Isolation of InsP⁴ and InsP⁶ binding proteins from human platelets: InsP⁴ promotes Ca2+ *efflux from inside-out plasma membrane vesicles containing 104 kDa GAP1IP4BP protein*

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A low-density membrane fraction from human platelets contained the plasma membrane marker glycoprotein Ib (GpIb) and selective binding sites for $\text{Ins}P_4$ and $\text{Ins}P_6$. It was separated from the bulk of $InsP_3$ -receptor-containing membranes, but was heterogeneous, probably also containing surface-connected canalicular system and some lighter elements of the internal dense tubule system. After loading with calcium oxalate and re-centrifugation on Percoll gradients, this mixed fraction was subfractionated into light membranes containing all of the GpIb, high-affinity Ins P_4 binding sites ($K_D = 18$ nM) and phosphatehigh-affinity Ins P_4 binding sites $(K_{\rm D} = 18 \text{ nM})$ and phosphate-
stimulated Ca²⁺ transport activity. Ins P_4 (EC₅₀ 0.6 μ M), but not
Ins P_3 or Ins P_6 , released up to 35% of the accumulated Ca²⁺ from $\text{Ins}P_{\scriptscriptstyle{3}}$ or $\text{Ins}P_{\scriptscriptstyle{6}}$ these vesicles, which were shown to be inside-out plasma membrane vesicles by a biotinylation labelling technique and selective removal of right-side-out plasma membrane vesicles with streptavidin–agarose. Most of the $\text{Ins}P_4$, and all of the $\text{Ins}P_6$, binding was present in the much denser calcium oxalate-loaded subfractions, which were free of GpIb. $\text{Ins}P_6$ binding activity was chromatographically purified as a 116 kDa protein $(K_D$ for $\text{Ins}P_6 = 5.9 \text{ nM}$, with an amino acid content and two internal peptide sequences identical to those of 116 kDa vinculin. A 104 kDa Ins P_4 binding protein $(K_D$ for Ins $P_4 = 12$ nM), probably 104 kDa Ins P_4 binding protein (K_{D} for Ins $P_4 = 12 \text{ nM}$), probably identical to GAP1^{TP4BP} described by Cullen, Hsuan, Truong, Letcher, Jackson, Dawson and Irvine [(1995) Nature (London) **376**, 527–530], was also isolated. This $\text{Ins}P_4$ receptor may mediate **376**, 527–530], was also isolated. This $\text{Ins}P_4$ receptor may mediate Ca^{2+} influx in platelets that occurs subsequent to receptor- Ca^{2+} influx in platelets that occurs subsequent to receptor-
stimulated production of $InsP_3$ and unloading of internal Ca^{2+} stores.

INTRODUCTION

The importance of $\text{Ins}(1,4,5)P_3$ as a second messenger for intracellular Ca^{2+} signalling is well documented in many cell types, including platelets. Other inositol phosphates such as Ins(1,3,4,5) P_4 and Ins P_6 are found in many cells, and it has been suggested that they are also involved in signal transduction processes, including the control of cytosolic Ca^{2+} levels and clathrin assembly, but their specific functions are largely either unclear or unknown. $InsP_4$ is formed intracellularly by the phosphorylation of $\text{Ins}P_3$, and $\text{Ins}P_4$ binding sites have been identified in cerebellum [1,2], HL-60 cells [3], adrenal cortex [4], liver [5] and platelets [6]. A specific $\text{Ins}P_4$ receptor has been purified from pig platelet plasma membranes [7], and recently its cDNA was sequenced and shown to code for a member of the GTPase-activating protein (GAP) protein family, and designated GTPase-activating protein (GAP) protein family, and designated
as GAP^{1IP4BP} [8]. Ins P_4 has various effects on Ca²⁺ in cells; e.g. it may (1) control Ca^{2+} entry into sea urchin eggs as a mechanism to replenish internal Ca²⁺ stores [9], (2) contribute to the release of Ca²⁺ from internal stores in brain [10], (3) enhance Ca²⁺ uptake into internal storage sites [11], and (4) activate a Ca^{2+} permeable channel in endothelial cell plasma membranes [12]. Several inositol polyphosphate binding proteins that bind Ins P_4 , but with lesser affinity than for $\text{Ins}P_{\epsilon}$, have also been described [13–15].

 $\text{Im} P_3$ releases Ca^{2+} from vesicles derived from the internal membrane system (internal dense tubule system; DTS) of human platelets [16–20], but nothing is known about the functions of either $\text{Ins}P_4$ or $\text{Ins}P_6$ in platelets. Here we report on the binding of Ins P_4 and Ins P_6 to platelet membranes, and the purification of a 104 kDa $\text{Ins}P_4$ receptor protein and its separation from a 116 kDa $\text{Ins}P_6$ binding protein. We also show that the $\text{Ins}P_4$

binding protein is found in two fractions, with the majority in a membrane fraction containing the $\text{Ins}P_6$ binding protein and exhibiting oxalate-stimulated Ca^{2+} transport. Lastly, we demexhibiting oxalate-stimulated Ca^{2+} transport. Lastly, we demonstrate the ability of $InsP_4$ to increase Ca^{2+} efflux across insideout membrane vesicles derived from the plasma membrane fraction of human platelets. Therefore the plasma membrane fraction of human platelets. Therefore the plasma membrane

Ins P_4 receptor may mediate Ca^{2+} influx in agonist-stimulated platelets, which occurs subsequent to the production of Ins*P*³ platelets, which occurs subsequent to the production of Ins P_3 and unloading of internally sequestered Ca²⁺ stores by Ins P_3 [21].

MATERIALS AND METHODS

Materials

Radiolabelled $[^{3}H]$ Ins P_4 (17 Ci/mmol), Ins P_6 (21 Ci/mmol) and adiolabelled $[^{3}H]$ Ins P_4 (17 Ci/mmol), Ins P_6 (21 Ci/mmol) and CaCl₂ were from New England Nuclear, $[^{3}H]$ Ins P_3 (35 Ci}mmol) was purchased from Amersham, and non-radioactive inositol phosphates were from the Rhode Island Chemical Group (University of Rhode Island, Kingston, RI, U.S.A.). The sources of other reagents were as follows: monoclonal antibody against glycoprotein Ib (GpIb) (Immunotech), peroxidaselabelled second antibodies (Boehringer Mannheim), sulphosuccinimidyl-6-(biotin amido)hexanoate (sulpho-NHS-LCbiotin), peroxidase-labelled streptavidin and Immunopure immobilized streptavidin linked to agarose (Pierce Chemical Co.), chemiluminescence reagents (Kirkegaard and Perry), concanavalin A (ConA)–agarose (Sigma Chemical Co.).

Assays of Ca2+ *uptake and release in platelet membrane vesicles*

Platelets obtained from the Connecticut Red Cross were washed in buffer containing 0.135 M NaCl, 5 mM KCl, 10 mM Hepes,

Abbreviations used: GAP, GTPase-activating protein; DTS, dense tubule system; GpIb, glycoprotein Ib; sulpho-NHS-LC-biotin, sulphosuccinimidyl-6-(biotin amido)hexanoate; DTT, dithiothreitol; ConA, concanavalin A; SCCS, surface-connected canalicular system.

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pH 7.6, and then washed in 0.125 M NaCl, 5 mM KCl, 10 mM Pipes, 0.2 mM EGTA, pH 6.8. Washed platelets were sonicated, and membrane fractions were separated on a 12 ml continuous 40% Percoll gradient by the method of O'Rourke and Feinstein [17] to yield 1.0 ml fractions numbered 1–11 from the top of the gradient. Membranes from the Percoll gradients were washed twice in a buffer of 100 mM KCl, 10 mM Hepes, 5 mM MgCl₂, 0.5 mM PMSF, 0.5 mM dithiothreitol (DTT) and 10 μ M each of pepstatin and leupeptin. Membranes $(0.2 \text{ mg of protein/ml})$ were incubated for 1 h at 23 $^{\circ}$ C in Ca²⁺ uptake buffer, i.e. the above incubated for 1 h at 23 °C in Ca²⁺ uptake buffer, i.e. the above wash buffer plus 0.5μ Ci/ml ⁴⁵CaCl₂, 0.56 mM EGTA, 0.4 mM CaCl₂, 10 mM potassium phosphate and 2 mM disodium ATP CaCl₂, 10 mM potassium phosphate and 2 mM disodium ATP (free Ca²⁺ = 1 μ M). Duplicate aliquots were added at various time points to $25 \mu l$ of a formalin/EDTA solution [17] to immediately stop all transport, and centrifuged for 2 min at 463000 *g* in a TL-100 centrifuge. Supernatants were aspirated and the pellets were extracted with 50 μ l of 50% (w/v) trichloroacetic acid and assayed for $45Ca^{2+}$ by liquid scintillation chloroacetic acid and assayed for ${}^{45}Ca^{2+}$ by liquid scintillation counting. Ca^{2+} release induced by $InsP_4$ was studied using vesicles counting. Ca^{2+} release induced by $InsP_4$ was studied using vesicles preloaded with $^{45}Ca^{2+}$. These reactions were also stopped by formalin/EDTA and the pellets analysed for $45Ca^{2+}$ as above.

Separation of plasma membrane vesicles from internal membrane vesicles by loading with calcium oxalate

Fractions 1–3 from Percoll gradients were pooled and incubated for 1 h at 25 °C in Ca²⁺ uptake buffer (without ${}^{45}Ca^{2+}$) plus 5 mM potassium oxalate and subfractionated into 'heavy' and 'light' membrane fractions by centrifugation on a 40% Percoll gradient for 50 min at 40000 *g* in a Sorvall centrifuge using an SS34 rotor. One-quarter of the total membranes were incubated in medium with $45Ca^{2+}$, which thereby served as a marker to locate on the gradient those membrane subfractions that were capable of oxalate-stimulated Ca^{2+} uptake. Fractions of 1.0 ml each, from the top of the gradient down, were removed and designated as subfractions 1a–11a. Non-radioactive subfractions isolated in the same way were washed twice and resuspended in Ca^{2+} uptake buffer supplemented with 10 mM phosphate, 1 mM ATP and uffer supplemented with 10 mM phosphate, 1 mM ATP and Ca^{2+} , and incubated for 60 min at 23 °C. The effect of $InsP_4$ on $45Ca^{2+}$ accumulation by these vesicles was measured as described above.

Ligand binding assays

Platelet sonicates were centrifuged on 12 ml Percoll gradients, the upper 3.0 ml (fractions 1–3) of the gradients was pooled, and 2.0 ml fractions were collected from the remaining gradient. All membranes were washed and resuspended at 1.0 mg of protein/ml. The binding of radioactive $\text{Ins}P_4$, $\text{Ins}P_6$ and $\text{Ins}P_8$ to membranes, at equilibrium, was evaluated over the pH range 5.8–8.3 at 4 °C. A pH 5.8 buffer (25 mM Mes, 1 mM EDTA, 0.5 mM DTT and 0.5 mM PMSF) was optimal for [\$H]Ins*^P* 0.5 mM DTT and 0.5 mM PMSF) was optimal for $[^3H]$ Ins P_4 0.5 mM DTT and 0.5 mM PMSF) was optimal for $[{}^3H]$ Ins P_4
binding, whereas $[{}^3H]$ Ins P_3 binding was greatest in bicarbonate binding, whereas [³H]Ins P_3 binding was greatest in bicarbonate
buffer at pH 8.3 [17] and [³H]Ins P_6 binding, which is unaffected by pH, was measured at pH 7.4. Non-specific binding was measured in the presence of 1μ M of the appropriate nonradioactive inositol phosphate. Duplicate aliquots of 100 μ l were centrifuged for 4 min in a Beckman TL-100 centrifuge at 463000 *g*. Supernatants were aspirated and the pellets were extracted with 50 μ l of 50% trichloroacetic acid. [³H]Inositol phosphate in the extracts was assayed by liquid scintillation counting.

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^{[3}H]Ins*P*₄</sub> binding to solubilized receptor protein was assayed using aliquots (75 μ l) of chromatographic fractions that were diluted with an equal volume of pH 5.8 Mes buffer without diluted with an equal volume of pH 5.8 Mes buffer without CHAPS and incubated with $[^3H] \text{Ins} P_4$ for 15 min at 4 °C,

followed by addition of 8 μ l of rabbit IgG (50 mg/ml) as carrier. Non-specific binding was determined in the presence of $1 \mu M$ non-radioactive Ins P_4 . Duplicate aliquots of 75 μ l were added to 100 μ l of 30 % poly(ethylene glycol) 6000 in pH 5.8 Mes buffer to precipitate proteins.The samples were held at 4 °C for 10 min, followed by centrifugation at 463000 *g* in a TL-100 Beckman centrifuge for 10 min. The protein pellets were extracted with 50% trichloroacetic acid and centrifuged to obtain supernatants that were assayed by liquid scintillation counting. Similarly, that were assayed by liquid scintillation counting. Similarly, binding of $[^{3}H]$ Ins $P_{\rm g}$ was measured at pH 7.4. All ligand binding data were analysed using the non-linear regression program BIOSOFT (Elsevier) and displayed as Scatchard plots.

Labelling of the platelet cell surface by sulpho-NHS-LC-biotin

All procedures were carried out at 25 °C. Three units of platelets (1 unit is 60 ml of platelet-rich plasma) were washed with 0.135 M NaCl, 5 mM KCl, 10 mM Hepes, pH 7.6, and then with 0.125 M NaCl, 5 mM KCl, 10 mM Pipes, 0.2 mM EGTA, pH 6.8. The platelet pellets were resuspended in PBS (138 mM NaCl, $1.2 \text{ mM } KH_2PO_4$, $8.1 \text{ mM } Na_2HPO_4$, $2.7 \text{ mM } KCl$, pH 7.4) with 5 mM sulpho-NHS-LC-biotin and incubated for 45 min. After two washes with PBS to remove unreacted biotin, the platelets were resuspended in 2 ml of ice-cold buffer containing 100 mM KCl , 10 mM Hepes , 5 mM MgCl_3 , 0.5 mM DTT, 0.5 mM PMSF, 10 μ M leupeptin and 10 μ M pepstatin, pH 7.1. The platelets were sonicated and the membranes were washed with the above buffer and then incubated with Immunopure immobilized streptavidin for 1 h. The suspensions were centrifuged for 10 min at 12000 *g* to remove the biotin-labelled membranes adhered to streptavidin–agarose beads. Unlabelled cells, treated in the same manner, served as a control. Thus the net result was to specifically remove biotin-labelled (right-sideout) vesicles, leaving inside-out vesicles plus internally derived membranes in the suspension. The latter were loaded with calcium oxalate, as described above, followed by centrifugation on a 40% Percoll gradient. Membrane subfractions (1b–11b) were washed and assayed for GpIb, $45Ca^{2+}$ uptake in the were washed and assayed for GpIb, $^{45}Ca^{2+}$ uptake in the presence of phosphate, and release of Ca^{2+} by Ins P_4 . The membrane vesicles that were not removed by streptavidin– agarose were subjected to SDS/PAGE (7.5% gels), blotting with peroxidase-labelled streptavidin and detection by enhanced chemiluminescence.

Western blotting for GpIb

Membrane proteins separated by $SDS/PAGE$ (7.5% gels) were semi-dry blotted on to Immobilon nylon membranes and incubated for 45 min with a blocking solution of 5% powdered milk and 1% goat serum in PBS/Tween (i.e. PBS, pH 7.4, with 0.1%) Tween 20). The blots were incubated with a 1:10000 dilution of anti-GP1b monoclonal antibody in blocking buffer for 1 h at 23 °C, and then washed with PBS/Tween for 2×15 min and 3×5 min. The blots were incubated for 45 min with peroxidaselabelled goat anti-mouse $\lg G_1$ diluted 1:15000 in PBS/Tween, followed by washing as described for the first antibody. The washed immunoblots were incubated with enhanced chemiluminescence reagent and exposed to BioMax-MR X-ray film (Kodak) for 1 min. The images were quantified by a Molecular Dynamics laser densitometer using Image Quant software.

Purification of InsP⁴ and InsP⁶ binding proteins

All procedures were carried out at 4 °C. Platelet membrane fractions 1–3 (80–100 mg of protein) were pooled from Percoll gradients and washed twice with buffer containing 1 M NaCl,

20 mM bicarbonate, 10μ M each of leupeptin and pepstatin, 0.5 mM PMSF, 0.5 mM DTT, pH 7.4, to remove non-integral membrane proteins. The membranes were washed twice more in the same buffer without added NaCl and then solubilized in 50 ml of the same buffer plus 5% CHAPS. The protease inhibitors and DTT stabilized the binding activity of detergentsolubilized protein. The solubilized membranes were stirred for 1 h and centrifuged for 1 h at 40000 *g* to remove particulate matter. The supernatant was passed through a 5 ml ConA– agarose column to remove glycoproteins. The ConA–agarose flow-through was adjusted to 0.025 M NaCl and pH 5.8 with Mes and applied to an HPLC anion-exchange column (Supelco) at a flow rate of 1 ml/min. Proteins were eluted with a gradient of 0.025–1.0 M NaCl in 1% CHAPS, 1 mM EDTA, 25 mM Mes at pH 5.8. Fractions (1.0 ml) were collected and assayed for at pH 5.8. Fractions (1.0 ml) were collected and assayed for
binding of $[^{3}H]$ Ins P_4 and $[^{3}H]$ Ins P_6 . The peak $[^{3}H]$ Ins P_4 and binding of $[^{3}H]$ Ins P_4 and $[^{3}H]$ Ins P_6 . The peak $[^{3}H]$ Ins P_4 and $[^{3}H]$ Ins P_6 binding fractions were pooled, concentrated and dialysed by a Centricon device (molecular mass cut-off of 30 kDa) and then applied to a heparin-TSK HPLC column (ToyoHaas) in the elution buffer described above (with 25 mM NaCl) at a in the elution buffer described above (with 25 mM NaCl) at a
flow rate of 0.2 ml/min. [³H]Ins P_6 binding activity was all found in the heparin column flow-through, which was concentrated using a 30 kDa cut-off Centricon device and chromatographed on an HPLC gel filtration column (Zorbax G450; DuPont). Protein adsorbed on to the heparin-TSK column was eluted with a $0.025-1.0$ M NaCl gradient at a flow rate of 0.5 ml/min and a 0.025–1.0 M NaCl gradient at a flow rate of 0.5 ml/min and
collected in 0.5 ml fractions. The peak [³H]Ins*P*₄ binding fractions were pooled, concentrated and dialysed overnight in elution buffer without NaCl, and assayed for ligand binding and analysis by SDS/PAGE.

RESULTS

The various inositol phosphates bound to sonicated platelet membranes with different dependencies on pH. Ins*P*³ binding was greatest at alkaline pH $[17]$, the binding of $InsP_4$ was greatest at moderately acid pH, whereas $\text{Ins}P_6$ binding was virtually unaffected from pH 5.8 to 8.3 (results not shown). Membranes isolated by centrifugation on Percoll gradients were divided into

Figure 1 Binding of inositol phosphates to platelet membrane fractions

Membrane fractions (100 μ g of protein) from a Percoll gradient were incubated with 10 nM $[^3H]$ Ins P_4 or $[^3H]$ Ins P_6 and specific binding was measured as described in the Materials and methods section. Data are from a single experiment repeated three times with similar results.

Figure 2 Displacement of bound [3 H]InsP⁶ from platelet membranes

Membrane fractions 1–3 (50 μ g of protein) were incubated with 5 nM $[^3H]$ Ins P_6 and various concentrations of non-radioactive displacer ligands, and analysed for bound radioactive ligand (% of control) as described in the Materials and methods section: \bullet , non-radioactive Ins P_6 ; \triangle , heparin; \blacktriangledown , Ins P_4 ; \Box , Ins P_3 . IC₅₀ values for displacement: Ins P_6 , 100 nM; heparin, 5 μ M; Ins P_4 and Ins P_3 , $> 10 \mu$ M.

 12×1 ml fractions and assayed for [8 H]Ins P_4 and [8 H]Ins P_6 12×1 ml fractions and assayed for $[^{8}H]\text{Ins}P_{4}$ and $[^{8}H]\text{Ins}P_{6}$ binding. A total of 52% of the total $[^{8}H]\text{Ins}P_{4}$ binding was found in combined fractions $1-3$, with a lesser amount in fractions $4+5$ in combined fractions 1–3, with a lesser amount in fractions $4+5$

(21%) and $5+6$ (17%) (Figure 1). Peak [³H]Ins P_6 binding (37%) was in fractions 1–3 (Figure 1). In contrast, most (50%) of Ins P_3 binding was concentrated in the heavier fractions $4+5$ $[17,22]$, suggesting that the $InsP_4$ and $InsP_6$ receptors might reside in a different membrane compartment than the Ins P_3 receptor.
The binding of β^3 Ullne *P* was bighly enoties for the Ins^{*P*}, γ^2 receptor. in a different membrane compartment than the $\text{Ins}P_3$ receptor
The binding of [³H]Ins*P*₄ was highly specific for the Ins(1,3,4,5)*P* The binding of $[^3H]$ Ins P_4 was highly specific for the Ins(1,3,4,5) P_4 isomer; e.g. IC₅₀ values for displacement of 10 nM $[^3H]$ Ins P_4 from fractions 1–3 were 40 nM for non-radioactive Ins P_4 , 8 μ M %for Ins(1,4,5,6)*P*₄, 50 μ M for Ins(1,3,4,6)*P*₄, 30 μ M for Ins*P*₃ and 6 μ M for Ins P_6 . The IC₅₀ for heparin was 1 μ M. Direct binding of [³H]Ins P_4 to membrane fractions 1–3, measured over a $\frac{1}{4}$ to membrane fractions 1–3, measured over a concentration range of 5–50 nM radioactive ligand, yielded an average K_D of 18 nM (results not shown). Similarly, the dis-
placement of 5 nM ^{[3}H]Ins $P₆$ from membranes was highly ⁶ from membranes was highly specific; i.e. IC₅₀s were 100 nM for Ins $P_6 > 10 \mu$ M for Ins P_4 and Ins P_3 , and 5μ M for heparin (Figure 2).

To test for functions of $\text{Ins}P_4$ and $\text{Ins}P_6$, we isolated membrane vesicle fractions $1-3$ and $4+5$ from 17 individual batches of human platelets and loaded them with $45Ca^{2+}$ in phosphatehuman platelets and loaded them with ⁴⁵Ca²⁺ in phosphate-
containing buffer plus ATP. Ins*P*₄ released 15–25% of the ⁴⁵Ca²⁺ from fractions 1–3, but had little or no effect on fractions $4+5$ (maximum 3–5% release by 10 μ M Ins P_4). In contrast, 5 μ M (maximum 3–5% release by 10 μ M Ins*P*₄). In contrast, 5 μ M
Ins*P*₃ released 25–40% of the accumulated ⁴⁵Ca²⁺ from fractions $4+5$ (results not shown). $45Ca^{2+}$ was released from fractions 1–3 by both Ins P_3 and Ins P_4 , but their effects were additive, suggesting that each acted on different compartments. For example, the maximum release induced by a combination of $\text{Ins}P_3 + \text{Ins}P_4$ was 40% , the maximum by Ins P_3 alone was 15% and the maximum
 40% , the maximum by Ins P_3 alone was 15% and the maximum 40%, the maximum by Ins P_3 alone was 15% and the maximum
by Ins P_4 alone was 25%. Ins P_6 (10–20 μ M) did not release Ca²⁺ from any vesicles.

Fractions 1–3 from the Percoll gradients also showed some Fractions 1–3 from the Percoll gradients also showed some

[³H]Ins*P*₃ binding and oxalate-stimulated Ca²⁺ uptake (results not shown). The latter is a specific characteristic of the Ca²⁺ transport system of the internal platelet membranes, but not that of the plasma membrane [23]. These findings, and the release of of the plasma membrane [23]. These findings, and the release of Ca^{2+} by both $InsP_4$ and $InsP_3$, indicated that fractions 1–3

Figure 3 Binding of [3 H]InsP⁴ and [3 H]InsP⁶ to platelet membrane subfractions obtained after loading with calcium oxalate

Membrane fractions $1-3$ were loaded with ${}^{45}Ca^{2+}$ in the presence of 5 mM oxalate and 1 mM ATP and recentrifuged on a Percoll gradient (see the Materials and methods section). Subfractions 1a–11a (30 μ g of protein) were assayed for binding of [³H]lns P_4 and [³H]lns P_6 , and for content of ⁴⁵Ca²⁺ and GpIb. (**a**) Bar graph: binding of [³H]Ins P_6 ; \bullet , ⁴⁵Ca²⁺ uptake. (**b**) Bar graph: specific activity of $[^{3}H]$ Ins P_{6} binding; Ψ , GP1b content of 10 μ g membrane protein samples (average of three experiments). (**c**) Bar graph: binding of [³H]Ins P_4 ; \bullet , ⁴⁵Ca²⁺ uptake. (d) Specific activity of Ins P_4 binding.

contained elements of both the surface and internal membranes. Plasma membranes were further separated from vesicles derived from the internal membrane system by taking advantage of the tendency of calcium oxalate to accumulate and precipitate within internal membrane vesicles, thereby increasing their specific gravity. This was confirmed by loading fraction 1–3 vesicles with %& $45Ca^{2+}$ in the presence of 5 mM oxalate and 1 mM ATP and ⁴⁵Ca²⁺ in the presence of 5 mM oxalate and 1 mM ATP and recentrifuging them on a Percoll gradient. ⁴⁵Ca²⁺ and Ins P_6 binding activity were found virtually exclusively in fractions 8a–11a, corresponding to a much denser part of the gradient (Figures 3a and 3b), whereas Gp1b was entirely confined to the lighter membranes in subfractions 3a–7a (Figure 3b). The dense membrane fractions also contained 90% of the total $InsP_4$ binding activity (Figure 3c), but the gradient had two areas with binding activity (Γ gate *set*), our the gradient had two dreas with high specific activity for $\text{Ins}P_4$ binding, i.e. the GpIb-containing fractions 3a–7a and the $45Ca^{2+}$ -labelled heavy fractions that contained all of the $\text{Ins}P_6$ binding activity (Figure 3d). In the latter fractions we determined that $\text{Ins}P_4$ and $\text{Ins}P_6$ were binding to different entities, because 200 nM Ins P_6 did not displace to different entities, because 200 nM Ins P_6 did not displace
bound [³H]Ins P_4 (Ins P_4 present at 10 nM; $K_p = 12$ nM) and bound $[^{3}H] \text{Ins} P_4$ (Ins P_4 present at 10 nM; $K_{\text{D}} = 12 \text{ nM}$) and 10 μ M Ins P_4 did not displace bound $[^{3}H] \text{Ins} P_6$ (the latter present at 10 nM; $K_{\text{D}} = 18$ nM).

The inositol phosphates were then tested for their effects on $Ca²⁺$ release from vesicles of the 'light' membrane fractions obtained after calcium oxalate loading as described above. Membrane fractions 1–3 were loaded with calcium oxalate (but no $45Ca^{2+}$) and centrifuged on Percoll to obtain fractions 1a–11a. The membrane fractions were individually washed and resus-

Figure 4 Phosphate-stimulated Ca2+ *uptake by GpIb-containing membrane vesicle fractions 1a–6a and release of accumulated* Ca^{2+} *by* $InsP_4$

Membrane subfractions (1a–11a) loaded with calcium oxalate (but no ${}^{45}Ca^{2+}$) were washed and resuspended in medium with 10 mM phosphate, 1 mM ATP and ${}^{45}Ca^{2+}$. \blacktriangledown , GP1b content of 10 μ g membrane protein samples (average of three experiments). The bar graph represents 45 Ca²⁺ content of membrane vesicles, and \bullet is the ⁴⁵Ca²⁺ released from membrane vesicles by 10 μ M Ins P_4 (average of three experiments). No Ca²⁺ was released from fractions 1a–6a by 10 μ M Ins P_3 .

Figure 5 Ca^{2+} *release from pooled subfractions 3a–5a by Ins* P_4

Membrane subfractions 3a–5a (15 μ g of protein) were incubated in assay medium with 10 mM phosphate, 1 mM ATP and ${}^{45}Ca^{2+}$ for 1 h as described in the Materials and methods section. The vesicles accumulated 77 nmol of Ca^{2+}/mg of protein, and 60% of the ${}^{45}Ca^{2+}$ was released by ionophore A23187. Ins P_4 was added and release of 45 Ca²⁺ was determined at the time points indicated. Data represent the means of four experiments. Inset: dose-response curve for Ca^{2+} release by Ins P_4 . Data are from a single experiment repeated four times with similar results.

pended in medium with 10 mM phosphate, 1 mM ATP and %& $45Ca^{2+}$. Phosphate-stimulated Ca^{2+} uptake was greatest in the light subfractions 1a–7a that contained virtually all of the GpIb. light subfractions 1a–7a that contained virtually all of the GpIb.
Ins P_4 (10 μ M) released Ca²⁺ from fractions 3a–6a (Figure 4). The latter were slightly denser on the gradient than the original fractions 1–3 from which they were derived, possibly due to some small accumulation of calcium oxalate. Ins P_3 (10 μ M) did not small accumulation of calcium oxalate. $\text{Ins}P_3$ (10 μ M) did not release ⁴⁵Ca²⁺ from fractions 3a–6a, whereas $\text{Ins}P_4$ consistently released 15–30% of the vesicle $^{45}Ca^{2+}$ within 30 s, and ionophore A23187 released 55% of the calcium (Figures 4 and 5). $^{45}Ca^{2+}$ release was maximal at $6 \mu M \ln sP_4$ (EC₅₀ = 0.6 μ M) (Figure 5, inset). Thapsigargin, an inhibitor of the internal membrane Ca^{2+} -

Table 1 Purification of an InsP⁴ binding protein in human platelets

Platelet membranes from fractions 1–3 were isolated and solubilized as described in the Materials and methods section. Samples from each purification step were incubated with 10 nM [³H]Ins*P*₄ (specific radioactivity 17 Ci/mmol) and assayed for the amount of specific ligand binding to protein (pmol/mg). Data shown are from a single purification repeated three times with similar results.

ATPase [24], blocked ATP-dependent Ca^{2+} uptake by the DTS membranes (fractions 4+5) and released 62% of the Ca²⁺ accumulated by this $\text{Ins}P_3$ -sensitive fraction. Thapsigargin also accumulated by this Ins P_3 -sensitive fraction. Thapsigargin also released 55% of accumulated ⁴⁵Ca²⁺ from the original fractions released 55% of accumulated ⁴⁵Ca²⁺ from the original fractions 1–3, but failed to release any ⁴⁵Ca²⁺ from the Ins P_4 -sensitive fractions $1a-6a$ ($n=3$ experiments).

The origin and orientation of vesicles exhibiting phosphate-The origin and orientation of vesicles exhibiting phosphate-
stimulated Ca²⁺ uptake and Ca²⁺ release by Ins P_4 was determined by labelling the surface proteins of intact platelets with sulpho-NHS-LC-biotin. This reagent has the advantages of reactivity with free protein amino groups at neutral pH and an inability to penetrate the cell membrane, resulting in specific labelling of plasma membrane proteins with low background and high sensitivity compared with other protein labelling reagents [25]. The procedure, described in detail in the Materials and methods section, involved biotinylation of intact platelets, washing to remove unreacted reagent, membrane sonication, and the selective precipitation and removal by streptavidin–agarose beads of membrane vesicles labelled with biotin on their outer surfaces. The remaining membranes were loaded with calcium oxalate and centrifuged on a Percoll gradient to obtain 1.0 ml subfractions designated 1b–11b and assayed for GpIb. Streptavidin–agarose beads (streptavidin concentration \lt biotin concentration) removed a maximum of 40 $\%$ of the GpIb-containing membranes from biotinylated platelets, but did not remove any GpIbcontaining membranes originating from platelets that had not been biotinylated. The remaining GpIb (60%) that was not removed by streptavidin–agarose was contained in the 'light' fractions 1b–5b of the gradients. GpIb was not present in the denser calcium oxalate-loaded internal membrane subfractions 6b–11b. Although not removed by streptavidin–agarose, many proteins in membrane fractions 1b–5b were found to be labelled with biotin by Western blot analysis after SDS/PAGE (see the Materials and methods section). From these data we conclude that: (1) fractions 1b–5b were largely of plasma membrane origin, and (2) since they were not precipitated by streptavidin– agarose beads, the biotin in them was oriented facing into the lumens of the vesicles, i.e. the membrane vesicles were inside-out. Subfractions 1b–5b took up $45Ca^{2+}$ from the medium when incubated with 10 mM phosphate plus ATP, and they released incubated with 10 mM phosphate plus ATP, and they released 15–35% of accumulated $^{45}Ca^{2+}$ when exposed to Ins P_4 (results not shown, similar to those in Figure 5).

Based on the evidence of specific and unique ligand binding sites for each of the inositol phosphates $\text{Ins}P_4$, $\text{Ins}P_3$ and $\text{Ins}P_6$, we undertook the purification of the individual binding proteins. Using a radioactive ligand binding assay for detergent-solubilized receptors, three proteins were purified from platelet membrane fractions 1–3 by a sequence of column chromatography steps. Isolation of the human platelet $\text{Ins}P_3$ receptor is described elsewhere $[22]$. The scheme for purification of the $\text{Ins}P_4$ (Table 1)

Figure 6 [3 H]InsP⁴ and [3 H]InsP⁶ binding to purified proteins

(a) Scatchard plot of $[^{3}H]$ Ins P_4 (5–50 nM) binding to 70 ng of solubilized 104 kDa protein. $B_{\text{max}} = 1.8$ nmol/mg of protein; $K_{\text{D}} = 12 \text{ nM}$. (**b**) Scatchard plot of [³H]Ins P_{6} (5–75 nM) binding to 250 ng of solubilized 116 kDa protein fraction. $B_{\text{max}} = 3$ nmol/mg of protein; $K_{\rm p} = 5.9 \text{ nM}.$

and $\text{Ins}P_6$ binding proteins (see the Materials and methods section) employed a ConA–agarose column as the first step to remove membrane glycoproteins, followed by application of the flow-through fraction, containing all of the ligand binding activity, to an HPLC anion-exchange column. Both Ins*P*₄ and Ins P_6 binding activities were adsorbed on to this column and were eluted by a salt gradient with a peak at 0.12 M NaCl. The inositol phosphate binding fractions were concentrated and chromatographed on a heparin-TSK HPLC column. At pH 5.8 chromatographed on a heparin-TSK HPLC column. At pH 5.8
the^{[3}H]Ins*P*₄ binding activity was adsorbed on to the column and was eluted by a salt gradient with a peak at 0.1 M NaCl. The peak binding fractions were combined and concentrated. This fraction bound $\text{Ins}P_4$ with a K_{D} of 12 nM and a B_{max} of 1.8 nmol/mg of protein (Figure 6), and contained a single polypeptide of molecular mass 104 kDa by SDS/PAGE analysis (Figure 7).

igure 7).
All $[^{3}H]InsP_6$ binding activity was found in the flow-through fraction of the heparin-TSK column at pH 5.8, and was subsequently concentrated and further purified by gel filtration. sequently concentrated and further purified by gel filtration.
^{[3}H]Ins*P*₆ binding peaked in fractions which chromatographed with retention times intermediate between those of standards phosphorylase b (97.5 kDa) and myosin (206 kDa) that were chromatographed independently. The concentrated gel filtration chromatographed independently. The concentrated gel filtration
fraction bound [³H]Ins P_6 with a K_{D} of 5.9 nM and a B_{max} of
3 nmol/mg of protein at pH 7.4 (Figure 6). There was no 3 nmol/mg of protein at pH 7.4 (Figure 6). There was no
displacement of bound $[^3H] \text{Ins} P_6$ (present at 10 nM concentration) by 10 μ M Ins P_3 , and only 20 % displacement by 10 μ M tration) by 10 μ M Ins*P*₃, and only 20 % displacement by 10 μ M
Ins*P*₄. Heparin inhibited the binding of 10 nM [³H]Ins*P*₆ with an

Figure 7 SDS/PAGE of purified InsP⁴ and InsP⁶ binding proteins from human platelets

Left lane, SDS/PAGE (7.5% gels) of $InsP₆$ binding fraction (1 μ g of protein) isolated by HPLC gel filtration (colloidal Coomassie Blue stain). Middle lanes, SDS/PAGE (7.5% gels) of Ins*P*⁴ binding fractions eluted from the heparin-TSK HPLC column (silver stain). Right lane, molecular mass markers (kDa): myosin, 206; β -galactosidase, 116; phosphorylase b, 97.5; BSA, 66 (positions indicated).

IC₅₀ of 2 μ M. The concentrated Ins P_6 binding fraction contained a single polypeptide band at 116 kDa by SDS/PAGE analysis (Figure 7). Bands were cut from gels and analysed for total amino acid content and for sequences of protease-generated peptides. The amino acid composition matched that of 116 kDa human vinculin [26], and two internal peptides (Val-Glu-Gly-Ile-Gln-Ala-Ser-Val-Lys and Ala-Arg-Met-Gln-Glu-Ala-Met-Thr-Gln-Glu-Val) were identical to vinculin amino acids 658–666 and 585–595 respectively.

DISCUSSION

As part of an endeavour for the concurrent purification of the various inositol phosphate receptors of human platelets we isolated the solubilized $\text{Ins}P_3$ receptor [22], and in the present paper we have described: (1) unique and specific ligand binding sites for $\text{Ins}P_4$ and $\text{Ins}P_6$, (2) the purification of a specific $\text{Ins}P_4$ receptor protein, and (3) the preliminary identification and partial purification of a specific $\text{Ins}P_6$ binding protein. Furpartial purification of a specific $\text{Ins}P_6$ binding protein. Fur-
thermore, we demonstrate that $\text{Ins}P_4$ promotes the efflux of Ca^{2+} across inside-out plasma membrane vesicles, further substantiating its putative role as a second messenger that promotes Ca^{2+} influx into cells.

Our findings are in agreement with Cullen et al. [6–8], who established the localization of $InsP₄$ binding in the plasma membrane fraction of human platelets. Those membranes were isolated from neuraminidase-treated platelets by a sequence of sonication, density gradient centrifugation and high-voltage free flow electrophoresis. The surface membrane, depleted of negatively charged surface sialic acid, undergoes a cathodal shift during electrophoresis due the change in the membrane zeta potential [27]. During the sonication process membrane vesicles of either right-side-out or inside-out orientations can be formed, and the electrophoretic method isolates vesicles of both orientations.

In our studies, the establishment of $\text{Ins}P_4$ binding and effects

on Ca^{2+} permeability also required methods to separate elements of the internal membranes from the plasma-membrane-containing fractions. In these procedures we employed GpIb as a specific marker for the plasma membrane and took advantage of the different properties of the Ca^{2+} pumps of the plasma membrane and the internal membranes [23]. The plasma membrane fraction, unlike the internal membrane fraction, was reported not to transport calcium in the presence of oxalate [23], a property that is shared by plasma membrane Ca^{2+} pumps from other cells [28,29]. Therefore we obtained membrane fractions 1–3 that were enriched in the plasma membrane marker GpIb, 1–3 that were enriched in the plasma membrane marker GpIb,
but released Ca^{2+} in response to both $InsP_4$ and $InsP_3$. Our but released Ca²⁺ in response to both Ins P_4 and Ins P_3 . Our strategy was to load the membrane vesicles with Ca²⁺ plus oxalate, and then recentrifuge them on a Percoll gradient to separate the denser membranes containing calcium oxalate deposits (fractions 6a–11a) from the 'light' plasma membrane vesicles (1a–5a). The latter subfractions (1a–5a) contained all of vesicles (1a–5a). The latter subfractions (1a–5a) contained all of
the membrane GpIb, had a high specific activity for $[{}^3H]$ Ins P_4 binding and were capable of phosphate (but not oxalate) stimulated Ca^{2+} transport. These more purified plasma membrane vesicles released a substantial amount of their Ca^{2+} when exposed to Ins*P*₄ (EC₅₀ = 0.6 μ M), but showed little or no response to Ins*P*₃ or Ins*P*₆. Furthermore, thapsigargin was unable to affect Ca²⁺ uptake or to cause release of Ca²⁺ from the Ins*P*₄-sensitive ϵ . The intermediate contract the sense of Ca^{2+} from the Ins P_4 -sensitive membrane vesicles. In contrast, thapsigargin blocked ATPdependent Ca²⁺ uptake by the DTS membranes (fractions $4+5$) dependent Ca²⁺ uptake by the DTS membranes (fractions $4+5$) and released 62 % of the Ca²⁺ accumulated by this Ins P_a -sensitive fraction. Thus the characteristics of the $\text{Ins } P_4$ -sensitive membrane fractions were distinctly different from those of the internal membranes.

The denser, calcium oxalate-loaded, membrane fractions (7a–11a), derived from fractions 1–3, contained the bulk of the total Ins P_4 binding activity (90%), and all of the Ins P_6 binding, but were devoid of GpIb. This finding suggests that $\text{Ins } P_4$ receptors are present in at least two different membrane compartments, but an alternative explanation (discussed below) is that these compartments may be two subdomains of the plasma membrane. The $\text{Ins}P_6$ receptor, on the other hand, appears to be entirely associated with one compartment that may be part of, or entity associated with one compartment that may be part of, or connected to, a major $InsP_4$ -receptor-containing compartment.

 We consider three hypotheses that could account for these results. The first hypothesis holds that one compartment for Ins P_4 receptors is in the plasma membrane, and the other compartment, containing most of the $InsP₄$ receptors and all of the Ins $P_{\rm g}$ receptors, is comprised of vesicles derived from internal DTS membranes that are capable of oxalate- and phosphatestimulated Ca^{2+} transport. The second hypothesis places all of the $\text{Ins}P_4$ and $\text{Ins}P_6$ receptors in the plasma membrane, with the bulk of them in the surface connected canalicular system (SCCS), and requires that the SCCS is devoid of GpIb and is capable of oxalate-stimulated Ca^{2+} transport. The SCCS is the site of the greatest cytochemically detectable $Ca^{2+}-ATP$ ase activity in the plasma membrane [30], and it is possible that its properties differ from those of the plasma membrane $Ca^{2+}-ATP$ ase activity described by Enouf et al. [23]; however, GpIb has been found in the SCCS [31], indicating that the second hypothesis is untenable. Lastly, the $\text{Ins}P_6$ receptor and most of the $\text{Ins}P_4$ receptors may be located in subdomains of the plasma membrane that are devoid of GpIb, adherent to regions of the DTS and tightly associated with each other even after sonication of whole platelets. Such plasma membrane–DTS complexes would become much denser when the DTS component is loaded with calcium oxalate, leading to their separation from vesicles that are derived purely from the plasma membrane. The SCCS, representing invaginations of the plasma membrane, may comprise this plasma membrane

domain, since such an intimate association of DTS and SCCS membranes has been demonstrated by electron microscopy in intact platelets [32]. Further work is necessary to resolve these different possibilities.

The plasma membrane location of $\text{Ins}P_4$ receptors and the The plasma membrane location of $\text{Ins}P_4$ receptors and the Ca²⁺-releasing effect of $\text{Ins}P_4$ were further established by biotinylation of platelet surface proteins with a reagent that does not penetrate the cells. After sonication of the platelets the membrane vesicles with biotin exposed on their surfaces (rightside-out vesicles) were removed with streptavidin–agarose beads. The remaining membranes were loaded with calcium oxalate and centrifuged on a density gradient to separate 'heavy' membrane vesicles from the 'light' membrane fractions 1b–5b. The latter were largely plasma membrane vesicles, based on the fact that they contained all the GpIb, and they were in an inside-out orientation since, although not removed by streptavidin–agarose, they contained biotinylated proteins as shown by SDS/PAGE analysis. These fractions 1b–5b exhibited phosphate (but not oxalate)-stimulated active uptake of Ca^{2+} , a plasma membrane property. These plasma membrane vesicles could release as much property. These plasma membrane vesicles could release as much
as one-third of their accumulated Ca²⁺ in response to Ins*P*₄. Since the lumen of the inside-out plasma membrane vesicles represents the 'extracellular space', the action of $\text{Ins}P_4$ is consistent with the 'extracellular space', the action of $\text{Ins}P_4$ is consistent with other findings that $\text{Ins}P_4$ promotes Ca^{2+} influx into cells [9,12].

Proteins capable of selective high-affinity $InsP_4$ binding have been isolated from platelets and brain [7,14,33]. The purified 104 kDa $\text{Ins}P_4$ binding protein of pig platelets [7] as well as that from human platelets is highly specific for $\text{Ins}(1,3,4,5)P_4$ from human platelets is highly specific for $\text{Ins}(1,3,4,5)P_4$
compared with other isomers, $\text{Ins}P_6$ or $\text{Ins}P_3$. [³H]Ins*P*₄ bound to the purified human platelet protein with a K_{D} of 12 nM and B_{max} of 1.8 nmol/mg of protein, compared with values of $K_{\text{D}} =$ 9.6 nM and $B_{\text{max}} = 2.5$ and 6.0 obtained by Cullen et al. [8]. The predicted B_{max} is 9.6 nmol/mg of protein assuming one ligand binding site per molecule. In all respects, including the pH dependence for ligand binding [34], the human platelet protein appears to be identical to the 104 kDa protein from pig platelet plasma membranes isolated by Cullen et al. [7]. These platelet proteins differ from all other putative $\text{Ins}P_4$ binding proteins, such as the two fractions from brain with a high specific affinity for Ins*P*₄, which contained polypeptides of 182 plus 123 kDa and 174 plus 84 kDa respectively [14].

The platelet 104 kDa Ins P_4 binding protein was recently identified as a member of the GAP family and designated GAP1^{IP4BP} [8]. Important regions of this protein include a Lys/Arg-rich sequence in the Ca^{2+} -independent phospholipid binding C2B domain, also found in GAP1 and GAP1^m, which comprises the selective ligand binding site, a C2A Ca^{2+} -dependent phospholipid binding domain, and a pleckstrin homology domain. GAP1^{IP4BP} stimulated the GTPase activity of the lowmolecular-mass GTP-binding proteins H-Ras, R-Ras and Rap1A, but not K-Ras, Q61L, Rap3A or Rac. GTPase activation exerted on Ras (but not Rap1A) by GAP1^{IP4BP} was inhibited by phospholipids commonly found in the inner leaflet of the plasma membrane, and this effect was reversed by $\text{Ins}P_4$. $\text{Ins}P_4$ did not affect Rap or Rap–GAP interactions. Platelets contain members of the Ras-related family such as Rap1A, Rap1B, Rap2B, Rac1 and Ral [35]. Rap1B is present in the plasma membrane and SCCS [36] and is a prominent substrate for protein kinase A. Rap1B has been implicated in cAMP-stimulated Ca^{2+} transport Rap1B has been implicated in cAMP-stimulated Ca^{2+} transport
by plasma membrane vesicles [37]. Since $InsP_4$ increases the Ca^{2+} permeability of plasma membrane vesicles, it is possible that permeability of plasma membrane vesicles, it is possible that Ins*P*₄–GAP1^{1P4BP}, in conjunction with a small G-protein, controls the opening of a plasma membrane channel that is permeable to $Ca²⁺$. Indeed, this is also suggested by the finding that in v-Kiras-transformed NIH/3T3 cells, but not in control cells, the

intracellular injection of 10 μ M Ins P_4 produced sustained Ca²⁺ oscillations requiring the presence of extracellular Ca^{2+} [38].

A number of proteins that bind inositol polyphosphates such as $\text{Ins}P_4$ have an even higher affinity for $\text{Ins}P_6$. Many of these proteins are involved in membrane cycling of secretory vesicles or clathrin-coated vesicles. Platelets contain clathrin which is associated with the plasma membrane, the SCCS and the surface of α -granules [39], so it was important to also characterize the $\text{Ins}P_6$ binding proteins in platelets, and to discriminate between them and the specific 104 kDa $\text{Ins}P_4$ binding protein. $\text{Ins}P_6$ binding proteins include 65 kDa synaptotagmin II [15,40], a synaptic vesicle membrane protein involved in exocytosis [41], and adaptins, which are components of the adaptor complexes that link clathrin to receptors in coated vesicles, i.e. the α -subunit (AP-2, α -c large chain, alpha adaptin) of the clathrin assembly heterotetramer protein AP-2 [42] and clathrin assembly protein 3 (AP-3, AP180). AP-2 cDNAs code for proteins of 108 and 104 kDa [43], and were isolated from rat brain membranes as an $\text{Ins}P_6$ receptor complex of 115, 105 and 50 kDa polypeptides with K_D values for $\text{Ins}P_6$ of 12 nM and 120 nM, and the same sequence of affinities as AP-3, i.e. $\text{Ins}P_6 > \text{Ins}P_5 > \text{Ins}P_4 > \text{Ins}P_8$ [44]. AP-3 is a 91.4 kDa protein from brain that runs anomalously at 155–185 kDa by SDS/PAGE and has a K_D for Ins $P₆$ of 1.2 μ M [45,46]. Some effects of inositol phosphates on the functions of these proteins have been described [45,47–49].

We identified a class of Ins_6 binding sites in human platelet membranes with the relative affinities: $\text{Ins}P_6 > \text{Ins}P_5 > \text{Ins}P_4 >$ Ins P_3 . By appropriate chromatographic methods the Ins P_6 binding activity was totally separated from the $104 \text{ kDa Ins } P_4$ binding protein. The final purified $\text{Ins}P_6$ binding activity had a nominal molecular mass by gel filtration chromatography that was greater than 90 kDa, but less than 200 kDa, and contained one band of than 90 kDa, but less than 200 kDa, and contained one band of 116 kDa by SDS/PAGE analysis.The protein bound $[^3H]$ Ins P_6 with a K_D of 5.9 nM and a B_{max} of 3 nmol/mg of protein. The expected B_{max} for a 116 kDa protein with one ligand binding site is 8.6 nmol/mg of protein, indicating that the $\text{Ins}P_6$ binding activity was highly purified. The total amino acid composition of the protein band corresponded to the 1066 amino acids of 116732 Da human vinculin, and two peptides generated from the protein by proteolysis were identical to sequences in human vinculin [26].

Vinculin is a component of the platelet plasma membrane cytoskeleton [50] that may associate with the membrane through myristoylation or palmitoylation [51,52]. Although the C-terminus of vinculin is extremely basic [53], which might confer ligand binding properties comparable with those of the Arg/Lysrich inositol polyphosphosphate binding regions in $GAP1^{\text{IP4BP}}$ and synaptotagmin II, its ability to bind $\text{Ins} P_6$ has not been reported previously. However, we cannot rule out the possibility that the actual $\text{Ins}P_6$ binding protein is another component of similar molecular mass that co-purified with vinculin, such as the heavy chain of AP-2. Further work is required to fully establish the identity of the high-affinity $\text{Ins}P_{\text{g}}$ binding protein in platelets.

In conclusion, human platelet plasma membranes contain a s binding protein of apparent molecular mass
specific Ins_4 binding protein of apparent molecular mass 104 kDa and a specific $\text{Ins}P_6$ binding protein with an apparent molecular mass of 116 kDa. Inside-out plasma membrane vesicles molecular mass of 116 kDa. Inside-out plasma membrane vesicles
containing the $\text{Ins}P_4$ receptor accumulated Ca^{2+} in the presence of phosphate anion and ATP, and they released a significant portion of that Ca^{2+} when exposed to submicromolar concentrations of $\text{Ins}P_4$, but not $\text{Ins}P_3$ or $\text{Ins}P_6$. This effect is consistent with other findings indicating that $\text{Ins}\, P_4$ can act as a second messenger to increase the Ca^{2+} permeability of the plasma membrane and permit entry of Ca^{2+} from the extracellular space. This action of $\text{Ins}P_4$ may be a significant mechanism in platelets

to account for the influx of Ca^{2+} that occurs subsequent to agonist-induced production of $\text{Ins}P_3$ and its release of internal Ca^{2+} stores [54].

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