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Embed Size (px) 344 x 292429 x 357514 x 422599 x 487GE HealthcareBiacore 3000Instrument HandbookContents1 Introduction1.1 1.2 1.3 Biomolecular interaction analysis	9 Safety information	10 Conformance with standards
112Description2.1 Biacore 3000 processing unit	132.1.1 2.1.2 2.1.3 2.1.4 2.1.5 2.1.6 2.1.7 2.1.8 2.1.9 Pumps.....	14 Autosampler
16 Integrated -Fluidic Cartridge (IFC)	16 The Surface Prep unit.....	20 Sensor chips.....
22 Temperature control	23 LED status indicators	232.2 2.3 2.4Biacore 3000 system control
253Installation3.1 3.2 Instrument placing	27 Moving Biacore 3000	273.2.1 Within the laboratory
273.3 3.4 3.5 3.6Connections	28 Software installation	28 Power up
294Operation4.1 Using the software	314.1.1 4.1.2 4.1.3 4.1.4 General Windows techniques	31 Starting the Control Software
34 Preparing solutions.....	34 Docking the sensor chip	35 Initiating the liquid system
344.2.1 4.2.2 4.2.3 4.2.4Biacore 3000 Instrument Handbook BR-1003-81 Edition AG14.2.5 Normalizing the signal response	35 Normalizing the signal response	37 4.2.6 Setting the temperature
394.4.1 4.4.2 4.4.3 4.4.4 4.4.5 4.4.6 4.4.7 4.4.8 4.4.9 4.4.10 4.4.11 4.4.12 4.4.13 Transferring, mixing and diluting samples.....	39 Data collection rate	39 Data collection rate
42 Setting the detection mode and flow path.....	43 Setting the flow rate.....	44 Injecting sample.....
49 Washing liquid handling system components	51 Saving the sensorgram.....	51 Stopping a sensorgram
52 Starting the command queue	53 Command queue window display	54 Managing the command queue.....
59 Creating a method	60 Checking and saving the method.....	61 Running a method
62 Stopping a method	634.5Queuing manual commands	634.5.1 4.5.2 4.5.3 4.5.4 4.5.5.4Method-controlled operation
634.7.1 Biacore 3000 Processing Unit.....	63 4.7.2 Control Software.....	644.8.1 4.8.2 4.8.3 4.8.4 4.8.5 4.8.6 4.8.7 4.8.8 4.8.9 4.8.10 Using multiple windows
64 Selecting sensorgrams.....	65 Viewing curve classes	66 Scaling the display
68 Report point and event log markers	69 Event log	69 Printing sensorgrams
705Application Wizards5.1 Using application wizards	725.1.1 Starting application wizards	722Biacore 3000 Instrument Handbook BR-1003-81 Edition AG5.1.2 Wizard templates
74 5.1.3 Common wizard functions	745.2 5.3Getting help on wizards	77 The surface preparation wizard
78 Immobilization pH scouting.....	79 Immobilization	82 Immobilization in Surface Prep
92 Troubleshooting surface preparation.....	935.4The analyte recovery wizard	955.4.1 Analyte recovery wizard functions
102 The kinetPage 28/14/2019 28-9617-44 AA Biacore X100 Brochure 1/14BiacoreGE HealthcareBiacoreX100The personal Biacore experience8/14/2019 28-9617-44 AA Biacore X100 Brochure 2/148/14/2019 28-9617-44 AA Biacore X100 Brochure 3/143Boost your protein interactionresearchBiacore X100 is a complete solution for biochemistry, molecular biology, or other research laboratories involved in the study of molecular interactions. The system contains all the key functionalities needed for day-to-day molecular interaction research with the purpose of understanding protein function and biological mechanisms. Biacore systems, used extensively in academic research worldwide, are cited in almost 10 000 peer-reviewed scientific publications. Real-time monitoring of binding events gives a deep understanding of the dynamics of molecular interactions, including valuable kinetic data. Biacore analysis allows or straightforward and rapid data generation, leading to dependable conclusions and enabling the design of new innovative studies. Biacore X100 can be used or a broad range of applications, including structure-uncion studies, pathway analysis, drug target identification and validation, and assay development. Versatility and flexibility, in combination with unparalleled support, make it easy to generate top-quality data or your publication. With Biacore X100 on your bench, take your experiments to the next level and boost your protein interaction research. 8/14/2019 28-9617-44 AA Biacore X100 Brochure 4/1448/14/2019 28-9617-44 AA Biacore X100 Brochure 5/145-50510152025303540-500 0 500 1000 1500 2000 2500 3000Response(RU)Time (s)1 nM5 nM10 nM20 nM30 nMRun successful assays rom day oneNo regeneration required Aibody molecules allowed to partially dissociate rom immobilized HER2 between injections (arrows) Sequential injection on increasing concentration sample in one continuous analysis cycle Biacore X100 uses workflow-oriented software that provides a support framework or assay development and data interpretation, building your expertise as you work. Researchers at Uppsala University used Biacore X100 to determine the binding characteristics of various Aibody molecules to HER2 with regard to specificity, ainity, and kinetic association- and dissociation-rates. Specificity was quickly established by comparing binding levels of the different Aibody molecules to immobilized HER2 and a reference protein. As a next step, the kinetics of high-ainity binders was studied. Aibody molecules turned out to be very difficult to regenerate. This problem was overcome with single-cycle kinetics which eliminates the need or inding regeneration conditions. Acknowledgement: Thuy Tran and Professor Jrgen Carlsson, Uppsala University, Sweden The software wizards were easy to use, and the help function was extremely useful to have. I got good at this very quickly! Thuy Tran, PhD student, Uppsala University, Sweden Guided workflows and software wizards enable generation or reliable data and rapid development or your expertise. Single-cycle kinetics sensorgram 8/14/2019 28-9617-44 AA Biacore X100 Brochure 6/146IdeSideSideCystatinC+IgG1000010020003000400050006000Response(RU)0 100 200 300 400 Time (s) Elucidate complex molecular mechanisms SideS is a papain-like cysteine protease rom the human pathogen Streptococcus pyogenes that specifically degrades IgG. The enzyme has been studied by Dr. Ulrich von Pawel-Rammingens group at Ume University in Sweden. They discovered that human cystatin C has an unexpected stimulatory effect on the IgG-endopeptidase activity of IdeS. Evidence of an interaction between the two proteins was first found using a combination of gel filtration and Western blotting. The mechanisms of the interactions between IdeS, cystatin C, and IgG were further investigated using Biacore X100. Their studies showed that cystatin C binds to IdeS, that IdeS can form homodimers, and that IdeS binding to IgG was not affected by cystatin C. The first research paper including data rom Biacore X100 was published five months after the system was installed. Having a Biacore X100 instrument in our own lab is or great value or our research and allows us to employ many new types of studies. Especially the possibility to run SPR experiments according to our own research agenda is a valuable tool in increasing the understanding of this sophisticated molecular interaction network. Dr. Ulrich von Pawel-Rammingen, Ume University, Sweden Vincents, B. et al. The human protease inhibitor cystatin C is an activating coactor of the streptococcal cysteine protease IdeS. Chemistry & Biology 15, 960-968 (2008). Acknowledgement: Dr. Ulrich von Pawel-Rammingen, Ume University, Sweden Activity assay or IdeS cleavage or IgG. IgG1 binding to immobilized Protein A is measured. Upper curve shows a sensorgram or uncleaved IgG1, while the lower curve shows a sensorgram or IgG1 cleaved by addition of IdeS. The precise mechanisms of this complex network of interactions are now being further investigated. To aid in this study, a standardized enzyme activity assay or IdeS cleavage or IgG is employed, which is run on Biacore X100. A schematic diagram showing the possible interactions between IdeS, cystatin C, and IgG. Red lines indicate a stimulatory effect on the interaction, illustrated by an arrow. 8/14/2019 28-9617-44 AA Biacore X100 Brochure 7/1470210-5410-5610-5810-5110-41-210-41-410-41-610-4Wild type Cys3Ser/His75GlyCys3Ser/Leu73GlyCys3Ser/Tyr97AlaCys3SerConcentration(M)Concentration from A280 measurementConcentration from CFCA11Wild type Cys3Ser Cys3Ser/His75GlyCys3Ser/Tyr97AlaCys3Ser/Leu73Gly105106107ka(M-1s-1)kaWild type Cys3Ser Cys3Ser/His75GlyCys3Ser/Tyr97AlaCys3Ser/Leu73Gly111kd1-1kd KD(KD(M)10-410-310-210-110-1010-910-810-7Increase the reliability of kinetic analysis Cystatin B is an inhibitor of papain-like cysteine proteases. Four mutants were produced in order to study the importance of three different amino acids at the C-terminal and second binding loop or its binding to papain. Since no standard was available, Calibration-free concentration analysis (CFCA) was used to assess protein concentrations. CFCA is an innovative tool to measure protein concentrations, based on specific binding activity, without using a standard curve. The combination of concentration, kinetics, and ainity analysis in a single study enabled the right interpretation of the interaction mechanism. Mutants Cys3Ser/His75Gly, Cys3Ser/Tyr97Ala, and Cys3Ser showed a good agreement between concentration values obtained with A280 and CFCA, while mutant Cys3Ser/Leu73Gly had a very low concentration as measured by CFCA. Introduction of mutations can destabilize protein folding and prolonged storage or freeze/thaw procedures may also decrease the amount of protein capable of binding. Kinetic analysis based on the A280 concentration measurement would lead to the conclusion that leucine 73 is important or the association rate, giving about ten times slower binding than the other mutants. In contrast, CFCA allowed or correct assessment of association rate (ka) and ainity (KD), allowing an appropriate interpretation of the interaction mechanism. The decreased ainity or all mutants were due to an increased dissociation rate (kd), while the association rate (ka) remained relatively constant. 8/14/2019 28-9617-44 AA Biacore X100 Brochure 8/148-10-200 300 800 1300 Time (s)Response(RU)H2NOO--OONHHNNNa+Na+OSSOOS-200 300 800 1300 Time (s)Response(RU)-5051015202530H2NNH2SO O-200 300 800 1300 Time (s)Response(RU)-5051015202530HHNNH2SOOHCIOOODevelop and run assays involving small molecule interactions Biacore X100 provides the sensitivity required or challenging applications. Low molecular weight (LMW) compounds represent one challenging application, because a small molecular size reduces the signal levels. In addition, LMW compounds often require organic solvents or solubility reasons. The optional Biacore X100 Plus PaPage 3		

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