The Mammalian Brain rsec6/8 Complex

lated exocytosis of chemical messengers (reviews:
Scheller, 1995; Südhof, 1995). Within the presynaptic
terminal, neurotransmitter is packed into synaptic vesi-
cles which are targeted to active zones at the nerve
terminal transmitter into the synaptic cleft. Modulation of the doubles the previous number of known proteins in the probability of neurotransmitter release is an important synapse which are similar to the yeast proteins critical m mechanism of synaptic plasticity; sites of such modula-
tion likely include molecules which mediate synaptic suppossible to further investigate the mechanisms tion likely include molecules which mediate synaptic
vesicle functioning. Thus, a major endeavor of current
neurobiological inquiry is to understand the biochemical
events which govern the synaptic vesicle life cycle.
leas

In the past few years, the convergence of three major experimental approaches, yeast genetics, in vitro vesi-
Results cle trafficking assays and purification and analysis of synaptic vesicle proteins, has brought forth the realiza- **rsec6 and rsec8 Are Components of a 17S** tion that although neurons have evolved a regulated **Complex in Brain**

University of Singapore, 10 Kent Ridge Crescent, Singapore 119260. mained unknown. To determine whether rsec6 and

Shu-Chan Hsu,* Anthony E. Ting,*‡ cells displays similarities to constitutive intracellular Christopher D. Hazuka,* Svend Davanger,* versicle trafficking pathways found in all cells (reviews: **James W. Kenny,† Yun Kee,*** Bennett, 1994; Rothman, 1994; Südhof, 1995). Many of **and Richard H. Scheller*** the proteins involved in synaptic transmission are con- *Department of Molecular and Cellular Physiology served from yeast Saccharomyces cerevisiae cells Howard Hughes Medical Institute to mammalian neurons. Specifically, SSO1 and SSO2 Stanford University Medical School (Aalto et al., 1993), SNC1 and SNC2 (Gerst et al., 1992), Stanford, California 94305-5428 and five of the twelve SEC genes (*SEC1, SEC4, SEC9,* †Hewlett-Packard Company *SEC17,* and *SEC18*; Novick et al., 1980) which are essen-California Analytical Division the the later stages of the yeast secretory pathway 1601 California Avenue have well characterized mammalian homologs (reviews: Palo Alto, California 94034 Bennett and Scheller, 1993; Pfeffer, 1994; Ferro-Novick and Jahn, 1994). Homologs of these yeast proteins include cytosolic factors (nsec1, NSF and α -SNAP), vesi-**Summary** cle proteins (Rab3A and VAMP/synaptobrevin), and plasma membrane proteins (SNAP-25 and syntaxin). **rsec6 and rsec8 are two components of a 17S complex** Some of these proteins interact with one another to form **in mammalian brain that is homologous to the yeast** the 7S and the 20S complexes, which are thought to **834 kDa Sec6/8/15 complex which is essential for exo-** mediate vesicle docking, activation and membrane fu**cytosis. Purification and partial amino acid sequencing** sion (Söllner et al., 1993b; Söllner et al., 1993a). Seven **of the mammalian rsec6/8 complex reveals that it is** of the twelve late-acting SEC mutants in yeast, however, **composed of eight novel proteins with a combined** still do not have well defined mammalian homologs. **molecular weight of 743 kDa. The complex is broadly** Interestingly, the proteins mutated in six of these seven **expressed in brain and displays a plasma membrane** mutants, Sec3, Sec5, Sec6, Sec8, Sec10 and Sec15, **localization in nerve terminals. Membrane associated** have been postulated to be components of a 19.5S com**rsec6/8 complex coimmunoprecipitates with syntaxin,** plex composed of eight polypeptides (TerBush and No**a plasma membrane protein critical for neurotrans-** vick, 1995). We recently identified rsec6 and rsec8, puta**mission. These data suggest a role for the mammalian** tive mammalian homologs of two members of this **rsec6/8 complex in neurotransmitter release via inter-** complex (Ting et al., 1995). Identification of these two **actions with the core vesicle docking and fusion appa-** mammalian SEC mutant homologs has provided a valu**ratus.** able stepping stone toward the isolation of the mammalian complex.

Here we demonstrate that, in brain, rsec6 and rsec8 **Introduction** are present together ina high molecular weight complex. Neurons communicate with target cells through regu-
lated executosis of chemical messengers (reviews: it is composed of eight proteins. Biochemical and immumembrane lipid bilayer, resulting in the release of neuro-
transmitter into the synaptic cleft. Modulation of the doubles the previous number of known proteins in the

Frevious studies demonstrated that rsec8 is a component of a 17S complex in rat brain (Ting et al., 1995). ‡Present address: Institute of Molecular and Cell Biology, National However, the biochemical associations of rsec6 re-

Proteins from rat brain supernatant were separated on a linear glyc-
Proteins from rat brain supernatant were separated on a linear glyc-
 erol gradient, and gradient fractions were collected and analysed immunoreactivity was concentrated and further purified by SDS–PAGE followed by Western blotting. using a strongly basic anion exchange resin, TMAE-

the top of the gradient. Size markers (indicated by the arrows) from HW55-S gel filtration chromatography. The rsec6 and left to right are bovine serum albumin (4.3S), β -amylase (11.2S) and rsec8 immunoreactivity was eluted in a single peak with

(C) Coimmunoprecipitation of rsec6 and rsec8. Immunoprecipitation At this stage of purification, eight polypeptides of molec-
The polyethylene glycol-fractionated rat brain supernatant was car-
Lar weights between 70 kDa a or polyemylene giycol-fractionated rat brain supernatant was car-

ried out with affinity-purified antibodies against rsec8 or with control

rabbit immunoglobulin. The immunoprecipitated sample was analyzed on a SDS polyac lysed for the presence of rsec6, rsec8 and nsec1 by Western blotting. Brain is the starting material; Ab represents proteins bound to the a second anion exchange chromatography utilizing anti-rsec8 antibody in the absence of brain homogenate; Ab + brain TMAE-Fractogel. Analysis of salt-eluted fractions from
1 represents proteins bound to the anti-rsec8 antibody following incu-
this column by SDS-PAGE revea represents proteins bound to the anti-rsec8 antibody following incu-
bation with brain homogenate; and Ig + brain represents proteins
bound to the control rabbit immunoglobulin following incubation
with brain homogenate. T

brain proteins were fractionated on a linear glycerol gra- eight proteins constitute at least 95% of the total prodient and the gradient fractions were analysed by both teins in this fraction (Figure 2A, lane TMAE2; Figure 2C). sodium dodecyl sulfate polyacrylamide gel electropho- Fractionation of the purified complex ona glycerol gradiresis (SDS–PAGE) and Western blotting (Figure 1A). ent demonstrated that all eight components comigrate Most of the proteins fractionated between the 4.3S and at the 17S position (data not shown). In addition, all eight 11.2S regions of the gradient. The migration of rsec6 proteins coimmunoprecipitate with rsec8 monoclonal

and rsec8 in the gradient was monitored by Western blot analysis using affinity-purified anti-rsec6 and antirsec8 antibodies. As demonstrated previously, rsec8migrated to the 17S position. Interestingly, rsec6 also migrated tothe 17S position (Figure 1B). In contrast, nsec1, another synaptosomal protein, migrated to the 4.3S position as previously observed (Pevsner et al., 1994b). This experiment indicates that all of the soluble rsec6 and rsec8 protein is in a large complex and that little or no protein is found in monomeric state. Because the Coomassie blue–stained glycerol gradient protein profile (Figure 1A) showed the presence of many proteins in the 17S region, it was necessary to determine whether the cofractionating rsec6 and rsec8 were in the same complex. Figure 1C shows an immunoprecipitation of rsec8 from soluble brain proteins using affinity-purified rabbit polyclonal anti-rsec8 antibodies. rsec6, but not nsec1, coimmunoprecipitated with rsec8. No rsec6, rsec8 or nsec1 were immunoprecipitated by control rabbit immunoglobulin, confirming the specific binding of the rsec6/8 complex to anti-rsec8 antibodies. These data demonstrate that both rsec6 and rsec8 are components of the same high molecular weight complex.

Purification of the Mammalian rsec6/8 Complex

The rsec6/8 complex was purified from rat brain by four sequential chromatographic steps to define other members of the complex (Figure 2A). The enrichment of the rsec6/8 complex following each chromatographic step was monitored by Western blot analysis (Figure 2B). Initially, cytosol prepared from frozen rat brains was applied to and step-eluted from hydroxyapatite. No significant amount of rsec6 and rsec8 was detected in the Figure 1. rsec6 and rsec8 Are Components of a 17S Complex flow-through from this column. The pooled hydroxyapa-(A) Coomassie blue–stained protein profile of glycerol gradient frac- Fractogel. All rsec6 and rsec8 immunoreactivity was tions. The positions of rsec8, rsec6 and nsec1 on the gel are indi-
cated on the right as 8, 6, and 1, respectively.
(B) Immunodetection of rsec6, rsec8 and nsec1 in gradient fractions
using immunoaffinity-purified antibod thyroglobulin (19.2S).
(C) Coimmunoprecipitation of rsec6 and rsec8. Immunoprecipitation
At this stage of purification. eight polypeotides of molecof rsec6 and rsec8 immunoreactivity (data not shown). SDS–PAGE analysis of pooled peak rsec6 and rsec8 rsec8 function together in a protein complex, soluble immunoreactivity fractions indicated that these same

antibodies (data not shown). Approximately 100–200 μ g of rsec6/8 complex was recovered from 50 rat brains after purification. Quantitation of the enrichment of the rsec6/8 complex by Western blot using 125I-labeled secondary antibodies suggest that the complex constitutes approximately 0.1% of the total soluble brain protein. All eight proteins were approximately equally stained by Coomassie blue (although p79 reproducibly appears to stain somewhat less intensely) suggesting a stoichiometry of one copy of each protein within the complex (Figure 2C). This 1:1 stoichiometry is further supported by the apparent molecular weight of 600–700 kDa of the native complex.

Peptide Sequencing of the rsec6/8 Complex Components

To further characterize individual components of the mammalian rsec6/8 complex, the purified complex was fractionated on an SDS polyacrylamide gel and each polypeptide band was individually subjected to in-gel proteolysis with trypsin, Lys C and/or Glu C. The digested peptides were eluted from the gel, fractionated by high performance liquid chromatography(HPLC), and in many cases, analysed by mass spectrometry for peptide purity and mass. Figure 3 shows the mass spectrometric analyses of HPLC peptide peaks from four proteins, p102, p96, p84 and p71. A single peptide peak in the mass spectrometry profile suggests the presence of one peptide species in the analysed HPLC peptide peak, as shown in (A), (B), and (C). The multiple peaks shown in (D) are due to the binding of different amounts of salt to the peptide. Amino acid sequence analysis of this peptide peak confirmed the presence of only one peptide species. Preselection of HPLC peaks for single peptide fractions by mass spectrometry greatly increases the clarity and confidence of obtained peptide sequences, as the observed and predicted masses differed by less than 0.1% (See Experimental Procedures and Figure 3 legend).

Figure 4 shows all the peptide sequences obtained from eight predicted members of the rsec6/8 complex. Peptide sequences from p110 and p86 confirmed that these two proteins are rsec8 and rsec6, respectively

Figure 2. Purification of Rat Brain rsec6/8 Complex

The rsec6/8 complex was purified from frozen rat brains using four sequential column chromatographic steps.

(A) Coomassie blue–stained SDS polyacrylamide gel analysis of pooled column fractions. Lys, starting soluble brain proteins; HT, hydroxyapatite eluant; TMAE, TMAE anion exchanger eluant; GF, HW55S gel filtration eluant; TMAE2, second TMAE anion exchanger eluant. Positions of rsec6 and rsec8 on the gel are indicated on the right as 6 and 8, respectively. Fifteen μ g of proteins were loaded in lane Lys, HT and TMAE; eight μ g of proteins were loaded in lane $GF:$ and three μ g of proteins were loaded in lane TMAE2.

(B) Western blot analysis of the column fractions shown in (A). The enrichment of the rsec6/8 complex following each column chromatography was monitored using mouse polyclonal antibodies against rsec6 and rsec8.

(C) Coomassie blue–stained SDS polyacrylamide gel analysis of purified rsec6/8 complex. Peptide sequences from protein bands 110 kDa and 86 kDa indicate that they are rsec8 and rsec6, respectively.

on SDS polyacrylamide gels, cut out and digested with Trypsin, Lys C and/or Glu C. The digested peptides were then subjected to HPLC spectively (Figure 6A). Similarly, in crude synaptosomes, fractionation and some HPLC peptide peaks were analysed by mass the majority of rsec6 and rsec8 was found associated
spectrometry for their mass and purity. Mass spectrometric analysis with synaptosomal membranes. Very lit spectrometry for their mass and purity. Mass spectrometric analysis with synaptosomal membranes. Very little rsec6 and
of peptides from p102, p96, p71 and p84 are shown in (A) to (D),
respectively. The mass of each peptide of each peptide determined by peptide sequencing and its mass (protonated form of peptide) calculated from the determined peptide (data not shown). The presence of rsec6 and rsec8 in sequence is shown beside corresponding peptide peak. In (A) to the membrane fraction was not due to the entrapment
(C) the calculated and observed masses matched with less than of the complex in intact cells or organelles (C) the calculated and observed masses matched with less than
0.1% difference. In (D), mass spectrometry analysis was used to
predict the last two amino acids (underlined) of the poptide. Amino
acids Y and K were the only be added to the peptide to result in a mass that agrees with the mogenized in hypotonic buffer with a Polytron. Likewise, mass spectrometry with less than 0.1% difference. Da $=$ dalton. the presence of these two proteins in the supernatant

(Figure 2C). Furthermore, all of the peptide sequences ATPase, a plasma membrane marker, were detected from these two protein bands match the amino acid only in synaptosomal membrane pellet and not in synapsequence predicted by rsec6 and rsec8 cDNAs demon- tosomal cytosol. strating that the bands are free of contaminating pro- To determine if the pool of the rsec6/8 complex teins and that the rsec6/8 complex is relatively pure. that pelleted with crude synaptosomal membranes at Comparison of remaining peptide sequences to Gen- $100,000 \times g$ was due to its association with synapto-Bank and a database of human expressed sequence somal membranes or with large proteinaceous aggretag (EST) cDNAs generated by the Institute for Genomic gates, we subjected crude synaptosomal membranes

Research found matches to two proteins p71 and p79. Overall the amino acid sequences match the sequences predicted from the cDNAs with an accuracy greater than 87%. Taken together, these results suggest that members of the rsec6/8 complex are novel proteins which have not been previously characterized.

The rsec6/8 Complex Is Ubiquitously Expressed

As a first step to determine the site of rsec6/8 complex function in brain, we examined the brain regional distribution of these proteins. Figure 5A shows that rsec8 is expressed in all regions of rat brain examined and there is no significant brain regional variation. A similar expression pattern is also observed for rsec6 (data not shown) suggesting that both proteins are required by all brain cells. To see whether the rsec6/8 complex functions in multiple exocytotic pathways in addition to the regulated pathway underlying neurotransmission, the presence of rsec8 in cell lines derived from kidney, ovary, pituitary and adrenal medulla tissues was investigated (Figure 5B). Western blot analysis using affinitypurified anti-rsec8 rabbit polyclonal antibodies detected rsec8 as a 110 kDa protein in all the cell lines examined. rsec6 was also observed in all cell lines examined (data not shown). Interestingly, the cells with the highest amounts of rsec8 were AtT-20 and PC-12 cells. Both cell lineshave regulated secretory pathways and contain numerous secretory vesicles as well as synaptic proteins, suggesting that the expression of the rsec6/8 complex parallels the level of secretory activity in cells.

Subcellular Localization of the rsec6/8 Complex

To understand better the biochemical properties of the rsec6/8 complex, we carried out cell fractionation studies to investigate its solubility properties. Upon homoge-Figure 3. Mass Spectrometric Analysis of rsec6/8 Complex Pep-
tides
Protein components of purified roof (8 complex were fractionsted and provimately 25% and 75% of rsec6 and rsec8 were Protein components of purified rsec6/8 complex were fractionated
on SDS polyacrylamide gels, cut out and digested with Trypsin Lys found in the supernatant and the membrane pellet, rewas not due to contaminating membrane fragments because both SV2, a synaptic vesicle marker, and Na/K

 β digestion; p86 or rsec6 peptide 1 was obtained from Lys C digestion and p86 or rsec6 peptides 2–3 were obtained from a combination of Lys C and Glu C digestion; p84 peptide 1 was obtained from Lys C digestion and p84 peptides 2–8 were obtained from a combination of Lys C and Glu C digestion; p79 peptides 1–4 were obtained from Lys C digestion and p79 peptides 5–8 were obtained from a combination of Lys C and Glu C digestion; p71 peptides were obtained from Lys C digestion.

rsec8 floated up into the sucrose gradient, as observed vesicles. While the synaptic vesicle–specific protein with both Na/K ATPase, and synaptophysin (a synaptic synaptotagmin was present in anti-SV2 antibody immuvesicle marker). Very little rsec6 and rsec8 were de- noprecipitated vesicles, no rsec8 was detected even tected at the bottom of the gradient as protein aggre- upon longer exposure. Neither protein was immunopregates. These data suggest that the insoluble pool of cipitated by control mouse immunoglobulin indicating rsec6/8 complex isassociated with synaptosomal mem- a specific association of synaptic vesicles with anti-SV2 branes. antibody. These results suggest that rsec6/8 complex is

tion with membranes, brain membranes were extracted leaving the plasma membrane as the likely site of its with 20 mM Tris buffer, 1.5 M NaCl, 4% Triton X-100, membrane localization. or 4 M urea (Figure 6C). The extracted membranes were centrifuged and the resulting supernatants and membrane pellets were subjected to Western blot analysis. **Localization of rsec8 in Cultured** The amount of complex extracted under these condi- **Hippocampal Neurons** tions was examined by probing the Western blots with To confirm the presence of the rsec6/8 complex in synantibodies against rsec8 and quantitating by phos- apses, its localization in primary hippocampal cultures phorimaging using ¹²⁵I-labeled secondary antibodies was studied by immunofluorescence microscopy. Syn-(See Experimental Procedures). Approximately 4%, aptic terminals in these cultures were identified by the 46%, 60% and 88% of the rsec6/8 complex were ex- presence of thesynaptic vesicle marker, synaptotagmin. tracted by Tris buffer, 1.5 M NaCl, 4% Triton X-100 and Figure 7A shows that rsec8 labeling was detected 4 M urea, respectively. The incomplete extraction of the throughout hippocampal neurons, including the cell rsec6/8 complex in the presence of a high concentration bodies, dendrites, axons and nerve terminals. Brighter of salt suggests that this complex may bind very tightly rsec8 staining at synapses suggests an accumulation to the membranes. Interestingly, a fraction of the native of the rsec6/8 complex in nerve terminals (Figures 7A rsec6/8 complex is found in the Triton X-100 insoluble and 7B). Although both synaptotagmin and rsec8 were pellet following membrane solubilization, contrary to the detected in synaptic terminals, staining of rsec8 was observation that purified soluble rsec6/8 complex is more concentrated near the plasma membrane than that completely soluble in Triton X-100, suggesting that the of synaptotagmin (Figures 7B, 7C, and 7D). Many termimembrane-bound complex may be associated with cy- nals displayed rsec8 labeling in peripheral areas where toskeletal elements. Taken together, these observations it did not colocalize with the more centrally positioned suggest that the insoluble pool of rsec6/8 complex may synaptotagmin staining. Glial and other non-neural cells be associated with cytoskeletal elements which, in turn, in the hippocampal neuron cultures were also stained, bind to membranes. Further studies will be required to although typically more weakly than the neurons (data

the sucrose gradient as synaptic vesicles and plasma bodies wereused as the primary antibodies. At the same cles. Synaptic vesicles were immunoprecipitated using gether, these biochemical and histochemical data sugspecific integral membrane protein. Figure 6D shows the membrane.

to sucrose gradient flotation (Figure 6B). Both rsec6 and Western blot analysis of immunoprecipitated synaptic To investigate the nature of rsec6/8 complex associa- not associated strongly or stably with synaptic vesicles

understand these issues. not shown). As controls, preimmune immunoglobulins Since rsec6 and rsec8 floated to the same region of of same protein concentrations as the anti-rsec8 antimembranes, we investigated the possibility of an associ- time exposures, no staining was observed in these neuation between the rsec6/8 complex and synaptic vesi- rons using identical labeling procedures. Taken toa monoclonal antibody against SV2, a synaptic vesicle– gest that the rsec6/8 complex is localized to the plasma

Figure 5. The rsec6/8 Complex Is Broadly Distributed (A) Western blot analysis of brain regional expression of the rsec 6/8 complex. Ten μ g of brain proteins were loaded per lane.

(B) Distribution of the rsec6/8 complex in cultured cell lines. Ten μ g (A) Western blot analysis of subcellular fractionation of the rsec6/8 complex. Ten

including its membrane association in brain, we gener-
ated monoclonal antibodies against rsec8. These anti-
bodies, with the exception of mAb15E12, recognize a
let a 100,000 × g spin to yield both soluble
bodies, with th single band of 110 kDa in brain postnuclear supernatant that of the corresponding supernatants. Five ul of each protein (Figure 8A). Monoclonal antibody 15E12 detected a ma-
ior band of 110 kDa in addition to two minor bands of these fractions were analysed by Western blotting. jor band of 110 kDa in addition to two minor bands of these ractions were analysed by western blotting.
65 kDa and 90 kDa. These two lower molecular weight can be considered with brain membranes.
bands are likely to be deg Of the seven monoclonal antibodies generated, only flotation of the rsec6/8 complex into the gradient was monitored mAbs 2E9 and 17A10 immunoprecipitate the rsec6/8 by Western blot analysis using mouse polyclonal antibodies. The complex. migration of plasma membrane andsynaptic vesicles was also mon-

to yield postnuclear supernatant (PNS).. The PNS was then subjected to either a 100,000 \times g spin to yield soluble (PNS sup) and **Coimmunoprecipitation of rsec8 Complex** membrane protein (PNS pellet) fractions or a 25,000 \times g spin to with Syntaxin
To better study the properties of the rsec6/8 complex (crude synaptosomes). The synaptosomal pellet was lysed in 2 mM To better study the properties of the rsec6/8 complex, (crude synaptosomes). The synaptosomal pellet was lysed in 2 mM
including its mombrane association in brain, we gener. Hepes, pH 7.4 and homogenized with a Polytron. T were resuspended in 20 mM Hepes, pH 7.4 to volumes equal to

Figure 7. The rsec6/8 Complex Is Present in Nerve Terminals of Cultured Primary Hippocampal Neurons Figure 8. Syntaxin Associates with the rsec6/8 Complex

and synaptotagmin (C). (D) shows a larger magnification of rsec8 brain postnuclear supernatant were loaded per lane. staining overlaid with that of synaptotagmin at two synaptic termi- (B) Coimmunoprecipitation of syntaxin with rsec8. Immunoprecipita-

rsec6/8 complex from 1% CHAPS or 1% Triton X-100 blotting. Ab represents proteins bound to the anti-rsec8 monoclonal
solubilized rat brain membranes. Interestingly, syntaxin antibodies. Ig represents proteins bound to cont both detergents (the association appears more stable

15- to 20-day-old cultures of primary hippocampal neurons were (A) The specificity of seven monoclonal antibodies generated fixed and immunostained with antibodies against rsec8 (A and B) against rsec8 was investigated by Western blot analysis. Ten μ g of

nals indicated by arrows. Bar = 7 μ m. tion of CHAPS or Triton X-100 solubilized rat brain membranes was carried out either with monoclonal antibodies 2E9 and 17A10 or with control mouse immunoglobulins. The immunoprecipitated sam-Figure 8B shows the immunoprecipitation of the ple was analysed for the presence of rsec8 and syntaxin by Westem
ec6/8 complex from 1% CHAPS or 1% Triton X-100 blotting. Ab represents proteins bound to the anti-rsec8 monoc

in the presence of CHAPS). Under these conditions

rsec8 is present in the 743 kDa complex (data not shown)

suggesting that the entire native complex is associated

with syntaxin. While more than 90% of rsec6/8 complex

p complex. Prolonged incubation of brain membranes in detergents or solubilization of brain membranes at itored using rabbit polyclonal antibodies against Na/K ATPase and higher detergent concentrations appears to weaken the a monoclonal antibody against synaptophysin, respectively. Frac-
syntaxin association with the rsec6/8 tion 1 corresponds to the top of the gradient.

(C) Nature of rsec8 association with brain membranes. Lysed brain

membranes were extracted with either 20 mM Tris. pH 8.0. 1.5 or N-ethylmaleimide-sensitive factor (NSF) coi and quantitated by phosphorimaging using anti-rsec8 primary and immunoglobulin. Together, these data indicate the spe-
¹²⁵I-labeled secondary antibodies (see Experimental Procedures). The colmmunoprecipitation of syntaxi --i-labeled secondary antibodies (see Experimental Procedures).

(D) Immunoprecipitation of synaptic vesicles from rat brain supernation of Syntaxin with the rsec

tant with anti-SV2 antibody or control mouse immunoglobuli examined for the presence of synaptotagmin and rsec8 by Western may serve as a plasma membrane receptor for the rsec

a monoclonal antibody against synaptophysin, respectively. Frac-

syntaxin association with the rsec6/8 complex. In the

same immunoprecipitation studies no n-sec1. Bab3A

M NaCl, 4% Triton X-100 or 4 M urea. Following extraction, the precipitated with the rsec6/8 complex confirming the membranes were centrifuged to yield soluble (s) and membrane (p) specificity of the immunoprecipitation. In addition, no fractions. The presence of rsec8 in these fractions was detected rsec8 or syntaxin were precipitated by control mouse

blotting. 6/8 complex.

are homologs of yeast Sec6p and Sec8p based on se- tion of an in vivo interaction between rsec8 and syntaxin quence identity (Ting et al., 1995). In this report, glycerol as revealed by the immunoprecipitation of syntaxin with gradient and immunoprecipitation analyses demon- anti-rsec8 antibodies. Additionally, staining of the Sec6/ strate that rsec6 and rsec8 are components of a 17S 8/15 complex in yeast appears enhanced at the site of protein complex. Purification of this mammalian rsec vesicle docking and fusion in the tip of the bud. This 6/8 complex by column chromatography revealed that observation is echoed in neurons stained with antibodit is composed of eight distinct proteins with a combined ies to rsec8. The area near the plasma membrane of the molecular weight of 743 kDa. Although the sequence nerve terminals, the site of exocytosis, are enriched in homology of Sec6 and Sec8 proteins between yeast and anti-rsec8 labeling. Thus, the yeast studies, along with rat is only in the 20%–25% range, the purified mamma-
lian rsec6/8 complex exhibits several striking physical support the proposal that the rsec6/8 complex, directly lian rsec6/8 complex exhibits several striking physical support the proposal that the rsec6/8 complex, directly
and biochemical similarities to its yeast counterpart. Or indirectly interacts with syntaxin and is a critical and biochemical similarities to its yeast counterpart. First, both mammalian and yeast complexes are rela-
tively large in size. The predicted molecular weights for
The data are consistent with a role for the rsc6/8 comtively large in size. The predicted molecular weights for the mammalian and yeast sec6/8 complexes are 743 plex in synaptic vesicle exocytosis upstream of the prekDa and 834 kDa, respectively (TerBush and Novick, viously proposed 7S and 20S synaptic vesicle docking/ 1995). Second, both complexes are composed of eight fusion machinery. However, at this early stage of analypolypeptides with similar molecular weights ranging sis we cannot rule out a role for the complex in later from 70 kDa to 140 kDa. Third, both complexes are stages of exocytosis as well.
unusually stable. Specifically, both Sec6 and Sec8 in stand and andition, a genetic interaction has also been obunusually stable. Specifically, both Sec6 and Sec8 in In addition, a genetic interaction has also been ob-
veast and rsec6 and rsec8 in rat brain are always found served between Sec8/Sec15 and Sec4, a yeast homolog yeast and rsec6 and rsec8 in rat brain are always found served between Sec8/Sec15 and Sec4, a yeast homolog as components of a large complex on glycerol gradients;
monomeric forms of these proteins are never observed terminals, Rab3A, a GTPase, is found associated with monomeric forms of these proteins are never observed
under nondenaturing conditions Unlike the 20S particle synaptic vesicles (Farnsworth et al., 1991; Fischer von under nondenaturing conditions. Unlike the 20S particle synaptic vesicles (Farnsworth et al., 1991; Fischer von
composed of syntaxin, VAMP, SNAP-25, α -SNAP and Mollard et al., 1990). Thus the data presented here are NSF, the 17S rsec6/8 complex does not dissociate in suggestive of a role for the rsec6/8 complex in a Rab response to ATP hydrolysis. In fact, this complex does mediated event at the plasma membrane, possibly innot dissociate in the presence of ATP, GTP, ATP_yS, tervening between the Rab and the 7S complex (Bowser $GTP_{\gamma}S$, complex (Bowser $GTP_{\gamma}S$, complex (Bowser GTP_YS , EGTA and/or Ca²⁺ (data not shown). Fourth, the equal of al., 1992). It is possible that one of the mechanisms grammation resection of the mechanisms grammation resection of the mechanisms of action of the r mammalian rsec6/8 complex displays solubility proper-
ties similar to its veast counterpart. In both organisms interaction with Rab3A on synaptic vesicles. Character-

teins, VAMP/synaptobrevin and synaptotagmin, and two **Experimental Procedures** presynaptic plasma membrane proteins, syntaxin 1A and SNAP-25 (Bennett et al., 1992b; Söllner et al., 1993a; **Glycerol Gradient Analysis** Söllner et al., 1993b). A role for the rsec6/8 complex at Rat brain supernatant was fractionated on a linear glycerol gradient
this step is suggested by studies of yeast secretory and analyzed by Western blotting as descri this step is suggested by studies of yeast secretory. mutants which have revealed genetic interactions be-
tween Sec8/Sec15 and the yeast homologs of syntaxin
and SNAP25, SSO1 and Sec9. Specifically, overexpres-
Bio-Gel HT Hydroxyapatite Chromatography sion of SSO1 can suppress mutations in the SEC15 gene Fifty frozen rat brains (Harlan, IN) were homogenized in 400 ml of (Aalto et al., 1993), while overexpression of Sec9 can homogenization buffer (20 mM Hepes, pH 7.4, 200 mM NaCl, 1 mM

Discussion suppress mutations in both the SEC8 and SEC15 genes (Brennwald and Novick, 1993). These observations in We previously identified two mammalian proteins that yeast can be extended to mammals with the demonstra-

ties similar to its yeast counterpart. In both organisms,

the raction with Rab3A on synaptic vesicles. Character-

the complex is found in soluble and membrane-bound in asso-

states. In yeast the Sec6/8/15 complex ins fo

and-down strokes with a Teflon/glass homogenizer. A postnuclear subjected to SDS–PAGE and Western blot analysis. supernatant was obtained by centrifuging the homogenate at 5000 For brain membrane extraction studies, lysed brain membranes supernatant was obtained by centrifuging the postnuclear superna- mg/ml) were incubated with equal volumes of either 20 mM Tris, tant at 36,000 rpm in a Ti45 rotor (Beckman, CA) for 1 hr. Following pH 8.0, 3 M NaCl in 20 mM Tris, pH 8.0, 8% Triton X-100 in 20 mM the centrifugation, a final concentration of 110 mM sodium phos-

Tris, pH 8.0, or 8 M urea in 20 mM Tris, pH 8.0. The incubations phate, pH 7.4 was added to the supernatant before it was applied were carried out at 4° C for 1 hr. Following the incubation, the memto a 25 ml hydroxyapatite (BioRad, CA) column equilibrated with branes were pelleted at 50,000 \times g. The resulting supernatants and the homogenization buffer containing 110 mM sodium phosphate membrane pellets were anal at a flow rate of 20 ml/hr at 18°C. The column was washed with 75 blot. The amount of rsec8 extracted from membranes were quanti-DTT, pH 7.4) and eluted stepwise with 5 ml aliquots of 0.2M to 0.65 The pixel values for 20 mM Tris extraction were 6713 for supernatant M phosphate in buffer A, with 50 mM phosphate increment per step. and 173171 for pellet; for 1.5 M NaCl extraction were 39189 for
Fractions containing rsec6 and rsec8 as determined by Western supernatant and 45414 for pell blot analyses were pooled and dialyzed twice against 2 liters of 20 56302 for supernatant and 37254 for pellet; and for urea extraction mM Tris, pH 8.0, 100 mM NaCl, 0.2 mM EDTA, and 0.5 mM DTT were 71419 for supernatant and 9999 for pellet. overnight. For sucrose gradient flotation analysis of rsec6/8 complex, lysed

of 20 mM Tris, pH 8.0 and loaded onto a 3 ml column of Fractogel DTT) at a protein concentration of 4 mg/ml. The resuspended mem-TMAE anion exchange resin (EM Separations Technology, NJ) equili-
brated with 20 mM Tris, pH 8.0, 50 mM NaCl, and 1 mM DTT at a gradient. After centrifugation at 42,000 rpm for 16 hrs in a TLS 55 flow rate of 15 ml/hr. The column was washed with 20 mM Tris, pH rotor (Beckman, CA), the gradient was fractionated and analysed 8.0, 50 mM NaCl, 1 mM DTT and eluted with a linear gradient of 0 by Western blot for rsec6, rsec8, Na/K ATPase (a plasma membrane to 350 mM NaCl in 20 mM Tris, pH 8.0 and 1 mM DTT. marker) and synaptophysin (a synaptic vesicle marker).

HW-55S Gel Filtration Chromatography

TMAE eluant fractions enriched in rsec6 and rsec8 were pooled and **Immunoprecipitation Studies** fractionated over a 180 ml HW-55S gel filtration column (TosoHaas, *Immunoprecipitation of the rsec6/8 Complex*

amide gel. Individual protein bands were cut out and subjected to in protein sample buffer, and subjected to Western blot analysis. in-gel proteolysis at the Stanford Pan facility by Lys C, trypsin and/ or Glu C using the method of Hwang et al. (1996). The digested **Immunoprecipitation of Synaptic Vesicles** peptides were fractionated by HPLC (Applied Biosystems, CA). Se-
Iected peptide peaks were then subjected to amino acid sequencing and a Waring blender. The powderized brain was then homogenized in 20 lected peptide peaks were then subjected to amino acid sequencing Waring blender. The powderized brain was then homogenized in 20 digestion, some peptides from p106, p96 and p79 were also fraction-
homogenizer. The homogenate was centrifuged at 100,000 \times g for

For brain regional Western blot analysis, various rat brain regions PAGE and analysed by Western blotting. were dissected from fresh brain and sonicated in 10 mM Hepes, pH 7.4, 2.5 mM KOAc, 1 mM MgCl₂, 0.1 mM EGTA, and 0.3 mM PMSF. **Coimmunoprecipitation of Syntaxin and the rsec6/8 Complex**
The homogenates were centrifuged at 10,000 × g for 5 min and the Anti-rsec8 monoclonal antibodies 2E

dithiothreitol (DTT), 0.1 mM EDTA and 0.3 mM PMSF) by eight up- in a TLS 55 rotor (Beckman, CA) at 4°C. All protein samples were

rpm in a JA-10 rotor (Beckman, CA) for 15 min. Soluble brain protein resuspended in 20 mM Tris, pH 8.0, 1 mM DTT and 10% sorbitol (2 membrane pellets were analysed for their rsec8 content by Western ml of 0.15 M sodium phosphate in buffer A (0.15 M NaCl, and 1 mM tated by phosphorimaging using 125I-labeled secondary antibodies. supernatant and 45414 for pellet; for Triton X-100 extraction were

Fractogel EMD TMAE-650 (S) Chromatography crude synaptosomal membranes were resuspended in 55% sucrose in gradient buffer (20 mM Hepes, pH 7.4, 150 mM NaCl and 1 mM gradient. After centrifugation at 42,000 rpm for 16 hrs in a TLS 55

Immunoaffinity purified anti-rsec8 antibodies (Ting et al., 1995) or DTT at a flow rate of 5 ml/hr.

Second Fractogel EMD TMAE-650 (S) Chromatography

a final concentration of 0.5 mg/ml as previously described (Peysner *Second Fractogel EMD TMAE-650 (S) Chromatography* a final concentration of 0.5 mg/ml as previously described (Pevsner rsec6 and rsec8-enriched fractions from HW-55S gel filtration col- et al., 1994a; Pevsneret al., 1994b). Three ml of rat brain supernatant
umn chromatography were pooled and diluted to a final buffer con- (Ting et al., 199 umn chromatography were pooled and diluted to a final buffer con-
centration of 20 mM Tris, pH 8.0 and 50 mM NaCl. The diluted at 4°C and centrifuged at 20.000 × q for 10 min. The pellet was at 4°C and centrifuged at 20,000 \times g for 10 min. The pellet was sample was applied to and eluted from a 0.5 ml Fractogel TMAE- dissolved in 1 ml 20 mM Tris, pH 8.0 and 50 mM NaCl and precleared 650 column as described above. Fractions containing purified rsec by incubation with 200 ul protein A beads for 4 hrs at 4°C. Following 6/8 complex were pooled and used for SDS–PAGE analyses and incubation, 500 μ of precleared brain supernatant was incubated peptide sequencing. with 30 μ of either anti-rsec8 antibody or rabbit immunoglobulin coupled to protein A beads overnight at 4° C. The beads were then **Mass Spectrometry and Peptide Sequence Analysis** washed three times with 200 μ l 20 mM Tris, pH 8.0, 150 mM NaCl Purified rsec6/8 complex was fractionated on an 8% SDS polyacryl- and 0.05% Tween 20. Proteins bound to the beads were solubilized

ml of 0.3 M sucrose and 10 mM Hepes, pH 7.5 with a Teflon-glass ated on a 1090 HPLC (Hewlett-Packard, CA). Selected HPLC frac-
tions were subjected to MALDI-TOF mass analysis (Hewlett-Pack-
of anti-SV2 monoclonal antibody or purified mouse immunoalopulin tions were subjected to MALDI-TOF mass analysis (Hewlett-Pack-of anti-SV2 monoclonal antibody or purified mouse immunoglobulin
ard, CA). Following mass spectrometric analysis, selected peptideogoupled Dynabeads M-500 (Dyna coupled Dynabeads M-500 (Dynal, Oslo; 16 μ g antibody/50 μ l fractions were subjected to amino acid sequencing (Hewlett Pack- beads) in 0.3 M sucrose, 10 mM Hepes, pH 7.5 and 0.15% bovine serum albumin. Following incubation, the beads were washed four times with 0.3 M sucrose, 10 mM Hepes, pH 7.5 and solubilized in **Brain Regional and Tissue Culture Cell Western Blot Analysis** protein sample buffer. Protein samples were subjected to SDS–

Anti-rsec8 monoclonal antibodies 2E9 and 17A10 or mouse immupostnuclear supernatants were collected.
For Western blot analysis of the rsec8 distribution in various cul-
of 2 mg/ml using the cross-linker dimethylpimelimidate as previously For Western blot analysis of the rsec8 distribution in various cul- of 2 mg/ml using the cross-linker dimethylpimelimidate as previously described (Pevsner et al., 1994a). Rat brain membranes prepared petri dishes, scraped, and dounce homogenized in 20 mM Hepes, as described above were resuspended in 20 mM Tris, pH 8.0, 150
pH 7.4. The homogenates were centrifuged at 5000 × g for 5 min mM NaCl and solubilized with eithe pH 7.4. The homogenates were centrifuged at 5000 \times g for 5 min mM NaCl and solubilized with either 1% CHAPS or Triton X-100 at and the supernatants were collected for Western blot analysis.
a final protein concentratio a final protein concentration of 2 mg/ml. The solubilized sample was incubated at 4°C for 30 min before centrifuging at 20, 000 \times g for **Subcellular Localization of rsec6/8 Complex** 20 min. Following centrifugation, the solubilized brain membranes For brain subcellular fractionation studies, postnuclear supernatant were precleared by incubation with protein G beads (1 ml solubilized and crude synaptosomal membrane fractions were prepared as membranes per 200 μ l protein G beads) for 30 min at 4°C. The described (Bennett et al., 1992a). Soluble brain proteins and brain precleared supernatant was then incubated with 20 ul protein G membranes were obtained by centrifuging the postnuclear superna- beads with either immobilized anti-rsec8 monoclonal antibodies tant or lysed crude synaptosomal fraction at 100,000 \times g for 20 min 2E9/17A10 or immobilized control mouse Ig for 4 hrs at 4 °C. The

beads were then washed three times with 300 μ l 20 mM Tris, pH a synaptic protein implicated in docking of synaptic vesicles at 8.0, 150 mM NaCl containing either 0.7% CHAPS or Triton X-100. presynaptic active zones. Science *257*, 255–259. Proteins bound to the beads were analyzed by Western blotting. Bowser, R., Müller, H., Govindan, B., and Novick, P. (1992). Sec8p

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tained as described by Malgaroli and Tsien, 1992. Immunocyto-

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