COMPOSITION OF THE SYNAPTIC PSD-95 COMPLEX

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ABSTRACT

PSD-95, a specialized scaffold protein with multiple protein interaction domains, forms the backbone of an extensive postsynaptic protein complex that organizes receptors and signal transduction molecules at the synaptic contact zone. Large, detergent-insoluble PSD-95-based postsynaptic complexes can be affinity-purified from conventional postsynaptic density (PSD) fractions using magnetic beads coated with a PSD-95 antibody. In the present study purified PSD-95 complexes were analyzed by liquid chromatography coupled to tandem mass spectrometry (LC/MS/MS). A semi-quantitative measure of the relative abundances of proteins in the purified PSD-95 complexes and the parent PSD fraction was estimated based on the cumulative ion current intensities of corresponding peptides. The affinity-purified preparation was largely depleted of presynaptic proteins, spectrin, intermediate filaments and other contaminants prominent in the parent PSD fraction. We identified 525 of the proteins previously reported in parent PSD fractions, but only 288 of these were detected after affinity purification. We discuss 26 proteins that are major components in the PSD-95 complex based upon abundance ranking and affinity co-purification with PSD-95. This subset represents a minimal list of constituent proteins of the PSD-95 complex and includes, in addition to the specialized scaffolds and NMDA receptors, an abundance of AMPA receptors, small G protein regulators, cell adhesion molecules and hypothetical proteins. The identification of two Arf regulators, BRAG1 and BRAG2b as co-purifying components of the complex implies pivotal functions in spine plasticity such as the re-organization of the actin cytoskeleton and insertion and retrieval of proteins to and from the plasma membrane. Another co-purifying protein, the hypothetical protein (Q8BZM2) with two SAM domains, may represent a novel structural core element of the PSD.
INTRODUCTION

The postsynaptic density (PSD) is a disk shaped protein complex lining the postsynaptic membrane. In a recent study its total mass was estimated to be around one million KDa (1). The function of this massive protein complex appears to be anchoring and organizing postsynaptic neurotransmitter receptors and corresponding signaling molecules at the active zone. Thus, it is expected that the extent and type of the postsynaptic response to neurotransmitter release will largely depend on the molecular composition and organization of the PSD.

The first tentative identification of PSD components was done in the late 1970s, when several laboratories developed methodology to isolate PSD fractions and started analyzing them by biochemical methods (2,3). The general strategy, still applied today, was treatment of synaptosomal fractions with detergents that solubilize membranes but leave the PSD relatively intact, and subsequent separation of membrane-free PSDs by further centrifugation. Analysis of PSD fractions continued to reveal additional putative PSD components in later years (4) and gained new momentum with the introduction of mass spectrometric techniques (5-14). The development of two hybrid screens and other methods to determine binding partners of already identified components added important complementary approaches [review: (15)].

The global proteomic analysis of isolated PSDs remains a crucial first step in the elucidation of the molecular structure of the PSD. Indeed, the strategy constitutes a relatively simple and convenient way for the identification of hundreds of proteins in a single run – one of the most recent studies identified a total of 1264 proteins (13). Also, unlike immunological approaches, the strategy is not based on any a priori notion of PSD constituents, and therefore can reveal hitherto unsuspected elements. A recent article (16) integrated data from seven proteomic studies (5-9,17), and other literature on the analysis of PSD fractions. Collins et al. report that altogether 1124 proteins were identified in these seven
studies. However, 58% of the proteins were detected in only one study, raising the possibility of a high rate of false positives. The authors also compiled a “consensus PSD” list of 467 proteins that were identified in at least two of the studies, thus reducing the probability of false positives linked to individual protocols.

While the 467 proteins in the “consensus PSD” list have a better probability of being genuine PSD components, detection in multiple studies does not necessarily prove that they are. In fact, there seem to be only a handful of proteins that were identified in all seven of the studies [(16) – supplementary Table 4)] and this high consensus group includes, in addition to the expected PSD components such as PSD-95, homer and CaMKII, likely contaminants such as synapsins and intermediate filaments. Moreover, because the probability of detection of a protein in a mixture increases with its relative abundance, it is likely that the contaminants in this group are among the most abundant in PSD fractions.

Detection of the same contaminants in all proteomic studies suggests systemic contamination problem in PSD fractions in general. The most widely applied protocol for the preparation of PSD fractions is the one originally developed by Carlin et al. (18) and uses the relatively mild detergent TritonX-100. Because TritonX-100 is mild, it appears to cause minimal loss of protein from the PSD as judged from morphological criteria. On the other hand, many proteins that are present in the synaptosomal fraction but are not part of the PSD also appear to be resistant to TritonX-100. Indeed, electron microscopic (EM) analyses of PSD fractions prepared by this method reveal various particulate contaminants including filamentous material and other protein complexes (19,20). Some of the filamentous materials that are not associated with the PSD have been identified as neurofilaments and spectrin (20).
Altogether these considerations indicate the need for a purer preparation as a basis for the identification of PSD components. The use of a stronger detergent such as N-lauryl sarcosinate [NLS, (21)] eliminates certain contaminants but also appears to dissociate some genuine PSD elements as well. In addition, certain contaminants such as the so-called “CaMKII clusters” that are resistant to the detergent become enriched in the NLS derived PSD fraction (19). On the other hand, because most particulate contaminants in the PSD fraction are membrane-free protein complexes like the PSDs themselves, they are expected to be of the same density as PSDs, excluding the possibility of further fractionation by conventional centrifugation-based techniques.

Affinity-based separation techniques targeting ubiquitous PSD components constitute an orthogonal approach for the isolation of postsynaptic protein complexes, a strategy expected to avoid the problem of detergent-insoluble particulate material contamination prevalent in conventional density based PSD preparations. Using this approach the isolation of NMDA receptor- and PSD-95-complexes from whole cell deoxycholate (DOC) extracts has been reported (22,23). However, because these preparations are from detergent-solubilized starting material, isolated complexes tend to be small. Indeed the molecular weight of NMDA receptor complexes was estimated to be around 2000 KDa, that is, about three orders of magnitude smaller than the whole PSD complex. Thus, the preparation presumably contains receptor complexes that become dissociated from the bigger PSD complex upon treatment with the relatively strong detergent DOC. In addition, because whole cell extracts are used as starting material, complexes that originate from extrasynaptic/ intracellular pools are expected to co-purify with complexes from the PSD. These may include extrasynaptic receptors and transport packages.

We evaluated an affinity-based strategy for the isolation of large PSD-95-containing complexes from the TritonX-100 derived PSD fraction (20). The strategy aims to minimize contribution from extrasynaptic/intracellular PSD-95
pools by starting with a PSD-enriched fraction from which such non-synaptic complexes have been largely eliminated. Importantly, by using magnetic beads coated with a PSD-95 antibody, large, insoluble complexes are separated without the use of additional detergents to solubilize particulates.

Postsynaptic PSD-95 complexes are likely to represent the bulk of the PSD observed by EM in intact cells. Indeed, PSD-95 is able to interact with a large number of proteins through its three PDZ domains, an SH3 domain and a GK domain and also can multimerize to form an extended scaffold [review: (15)]. Moreover, proteins that bind PSD-95, in turn, interact with yet other postsynaptic components, thus extending the network. The complexes isolated using PSD-95 antibody-coated magnetic beads resemble in situ PSDs (20), suggesting that most, if not all of the original components have been retained. These considerations suggested that analysis of the isolated PSD-95 complexes would identify most, if not all of the components of the in situ PSD.

In the present study, isolated PSD-95 complexes and the parent PSD fraction were analyzed in parallel by liquid chromatography coupled to tandem mass spectrometry. For each fraction, identified proteins were ranked according to cumulative ion current intensities of corresponding peptides as a semi-quantitative measure of relative abundance. Comparison of the ranks of proteins in the parent and affinity-purified preparations allowed identification of those that co-purify with PSD-95 and, importantly, those that are likely contaminants.

MATERIALS and METHODS

Preparation of the PSD fraction and isolation of PSD-95 complex:
The PSD fraction was prepared essentially by the method of Carlin et al. (18) with modifications as described previously (19). Brains from adult Sprague Dawley rats were custom collected by Pel Freez Biologicals (Rogers AR) and frozen immediately in liquid nitrogen and shipped on dry ice. Brains were thawed
by a 1 min immersion in isotonic sucrose at 37 °C, dissected on ice to remove white matter and cerebral cortices were then rapidly homogenized. A synaptosomal fraction was obtained and treated with 0.5% TritonX-100. Detergent-insoluble pellets were collected and a PSD-enriched fraction was separated by sucrose density centrifugation. This fraction was extracted once more with 0.5% TritonX-100, 75 mM KCl.

Isolation of PSD-95 complexes was as described previously (20) with some modifications. Dynabeads (M-450 coated with goat anti-mouse IgG) were obtained from Dynal (Oslo, Norway) and were further coated with a monoclonal PSD-95 antibody (MA1-046; ABR, Golden CO). PSD fraction (200 µg protein) was resuspended in 10 ml of 2% BSA (of 99% purity to minimize contamination of the preparation by the blocker), 0.01 % Tween-20 in phosphate buffered saline, using a probe sonicator. Sonication (3X1min, with ~3 min cooling intervals in ice) was done at the lowest power setting (<5W) taking care not to warm the samples. Resuspended PSD fraction (200µg) was incubated with antibody-coated magnetic beads (2X10^8 beads) in a final volume of 10 ml for 2h at 4°C with continuous rotation. Unbound material was removed and the beads were washed 3X with 2% BSA, 0.01 % Tween-20 in phosphate buffered saline and 5X with 0.01 % Tween-20 in phosphate buffered saline for a total of ~3 hrs.

Fractionation and mass spectrometric analysis of preparations: Parent PSD fraction or washed beads with attached complexes were treated with SDS-containing electrophoresis sample buffer and were incubated in boiling water for 5 min. Solubilized affinity-purified samples corresponding to the yield from ~100 µg starting PSD fraction were loaded onto individual gel lanes. Gels were stained with Coomassie Brilliant Blue to visualize bands for imaging, and then sectioned from the top of the gel to the bottom in 2mm increments, and the pieces placed in clean Eppendorf tubes. In-gel tryptic digestion was performed after two washes with 50% acetonitrile in 100 mM ammonium bicarbonate, and dehydration of gel slices with the addition of 100% acetonitrile. Disulfides were
reduced with 45mM dithiothreitol in 50 mM ammonium bicarbonate, and alkylated with 100mM iodoacetamide in 50 mM ammonium bicarbonate. Gel pieces were again dehydrated with 100% acetonitrile. Trypsin (260 ng/gel piece) was added and incubated overnight at room temperature. Peptides were extracted from the gel pieces by subsequent additions of 30% acetonitrile in 0.1% TFA and 80% acetonitrile in 0.1% TFA. Samples were dried, re-dissolved in 0.1% formic acid and injected into a Shimadzu HPLC system coupled to a Thermo Finnigan LCQ Classic (24). HPLC separation was performed on a New Objectives Pico-frit column filled with BetaBasic C18. A linear gradient was developed from 10-60% B (A, 5% acetonitrile, 95% aqueous 0.1% formic acid; B, 80% acetonitrile, 20% aqueous 0.1% formic acid) at a rate of 1.5%/minute. Data was collected continuously for 60 minutes, selecting the 3 most intense ions (exceeding 3X10E6 intensity units) in a MS survey scan to subsequent MS/MS analyses using collisionally induced dissociation. Selected precursors were analyzed for 2 MS/MS cycles and then excluded for redundant analyses for a 90 sec interval. Thermo-Finnigan Excalibur 2.0 utility extract_msn was used to retrieve peak lists without any added smoothing or S/N criteria. The recorded MS/MS files were searched with the Mascot search engine 2.1.04 (Matrix Sciences, London, UK) against the Swiss-Prot database (Sp_Trembl_122406.fas) with the limitation of mammalian species for protein database records; precursor ion mass tolerance 2.0; fragment-ion mass tolerance 0.8; methionine oxidation and carbamido methylation of cysteine allowed; trypsin specificity with one missed cleavage allowed.

Mascot assigned peptides with Ion Score exceeding their Identity Score were then grouped using the software tool DBParser 2.0 (25) and reports were generated for each lane from the concatenated Mascot files. DBParser 2.0 was also used to compare data from multiple lanes at both the peptide and protein level. DBParser 3.0 was used to extract ion current intensity values for peptides with Mascot Ion Scores greater than Identity Scores (DBParser 3.0 is further described in Supplement 1).
RESULTS

PSD-95 complexes were affinity-purified from the conventional PSD fraction using magnetic beads coated with an antibody against the core PSD protein PSD-95. Parent and affinity-purified samples were separated by 1D-SDS gel electrophoresis and analyzed in parallel. The control sample (Figure 1, lane 3) shows no visible band except the secondary antibody used to coat the magnetic beads, indicating the absence of non-specific binding. The protein profiles of the parent PSD fraction (Figure 1, Lane 1) and of the affinity-purified PSD-95 complex (Figure 1, Lane 2) are different, indicating removal of several proteins during purification.

Gel lanes in their entirety were cut into 40 fractions, digested with trypsin and analyzed by LC/MS/MS. The resulting mass spectra were assigned probable peptide sequences using the Mascot search engine (Matrix Sciences, UK). For these studies, the Swiss-Prot mammalian protein reference library was selected, and peptides with Mascot Ion Scores exceeding their Identity Scores were analyzed and grouped using DBParser 2.0. This software applies parsimony analysis to reduce the thousands of identified peptides to a minimal protein list (25). Only proteins from the minimal protein list were considered for further evaluation (Tables I-IV). The results from the two preparations include protein assignments from homologous mammalian proteins other than rat as indicated in the tables of results.

Altogether, three sets of samples were analyzed, corresponding to two independent parent and affinity-purified preparations. The concatenated parent (from 133 LC/MS/MS runs) and affinity-purified (125 LC/MS/MS runs) files correspond to summed and integrated analyses. Identified proteins were ranked according to summed ion current intensities of their constituent peptides as a relative abundance index. DBParser 3.0 extracts retention time and peak
intensity from raw data based on the precursor mass identified by the search engine as described previously for ion trap LC/MS/MS data (26). The corresponding maximum intensity, peak area and number of scans for each identified peptide were then calculated from respective selected ion chromatograms recorded during the survey scan cycle (see Supplement 1 for DBParser 3.0 details).

Known contaminants, originating from sources other than brain tissue, including immunoglobulins (antibodies used for affinity purification), serum albumin (blocker), trypsinogen, and human keratin were deleted from the lists. The lists were condensed further by reporting certain related proteins with multiple isoforms as a single family. Families of proteins are represented by their most abundant member. For example, although α-, β-, δ- and γ-isoforms of CaMKII were identified, CaMKII is reported by a single entry corresponding to its most abundant α-isoform.

Tables I and II list the highest ranking 50 proteins from the simplified lists corresponding to affinity-purified and parent samples respectively. The tables include only those proteins detected in both fractions and thus allow a fair comparison by rank order. The proteins are listed in descending rank order (highest ion current intensity at the top). Only proteins identified by two or more peptides were included in determining rank order. The second columns on Tables I and II show the rank of the same protein in the other group. Although a number of factors in addition to a protein’s abundance may influence the ion current intensity, these other factors are expected to remain the same for the two fractions so that a change in rank order may be used as an indication of a change in relative abundance. The last column in Tables I and II indicate the number of peptides identified by MS/MS exclusively associated with the assigned proteins and used for intensity determinations. There is no direct correlation between the number of peptides and total ion current intensity, as the number of
peptides detectable is a function of both the number of possible tryptic products compatible with mass spectrometric detection and their relative abundance.

As a measure of co-purification with PSD-95, the ratios of normalized ion current intensities in the affinity-purified group over that in the parent group were calculated for individual proteins (Tables III and IV, last columns). To compensate for variable total protein contents of samples applied to gels, ion current intensities for individual proteins were normalized with respect to the ion current intensity for PSD-95 in the same sample. For certain proteins, the ratios of normalized ion current intensities were greater than 1 implying that immunoaffinity capture of PSD-95 resulted in the capture of additional specific proteins with higher efficiency than the targeted PSD-95. However, this phenomenon is more likely the result of S/N differences between the parent and affinity-purified protein mixtures. Chemical noise from peptides from contaminant proteins masks co-eluting peptides from constitutive proteins present in the parent mixture. Thus, peptides from some proteins are observable only after affinity purification. Comparable amounts of PSD-95 (DLG4) were analyzed in each preparation, (24 peptides observed in the parent preparation, summed intensity $7 \times 10^8$; 25 peptides in the affinity-purified, summed intensity $9 \times 10^8$).

After removal of interfering peptides from contaminants, signals from peptides from the constituents of the PSD-95 complex were detected more readily. For example, GluR1 (GRIA1_RAT) was characterized by 3 peptides in 113 MS scans (summed intensity $2 \times 10^8$) in the parent mixture, and by 7 peptides in 274 MS scans ($9 \times 10^8$) after affinity purification. The semi-quantitative nature of this method assesses relative ranking but cannot be used to infer stoichiometry.

Table III lists those proteins that co-purify with PSD-95 by two criteria presented in the last two columns: change in rank order and normalized ion current intensity ratio (purified/parent). Only the 50 top ranking proteins from the affinity-purified group (Table I) were considered and the cut-off point for inclusion in the list was a normalized ion current intensity ratio of 0.5. It can be observed that 26 out of
the 50 top ranking proteins met these criteria and also demonstrated a substantial decrease in rank order (Table III). The 26 proteins shown in Table III are relatively abundant components that are substantially co-purified with PSD-95 and thus most likely represent a minimal list of constitutive PSD-95 complex proteins.

Table IV lists those proteins that are depleted or greatly reduced in the affinity-purified sample, with the same indexes as in Table III. For this list, those proteins from Table II (top ranking proteins from the parent group) with normalized ion current intensity ratios of parent/purified below 0.1 were selected. Also 5 additional top ranking proteins that were detected in the parent group only were included. Out of the 21 proteins that show significant reduction/depletion in purified samples, 7 are presynaptic elements and 6 are cytoskeletal elements.

DISCUSSION
The molecular architecture of the PSD-95 complex is less readily definable than that of the synaptic vesicle, elegantly described by Takamori et al. (27). In the course of that work, the value of immunoaffinity assisted isolation was recognized in the proteomic analyses of light and heavy synaptic vesicles by Morciano et al. (28). Both heavy and light sucrose density gradient separated vesicles contain many proteins in common, but the sedimented heavy fraction was contaminated with PSD proteins until separated with anti-SV2 mAb-coated magnetic beads. The heavy fraction was then found to consist of synaptic vesicles docked to pre-synapse plasma membranes, but free of PSD proteins (28). In an analogous manner, we sought to demonstrate that the immunoaffinity assisted isolation of the PSD-95 complex developed by Vinade et al. (20) provides an isolate more relevant to defining the composition of the PSD-95 complex because it is substantially freer from co-sedimenting components than attainable by sucrose density centrifugation alone.
Because the identification of proteins in the PSD fraction has been the subject of multiple reports, we have reconciled our findings with those of others. Repeated observation of the same proteins by multiple investigators adds certainty to the identified constituents of the PSD fraction. Collins et al. (16) collected and correlated reports from seven laboratories and the literature to assemble a non-redundant set of 1124 accession numbers of proteins. The task of comparing protein identifications is not possible without access to either the original tandem mass spectrometry data or the peptide sequences ascribed to that data. Protein accession numbers and entry names change when protein databases are curated, so that differences in published lists of proteins are sometimes due to differences in the versions of the protein reference libraries used for sequence assignment. Consequently, we compiled protein sequence fasta files for the entries tabulated by Collins et al. (16) and used these reference sub-libraries for Mascot to re-search and identify proteins. The use of the Collins et al. sub-library (kindly provided by the authors) ensures that peptide sequences recognized can be mapped to the same protein names, eliminating ambiguity of naming conventions or isoform selection. Table V summarizes these results parsed and analyzed using MassSieve software.

The agreement between proteins identified in our parent preparation is consistent with those reported by others. Of 134 proteins observed by 4 or more labs, we identified peptides from 124 (92%). Of greater importance are differences observed after affinity purification - only 88 (57%) of the 134 proteins observed by 4 or more labs were observed after affinity purification presumably due to removal of contaminating proteins.

In the present study large, affinity-purified PSD-95 complexes derived from the synapse were analyzed and, on the basis of rank order changes with respect to the parent PSD fraction, a subset of the identified proteins were selected as likely

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to be consistent, integral components of the complex. It should be noted that the 26 proteins included in Table III constitute a minimal list of relatively abundant constituents of the PSD-95 complex. The PSD-95 complex undoubtedly includes additional components. Indeed a much larger number of proteins than those listed in Table III have been identified in the affinity-purified preparation (see Table V and Supplemental Tables for a complete lists of proteins and constituent identified peptides) and many of these appear to be more prominent than in the parent PSD fraction. However, we have chosen to apply stringent criteria (2 or more peptides within the top 50 rank order by intensity, normalized ion current ratios greater than 0.5 relative to PSD-95) that would select only for the relatively abundant proteins that co-purify with PSD-95.

A minimal list of constituent proteins of the synaptic PSD-95 complex (Table III) includes specialized PSD scaffolds with multiple protein interaction sites, receptors as well as several proteins likely to be involved in aspects of spine structure and dynamics such as trafficking of receptors, actin dynamics and cell adhesion. On the other hand, many of the proteins that are greatly reduced or eliminated upon affinity purification are presynaptic or extra-synaptic in origin (Table IV). Effective removal of these known contaminants attests to the success of the affinity-based strategy and establishes the preparation as a good base for the elucidation of the composition of the PSD complex.

Electron microscopy of the affinity-purified preparation shows many particulate structures that look like PSDs (20), suggesting that the isolated PSD-95 complex retains the bulk of the proteins that make up the in situ PSD. However, there are a few proteins, including N-cadherin, catenins and α-actinin which have been observed at the contact zone by immuno EM (29-31), but whose levels decrease with respect to the parent PSD fraction upon affinity purification. This could be due to the dissociation of some loosely bound components during purification as well as the existence of physically separate complexes that co-localize in situ with the PSD-95 complex. It is interesting to note that all the above-mentioned
proteins are associated (either directly or indirectly) with the actin cytoskeleton and may be linked to the PSD-95 complex through actin. Partial disassembly of the actin during the purification protocol may have caused their release. Thus, the affinity-purified preparation appears to include the majority but not all of the components of the in situ PSD.

Two measures for affinity co-purification (change in rank order, and ratio of normalized ion current intensities) - were used to identify integral elements of the PSD-95 complex. The 26 proteins in Table III are thus likely to represent a subset of constituent elements. As discussed below, some of the proteins in the list are expected components of the PSD-95 complex such as specialized PSD scaffolds and NMDA receptors, while the involvement of some of the other identified proteins had been somewhat controversial. Definitive stoichiometry of constitutive PSD-95 complex proteins will require either orthogonal techniques such as quantitative Western blotting or stable isotope mass spectrometric standards, and this study refines the list of proteins that should be targeted as well as identifying their proteotypic peptides for synthesis of labeled standards. Most interestingly, the list spotlights certain proteins that had not been generally acknowledged up to now as part of the PSD-95 complex. We discuss below particular proteins in functional groups.

**Scaffolds:**
Most specialized PSD scaffolds are identified as constituents of the PSD-95 complex. Co-purification of PSD-93 with PSD-95 -two homologous proteins, each with a guanylate kinase, an SH3 and three PDZ domains [review: (15)] - argues against their differential localization in different synapses and indicates that they are part of the same complex. In addition, SAPAPs (GKAPs) that bind directly to PSD-95, Shanks that bind to SAPAPs and homer that binds to Shanks [review: (15)] all copurify with PSD-95 suggesting that the entire PSD scaffold is preserved in the purified complex.
Shank3, together with PSD-95 and PSD-93, is among the 10 top ranking proteins in the purified fraction. Shanks are thought to multimerize through association of their sterile alpha motif (SAM) domains (32). Indeed SAM domains that typically spread over ~70 residues have been described to homo- and hetero-oligomerize [review: (33)]. A recent report (34) described large sheets made of stacked helical fibers being formed by the SAM domains of Shank3, which, they suggest, may constitute a core platform for the PSD organization. The present analysis identifies a hypothetical protein (Q8BZM2) with two SAM domains as a constituent of the PSD-95 complex. In analogy to other SAM containing proteins, this protein is expected to homo- and hetero- oligomerize and thus participate in the formation of the PSD scaffold.

**Adhesion molecules:**
In contrast to cadherin/catenin, another group of cell adhesion molecules, neuroligins, are identified as constituents of the PSD-95 complex. This finding is in agreement with reports on direct binding of the two proteins (35). In addition, the present analysis reveals the presence of yet another putative adhesion molecule, LRTM1, of the leucine rich repeat transmembrane protein family in the PSD-95 complex (36).

**Cytoskeletal elements:**
Cytoskeletal elements make up a major proportion of the proteins in the conventional PSD fraction and were observed to be enriched in the PSD fraction compared to the synaptosome fraction (10). However, with the exception of actin and tubulin most cytoskeletal proteins are substantially reduced/depleted in the affinity-purified PSD-95 complex. Actin constitutes the main cytoskeleton of the dendritic spine and interacts with the PSD in situ (37). The present data, demonstrating slight tendency for actin to co-purify with PSD-95, is in agreement with the notion that actin is an integral element of the PSD. Another cytoskeletal protein tubulin, also appears to be present in large quantities in the affinity-purified fraction. This is somewhat surprising since microtubules are rarely
observed near the PSD of mature spines. One explanation may be that tubulin is attached to the PSD either in monomeric or a different polymeric form— for example, it has been proposed that NMDA receptors have a preferential affinity for soluble forms of tubulin [review: (38)]. On the other hand immunoEM studies do not support the presence of large quantities of tubulin at the in situ PSD\(^2\). Thus, the possibility remains that at least part of the detected tubulin becomes associated with the PSD-95 complex post-mortem, when large quantities of depolymerized tubulin become available during homogenization.

In contrast to actin and tubulin, other cytoskeletal elements such as spectrins and intermediate filaments that are prominent in conventional PSD fractions (5,9,10) are virtually eliminated upon affinity-purification. The removal of spectrin and intermediate filaments suggests that these proteins are not components of the PSD, consistent with the observation of non-associated spectrin filaments and neurofilaments in the parent PSD preparation (20).

**Glutamate receptors and related molecules:**

Glutamate receptors of both NMDA- and AMPA-type appear to be prominent components of the PSD-95 complex. Our previous work demonstrated by western immunoblotting the presence of AMPA-type glutamate receptors in the affinity-purified preparation (20). Comparative analysis of the parent and purified fractions in the present study shows that AMPA receptors co-purify with PSD-95. Earlier reports had indicated that NMDA receptor complexes isolated from detergent extracts do not contain AMPA-type receptors (22,23), an observation which led the authors to conclude that AMPA receptors at the PSD are physically separate from the PSD-95 complex. It is possible that these small NMDA complexes (2000 KDa as compared to one million KDa for the PSD) are sub-complexes dissociated from the PSD by the relatively strong detergent (DOC) used. Alternatively they may represent a distinct group of receptors of either synaptic or extra-synaptic origin.

\(^2\) J-H. Tao-Cheng, NINDS, NIH, personal communication
Our observation that AMPA-type receptors are an integral part of the PSD-95 complex is in agreement with accumulated evidence on the regulation of synaptic AMPA receptor levels by PSD-95 (39-42). On the other hand, because direct binding of AMPA receptors to PSD-95 has not been demonstrated, an indirect association through at least one bridging molecule has to be assumed. SAP-97 has been detected by western immunoblotting to be present in affinity-purified complexes (20), but this protein would be able to anchor only those receptors that contain GluR1 subunits. Also, the present semi-quantitative analysis indicates that SAP-97 is not particularly enriched in the PSD-95 complex while GluR1 is. A good candidate for bridging all types of AMPA receptors to the core PSD complex is the TARP (Stargazin) family of proteins, reported to bind very strongly to AMPA receptors and also to PSD-95 (43). Our results identify TARP gamma 8 (CCG8_RAT) as a component of the PSD-95 complex. However, at this stage it is not clear whether the amount of TARP found in the PSD-95 complex is sufficient to support the binding of all AMPA receptors – at least one TARP per five AMPA receptor subunit. Future quantitative studies that assess stochiometric relationships would clarify that point.

CPG2, a protein that has been proposed to be involved in the constitutive internalization of NMDA and AMPA-type glutamate receptors and in the activity-induced internalization of AMPA receptors (44) is also a component of the PSD-95 complex. Immuno-EM studies demonstrated that the protein is located lateral and underneath the cytosolic side of the PSD (44). These results, together with our data indicating physical attachment of the protein to the PSD-95 complex suggests that CPG2 may be associated as an appendage to the PSD, rather than being integrated within the core structure.

CaMKII:
The Ca2+-regulated protein kinase, CaMKII appears to be the major protein in the PSD-95 complex as judged by its abundance ranking and relative band
intensity in Coomassie-stained gels. We had previously demonstrated that part of the CaMKII present in conventional PSD preparations is contributed by contaminating CaMKII clusters, spherical structures, ~100 nm in diameter (19). Thus, it is remarkable that even after the elimination of these CaMKII clusters in affinity-purified samples, CaMKII still remains the most abundant protein. However, it should be noted that this may not hold true for in situ PSD-95 complexes at inactive synapses. Indeed, the amount of CaMKII associated with the PSD is regulated by synaptic activity. Previous immunoEM studies have shown that excitatory and ischemia-like conditions cause several fold increases in CaMKII labeling of the PSD (19,45,46). Ischemia-like conditions that prevail during the dissection of brain tissue likewise cause an increase in the CaMKII content of PSD fractions (47). Thus, for the case of CaMKII, and certain other variable / transient components of the postsynaptic complex such as GluR1, the abundance is likely to be determined by factors such as the level of neuronal activity and anesthesia prior to sacrifice as well as by postmortem handling.

**Small G-protein regulators:**

A substrate for CaMKII, the synaptic Ras GTPase activating protein SynGAP (48) is also among the abundant proteins in the purified PSD-95 complexes. SynGAP can directly bind to PSD-95 (49). Parallel analysis of parent and affinity-purified fractions highlighted the presence of two additional small G-protein regulators of the Brefeldin A-resistant ArfGEF family (BRAG) in the PSD-95 complex. One of these (KIAA0522, O60275_HUMAN, IQEC2_HUMAN, gi|62666747|ref|XP_228841.3|) has been classified as BRAG1 (50). A recent study (51), published during the preparation of this manuscript identifies an error in the sequence of KIAA0522 and demonstrates *in situ* co-localization of BRAG1 and PSD-95. BRAG1 is enriched in the PSD-95 fraction compared to the synaptosome fraction (10,51). BRAG1 is a 190 KDa protein with a calmodulin binding IQ domain and a sec7 domain, a ~200 amino acid signature sequence for ArfGEFs that confers guanine nucleotide exchange activity. BRAG1 has been
shown to regulate Arf1 (51) and from the sequence similarity, it is probable that it also acts on Arf6 (49).

Surprisingly, another member of the same family, BRAG2b (Q6DN90_HUMAN, IQEC1_HUMAN) is also identified in the PSD-95 complex. BRAG1 and BRAG2b are distinguishable proteins and were identified by two entirely different sets of peptides with no overlapping assignments. BRAG2b, is a splice isoform of a previously identified ArfGEF (Arf-GEP100, (52) and has been shown to regulate Arf6 (53). Another ArfGEF called synArfGEF (Q76M68) has recently been reported by Inaba et al. (54) to be enriched in the PSD fraction and is suggested to act on Arf1. SynARFGEF was not observed in this study, and differs from either BRAG1 and BRAG2b (63% and 48% homology, respectively).

Arfs are from the Ras family of small G-proteins that regulate membrane trafficking and the actin cytoskeleton. Different types of Arfs appear to be targeted to different subcellular locations [reviews: (55,56)]: Arf1 is preferentially targeted to the Golgi while Arf6 is localized at the plasma membrane and, to some extent on endosomes [reviews: (56,57)]. Interestingly, Arf6 has been implicated in the insertion of and retrieval of membrane proteins at defined sites as well as in the reorganization of the actin cytoskeleton that results in various forms of membrane remodeling [review: (57)]. Considering that synaptic strength is largely regulated by the insertion and retrieval of receptors to and from the postsynaptic contact zone and that the cytoskeleton at the spine constitutes of actin, the potential relevance of Arf6 to spine structure and function becomes obvious. In fact, two recent studies (58,59) already reported involvement of Arf6 on spine formation and stability, although with somewhat contradictory conclusions. The finding in the present study that activators of Arf6 are specifically concentrated at the PSD opens the way for the unraveling of new mechanisms for the modification of spine morphology and function.
REFERENCES


architectural framework that may lie at the core of the postsynaptic density. *Science.* 311, 531-535.


Table I: 50 top ranking of proteins in the affinity-purified PSD-95 complex

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<th>Aff. purif. rank</th>
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<th>Unique peptides</th>
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Proteins are ranked in descending order of summed ion current intensity. For complete peptide sequences and statistical confidence scores, refer to Supplemental Table 1.

### Table II: 50 top ranking of proteins in the conventional (parent) PSD fraction

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Proteins are ranked in descending order of summed ion current intensity. For complete peptide sequences and statistical confidence scores, refer to Supplemental Table 2.
Table III: Proteins co-purifying with PSD-95

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<td>SynGAP</td>
<td>SYGP1_RAT</td>
<td>7/4</td>
<td>0.64</td>
</tr>
<tr>
<td>BRAG1 (KIAA0522)</td>
<td>O60275_HUMAN</td>
<td>22/10</td>
<td>&gt;1</td>
</tr>
<tr>
<td>BRAG2b</td>
<td>Q6DN90_HUMAN</td>
<td>49/17</td>
<td>&gt;1</td>
</tr>
<tr>
<td><strong>Other</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Neuroligin</td>
<td>NLGN3_RAT</td>
<td>76/30</td>
<td>&gt;1</td>
</tr>
<tr>
<td>Hypothetical (FAM81A)</td>
<td>Q8TBF8_HUMAN</td>
<td>87/31</td>
<td>&gt;1</td>
</tr>
<tr>
<td>Rp1 protein (ubiquit.</td>
<td>Q66H62_RAT</td>
<td>84/33</td>
<td>&gt;1</td>
</tr>
<tr>
<td>t.e.)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leu rich repeat tm. n. 1</td>
<td>LRTM1_HUMAN</td>
<td>92/41</td>
<td>&gt;1</td>
</tr>
<tr>
<td>Hypothetical (FLJ35778)</td>
<td>Q8NA73_HUMAN</td>
<td>59/42</td>
<td>0.73</td>
</tr>
<tr>
<td>TARP (gamma 8)</td>
<td>CCG8_RAT</td>
<td>58/46</td>
<td>0.62</td>
</tr>
<tr>
<td>CPG2 protein</td>
<td>Q63128_RAT</td>
<td>69/50</td>
<td>0.95</td>
</tr>
</tbody>
</table>

Proteins from Table I (50 top ranking proteins in the affinity-purified preparation) with a normalized ion current intensity ratio greater than 0.5 are included.
Table IV: proteins greatly reduced/depleted in the affinity-purified PSD-95 complex

<table>
<thead>
<tr>
<th>Protein (family) name</th>
<th>ID</th>
<th>Change in rank (parent/purified)</th>
<th>Normalized ion current int. ratio (purified/parent)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Presynaptic proteins</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bassoon</td>
<td>BSN_RAT</td>
<td>8/69</td>
<td>0.01</td>
</tr>
<tr>
<td>SNIP</td>
<td>SNIP_RAT</td>
<td>12/35</td>
<td>0.06</td>
</tr>
<tr>
<td>Synapsin 2</td>
<td>SYN2_RAT</td>
<td>21/74</td>
<td>0.02</td>
</tr>
<tr>
<td>ERC protein 2</td>
<td>ERC2_RAT</td>
<td>31/71</td>
<td>0.04</td>
</tr>
<tr>
<td>Synapsin 1</td>
<td>SYN1_RAT</td>
<td>NA/ *</td>
<td>0.00</td>
</tr>
<tr>
<td>Piccolo</td>
<td>PCLO_RAT</td>
<td>NA/ *</td>
<td>0.00</td>
</tr>
<tr>
<td>RIM</td>
<td>RIMS_RAT</td>
<td>N/A/*</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Cytoskeletal elements</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>spectrin</td>
<td>SPTA2_RAT</td>
<td>5/59</td>
<td>0.01</td>
</tr>
<tr>
<td>Plectin</td>
<td>PLEC1_RAT</td>
<td>9/36</td>
<td>0.04</td>
</tr>
<tr>
<td>internexin</td>
<td>AINX_RAT</td>
<td>11/67</td>
<td>0.01</td>
</tr>
<tr>
<td>spectrin</td>
<td>SPTN2_RAT</td>
<td>NA/*</td>
<td>0.00</td>
</tr>
<tr>
<td>Neurofilament-L</td>
<td>NFL_RAT</td>
<td>NA/*</td>
<td>0.00</td>
</tr>
<tr>
<td>Neurofilament-M</td>
<td>NFM_RAT</td>
<td>NA/*</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Different organelle/cell type</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>VDAC1(mitochondrial)</td>
<td>VDAC1_RAT</td>
<td>15/43</td>
<td>0.06</td>
</tr>
<tr>
<td>VDAC2 (mitochondrial)</td>
<td>VDAC2_RAT</td>
<td>34/73</td>
<td>0.04</td>
</tr>
<tr>
<td>Myelin basic protein</td>
<td>MBP_RAT</td>
<td>NA/*</td>
<td>0.00</td>
</tr>
<tr>
<td>Ribosomal proteins</td>
<td>RLA0_RAT</td>
<td>NA/*</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Other</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>actinin</td>
<td>Q6GMN8_RAT</td>
<td>18/47</td>
<td>0.06</td>
</tr>
<tr>
<td>Synaptopodin</td>
<td>SYNPO_RAT</td>
<td>NA/*</td>
<td>0.02</td>
</tr>
<tr>
<td>catenin</td>
<td>CTNB1_HUMAN</td>
<td>33/52</td>
<td>0.09</td>
</tr>
<tr>
<td>N-cadherin</td>
<td>CADH2_RAT</td>
<td>42/63</td>
<td>0.09</td>
</tr>
</tbody>
</table>

Proteins from Table II with a normalized ion current intensity ratio of 0.1 or smaller were included. Certain proteins (NA) were abundant in the parent fraction with intensities that would rank them in the top 50 proteins but were not detected after affinity purification.

*Proteins identified with 2 or more peptides in parent fraction only
Table V – Comparison of proteins observed with literature data. Shaded columns are data from present study. For complete protein information and peptide sequences and statistical confidence scores, refer to Supplemental Tables 3-6.

<table>
<thead>
<tr>
<th>Confidence*</th>
<th>Proteins Reported**</th>
<th>Parent Preparation</th>
<th>Affinity Purification</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>10</td>
<td>10</td>
<td>8</td>
</tr>
<tr>
<td>7</td>
<td>13</td>
<td>13</td>
<td>12</td>
</tr>
<tr>
<td>6</td>
<td>15</td>
<td>15</td>
<td>12</td>
</tr>
<tr>
<td>5</td>
<td>34</td>
<td>30</td>
<td>25</td>
</tr>
<tr>
<td>4</td>
<td>62</td>
<td>56</td>
<td>31</td>
</tr>
<tr>
<td>3</td>
<td>135</td>
<td>91</td>
<td>50</td>
</tr>
<tr>
<td>2</td>
<td>198</td>
<td>112</td>
<td>45</td>
</tr>
<tr>
<td>1</td>
<td>657</td>
<td>192</td>
<td>101</td>
</tr>
<tr>
<td>Totals</td>
<td>1124</td>
<td>525</td>
<td>288</td>
</tr>
</tbody>
</table>

*Consensus number of studies reporting identification of the same set of proteins; **number of proteins in the set (Collins et al. (16))
Figure 1: Coomassie blue stained SDS gel (7.5% acrylamide)
(1) Parent PSD fraction; (2) PSD-95 complex, affinity-purified with antibody coated magnetic beads; (3) control, eluant when beads coated with secondary antibody only were incubated with PSD fraction. The position of the antibody heavy chain is shown with an arrow. Sample 2 contains PSD-95 antibody and secondary antibody whereas sample 3 contains secondary antibody only. Positions of molecular weight standards (in KDa) are indicated on the left.