

## Supporting Information

### Rapid 3-dimensional Shape Determination of Globular Proteins by Mobility Capillary Electrophoresis and Native Mass Spectrometry

Haimei Wu,<sup>1#</sup> Rongkai Zhang,<sup>1#</sup> Wenjing Zhang,<sup>1</sup> Jie Hong,<sup>1</sup> Ye Xiang<sup>2\*</sup> and Wei  
Xu<sup>1\*</sup>

<sup>1</sup>Department of Biomedical Engineering, School of Life Science, Beijing Institute of  
Technology, Beijing 100081, China

<sup>2</sup>Beijing Advanced Innovation Center for Structural Biology, Department of Basic  
Medical Sciences, School of Medicine, Tsinghua University, Beijing 100084, China

\*Corresponding Authors:

Wei Xu School of Life Science Beijing Institute of Technology Haidian, Beijing, 100081, China Email: <a href="mailto:weixu@bit.edu.cn">weixu@bit.edu.cn</a> Web: <a href="http://www.escience.cn/people/weixu">http://www.escience.cn/people/weixu</a>	Ye Xiang Department of Basic Medical Sciences, School of Medicine Tsinghua University Beijing, 100084, China Email: <a href="mailto:yxiang@mail.tsinghua.edu.cn">yxiang@mail.tsinghua.edu.cn</a>
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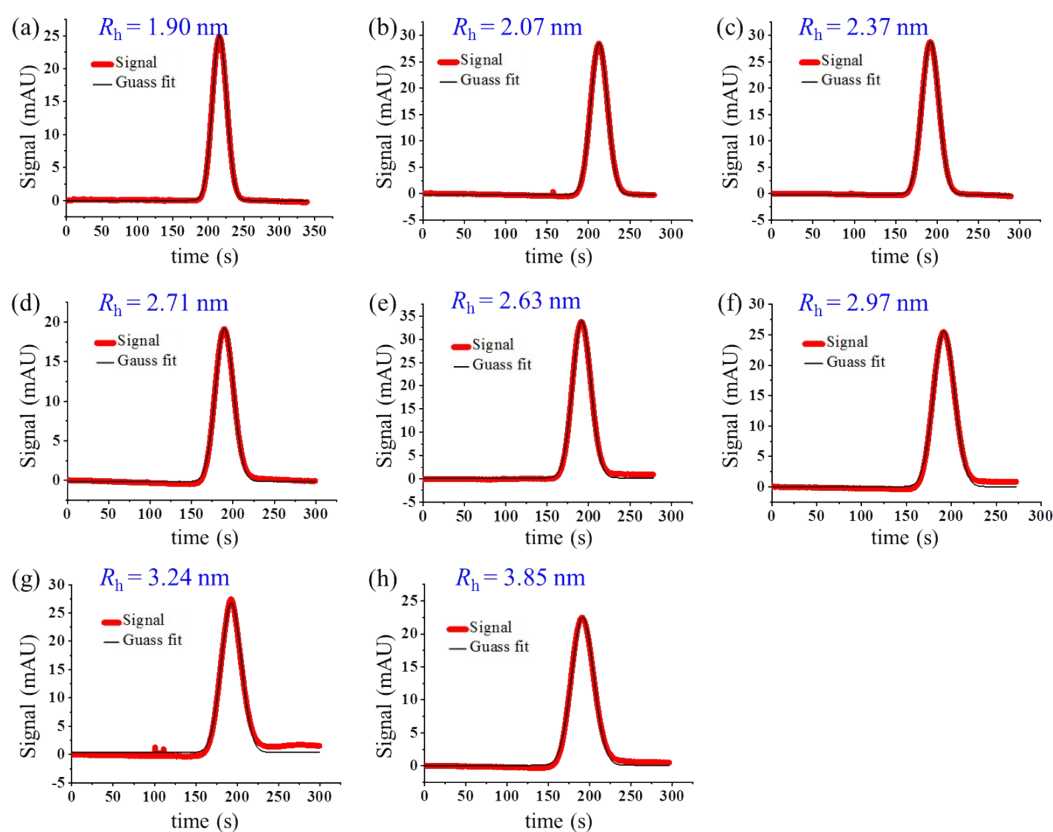
#Equal contribution

**Table S1.** Measured and calculated parameters of 52 globular proteins ranging in size from 4.7 to 68.7 kDa.

Protein name	PDB id	SASA (nm <sup>2</sup> )	a <sub>SASA</sub> (nm)	a <sub>MD</sub> (nm)	b <sub>MD</sub> (nm)	c <sub>MD</sub> (nm)
Zinc-finger domains	1zfd	30.19	1.55	1.78	1.18	0.66
Agglutinin-toxin motif	1hev*	32.17	1.60	1.45	1.20	0.91
Ferredoxin(A)	1vjw	35.89	1.69	1.59	1.19	1.10
Chymotrypsin inhibitor II	1ciq*	40.72	1.80	1.68	1.48	0.97
Ribosomal protein L7/L12	1ctf	41.62	1.82	1.87	1.23	1.13
Ubiquitin	1ubq	47.78	1.95	1.86	1.41	1.21
P13K SH3 domain	1pht	52.30	2.04	1.88	1.52	1.27
Oxidized uteroglobin	1utg*	52.81	2.05	2.14	1.69	1.00
Pyruvate dehydrogenase complex	1iyv	53.85	2.07	2.25	1.26	1.24
Translation initiation factor	1tig	54.89	2.09	2.19	1.42	1.17
Cellulose domain (Cellulomonas fimi)	1exg	57.55	2.14	2.32	1.47	1.19
Llama heavy chain variable domain	1hcv	60.82	2.20	2.24	1.40	1.35
Hepatocyte growth factor	2hgf	62.49	2.23	2.00	1.62	1.24
HIT protein substrate	1kpf	68.81	2.34	2.10	1.68	1.49
Yeast cofilin	1cof	72.38	2.40	2.43	1.76	1.32
Cellular retinoic acid binding protein I	1cbi	73.59	2.42	2.21	1.85	1.50
Glycera dibranchiata hemoglobin	1hbg*	74.82	2.44	2.31	1.90	1.28
Avian sarcoma virus integrase	1vsd	81.07	2.54	2.63	1.73	1.43
Biliverdin apomyoglobin complex	1bvc*	81.71	2.55	2.35	2.10	1.32
Ribonuclease H	2rn2*	88.25	2.65	2.43	2.02	1.44
Dextrin	1ak6	90.26	2.68	2.72	1.74	1.45
Scytalone dehydratase	1std	90.26	2.68	2.78	1.63	1.60
Trypsin	2blv*	92.97	2.72	2.50	2.07	1.57
Peptide deformylase	1dff	95.03	2.75	2.54	1.96	1.50
Human growth hormone	1huw	95.03	2.75	2.95	1.82	1.43
Yellow fluorescent protein	2yfp	101.36	2.84	2.74	1.91	1.68
GroEL-polypeptide recognition	1kid	102.07	2.85	2.80	1.91	1.54
Green fluorescent protein	1w7s	107.88	2.93	2.79	1.95	1.70
Xylanase from Penicillium simplicissimum	1bg4	107.88	2.93	2.98	2.23	1.66
Phospholipase C (Bacillus cereus)	1ah7	108.62	2.94	3.03	1.97	1.66
L-2-haloacid dehalogenase	1jud	108.62	2.94	2.89	2.00	1.68
The periplasmic -binding protein	1lst	108.62	2.94	3.06	1.91	1.63
Uracil-DNA glycosylase	1udg	110.10	2.96	2.78	2.12	1.66
Human nuclear receptor RAR gamma.	3lbd	112.34	2.99	2.97	2.15	1.55
Recombinant ricin A-chain	1ift	117.67	3.06	2.87	2.28	1.71
Porcine pepsin	5pep	133.55	3.26	3.35	2.25	1.78
Complex of Y216F D-ALA	1iow	136.02	3.29	3.29	2.32	1.73
Arthromyces ramosus peroxidase	1arv	136.02	3.29	3.22	2.21	1.92
Holotransferrin,N-lobe(human)	1a8e	139.35	3.33	3.30	2.30	1.85

Calmodulin-dependent protein kinase	1a06	140.19	3.34	3.51	2.15	1.75
Lactate dehydrogenase	1ldg	142.72	3.37	3.12	2.26	2.00
Cyclin MCS2	1jkw	148.71	3.44	3.66	2.23	1.67
Exo-amylase	1jdd	152.18	3.48	3.53	2.39	1.98
TRNA-guanine transglycosylase	1pud	153.94	3.50	3.28	2.48	2.05
Maltodextrin binding protein	1anf	155.70	3.52	3.44	2.50	1.83
CU-nitrite reductase	1nif*	156.59	3.53	3.29	2.94	1.57
Dihydrolipoamide dehydrogenase	1ojt*	159.26	3.56	3.84	3.15	2.14
HhaI methyltransferase with adohcy and DNA	6mht	161.06	3.58	3.58	2.20	2.05
Human salivary alpha-amylase	1smd	180.50	3.79	3.97	2.39	2.20
Photolyase	1qnf	210.21	4.09	4.13	2.40	2.37
Benzoylformate decarboxylase	1bfd*	211.24	4.10	3.84	3.18	2.10
Galactose oxidase	1gof	219.56	4.18	4.18	2.74	2.38

\*oblate protein



**Figure S1.** TDA spectra of eight proteins. (a) insulin; (b) cytochrome C; (c) myoglobin; (d) carbonic anhydrase I; (e)  $\alpha$ 1-chymotrypsinogen; (f)  $\beta$ -lactoglobulin dimer; (g) ovalbumin; (h) human serum albumin.