established a novel method to quantify SCFAs by coupling amidation derivatization of SCFAs with paper-loaded direct analysis in real time mass spectrometry (pDART-MS). Remarkably, SCFAs of a biological sample were quantitatively determined within a minute using the pDART-MS platform, which showed a limit of detection at the μM level. This platform was applied to quantify SCFAs in various biological samples, including feces from stressed rats, sera of patients with kidney disease, and fermentation products of metabolically engineered cyanobacteria. Significant differences in SCFA levels between different groups of biological practices were promptly revealed and evaluated. As there is a burgeoning demand for the analysis of SCFAs due to an increasing academic interest of gut microbiota and its metabolism, this newly developed platform will be of great potential in biological and clinical sciences as well as in industrial quality control.



Abstract
是最重要的通關文件

- ✓ (至少看起來) New method
- ✓ Significant advancement
- ✓ Analytical merits
- ✓ New information

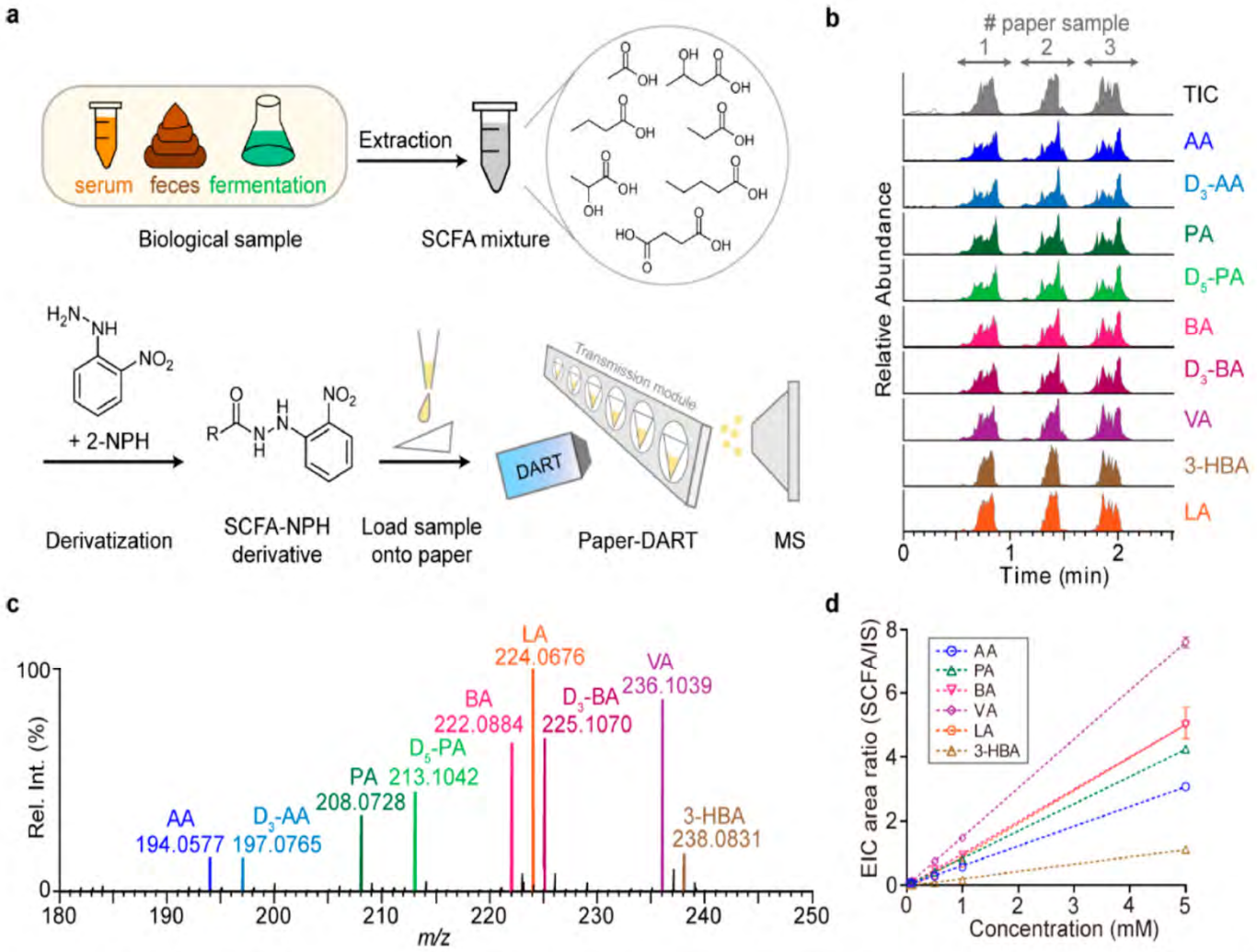


Figure 1. Rapid quantification of SCFAs by coupling NPH derivatization with pDART-MS. (a) pDART-MS workflow of quantifying SCFAs.

Figure, Table

展現文章品質的門面

- ✓ Clear visibility
- ✓ Profession
  - --X-Y axis
  - -- data presentation
  - -- spectra annotation
  - -- .....
- ✓ Avoid complication

精美包裝

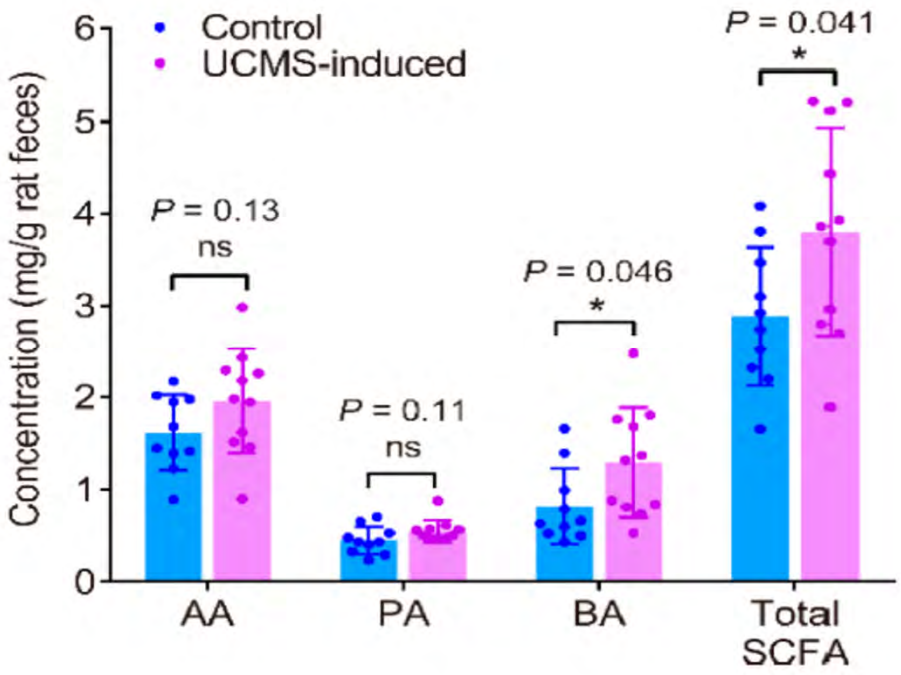


Figure 2. Fecal SCFAs of the UCMS-induced and control rats. Fecal SCFAs of control (n = 10) and UCMS-induced of rats (n = 11) quantified with the pDART-MS platform. Total SCFA refers to the summed concentration of AA, PA, and BA. Statistical significance was evaluated by an unpaired Student's t test. (*P value < 0.05). Error bars represent standard deviation. Numeric data are given in Table S3.

Figure, Table

展現文章數據的專業

- ✓ Profession
  - --Statistics
  - -- X-Y axis
  - -- data presentation
  - -- spectra annotation
  - -- .....
- ✓ Provide raw data in supplementary infor. or public data repository
- ✓ Artistic figure
- ✓ Avoid complication

慎選 Suggested Reviewer

1. (**非常**)相關領域
2. 學術名聲
3. 發表相關並高品質成果

系統推薦審查委員

External Searches

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- ☐ Online 2D high-pH and low-pH reversed-phase nano-L
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- ☐ [redacted] (Preferred Reviewer)
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慎選 文章標題

會決定系統推薦審查委員

ACS Reviewer Recommender

Web of Science Reviewer Locator

The matching algorithm compares metadata such as author names, manuscript titles, abstracts, and journal of the submission to the same metadata for publications indexed in Web of Science and generates a list of authors of relevant publications who could serve as potential reviewers.

TWO reviews for minor revision

1. The manuscript details optimization, control experiments and application of this quantitative method in biological samples.
2. The importance of SCFAs in microbiota metabolism justifies the development of this method for fast analysis of these volatile compounds. The comparison with a common HPLC method is very convincing that the method is fast and robust.
3. The data and statistical analysis is outlined nicely in the manuscript and the SI.
4. This well-structured manuscript is of high interest for the readership of Analytical Chemistry.

1. The manuscript describes a new method using paper Direct Analysis in Real Time (pDART) MS for short chain fatty acid analysis.
2. Overall, the experiments are well-done and the data support the conclusions.
3. The reproducibility between HPLC quantitation and pDART is remarkable.
4. I also appreciated the use of multiple sample types.
5. The paper is very well-written.

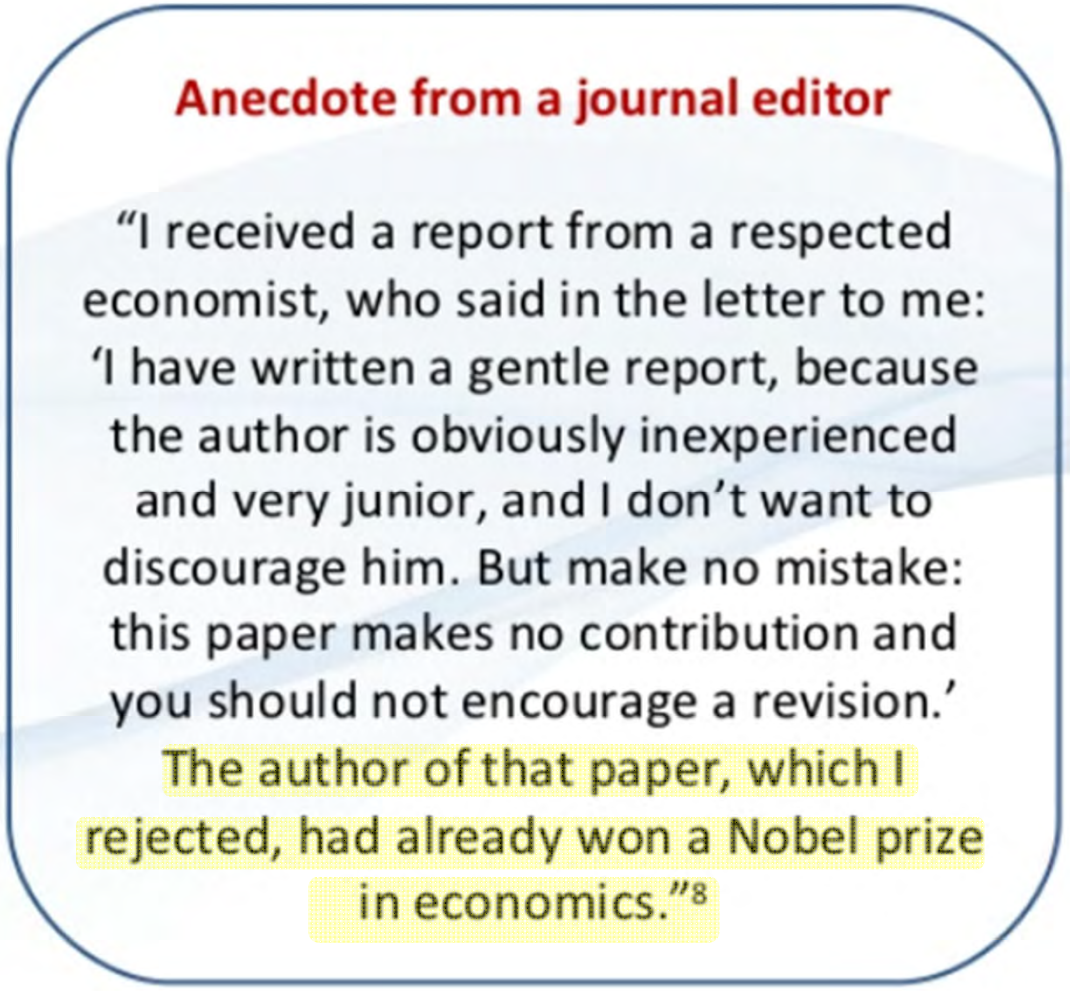
廣結善緣

Establish your reviewer network

- 你推薦的審查委員願意審查嗎?
- 同領域的人認識你嗎?

" Dear Dr. Chen.
"I am sorry to inform you……"

Rejection is the normal in academia publishing



http://www.slideshare.net/editage/most common-reasons-for-journal-rejections

The Paper Rejection Repository

Posted On	Title	Rejected By	Ultimately Published In	
10 Jun 2014	Taura syndrome virus IRES initiates translation by binding its tRNA-mRNA-like structural element in the ribosomal decoding center	Nature	2014, PNAS	@
13 Dec 2013	Opposing dopaminergic and GABAergic neurons control the duration and persistence of copulation in Drosophila	Science, Nature, Neuron	2013, Cell 155:881-93	@
13 Dec 2013	Structure of the Ribosome with Elongation Factor G Trapped in the Pre-Translocation State	Nature, NSMB	2013, PNAS 110:20994–20999	@
14 Se 2012			NAS 067-76	@
31 Au 2012			tructure 3–1828	@
2 Ma 2012			NAS 53–3358	@
14 De 2010			MBO J. 416	@
29 Jul 2010	Aβ(1-40) Fibril Polymorphism Implies Diverse Interaction Patterns in Amyloid Fibrils	EMBO J, PLoS, JBC, JACS	2009, J. Mol. Biol. 386:869–877	@
28 Jul 2010	Molecular interactions in rotavirus assembly and uncoating seen by high-resolution cryo-EM	Science	2009, PNAS 106:10644–10648	@
28 Jul 2010	Paired β-sheet structure of an Aβ(1-40) amyloid fibril revealed by electron microscopy	Nature, Science	2008, PNAS 105:7462–7466	@

Rejected without review at ***Science***,
Rejection by ***Nature*** and ***Neuron***.
Published more than a year later in ***Cell***
(155:881-893).

https://grigoriefflab.umassmed.edu/paper_rejection_repository

My experiences (100% successful rate)

期刊	理由	結果	時間
Mol. Cell. Proteomics	實驗寫不清楚 英文不好 Negative (major) x 1 Positive x (minor) 1	成功	**2.5** 個月 **8** 個月
J. Proteome. Res.	Rejection after 2 rounds of revisions （兩次問題截然不同）	成功	**16** 小時 **5** 個月
Nat. Commun.	沒有應用價值 分析方法有問題 Negative (rejection) x 1 Positive (minor) x 1	成功	2.5 個月 6 個月
Nat. Commun.	晶片沒有發展價值 很多實驗設計不對 Negative (rejection) x 1 Positive (major, Major) x 2	成功	1.5 個月 8 個月

Since 2005

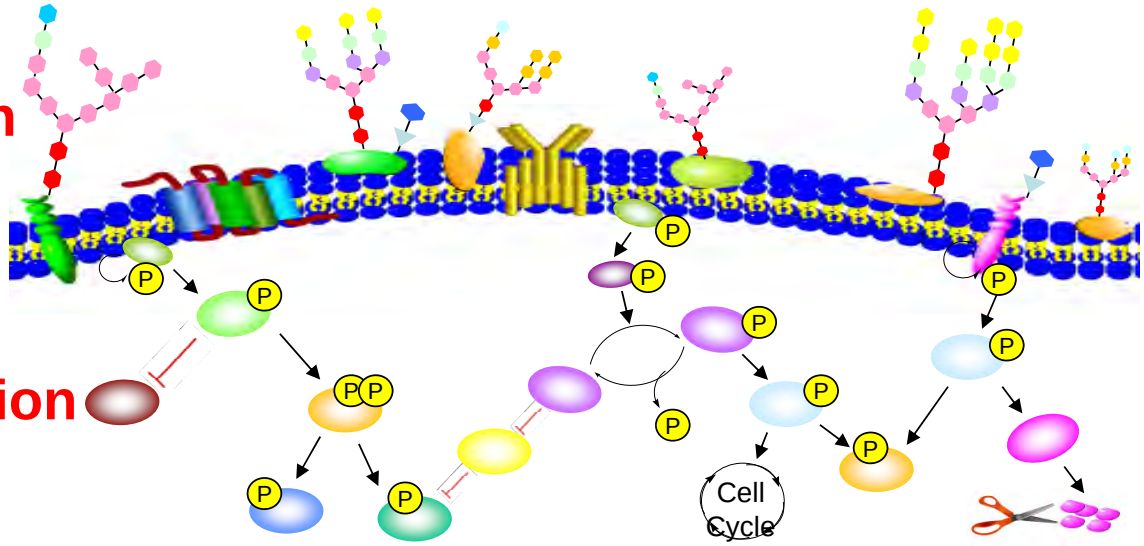
Membrane Proteome and Modification

Opportunity for Disease Biomarker and Drug Target

Immuno-modulation, Molecular recognition , Cell surface adhesion

Glycosylation

Phosphorylation



Signal transduction

Differentiation, proliferation

Protein degradation Apoptosis

Hydrophobic, Low abundant, Labile, Dynamic and heterogeneous modification, Low MS signal

On the journey of rebuttal……

韓嘉莉
副教授
臺北醫學大學

簡芷薇
Stanford U.
Postdoc. & Wife

Shot-gun Membrane Proteomics

Trial started in **2004**……. By 1 MS student

Date	Manuscript status	Note
2007-8-20	First Submission	
2007-11-25	Rejection	One-major revision One-rejection
2008-2-14	Rebuttal	Re-submission as a new manuscript 11-page letter
2008-3-19	Received response --Major revision	Only one new reviewer Ask for new analysis
2008-5-2	Submitted revision	
2008-June	Accepted	

Reviewer 1 (major revision?)

" The authors put forward two advances:

1. Gel assisted digestion ***is a powerful tool*** *for analyzing the membrane proteome.*

2. Coupling this approach to iTRAQ MDLCMSMS

The data from 2. gives reproducibility that's ***as good as any reported before, if not better. "***

Other comments:

Q: An experiment required is to compare two identical samples

Q: Overall the text is too long, especially the Discussion

Q: How much material was used for western blots?

……

……

Reviewer 2 (rejection)

" The manuscript by Han et. al. Describes the use of polyacrylamide gel formation to assist with sample clean-up and digestion followed by iTRAQ labeling to perform deferential proteomics on membrane protein samples.

*While I find the **topic interesting and the approach compelling,** I can not recommend this paper for publication due to the **grammatic errors** and **lack of experimental detail.** A few examples are given below. "*

1. **Summary**: The last sentence of this section is run on and confusing
2. **Methods:** "Incorporated into gel matrix" What are the details? Percent TEMED used? or all according to the previously published method?
3. **Methods:** "TFA in ACN, and can, and.." auto correction of neat ACN?
4. Q: Methods: "10% APS, and TEMED.." what %?

陳儀莊　教授
中研院生醫所

A Successful Story !

MCP MOLECULAR & CELLULAR PROTEOMICS

Jan. 3rd, 2007

Dear Dr. Bradshaw:

Enclosed is a revision of our manuscript entitled "Systematic uncovering of multiple pathways underlying the pathology of Huntington's disease by an acid-cleavable isotope-coded affinity tag approach" (M6:00356-MCP). New experimental evidence (Figs. 6, S1, S2, S3) and data analyses (Tables 2, S2, S3) were provided to satisfy the concerns raised in reports #1 and #2. The major problem raised in report #3 was due to a misunderstanding of the lamin isoforms involved in the ICAT and Western blot analyses. We would like to emphasize that we used Western blotting to confirm the ICAT results and to fine-tune the normalization of the ICAT experiments because no other normalization procedure for large-scale quantitative analyses of severe degeneration diseases has yet been reported, while a proper internal control (lamin A/C) for Western blotting under the experimental conditions tested in the present study is available. Because we only analyzed proteins that showed alterations in the same direction in the two independent ICAT experiments, our Western blot analyses of the 10 different proteins (including 3 which were upregulated and 5 which were downregulated; comprising 12% of the total proteins which exhibited changes) verified that when using the analytical protocol presented herein, changes larger than the average RSD (0.23) may have differed from "1" and were meaningful (Fig. 2). Our study provides a careful and reliable application of ICAT to the large-scale proteomic analysis of severe degeneration diseases. The majority of the proteins with changes revealed in the present study have never been reported in Huntington's disease (HD) before, and this is expected to facilitate the identification of novel pathological pathways of HD. It is on these bases that we believe that publication of this work is appropriate in *Molecular and Cellular Proteomic*. We summarize our point-by-point responses to the reviewers in the following letter.

STEP 1

A polite Rebuttal Letter (不卑不亢）

再以數據/結果強調此工作超級棒的地方

申訴的2-3個主要理由(不要重複摘要)

Dear Prof. Burlingame:

We would like to submit our manuscript entitled "*A Multiplexed Quantitative Strategy for Membrane Proteomics: Opportunities for Mining Therapeutic Targets for Autosomal-Dominant Polycystic Kidney Disease*" ...teomics. We report a multiplexed qu... ides high accuracy (< 9% error), prec... nong 945 quantified proteins with kn... s, and an average of 5.4 peptides per... y, topological analysis revealed ... ieved with transmembrane peptic... helices. To the best of our knowled... mass spectrometry and provides ... on these bases that we believe this work is appropriate for publication in *Molecular and Cellular Proteomics*.

當你找不出審查委員有任何錯誤時 -
一切永遠都是自己的錯，

- 沒有寫出研究成果的優點 ？
- 缺乏細節 ？
- 結果不吸引人 ？

The work was originally submitted to *Molecular and Cellular Proteomics* on Sep 2, 2007 (M7:00337-MCP). **Because of the lack of partial experimental details and grammatical errors** (see the following original reviewer statements), **our previous manuscript did not clearly and completely demonstrate the advantages of our new methodology**. However, we have now taken into account the reviewers' comments when revising our paper, and we offer point-by-point responses to those comments below.

STEP 2 – Emphasize novelty from other reviewer's comments (借力使力）

Reviewer 1:

*The authors **put forward two advances**: 1. Gel assisted digestion is a powerful tool for analysing the membrane proteome. 2. Coupling this approach to iTRAQ MDLCMSMS The data from 2. gives reproducibility that's as good as any reported before, if not better.*

引用審查意見的稱讚

Reviewer 2:

*"While I find the **topic interesting and the approach compelling** I can not recommend this paper for publication due to the grammatic errors and lack of experimental detail."*

– Incorporate relevant revision, Add new data (改頭換面）

The detailed **point-by point revisions** are listed in the accompanying response letter

Compared with the reported 20-30% standard deviation in **xxx** methods (**cite previous GOOD literatures**), **our xxxx result** demonstrated the superior accuracy and reproducibility of our platform.

比較現有情形

To further demonstrate the efficient identification and quantification of our method, we have added **NEW results** for the first membrane proteomic study of

可以加上新結果

Although our previous manuscript was edited by a professional English editing service before submission, it did not meet the language criteria due to some grammatical errors. To ensure readability and correct grammar, the new manuscript has been revised by a **scientific revision service** (***company name, http://www.xxxxx.com/)---- attach certificate***

專業英文修改

MCP MOLECULAR & CELLULAR PROTEOMICS

2.5 months later……

A Multiplexed Quantitative Strategy for Membrane Proteomics

OPPORTUNITIES FOR MINING THERAPEUTIC TARGETS FOR AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE[S]

Chia-Li Han‡, Chih-Wei Chien§, Wen-Cheng Chen¶, Yet-Ran Chen‖, Chien-Peng Wu‖, Hung Li**, and Yu-Ju Chen‡‡§§

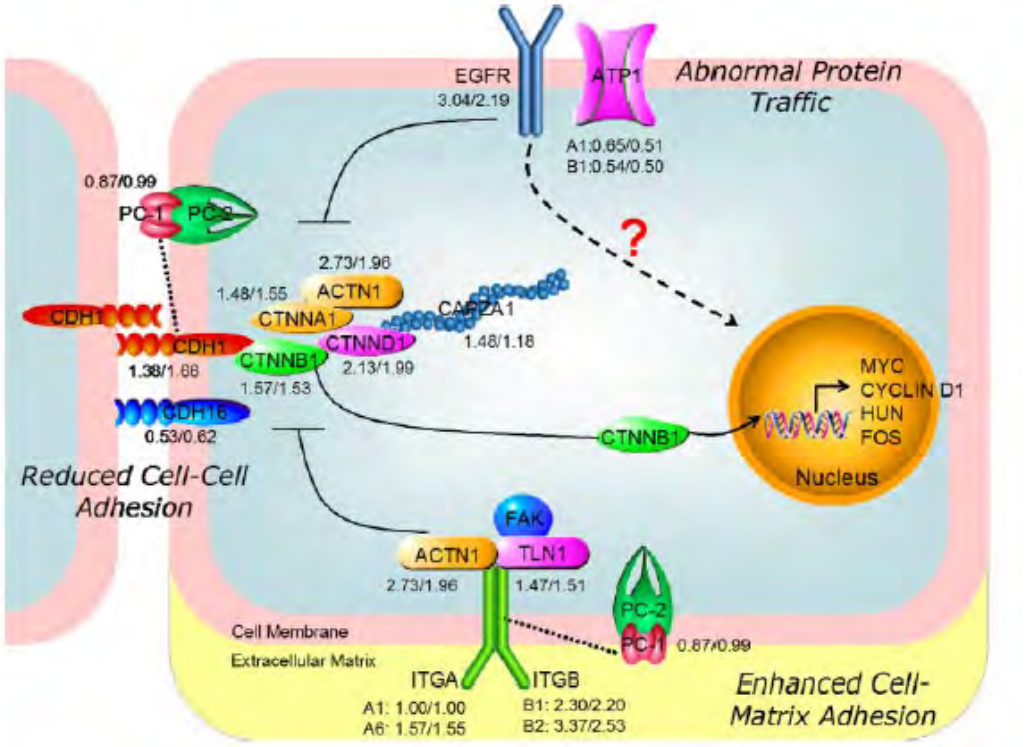
Mol. Cell. Proteomics, **7**, 1983–1997**(2008)**

Dr. Hung Li 李鴻研究員

1963.11.9 - 2009.3.7

任分生所研究員 1996 - 2009

Partial pathways in polycystic kidney disease



1. First milestone of developing proteomics strategy in my group
2. Selected as top **2% of published articles in biology and medicine** by *Faculty of 1000*
3. Selected as 中央研究院重要研究成果
4. 105 citations
5. Received invitation to join Editor Board of journal "*Kidney International* (**IF: 8.536**)"

nature COMMUNICATIONS

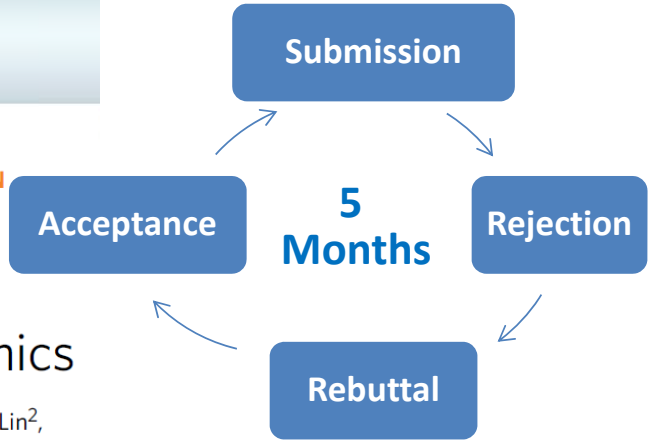
ARTICLE

Received 9 Jul 2014 | Accepted 12 Feb 2015 | Published 27 Mar 2015

DOI: 10.1038/ncomms7622 OPEN

Large-scale determination of absolute phosphorylation stoichiometries in human cells by motif-targeting quantitative proteomics

Chia-Feng Tsai[1,2], Yi-Ting Wang[2,3,4], Hsin-Yung Yen[4,5], Chih-Chiang Tsou[6], Wei-Chi Ku[7], Pei-Yi Lin[2], Hsuan-Yu Chen[8], Alexey I. Nesvizhskii[6], Yasushi Ishihama[9] & Yu-Ju Chen[1,2,3]



2014/7/14	First submission
2014/9/29	**Rejection** from Nature Communications (one minor revision, one rejection)
2014/9/30	內部討論, 不認同其中一位**reviewer**意見 **(**總共只有兩位**)**
2014/11/13	Appeal request for NCOMMS-14-10342-T
2014/11/14	正式 submit Appeal
2014/12/5	Editor 同意將Rebuttal revision & revised manuscript 送給原本的 reviewer
2014/12/6	YuJu replied 希望Editor送給另一個具足夠專業的Reviewer審查
2015/12/9	Editor同意送給第三個Reviewer審查
2015/2/12	Acceptance of NCOMMS-14-10342B

"I am sorry to inform you……"

How to deal with paper rejection ?

- Keep your emotions at bay
- Keep an open mind
  - Is this comment correct and relevant? Have the referee got to the bottom of the experiment/claim?
  - How much weight this comment has on the overall rejection decision?
  - Assuming this comment is correct and in place, can I supply data/claim to defer it?
- Keep your team posted
- Should I write a rebuttal letter?
- Should I consider a different set of suggested reviewers?

To rebut or not to rebut?