1	GLUTARALDEHYDE IN BIO-CATALYSTS DESIGN:
2	A useful crosslinker and a versatile tool in enzyme immobilization
3	Oveimar Barbosa ^a , Claudia Ortiz ^b , Ángel Berenguer-Murcia ^c , Rodrigo Torres ^a ,
4	Rafael C. Rodrigues*, ^d Roberto Fernandez-Lafuente ^{e,*} .
5	
6	^a Escuela de Química, Grupo de investigación en Bioquímica y Microbiología (GIBIM), Edificio
7	Camilo Torres 210, Universidad Industrial de Santander, Bucaramanga, Colombia.
8	^b Escuela de Bacteriología y Laboratorio Clínico, Universidad Industrial de Santander,
9	Bucaramanga, Colombia.
10	^c Instituto Universitario de Materiales, Departamento de Química Inorgánica, Universidad de
11	Alicante, Campus de San Vicente del Raspeig, Ap. 99 - 03080 Alicante, Spain.
12	^d Biocatalysis and Enzyme Technology Lab, Institute of Food Science and Technology, Federal
13	University of Rio Grande do Sul, Av. Bento Gonçalves, 9500, P.O. Box 15090, ZC 91501-970,
14	Porto Alegre, RS, Brazil.
15	^e Departamento de Biocatalisis. ICP-CSIC. Campus UAM-CSIC. Cantoblanco. 28049 Madrid.
16	Spain.
17	* Co-corresponding authors.
18	Dr Rafael Costa Rodrigues
19	Biocatalysis and Enzyme Technology Lab, ICTA-UFRGS
20	Av. Bento Gonçalves, 9500, P.O. Box 15090, ZC 91501-970, Porto Alegre, RS, Brazil.
21	e-mail: <u>rafaelcrodrigues@ufrgs.br</u>
22	Prof. Dr Roberto Fernández-Lafuente
23	Departamento de Biocatálisis. Instituto de Catálisis-CSIC.
24	C/ Marie Curie 2. Campus UAM-CSIC. Cantoblanco.
25	28049 Madrid (Spain).
26	e-mail: rfl@icp.csic.es

27 Abstract

28 Glutaraldehyde is one of most widely used reagents in the design of biocatalysts. It is a powerful crosslinker, able to react with itself, with the advantages that this may bring forth. In 29 30 this review, we intend to give a general vision of its potential and the precautions that must be 31 taken when using this effective reagent. First, the chemistry of the glutaraldehyde/amino 32 reaction will be commented. This reaction is still not fully clarified, but it seems to be based on 33 the formation of 6-membered heterocycles formed by 5 C and one O. Then, we will discuss the 34 production of intra and inter-molecular enzyme crosslinkings (increasing enzyme rigidity or 35 preventing subunit dissociation in multimeric enzymes). Special emphasis will be placed on the 36 preparation of cross-linked enzyme aggregates (CLEAs), mainly in enzymes that have low density of surface reactive groups and, therefore, may be problematic to obtain a final solid 37 38 support. Next, we will comment on the uses of glutaraldehyde in enzymes previously 39 immobilized on supports. First, the treatment of enzymes immobilized on supports that cannot 40 react with glutaraldehyde (only inter and intramolecular cross-linkings will be possible) to 41 prevent enzyme leakage and obtain some enzyme stabilization via cross-linking. Second, the 42 cross-linking of enzymes adsorbed on aminated supports, where together with other reactions 43 enzyme/support crosslinking is also possible; the enzyme is incorporated to the support. Finally, 44 we will present the use of aminated supports preactivated with glutaraldehyde. Optimal 45 glutaraldehyde modifications will be discussed in each specific case (one or two glutaraldehyde 46 molecules for amino group in the support and/or the protein). Using preactivated supports, the 47 heterofunctional nature of the supports will be highlighted, with the drawbacks and advantages 48 that the heterofunctionality may have. Particular attention will be paid to the control of the first 49 event that causes the immobilization depending on the experimental conditions to alter the 50 enzyme orientation regarding the support surface. Thus, glutaraldehyde, an apparently old 51 fashioned reactive, remains as the most widely used and with broadest application possibilities 52 among the compounds used for the design of biocatalyst.

Key words: enzyme immobilization, enzyme stabilization, inter and intramolecular
 crosslinking, CLEAs, heterofunctional supports, glutaraldehyde.

56 1. Introduction

Enzymes are biocatalysts which catalyze most metabolic reactions in living beings. *In vivo*, they are highly specific (modifying just one substrate among a collection of similar ones), chemo/enantio/regio-selective (yielding just one substrate among several possible) and very active under very mild environmental conditions (atmospheric pressure, room temperature, aqueous medium). Thus, enzymes have been considered the ideal catalyst from an environmental point of view, in reactions involving complex or labile compounds.¹⁻⁵

63 However, enzymes perform their function inside living beings, under complex 64 regulations and stress. This causes enzymes to become inhibited by many compounds. Thus, 65 their in vivo stability can hardly be measured in days, and their exceptional properties may not 66 be found when they are utilized for modifying other substrates (different to the physiological 67 ones) or even performing other reactions (e.g., using hydrolases as transferases in kinetically 68 controlled synthesis). Moreover, the soluble nature of the enzymes avoids their extended use 69 (and subsequent re-use) in industry. These properties are far from the requirements of an industrial catalyst.⁶ 70

The solution to these limitations is the main subject of enzyme technology. The researcher may use a handful of different tools, such as microbiology,² genetic approaches,⁷⁻¹⁰ immobilization,¹¹⁻¹⁷ chemical modification,^{18,19} and medium and reactor engineering to shortcut these enzyme limitations. Many of these tools may be used in an integrated way.²⁰⁻²³

Physicochemical tools, such as chemical modification or enzyme immobilization, have special interest in this context. Due to the requirements of producing a heterogeneous catalyst, enzyme immobilization becomes a necessity from this perspective.¹⁴ This strategy has been investigated by many authors as a way to improve enzyme properties. It has been shown that enzyme stability may be significantly improved if an intense multipoint covalent attachment (MCA) between an enzyme molecule and a rigid support, via a short spacer arm, is achieved.¹⁷ 81 This phenomenon causes all groups involved in the immobilization to keep their relative 82 positions when the enzyme is submitted to any conformational change. The area of the enzyme involved in the immobilization may be also critical to maximize the stabilizing effect of the 83 MCA.²² Immobilization may also tune some other enzyme properties, such as activity, 84 resistance to inhibition, selectivity or specificity.¹⁷ Chemical modification of enzymes may be 85 used to further improve enzyme stability (e.g., via chemical crosslinking),²⁴ and may be also 86 used as another tool to alter enzyme catalytic features.¹⁸ Moreover, as it has been revised, 87 88 chemical modification or immobilization of enzymes may be designed to simplify or improve one another.²¹ 89

Glutaraldehyde is the reagent that the present review is devoted to. It has been used in many instances as protein cross-linker, as an activator of supports, and as crosslinker of enzymes and supports.^{25,26} In this review, we intend to give a wide vision of the prospects of this very interesting and versatile molecule in the design of biocatalysts.

94

95 **2.** Chemistry of glutaraldehyde

Glutaraldehyde is a bi-functional reagent with the capacity to polymerize.^{27,28} 96 97 Glutaraldehyde may react with different enzyme moieties, mainly involving primary amino 98 groups of proteins, although it may eventually react with other groups (thiols, phenols, and imidazoles).²⁷⁻³⁰ However, the exact structure of the main structures related to protein 99 100 crosslinking or enzyme immobilization is still not fully clarified. Figure 1 shows some of these 101 proposed structures. It is clear that the structure of the glutaraldehyde relevant for the 102 modification of enzymes and supports is not a linear one, but some kind of fairly stable cycles 103 (activated support may be washed with an excess of distilled water without losing 104 glutaraldehyde moieties).

105

107 The reaction mechanism of glutaraldehvde with proteins implies that it is not limited to just one 108 mechanism. This is because the main reactive species of glutaraldehyde are found in equilibrium between their monomeric and polymeric conformations.^{27,28,31,32} Moreover, every structure can 109 110 react in a different way with the protein. For instance, under both acidic and neutral conditions, 111 aldehvde groups from glutaraldehvde can react with proteins by formation of Schiff bases. In 112 this case, a nucleophilic attack takes place by the ε-amino group from lysine to glutaraldehyde 113 (See Figure 2a). However, Schiff bases are unstable at acidic conditions and are broken up, 114 regenerating both the aldehyde and the amine groups. For this reason, several procedures have 115 recommended reduction by NaBH₄ or NaBCNH₃ as a final step in order to stabilize the Schiff 116 base into a secondary amine. Nevertheless, some studies suggest that protein preparations treated with a reducing agents does not cause an striking increase in the enzyme stability.³³ 117 118 Additionally, lysine residues of protein treated with glutaraldehyde without further chemical reduction are not regenerated by incubation in HCl 6M at 110 °C by 24 h.³⁴ Consequently, it is 119 120 possible that a mechanism of formation of Schiff bases between proteins and glutaraldehyde 121 could not be carried out. In this sense, an additional reduction step would not be necessary in order to stabilize the reaction product.^{27,28,35} Therefore, the mechanism of glutaraldehyde at 122 123 neutral and acidic conditions would be mediated by hemiacetal cyclic conformations from both 124 the monomer and polymer of glutaraldehyde. This cyclic hemiacetal of glutaraldehyde reacts by 125 nucleophilic substitution of the amino groups from lysines with the hydroxy group of 126 glutaraldehyde according to the Figure 2.

127 On the other hand, under basic conditions it has been proposed that glutaraldehyde quickly 128 suffers intramolecular aldolic condensations, producing a polymeric form of an a α , β -129 unsaturated aldehyde, which may react with amino groups from proteins through two 130 mechanisms: Firstly by formation of Schiff bases between internal aldehyde groups from the 131 polymeric form of glutaraldehyde and primary amino groups from the protein (Figure 3, 132 reaction 1). In this case, the obtained product could be stabilized by a resonance effect of

133 conjugated double C-C bonds.³² The second mechanism involves a Michael addition to the 134 double C-C linkage.²⁷ However, this reaction results in a less stable product due to loss of 135 resonance effect of the conjugated double C-C bonds, which would be labile under acidic 136 conditions (Figure 3,).

Prof. Monsan,^{36,37} has shown that it is relatively simple to only have one or two 137 138 molecules of glutaraldehyde per amino group in a support. This result, coupled to some more 139 recent ones that confirm this, suggested a different reactivity of the amino/glutaraldehvde 140 moiety with free glutaraldehyde compared to the capacity of free glutaraldehyde molecule to 141 polymerize, as under the described conditions to get this amino/glutaraldehyde/glutaraldehyde moiety there is not a massive precipitation of glutaraldehyde polymers.³⁸ Amino/glutaraldehyde 142 143 reacted with free glutaraldehyde much more rapidly that free glutaraldehyde with free 144 glutaraldehyde molecules. It also showed that the two glutaraldehyde molecules/amino moiety 145 groups in the support possessed the structure that exhibited the highest reactivity versus amino 146 groups in a protein. If just one glutaraldehyde molecule was attached to the amino group, this 147 moiety exhibited a low reactivity versus amino groups. However, this group, together with the 148 already commented reactivity versus free glutaraldehyde molecules, exhibited a vey high 149 reactivity versus other similar amino/glutaraldehyde moieties, being the activation of a protein 150 the preferred way to get crosslinkings as we will discuss later. This different reactivity of the 151 amino/glutaraldehyde moiety compared the glutaraldehyde or the to 152 amino/glutaraldehyde/glutaraldehyde moiety should be found in the presence of an amino group in the heterocycle of the glutaraldehyde ring.^{39,40} Amino/glutaraldehyde/glutaraldehyde has a 153 154 similar reactivity when compared to free glutaraldehyde, as the second glutaraldehyde group 155 will be very similar to free glutaraldehyde. If the conditions were forced (e.g., increasing the pH 156 value or the glutaraldehyde concentration) to get a higher degree of polymerization on the amino 157 group, the free glutaraldehyde may also react; giving large glutaraldehyde aggregates that may 158 precipitate and the suspension will turn white.

159

160 **3. Glutaraldehyde as protein crosslinker**

161 The first use of glutaraldehyde was to preserve and fix tissues^{41,42} in some instances 162 combined with formaldehyde.²⁵ This is achieved through the formation of intermolecular 163 crosslinking. Nowadays, glutaraldehyde remains as one of the most potent crosslinker reagents, 164 even with clinical applications.⁴³⁻⁴⁵ In part, these very good crosslinker features are a 165 consequence of the capacity of glutaraldehyde to react with itself or with protein groups already 166 modified with a glutaraldehyde molecule.²⁸

167 The protein crosslinkings may be among groups placed on different protein molecules 168 (intermolecular crosslinking) or between groups placed in the same molecule (intramolecular 169 crosslinkings).^{24,46} Both kinds of crosslinkings have interest in specific cases.

170

171

3.1- Glutaraldehyde as intermolecular crosslinker of proteins

As previously commented, this was the first use of glutaraldehyde, using its crosslinker potential to fix tissues.⁴¹ However, in this review we will focus on the use of glutaraldehyde in the design of biocatalysts.

175 The addition of glutaraldehyde to a protein solution may produce the chemical 176 aggregation of the enzyme, causing protein molecules to react among themselves, and can directly yield a "solid biocatalyst" (Figure 4). Although this immobilization strategy has not 177 178 been widely used, it is possible to find diverse examples in literature. For example, insoluble 179 trypsin was prepared by the use of glutaraldehyde to produce intermolecular crosslinks and the insoluble trypsin thus prepared exhibited enzymatic activity toward casein.⁴⁷ Later, 180 181 glutaraldehyde was reacted in aqueous solutions with papain to form a water-insoluble product 182 with enzymatic activity after activation by reducing agents. A rapid reaction of glutaraldehyde 183 with the essential sulfhydryl of papain was not involved in the reaction since after activation the insoluble enzyme retained esterolytic and proteolytic activity.⁴⁸ 184

In another example, a purified preparation of extracellular alkaline proteinase of *Trichoderma koningii* was insolubilized by intermolecular crosslinking with glutaraldehyde.⁴⁹ The optimum operational temperature of the insolubilized enzyme increased by 20 °C. The immobilized enzyme was also relatively more stable and activity was less depended on the presence of ions or detergents than the soluble enzyme. More surprisingly, an enhanced affinity to casein, hemoglobin and bovine serum albumin was found, although with a lower V max values.

192 Intermolecular cross-linking of the protease stem bromelain with 0.25 and 1.25% glutaraldehyde results in the formation of a large molecular mass, multimeric and 193 194 soluble aggregate having comparable activity to the unmodified bromelain. Both 0.25 and 195 1.25% glutaraldehyde cross-linked bromelain preparations were more stable against urea, 196 guanidine hydrochloride and temperature-induced inactivation, and exhibited slightly better 197 storage stability compared to the unmodified protease. Such a high molecular weight, soluble, 198 active and stable preparation may be useful in industry, i.e. in the textile industry for improving the properties of a fabric without loss of fabric strength and shape.⁵⁰ 199

200 On the other hand, glutaraldehyde is the intermolecular crosslinker of some of the recent carrier-free immobilization protocols, such as crosslinked enzyme crystals (CLECs)^{51,52} 201 (Figure 5) or aggregates (CLEAs) (Figure 6).⁵³⁻⁵⁶ While using a conventional homo-bi-202 203 functional reagent the ideal strategy seems to modify around 50% of the reactive groups of the 204 protein to maximize the possibility of crosslinking, the chemistry of glutaraldehyde causes this 205 option not to be the optimal one, as amino/glutaraldehyde moieties reacts better with other group.³³ 206 amino amino/glutaraldehyde groups than one Moreover, 207 amino/glutaraldehyde/glutaraldehyde did not react easily with other amino/ (glutaraldehyde)₂ 208 groups, making it inconvenient to excessively modify the proteins. Thus, to reach protein 209 crosslinking using glutaraldehyde, it seems adequate to use moderate concentrations of 210 glutaraldehyde, high enough to ensure the activation of most amino groups with one molecule of

211 glutaraldehyde, but not too high so as not to reach activations with two molecules of 212 glutaraldehyde per amino group (e.g., 0.1-1% (v/v) glutaraldehyde at pH 7 for 1 hour).³⁶ Milder 213 activation of the amino groups of the enzyme may produce a milder crosslinking. However, in 214 some instances it may be necessary to use suboptimal crosslinking conditions if the protein is 215 especially sensible to glutaraldehyde modifications. In certain cases, as if the enzyme has a Lys 216 group in its catalytic site (e.g., some aldolases), glutaraldehyde must be discarded and other 217 crosslinking reagent should be used, such as aldehyde dextran.⁵⁷

218 To achieve a proper crosslinking in this kind of immobilization strategies may be a 219 problem, mainly if the protein has not many Lys on its surface (Figure 7). This may make the 220 formation of large aggregates difficult and enable the release of enzyme molecules (individual 221 molecules or small aggregates) from the solid. In some cases, it is even not possible to get a 222 solid in aqueous medium. Using CLEAs some solutions have been offered to overcome this 223 situation. Taking advantage of the fact that the enzyme did not need to be pure to prepare 224 CLEAs, the co-precipitation of the target enzyme with inert proteins having a high density of superficial Lys groups (e.g. bovine serum albumin)⁵⁸⁻⁶³ or with polymers having many amino 225 groups (e.g., polyethylenimine)⁶⁴⁻⁶⁷ has been proposed (Figure 8). Both strategies permit the 226 227 formation of physically stable CLEAs, but they also produce a decrease in the volumetric 228 loading of the target enzyme, as part of the volume will be occupied by the inert protein or the 229 polymer. As an alternative, a strategy based on the use of chemically aminated enzymes with their protein surface enriched on reactive groups has been proposed (Figure 9).⁶⁸ This way, it is 230 231 not necessary to mix the target protein with any other molecule or polymer and the volumetric 232 loading of the CLEA is similar to that of proteins that may be directly used to prepare CLEAs.

233

234 **3.2.** Glutaraldehyde as intramolecular crosslinker of proteins

The introduction of intramolecular crosslinkings in an enzyme structure is one of the most widely used techniques to increase enzyme stability, using genetic or chemical routes.^{24,69,70} If the crosslinking agent is short enough, the relative mobility of one group relative to the other crosslinked group should be minimized.⁷¹ Furthermore, if the researcher is able to introduce several crosslinkings on the enzyme surface, the final result should be a global rigidification of the overall structure of the enzyme (Figure 10).

However, to introduce several intramolecular crosslinkings in a protein molecule and to get a significant stabilization effect is not a simple task, as many problems may rise. We will detail some of the most relevant ones.

- Distance between reactive groups in the protein. The crosslinking formation requires the 244 existence of at least two reactive moieties in the protein surface at the adequate distance.^{72,73} If 245 246 there are no groups in the range of distances covered by the crosslinker, crosslinking will not be 247 possible. This may be solved if the researcher somehow increases the number of reactive groups 248 on the protein surface, e.g. via amination (Figure 11). Site-directed mutagenesis, changing an 249 aminoacid of the protein by Lys next to other Lys or the terminal amino group, may permit to 250 increase the prospects of crosslinking just in a desired place (e.g., an unstable area of the 251 protein). However, although the site directed introduction of Cys residues has been used to establish disulfide bonds in a protein,⁷⁴⁻⁷⁶ these reviewers have been unable to find the use of 252 253 introduce Lys to improve the chemical crosslinking with glutaraldehyde, only to improve the multipoint covalent attachment via immobilization.^{77,78} Another possibility is the chemical 254 255 amination of the enzyme with ethylenediamine via activation of the carboxylic groups of the protein with carbodiimide.^{79,80} This strategy implies the general modification of the enzyme 256 257 surface, but the number of reactive groups may be increased by a factor between 2 and 5, augmenting the possibilities that several groups in the protein surface may be at an adequate 258 259 crosslinking distance. This strategy has been utilized to introduce intramolecular crosslinking in immobilized penicillin G acylase, with stabilization factor of 30-50, depending on the 260 crosslinking conditions and inactivation cause.³³ 261

262 - Competition between one-point chemical modification and crosslinking. The first one-point 263 chemical modification involves a soluble reactive that must modify a group placed in the surface of a protein. In principle, this one-point modification may be very rapid. However, the 264 265 crosslinking reaction involves the correct alignment of two groups located on a moderately rigid 266 surface, such as that of an enzyme. Using other homo-bifunctional crosslinkers, this competition may produce serious hindrances to the promotion of an intense crosslinking in the enzyme 267 268 surface, using glutaraldehyde, as stated above, there is not a real competition between one-point 269 modification and crosslinking, as the best solution is an activation of all amines in the protein 270 with just one glutaraldehyde group. However, there is no guarantee that the modified amino 271 groups participate in crosslinking. In the best scenario, the final effect of the glutaraldehyde treatment will be a mixture of crosslinking and chemical modification. The first one should 272 273 produce a rigidification of the enzyme surface; the second may have unpredictable effects on the 274 enzyme features. Some times these effects may be very negative, even overcoming the positive 275 effects of the crosslinking bridges. Some times, it may be very positive, increasing enzyme stability even without the formation of any crosslinking.^{81,82} This effect of the one-point 276 chemical modification needs to be considered when explaining the effects of the glutaraldehyde 277 278 treatment on the stability of a particular enzyme.

279 - Competition between inter and intra molecular crosslinking. Another possibility is the 280 competition between intra and intermolecular crosslinking. In fact, using free enzyme, to just 281 have the desired intramolecular crosslinking may be nearly impossible, as inter molecular 282 crosslinking is a faster reaction. Although this may also produce enzyme stabilization (see 283 above), it may complicate the understanding of the results, and also make reproducibility 284 complex, because the intermolecular crosslinking will depend on the protein concentration, kind 285 and percentage of contaminant proteins, etc. The use of simple analytical techniques applied to 286 glutaraldehyde treated samples after reduction with borohydride, such as SDS-PAGE, may 287 permit to visualize the presence and extension of the intermolecular crosslinking.

288 Even when using immobilized enzymes, to fully prevent enzyme crosslinking may be 289 hard. Using porous supports, if the immobilization rate is much higher than the diffusion rate, 290 the enzymes may be packed so near each other that the enzyme molecules may be crosslinked 291 with each other even using short reagents like glutaraldehyde (Figure 12). If the immobilization rate is slow enough, the distance between enzyme molecules may be enough to almost fully 292 prevent enzyme intermolecular crosslinking.⁸³ Recently, by changing the immobilization 293 conditions, a lipase has been immobilized on octyl agarose and treated with glutaraldehyde.⁸⁴ 294 295 Under one immobilization condition, immobilization was quite slow (in presence of ethanol) 296 and intermolecular crosslinking was almost negligible and it was possible to analyze the effect 297 of intramolecular modifications. Under another condition, immobilization rate was vey high and 298 the enzyme molecules were so near that both modifications could be achieved. The comparison 299 between both derivatives (one having only intramolecular modifications, the other having both 300 intramolecular and intermolecular modifications) permitted to determine the positive effects of 301 the intermolecular crosslinking in the enzyme stability.

302

303 3.3. Crosslinking of multimeric enzymes.

Many enzymes are formed by several subunits, which are in association/dissociation 304 equilibrium, usually being the associated form the most active and stable.⁸⁵⁻⁸⁷ In other cases, 305 306 some cascade reactions may require the joint action of several different enzymes that require their being associated.⁸⁸⁻⁹⁰ If the researcher is able to crosslink these structures, the system will 307 308 work in a more adequate fashion. However, the difficulties commented for the intramolecular 309 crosslinking remain valid here, even with one additional key point: the reactive groups at the crosslinking distance need to be placed in different enzyme subunits (Figure 13).²³ This is why 310 311 crosslinking of these structures may be achieved in a better way using polymers, as they should 312 not confer an intense structural rigidity, but may be useful to keep together the different enzyme subunits or maintain the multi enzymatic complex assembled (e.g., dextran aldehyde,⁹¹ 313

polyehtylenimine^{92,93}). Nevertheless, glutaraldehyde has been used in certain cases to stabilize. 314 315 even though only in a small percentage of the total enzyme structures, the subunit-subunit 316 interactions. For example, the crosslinking of the hetero-oligomeric glucose dehydrogenase from 317 a moderate thermophilic bacterium, SM4, using glutaraldehyde as crosslinking reagent has been reported.⁹⁴ The treatment permitted glucose dehydrogenase to gain high thermal stability 318 319 without loss of its catalytic activity and thus increase the activity of the enzyme at high 320 temperature. The authors concluded that by chemical cross-linking of the subunits, the 321 dissociation of alpha and beta subunits was prevented. Consequently, its quaternary structure 322 was stabilized, and thus the thermal stability of the glucose dehydrogenase was enhanced. Also, 323 D-Lactate dehydrogenase from Limulus polyphemus is a homodimer which is composed of identical subunits that has been crosslinked with glutaraldehyde to show a relation of 324 reactivation with reassociation of the dimer.95 325

In another paper, primase/helicase produced by bacteriophage T7 that can form both hexamers and heptamers. These oligomers were stabilized via cross-linking with glutaraldehyde and purified.⁹⁶ The authors detected how the percentage of each oligomeric form could be altered by the presence of either dTTP or β , γ -methylene. Heptamers are unable to efficiently bind either single-stranded DNA or double-stranded DNA, thus the authors postulated that a switch between heptamer to hexamer may provide a ring-opening mechanism for the singlestranded DNA binding pathway.

333 NTPDase1 and NTPDase2 enzymes from rats were expressed in *Xenopus laevis* 334 oocytes and their quarternary structure was analyzed.⁹⁷ The treatment with glutaraldehyde 335 permitted to detect that native NTPD-ase1 and NTPD-ase2 occur in oligomeric form. Dynamic 336 alterations in oligomeric state may induce changes in substrate preference and thus influence the 337 pattern of *in situ* extracellular nucleotide degradation.

In some instances, glutaraldehyde may have an indirect use to stabilize a multimeric enzyme, by crosslinking a polymer to the enzyme surface avoiding the polymer release. The

340 coating of the surface of multimeric enzymes with a poly-ionic polymer that may 341 simultaneously interact with several enzyme subunits, preventing enzyme dissociation has proved to prevent enzyme subunit dissociation if the polymer can become adsorbed on the 342 enzyme (Figure 14).⁹³ This strategy has been recently utilized to stabilize the enzyme glutamate 343 344 dehvdrogenase from *Thermus thermophilus* and formate dehvdrogenase from *Pseudomonas* sp., 345 using polyethyleneimine as the "crosslinking" polymer. Both enzymes were inactivated by 346 dissociation at acidic pH value, and the coating of their surface with polyethyleneimine 347 prevented this (Figure 14). However, the reversible nature of the polymer adsorption permitted 348 the polymer to become desorbed under certain conditions (e.g., high ionic strength, drastic pH 349 value), and the protective effect of the polymer coating was lost. This problem was solved by a 350 further treatment with glutaraldehyde, crosslinking the enzyme and the polymer: the new 351 composite was fully stable under enzyme dissociation conditions. This composite could be used in soluble form, or ionically exchanged on a cation exchanger.⁹³ When a similar strategy was 352 353 applied to the hexameric glutamate dehydrogenase from E. coli, the polymer protection was successful, but the enzyme was rapidly inactivated by incubation with glutaraldehyde.⁹² Thus, 354 355 this strategy not only requires that the polyethyleneimine may stabilize the multimeric structure 356 of the enzyme without inactivating it, but also requires that the enzyme was resistant to the 357 treatment with glutaraldehyde.

358

4. Intermolecular crosslinking of immobilized proteins via reversible immobilization using supports unreactive towards glutaraldehyde

Enzyme immobilization by physical adsorption (using ion exchange, immobilized chelates or hydrophobic adsorption) is the simplest protocol to immobilize enzymes, does not require enzyme nor support treatment, immobilization is rapid, and the support does not require special storage conditions.¹⁴ However, this enzyme immobilization strategy has two disadvantages. The first one, the enzyme may be released from the support under certain experimental conditions.^{98,99} Using ion exchangers, this may occur when changing the pH value or increasing the ionic strength. Using hydrophobic adsorption, if the reaction requires the presence of co-solvents or detergents the enzyme may be released to the medium. The second problem is that physical adsorption may have no positive effects on enzyme stability, even as the support retains its capacity to interact with the enzyme, the immobilization may produce a certain destabilization of the enzyme.¹⁴

372 Thus, to prevent enzyme desorption and improve enzyme stability, it is relatively 373 common to find reports where the researcher, after enzyme reversible immobilization, treats the 374 immobilized enzyme with glutaraldehyde. In most cases, a certain enzyme stabilization is 375 observed and enzyme desorption is at least partially avoided under conditions where previously 376 all the immobilized enzyme became desorbed (Figure 12). Furthermore, this occurs using 377 supports with which the glutaraldehyde can not react, thus the enzyme cannot become 378 immobilized on the support. This is the case of supports having aliphatic acyl moieties or 379 quaternary amine groups as active groups on the support; glutaraldehyde hardly can react with 380 these groups in the support.

381 To explain these results, we should go back to point 3.2 of this review. Immobilization 382 via physical adsorption is usually much faster than enzyme diffusion inside the support pores 383 and in most cases the treatments of the biocatalyst involving glutaraldehyde described in the 384 literature are performed using fully protein loaded biocatalysts. Under these conditions, the 385 enzymes are packed together, so close to each other that the distance is in the range of 386 glutaraldehyde crosslinking. Furthermore, if two reactive groups are conveniently confronted, intermolecular crosslinking will occur (Figure 12).⁸⁴ Moreover, intramolecular modifications 387 388 (one point or crosslinkings) will also take place, reinforcing in some cases the stabilization 389 effects. Regarding enzyme release, it now becomes necessary to simultaneously release all 390 adsorbed enzymes, otherwise the aggregate will remain adsorbed. This makes that the "strength" 391 of the adsorption increases exponentially with the size of the aggregate, and under conditions

where individual molecules were fully desorbed, now the enzyme remains fully adsorbed on the
 support.⁸⁴

394 As in certain cases the reactivity of the support with the glutaraldehyde cannot be fully 395 discarded due to its unknown nature, the lack of glutaraldehyde reaction with the support may be 396 verified via different strategies. For example, it is possible to check if we can "preactivate" the 397 support, to achieve a covalent attachment between the enzyme molecules and the support after 398 washing the support with an excess of water to eliminate all free glutaraldehyde molecules and 399 later offering the enzyme. The use of Schiff reactive may also help to verify if some reactive 400 glutaraldehyde remain bound to the support after the washings. Second, slowing down the 401 immobilization rate of the enzyme to increase the distance between enzyme molecules, and 402 checking if the glutaraldehyde treatment still avoids desorption of a significant percentage of the 403 enzyme molecules.

One drawback of this strategy is that desorption of very large chemical aggregates may be fully impossible even under the most drastic conditions, transforming a reversible immobilization method in an irreversible one. The researcher should carefully evaluate the convenience of this treatment, considering the stability requirements of the enzyme and the real risks of enzyme desorption during the use of the biocatalyst versus the possibility of having to discard the support after enzyme immobilization.¹⁴

410 This strategy has been used in several examples to prepare crosslinked enzyme 411 aggregates in an immobilized form, that some authors call CLEAs (see above), but which really 412 are an altogether different thing. Hierarchically ordered mesocellular mesoporous carbon was used as a host for enzyme immobilization.¹⁰⁰ To improve the retention of enzymes, the adsorbed 413 414 enzymes were cross-linked using glutaraldehyde. The resulting preparation showed a significant 415 stabilization with high enzyme loadings. For example, 0.5 g chymotrypsin could be loaded in 1 416 g of silica with no activity decrease observed with rigorous shaking over one month. In contrast, 417 adsorbed chymotrypsin without any crosslinking treatment resulted in a lower loading, which 418 further decreased due to continuous leaching of adsorbed chymotrypsin under shaking. The 419 activity of crosslinked enzyme aggregates was 10 times higher than that of the adsorbed 420 chymotrypsin..

In two papers, both α -chymotrypsin and a lipase were immobilized in SBA-15 mesoporous silica by crosslinking adsorbed enzymes to give the so-called one-dimensional crosslinked enzyme aggregates.^{101,102} This simple approach resulted in one-dimensional crosslinked enzyme aggregates in the linear pore channels of SBA-15, which was very effective in preventing the enzyme leaching and consequently improving the enzyme stability.

In another research effort, meso-structured onion-like silica was produced with a 200-300 nm sized primary meso-structured onion building unit, with each onion unit having highly curved mesopores of 10 nm diameter in a multishell structure.¹⁰³ Nanoscale enzyme reactors in these supports were prepared via a two-step process of enzyme adsorption and subsequent enzyme cross-linking with glutaraldehyde, which effectively prevents the leaching of crosslinked enzyme aggregates from highly curved mesopores. This improved the enzyme stability as well as the enzyme loading.

In another example, β -glucosidase was immobilized onto mesocellular silica foams and later crosslinked with glutaraldehyde.¹⁰⁴ This resulted in the formation of crosslinked enzyme aggregates of nanometer scale. The final catalyst was more stable and presented a lower Km than that of its free counterpart.

Other authors really produced CLEAs inside the pores of supports, taking advantage of the increase in size of the enzyme when an aggregate was formed. However, they are neither real CLEAs, as the enzyme is not previously precipitated (Figure 15). This is the case of the examples described by Prof Hartman's group. Using chloroperoxidase, they showed that the formation of cross-linked chloroperoxidase aggregates in the pores of mesocellular foam materials results in active biocatalysts that are more resistant to leaching than the conventional catalyst prepared by physisorption of chloroperoxidase. Small-angle neutron scattering

444 experiments clearly confirm that the chloroperoxidase -CLEAs are located in the pores of the mesocellular foams.¹⁰⁵ Later, they extended the studies to glucose oxidase. The formation of 445 446 cross-linked enzyme aggregates of glucose oxidase in the pores of mesocellular foams was 447 obtained. The enzymes can enter the ultra-large cavities connected through the smaller windows, 448 where their agglomeration and cross-linking with glutaraldehyde will take place. After cross-449 linking, the diameter of the aggregates is larger than the diameter of the pore entrance and, thus, the enzymes are trapped in the pores of the support.¹⁰⁶ Finally, glutaraldehyde cross-linked 450 451 enzyme aggregates of chloroperoxidase and glucose oxidase were grown in large-pore mesocellular foams, improving operational stability in the oxidation of indol.¹⁰⁷ 452

453

454 5. Crosslinking of supports bearing primary amino groups and ionically exchanged 455 proteins

In this new example of use of glutaraldehyde to immobilize enzymes in preexisting supports, as in the case explained above, the treatment with glutaraldehyde is performed after the enzyme is adsorbed in the support, in this case via ion exchange. However, this is a fully different case from the one described above. Now, the researcher knows that the support has primary amino groups, and that, therefore, it is likely to modify the support with glutaraldehyde, and finally obtain enzyme-support covalent bonds.¹⁰⁸ Thus, in this case, the enzyme may experience three different kinds of modifications caused by glutaraldehyde (Figure 16):

463

1- Intramolecular modifications (one point modifications or crosslinking, see above).

464 2- Interprotein crosslinking. If the ion exchange immobilization has been rapid enough,
465 the enzymes will be very near each other and it is likely to have enzyme-enzyme crosslinking
466 (see above).

3- Support-enzyme reaction. The support and the enzyme molecules may react with each
other. In fact, if the treatment with glutaraldehyde is performed in a way that enables the
modification of each reactive group in the support and the enzyme with one glutaraldehyde

470 molecule, we will have the situation where the highest prospects of enzyme support reaction 471 may occur. And this reaction will take place in a relative wide range of pH value, as the reaction will occur between amino/glutaraldehvde moieties; although considering the stability of the 472 473 groups and its reactivity, some reports suggest that pH values around 8.5 may be the most adequate.³³ That way, the support will behave as a large multi-crosslinking reagent, fixing the 474 475 positions of all the protein groups involved in the reaction with the support, whose relative 476 position must remain unaltered under any distorting condition, promoting an increase of the 477 overall enzyme structure, which becomes more intense when a more intense multipoint covalent attachment is achieved.^{17,109-111} 478

479 Thus, this strategy has some positive points, as the good reactivity of the amino 480 glutaraldehyde moieties with similar groups in a relatively wide range of pHs, that include 481 neutral pH, the fact that the glutaraldehyde treatment is performed on a previously immobilized 482 enzyme, and the possibilities of having some positive inter or intra-modifications. This last point 483 is also the drawback of the strategy, as the enzyme should be fully modified, not only in the 484 groups involved in the immobilization, and in some cases these modifications may be negative 485 for enzyme stability or activity. However, in many instances when there is a comparison between immobilization on preactivated supports (see below) or treatment with glutaraldehyde 486 487 after enzyme in exchange, stabilization improves using this strategy.^{108,112,113}

In other many cases, a comparison was not performed but results using the treatment of previously adsorbed enzymes were very positive regarding stabilization and prevention of enzyme leakage.¹¹⁴⁻¹¹⁹

The treatment of lipases adsorbed on anion exchanger supports has been in some cases used to modulate enzyme properties. Thus, the open form of some lipases was fixed by glutaraldehyde treatment of adsorbed lipases in the presence of detergents.¹²⁰ In other cases, the random chemical modification was enabled to modulate the lipase selectivity or specificity.¹²¹

495 This strategy may be only used when the support is able to immobilize the protein via 496 ionic exchange. That means that the support should present a high enough number of ionic 497 groups to permit the adsorption of the enzyme on the support. Moreover, the enzyme should 498 have the capacity to become adsorbed to anion exchangers. Considering that this is a multipoint process (several ion bridges need to be produced to fix the enzyme to the support).¹²²⁻¹²⁴ the 499 500 strategy presents the problem that the support should never be physically inert. Furthermore, the 501 inertness of the support surface may be in many instances a desired feature of the support, to 502 prevent uncontrolled support-enzyme interactions that may affect enzyme stability (sometimes in a positive sense, but in another may have a negative impact in the enzyme stability).^{14,125} 503 504 Another negative point to be considered is the possibility of reactivating the enzyme after inactivation, the folding-unfolding strategy may not work if the unfolded enzyme may interact 505 with the support.¹⁴ 506

Moreover, the strategy does not offer a large versatility. It may be possible that the immobilization via ionic exchange under different conditions of pH and ionic strength may involve different areas, but that is the only way of altering the enzyme orientation regarding the support.¹²⁶⁻¹²⁸ The immobilization of an enzyme via different areas may be interesting to reach optimum stabilization (involving the most labile area of the protein in the immobilization)^{22,129-} ¹³² or to tune the enzyme catalytic properties (selectivity, specificity, activity).¹⁷

513

514 6. Activation of supports with glutaraldehyde

In this last case, the support is pre-activated with glutaraldehyde. Following the results from Monsan, the optimal activation regarding the chemical reactivity of the support should be two molecules of glutaraldehyde per amino group in the support (obtained, e.g., by incubating the support in 1 M glutaraldehyde at pH 7 by 12-16 h).³⁷ It is very likely the most widespread form of using glutaraldehyde to immobilize enzymes (see for example¹³³⁻¹⁴¹) and one of the first papers concerning the use of glutaraldehyde to prepare immobilize enzymes may be found in .¹⁴² 521 Compared to the strategy described above, this method has some advantages and 522 drawbacks. As a drawback, we can consider the higher difficulty on having an intense 523 multipoint covalent attachment. the reaction between as now is 524 amino/glutaraldehyde/glutaraldehyde moieties and the ε amino groups of the Lys residues (and 525 the terminal amino group). The Lvs groups have a pK of 10.7, and the stability of the 526 glutaraldehyde groups in the support is not good at alkaline pH value while at neutral pH value 527 the reactivity of the amino groups is relatively low. At neutral pH value, the most reactive amino 528 group is the terminal one, with a pK value between 7 and 8, being much more reactive that the addition of the reactivities of all Lys external groups.¹⁴³ However, it should be considered that 529 530 after the first immobilization, if some nucleophiles of the protein are in the area exposed to the 531 support, the high apparent concentration of the different groups may permit the establishment of some new covalent enzyme-support bonds.¹⁴⁴ Moreover, the preactivated support may not be 532 533 stored for a long time under wet conditions due to the relatively low stability of the groups.

534 The first advantage compared to the case described in Section 5, is that now only the 535 groups involved in the covalent immobilization are modified by glutaraldehyde. Moreover, the 536 support may immobilize enzymes even if they are very poorly activated, because the enzyme is 537 covalently fixed to the support just with one point as the glutaraldehyde-protein bonds are 538 stable. Thus, using very lowly activated amino supports (e.g., 1 reactive group under each 539 projected area of the protein) immobilization using glutaraldehyde activated supports will be 540 directly performed by a covalent reaction by the most reactive amino group on the enzyme (very likely the amino group of the enzyme if immobilization is performed at neutral pH value).¹⁴³ 541 542 However, immobilization will be very slow due to the low activation of the support, and will offer no chance of reaching an intense multipoint covalent attachment.¹⁴ 543

544 On the other hand, using highly activated supports; the features of the spacer arm 545 (amino/glutaraldehyde/glutaraldehyde) convert the supports in a heterofunctional support. The 546 term "heterofunctional support" may be applied to supports that present several functionalities on its surface that are able to interact with different groups of an enzyme, and these interactions
may be different under different conditions (Figure 17).^{145,146}

Immobilization of enzymes on a heterofunctional support may be more versatile. If the researcher is able to benefit from this fact it may be an advantage, but if this fact is not considered, the understanding of the results may be really complex. The use of heterofunctional supports to immobilize proteins has been recently discussed in the literature.¹⁴⁷ In this review we will focus on glutaraldehyde activated supports.

The multifunctionality of the supports having a high surface density of amino groups and activated with glutaraldehyde is a direct consequence of the way they are prepared. Their preparation requires the modification of supports bearing primary amino groups with two glutaraldehyde molecules, if the optimal protocol is followed.^{28,36,37} The final result is a support having spacer arms bearing one or two amino groups (cationic groups that may function as anion exchangers), a fairly hydrophobic moiety formed by the glutaraldehyde dimer and the covalent reactive group.

561 In this way, a support highly activated with glutaraldehyde may give three different kinds of interactions with a protein: hydrophobic, anionic exchange and covalent (Figure 18).⁸⁴ 562 563 Biomacromolecules are only immobilized on supports via ionic exchange or hydrophobic 564 interactions when several enzyme-support interactions may be established, being the one point interaction insufficient to immobilize a protein.¹²⁸ Thus, these interactions will only have a real 565 impact on enzyme immobilization when using supports bearing several amino-(glutaraldehyde)_n 566 moieties under each enzyme molecule (Figure 18). 148-153 Thus, using highly activated 567 568 glutaraldehyde supports, the three immobilization causes may be able to immobilize a protein 569 molecule. If the researcher is aware of this fact, it is possible to permit that one or the other immobilization cause may be the dominant one, by playing with the experimental conditions.³⁸ 570 571 This permits to immobilize enzymes following different orientations regarding the support 572 surface. If there is a very small amount of groups on the support, (e.g. just one spacer arm per

573 projected area of the enzyme), this multi-interaction will no longer be possible or will be so 574 slow, that the only relevant cause of immobilization will be the one point covalent 575 immobilization, as explained above.^{143,148-153}

576 This means that even if all enzyme molecules are immobilized (incorporated to the 577 support) in a very rapid fashion using a highly activated glutaraldehyde support, there is no 578 guarantee that covalent immobilization of the enzyme on the support has taken place. In fact, the 579 immobilization may be very strong, and the enzyme may remain immobilized under conditions 580 where the enzyme may be fully released from the mother amino support, and still the enzyme molecules may be just adsorbed, as now the adsorption may be mixed, ionic/hydrophobic.⁸⁴ To 581 582 ensure that covalent immobilization has taken place, the enzyme should remain immobilized 583 under conditions where both ionic and hydrophobic interactions may be broken (e.g., using 584 cationic detergents, using guanidine, increasing the ionic strength in the presence of non-ionic detergents).⁸⁴ 585

586 Using highly activated supports, it has been shown that in most cases an ionic exchange 587 with the amino groups in the support is the first step in the immobilization of most 588 enzymes.^{22,38,84,154-156}

589 One effect of this first ionic adsorption is that, even though glutaraldehyde is able to 590 immobilize enzymes via just one attachment due to the stability of the bond formed, the 591 activation degree of the support has an exponential effect on the immobilization reaction rate of 592 proteins, not the expected linear effect using reactive groups in the support able to immobilize the proteins via just one point.¹⁴³ This is because the researcher is measuring the rate of ionic 593 594 exchange of the enzyme on the support, which requires the establishment of several enzyme-595 support interactions, and thus it is exponentially dependent on the surface density of amino groups on the support although the covalent reaction should be of order 1.^{38,148-153} This 596 597 immobilization mechanism is much faster that the direct covalent attachment via

598 glutaraldehyde-enzyme covalent reaction, being this way the first cause of immobilization for 599 most enzyme molecules.

This multifunctionality of the glutaraldehyde supports is an advantage in certain cases. The rapid ionic exchange of the enzyme on the support keeps the enzyme from being in soluble form before being covalently immobilized (thus avoiding some inactivation causes, such as interaction with interfaces or autolysis).^{16,17} If enzyme immobilization via ion exchange has a positive effect on enzyme stability, enzyme inactivation by distortion will also be slowed down.

However, the main advantage of the multifunctionality of glutaraldehyde is that we can alter the enzyme orientation on the support by changing the immobilization conditions, favoring one mechanism or another as the first immobilization cause (Figure 18).

608 If the researcher wishes to have a first hydrophobic adsorption, this can be achieved 609 using a high enough ionic strength. The glutaraldehyde dimer is not very hydrophobic, but may 610 be hydrophobic enough if the surface density of the groups in the support is high enough. Using 611 very high ionic strength, the ionic exchange will be rolled out, and the areas of the protein with 612 high concentration of external hydrophobic groups may be involved in the first enzyme adsorption and delimit the area where the reactive groups of the enzyme which will react with 613 614 the support should be located. After enzyme hydrophobic adsorption, the reactive groups of the 615 enzyme near the support surface may produce some covalent reactions. However, this will be 616 produced *after* enzyme immobilization, and there is no guarantee that the enzyme will finally 617 have any covalent attachment with the support (e.g., if there are no reactive groups on the 618 enzyme surface in that area).

The second possibility is to permit ionic exchange of the enzyme prior to covalent immobilization. Using most enzymes, the use of low ionic strength is enough to reach this situation (an ionic strength that permits ionic exchange of the proteins on the non-activated glutaraldehyde amino support).^{38,84} In this case, the enzyme will be first immobilized on the support by ionic exchange and this area will be the one where nucleophiles capable of reacting with the glutaraldehyde moieties should be located. Ionic exchange may also involve different enzyme regions depending on the experimental conditions and activation degree of the support. Ionic exchange at different pH values may in certain enzymes change the area where the highest concentration of available anionic charged groups may be found. Furthermore, the ionic strength may determine the area involved because the higher the ionic strength, the more restrictive the immobilization becomes (requiring more enzyme support-interactions).^{126,127}

Finally, it is possible to immobilize the enzyme via a direct first covalent attachment, involving the most reactive exposed group of the enzyme (usually the terminal amino group). Using most enzymes, the moderate ionic strength used to prevent ionic exchange (100-250 mM of NaCl) is not enough to force the hydrophobic adsorption of the protein on the support (that is not very hydrophobic) and a direct covalent immobilization may be the first cause for the enzyme immobilization.^{38,84}

Lipases are a special case of enzymes that permit a new alternative to the immobilization on glutaraldehyde activated supports. This has special interest as they are perhaps the most used enzymes in industry and academic studies due to their broad range of substrates and reactions, accompanied of a high enantio- and regio- selectivity or specificity, together to good stability in different reaction medium and wide availability.¹⁵⁷⁻¹⁵⁹

641 Lipases are complex enzymes that usually have two conformations, a closed one where 642 the active center is secluded from the medium by a polypeptide chain (lid or flap), and an open 643 form, where the lid is displaced and the active center of the lipase is exposed to the medium (Figure 19).¹⁶⁰ This open form presents a very large hydrophobic area exposed to the medium, 644 645 formed by the hydrophobic residues around the active center of the lipase and the hydrophobic groups in the internal face of the lid.¹⁶¹ The exposition to a hydrophilic medium (e.g., an 646 647 aqueous buffer) of this large hydrophobic area is unfavorable, thus the enzyme in aqueous 648 homogeneous media will be mainly in the closed form. However, this open form is readily adsorbed on the hydrophobic surface of the oil drops even at very low ionic strength (interfacial
 activation) (Figure 19)..^{162,163}

It has been shown that lipases may become adsorbed via a similar mechanism on any 651 652 other hydrophobic surface (hydrophobic supports, hydrophobic proteins, other "open" lipases). ¹⁶⁴⁻¹⁶⁶ Thus, the use of hydrophobic supports to immobilize lipases at low ionic strength has been 653 suggested as a simple way to obtain the open and stabilized form of the immobilized lipases.¹⁶⁷ 654 655 Although this interfacial activation is the specific feature of lipases, the lid may be quite 656 different from one lipase to another, e.g., lipase B from Candida antarctica has a very small lid that can not fully seclude the active center from the medium,¹⁶⁸ while the lipase from *Bacillus* 657 thermocatenulatus has a double lid and a very complex movement governing its activation.¹⁶⁹ 658 659 This immobilization is based on the fact that the hydrophobic support mimics the natural 660 substrate of lipases. And highly activated glutaraldehyde activated supports offers a fairly 661 hydrophobic surface to this interfacial activation of lipases.

662 In fact, it has been shown that using lipases, it is at least possible to immobilize the 663 enzyme via 4 different mechanisms on highly activated glutaraldehyde supports.⁸⁴

664 Thus, the control of the immobilization on these supports using lipases is more 665 complex, but the support offers a new immobilization orientation.

666 Due to the tendency of the open form of the lipases to become adsorbed versus hydrophobic interfaces,^{164,170,171} if the immobilization is just performed at low ionic strength, the 667 enzyme will be immobilized by both immobilization mechanisms: interfacial activation and 668 ionic exchange (Figure 20).⁸⁴ Depending on the enzyme, the support and the immobilization 669 670 conditions, one or the other immobilization cause may be predominant, but most likely the other 671 cause will always be present in a major or minor percentage. This mixture of lipase orientations 672 is not the ideal situation if the researcher wishes to tune lipase properties via immobilization and 673 may also make difficult to understand the results. In fact, this is the usual situation that we may 674 find in the literature.

This situation may be avoided by using non-ionic detergents, which prevent the interfacial activation of the lipase versus a hydrophobic support (Figure 21). ¹⁶⁴ Performing the immobilization in the presence of Triton X-100 at low ionic strength, lipases are mainly immobilized on the glutaraldehyde supports via a first ionic exchange.⁸⁴ Using moderate ionic strength, the enzyme immobilization will mainly proceed via interfacial activation (Figure 22).

The use of very high ionic strength will cause the lipase to adopt mainly the closed form, permitting as a first immobilization step the conventional hydrophobic adsorption via hydrophobic groups located on the lipase surface (Figure 23). It has been reported that interfacial activation of lipases on hydrophobic supports is slowed at high ionic strength.¹⁶⁴ That way, using an ionic strength just high enough able to prevent the ionic exchange of the lipase, lipases will become immobilized on the support first via a rapid interfacial activation on the support, which is much faster than the direct covalent attachment.⁸⁴

The only way to ensure that the first step in the immobilization of a lipase in these supports is a covalent attachment is to simultaneously prevent ionic exchange and interfacial activation. This may be achieved using simultaneously moderately high ionic strength and detergents, or ionic detergents (Figure 24).⁸⁴

Whatever the enzyme used, if we have a situation where the first phenomenon is covalent immobilization, the surface density of groups in the support will have a first order effect on the rate of enzyme immobilization.¹⁴³ If this is not the case (mainly at the highest support activation degree), another cause may be the responsible for the first enzyme immobilization.

Thus, it is possible to immobilize enzymes on glutaraldehyde supports via different first events. This may lead to different orientations of the enzyme on the support, offering different stabilities.³⁸ In the case of lipases, they also exhibited different catalytic behavior (e.g., specificity was altered).⁸⁴ This way, it is possible to have, using the same immobilization support, enzymes immobilized by different areas, with different numbers of enzyme moleculesupport covalent bonds and different enzyme-support unspecific interactions.¹⁴⁷ We should bear in mind that, due to the proximity between the groups of the support and of the enzyme, interactions between immobilized enzyme and support will be produced over time even though they may not be enough to be the only cause for immobilization.¹⁴⁴

In other, more difficult to classify cases, a lipase was immobilized on electrospun and ethanol-dispersed polystyrene-poly(styrene-co-maleic anhydride) nanofibers in the form of enzyme precipitate coatings.¹⁷² Lipase precipitate coatings were prepared in a three-step process, consisting of lipase covalent attachment, lipase precipitation, and crosslinking of precipitated lipases onto the covalently attached lipases via glutaraldehyde treatment.

710 A similar approach was used to immobilize β -glucosidase. The enzyme was 711 immobilized on polymer nanofibers. Then, additional enzyme molecules were crosslinked onto 712 the covalently attached enzyme molecules via glutaraldehyde treatment.¹⁷³

713

714 Conclusions

715 Glutaraldehyde, an apparently old fashioned reagent use for a long time in design of 716 biocatalyst, remains as one of the most interesting tools in enzyme crosslinking and 717 immobilization (Figure 25). However, to achieve optimal results, it is necessary to understand 718 the different reactivities of the amino/glutaraldehyde and amino/glutaraldehyde/glutaraldehyde, 719 together with the fact that, in immobilization of enzymes on glutaraldehyde pre-activated 720 supports, it is a heterofunctional support that permits altering the enzyme orientation on the 721 support surface. Thus, glutaraldehyde remains one of the most potent and versatile tools in 722 Enzyme technology, and the new knowledge on its reactivity and possibilities open even new 723 opportunities for the future.

724

725 ACKNOWLEDGMENTS

This work has been supported by grant CTQ2009-07568 from Spanish Ministerio de Ciencia e
Innovacion, Grant No.1102-489-25428 from COLCIENCIAS and Universidad Industrial de
Santander (VIE-UIS Research Program) and CNPq and FAPERGS (Brazil). Á. BerenguerMurcia thanks the Spanish Ministerio de Ciencia e Innovacion for a Ramon y Cajal fellowship
(RyC-2009-03813). The authors would like to thank Mr Ramiro Martinez (Novozymes, Spain
S.A) for his kind support to our research.

733 References

- A. Schmid, J. S. Dordick, B. Hauer, A. Kiener, M. Wubbolts and B. Witholt, *Nature*, 2001, 409, 258-268.
- 736 2. S. G. Burton, D. A. Cowan and J. M. Woodley, *Nat. Biotechnol.*, 2002, 20, 37-45.
- 737 3. J. M. Woodley, *Trends Biotechnol.*, 2008, **26**, 321-327.
- 738 4. A. Liljeblad and L. T. Kanerva, *Tetrahedron*, 2006, **62**, 5831-5854.
- 5. S. Panke, M. Held and M. Wubbolts, *Curr. Opin. Biotechnol.*, 2004, **15**, 272-279.
- 740 6. H. E. Schoemaker, D. Mink and M. G. WubboLts, *Science*, 2003, 299, 1694-1697.
- 741 7. F. H. Arnold, *Nature*, 2001, **409**, 253-257.
- 742 8. F. H. Arnold, *Chem. Eng. Sci.*, 1996, **51**, 5091-5102.
- 743 9. J. M. Woodley, Curr. Opin. Chem. Biol., 2013, 17, 310-316.
- 744 10. A. R. Fersht and L. Serrano, *Curr. Opin. Struct. Biol.*, 1993, **3**, 75-83.
- R. C. Rodrigues, C. Ortiz, A. Berenguer-Murcia, R. Torres and R. Fernandez-Lafuente,
 Chem. Soc. Rev., 2013, 45, 6290-6307.
- 12. M. L. Verma, C. J. Barrow and M. Puri, Appl. Microbiol. Biotechnol., 2013, 97, 23-39.
- 748 13. E. T. Hwang and M. B. Gu, *Eng. Life Sci.*, 2013, **13**, 49-61.
- 749 14. C. Garcia-Galan, A. Berenguer-Murcia, R. Fernandez-Lafuente and R. C. Rodrigues,
 750 Adv. Synth. Catal., 2011, 353, 2885-2904.
- 751 15. D. Brady and J. Jordaan, *Biotechnol. Lett.*, 2009, **31**, 1639-1650.
- 752 16. P. V. Iyer and L. Ananthanarayan, *Process Biochem.*, 2008, **43**, 1019-1032.
- 753 17. C. Mateo, J. M. Palomo, G. Fernandez-Lorente, J. M. Guisan and R. Fernandez-T54 Lafuente, *Enzyme Microb. Technol.*, 2007, 40, 1451-1463.
- 755 18. A. Díaz-Rodríguez and B. G. Davis, Curr. Opin. Chem. Biol., 2011, 15, 211-219.
- J. M. Chalker, G. J. L. Bernardes, Y. A. Lin and B. G. Davis, *Chem.-Asian J.*, 2009, 4, 630-640.
- 758 20. D. A. Cowan and R. Fernandez-Lafuente, *Enzyme Microb. Technol.*, 2011, 49, 326-346.
- R. C. Rodrigues, Á. Berenguer-Murcia and R. Fernandez-Lafuente, *Adv. Synth. Catal.*,
 2011, 353, 2216-2238.
- 761 22. K. Hernandez and R. Fernandez-Lafuente, *Enzyme Microb. Technol.*, 2011, 48, 107-122.
- 762 23. R. Fernandez-Lafuente, Enzyme Microb. Technol., 2009, 45, 405-418.
- 763 24. S. S. Wong and L. J. C. Wong, *Enzyme Microb. Technol.*, 1992, 14, 866-874.
- 764 25. E. A. Woodroof, J. Bioeng., 1978, 2, 1-9.
- A. D. Russell, Infection control and hospital epidemiology : the official journal of the
 Society of Hospital Epidemiologists of America, 1994, 15, 724-733.
- 767 27. I. Migneault, C. Dartiguenave, M. J. Bertrand and K. C. Waldron, *Biotechniques*, 2004,
 768 37, 790-802.
- 769 28. D. R. Walt and V. I. Agayn, *TrAC*, *Trends Anal. Chem.*, 1994, **13**, 425-430.
- 770 29. A. F. S. A. Habeeb and R. Hiramoto, Arch. Biochem. Biophys., 1968, 126, 16-26.
- Y. Wine, N. Cohen-Hadar, A. Freeman and F. Frolow, *Biotechnol. Bioeng.*, 2007, 98, 711-718.
- 773 31. C. Aso and Y. Aito, *Die Makromolekulare Chemie*, 1962, **58**, 195-203.
- 774 32. F. M. Richards and J. R. Knowles, J. Mol. Biol., 1968, **37**, 231-233.
- R. Fernandez-Lafuente, C. M. Rosell, V. Rodriguez and J. M. Guisan, *Enzyme Microb. Technol.*, 1995, 17, 517-523.
- 777 34. A. H. Korn, S. H. Feairheller and E. M. Filachoine, J. Mol. Biol., 1972, 65, 525-529.
- 778 35. T. J. Johnson, Eur. J. Cell Biol., 1978, 45, 160-169.
- 779 36. P. Monsan, G. Puzo and H. Mazarguil, *Biochimie*, 1975, **57**, 1281-1292.
- 780 37. P. Monsan, J. Mol. Catal., 1978, **3**, 371-384.

38.	L. Betancor, F. López-Gallego, A. Hidalgo, N. Alonso-Morales, G. Dellamora-Ortiz, C.
	Mateo, R. Fernández-Lafuente and J. M. Guisán, <i>Enzyme Microb. Technol.</i> , 2006, 39 ,
20	877-882.
39.	K. Ziegler, I. Schits and H. Zahn, in Protein Crosslinking: Biochemical and Biological
4.0	Aspects, ed. M. Friedman, Plenum, New York, 1977, vol. 86a, pp. 345-354.
40.	T. Imoto and H. Yamada, in Protein Function: A Practical Approach, ed. T. E.
	Creighton, IRL Press, Oxford, UK, 1989, pp. 247–278.
41.	D. T. Cheung, N. Perelman, E. C. Ko and M. E. Nimni, Connect. Tissue Res., 1985, 13,
	109-115.
42.	E. A. Talman and D. R. Boughner, Ann. Thorac. Surg., 1995, 60, S369-S373.
43.	S. Mathapati, D. K. Bishi, S. Guhathakurta, K. M. Cherian, J. R. Venugopal, S.
	Ramakrishna and R. S. Verma, <i>Mater. Sci. Eng., C</i> , 2013, 33 , 1561-1572.
44.	Y. Liu, L. Ma and C. Gao, <i>Mater. Sci. Eng.</i> , C, 2012, 32 , 2361-2366.
45.	P. Sinha, D. Zurakowski, T. K. Susheel Kumar, D. He, C. Rossi and R. A. Jonas, J.
	Thorac. Cardiovasc. Surg., 2012, 143 , 224-227.
46.	C. P. Govardhan, Curr. Opin. Biotechnol., 1999, 10, 331-335.
47.	A. F. S. A. Habeeb, Arch. Biochem. Biophys., 1967, 119, 264-268.
48.	E. F. Jansen and A. C. Olson, Arch. Biochem. Biophys., 1969, 129, 221-227.
	H. K. Manonmani and R. Joseph, Process Biochem., 1993, 28, 325-329.
	T. Anwar, B. Ahmad and H. Younus, <i>Biocatal. Biotransform.</i> , 2007, 25, 453-458.
	F. A. Quiocho and F. M. Richards, <i>Proc. Natl. Acad. Sci. U. S. A.</i> , 1964, 52 , 833-839.
	N. L. St. Clair and M. A. Navia, J. Am. Chem. Soc., 1992, 114 , 7314-7316.
	L. Cao, F. Van Rantwijk and R. A. Sheldon, <i>Org. Lett.</i> , 2000, 2 , 1361-1364.
	R. A. Sheldon, <i>Adv. Synth. Catal.</i> , 2007, 349 , 1289-1307.
	R. A. Sheldon, R. Schoevaart and L. M. Van Langen, <i>Biocatal. Biotransform.</i> , 2005, 23,
55.	141-147.
56	R. A. Sheldon, <i>Appl. Microbiol. Biotechnol.</i> , 2011, 92 , 467-477.
	C. Mateo, J. M. Palomo, L. M. Van Langen, F. Van Rantwijk and R. A. Sheldon,
57.	Biotechnol. Bioeng., 2004, 86, 273-276.
50	S. Shah, A. Sharma and M. N. Gupta, <i>Anal. Biochem.</i> , 2006, 351 , 207-213.
39.	I. Matijošyte, I. W. C. E. Arends, S. de Vries and R. A. Sheldon, J. Mol. Catal. B:
60	Enzym., 2010, 62 , 142-148.
60.	F. Šulek, D. P. Fernández, Z. Knez, M. Habulin and R. A. Sheldon, <i>Process Biochem.</i> , 2011. 46, 765, 760
(1	2011, 46 , 765-769.
	T. Dong, L. Zhao, Y. Huang and X. Tan, <i>Bioresour. Technol.</i> , 2010, 101 , 6569-6571.
62.	J. J. Karimpil, J. S. Melo and S. F. D'Souza, J. Mol. Catal. B: Enzym., 2011, 71, 113-
()	
63.	J. Cruz, O. Barbosa, R. C. Rodrigues, R. Fernandez-Lafuente, R. Torres and C. Ortiz, J.
	Mol. Catal. B: Enzym., 2012, 80, 7-14.
64.	J. Pan, X. D. Kong, C. X. Li, Q. Ye, J. H. Xu and T. Imanaka, J. Mol. Catal. B: Enzym.,
	2011, 68 , 256-261.
65.	L. Wilson, G. Fernández-Lorente, R. Fernández-Lafuente, A. Illanes, J. M. Guisán and J.
	M. Palomo, Enzyme Microb. Technol., 2006, 39 , 750-755.
66.	F. López-Gallego, L. Betancor, A. Hidalgo, N. Alonso, R. Fernández-Lafuente and J. M.
	Guisán, Biomacromolecules, 2005, 6, 1839-1842.
67.	J. Yan, X. Gui, G. Wang and Y. Yan, Appl. Biochem. Biotechnol., 2012, 166, 925-932.
68.	M. Galvis, O. Barbosa, M. Ruiz, J. Cruz, C. Ortiz, R. Torres and R. Fernandez-Lafuente,
	Process Biochem., 2012, 47, 2373-2378.
69.	V. P. Torchilin and K. Martinek, Enzyme Microb. Technol., 1979, 1, 74-82.
70.	A. E. Habibi, K. Khajeh, H. Naderi-Manesh, B. Ranjbar and M. Nemat-Gorgani, J.
	Biotechnol., 2006, 123 , 434-442.
	 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69.

832 71. K. Martinek and V. P. Torchilin, in *Methods Enzymol.*, 1988, vol. 137, pp. 615-626. 833 72. V. P. Torchilin, A. V. Maksimenko, V. N. Smirnov, I. V. Berezin, A. M. Klibanov and 834 K. Martinek, Biochim. Biophys. Acta, 1978, 522, 277-283. 835 V. P. Torchilin, A. V. Maksimenko, V. N. Smirnov, I. V. Berezin and K. Martinek, 73. 836 Biochim. Biophys. Acta, Enzymol., 1979, 568, 1-10. N. M. Young, C. R. MacKenzie, S. A. Narang, R. P. Oomen and J. E. Baenziger, FEBS 837 74. 838 Lett., 1995, 377, 135-139. U. Arnold and M. Sch $\sqrt{\partial p}$ fel, *FEBS J.*, 2012, **279**, 2508-2519. 839 75. 840 V. G. H. Eijsink, A. Bjork, S. Gaseidnes, R. Sirevag, B. Synstad, B. V. D. Burg and G. 76 841 Vriend, J. Biotechnol., 2004, 113, 105-120. 842 77. V. Grazu, F. López-Gallego and J. M. Guisán, Process Biochem., 2012, 47, 2538-2541. 843 78. O. Abian, V. Grazú, J. Hermoso, R. González, J. L. García, R. Fernández-Lafuente and 844 J. M. Guisán, Appl. Environ. Microbiol., 2004, 70, 1249-1251. K. L. Carraway and D. E. Koshland Jr, Methods Enzymol., 1972, 25, 616-623. 845 79. K. L. Carraway, P. Spoerl and D. E. Koshland Jr, J. Mol. Biol., 1969, 42, 133-137. 846 80. 847 V. P. Torchilin, A. V. Maksimenko, V. N. Smirnov, I. V. Berezin, A. M. Klibanov and 81. 848 K. Martinek, Biochim. Biophys. Acta, Enzymol., 1979, 567, 1-11. 849 82. R. Tyagi and M. N. Gupta, Biochemistry (Mosc.), 1998, 63, 334-344. J. M. Bolivar, A. Hidalgo, L. Sánchez-Ruiloba, J. Berenguer, J. M. Guisán and F. López-850 83. 851 Gallego, J. Biotechnol., 2011, 155, 412-420. 852 O. Barbosa, R. Torres, C. Ortiz and R. Fernandez-Lafuente, Process Biochem., 2012, 47, 84. 853 1220-1227. 854 85. O. M. Poltorak, E. S. Chukhray and I. Y. Torshin, Biochemistry (Mosc.), 1998, 63, 303-855 311. 856 R. W. Lencki, J. Arul and R. J. Neufeld, Biotechnol. Bioeng., 1992, 40, 1427-1434. 86. 857 O. M. Poltorak, E. S. Chukhrai and I. Y. Torshin, Russ. J. Phys. Chem. A, 2000, 74, 87. 858 S400-S410. 859 A. J. D. Silva, D. P. Gómez-Mendoza, M. Junqueira, G. B. Domont, E. Ximenes Ferreira 88. 860 Filho, M. V. de Sousa and C. A. O. Ricart, Proteomics, 2012, 12, 2729-2738. 861 89. T. Ohtsuki, Suyanto, S. Yazaki, S. Ui and A. Mimura, Lett. Appl. Microbiol., 2005, 40, 862 111-116. 863 90. H. Schagger, W. A. Cramer and G. Von Jagow, Anal. Biochem., 1994, 217, 220-230. 864 91. M. Fuentes, R. L. Segura, O. Abian, L. Betancor, A. Hidalgo, C. Mateo, R. Fernandez-Lafuente and J. M. Guisan, Proteomics, 2004, 4, 2602-2607. 865 C. Garcia-Galan, O. Barbosa and R. Fernandez-Lafuente, Enzyme Microb. Technol., 866 92. 867 2013, 52, 211-217. 93. J. M. Bolivar, J. Rocha-Martin, C. Mateo, F. Cava, J. Berenguer, R. Fernandez-Lafuente 868 869 and J. M. Guisan, Biomacromolecules, 2009, 10, 742-747. 870 94. T. Yamazaki, W. Tsugawa and K. Sode, Biotechnol. Lett., 1999, 21, 199-202. M. Gerl, R. Rudolph and R. Jaenicke, Biol. Chem. Hoppe. Seyler, 1985, 366, 447-454. 871 95. 872 D. J. Crampton, M. Ohi, U. Qimron, T. Walz and C. C. Richardson, J. Mol. Biol., 2006, 96. 873 **360**, 667-677. 874 B. U. Failer, A. Aschrafi, G. Schmalzing and H. Zimmermann, Eur. J. Biochem., 2003, 97. 875 270, 1802-1809. 876 98. R. A. Sheldon and S. Van Pelt, Chem. Soc. Rev., 2013, 42, 6223-6235. 99. P. Jochems, Y. Satyawali, L. Diels and W. Dejonghe, Green Chem., 2011, 13, 1609-877 878 1623. 879 100. J. Lee, J. Kim, H. Jia, M. I. Kim, J. H. Kwak, S. Jin, A. Dohnalkova, H. C. Park, H. N. Chang, P. Wang, J. W. Grate and T. Hyeon, Small, 2005, 1, 744-753. 880 881 101. M. I. Kim, J. Kim, J. Lee, S. Shin, H. B. Na, T. Hyeon, H. G. Park and H. N. Chang, 882 Microporous Mesoporous Mater., 2008, 111, 18-23.

- 883 102. I. K. Moon, J. Kim, J. Lee, H. Jia, B. N. Hyon, K. Y. Jong, H. K. Ja, A. Dohnalkova, J.
 884 W. Grate, P. Wang, T. Hyeon, G. P. Hyun and N. C. Ho, *Biotechnol. Bioeng.*, 2007, 96, 210-218.
- 886 103. S. H. Jun, J. Lee, B. C. Kim, J. E. Lee, J. Joo, H. Park, J. H. Lee, S. M. Lee, D. Lee, S.
 887 Kim, Y. M. Koo, C. H. Shin, S. W. Kim, T. Hyeon and J. Kim, *Chem. Mater.*, 2012, 24, 924-929.
- 889 104. R. Reshmi and S. Sugunan, J. Mol. Catal. B: Enzym., 2013, 85-86, 111-118.
- 890 105. D. Jung, M. Paradiso, D. Wallacher, A. Brandt and M. Hartmann, *ChemSusChem*, 2009,
 891 2, 161-164.
- 892 106. D. Jung, M. Paradiso and M. Hartmann, J. Mater. Sci., 2009, 44, 6747-6753.
- 893 107. D. Jung and M. Hartmann, Catal. Today, 2010, 157, 378-383.
- 894 108. F. López-Gallego, L. Betancor, C. Mateo, A. Hidalgo, N. Alonso-Morales, G.
 895 Dellamora-Ortiz, J. M. Guisán and R. Fernández-Lafuente, *J. Biotechnol.*, 2005, 119, 70896 75.
- 897 109. A. S. Bommarius and M. F. Paye, Chem. Soc. Rev., 2013, 42, 6534-6565.
- 898 110. U. Hanefeld, L. Cao and E. Magner, *Chem. Soc. Rev.*, 2013, **42**, 6211-6212.
- 899 111. S. Cantone, V. Ferrario, L. Corici, C. Ebert, D. Fattor, P. Spizzo and L. Gardossi, *Chem. Soc. Rev.*, 2013, 42, 6262-6276.
- 901 112. L. Betancor, F. López-Gallego, A. Hidalgo, N. Alonso-Morales, G. Dellamora-Ortiz, J.
 902 M. Guisán and R. Fernández-Lafuente, *J. Biotechnol.*, 2006, **121**, 284-289.
- 903 113. M. Filho, B. C. Pessela, C. Mateo, A. V. Carrascosa, R. Fernandez-Lafuente and J. M.
 904 Guisán, *Enzyme Microb. Technol.*, 2008, 42, 265-271.
- 905 114. D. Radva, J. Spanyol and J. Kosáry, Food Technol. Biotechnol., 2011, 49, 257-262.
- 906 115. C. Z. Guidini, J. Fischer, L. N. S. Santana, V. L. Cardoso and E. J. Ribeiro, *Biochem.* 907 Eng. J., 2010, 52, 137-143.
- 908116.C. Pan, B. Hu, W. Li, Y. Sun, H. Ye and X. Zeng, J. Mol. Catal. B: Enzym., 2009, 61,909208-215.
- 910 117. C. Sisak, Z. Csanádi, E. Rónay and B. Szajáni, *Enzyme Microb. Technol.*, 2006, 39, 1002-1007.
- 912 118. A. Kumar and S. S. Kanwar, *Enzyme Research*, 2011, 2011, 718949.
- 913 119. A. Kumar and S. S. Kanwar, *Bioresour. Technol.*, 2011, **102**, 2162-2167.
- 914 120. G. Fernández-Lorente, J. M. Palomo, C. Mateo, R. Munilla, C. Ortiz, Z. Cabrera, J. M.
 915 Guisán and R. Fernández-Lafuente, *Biomacromolecules*, 2006, 7, 2610-2615.
- 916 121. J. M. Palomo, R. L. Segura, G. Fernandez-Lorente, R. Fernandez-Lafuente and J. M.
 917 Guisán, *Enzyme Microb. Technol.*, 2007, 40, 704-707.
- 918 122. M. Filho, B. C. Pessela, C. Mateo, A. V. Carrascosa, R. Fernandez-Lafuente and J. M.
 919 Guisán, *Process Biochem.*, 2008, 43, 1142-1146.
- M. Fuentes, P. Batalla, V. Grazu, B. C. C. Pessela, C. Mateo, T. Montes, J. A. Hermoso,
 J. M. Guisan and R. Fernandez-Lafuente, *Biomacromolecules*, 2007, 8, 703-707.
- 922 124. B. C. C. Pessela, R. Munilla, L. Betancor, M. Fuentes, A. V. Carrascosa, A. Vian, R.
 923 Fernandez-Lafuente and J. M. Guisán, *J. Chromatogr. A*, 2004, **1034**, 155-159.
- 125. C. Mateo, O. Abian, G. Fernández-Lorente, J. Pedroche, R. Fernández-Lafuente, J. M. Guisan, A. Tam and M. Daminati, *Biotechnol. Prog.*, 2002, 18, 629-634.
- B. C. C. Pessela, M. Fuentes, C. Mateo, R. Munilla, A. V. Carrascosa, R. FernandezLafuente and J. M. Guisan, *Enzyme Microb. Technol.*, 2006, **39**, 909-915.
- B. C. C. Pessela, L. Betancor, F. Lopez-Gallego, R. Torres, G. M. Dellamora-Ortiz, N.
 Alonso-Morales, M. Fuentes, R. Fernández-Lafuente, J. M. Guisán and C. Mateo, *Enzyme Microb. Technol.*, 2005, 37, 295-299.
- 931 128. M. Fuentes, C. Mateo, B. C. C. Pessela, P. Batalla, R. Fernandez-Lafuente and J. M.
 932 Guisán, J. Chromatogr., B: Anal. Technol. Biomed. Life Sci., 2007, 849, 243-250.
- 933 129. A. Schellenberger and R. Ulbrich, Biomed. Biochim. Acta, 1989, 48, 63-67.

- J. Mansfeld, G. Vriendl, O. R. Veltman, B. Van Den Burg, G. Venema, V. G. H. Eijsink
 and R. Utbrich-Hofmann, *FASEB J.*, 1997, 11.
- R. Ulbrich-Hofmann, U. Arnold and J. Mansfeld, J. Mol. Catal. B: Enzym., 1999, 7, 125131.
- J. Mansfeld, G. Vriend, B. Van Den Burg, V. G. H. Eijsink and R. Ulbrich-Hofmann, *Biochemistry*, 1999, **38**, 8240-8245.
- 940 133. S. Pahujani, S. S. Kanwar, G. Chauhan and R. Gupta, *Bioresour. Technol.*, 2008, 99, 2566-2570.
- 942 134. A. Pal and F. Khanum, *Process Biochem.*, 2011, 46, 1315-1322.
- 943 135. S. Nagar, A. Mittal, D. Kumar, L. Kumar and V. K. Gupta, *Process Biochem.*, 2012, 47, 1402-1410.
- 945 136. T. N. Nwagu, B. N. Okolo and H. Aoyagi, J. Microbiol. Biotechnol., 2012, 22, 628-636.
- 946 137. G. Yang, J. Wu, G. Xu and L. Yang, *Colloids and Surfaces B: Biointerfaces*, 2010, 78, 351-356.
- 948 138. M. Yiitolu and Z. Temo√Bin, J. Mol. Catal. B: Enzym., 2010, 66, 130-135.
- M. P. Klein, L. P. Fallavena, J. D. N. Schöfer, M. A. Z. Ayub, R. C. Rodrigues, J. L. Ninow and P. F. Hertz, *Carbohydr. Polym.*, 2013, 95, 465-470.
- M. P. Klein, M. R. Nunes, R. C. Rodrigues, E. V. Benvenutti, T. M. H. Costa, P. F.
 Hertz and J. L. Ninow, *Biomacromolecules*, 2012, 13, 2456-2464.
- 953 141. S. G. Valerio, J. S. Alves, M. P. Klein, R. C. Rodrigues and P. F. Hertz, *Carbohydr. Polym.*, 2013, 92, 462-468.
- W. L. Stanley, G. G. Watters, S. H. Kelly, B. G. Chan, J. A. Garibaldi and J. E. Schade, *Biotechnol. Bioeng.*, 1976, 18, 439-443.
- 143. C. Mateo, O. Abian, M. Bernedo, E. Cuenca, M. Fuentes, G. Fernandez-Lorente, J. M.
 Palomo, V. Grazu, B. C. C. Pessela, C. Giacomini, G. Irazoqui, A. Villarino, K.
 Ovsejevi, F. Batista-Viera, R. Fernandez-Lafuente and J. M. Guisán, *Enzyme Microb. Technol.*, 2005, 37, 456-462.
- 961 144. J. M. Bolivar, C. Mateo, C. Godoy, B. C. C. Pessela, D. S. Rodrigues, R. L. C. Giordano,
 962 R. Fernandez-Lafuente and J. M. Guisan, *Process Biochem.*, 2009, 44, 757-763.
- 963 145. C. Mateo, G. Fernández-Lorente, O. Abian, R. Fernández-Lafuente and J. M. Guisán,
 964 *Biomacromolecules*, 2000, 1, 739-745.
- 965 146. C. Mateo, V. Grazu, J. M. Palomo, F. Lopez-Gallego, R. Fernandez-Lafuente and J. M. Guisan, *Nat. Protoc.*, 2007, 2, 1022-1033.
- 967 147. O. Barbosa, R. Torres, C. Ortiz, Á. Berenguer-Murcia, R. C. Rodrigues and R.
 968 Fernandez-Lafuente, *Biomacromolecules*, 2013, in press, DOI: 10.1021/bm400762h.
- 969 148. A. Kumar, I. Y. Galaev and B. Mattiasson, J. Chromatogr. B Biomed. Sci. Appl., 2000,
 970 741, 103-113.
- 971 149. B. C. C. Pessela, R. Torres, M. Fuentes, C. Mateo, R. Munilla, A. Vian, A. V.
 972 Carrascosa, J. L. Garcia, J. M. Guisán and R. Fernandez-Lafuente, *J. Chromatogr. A*, 973 2004, **1055**, 93-98.
- 974 150. F. H. Arnold, Biotechnology. (N. Y.), 1991, 9, 151-156.
- 975 151. E. Hochuli, H. Döbeli and A. Schacher, J. Chromatogr. A, 1987, 411, 177-184.
- 976 152. V. Gaberc-Porekar and V. Menart, J. Biochem. Biophys. Methods, 2001, 49, 335-360.
- 977 153. M. Fuentes, C. Mateo, R. Fernández-Lafuente and J. M. Guisán, *Biomacromolecules*, 2006, 7, 540-544.
- 979 154. W. S. Adriano, E. H. C. Filho, J. A. Silva, R. L. C. Giordano and L. R. B. Gonçalves,
 980 *Brazilian Journal of Chemical Engineering*, 2005, 22, 529-538.
- 981 155. W. S. Adriano, E. H. C. Filho, J. A. Silva and L. R. B. Gonçalves, *Biotechnol. Appl.* 982 *Biochem.*, 2005, 41, 201-207.
- W. S. Adriano, D. B. Mendonça, D. S. Rodrigues, E. J. Mammarella and R. L. C. Giordano, *Biomacromolecules*, 2008, 9, 2170-2179.

- 985 157. K. E. Jaeger and T. Eggert, *Curr. Opin. Biotechnol.*, 2002, **13**, 390-397.
- 986 158. K. E. Jaeger and M. T. Reetz, Trends Biotechnol., 1998, 16, 396-403.
- 987 159. R. D. Schmid and R. Verger, Angew. Chem., Int. Ed., 1998, 37, 1609-1633.
- 988 160. R. Verger, *Trends Biotechnol.*, 1997, **15**, 32-38.
- 989 161. Z. S. Derewenda, U. Derewenda and G. G. Dodson, J. Mol. Biol., 1992, 227, 818-839.
- 990 162. N. Miled, F. Beisson, J. De Caro, A. De Caro, V. Arondel and R. Verger, *J. Mol. Catal.* 991 *B: Enzym.*, 2001, 11, 165-171.
- 992 163. P. Reis, K. Holmberg, H. Watzke, M. E. Leser and R. Miller, *Adv. Colloid Interface Sci.*,
 993 2009, 147-148, 237-250.
- 164. R. Fernandez-Lafuente, P. Armisén, P. Sabuquillo, G. Fernández-Lorente and J. M.
 Guisán, *Chem. Phys. Lipids*, 1998, 93, 185-197.
- 996 165. J. M. Palomo, C. Ortiz, M. Fuentes, G. Fernandez-Lorente, J. M. Guisan and R.
 997 Fernandez-Lafuente, J. Chromatogr. A, 2004, 1038, 267-273.
- 998 166. J. M. Palomo, M. M. Peñas, G. Fernández-Lorente, C. Mateo, A. G. Pisabarro, R.
 999 Fernández-Lafuente, L. Ramírez and J. M. Guisán, *Biomacromolecules*, 2003, 4, 204-210.
- 1001 167. J. M. Palomo, G. Muoz, G. Fernández-Lorente, C. Mateo, R. Fernández-Lafuente and J.
 1002 M. Guisán, J. Mol. Catal. B: Enzym., 2002, 19-20, 279-286.
- 1003 168. J. Uppenberg, S. Patkar, T. Bergfors and T. A. Jones, J. Mol. Biol., 1994, 235, 790-792.
- 1004 169. C. Carrasco-López, C. Godoy, B. de las Rivas, G. Fernández-Lorente, J. M. Palomo, J.
 1005 M. Guisán, R. Fernández-Lafuente, M. Martínez-Ripoll and J. A. Hermoso, J. Biol.
 1006 Chem., 2009, 284, 4365-4372.
- 1007 170. J. M. Palomo, M. Fuentes, G. Fernández-Lorente, C. Mateo, J. M. Guisan and R.
 1008 Fernández-Lafuente, *Biomacromolecules*, 2003, 4, 1-6.
- 1009 171. G. Fernández-Lorente, J. M. Palomo, M. Fuentes, C. Mateo, J. M. Guisán and R.
 1010 Fernández-Lafuente, *Biotechnol. Bioeng.*, 2003, 82, 232-237.
- 1011
 172.
 H. J. An, H. J. Lee, S. H. Jun, S. Y. Hwang, B. C. Kim, K. Kim, K. M. Lee, M. K. Oh

 1012
 and J. Kim, *Bioprocess Biosyst. Eng.*, 2011, **34**, 841-847.
- 1013 173. S. M. Lee, L. H. Jin, J. H. Kim, S. O. Han, H. B. Na, T. Hyeon, Y. M. Koo, J. Kim and J. H. Lee, *Bioprocess Biosyst. Eng.*, 2010, 33, 141-147.
- 1015 1016

1017 FIGURE LEGENDS

- 1019 **FIGURE 1.** Possible structures of glutaraldehyde in aqueous solution.
- 1020 FIGURE 2. Reactions of glutaraldehyde with proteins under acidic or neutral conditions.
- 1021 FIGURE 3. Schiff base (1) and Michael-type (2) reactions of glutaraldehyde with proteins
- 1022 under basic conditions
- 1023 FIGURE 4. Immobilization of enzyme via copolymerization with glutaraldehyde.
- 1024 FIGURE 5. Preparation of Crosslinked Enzyme Crystals (CLECs).
- 1025 FIGURE 6. Preparation of Crosslinked Enzyme Aggretates (CLEAs).
- 1026 FIGURE 7. Problems in the crosslinking step during CLEAs preparation using enzymes poor1027 in Lys residues.
- 1028 FIGURE 8. Preparation of combi-CLEAs using proteins having many Lys residues to1029 facilitate the crosslinking step.
- 1030 FIGURE 9. Amination of enzymes that are poor in Lys residues to facilitate the crosslinking1031 step in CLEA preparation.
- 1032 FIGURE 10. Effect of intramolecular crosslinking on the stability of enzymes.
- FIGURE 11. Amination of enzyme surfaces to facilitate the promotion of an intenseintramolecular crosslinking.
- FIGURE 12. Effect of the immobilization rate on the possibilities of intermolecular
 crosslinking between immobilized enzyme molecules.
- 1037 **FIGURE 13**. Chemical crosslinking of subunits in multimeric enzymes.
- 1038 FIGURE 14. Stabilization of polyethyleneimine/enzyme composites via glutaraldehyde1039 crosslinking to prevent subunit dissociation.
- 1040 FIGURE 15. Production of enzyme chemical aggregates to prevent enzyme leakage on mildy1041 adsorbed enzymes.
- 1042 **FIGURE 16**. Crosslinking of enzymes and aminated supports after enzyme ionic adsorption.

- 1043 **FIGURE 17**. Multifunctional supports.
- 1044 FIGURE 18. Effect of the superficial density of glutaraldehyde groups on the possibilities of
- 1045 physical adsorption of the enzyme on the support surface.
- 1046 **FIGURE 19**. Interfacial activation of lipases.
- 1047 FIGURE 20. Immobilization of lipases at low ionic strength on glutaraldehyde activated1048 supports.
- FIGURE 21. Immobilization of lipases at low ionic strength in the presence of a detergent onglutaraldehyde activated supports.
- 1051 FIGURE 22. Immobilization of lipases at high enough ionic strength to prevent ionic exchange
- 1052 on glutaraldehyde activated supports.
- FIGURE 23. Immobilization of lipases at very high ionic strength (more than 1 M) onglutaraldehyde activated supports.
- FIGURE 24. Immobilization of lipases at moderate ionic strength and in the presence ofdetergents on glutaraldehyde activated supports.
- 1057 FIGURE 25. Glutaraldehyde, a versatile reagent in enzyme biocatalyst design.1058

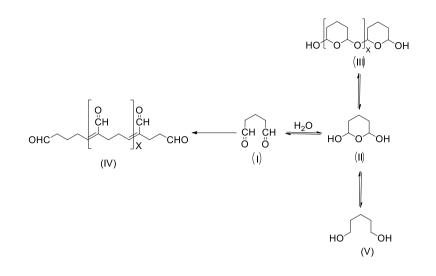
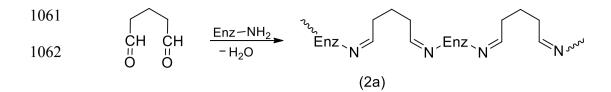
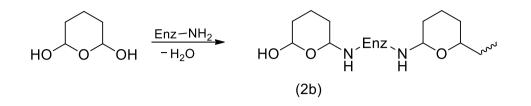


Figure 1





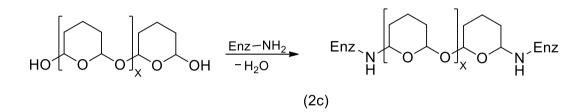


Figure 2

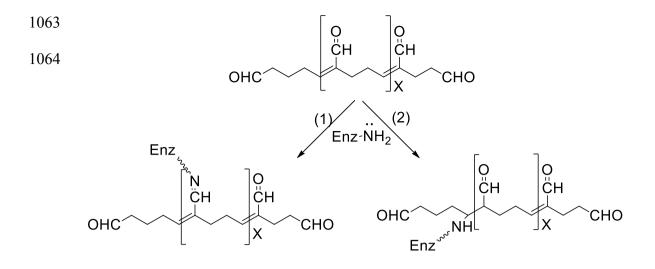
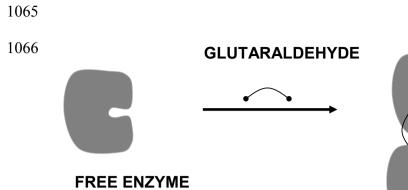
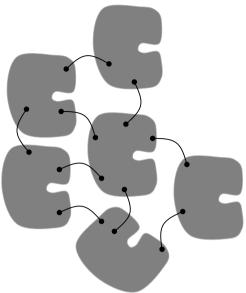
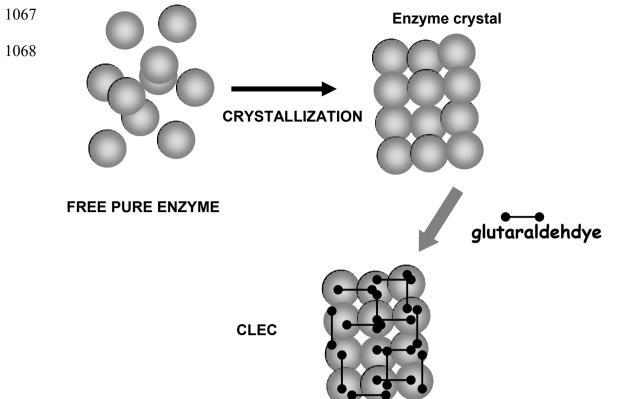


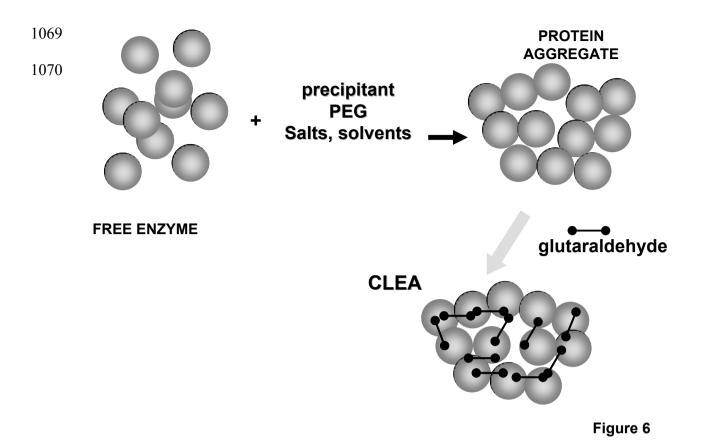
Figure 3

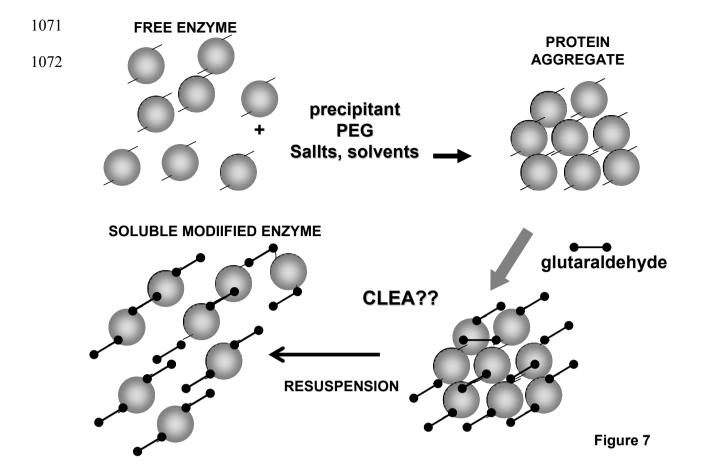


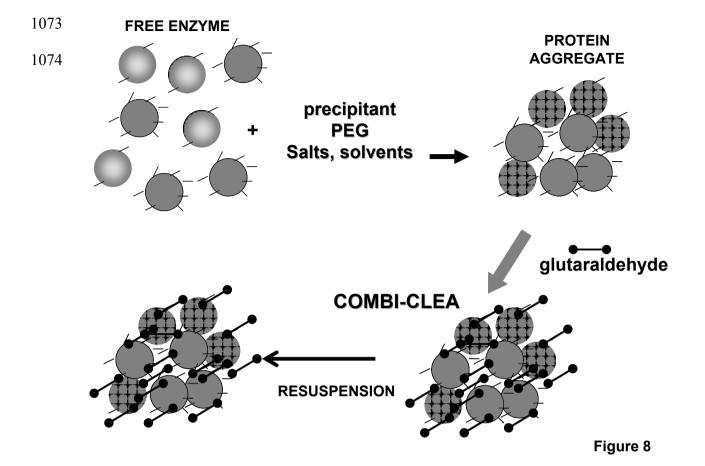


COPOLYMER GLUTARALDEHYDE-ENZYME









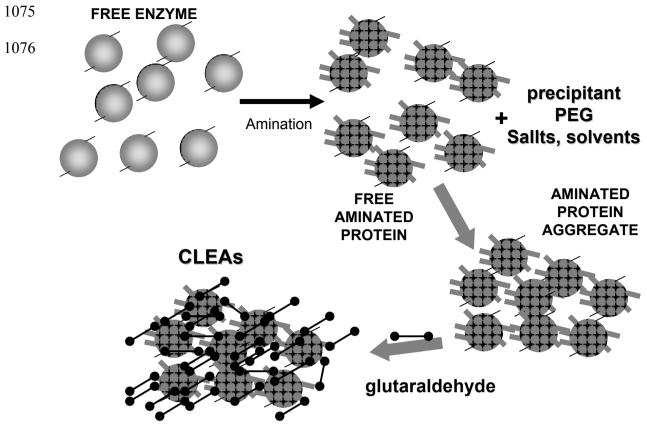
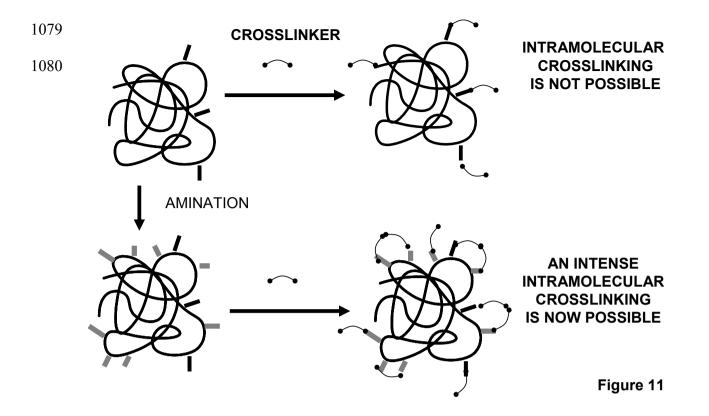
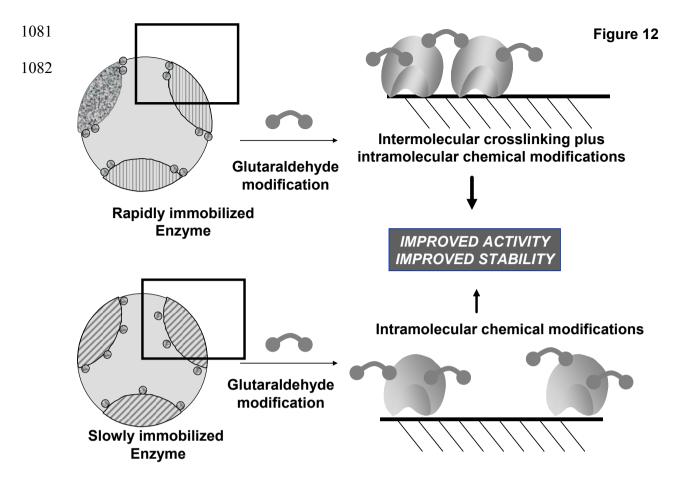
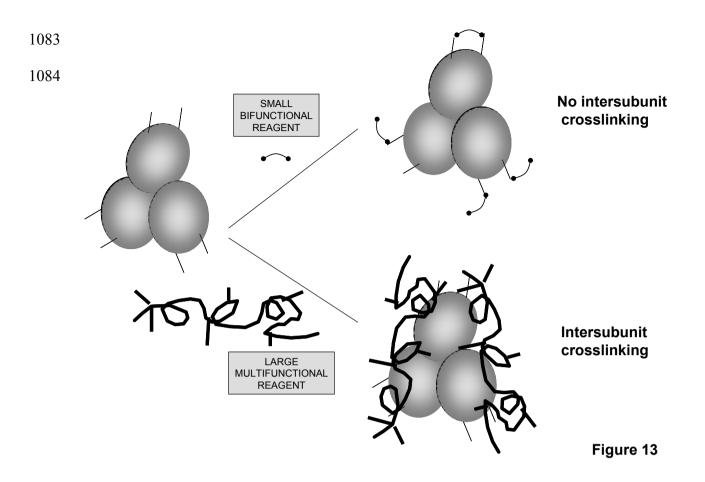


Figure 9

1077 1078 NATIVE ENZYME DISTORTED ENZYME DISTORTED ENZYME DISTORTED ENZYME DISTORTED ENZYME DISTORTED ENZYME CONFORMATIONAL CHANGES Enzyme crosslinking CONFORMATIONAL CHANGES ARE RESTRICTED







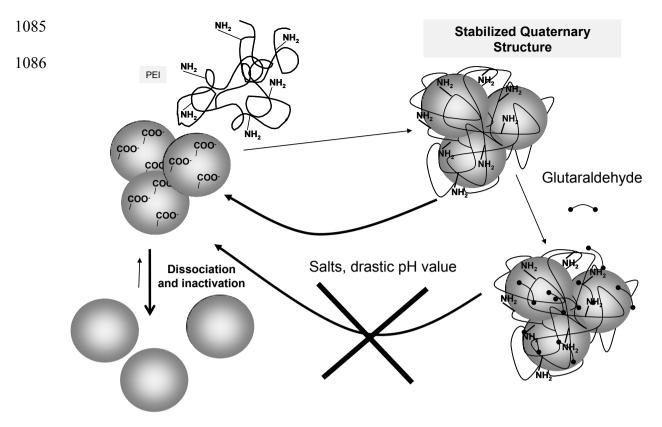


Figure 14

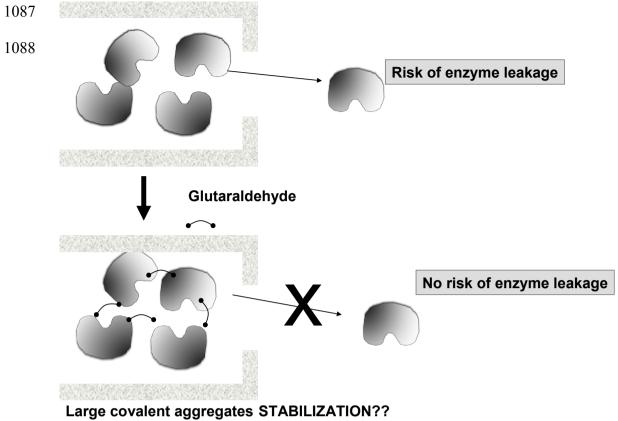


Figure 15

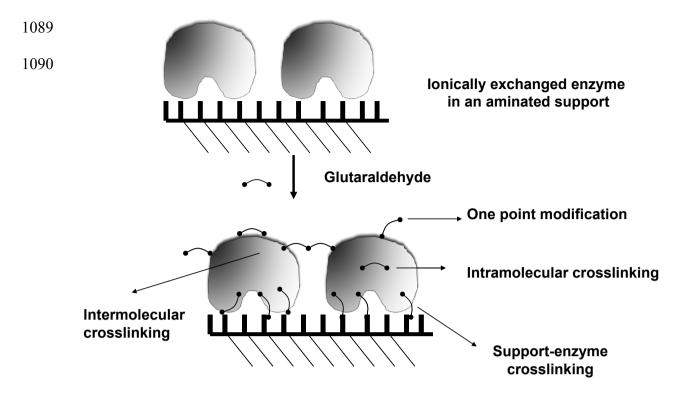


Figure 16



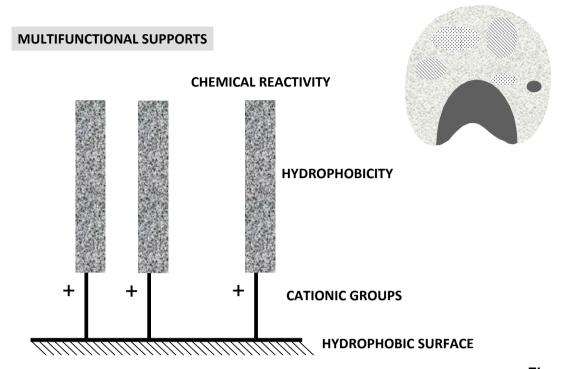
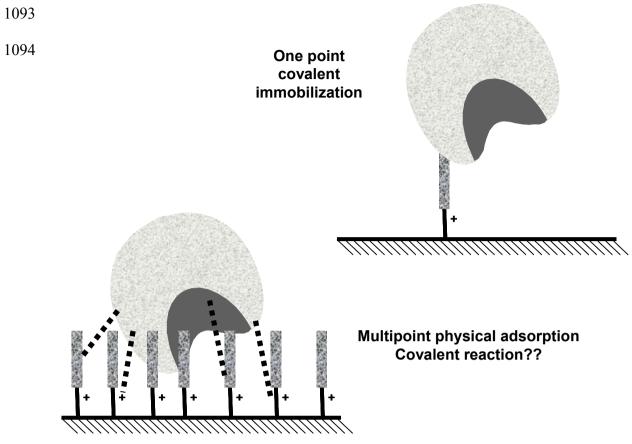


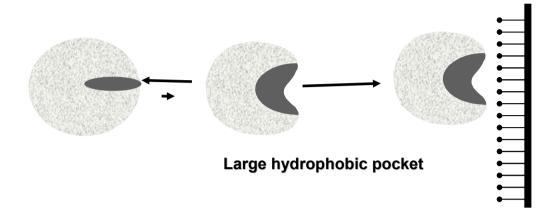
Figure 17



THE CASE OF LIPASES

1095 1096

Interfacial adsorption on hydrophobic supports



LOW IONIC STRENGTH

LIPASE ADSORPTION VIA INTERFACIAL ACTIVATION IONIC EXCHANGE NO INSPECIFC HYDROPHOBIC ADSORPTION

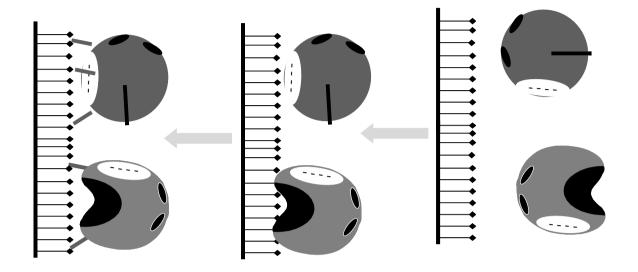


Figure 20

1097

1098

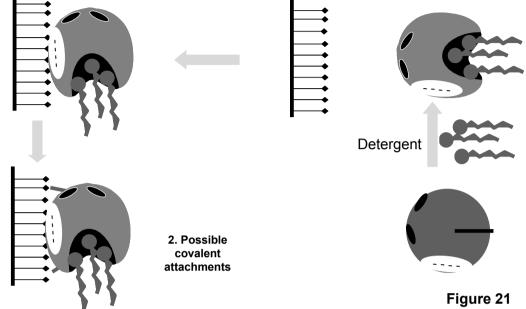
Possible covalent attachments

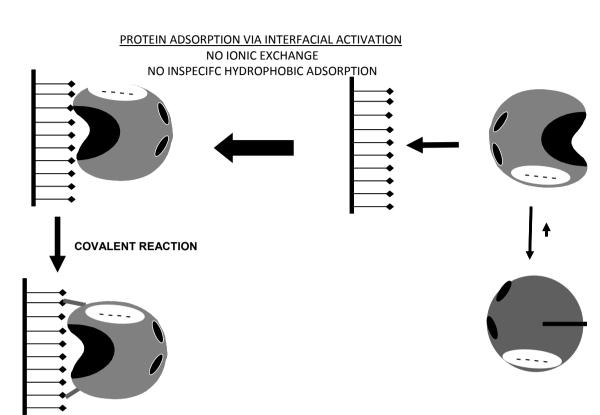




1. Ionic exchange

IONIC EXCHANGE NO INSPECIFC HYDROPHOBIC ADSORPTION NO ADSORPTION VIA INTERFACIAL ACTIVATION





IONIC STRENGTH HIGH ENOUGH TO PREVENT IONIC EXCHANGE

Figure 22

