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**Directed evolution of artificial repeat proteins as habit modifiers for the morphosynthesis of (111)-terminated gold nanocrystals**

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7 **Directed evolution of artificial repeat proteins as**  
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11 **habit modifiers for the morphosynthesis of (111)-**  
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15 **terminated gold nanocrystals**  
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49 **KEYWORDS:**  $\alpha$ Rep proteins, anisotropic gold nanoparticles, phage display screening,  
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52 Au (111) selectivity.  
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19 **ABSTRACT.** Natural biocomposites are shaped by proteins that have evolved to  
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22 interact with inorganic materials. Protein directed evolution methods which mimic  
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26 Darwinian evolution have proven highly successful to generate improved enzymes or  
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29 therapeutic antibodies but have rarely been used to evolve protein-material interactions.  
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33 Indeed, most reported works have focused on short peptides and a wide range of  
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36 oligopeptides with chemical binding affinity for inorganic materials have been uncovered  
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40 by phage display methods. However, their small size and flexible unfolded structure  
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43 prevent them to dictate the shape and crystallinity of the growing material. In the  
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47 present work, a specific set of artificial repeat proteins ( $\alpha$ Rep), that exhibit highly stable  
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51 3D folding with a well-defined hypervariable interacting surface, is selected by directed  
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54 evolution of a very efficient home-built protein library for their high and selective affinity  
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3 for the Au(111) surface. The proteins are built from the extendable concatenation of  
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7 self-compatible repeated motifs idealized from natural HEAT proteins. The high-yield  
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10 synthesis of Au(111)-faceted nanostructures mediated by these  $\alpha$ Rep demonstrates  
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12  
13 their chemical affinity and structural selectivity that endow them with high crystal habit  
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16 modification performances. Importantly, we further exploit the protein shell  
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19 spontaneously assembled on the nanocrystal facets to drive protein-mediated colloidal  
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22 self-assembly and on-surface enzymatic catalysis. Our method constitutes a generic  
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27 tool for producing nanocrystals with determined faceting, superior biocompatibility and  
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31 versatile bio-functionalization towards plasmon-based devices and (bio)molecular  
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35 sensors.  
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4       Natural protein evolution is remarkably efficient to foster the emergence of specific  
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7 interactions between proteins and targeted molecules <sup>1</sup> or biomineral surfaces.<sup>2-3</sup>  
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10 Indeed, most inorganic structures found in living organisms such as diatom cell wall,  
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13 magnetosome, sea urchin spicule, nacre, to cite a few, are shaped and organized at the  
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16 molecular level through the intimate interactions with proteins. The efficiency of such  
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19 molecular interactions in natural systems does not rely on prior knowledge of rules  
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22 governing interaction between polypeptides and material surfaces but rather on  
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25 combinatorial selection and optimization. Mimicking the evolutionary exploration of the  
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28 protein sequence space is therefore a promising strategy to create new proteins  
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32 endowed with new tailored interaction properties. Directed evolution approaches, that  
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35 have originally been developed and broadly used to address biological questions,<sup>4-5</sup> can  
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38 be a powerful tool to create new artificial proteins with specific chemical affinity and  
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41 structural selectivity for crystalline material surfaces. Surprisingly, these methods have  
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44 not yet attracted the general attention in nanomaterial sciences with the remarkable  
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47 exception of short peptides.<sup>6-10</sup> Oligopeptides with chemical affinity for a chosen  
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50 inorganics surfaces (for example Au,<sup>6</sup> ZnS,<sup>8</sup> Co<sub>3</sub>O<sub>4</sub><sup>11</sup>) or, even, facet-specific adsorption  
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3 (Pt(100) vs Pt(111),<sup>12</sup> GaAs(100) vs GaAs(111A),<sup>7</sup> Au(111)<sup>13</sup>) have been discovered by  
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7 genetic sorting methods such as phage display or cellular display.  
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11 Remarkably, in nature, the overwhelming majority of material-specific biomolecules  
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13 are proteins, not peptides owing to the very distinct molecular recognition potential of  
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15 these two classes of molecules. Peptides are too short to have a stable hydrophobic  
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17 core and hence are usually not able to reach a stable folded tertiary structure. The  
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19 molecular recognition capacities of peptides are therefore inherently limited which  
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21 translates, for peptides selected for a high chemical affinity towards inorganic materials,  
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23 into a lack of structural selectivity. Single crystals grown in the presence of such  
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25 peptides do not exceed a few nanometers in size, involving a few tens of peptides per  
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27 crystalline facets,<sup>12</sup> beyond which their small size and lack of stable folding cannot  
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29 prevent serendipitous polycrystalline growth.  
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47 This intrinsic shortcoming of peptides is well established in biology and has motivated  
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49 the development of combinatorial libraries of folded proteins rather than peptides which  
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51 has had a major impact for biological applications. Antibodies possess a protein  
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3 architecture known for its versatile binding capabilities and in-vitro evolved antibodies  
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7 have revolutionized the field of targeted therapeutics.<sup>14-15</sup> Yet, the non-biological  
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10 applications of antibodies are severely hampered by their strong propensity to  
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14 aggregate and the low efficiency of their production in bacterial expression systems.  
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17 Phage display libraries of antibody fragments have nevertheless been successfully used  
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21 to identify proteins with binding properties for polymeric<sup>16</sup> or inorganic surfaces<sup>17-19</sup> but  
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24 the binding site of being a flexible amino-acid loop, their interaction is also essentially  
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28 driven by chemical affinity and lack structural selectivity.<sup>19</sup>  
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32       Unfortunately, no effective alternative approach is available to design material-binding  
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35 proteins. The trial-and-error identification of surface-binding molecules remains  
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38 essentially serendipitous<sup>20-23</sup> leading to some successful systems exploiting natural  
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42 globular<sup>20, 24</sup> and fibrillary<sup>25-26</sup> proteins or complex plant and microbial extracts.<sup>27-28</sup>  
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47       However, efficiently produced and highly evolvable artificial proteins have recently  
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51 been constructed from naturally stable proteins scaffolds.<sup>29</sup> Extremely efficient protein  
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54 libraries have been designed by the concatenation of self-compatible repeated motifs  
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3 idealized from natural protein families such as ankyrin, HEAT or Leucine-rich repeats.<sup>30-</sup>  
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7 <sup>32</sup> Such artificial repeat proteins are particularly promising since their interaction surface  
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10 can be extended by additional motifs without compromising the stability of the folded  
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13 protein scaffold. Our goal is to extend, at the interface with inorganic nanomaterials, the  
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16 directed evolution strategy so far limited to short and unstructured peptides to the  
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19 growing field of artificial proteins libraries.  
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25 Here, we demonstrate a new scalable strategy whereby a library of fully folded and  
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28 designable proteins is exposed to crystalline Au(111) prior to the identification of the  
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31 selected proteins and their use as habit modifiers in a seed-mediated nanocrystal  
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34 growth approach. Robustness, to favor epitaxial facet binding, and chemical diversity, to  
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37 optimize the affinity towards the chosen material, are successfully combined by  
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40 exploiting the stable and rigid artificial alpha helical repeat ( $\alpha$ Rep)<sup>33</sup> that comprise a  
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43 fixed rigid multi- $\alpha$ -helical scaffold and a binding surface with random sequence changes  
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47 in designed positions.<sup>33-35</sup> This variable surface is optimized, without altering the global  
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50 protein structure, for the specific binding of the non-biological Au(111) target by  
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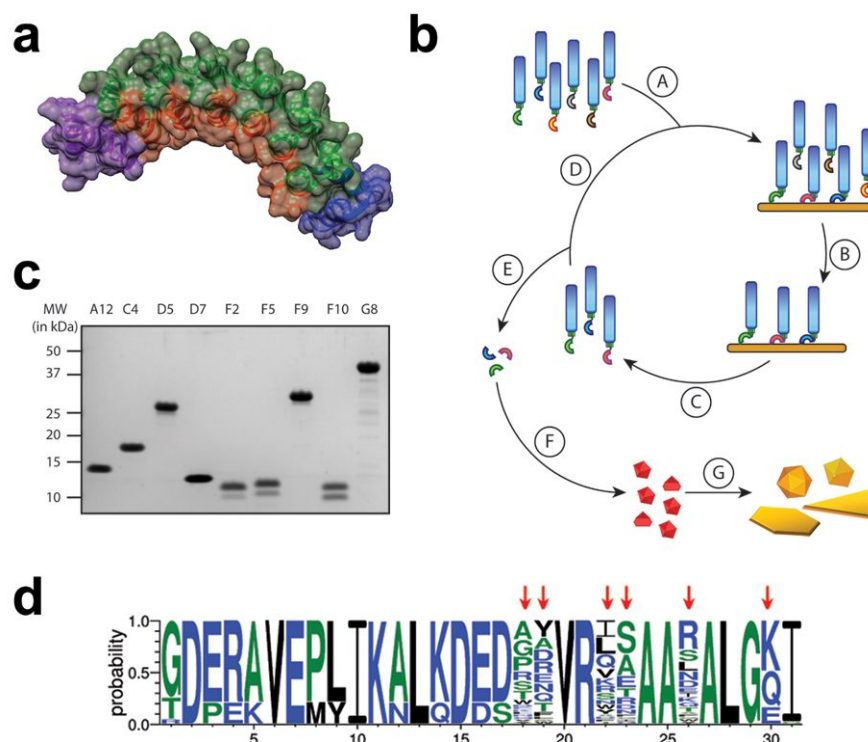


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3 evolutionary selection and therefore offers a unique possibility for an optimal design of  
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7 gold nanocrystal habit modifiers.<sup>31</sup> Importantly, the selection is performed against  
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10 atomically smooth, (111)-oriented gold surface unlike peptides and protein selections  
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13 which are usually performed against polycrystalline<sup>9, 19</sup> or amorphous<sup>6, 21</sup> inorganic  
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16 targets leading to material- but not facet-specific biomolecules. The selected  $\alpha$ Reps  
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19 govern efficiently the synthesis of purely (111)-faceted crystals. Additionally, the  
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22 presence of the capping proteins enable the directed self-assembly of stacked  
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25 ensembles and satellites superstructures, or the surface confinement of enzymatic  
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28 production of electroactive species.<sup>36</sup>  
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## RESULTS AND DISCUSSION

**Selection of anti-Au(111)  $\alpha$ Rep by  $\alpha$ Rep protein phage display.** The native structure of  $\alpha$ Rep proteins is illustrated in Figure 1a and consists in the concatenation of internal repeats composed of two antiparallel  $\alpha$ -helices. The first (N-cap) and last (C-cap) motifs have a similar topology but their sequence is adapted to shield the hydrophobic core. The internal repeats comprise 31 amino-acids (AA) were defined by sequence analysis of a group of homologous HEAT-like repeat proteins found in thermophilic organisms.<sup>33</sup> The resulting consensus sequence combines twenty-five highly conserved positions (green region in Fig. 1a) that ensure the robust structure of the folded  $\alpha$ Rep proteins with six specific hypervariable positions that can accommodate a wide range amino acid substitutions. Interestingly, all the hypervariable positions are gathered in the same concave surface of the proteins (brown region in Fig. 1a) allowing to choose them in order to confer the proteins specific interaction properties.<sup>34</sup> To exploit the combined asset of structural robustness and functional interaction specificity of these proteins, we have built a large combinatorial phage library of  $\alpha$ Reps distinct from each other by (i)

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3 the number of internal repeats and (ii) the random nature of the AA in the hypervariable  
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7 positions.<sup>34</sup> Such a library of  $1.7 \times 10^9$  unique clones is sufficiently diverse to allow  
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10 selection of new  $\alpha$ Rep proteins binding tightly and specifically to almost any other  
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13 protein defined *a priori*. The  $\alpha$ Rep library was initially developed for biological  
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16 applications such as the generation of crystallization chaperones,<sup>37</sup> cell tracking<sup>38</sup> or in  
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19 protein interference experiments.<sup>39</sup> In this work, we apply it, for the first time, to optimize  
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22 the protein-metal surface affinity and to identify  $\alpha$ Rep proteins that can act as habit  
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25 modifiers for the growth of crystalline gold nanoparticles by strong and specific  
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28 adsorption to pre-determined Au(111) crystal facets.  
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**Figure 1. Construction and directed evolution of Au(111)-binding artificial repeat proteins.** (a) 3D representation of the crystallographic structure of a 4-repeat  $\alpha$ Rep protein depicting the internal repeats comprising the hypervariable positions (brown) with their conserved scaffold regions (green), N- and C-cap (blue). (b) Schematic flowchart showing the phage display design and selection of  $\alpha$ Rep's (A-D) and the  $\alpha$ Rep directed Au nanocrystal morphosynthesis (I-J) process. These steps involve: (A) Construction of the phage display library; (B)  $\alpha$ Rep selection on planar Au(111) substrate on mica and elution of unbound phage at pH5; (D) acid elution of Au-bound phages and bacterial amplification of selected phages (E) proteolytic isolation of  $\alpha$ Rep from phage body and large scale production. The morphosynthesis of Au nanocrystals by seeded growth process comprises: (F)  $\alpha$ Rep directed Au seed synthesis; (G) nanocrystal growth in the presence of excess  $\alpha$ Rep through hydroxylamine-mediated disproportionation mechanism. (c) Coomassie blue stained SDS-PAGE profiles of 9 different Au(111)-selected  $\alpha$ Rep after cleavage digestion. The position of the major bands represents the molecular weight of respective  $\alpha$ Rep. (d) Sequence logo obtained

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4 by multi-alignment of the sequences of all the repeats from the selected  $\alpha$ Rep, including  
5 those of the N-cap that have the same second helix as the internal repeats, hence the  
6 apparent variability observed in positions (1,3,4,8,9,12,14,17). The binding  
7 hypervariable surface is generated by the position indicated by red arrows.  
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14 First,  $\alpha$ Reps with high affinity for Au(111) surface are selected by exposing the  
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17 combinatorial phage library to a planar Au(111) film and following the steps depicted in  
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21 Figure 1b (See Materials and Methods and Section A in Supplementary Information).  
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24 The phage population bearing  $\alpha$ Reps is incubated at pH 7.5 with freshly prepared  
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27 Au(111) surfaces (Step A). Weakly bound phages are eluted (Step B) while the  
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30 Au(111)-bound clones are collected by acidic elution (Step C) and amplified in bacteria  
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33 (step D). This iterative biopanning procedure was repeated three time before 96  
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36 Au(111)-interacting clones were randomly picked from the emerging sub-population,  
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39 expressed, isolated and tested by standardized ELISA assays against similar freshly  
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42 prepared Au(111) substrates (See Supplementary Information Figure S1a). 18 clones  
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45 showed positive ELISA response, however after sequencing a total of 9 different  
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48 Au(111)-binders with internal repeat numbers (n) comprised between 1 and 10 and pI  
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51 ranging from 5.3 to 9.05 were identified and will be labeled A12, C4, D5, D7, F2, F5, F9,  
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3 F10, G8 in the following (Fig. S1). The chemical diversity of the hypervariable positions  
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7 (Figure 1d) indicates that the interaction between the protein and the Au(111) surface is  
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10 complex and does not yield a single optimal configuration. Yet, the selected  
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13 hypervariable AA are the same as the AA found in non-thiolated gold-binding  
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16 polypeptides.<sup>6, 13</sup> Recent modeling of the peptide-Au interface have indeed shown that  
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19 optimal adsorption could be attained with sp<sup>2</sup> conjugated (Trp, Tyr, Arg), polar (Gln,  
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22 Asn, Ser), positively (Arg, Lys) and negatively (Glu, Asp) charged amino acids, thus  
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27 suggesting a large variety of possible adsorption scenarii for gold-binding proteins.<sup>40-43</sup>  
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31 The molecular weight of the proteins ranges between 12 and 42 kDa as shown in the  
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34 SDS-PAGE profile shown in Figure 1c and correspond to 1 to 10 internal repeats. The  
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37 large size variation of the selected  $\alpha$ Reps is also consistent with the concomitance of  
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41 several different gold-binding mechanisms.  
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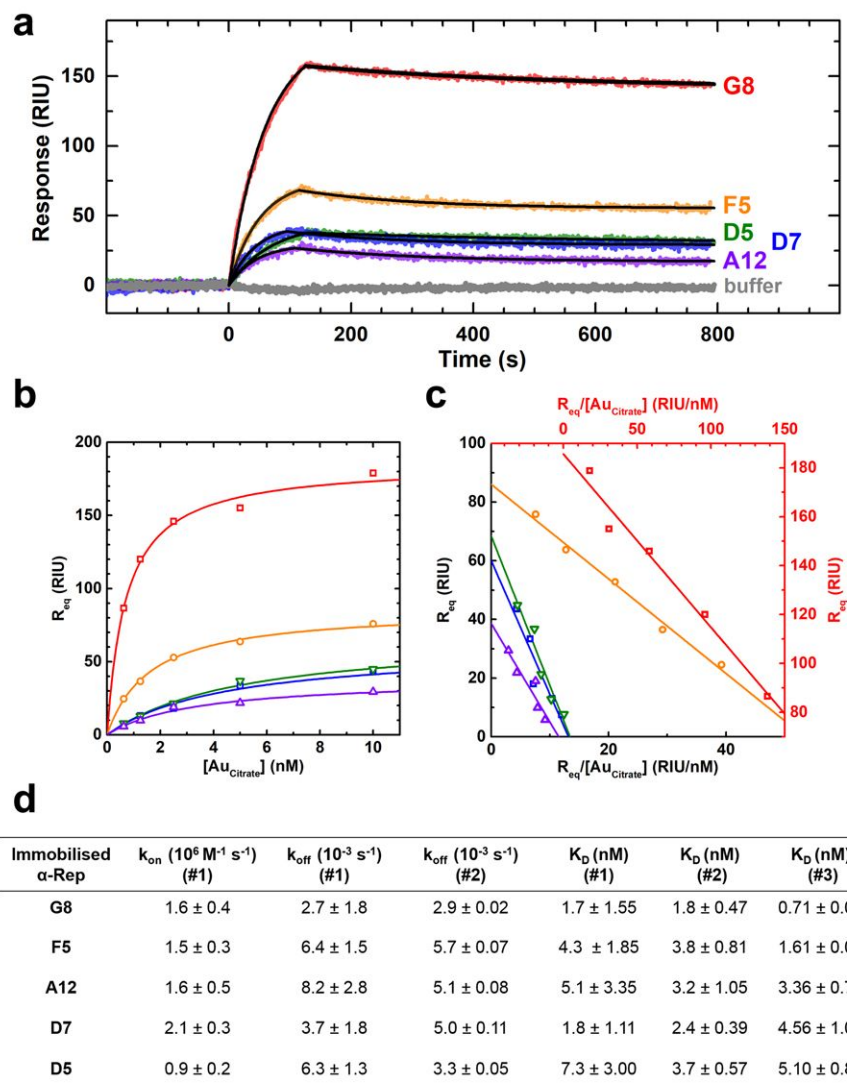
46 **SPR characterization of the gold affinity of the selected proteins.** To further assess the  
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49 gold-binding specificity and estimate the affinity constants, each of the nine binders was  
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53 immobilized on Surface Plasmon Resonance (SPR) sensor chips and subjected, first, to  
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3 a high influx of citrate-stabilized, decahedral gold nanoparticles exposing primarily (111)  
4 facets<sup>44</sup> and, second, to an influx of pure buffer, as described in Materials and Methods.  
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10 The sensograms for A12, D5, D7, F5 and G8 and buffer are shown in Figure 2a (See  
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13 also Supplementary Information Figure S2a for C4, F9, F10, F2 and extra controls). A  
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16 significant positive association phase is observed, which shows a maximal response for  
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20 G8 followed by F5, D5, D7 and, at a lower level, by A12. When the nanoparticles bound  
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24 to the protein-coated substrates are washed with a pure buffer a small reduction of the  
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28 SPR response is observed indicating that some dissociation occurs leading, in first  
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32 approximation, to a new equilibrium state. No association is observed during control  
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35 experiments performed either by replacing the Au nanoparticle with buffer during the  
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38 initial influx or by immobilizing an  $\alpha$ Rep protein of identical structure but with no specific  
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42 affinity for gold such as a GFP-binder with 4 internal repeat (bGFPa).<sup>34</sup> The maximal  
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46 SPR response is observed with the largest protein containing 10 internal repeat (G8). A  
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49 control sensogram was performed with a non-selected  $\alpha$ Rep with 10 internal repeats  
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52 (N10) and is shown in Figure S2a. The low binding signal observed for N10 is clearly  
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56 marginal compared to the one of G8, which precludes the control of the protein-gold  
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3 surface simply by the protein size and confirms the role of the AA selection in the  
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7 variable positions. The general behavior indicates that G8, F5, D5, D7 and A12 gold-  
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10 binding proteins have the ability to capture citrate-stabilized gold nanoparticles, while  
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13 the other proteins show no significant detectable affinity during SPR tests. More  
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17 quantitative insight can be gained by extracting dissociation constants from the  
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21 sensograms using the three approaches detailed in the supplementary section (Section  
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24 S2). The first dataset ( $K_D\#1$ ) is derived from the kinetic constants of the association  
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27 phase,  $k_{on}$  and  $k_{off\#1}$  (Figure 2d). The second dataset ( $KD\#2$ ) takes into account the  
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31 corrected  $k_{off\#2}$  values from the dissociation phase.  
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**Figure 2. Gold affinity of the selected anti-Au(111) repeat proteins. (a)** SPR sensograms during adsorption and desorption phases monitoring the interactions between immobilized  $\alpha$ Rep proteins (see labels) and citrate-stabilized Au nanoparticles ( $[Au_{cit}]=10$  nM). Solid black lines are exponential fits to the association and dissociation phases. The exponent of the association fits provides the association ( $k_{ON}$ ) and dissociation ( $k_{OFF}$  #1) kinetic constants tabulated in (d). The dissociation phase fits provide the  $k_{OFF}$  #2 kinetic constant in Table (d). Each protein data is associated to the same color throughout the figure. **(b)** SPR equilibrium analysis along with Langmuir fits (continuous lines). **(c)** Scatchard plot for the empirical estimation of the dissociation

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4 constants labelled  $K_D$  #3 which is obtained from the slopes of the linear fits. G8 data  
5 (red) are plotted on the red x-y axis while all other data share the black x-y axis. (d)  
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7 Summary table of all association ( $k_{ON}$ ) and dissociation ( $k_{OFF}$  #1 and  $k_{OFF}$  #2) alongside  
8  
9 the dissociation constant ( $K_D$ ) values obtained from the ratio of kinetic constants ( $K_D$ #1=  
10  $k_{OFF}$  #1 /  $k_{ON}$ ,  $K_D$ #2=  $k_{OFF}$  #2 /  $k_{ON}$ ) and from the Scatchard plot ( $K_D$ #3).

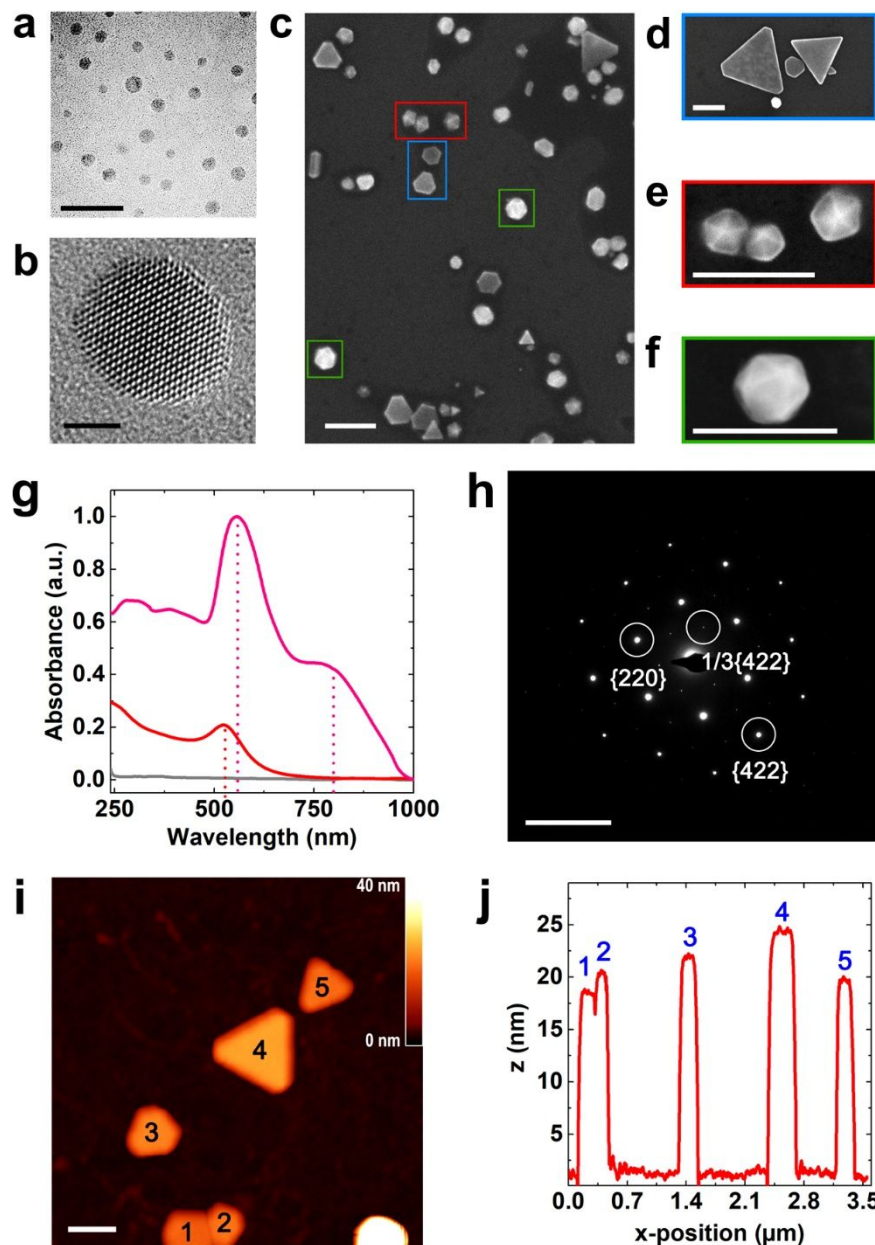
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13 The third dataset ( $K_D$ #3) is obtained by fitting the data with the Langmuir isotherm  
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16 model (Figure 2b) followed by a Scatchard linearization (Figure 2c). All three  
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20 quantitative analyses consistently yield sub-10 nM dissociation constants similar to the  
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23 ones routinely measured in protein pairs involving at least one  $\alpha$ Rep binder.<sup>34</sup> This SPR  
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27 study demonstrates that the selected  $\alpha$ Rep proteins readily associate with the solid gold  
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30 surface and quantifies the Au(111)-binding strength, which is maximal for G8.

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34 Furthermore, taking into consideration their intrinsic rigid tridimensional folded shape,  
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37 their high pH and thermal stability and their high expression potential that allows the  
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40 production of mM solutions, these proteins possess a strong potential as selective  
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44 Au(111) capping agents and even as crystal habit modifiers in the synthesis of Au  
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48 nanoparticles.

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3 **Protein-controlled nanocrystal morphosynthesis.** This unique feature is revealed by  
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7 the reduction of a gold precursor in the presence of  $\alpha$ Rep-capped seeds and free  $\alpha$ Rep  
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10 which results in the morphosynthesis of protein-capped gold nanoparticles exclusively  
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12  
13 terminated with (111) facets (Figure 1b, steps F and G). First, gold seeds ( $7 \pm 1$  nm) are  
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16 produced by the reduction of  $\text{Au}^{3+}$  to  $\text{Au}^0$  with an extrinsic mild reducing agent, sodium  
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19 formaldehyde sulfoxylate (SFS),<sup>45</sup> in a buffered (pH 7.5) solution of  $\alpha$ Rep protein acting  
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22 as capping agents (Fig. 3a and Fig. S3a). The bright red seed solution is produced  
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25 within two hours after SFS addition, ten times faster than known protein-free methods,<sup>20-</sup>  
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32 <sup>21, 24</sup> probably thanks to the stabilization by the protein capping. The seeds are  
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35 crystalline with frequent single or penta twin boundaries and occasionally polycrystalline  
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38 (Fig. 3b and Figs. S3d-h). The presence of a protein shell is confirmed by a 7-nm red  
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41 shift of the plasmon resonance peak of the  $\alpha$ Rep-capped seeds compared to protein-  
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44 free seeds (Fig. S4b), by the light organic halo surrounding the Au seeds in TEM  
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47 micrographs (Fig. S3a) and by the prolonged colloidal stability with no sign of  
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50 aggregation after several months at 4°C. Furthermore, the electrophoretic mobility of  
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53 seeds synthesized with any selected  $\alpha$ Rep proteins having different number of internal  
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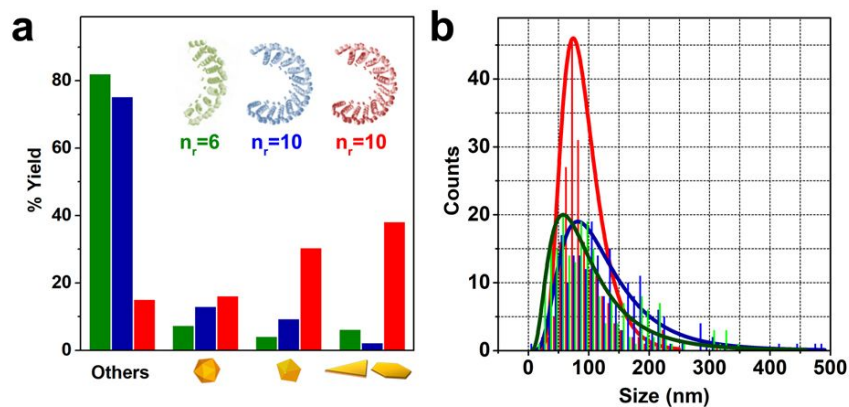
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3 repeats (n) varies consistently with the net surface charge of the corresponding protein  
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7 in pH 8.5 tris-borate buffer (Fig. S3c). In spite of the presence of the proteins, the seeds  
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10 are systematically spherical, which suggest that the proteins, at the seed stage, do not  
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13 induce faceting but merely act as surface stabilizers when the direct reduction is  
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16 performed with SFS. The seeds are then injected in a fresh solution set at pH 5 and  
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19 containing  $\text{Au}^{3+}$ , one of the selected  $\alpha\text{Rep}$  and hydroxylamine, which is not able to fully  
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22 reduce gold at this pH and in the absence of seeds (See Section S4 in Supplementary  
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25 Information).<sup>46</sup> The appearance of a pink-to-purple color in the different solutions  
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27  
28 confirms the surface-mediated growth through disproportionation reaction<sup>47</sup> onto the  
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30  
31 pre-formed Au seeds, as demonstrated for G8 in Figure 3 and generalized to all  
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34 selected  $\alpha\text{Rep}$  proteins in Figures 5i-l and in Sections S5 and S6 of Supplementary  
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37 Information. Detailed electron microscopic examination reveals that the resulting colloid  
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40 is composed of three (111)-terminated subpopulations of 2D nanoplates (38.2%),  
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43 decahedra (30.4%) and icosahedra (16.2%) with only 15.2% of other random structures  
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49 (Figs. 3a and 4a). The ensemble absorption spectrum of as-synthesized nanostructures  
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52 displays two peaks centered at 556 nm and 804 nm (Fig. 3b), suggesting a composite  
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3 nanocrystal population. The former one dominates and is associated to a plasmon  
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7 resonance in quasi-isotropic nanoparticles (decahedra and icosahedra). The latter peak  
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10 shouldering at 780 nm arises from the in-plane higher order plasmon modes of  
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13 prismatic nanoplates.<sup>48</sup> Selected area electron diffraction (SAED) patterns recorded on  
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17 the nanoplates exhibit three sets of spots of decreasing intensity that are indexed to  
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21 (220), (422) and  $1/3(422)$  planes of fcc gold (Fig. 3c).<sup>49</sup> The 2D prisms are single  
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23  
24 twinned crystals sharing the same [111] zone axis aligned with the electron beam and  
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28 thus exposing two extended (111) basal facets.  
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**Figure 3. Morphological and structural characterization of  $\alpha$ Rep-coated, (111)-terminated Au nanocrystals. (a,b)** High resolution TEM of spherical G8-stabilized seeds showing a high degree of crystallinity. The seed in (b) is single crystalline and oriented along the [011] zone axis (c) Representative SEM micrograph of G8-capped, (111)-facet terminated Au nanostructures showing nanoplates (blue box), decahedrons (red box) and icosahedrons (green box) morphologies. (g) Characteristic UV-visible spectra of G8 templated Au seeds (red,  $\lambda_{\text{max}} = 524$  nm), seedless growth solution (grey) and Au nanostructures synthesized by the G8-templated, seeded growth approach (pink), which

exhibit two peaks at  $\lambda_{\max} = 556$  nm and  $\lambda_{\max} = 804$  nm. **(h)** Selected area electron diffraction of an Au nanoplate showing diffraction spots along the [111] zone axis. **(i)** Tapping mode AFM image of five Au nanoplates. **(j)** Height profile of the five nanoplates shown in (i), which all have a thickness of  $21 \pm 3$  nm. Scale bars are (a) 20 nm, (b) 2 nm, (c-f, i) 200 nm, (h)  $10 \text{ nm}^{-1}$ .



**Figure 4: Comparative analysis of nanocrystal shapes and sizes obtained in the presence of control proteins, anti-GFP and N10, or anti-Au(111) G8.** (a) Histogram showing the relative occurrence of nanoprisms, decahedra, icosahedra and other shape (spheroidal, and irregular shapes) obtained by morphosynthesis with anti-GFP  $\alpha$ Rep (green), of consensus sequence N10  $\alpha$ Rep (blue) and the isomorphous anti-Au(111) G8  $\alpha$ Rep (red). (b) Size distribution histograms and log-normal fits of as-synthesized nanocrystals with anti-GFP (green), N10 (blue) and G8 (red)  $\alpha$ Rep proteins (200 measurements for each set).

While the lateral dimensions of the nanoplates vary between ca. 50 and 500 nm, they show a fairly uniform thickness of 22 nm as evidenced by atomic force microscopy

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3 (AFM) measurements displayed in Figures 3d and 3e, in good agreement with twinned  
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7 nanoprisms of similar morphology produced by other methods.<sup>50-52</sup>  
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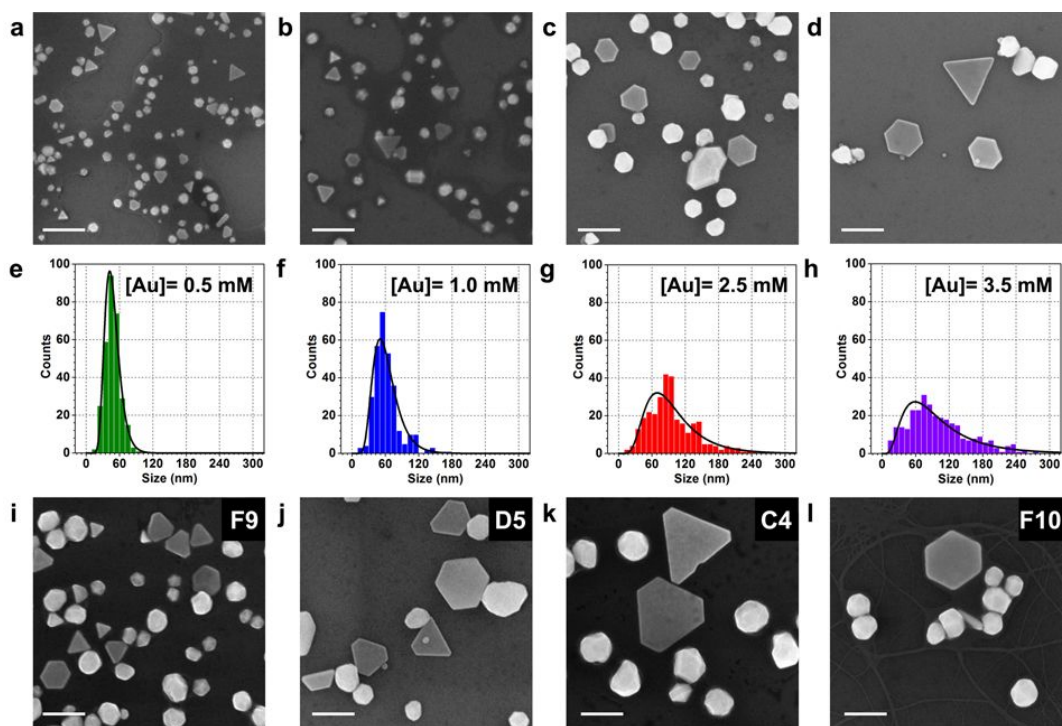
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11 Figure 4 demonstrates that the direct effect of the facet-specific gold affinity of  
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14 Au(111)-selected G8 proteins on the morphology and structure of the gold nanocrystals  
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17 is absent for analogous proteins that have not been selected against Au(111). The exact  
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22 same synthesis conditions used with G8 in Figure 3 are performed with the two control  
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25  $\alpha$ Rep proteins, N10 and bGFPa, that have no specific affinity for Au(111) surfaces  
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28 (Fig. S7).<sup>34</sup> Figure 4a clearly illustrates that the (111)-faceted nanoplates, icosahedrons  
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32 and decahedrons represent only 25% and 18% of the particles produced in the  
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36 presence of bGFP and N10 respectively while they amount to 85% when the  
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39 morphosynthesis is performed with G8. The vast prevalence of (111)-terminated  
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42 nanoparticles in the latter case results from the specific and strong binding of the  
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46 designed proteins to emerging (111) facets as the metal growth proceeds in pH  
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50 conditions similar to the one corresponding to the binding step during the protein  
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53 selection (Fig. 1, step B). The strong protein-surface affinity hinders the build-up on  
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3 (111) facets, which are thus stabilized, and results in enhanced growth rates in other  
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7 available crystallographic directions. Decahedra and icosahedra only expose (111)  
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10 facets and thus are fully coated with  $\alpha$ Rep proteins leading to a rapid inhibition of their  
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13 growth. As a consequence of the seed-mediated protocol and of the effective growth  
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16 inhibition of the (111) facets, the size distribution of the G8-driven synthesis is twice  
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19 narrower ( $92 \text{ nm} \pm 35 \text{ nm}$ ) than the two control experiments ( $130 \text{ nm} \pm 77 \text{ nm}$  for N10  
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22 and  $106 \text{ nm} \pm 75 \text{ nm}$  for bGFP) as seen in Figure 4b.  
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29 Interestingly, nanoplates are formed by inhibiting the two basal (111) facets of single  
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32 twinned seeds but their edges expose (100) and (110) facets that keep growing even in  
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35 the presence of the selected proteins as witnessed by the larger edge length distribution  
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38 (Figs. 3 and 4b), which further confirms the (111) binding specificity of the selected  
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42  $\alpha$ Rep proteins. The kinetic control obtained by performing the hydroxylamine reduction  
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45 at pH 5 allows to tune the nanocrystal size distribution by adjusting the  $\text{Au}^{3+}$  ions flux in  
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48 the growth solution. In Figures 5a-h, the G8-mediated nanocrystal synthesis is  
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52 performed with increasing  $\text{Au}^{3+}$  concentrations and shows the same types of structures  
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with a marked increase of the nanoplate edge length. The overall size distributions shift from  $48 \pm 14$  nm for  $[\text{Au}^{3+}] = 0.5\text{mM}$  to  $105 \pm 72$  nm for  $[\text{Au}^{3+}] = 3.5\text{mM}$  and is accompanied by a red-shift of both plasmon resonances (Figs. S8a,b).



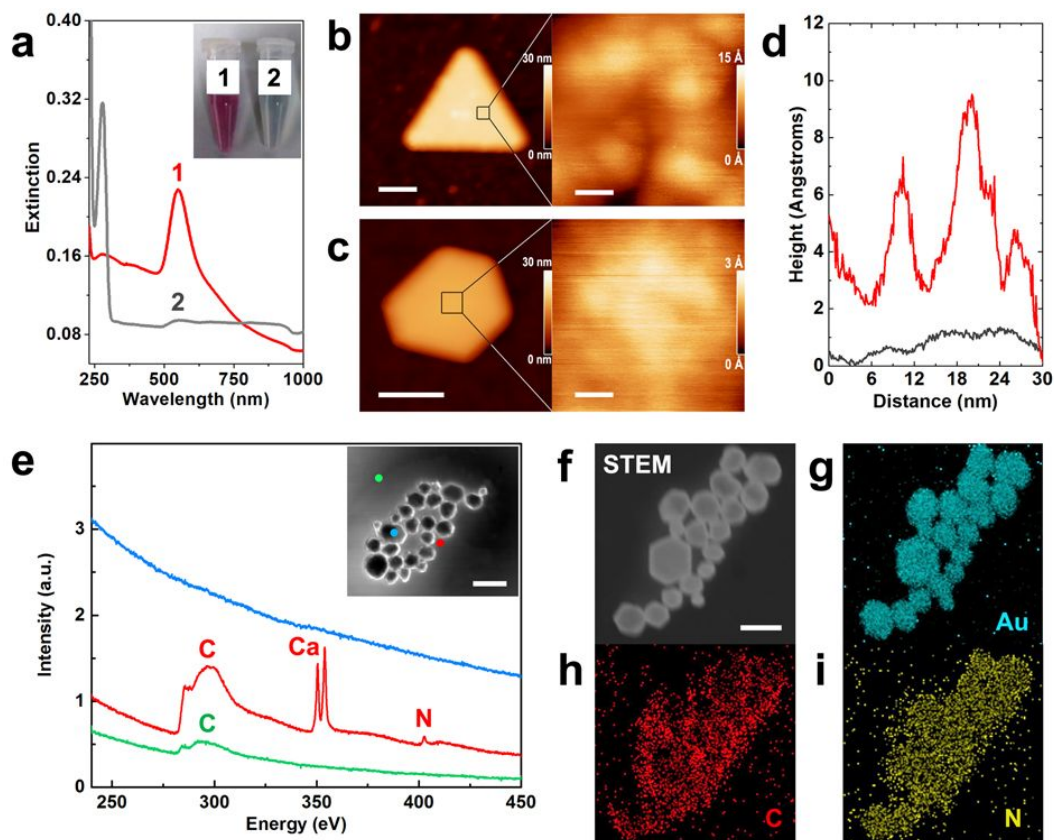
**Figure 5: Nanocrystal size adjustment by varying the initial  $\text{Au}^{3+}$  concentration and generalized synthesis with other selected proteins.** (a-h) SEM micrographs and nanocrystal size distribution of kinetically controlled G8-capped Au nanostructures for four different  $\text{Au}^{3+}$  concentrations: (a, e) 0.5 mM; (b,f) 1.0 mM; (c,g) 2.5 mM; (d, h) 3.5 mM. The histograms follow lognormal distributions (black lines) with sizes of (e)  $48 \pm 14$  nm, (f)  $62 \pm 24$  nm, (g)  $99 \pm 50$  nm and (h)  $105 \pm 72$  nm. (i-l) SEM micrographs of nanostructures synthesized in the presence of different  $\alpha\text{Rep}$  at the same  $\text{Au}^{3+}$  concentration of 2.5 mM: (i) F9; (j) D5; (k) C4; (l) F10. Scale bars: 200 nm.

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4 This shift is more pronounced for the higher order plasmon mode peak in agreement  
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7 with the significant increase of the nanoplate edge length (from  $54 \pm 4$  nm for  
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10  $[\text{Au}^{3+}] = 0.5\text{mM}$  to  $180 \pm 7$  nm for  $[\text{Au}^{3+}] = 2.5\text{mM}$ ) compared to the moderate growth of  
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12  
13 the spheroidal nanocrystals (from  $46 \pm 2$  nm to  $78 \pm 3$  nm) and the quasi negligible  
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16 thickening of the nanoplates (Figs. S8c,d). Indeed, at the lowest concentrations, the in-  
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19 plane size of the nanoplates is similar to the diameter of the decahedra and icosahedra  
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22 (Figs. 5a). However, as  $[\text{Au}^{3+}]$  increases, the overall increase of mean size and size  
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25 spread is predominantly ascribed to the lateral growth of the nanoplate subpopulation,  
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28 with an in-plane size reaching ca. 3-4 times the spheroidal diameter at  $[\text{Au}^{3+}] = 3.5\text{mM}$   
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31 (Fig. 5d). This further illustrates that the (111) growth inhibition by the proteins does not  
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34 apply to other crystallographic directions, like (100) and (110). Very similar results,  
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37 albeit with specific nanocrystal size distributions, were obtained for several of the  
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40 selected proteins: F9, D5, C4 and F10 as shown, for  $[\text{Au}^{3+}] = 2.5\text{mM}$ , in Figures 5i to 5l  
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42  
43 respectively. Contrary to previous studies<sup>20-21, 53</sup> where pH and temperature are  
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46 commonly used to control the shape and yield of nanocrystal morphosynthesis, these  
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49 parameters have no marked influence on the growth process (see sections S9 and S10  
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4 in Supporting Information), which indicates that our approach is predominantly  
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7 determined by the effective design of the protein-gold interactions.  
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11 **Structural and interfacial characterization of the protein-coated (111)-faceted**  
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13 **nanocrystals.** Remarkably, at elevated temperatures ( $T > 37^{\circ}\text{C}$ ), basal stacking of  
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15 nanoplates is observed suggesting an inter-particle assembly process mediated by  
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17 interactions between proteins strongly tethered to the basal surfaces.<sup>54</sup> Since the direct  
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19 evidence of robust protein attachment to the nanocrystal surface is challenging for low  
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21 molecular weight proteins like  $\alpha\text{Rep}$ 's ( $\sim 12 - 42$  kDa), we have performed a series of  
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23 analysis of the  $\alpha\text{Rep}$ -gold interface, which are gathered in Figure 6. Proteolytic  
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25 trypsinization of G8-coated gold nanocrystals was conducted by addition of  $20\ \mu\text{M}$   
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27 trypsin in  $0.01\ \text{M}$  phosphate buffer at pH 8 (Fig. 6a). The originally clear red solution  
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29 (tube 1) rapidly turns grey with the appearance of a small black precipitate (tube 2) as  
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31 the proteins are degraded. This correlates to the complete disappearance of the  $530\ \text{nm}$   
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33 plasmon peak in the absorbance spectrum. Non-contact AFM (nc-AFM) was performed  
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35 in ultrahigh vacuum (UHV) on individual nanoplates deposited onto smooth silica  
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substrate (Figs. 6b-d). This AFM mode is used for atomic resolution imaging and it ensures that the proteins are not distorted during the raster scanning of the tip.



**Figure 6: Chemical analysis of the  $\alpha$ Rep-Au interface on the surface of the G8-coated nanocrystals.** (a) Trypsinization test on G8-capped nanocrystals monitored by UV-visible spectrometry. Sample in tube1 consists in stable nanocrystals produced with G8 that show a clear plasmon resonance at 520 nm (spectrum 1). In tube 2, trypsin is used to degrade the protein shell resulting in nanocrystal aggregation and the disappearance of the resonance peak (spectrum 2). (b, c) nc-AFM images of (b) G8-capped and (c) O<sub>2</sub> plasma cleaned nanoplates. The black squares indicate the areas zoomed in the right panels. Scale bars are 100 nm and 6 nm for the left and right panels respectively. (d) nc-AFM height profiles of the G8-coated triangular nanoprism (red) and of the plasma-

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4 cleaned hexagonal nanoprisms (black) shown in (b) and (c) respectively. (e) EELS  
5 spectra taken from three locations in the TEM image of streptavidinylated G8-capped  
6 nanocrystals shown in inset. The background spectrum (green) shows only the carbon  
7 peak. The blue spectrum taken at the center of a Au nanocrystal shows a large uniform  
8 background due to a very low energy Au peak located out of the spectral window. The  
9 red spectrum recorded tangentially to the nanocrystal reveals the presence of Nitrogen,  
10 Carbon, and Calcium. Note that the Ca signal is ascribed from the calcium-based  
11 purification method of commercial streptavidin. Scale bar in inset is 200 nm. (f) STEM  
12 image and (g-i) corresponding EDS maps showing elemental distribution of (g) gold (h)  
13 carbon (i) nitrogen. Scale bar in (f) is 400 nm.

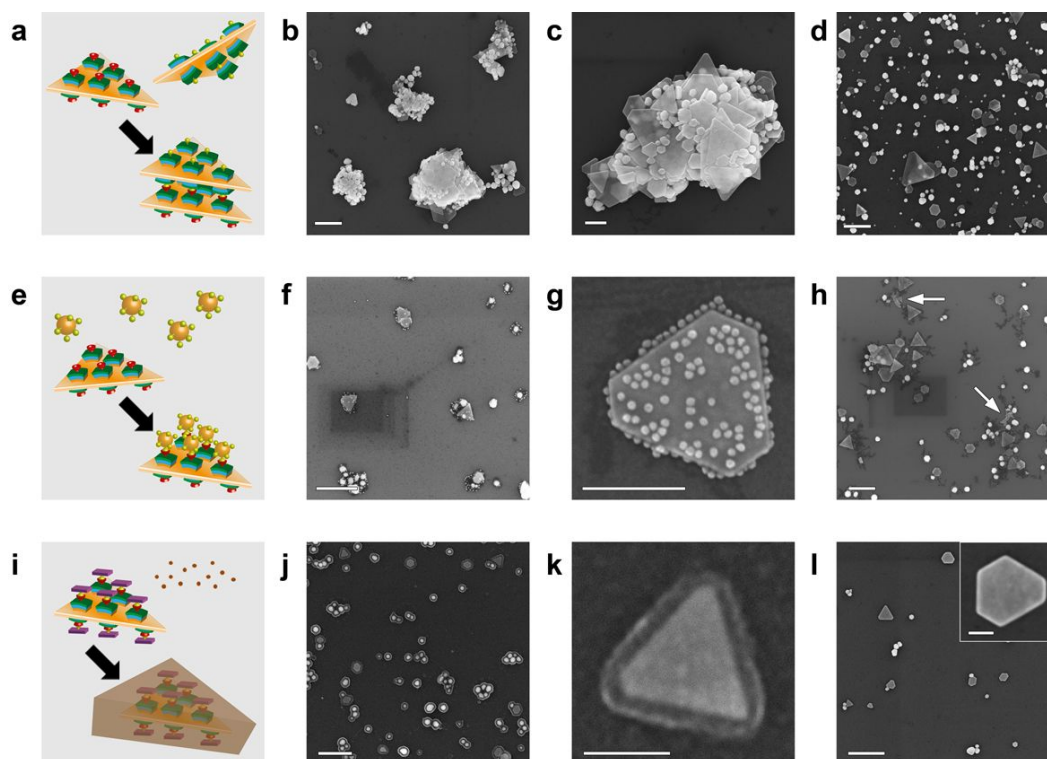
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22 When performed on the as-synthesized nanoplates, a uniform surface is observed  
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24 which is constellated with globular objects of typical lateral sizes of 5-15 nm (Fig. 6b)  
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26 and a height corrugation of about 5-7 Å (Fig. 6d, red line). This is consistent with an  
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28 irregular protein coating surface. The sample was then treated with a r.t. O<sub>2</sub> plasma to  
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30 remove all organic adsorbates and re-introduced in UHV, outgassed for 24 h before  
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32 resuming nc-AFM imaging (Fig. 6c). The apparent total height of the nanoplates is  
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34 about 5 nm smaller after plasma cleaning, which is consistent with the removal of the  
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36 protein capping layer. Moreover, the upper surface is extremely smooth (Fig. 6c) with a  
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38 corrugation reduced down to 1-1.5 Å, which corresponds to atomically flat Au terraces  
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40 (Fig. 6d, black line). Similar samples drop-casted onto electron microscopy grids were  
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3 analyzed by electron energy loss spectroscopy (EELS) in the 250-450 eV energy loss  
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7 window as shown in Fig. 6e. The EELS signal from the core of the nanocrystals (cyan  
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10 spot and line) is dominated by the tail-off of the low energy peak of gold. However,  
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14 spectra recorded just on the edge of the nanocrystal (red spot and line) reveal the  
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17 peaks associated to carbon and nitrogen loss energies, as expected from a thin protein  
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20 coating. The supporting carbon film (green spot and line) only accounts for a small  
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24 fraction of the carbon signal, which can be predominantly ascribed to the proteins.  
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28 Finally, STEM/EDS elemental analysis performed on nanocrystals drop-casted onto  
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31 ultrathin SiO<sub>2</sub> membranes are shown in Figures 6f-i and S11. The gold (Fig. 6g), carbon  
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34 (Fig. 6h) and nitrogen (Fig. 6i) EDS maps perfectly match the STEM image with very  
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38 little background signal. Taken together, these analyses clearly demonstrate that the  
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42 nanocrystals are coated by proteins which remain on the surface after the  
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46 morphosynthesis and purification steps. We expect the hyper-variable side, which is the  
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50 only one able to discriminate the Au(111) surface during the selection process, to be  
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54 strongly interacting with the nanocrystal surface and thus probably exposing the non-  
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60 variable backside of the proteins to the surrounding medium.

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3 **Versatile functionalization of the  $\alpha$ Rep-coated nanocrystals.** To fully exploit the  
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7 potential of these protein-coated nanoparticles, we use the displayed  $\alpha$ Reps as  
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10 modules to directly integrate functional bioactive elements onto anisotropic nanocrystals  
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13 without resorting to tedious ligand exchange procedures.<sup>35</sup> One first option is to  
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16 incorporate a secondary streptavidin (STV) layer through biotinylation of the Lys  
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19 residues present in the exposed  $\alpha$ Rep backside via the standard NHS-NH<sub>2</sub> coupling  
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22 method. This streptavidinylation of  $\alpha$ Rep offers a versatile platform to confer the gold  
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25 nanocrystals with targeted self-assembly and catalysis functionalities. The feasibility of  
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28 this approach is demonstrated in Figures 7a-c where streptavidinylated  $\alpha$ Rep gold  
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31 nanocrystals are coupled to NHS-biotin modified  $\alpha$ Rep gold nanocrystals resulting in  
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34 large 3D self-assemblies mostly driven by the face-to-face stacking of the nanoplates by  
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37 streptavidin-biotin recognition. Beyond this direct basal stacking, a detailed examination  
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40 of micrographs suggests that the platonic nanostructures, which probably exhibit  
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43 accessible biotin and streptavidin molecules on all facets, also contribute to the  
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46 crosslinking of the large assemblies and are often found inserted between nanoplates.  
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49 UV-visible spectroscopy monitoring on equimolar mixtures of streptavidinylated and  
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4 biotinylated gold nanocrystals shows a marked decrease of the plasmon resonance  
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7 peak and suggests that self-assembly occurs in solution. In the absence of biotin (bn)  
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10 on the second partner, the nanocrystals remain isolated from each other and no  
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13 aggregation is observed (Fig. 7d). This first scheme demonstrates that fully functional  
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16  $\alpha$ Rep proteins are present on the (111) facets of nanocrystals where they can be freely  
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21 coupled to other biomolecules to create patch antenna-like stacks.<sup>55</sup>  
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52 **Figure 7: Functional surface derivatization of  $\alpha$ Rep protein coated nanocrystals. (a)**  
53 **Scheme and (b, c) SEM images of basal stacking of G8-capped Au nanocrystals**  
54 **obtained by self-assembly between streptavidinylated and biotinylated nanocrystals. (d)**  
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4 Control experiment in absence of biotin shows no stacking. **(e)** Scheme and **(f, g)** SEM  
5 images of core-satellite hybrid assemblies obtained by combining streptavidinylated G8  
6 nanocrystals and biotin-PEG Au nanospheres which results in the decoration of the top  
7 and bottom prism facets by the nanospheres. **(h)** Control experiment with non-  
8 streptavidinylated G8-capped Au nanocrystals. No satellite is observed even though  
9 segregated nanosphere clumps can be found (white arrows). **(i)** Scheme and **(j, k)** SEM  
10 images of on-surface DAB catalysis by HRP-Biotin tagged streptavidinylated G8  
11 nanocrystals results in a uniformly wrapping polymer corona. **(l)** Control experiment run  
12 with simply streptavidinylated nanocrystal in the absence of HRP. No polymer capping  
13 layer as shown also in the inset. Scale bars are (b, d, f, h, j, l) 500 nm, (c, g) 200 nm, (k)  
14 100 nm and inset of (l) 50 nm.  
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28 Replacing the biotinylated nanoplates by PEG-biotin functionalized 30-nm gold  
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31 nanospheres leads to core-satellite assemblies as shown in Figures 7e-g and Fig. S12.  
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35 Such structures have been predicted to modulate the native spatial and spectral  
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38 plasmonic properties of the core nanoplates.<sup>19, 56</sup> The decoration of the nanoplates by  
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41 the nanospheres occurs preferentially on both basal (111) facets but structure with a  
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44 core decahedron or icosahedron are also easily identified. No core-satellite structure is  
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47 formed upon incubation of streptavidinylated  $\alpha$ Rep gold nanocrystals with non-  
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52 biotinylated nanospheres, which remains randomly segregated (Fig. 7h, white arrows).  
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4 Finally, we have converted the streptavidinylated  $\alpha$ Rep gold nanocrystals into catalytic  
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7 nano-platforms by adding a tertiary layer of biotin-HRP enzyme (Fig. 7i-k). HRP  
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10 catalyzes the oxidation of benzidines to form water insoluble polymer aggregates. Here,  
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13 we show that the HRP-tagged gold nanocrystals trigger the polymerization of 1 mM 3,3'-  
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16 diaminobenzidine (DAB), in the presence of  $H_2O_2$ .<sup>57</sup> Since the catalytic reaction occurs  
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18  
19 locally at the nanocrystal surface, a uniform layer of polymerized DAB is grown around  
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21  
22 the nanocrystals as seen in Fig. 7j,k and Figs. S13a,b. The thickness can be adjusted  
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24  
25 by the amount of DAB or the reaction time and is about 25 nm in the displayed sample.  
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31 When simply streptavidinylated  $\alpha$ Rep gold nanocrystals are used, no polymerization  
32  
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34 reaction takes place and the surface of the nanostructures remains free of polymer  
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37 over-coating (Fig. 7l). This form of catalysis reflects the stability of the  
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41 Au /  $\alpha$ Rep /enzyme construction as no side polymer particles were found in the sample,  
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44 away from the nanocrystals as it should have been expected if HRP had been grafted to  
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48  $\alpha$ Rep loosely bound to the Au surface. The local production of polymer near plasmonic  
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51 structures allows to tune the local dielectric constant, to envision embedding more  
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55 complex optically active moieties<sup>58</sup> and could be harnessed for sensing applications.<sup>59</sup>  
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## Conclusions

The design and combinatorial selection of fully folded artificial proteins is applied here for the first time to the construction of crystal habit modifiers able to shape noble metals such as gold at the nanoscale. Nine new Au(111) binding proteins have been isolated, sequenced, mass produced and used as habit modifiers in a gold nanocrystal seeded growth synthesis. All proteins demonstrated a high chemical affinity for gold and structural selectivity for (111) facets, which result in an effective morphosynthetic action yielding > 85% of (111)-terminated Au nanoplates, icosahedra and decahedra. The thin nanoplate size could be tuned up to 500 nm that requires the recruitment of thousands of proteins per crystalline facet. The detailed structural characterization of the nanocrystals has established the crystalline structure of the gold nanoparticles and the functional activity of the capping protein layer. We further demonstrated the benefit of the artificial protein coating by derivatizing them with streptavidin, biotin and HRP enzyme therefore incorporating extra surface functionalities such as self-assembling or on-surface catalytic capabilities. Our approach presents several assets compared to the

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3 design of gold-binding peptides or antibodies fragments and hence offers a promising  
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7 generic tool for the rational morphosynthesis of high-index facet nanocrystals with  
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10 superior biocompatibility and versatile *in-situ* construction of (bio)molecular platforms at  
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13 the solid interface, which could be capitalized towards plasmon-based optical devices<sup>51</sup>,  
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17 <sup>55</sup> and (bio-) molecular sensing applications <sup>60-62</sup> on individual or 2D/3D arrayed  
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21 nanoparticles.<sup>35</sup>  
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## Methods

**Selection of Au(111)-binding  $\alpha$ Rep proteins.**  $\alpha$ Rep proteins exhibiting binding affinity to Au(111) coated mica substrate are selected by phage display. Typically, (111)-oriented Au films are produced by thermal evaporation on freshly cleaved mica slides according to a well-established procedure. The protein library 2.1 comprising  $1.7 \times 10^9$  variants of  $\alpha$ Rep proteins fused with phage coat protein pIII is exposed to the Au(111) film at pH 7.5 and room temperature (r. t.).<sup>34</sup> Phages from the library are loaded on a 96-well Elisa plate exposing the Au(111) surface using the MicroArrayIt system ([www.arrayit.com](http://www.arrayit.com)) and incubated for 2 h at 20°C and 300 rpm. Non-specific phages are removed by ten TBS 0.05% Tween 20 and ten TBS washing steps. Bound phages are eluted in a glycine solution (0.1 M pH 2.5) for 10 min at 20°C and recovered by infecting a suspension of growing XL1blue MRF' bacteria. This selection round is performed 3 times. 96 clones are analyzed by ELISA Soluble bacterial extracts are incubated on the Au(111) film and specific binding is revealed by an antitag-tag HRP-antibody. 18 positive hits from the ELISA test were sequenced and 9 different  $\alpha$ Reps were identified

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3 and labelled A12, C4, D5, D7, F2, F5, F9, F10, G8. The expression and purification of  
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7 these proteins is performed according to a standard procedure detailed in  
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10 Supplementary Information.

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13 **Surface Plasmon Resonance (SPR) analysis.** SPR data are recorded using the  
14  
15 ProteOn XPR36 (Bio-rad).  $\alpha$ Rep proteins are immobilized on HTG ProteOn sensor  
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18 chips until reaching a response signal around 200 RU in 10 mM phosphate buffer pH  
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21  
22 7.5, 137 mM KCl, 2.7 mM KCl and 0.005% Tween 20. Interactions are recorded at a  
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29 100  $\mu$ L/min flow rate and a 120 s contact time followed by a dissociation of 600 s with  
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32 citrate stabilized 5-nm diameter gold nanoparticles at different concentrations (10, 5,  
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36 2.5, 1.25 and 0.625 nM). The interspot signal is removed from the sensograms.

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40  **$\alpha$ Rep stabilized Au seed synthesis.** 50  $\mu$ l of 20  $\mu$ M  $\alpha$ Rep protein solution in 0.1 M  
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43 phosphate buffer (pH 7.5) is mixed with 10  $\mu$ l aqueous solution of 20 mM sodium  
44  
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46  
47 formaldehyde sulfoxylate at r. t.. This solution is immediately injected into 100  $\mu$ l of  
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51 2 mM HAuCl<sub>4</sub> solution under vigorous stirring at 900 rpm at r. t.. After stirring for 2 min,  
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3 the resulting red solution is left to grow for 2 hours until full completion of the reduction  
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7 process. The seed solution is stored at 4°C.  
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11  **$\alpha$ Rep mediated seeded growth of nanocrystals.** The growth of  $\alpha$ Rep capped Au  
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15 nanocrystals is performed by adapting the hydroxylamine reduction method.<sup>46</sup> Briefly,  
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18 2.5  $\mu$ l Au seeds are mixed with 20  $\mu$ l of 100  $\mu$ M  $\alpha$ Rep protein solution (0.1 M phosphate  
19  
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21 buffer, pH 7.5) and diluted to a final volume of 245  $\mu$ l with MilliQ water. Concomitantly,  
22  
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25 5  $\mu$ l of freshly prepared 200 mM hydroxylamine hydrochloride is injected to the seed  
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29 and  $\alpha$ Rep solution. The resulting solution is promptly injected to a series of 250  $\mu$ l  
30  
31  
32 H<sub>2</sub>AuCl<sub>4</sub> solutions with final [Au<sup>3+</sup>] concentrations of 1 mM, 2 mM and 5 mM. The pH  
33  
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36 value of the reaction mixture is adjusted to the desired values by adding aliquots of  
37  
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39 0.1 M HCl or NaOH solutions. The final reaction volume is homogenized by stirred at  
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43 900 rpm for 2 min, followed by incubation at r. t. for 2 h. After synthesis, the final  
44  
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47 products are washed 4 times by centrifugation at 8000 rpm for 5 min and re-suspended  
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49  
50 in 1 mL MilliQ water in order to remove the uncoordinated  $\alpha$ Rep proteins.  
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3 **Structural characterization of as-synthesized gold nanocrystals.** Absorbance of as-  
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7 synthesized gold nanocrystals is recorded on a Cary-5000 UV–vis NIR  
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10 spectrophotometer in the range 200–1200 nm and at 600 nm/min scan rate. Structural  
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13 analyses of the nanocrystals are carried out by scanning electron microscopy (SEM),  
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16 transmission electron microscopy (TEM), selected area electron diffraction (SAED) and  
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19 atomic force microscopy (AFM). Samples for SEM and AFM analyses are prepared by  
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21  
22 drop casting 20  $\mu$ L of the nanocrystal suspension in milliQ water on an oxide-coated  
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27 silicon wafer followed by overnight drying in air. FEG-SEM images are recorded on a  
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30  
31 Zeiss 1540XB system operated at 20 kV. Tapping mode AFM is conducted using a  
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33  
34 Bruker Dimension 3000 microscope. Extra topological information of the corrugation of  
35  
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37 the flat prismatic nanocrystals is obtained from non-contact AFM (nc-AFM) imaging in  
38  
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40  
41 ultrahigh vacuum (UHV).<sup>63</sup> The samples are introduced in a Scienta Omicron  
42  
43  
44 Nanotechnology UHV-STM/nc-AFM microscope and probed with Pt-Ir coated silicon  
45  
46  
47 cantilevers (Nanosensors PPP-QNCHR) at 280-300 kHz resonance frequency and  
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49  
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52 quality factors of 32000-40000. With an overall oscillation amplitude fixed at 5 nm, this  
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56 attractive mode obviates protein distortion under the AFM tip and so provides accurate  
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3 height measurements and sub-molecular resolution on organic molecules.<sup>64</sup> Bright field  
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7 TEM and SAED analyses are conducted on a Philips CM20FEG TEM operated at  
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10 200 kV accelerating voltage and equipped with a Gatan CCD camera and Digital  
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12  
13 Micrograph acquisition software. Size and shape distribution analyses of the electron  
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17 micrographs are performed by ImageJ software. Electron energy loss spectroscopy  
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20 (EELS) is carried out in a Hitachi HF3300 microscope equipped with a GIF (Gatan  
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23 Imaging Filter) Quantum. STEM-EDS was performed in a Phillips CM20FEG equipped  
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27 with a Brücker SDD detector. Samples for TEM are prepared by drop-casting and air-  
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31 drying a 10  $\mu$ L droplet of aqueous suspension onto 300 mesh carbon film copper grids,  
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35 for TEM, SAED and EELS, or 10 nm thick SiO<sub>2</sub> membranes, for STEM-EDX.  
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39 **Streptavidinylation of  $\alpha$ Rep capped nanocrystals.** To integrate streptavidin to  $\alpha$ Rep-  
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41  
42 capped gold nanocrystals, the lysine residues present in the  $\alpha$ Rep backbone are  
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45  
46 biotinylated. 500  $\mu$ l of as-synthesized and washed gold nanocrystals are mixed with  
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50 20  $\mu$ l of 2 mg/ml NHS-biotin dissolved in DMF and incubated at r. t. for 2 hours.  
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54 Following incubation, the biotinylated gold nanocrystals are washed four times with a  
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3 0.01% Tween 20 solution adjusted at pH 7 to remove free NHS-biotin molecules and re-  
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7 suspended in PBST solution. 50  $\mu$ l of 1 mg/ml Streptavidin solution is added to the  
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9  
10 biotinylated,  $\alpha$ Rep-capped gold nanocrystals. The suspension is incubated at r. t. for 3  
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14 hours and subsequently washed 4 times with a 0.01% Tween 20 solution adjusted at  
15  
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17 pH 7. The streptavidin-coupled gold nanocrystals assemblies are stored at 4°C.  
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22 **Synthesis and PEGylation of 15-nm citrate stabilized Au nanospheres.** Citrate  
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25 stabilised gold nanospheres (AuNP) are synthesised using Turkevich's method.<sup>65</sup>  
26  
27  
28 Briefly, 20 ml of 0.25 mM HAuCl<sub>4</sub> solution is heated to boiling point prior to the rapid  
29  
30  
31  
32 addition of 120  $\mu$ l of a 50 mg/ml sodium citrate solution under vigorous stirring. The  
33  
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36 solution is continuously stirred for 30 min, until it turns to ruby red. The AuNP  
37  
38  
39 suspension is allowed to cool down at RT over 4 hours. 2 ml of AuNP suspension are  
40  
41  
42  
43 centrifuged at 14,500 rpm for 15 min. The supernatant is discarded and the pellet is re-  
44  
45  
46  
47 suspended in 500  $\mu$ l of a 2 mg/ml biotin-PEG-SH solution and incubated for 6 h.  
48  
49  
50 PEGylated AuNP are washed eight times with MilliQ water at 14,500 rpm for 15 min  
51  
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54 and, finally, re-suspended in 100  $\mu$ l MilliQ water before storage at 4°C.  
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3 **Peroxidase-catalyzed 3,3' diaminobenzidine polymerization.** A 2 mg/ml solution of  
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7 horseradish peroxidase (HRP) in PBS buffer is mixed with 20  $\mu$ l of a 2 mg/ml NHS-biotin  
8  
9  
10 dissolved in DMF. Biotinylation of HRP is allowed to proceed for 2 h. Excess NHS-biotin  
11  
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14 is removed by passing the solution through a Zepa spin desalting column  
15  
16  
17 (ThermoFisher Scientific). Next, 500  $\mu$ l of streptavidinylated,  $\alpha$ Rep-capped gold  
18  
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20 nanocrystals are reacted with biotinylated HRP enzyme at RT for 2 h. The HRP-coupled  
21  
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23  
24 gold nanocrystals are washed four times at 8,000 rpm for 5 min with a 0.01% Tween 20  
25  
26  
27  
28 solution adjusted at pH 7 to eliminate unconjugated biotin-HRP. 5  $\mu$ l of HRP-gold  
29  
30  
31 nanocrystals are drop-casted on silicon substrates and allowed to dry for 3 hrs.  
32  
33  
34  
35 Enzyme-catalyzed polymerisation and precipitation (ECP)<sup>66</sup> of 3,3'-diaminobenzidine  
36  
37  
38 (DAB) is triggered locally by drop-casting 30  $\mu$ l of a freshly prepared 1 mM aqueous  
39  
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41  
42 solution of DAB on top of the silicon-immobilized HRP-gold nanocrystals, in the  
43  
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45 presence of 5  $\mu$ l 30%w/w H<sub>2</sub>O<sub>2</sub> solution. The DAB polymerization reaction by HRP is  
46  
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49 allowed to proceed for 3 h. Finally, the silicon substrate is washed 6 times with 100  $\mu$ l of  
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52 MilliQ water and air dried.  
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## ASSOCIATED CONTENT

### Supporting Information.

The following files are available free of charge. Materials and Methods. Screening and biochemical characterization of  $\alpha$ Rep (Fig. S1). Determination of Au(111)] binding affinities (Figs. S2a-d). TEM and gel electrophoresis on AU seeds (Fig. S3). Two-stage seeded growth details (Fig. S4). SEM characterization of  $\alpha$ Rep coated Au nanocrystals (Fig. S5). UV-visible spectral characterization (Fig. S6). Control experiments with non-selected  $\alpha$ Rep (Fig. S7). Au nanocrystal size tenability (Fig.S8). Effect of pH (Fig; S9) and temperature (Fig. S10). Chemical analysis of G8-capped nanocrystals (Fig.S11). SEM images of core-satellite self-assembled nanostructures (Fig.S12). SEM images of in-situ DAB encapsulated Au nanocrystals (Fig.S13a,b). (PDF)

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## Author Contributions

E.D. and P.M. conceived the initial ideas. P. M. A.U., M.V.L. and S.V. designed the  $\alpha$ Rep protein library and proceeded to phage display library selection with the contribution of A.F.  $\alpha$ Rep proteins were produced and characterized by S.V., A.U. and M.L.V. SPR characterization was performed by S.V, and A. U. and interpreted by J.P., S.V., P.M and E.D. Morphosynthesis and further functionalization experiments were designed and performed by E.D. J.P., K.L.G. and A.F. J. P., C.M. and B. B. performed sample analysis by TEM/EDX/EELS and nc-AFM. J.P., S. V., P. M. and E. D drafted the paper. All authors discussed the results and contributed to the manuscript.

‡These authors contributed equally.

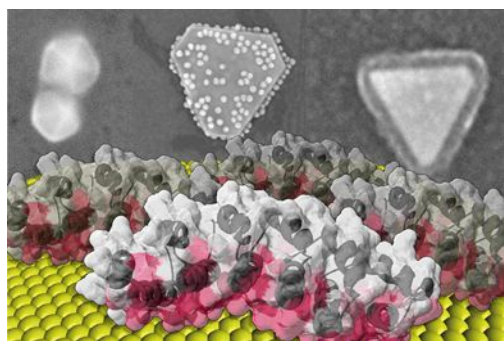
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8  
9  
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4 **Table of Content illustration**  
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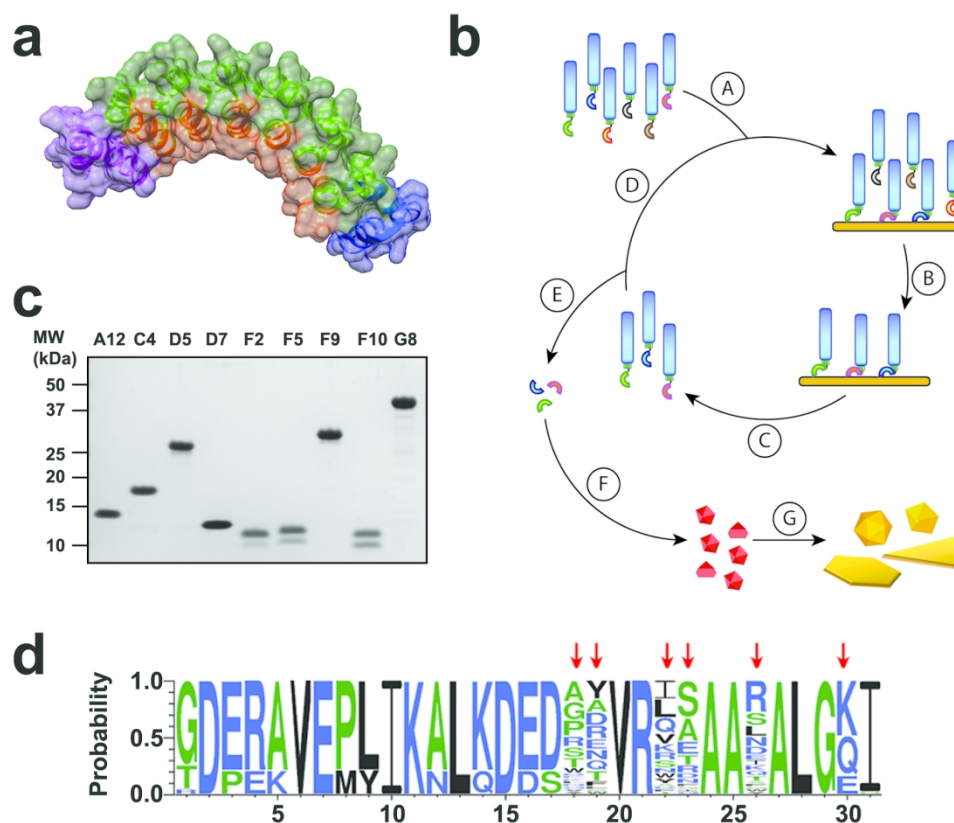
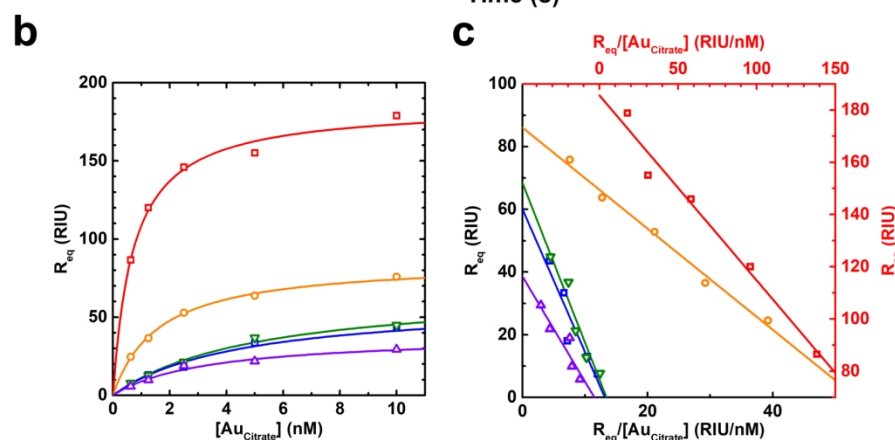
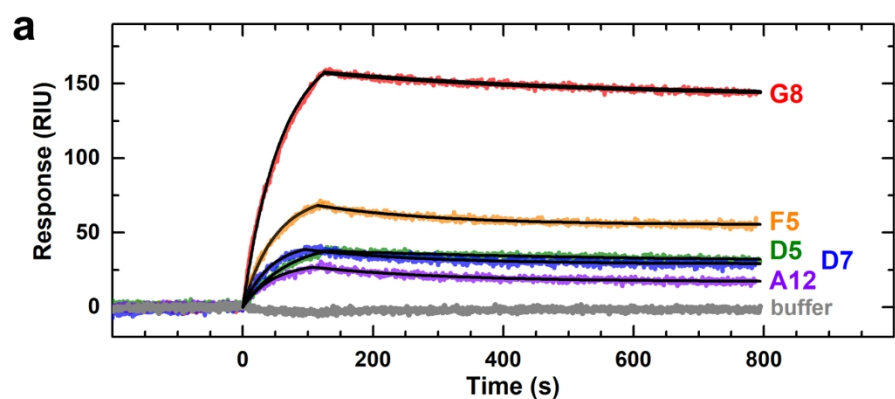


Figure 1. Construction and directed evolution of Au(111)-binding artificial repeat proteins. (a) 3D representation of the crystallographic structure of a 4-repeat aRep protein depicting the internal repeats comprising the hypervariable positions (brown) with their conserved scaffold regions (green), N- and C-cap (blue). (b) Schematic flowchart showing the phage display design and selection of aRep's (A-D) and the □Rep directed Au nanocrystal morphosynthesis (I-J) process. These steps involve: (A) Construction of the phage display library; (B) □Rep selection on planar Au(111) substrate on mica and elution of unbound phage at pH5; (D) acid elution of Au-bound phages and bacterial amplification of selected phages (E) proteolytic isolation of aRep from phage body and large scale production. The morphosynthesis of Au nanocrystals by seeded growth process comprises: (F) aRep directed Au seed synthesis; (G) nanocrystal growth in the presence of excess aRep through hydroxylamine-mediated disproportionation mechanism. (c) Coomassie blue stained SDS-PAGE profiles of 9 different Au(111)-selected □Rep after cleavage digestion. The position of the major bands represents the molecular weight of respective aRep. (d) Sequence logo obtained by multi-alignment of the sequences of all the repeats from the selected aRep, including those of the N-cap that have the same second helix as the internal repeats, hence the apparent variability observed in positions (1,3,4,8,9,12,14,17). The binding hypervariable surface is generated by the position indicated by red arrows.





**d**

Immobilised $\alpha$ -Rep	$k_{on}$ ( $10^6 M^{-1} s^{-1}$ ) (#1)	$k_{off}$ ( $10^{-3} s^{-1}$ ) (#1)	$k_{off}$ ( $10^{-3} s^{-1}$ ) (#2)	$K_D$ (nM) (#1)	$K_D$ (nM) (#2)	$K_D$ (nM) (#3)
G8	$1.6 \pm 0.4$	$2.7 \pm 1.8$	$2.9 \pm 0.02$	$1.7 \pm 1.55$	$1.8 \pm 0.47$	$0.71 \pm 0.06$
F5	$1.5 \pm 0.3$	$6.4 \pm 1.5$	$5.7 \pm 0.07$	$4.3 \pm 1.85$	$3.8 \pm 0.81$	$1.61 \pm 0.09$
A12	$1.6 \pm 0.5$	$8.2 \pm 2.8$	$5.1 \pm 0.08$	$5.1 \pm 3.35$	$3.2 \pm 1.05$	$3.36 \pm 0.75$
D7	$2.1 \pm 0.3$	$3.7 \pm 1.8$	$5.0 \pm 0.11$	$1.8 \pm 1.11$	$2.4 \pm 0.39$	$4.56 \pm 1.01$
D5	$0.9 \pm 0.2$	$6.3 \pm 1.3$	$3.3 \pm 0.05$	$7.3 \pm 3.00$	$3.7 \pm 0.57$	$5.10 \pm 0.80$

Figure 2. Gold affinity of the selected anti-Au(111) repeat proteins. (a) SPR sensograms during adsorption and desorption phases monitoring the interactions between immobilized  $\alpha$ Rep proteins (see labels) and citrate-stabilized Au nanoparticles ( $[Au_{cit}] = 10$  nM). Solid black lines are exponential fits to the association and dissociation phases. The exponent of the association fits provides the association ( $k_{ON}$ ) and dissociation ( $k_{OFF}$  #1) kinetic constants tabulated in (d). The dissociation phase fits provide the  $k_{OFF}$  #2 kinetic constant in Table (d). Each protein data is associated to the same color throughout the figure. (b) SPR equilibrium analysis along with Langmuir fits (continuous lines). (c) Scatchard plot for the empirical estimation of the dissociation constants labelled  $K_D$  #3 which is obtained from the slopes of the linear fits. G8 data (red) are plotted on the red x-y axis while all other data share the black x-y axis. (d) Summary table of all association ( $k_{ON}$ ) and dissociation ( $k_{OFF}$  #1 and  $k_{OFF}$  #2) alongside the dissociation constant ( $K_D$ ) values obtained from the ratio of kinetic constants ( $K_D$  #1 =  $k_{OFF}$  #1 /  $k_{ON}$ ,  $K_D$  #2 =  $k_{OFF}$  #2 /  $k_{ON}$ ) and from the Scatchard plot ( $K_D$  #3).

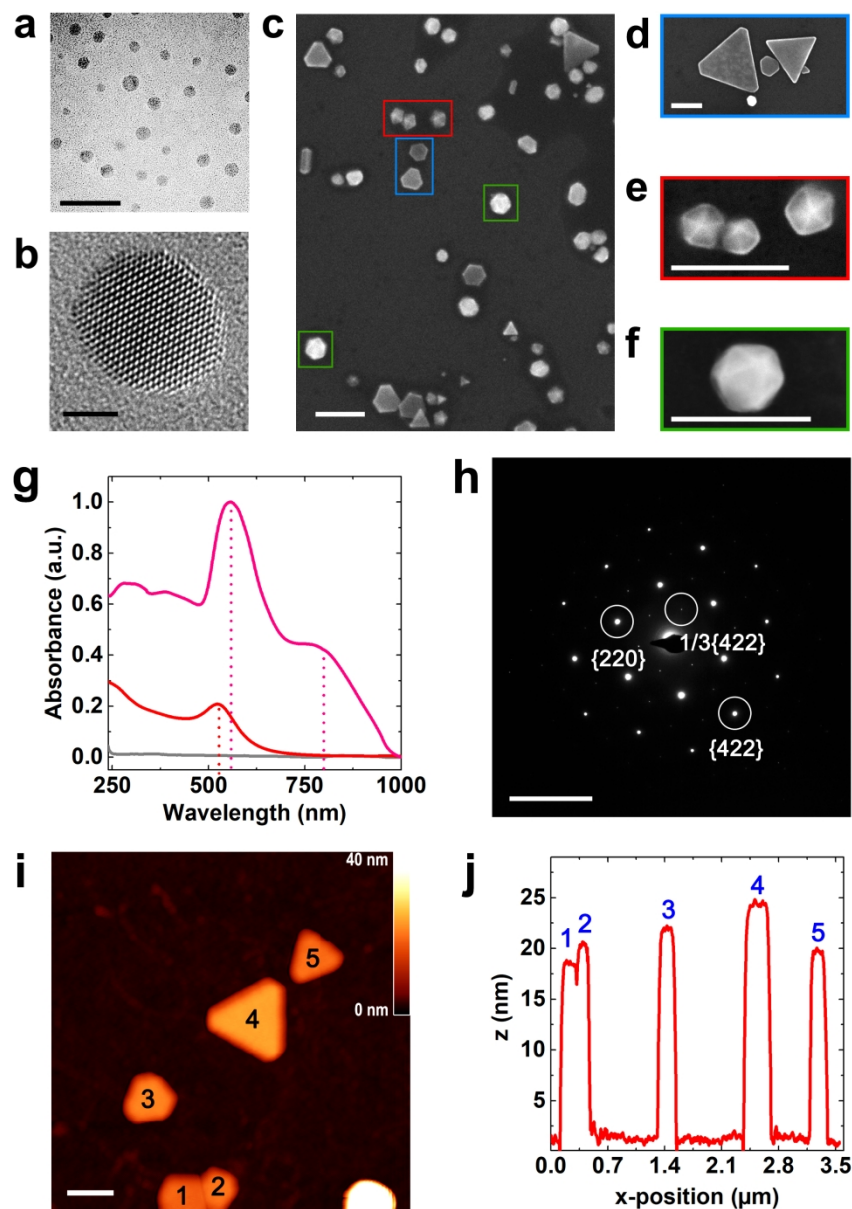


Figure 3. Morphological and structural characterization of aRep-coated, (111)-terminated Au nanocrystals. (a,b) High resolution TEM of spherical G8-stabilized seeds showing a high degree of crystallinity. The seed in (b) is single crystalline and oriented along the [011] zone axis (c) Representative SEM micrograph of G8-capped, (111)-facet terminated Au nanostructures showing nanoplates (blue box), decahedrons (red box) and icosahedrons (green box) morphologies. (g) Characteristic UV-visible spectra of G8 templated Au seeds (red,  $\lambda_{\text{max}} = 524$  nm), seedless growth solution (grey) and Au nanostructures synthesized by the G8-templated, seeded growth approach (pink), which exhibit two peaks at  $\lambda_{\text{max}} = 556$  nm and  $\lambda_{\text{max}} = 804$  nm. (h) Selected area electron diffraction of an Au nanoplate showing diffraction spots along the [111] zone axis. (i) Tapping mode AFM image of five Au nanoplates. (j) Height profile of the five nanoplates shown in (i), which all have a thickness of  $21 \pm 3$  nm. Scale bars are (a) 20 nm, (b) 2 nm, (c-f, i) 200 nm, (h) 10 nm.

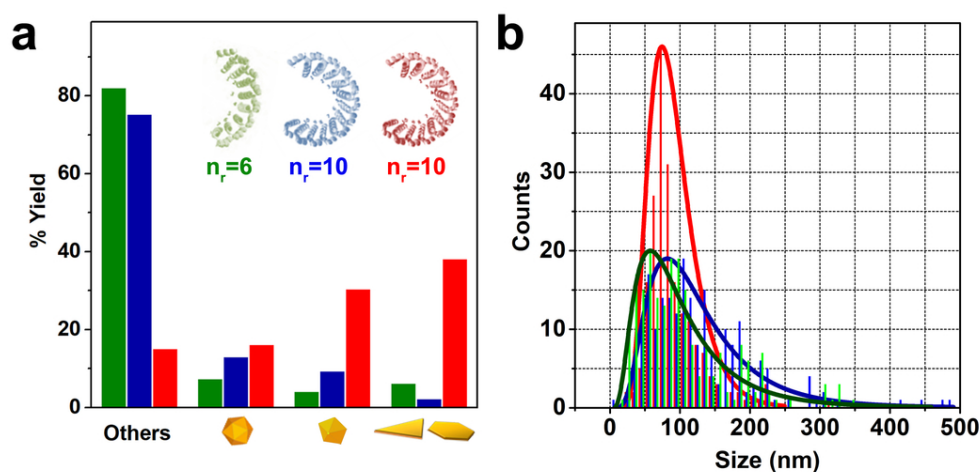


Figure 4: Comparative analysis of nanocrystal shapes and sizes obtained in the presence of control proteins, anti-GFP and N10, or anti-Au(111) G8. (a) Histogram showing the relative occurrence of nanoprisms, decahedra, icosahedra and other shape (spheroidal, and irregular shapes) obtained by morphosynthesis with anti-GFP  $\square$ Rep (green), of consensus sequence N10  $\square$ Rep (blue) and the isomorphous anti-Au(111) G8  $\square$ Rep (red). (b) Size distribution histograms and log-normal fits of as-synthesized nanocrystals with anti-GFP (green), N10 (blue) and G8 (red)  $\square$ Rep proteins (200 measurements for each set).

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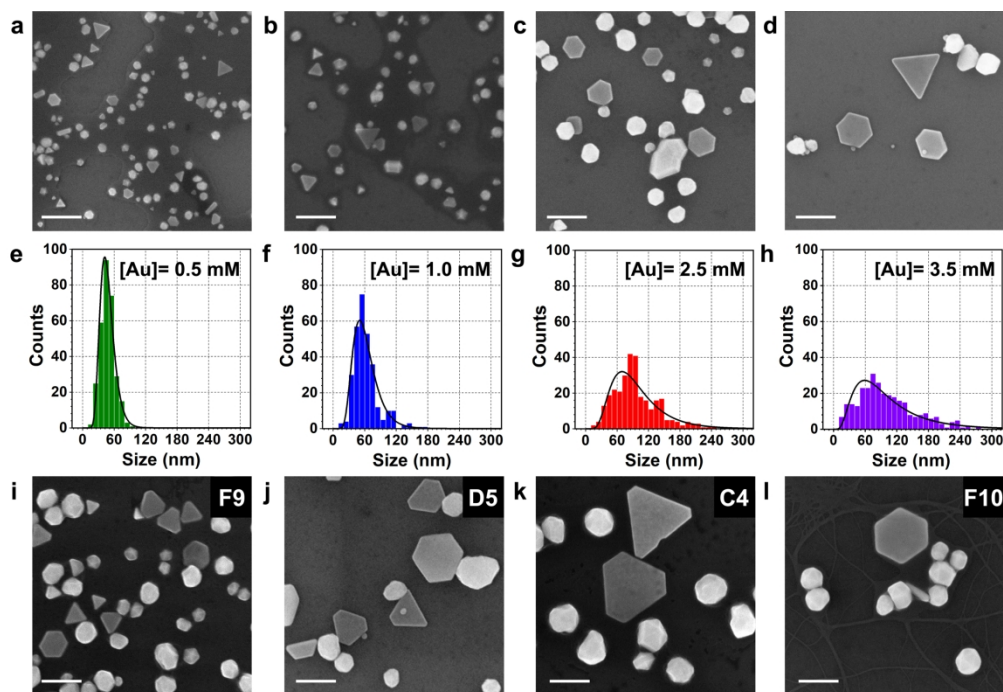


Figure 5: Nanocrystal size adjustment by varying the initial Au<sup>3+</sup> concentration and generalized synthesis with other selected proteins. (a-h) SEM micrographs and nanocrystal size distribution of kinetically controlled G8-capped Au nanostructures for four different Au<sup>3+</sup> concentrations: (a, e) 0.5 mM; (b, f) 1.0 mM; (c, g) 2.5 mM; (d, h) 3.5 mM. The histograms follow lognormal distributions (black lines) with sizes of (e)  $48 \pm 14$  nm, (f)  $62 \pm 24$  nm, (g)  $99 \pm 50$  nm and (h)  $105 \pm 72$  nm. (i-l) SEM micrographs of nanostructures synthesized in the presence of different  $\alpha$ Rep at the same Au<sup>3+</sup> concentration of 2.5 mM: (i) F9; (j) D5; (k) C4; (l) F10. Scale bars: 200 nm.

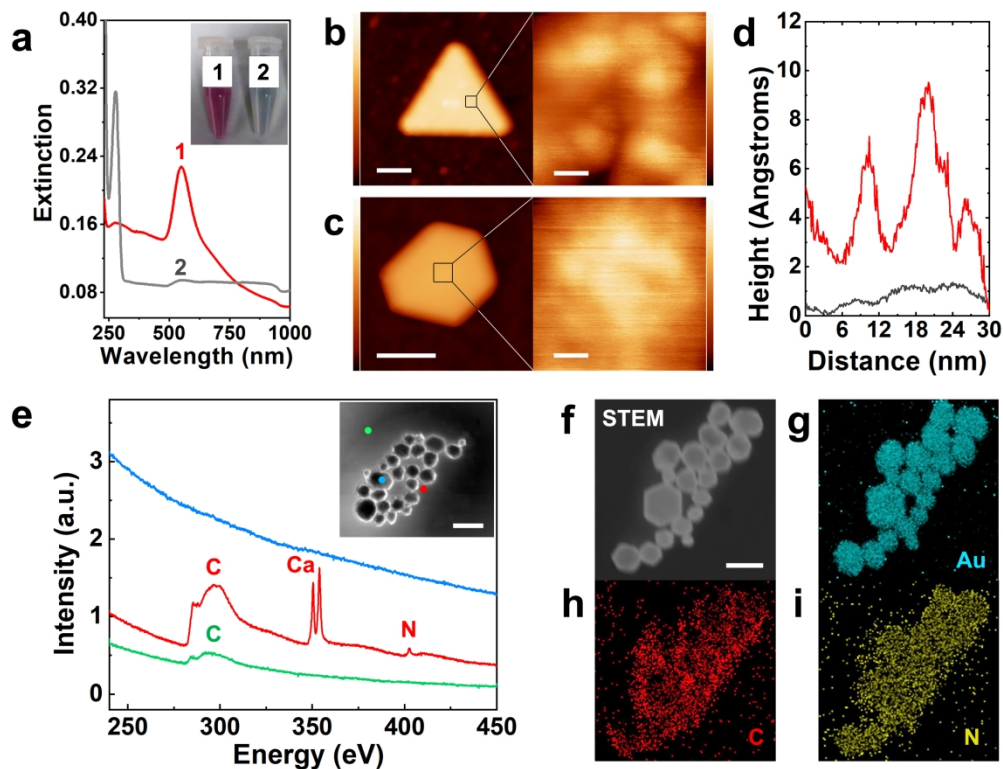


Figure 6: Chemical analysis of the aRep-Au interface on the surface of the G8-coated nanocrystals. (a) Trypsinization test on G8-capped nanocrystals monitored by UV-visible spectrometry. Sample in tube 1 consists in stable nanocrystals produced with G8 that show a clear plasmon resonance at 520 nm (spectrum 1). In tube 2, trypsin is used to degrade the protein shell resulting in nanocrystal aggregation and the disappearance of the resonance peak (spectrum 2). (b, c) nc-AFM images of (b) G8-capped and (c) O<sub>2</sub> plasma cleaned nanoplates. The black squares indicate the areas zoomed in the right panels. Scale bars are 100 nm and 6 nm for the left and right panels respectively. (d) nc-AFM height profiles of the G8-coated triangular nanoprism (red) and of the plasma-cleaned hexagonal nanoprisms (black) shown in (b) and (c) respectively. (e) EELS spectra taken from three locations in the TEM image of streptavidinylated G8-capped nanocrystals shown in inset. The background spectrum (green) shows only the carbon peak. The blue spectrum taken at the center of a Au nanocrystal shows a large uniform background due to a very low energy Au peak located out of the spectral window. The red spectrum recorded tangentially to the nanocrystal reveals the presence of Nitrogen, Carbon, and Calcium. Note that the Ca signal is ascribed from the calcium-based purification method of commercial streptavidin. Scale bar in inset is 200 nm. (f) STEM image and (g-i) corresponding EDS maps showing elemental distribution of (g) gold (h) carbon (i) nitrogen. Scale bar in (f) is 400 nm.



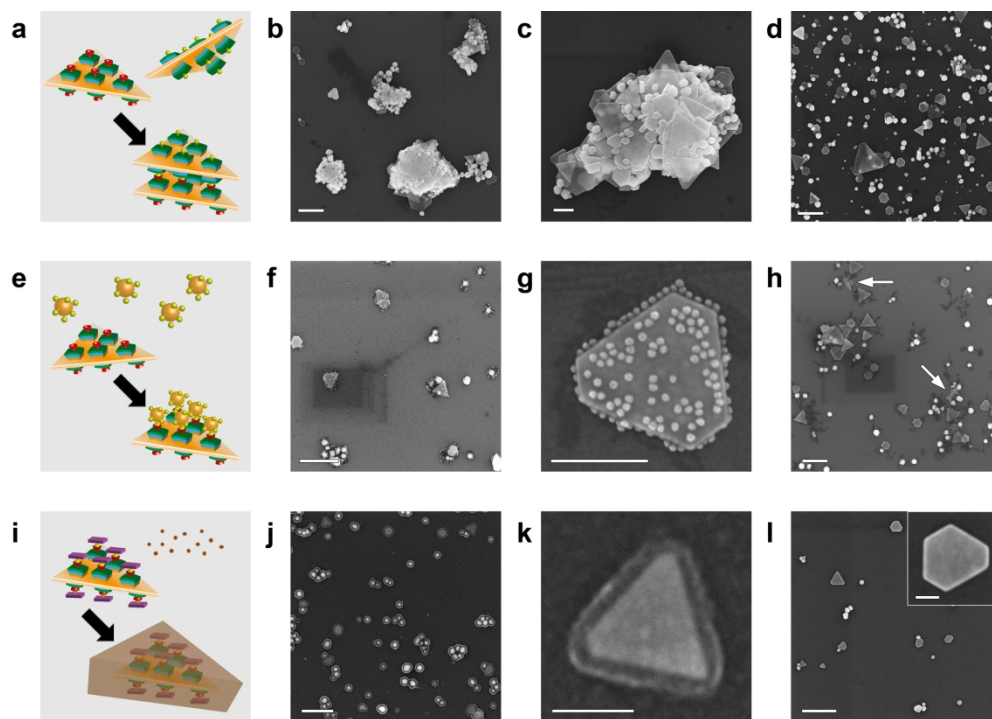


Figure 7: Functional surface derivatization of aRep protein coated nanocrystals. (a) Scheme and (b, c) SEM images of basal stacking of G8-capped Au nanocrystals obtained by self-assembly between streptavidinylated and biotinylated nanocrystals. (d) Control experiment in absence of biotin shows no stacking. (e) Scheme and (f, g) SEM images of core-satellite hybrid assemblies obtained by combining streptavidinylated G8 nanocrystals and biotin-PEG Au nanospheres which results in the decoration of the top and bottom prism facets by the nanospheres. (h) Control experiment with non-streptavidinylated G8-capped Au nanocrystals. No satellite is observed even though segregated nanosphere clumps can be found (white arrows). (i) Scheme and (j, k) SEM images of on-surface DAB catalysis by HRP-Biotin tagged streptavidinylated G8 nanocrystals results in a uniformly wrapping polymer corona. (l) Control experiment run with simply streptavidinylated nanocrystal in the absence of HRP. No polymer capping layer as shown also in the inset. Scale bars are (b, d, f, h, j, l) 500 nm, (c, g) 200 nm, (k) 100 nm and inset of (l) 50 nm.