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# The proteomes of neurotransmitter receptor complexes form modular networks with distributed functionality underlying plasticity and behaviour

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Neuronal synapses play fundamental roles in information processing, behaviour and disease. Neurotransmitter receptor complexes, such as the mammalian *N*-methyl-D-aspartate receptor complex (NRC/MASC) comprising 186 proteins, are major components of the synapse proteome. Here we investigate the organisation and function of NRC/MASC using a systems biology approach. Systematic annotation showed that the complex contained proteins implicated in a wide range of cognitive processes, synaptic plasticity and psychiatric diseases. Protein domains were evolutionarily conserved from yeast, but enriched with signalling domains associated with the emergence of multicellularity. Mapping of protein–protein interactions to create a network representation of the complex revealed that simple principles underlie the functional organisation of both proteins and their clusters, with modularity reflecting functional specialisation. The known functional roles of NRC/MASC proteins suggest the complex co-ordinates signalling to diverse effector pathways underlying neuronal plasticity. Importantly, using quantitative data from synaptic plasticity experiments, our model correctly predicts robustness to mutations and drug interference. These studies of synapse proteome organisation suggest that molecular networks with simple design principles underpin synaptic signalling properties with important roles in physiology, behaviour and disease.

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*Subject Categories:* neuroscience; signal transduction

*Keywords:* LTP; NMDA receptor; protein complex; synaptic plasticity

## Introduction

In the last 5 years, proteomic studies of brain synapses have increased the number of known synaptic proteins by a factor of 5–10 revealing a surprisingly high molecular complexity (Husi *et al.*, 2000; Collins *et al.*, 2005). Comprising over 1000 proteins, the macromolecular complexes of neurotransmitter receptors connected with the postsynaptic density (PSD) are perhaps the most complex molecular structures known in mammals. Since many of these proteins participate in information processing in the brain, and also play roles in disease, it is of fundamental importance to ask if there is a molecular logic or organisation of the synapse proteome.

Synapses not only transmit information between neurons, but also process information by detecting patterns of neural activity that activate intracellular biochemical pathways, changing the properties of the neuron (Greengard, 2001; Kandel, 2001). Current molecular models focus on the excitatory neurotransmitter glutamate, which activates postsynaptic receptors that can be broadly categorised into those that transmit the electrical depolarisation ( $\alpha$ -amino-3-hydroxy-5-methylisoxazole-4-propionic acid (AMPA) receptors)

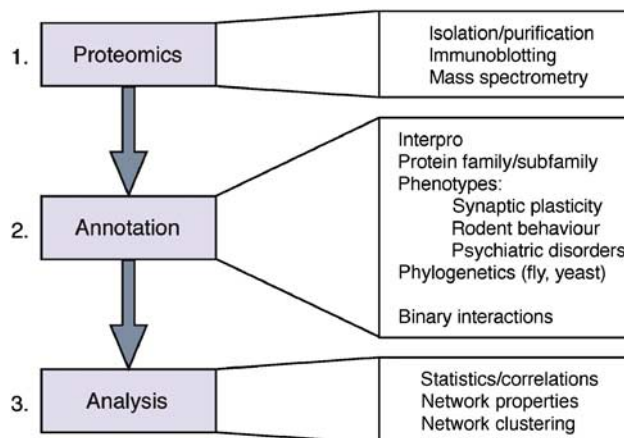
and those that activate signalling and plasticity mechanisms (*N*-methyl-D-aspartate receptor (NMDA) and metabotropic receptors (mGluR)). Proteomic profiling of glutamate receptors isolated from brain reveal that NMDA and mGluR are assembled into large complexes of 186 proteins measuring 2–3 MDa and AMPA receptors into much smaller complexes of ~10 proteins (Husi *et al.*, 2000; Husi and Grant, 2001; Farr *et al.*, 2004; Collins *et al.*, 2005). These neurotransmitter receptor complexes are embedded within the PSD, which is visible with electron microscopy and comprises 1124 identified proteins (Collins *et al.*, 2005). Studies of binary protein–protein interactions show that the NMDA–mGluR receptors are linked via adaptor proteins that also link the receptors to signalling enzymes and structural proteins (Tu *et al.*, 1999). The adaptor proteins include Membrane-Associated Guanylate Kinase (MAGUK) proteins such as PSD-95 and SAP 102, which directly bind the cytoplasmic domains of NMDA receptors. These 186 protein complexes of NMDA receptors, mGluR receptors, MAGUK proteins and associated molecules, referred to as the NMDA receptor complex/MAGUK-associated signalling complex (NRC/MASC), are the subject of our analysis.

Functional studies of synaptic signalling have centred on the cellular mechanisms and behavioural roles of synaptic plasticity. Electrophysiological studies show that particular patterns of neuronal activity can induce changes in synaptic strength (e.g. long-term potentiation (LTP)) and other neuronal properties, which are currently thought to contribute to learning (mediated in the hippocampus), fear conditioning (mediated in the amygdala) and other forms of behavioural plasticity. Early pharmacological studies of synaptic plasticity revealed a role for glutamate receptors and subsequent knockout studies of MAGUK proteins revealed that these receptors require the assembly of signalling complexes for LTP and learning (Migaud *et al*, 1998). However, the progression of this field of research has been confused by the high number of molecules that are essential for normal forms of LTP (Sanes and Lichtman, 1999; A Howell *et al*, unpublished). In excess of 100 mouse gene knockouts show impairments in LTP and a similarly high number are involved with forms of behaviour involving glutamate receptors (Howell *et al*, in preparation). A second, and perhaps not unrelated problem, is that these single-gene perturbations do not usually completely block LTP (Howell *et al*, in preparation). The apparent robustness of synaptic plasticity may reflect its intrinsically important role as a necessary biological process. How this complexity and robustness can be related to the physiology of plasticity and learning is an important problem requiring new approaches.

In this paper, we utilise synapse proteomic data and present a detailed analysis of the NRC/MASC complex using annotation, network and statistical approaches. Using information on the function, interactions and phylogeny of individual proteins, their roles in synaptic plasticity and behavioural plasticity in the hippocampus and amygdala, and their roles in human diseases, we develop a model that explains many of the features of synaptic signalling. We find that the model explains the structural and functional aspects of synapse molecular complexity and why mutations in many genes have only partial effects on synapse plasticity. We suggest general principles of functional organisation that should provide a basis for new functional genomic approaches to synapse function and behaviour and be applicable to other cellular models of signal transduction.

## Results

We adopted a three-step strategy of proteomics, annotation and analysis of synapse proteins (Figure 1). The proteomic step consisted of profiling of protein components of the synapse proteome, and is reported elsewhere (Husi *et al*, 2000; Collins *et al*, 2005). Step 2 involved the annotation of protein structure and function, including physiological and disease roles. Here we classify proteins according to function and molecular features (e.g. kinases, phosphatases) and known binding partners, as this informs on biochemical pathways. The physiological data were obtained from rodent experimental systems, where mutations or drugs that specifically interfere with a given protein have been tested for their effects on synapse physiology and animal behaviour. Finally, we have searched the literature for information on the involvement of specific molecules in human diseases. Step 3 comprised



**Figure 1** A three-step strategy for analysis of synapse proteome organisation. Step 1 (Proteomics) was the collection of proteomic data identifying specific proteins. Step 2 (Annotation) was the collection of specific structural and functional data on individual proteins from Step 1, which was followed by Step 3 (Analysis) using statistical and network approaches.

statistical and network analyses, where we ask if there are correlations and connections between proteins and functions. Integration of these data allows us to search for underlying principles of organisation and generate new models.

### Functional annotation of MASC

MASC proteins were assigned to functional families/sub-families (Table I and Supplementary Table 1). Membrane-spanning channels, receptors and adhesion proteins, together with their associated signal transduction machinery, including adaptors and enzymes, account for 83% of the complex. Interpro annotations were retrieved via SwissProt (Supplementary Table 2). The protein domains most commonly found in MASC proteins (Table II) were highly enriched (3–12-fold) when compared to their frequency in the proteome as a whole. These top 10 domains represent key functionality associated with synaptic signalling: calcium binding (calcium-binding EF hand, C2, IQ calmodulin-binding region), G-protein-coupled signal transduction (small GTP-binding protein domain), phosphorylation (protein kinases, serine/threonine protein kinase), scaffolding (SH3, PDZ/DHR/GLGF) and membrane localisation (Pleckstrin homology type, Pleckstrin type, C2). These functional family and domain annotations clearly reflect specialisation for intercellular signalling.

We next searched the literature for evidence that MASC proteins were involved in synaptic physiology and rodent behaviour. The systematic text searching and manual curation of the published literature that was utilised is described in detail elsewhere (Grant *et al*, 2005; Howell *et al*, in preparation). We specifically searched for genetic and pharmacological evidence that disruption of MASC proteins interferes with LTP and long-term depression (LTD), forms of synaptic plasticity found at most central nervous system synapses (Supplementary Table 3). In total, 44 (24%) proteins represented in MASC were known to be essential: without the function of these proteins, synaptic plasticity was impaired. We also searched for studies reporting the

involvement of specific proteins/genes in behavioural plasticity, focusing on rodent learning and conditioning paradigms, as these represent the largest body of molecular data (Supplementary Table 3). We annotated papers into those affecting spatial learning (primarily mediated by the hippocampus), cue/context conditioning (primarily mediated by the amygdala) and other behavioural paradigms (Kandel *et al.*, 2000). Overall there were 48 (26%) MASC proteins involved with behaviour, of which 42 (23%) were important for learning. Of those involved in learning, 32 (17%) were involved with spatial learning and 25 (13.5%) with cue/contextual conditioning.

Although it is generally accepted on the basis of anatomical homology and lesion data that cognitive mechanisms are conserved between mice and humans, it is unclear to what degree the rodent molecular studies map onto human psychiatric conditions. We therefore examined the possibility that MASC proteins may be involved in human psychiatric and neurological disorders. We identified 54 (29%) MASC proteins implicated in mental illness (Supplementary Table 3). Although we searched all mental disorders, we found 33 (18%) in schizophrenia, 23 (12%) in mental retardation, 12 (6.5%) in bipolar disorder and 14 (7.5%) in depressive illness. This apparent bias toward schizophrenia and mental retardation may be biologically relevant as they both have a major cognitive component to their primary symptoms. In total, 49 (26%) proteins were linked to cognitive disorders (schizophrenia, mental retardation), compared to only 22 (12%) implicated in affective disorders (bipolar, depression).

**Table I** Functional families present in MASC

Family	n MASC <sup>a</sup>	% MASC <sup>b</sup>
Channels and receptors	12	6.4
Cell adhesion and cytoskeletal	35	18.8
G-proteins and modulators	19	10.2
Kinases	22	11.8
MAGUKs/adaptors/scaffolders	20	10.8
Protein phosphatases	8	4.3
Signalling molecules and enzymes	39	21.0
Synaptic vesicles/protein transport	23	12.4
Transcription and translation	5	2.7
Uncharacterised/novel	3	1.6

<sup>a</sup>Number of MASC proteins assigned to family.

<sup>b</sup>Percentage of MASC proteins assigned to family.

**Table II** Domain profile of MASC—10 most common

Domain	Accession	% MASC <sup>a</sup>	% Proteome <sup>b</sup>	Ratio <sup>c</sup>
Protein kinase	IPR000719	11.8	3.75	3.16
Serine/threonine protein kinase	IPR002290	10.2	1.69	6.05
SH3	IPR001452	8.06	1.51	5.33
Pleckstrin-like	IPR001849	5.91	1.25	4.72
PDZ/DHR/GLGF	IPR001478	5.91	0.74	8.04
Small GTP-binding protein domain	IPR005225	5.38	1.49	3.62
Pleckstrin homology-type	IPR011993	4.84	1.08	4.49
Calcium-binding EF-hand	IPR002048	4.84	1.65	2.93
C2	IPR000008	4.84	0.82	5.92
IQ calmodulin-binding region	IPR000048	3.76	0.31	12.0

<sup>a</sup>Percentage of MASC proteins possessing domain annotation.

<sup>b</sup>Percentage of mouse proteome possessing domain annotation.

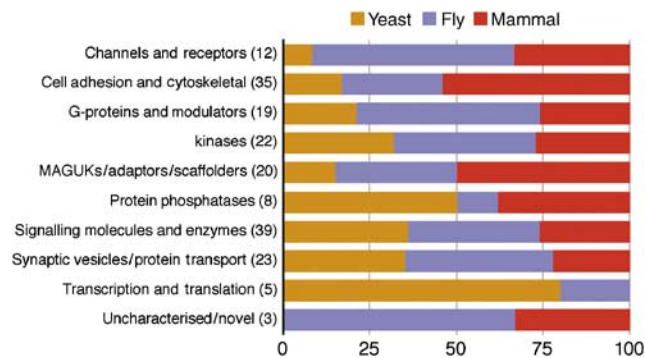
<sup>c</sup>Ratio of MASC to proteome (measure of enrichment in MASC).

To investigate the evolutionary conservation of MASC proteins in invertebrates and unicellular eukaryotes, we searched for orthologues in the genomic databases of yeast (*Saccharomyces cerevisiae*) and fruit fly (*Drosophila melanogaster*) (see Materials and methods). In total, 117 (63%) MASC proteins were identified in fly and 51 (27.5%) in yeast (Supplementary Table 4). Overall, 63 (34%) were found only in mouse (i.e. have no identified orthologues in yeast or fly), 135 (72.5%) were metazoan (not found in yeast) and 45 (24%) conserved (present in both fly and yeast). While transcription/translation proteins were generally conserved from yeast (Figure 2), those protein families involved in intercellular signalling were primarily metazoan, consistent with previous observations (Manning *et al.*, 2002). Although all functional families were found in yeast, and thus predate the evolution of the nervous system, there were distinct patterns among these families relevant to synapse specialisation. For example, significant expansion of most families arises at the metazoan transition (yeast to fly) and there is additional expansion from fly to mammals in specific classes (Cell Adhesion and Cytoskeletal, MAGUKs/Adaptors/Scaffolders). This is supported by more detailed statistical analysis described in the following section. These expansions toward the mammalian lineage may be relevant to the more complex range of behaviours and neuroanatomy of the mammalian nervous system and the physiological role of MASC proteins.

## Statistical analysis of annotations

The entire set of functional, phenotypic and phylogenetic annotations (Supplementary Tables 1–6) were subjected to a statistical analysis, looking at their distribution and overlap (see Materials and methods). For each pair of annotations (e.g. *glutamate receptors* and *schizophrenia*), we identified the number of common proteins, calculating the probability of an overlap as or less likely occurring by chance. As an example, of the 32 MASC proteins implicated in schizophrenia, five are glutamate receptor proteins. In total, there are only six glutamate receptor proteins in MASC—if 32 MASC proteins are selected at random, it is most likely that only one of them will be a glutamate receptor. The probability of finding five or more glutamate receptors in a random sample of 32 taken from MASC is  $\sim 0.0007$ . This suggests that the overlap between glutamate receptors and schizophrenia is of biological





**Figure 2** Evolutionary expansion of protein families in MASC. Functional classes of proteins are represented as a horizontal line and the number of these proteins found in mouse MASC is shown in parenthesis. The percentage of each functional family making its earliest appearance in yeast (brown), fly (blue) or mammal (mouse, rat, human) (red) is indicated using the species-specific colour scheme. For example, only one out of 12 (8.5%) mammalian channels and receptors were found in yeast, in contrast to transcription and translation regulators, where four out of five (80%) were found in yeast. It is interesting to note that the novel/uncharacterised proteins arise in metazoans.

relevance. Only probabilities  $<0.01$  were considered as potentially significant (Supplementary Table 7). In both this and the following section, references to annotations are indicated in italics, brief descriptions of which are collected below.

*Glutamate receptors* showed a striking correspondence with all studies of synaptic plasticity (*drug*  $P < 10^{-4}$ , *mutation*  $P < 10^{-3}$ , *synaptic plasticity*  $P < 10^{-3}$ ), all behavioural assays (*spatial learning*  $P < 10^{-2}$ , *cue/contextual conditioning*  $P < 10^{-3}$ , *behavioural (other)*  $P < 10^{-3}$ , *behavioural plasticity*  $P < 10^{-2}$ ), *cognitive disorders* in general ( $P < 10^{-2}$ ) and *schizophrenia* in particular ( $P < 10^{-3}$ ). The only proteins to occur in all of these categories were the NMDA receptor subunits NR1, NR2A and NR2B: evidence of a strong link between NMDA receptor signalling and cognitive function. Notable overlaps were also found between *phosphatases* and synaptic plasticity (*drug*  $P < 10^{-2}$ , *synaptic plasticity*  $P < 10^{-2}$ ), between *G- $\alpha$  proteins* and affective disorders (*affective*  $P < 10^{-2}$ , *bipolar*  $P < 10^{-2}$ , *depressive*  $P < 10^{-2}$ ) and between C2 (Ca-dependent membrane-targeting) domain proteins and behavioural phenotypes (*behavioural plasticity*  $P < 10^{-3}$ , *cue/contextual conditioning*  $P < 10^{-3}$ , *spatial learning*  $P < 10^{-2}$ ). While the functional subfamily of *other enzymes* had a significant overlap with *mental retardation*, four of the five proteins responsible for this overlap (a lactate dehydrogenase, phosphofructokinase, pyruvate kinase and triosephosphate isomerase) are metabolic enzymes involved in glycolysis. As such, the phenotypes of these enzymes are more likely to be due to widespread disruption of electrophysiological properties than the perturbation of specific signalling pathways.

*Synaptic plasticity* and *behavioural plasticity* were intimately connected within MASC ( $P < 10^{-11}$ ), which strongly supports the model that the overall complex is a molecular machine underpinning cellular and behavioural plasticity. The close correspondence found between *spatial learning* and *cue/contextual conditioning* ( $P < 10^{-6}$ ) indicates a common molecular basis for learning in the amygdala and hippocampus. *Synaptic plasticity* showed a high degree of overlap with studies of cognitive and to a lesser extent affective disorders

(*cognitive*  $P < 10^{-8}$ , *schizophrenia*  $P < 10^{-6}$ , *mental retardation*  $P < 10^{-2}$ , *affective*  $P < 10^{-2}$ , *bipolar*  $P < 10^{-2}$ ). In contrast, *behavioural plasticity* displayed a high degree of overlap with both (*cognitive*  $P < 10^{-9}$ , *affective*  $P < 10^{-6}$ , *bipolar*  $P < 10^{-4}$ , *depressive*  $P < 10^{-3}$ ). In addition, *cognitive* and *affective disorders* showed a significant overlap ( $P < 10^{-6}$ ). Within the cognitive disorders, *schizophrenia* showed a significant overlap with both affective disorders (*depressive*  $P < 10^{-7}$ , *bipolar*  $P < 10^{-4}$ ) and *mental retardation* with *bipolar* ( $P < 10^{-2}$ ). However, the overlap between *schizophrenia* and *mental retardation* was not significant ( $P > 0.1$ ). In general, the degree of commonality between *mental retardation* and other annotations tended to be among the least significant of all phenotypes. Together, these results validate the use of rodent models of human mental illness, particularly schizophrenia, and promote the perturbation of MASC and its effect on synaptic plasticity as a major underlying factor.

The physiological and behavioural annotations did not have significant overlap with the phylogenetic annotations. Nevertheless, consistent with Figure 2 and earlier results, *cell adhesion and cytoskeletal* proteins were under-represented in fly ( $P < 10^{-2}$ ) and significantly expanded in mammals (*mammalian*  $P < 10^{-2}$ ). All *ATP synthases* were conserved ( $P < 10^{-2}$ ) and all *Ser/Thr-specific phosphatases* were found in yeast. All MASC proteins containing L27 domains (found in receptor-targeting proteins) appeared to be *mammalian* specific ( $P < 10^{-2}$ ).

Drawing these analyses together, MASC appears to be a highly specialised signal transduction complex, whose evolutionary expansion reflects a role in neural information processing unique to higher organisms. The composition of MASC suggests that diverse cell-biological responses are coordinated within the complex. The coupling of these responses to glutamatergic signalling induces synaptic plasticity, which results in behavioural learning. Disruption of the complex perturbs the orchestration of responses, causing altered synaptic plasticity. This manifests as impaired behavioural plasticity in rodents and psychiatric disorders in humans. To the limited extent to which they can be separated, cognitive disorders appear intimately linked to signal transduction via the NMDA receptor, while affective disorders show closer correspondence to G-protein-coupled signalling and mGluRs. On balance, information processing within MASC appears primarily related to cognitive function. The relatively weak correlation between mental retardation and other annotations (i.e. essentially random overlap) suggests that it involves random disruption within MASC, and that the major cognitive component to its symptoms simply reflects the primary role of the complex.

## Protein interaction network analysis

The annotation studies presented above only consider the list of components and do not take into consideration their organisation or assembly into a complex through protein-protein interactions. We therefore obtained high-quality interaction data, curated from the literature, in order to generate a network representation of the complex (see Materials and methods) and analyse its features.

We identified 248 binary interactions between 105 of the MASC proteins (Supplementary Table 8). This number excludes self-interactions, which were not used in network construction. No interaction data were found for the remaining 77 proteins (apart from self-interactions). When represented as an undirected graph, the largest network component consisted of 101 proteins linked by 246 interactions. This connected component constitutes core functional elements of the complex. It links together all glutamate receptors and a high proportion of the signal transduction machinery responsible for the reception and integration of calcium and G-protein-coupled synaptic signalling (Table IIIa). That the component captures key functional processes is supported by the fact that it contains the majority of all phenotypically linked proteins (Table IIIb). The sole exception to this is mental retardation, whose representation within the connected component (65%) is close to that of MASC proteins as a whole. This supports the hypothesis that mental retardation entails general disruption of the complex, and argues against enrichment of the component with other phenotypic annotations being solely due to bias in the literature. All further analysis concerns this 101-protein component.

The average number of interactions separating any pair of proteins was very low (average shortest path length=3.3), implying a high level of crosstalk between signal transduction pathways. While this suggests an ability to rapidly integrate disparate sources of information and orchestrate coherent responses, it does not sit comfortably with a model of well-defined linear pathways of limited overlap. It suggests instead

that functional roles are distributed over sets, or clusters of proteins within MASC. We therefore sought to identify and evaluate any clustering inherent in the network (see Materials and methods).

The connected component was found to possess a clearly modular structure (Figure 3 and Supplementary Table 9), with ~75% of its proteins contained in the five largest clusters. To evaluate the functional significance of these clusters, their overlap with each functional and phenotypic annotation (such as those shown in Figure 4) was analysed using the statistical method introduced earlier (Supplementary Table 10).

Cluster 1 contains all *ionotropic glutamate receptor* proteins ( $P < 10^{-3}$ ) and a large number of *PDZ/DHR/GLGF* scaffolding molecules ( $P < 10^{-3}$ ), particularly MAGUKs. In total, ~50% of its proteins are essential to normal *synaptic plasticity* ( $P < 10^{-2}$ ) and ~40% are implicated in *schizophrenia* ( $P < 10^{-2}$ ). Within MASC, these features have a strong association with cognitive function.

Cluster 2 appears specialised for metabotropic/G-protein-coupled signalling (*G-proteins*  $P < 10^{-2}$ , *metabotropic glutamate receptor*  $P < 10^{-2}$ ). Half of its proteins have known behavioural phenotypes (*behavioural (other)*  $P < 10^{-2}$ ) and it contains a third of all MASC proteins implicated in *depressive illness* ( $P < 10^{-2}$ ). With Homer coupling mGluRs to IP3 receptors in the endoplasmic reticulum and PLC  $\beta$  localised to the membrane via PH and C2 domains, the cluster is capable of directly regulating  $Ca^{2+}$  release from internal stores. Also present are several proteins closely associated with vesicular release. These link to cluster 8, which contains proteins

**Table III** Composition of the largest network component

Annotation	n Ccpt <sup>b</sup>	% Ccpt <sup>b</sup>	+ / - <sup>c</sup>	Probability <sup>d</sup>
<b>(a) Functional family<sup>a</sup></b>				
Channels and receptors (12)	8	67	~	0.6
Cell adhesion and cytoskeletal (35)	19	54	~	1.
G-proteins and modulators (20)	17	85	+	0.007
Kinases (21)	19	90	+	0.0007
MAGUKs/adaptors/scaffolders (17)	15	88	+	0.004
Protein phosphatases (7)	6	86	~	0.1
Signalling molecules and enzymes (39)	10	26	-	0.00004
Synaptic vesicles/protein transport (23)	7	30	-	0.01
Transcription and translation (5)	0	0	-	0.02
Uncharacterised/novel (3)	0	0	-	0.09
Glutamate receptors (6)	6	100	+	0.03
<b>(b) Phenotype<sup>a</sup></b>				
Synaptic plasticity (44)	38	86	+	10 <sup>-6</sup>
Behavioural plasticity (41)	35	85	+	10 <sup>-5</sup>
Psychiatric disorder (53)	40	75	+	0.0005
Schizophrenia (32)	27	84	+	0.0003
Mental retardation (23)	15	65	~	0.4
Bipolar (13)	11	85	+	0.04
Depressive (13)	11	85	+	0.04

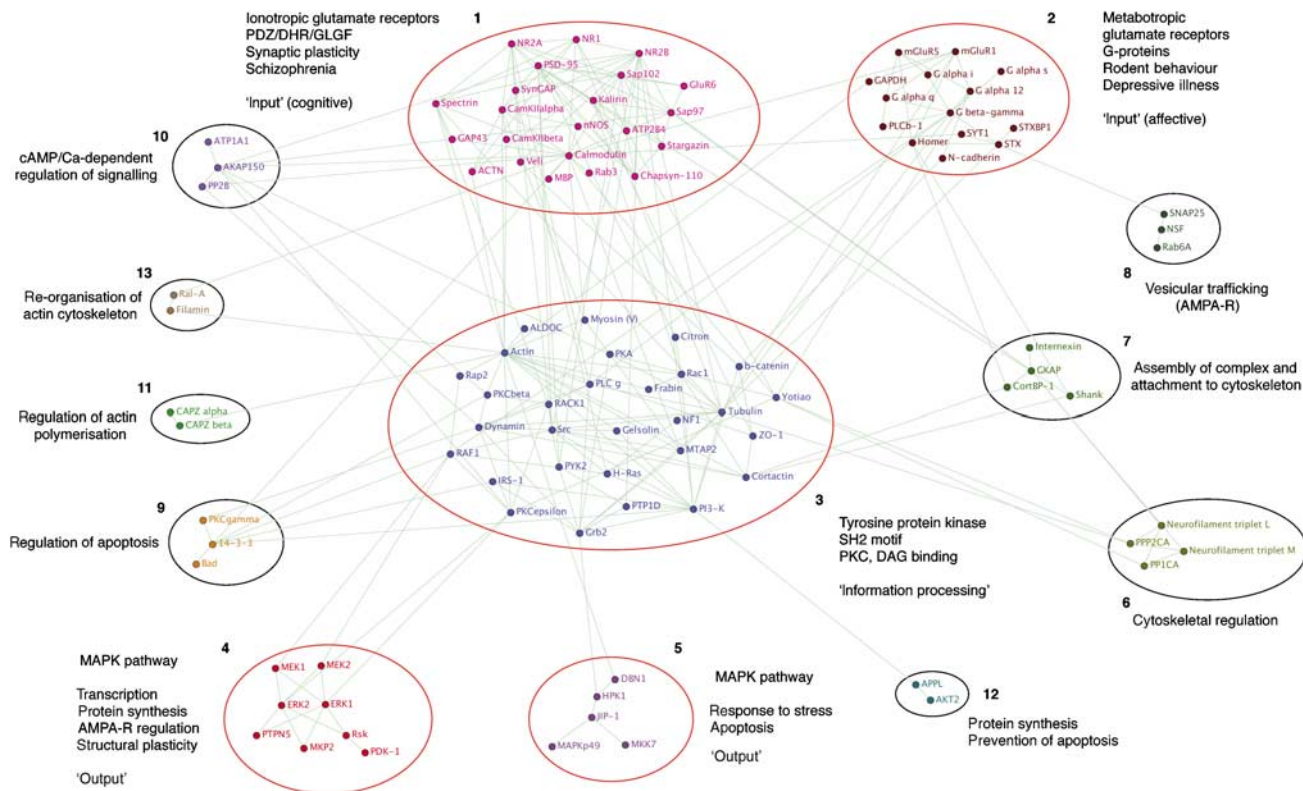
<sup>a</sup>Number of MASC proteins contained in each family or implicated in each phenotype indicated in brackets. Also shown in (a) is the representation of glutamate receptors, a subfamily of channels and receptors.

<sup>b</sup>Number and percentage of each annotation present in the largest connected component of network.

<sup>c</sup>Annotations over/under-represented in the connected component denoted by (+/-). The representation of an annotation is considered to be indistinguishable from a random sample (~) if the probability given in the final column is >0.1.

<sup>d</sup>Probability of this overlap (n Ccpt) between annotation and network component using the statistical method described in the text.

Summarised are the representation of (a) functional family and (b) phenotype annotations within the largest network component. The number of MASC proteins contained in each family (or implicated in each phenotype) is indicated in brackets. Subsequent columns show the number (n Ccpt) and percentage (% Ccpt) of these present in the largest connected component, whether this is more or less than expected by chance (+/-) and the probability of this overlap between annotation and connected component using the statistical method described in the text. The representation of an annotation is considered to be indistinguishable from a random sample (~) if this probability is >0.1. Also shown in (a) is the representation of glutamate receptors, a subfamily of channels and receptors.



**Figure 3** Network cluster analysis. Clustering of the largest connected component of the MASC network identified 13 clusters. Significant overlap with functional and phenotypic annotations is indicated for the largest clusters, 1–3. Clusters 4 and 5 both correspond to MAPK signalling pathways regulating various functional processes (briefly summarised). All five are followed by a brief descriptive phrase indicating their general functional role. Functional roles suggested by composition and interactions are indicated for the remaining clusters. Graphical representation of network produced using BiLayout (Enright and Ouzounis, 2001).

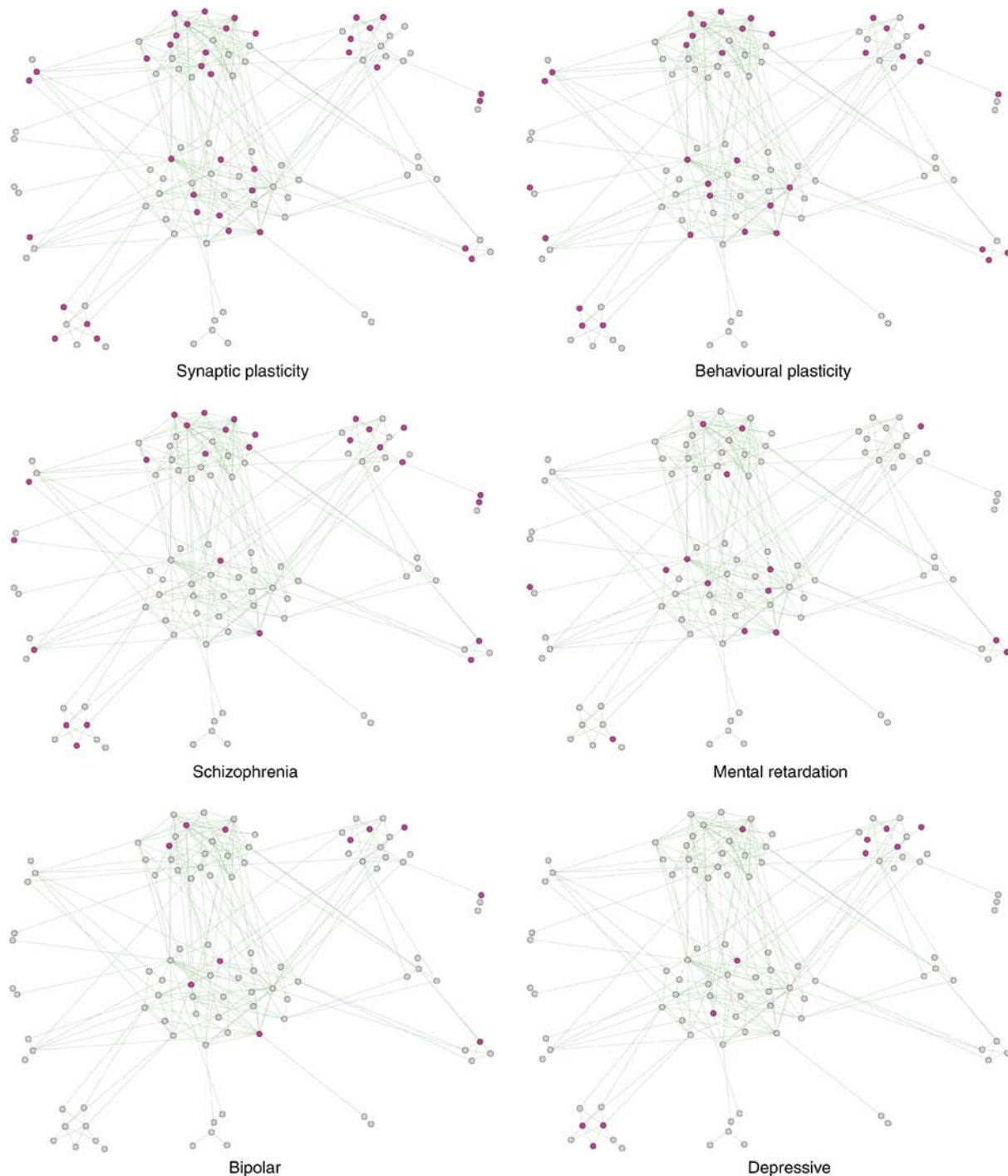
implicated in the postsynaptic trafficking of AMPA receptors, for example, NSF (Nishimune *et al*, 1998).

Cluster 3, the largest, is strongly connected to clusters 1 and 2. Its size and centrality within the network (see Figure 3) suggest that it assimilates signals from various sources and co-ordinates common effector mechanisms. This seems to be borne out by its composition. The well-studied Ser/Thr kinase PKA, known as an integrator of signals in synaptic plasticity, is found within the cluster. The cluster also contains a concentration of *tyrosine kinases* ( $P < 10^{-3}$ ) and *SH2 motif* proteins ( $P < 10^{-3}$ ). SH2 domains bind specifically to phosphotyrosine in a wide range of substrates, interactions known to regulate diverse signal transduction pathways (Pawson, 2004). The tyrosine kinases are themselves a point of convergence for multiple signalling pathways regulating NMDA receptor activity (Salter and Kalia, 2004). These data suggest that cluster 3 integrates the ionotropic and metabotropic signals of clusters 1 and 2 with modulatory sources external to MASC. This is supported by the concentration of Ser/Thr kinases sensitive to the second messenger diacylglycerol (DAG), another route for external modulation (*PKC, phorbol ester/DAG binding*  $P < 10^{-2}$ ). These processes are closely interconnected: Citron, a dual-specificity kinase, contains a DAG-binding motif, while PLC  $\gamma$  hydrolyses PI(4,5)P<sub>2</sub> to form DAG and IP<sub>3</sub> (another link to Ca<sup>2+</sup> signalling) when activated by tyrosine phosphorylation.

Cluster 4 encapsulates the well-studied MAPK–ERK signalling pathway (*Ser/Thr kinases*  $P < 10^{-4}$ , *Erk1/2 MAP kinase*  $P < 10^{-2}$ , *tyrosine & dual-specificity phosphatase*  $P < 10^{-2}$ ). ERK activation has been linked to transcription, protein synthesis, regulation of AMPA receptors and structural plasticity (Thomas and Huganir, 2004). Cluster 5 is another MAPK pathway (*Ser/Thr kinases*  $P < 10^{-2}$ ), mediating response to stress through JNK3 (MAPKp49). It may be of note that cluster 4 interacts with cluster 3 via proteins containing DAG-binding motifs (RAF1 and PKC  $\epsilon$ ), while cluster 5 interacts through Grb2—an SH2 domain adapter protein. With reference to clusters 4 and 5, it is interesting to note the existence of the small cluster 12 linking AKT2 (PKB  $\beta$ ) to PI3-K via the scaffolding protein APPL. Interplay between PI3-K and MAPK signalling has a complex effect on LTP, the mechanisms of which are still unclear (Opazo *et al*, 2003). PI3-K has been implicated in vesicular trafficking and cytoskeletal rearrangement, while PI3-K-dependent activation of PKB contributes to the control of protein synthesis and the prevention of apoptosis (Rogers and Theibert, 2002).

For the smaller clusters still to be discussed, we indicate functional roles suggested by their composition and interactions (Supplementary Tables 8 and 9). Clusters 6, 7, 11 and 13 mediate interactions with the cytoskeleton. Three of these regulate cytoskeletal structure and its rearrangement: cluster 6 via neurofilaments, clusters 11 and 13 via actin. Assembly and





**Figure 4** Network clustering—phenotypic overlay. Proteins with various phenotypes (electrophysiological, behavioural and human psychiatric) are highlighted within the MASC network. The layout of proteins, identical to that of Figure 3, reflects network clustering.

localisation of the complex are influenced by cluster 7, which mediates colocalisation of receptor subcomplexes (clusters 1 and 2) and their attachment to the cytoskeleton. Cluster 10 controls channel and kinase activity through the integration of cAMP and Ca signals. Regulation of Na/K channel ATP1A1 alters the postsynaptic resting potential,

while control of PKA and PKC isoforms strongly modulates MASC signalling. Cluster 9 regulates the induction of apoptosis through the phosphorylation and sequestration of Bad. These clusters reflect the role of the NMDA receptor in structural plasticity, cell death and the synaptic localisation of proteins.



In general terms, the network seems to be organised into a few large, highly connected clusters directing MASC function (clusters 1–3) and a greater number of smaller, more sparsely connected clusters dedicated to specific functional processes (clusters 6, 7, 8, 9, 11 and 13). Other clusters are intermediate between the two (clusters 4, 5, 10 and 12).

### Topology and functional robustness of the MASC network

Synaptic plasticity is surprisingly robust, with disruption by mutation or drugs only partially impairing rather than completely abolishing plasticity in most cases (e.g. see Grant *et al*, 1992; Watabe *et al*, 2000; Komiyama *et al*, 2002; Opazo *et al*, 2003; Yasuda *et al*, 2003). A potential source of robustness lies in the pattern of connectivity within the network. The degree distribution of the network (the probability  $\rho(k)$  of a protein being involved in  $k$  interactions) was found to be well fitted by a power law, with  $\rho(k) \sim k^{-1.2}$  ( $P < 10^{-5}$ ). This reflects the presence of a few highly connected proteins mediating interaction between the more sparsely connected proteins that constitute the bulk of the network. It provides a level of structural robustness whereby the degree of a protein (the number of interactions it is involved in) correlates with the structural disruption caused by its removal (Albert *et al*, 2000). In yeast this has been shown to translate into functional robustness—while highly connected proteins form a small percentage of the proteome, their disruption is more likely to prove lethal (Jeong *et al*, 2001). Of the eight MASC proteins with  $>10$  interactions, there are five (62.5%) with phenotypes in all three major categories (synaptic plasticity, behavioural plasticity and psychiatric disorder), while of the 61 MASC proteins with  $<5$  interactions, there are only nine (14.8%).

Given that the more interactions a protein has the more likely it is to influence multiple processes (e.g. effector mechanisms), correlation between protein connectivity and severity of effect on disruption naturally arises. When combined with a power-law degree distribution, this suggests a loose functional hierarchy composed of a few highly interacting proteins, largely responsible for overall functional co-ordination, a broad range of lower degree proteins influencing various aspects of functionality and a large number of low interacting proteins specific to individual functional processes. This has clear parallels with the modular organisation of MASC, discussed above. Our analysis up to this point led us to propose the following model for the structural and functional organisation of MASC.

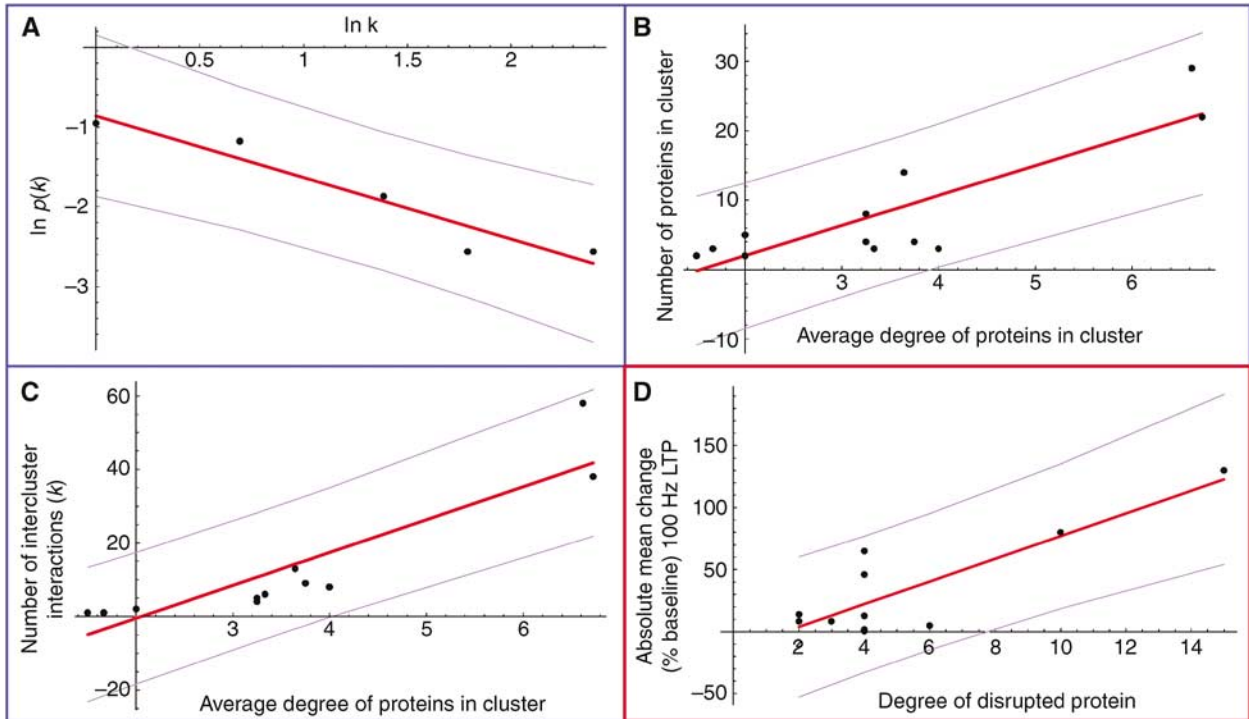
Each functional process is the net result of complex interactions within a subset of MASC proteins. These subsets overlap, with some proteins being involved in multiple functions: there is a positive correlation between the degree of a protein and the number of functional processes it influences. This correlation is intimately connected with the emergence of a power-law degree distribution and low average path length. Physical interactions cluster MASC proteins into functional modules. The network formed by these modules is subject to the same organisational principles: the mean shortest path length between modules is low; the size and

intercluster connectivity (degree of interaction with other clusters) of each module correlates with the extent of its functional influence; and module–module interactions possess a roughly power-law degree distribution. These common principles facilitate co-ordination and impart robustness to functional processes at both levels. Individual modules are specialised for functional roles including signal reception, signal integration and processing and the regulation of effector mechanisms. Through the dynamic balance of interactions within and between modules, MASC integrates multiple streams of information and co-ordinates diverse cell-biological processes in response, regulating the induction of synaptic plasticity.

While more data are needed to properly evaluate this model, some preliminary observations can be made. The low average path length separating proteins and the power-law distribution of their interactions have already been demonstrated. The mean shortest path length between modules was 1.86. Limited by the low number of modules, the probability  $\rho(k)$  of a module interacting with  $k$  others showed a marginally significant fit to a power law:  $\rho(k) \sim k^{-0.77}$  ( $P=0.010$ , see Figure 5A). Functional influence is positively correlated with properties at two levels: the degree of individual proteins and the size and connectivity of clusters of proteins. Compatibility between the two requires the degree of a protein to be correlated with the size/intercluster connectivity of the module in which it is found. The average degree of proteins belonging to each cluster of the MASC network was found to have a significant correlation with both cluster size (linear fit:  $P < 10^{-3}$ , Pearson correlation=0.87; see Figure 5B) and intercluster connectivity (linear fit:  $P < 10^{-4}$ , Pearson correlation=0.90; see Figure 5C). Correlation was also found between cluster size and intercluster connectivity (linear fit:  $P < 10^{-6}$ , Pearson correlation=0.96). These correlations persist when data are restricted to the five largest, most clearly defined clusters, and also when connections between clusters are taken to be binary (data not shown). The relationship with functional influence is reflected in the concentration of highly interacting, influential proteins (e.g. NR2A/B, PSD-95, calmodulin, CamKII  $\alpha$ , PI3-K, actin) within the largest, most highly connected clusters, 1 and 3.

Most significantly, the model makes the following prediction: if MASC controls the induction of synaptic plasticity, then a correlation between protein degree and extent of functional influence entails a correlation between protein degree and quantitative perturbation of LTP/LTD on disruption.

Quantitative data on the perturbation of LTP/LTD caused by disruption of individual proteins were available for a subset of MASC proteins with synaptic plasticity phenotypes. As LTP varies with the frequency of presynaptic stimulation, we considered only experimental data obtained using 100 Hz stimulation protocols, by far the most common. Such data are available for 36 experiments covering 11 MASC proteins, all of which are present in the connected component (Supplementary Table 11). Despite the inherent variability of this data due to differences in experimental protocols, protein degree and quantitative perturbation of LTP on disruption were found to be strongly correlated (linear fit:  $P < 10^{-3}$ , Pearson correlation=0.85, see Figure 5D).



**Figure 5** Support for model of MASC organisation. The model of MASC functional organisation makes several predictions: interconnectivity between modules follows a power law; protein degree is correlated with the size and interconnectivity of the enclosing module; and the degree of a protein is correlated with the perturbation of synaptic plasticity caused by its disruption. In all plots, the best linear fit is shown in red, with magenta lines at one standard deviation. **(A)** The probability  $p(k)$  of a cluster being connected to  $k$  other clusters is shown as a function of  $k$  in a log–log plot, a power-law distribution being characterised by a straight-line plot. **(B)** The number of proteins contained in a cluster is plotted as a function of their average degree. **(C)** The number of interactions with proteins external to a cluster is shown as a function of the average degree of proteins within the cluster. **(D)** The absolute change (% baseline) in 100 Hz LTP is shown as a function of the degree (number of interaction partners) of the protein disrupted. Where multiple sets of experimental data were available for a single protein, the absolute value of the mean experimentally recorded change was used (a significant linear fit was also evident for the full data set of 36 points).

## Discussion

Here we present an integrated analysis of molecular organisation, signal transduction, physiology and diseases of a neurotransmitter receptor signalling complex as a step toward synapse systems biology. We also present a new model for understanding the molecular complexity of the synapse proteome and its relationship to synapse physiology (Figure 6). In addition to its specific features relevant to neurobiology, this model has some general properties applicable to other areas of signal transduction and receptor biology. Below we discuss the elements of this model progressing from signal transduction, to physiology and finally to behaviour and disease. We then compare our model of network organisation to other descriptions of network topology, before placing our analysis in perspective with some general observations.

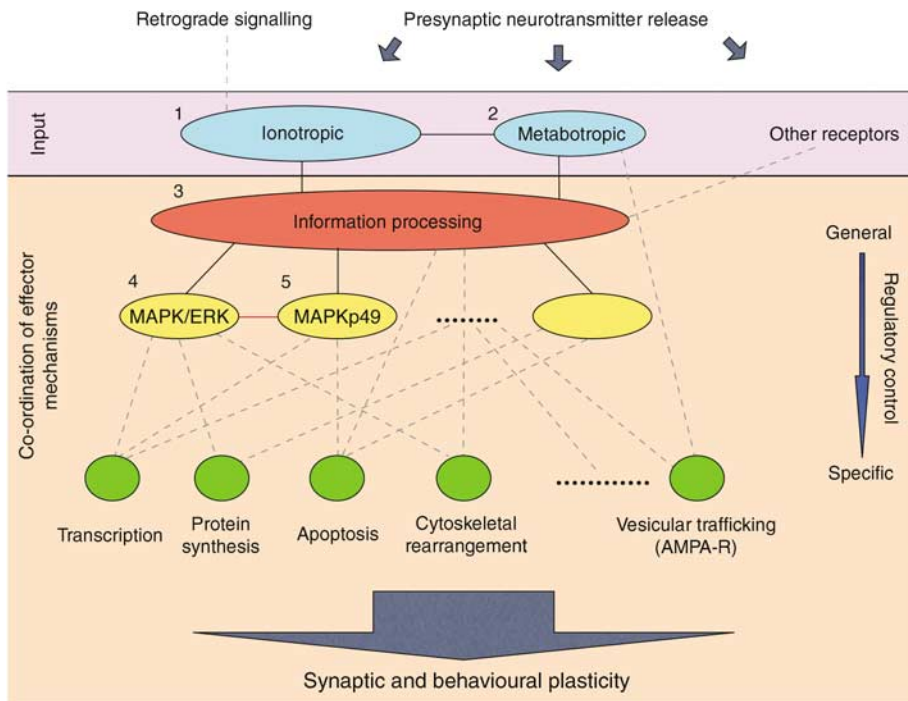
### Signal transduction

Analysis of protein interactions leads us to propose the following view of signal transduction within the complex, summarised in Figure 6. Clusters of proteins around ionotropic and metabotropic glutamate receptors (modules 1 and 2) form the primary sites for signal reception. The density of interactions surrounding NMDA receptor subunits and the extent of their phenotypic involvement suggest that ionotropic

signalling dominates. Indeed, this is supported by electrophysiological studies using blockers of NMDA and metabotropic receptors, where the NMDA receptors have a severe phenotype (Bliss and Collingridge, 1993). These clusters may directly regulate effector mechanisms such as retrograde signalling (ionotropic) and release of calcium from internal stores (metabotropic). The latter generates a second calcium signal with a spatiotemporal profile quite distinct to that of the ionotropic current. The relative timing, strength and duration of these signals are likely to be important factors in the initiation of downstream signalling events. These signals are modulated by other sources of information, both internal and external to the complex. The main body of proteins (module 3) integrates these disparate sources, co-ordinating common effector pathways via a cascade of smaller clusters (modules 4, 5 and others). This integrated model fits well with classical reductionist studies of molecular plasticity, where, for example, these output clusters, such as the ERK pathway, are well known as important outputs of glutamate receptor-mediated synaptic plasticity (Sweatt, 2004).

### Physiology

At the physiological level, our analysis suggests that MASC is central to the postsynaptic processing of information encoded in neural activity, orchestrating the cellular responses under-



**Figure 6** Modular structure and functional organisation within MASC. MASC proteins are clustered into modules with well-defined functional roles. Primary signal reception modules (blue) are formed around ionotropic and metabotropic receptors. These inputs are integrated within a large signal-processing module (red) responsible for overall co-ordination of functional processes. Other sources of input ('other receptors') may feed into this module directly, or through smaller input/processing modules (such as cluster 10, Figure 3). Note that, within this general structure, individual modules may play multiple functional roles (e.g. regulation of effector mechanisms by input modules 1 and 2). In this way, information processing and regulation of effector pathways are distributed over multiple modules. The general principles underlying functional organisation within MASC are apparent in the co-ordinated regulation of common downstream effector pathways: a single, large module (red) is responsible for overall co-ordination; several intermediate modules (yellow) regulate overlapping sets of pathways, while numerous small modules (green) are specific to individual effector responses. Note that this is not a simple feed-forward mechanism, rather a dynamical balance between multiple functional processes. The resulting synchronisation of multiple cell-biological processes induces synaptic plasticity, manifest at a higher level of neurological function through behavioural learning. Numbering of the five largest clusters reflects that of Figure 3, as do the interactions between them (solid black lines). Internal/external modulation of MASC function and the regulation of effector mechanisms are denoted by dashed lines. The red line between clusters 4 and 5 denotes the fact that other interactions (e.g. phosphorylation) play an important role in MASC function.

lying synaptic plasticity. We propose that the complex as a whole is responsible for the induction of synaptic plasticity. The strongest case can be made for hippocampal LTP/LTD, with MASC containing a large number of proteins implicated through study of CA3-CA1 synapses. While it was obvious that NMDA receptors were involved in both plasticity and learning, it was not obvious that so many of the other proteins were involved with both synaptic plasticity and behaviour and could be 'unified' in the complex. Thus, the fact that there was such an extremely high overlap (probability of an overlap as or more extreme occurring by chance  $< 10^{-11}$ ) is indeed very striking. The physiological role of the complex is strongly reinforced by the correlation between protein connectivity within the complex and quantitative perturbation of LTP on disruption (Figure 5D).

### Behaviour and disease

Extending from the physiology to behaviour and disease, we see marked evidence of a common molecular foundation to synaptic plasticity, rodent behaviour and human mental illness. Of the psychiatric disorders, the complex is most

closely associated with schizophrenia, which itself shows the highest correlation to synaptic and behavioural plasticity. Mouse genetic studies have been used to dissect distinct cognitive subprocesses (such as strategy choice, perception and learning) and show that these processes can be separated by mutations in different genes in NRC/MASC (Migaud *et al*, 1998; Cuthbert *et al*, submitted). This is consistent with the modularity within MASC mapping onto these distinct cognitive processes. For example, signal reception modules (clusters 1 and 2) were clearly specialised for different streams of information transmitted by distinct mechanisms (ionotropic and metabotropic receptors) that map onto cognitive and affective disorders and processing, respectively. The fact that cognitive and affective disorders display contrasting associations at the level of input should not be taken as indicating a sharp separation, as they appear closely intertwined, with elements of ionotropic and metabotropic signalling implicated in both. On balance, the evidence argues for a primarily cognitive role to MASC function. It is interesting to note that although schizophrenia and mental retardation/learning disability are both cognitive disorders, mental retardation genes are found scattered throughout the genome in large numbers,

whereas schizophrenia genes are found in a small number of regions, and that schizophrenia is likely to entail more specific disruption within the complex.

A potentially exciting feature of our model for the aetiology of human psychiatric diseases arises from our study of molecular complexity and robustness, which helps explain why many molecules participate in a phenotype. We speculate that the genetic complexity of schizophrenia or other diseases affecting this complex (Grant *et al*, 2005) may emerge from combinations of common polymorphisms in the many genes encoding MASC. These polymorphisms alone may have no clear phenotype, until they are in combination with others, which together have a cumulative effect on MASC function. Complementary to this aetiological model is the possibility of using the network to identify disease-modifying pharmaceuticals that target specific proteins.

### Network organisation

We observed evidence for simple principles underlying the functional organisation of MASC at the level of both proteins and clusters: the characteristic path length (average shortest path length) separating elements (proteins/modules) is low; the connectivity of elements follows an approximately power-law distribution and the connectivity of each element is correlated with the extent of its functional influence. These imply a functional hierarchy ranging from a few highly connected elements responsible for overall coordination, to numerous sparsely connected elements specific to individual functional processes. In between these extremes lies a range of elements through which particular sets of functional processes are coordinated. We suggest that these principles extend to all levels of organisation within the postsynaptic proteome.

The properties of this model are best understood through comparison with other models of network topology—small-world, scale-free and bow-tie architectures—all of which have been identified in biological networks. The small-world models of Watts and Strogatz (1998) combined local clustering and a low characteristic path length. Both of these properties are present in our model, where we would expect them to reproduce the enhanced signal propagation and functional coordination with which they were associated. Many biological networks have been described as scale-free due to their approximately power-law degree distribution (Jeong *et al*, 2000), another component of our model. This reflects the presence of a few highly connected nodes (molecules/clusters) that mediate interaction within the less-well-connected bulk of the network. Such networks are structurally robust to random deletions, but fragile to targeted removal of highly interacting nodes (Albert *et al*, 2000). Given that the more interactions a node has the more likely it is to influence multiple functional processes (as in our model); this naturally extends to a correlation between node connectivity and severity of functional effect on disruption, a correlation also observed in the yeast proteome (Jeong *et al*, 2001). Higher-level structure has been modelled as a 'bow-tie' (Ma and Zeng, 2003; Csete and Doyle, 2004) in which multiple inputs converge on a tightly integrated core of processes that drive an array of output pathways. While it is tempting to identify the MASC network (Figures 3 and 6) as a bow-tie structure—modules 1 and 2 as

input, 3 as core functional processing, and 4, 5 and others as outputs—this would be overly simplistic. Input clusters 1 and 2 are directly linked to output pathways (retrograde signalling, vesicular trafficking), while cluster 10 (Figure 3) integrates second messenger signals, strongly modulates information processing in cluster 3 and directly regulates ion channel properties. In effect, the core functionality of information processing and integration is distributed rather than centralised. As we have shown, higher-level structure is better described by a network of modules with power-law degree distribution.

The proposal that all levels of organisation follow the same structural pattern is supported by evidence of self-similarity in biological networks (Song *et al*, 2005). By identifying this common pattern as a power-law distribution, each level is endowed with structural and functional robustness. The combination of modularity and distributed function also appears to be a novel feature of the model. Each cluster integrates a particular set of inputs (either external or internally processed signals) and influences a particular set of functional processes (e.g. other modules, effector pathways). Stated another way, each module reflects the correlation between a particular set of functions in response to a specific range of stimuli. This implies that different sets of signals (e.g. different patterns of action potentials) are processed by different sets of modules, and that the relative importance of each module varies according to the information being processed.

Predictions arising from the model have been confirmed, most significantly in the correlation between protein connectivity and quantitative perturbation of LTP. The fact that this correlation emerges with current interaction data suggests that the network used in our analysis and the organisation apparent within it accurately reflects the general structure of the complete network.

### General observations

Although we have referred to the complex as if it were identical at all synapses, this is known not to be the case in all parts of the central nervous system (Porter *et al*, 2005). Ongoing systematic studies of MASC proteins using microarray data and protein localisation show a high degree of coexpression for most MASC proteins in forebrain structures, including hippocampus, cortex, striatum and amygdala (Zapala *et al*, 2005). Given the number of different proteins involved and the complexity of their interactions, it seems most likely that any given synapse will contain a distribution of complexes of varying composition. This implies that the coordination of signalling responses takes place both within individual complexes and as a function of the distribution as a whole. Dynamic interactions could be factored into future analysis both at the level of protein turnover and phosphorylation. We also recognise the incompleteness of some of our data sets that ideally would be obtained in systematic unbiased studies and such programs are underway (e.g. [www.genes2cognition.org](http://www.genes2cognition.org); [www.gensat.org](http://www.gensat.org); [www.brainatlas.org](http://www.brainatlas.org)). Not only will the availability of this data refine our 'draft' maps of synapse proteome organisation, but our maps can also be used to prioritise areas for data acquisition and development of



analytical techniques relevant to the nervous system. Future directions will not only include refinements based on more systematic data availability, but also act as a starting point for systems biology approaches to the synapse. This presents an attractive approach within the overall complexity of the brain proteome and transcriptome, as it has defined functional roles amenable to genetic and pharmacological manipulation. This model of MASC can now be extended to the synapse proteome as a whole and encompass neurological and psychiatric disease genes. This model also presents an exciting new avenue for the integration of the molecular networks presented here with synapse models of neural networks.

## Materials and methods

### Functional annotation

Throughout this study, we have stressed the use of high-quality, manually curated data sets. While bioinformatic tools are invaluable for extensive literature searches, subsequent manual curation is indispensable. The inadequacy of fully automated annotation methods is perhaps most acute when searching for complex disease associations. These human data include evidence of mendelian inheritance of polymorphisms and changes in protein or mRNA levels in brain tissue. It is generally unknown if any of these molecular changes alone produce mental illness. To compound this level of uncertainty with artefacts inevitably thrown up by automated methods is to risk losing all information to noise. The use of GO annotation has also been avoided, as its coverage of experimental data is generally incomplete. Given the partial nature of this data itself, comprehensive (automated and manual) literature searching and expert curation was felt to be the only means of obtaining a data set of minimal inherent bias.

Interpro annotations for all proteins were taken from SwissProt (Supplementary Table 2). To compare the frequency of domain occurrence within mouse, SwissProt identifiers for the NCBI33 mouse gene data set were obtained from Ensembl. Out of 24461 entries, identifiers were available for 7338 genes. Interpro annotations available through Ensembl were not used, as these were found to contain a large number of spurious entries (e.g. tyrosine kinases and nuclear localisation signals: IPR001245 and IPR001472). The annotation provided by SwissProt was found to contain significantly fewer such entries.

Ensembl was used to identify orthologues in the BDGP3.2.1 *Drosophila* and SGD1 yeast data sets (Supplementary Table 4). Human, mouse and rat Ensembl Gene Ids (Supplementary Table 1) were used for the search, and their results combined—a protein was deemed to possess an orthologue if at least one of its gene ids returned an orthologue.

In presenting the number and percentage of MASC proteins with a particular phenotypic annotation, a protein was counted as having that annotation if identified directly in the literature, or if a corresponding generic protein entity was referred to (e.g. a reference to 'PKA' would be taken as implicating PRKACB and PKA-R2b).

### Generic protein entities

The specificity with which interactions and phenotypes are reported varies considerably, and it is not uncommon to find references to classes of molecules (e.g. 'G- $\alpha$ s'). In order to make use of such data, a number of generic proteins were defined (Supplementary Table 5). This was strictly limited to cases where isoforms were judged to be functionally identical, or where the level of resolution was most appropriate to the analysis. These were as follows: G- $\alpha$  proteins treated as four classes (s/i/q/12); G  $\beta/\gamma$  treated as a single entity; 14-3-3 isoforms treated as a single entity; PKA subunits fused into a single entity and PP2a isoforms fused into a single entity. Prior to this, the MASC set was supplemented with a minimal number of additional proteins: the catalytic subunit of PKA (the regulatory subunit having been found in MASC) and G- $\alpha$  i/q/12. While only G- $\alpha$ s was identified

by proteomic studies, all classes are known to interact with MASC proteins, and all have been identified in the PSD. For a complex involved in signal transduction via ionotropic and metabotropic receptors, their inclusion seems natural. The manipulations described above, resulting in a final set of 182 proteins, were carried out prior to the statistical and network analyses described in the text.

### Functional correlation

The significance of the overlap between a pair of annotations was evaluated by calculating its probability of occurrence under a random distribution. Suppose that within a set of  $N$  proteins,  $n_a$  and  $n_b$  possess annotations  $a$  and  $b$ , respectively. If both annotations are distributed randomly throughout the set, the probability of  $n_{ab}$  proteins possessing both annotations is given by the function:

$$h(n_{ab}, n_a, N, n_b) = \frac{n_a!(N - n_a)!n_b!(N - n_b)!}{[N!(n_a - n_{ab})!n_b!(N - n_a - n_b + n_{ab})!(n_b - n_{ab})!]}$$

Given the actual number of proteins possessing both annotations,  $\mu_{ab}$ , we estimate its significance by calculating the probability  $P(\mu_{ab})$  of an overlap as or less likely under the random distribution:

$$P(\mu_{ab}) = \sum h(n_{ab}, n_a, N, n_b) : h(\mu_{ab}, n_a, N, n_b)$$

These values were used without any further adjustment to account for the number of comparisons made. This was done for several reasons. Annotations are not independent, with many correlated to a significant degree (see, e.g. the Interpro annotations of Table I). It was also felt that, due to the incomplete and potentially uneven nature of much of the data, it was better policy to retain sensitivity. As a consequence, we have tried to avoid placing undue stress on isolated scores unsupported by other evidence.

### Network analysis

Protein-protein binding data were mined from studies describing protein interactions in any relevant mammalian source (cell or specific organ) and has been described elsewhere (Husi and Grant, 2002). Protein sequence alignment was used to identify splice variants and orthologues across the mouse, rat and human genomes and synonyms were collected for each protein entity. The synonym list was used to search PubMed for scientific reports that may describe protein interactions. Interactions described in BIND, GRID and the commercial database NetPro (<https://www.molecularconnections.com/home.html>) were also identified. All interaction data were manually curated: evidence for binary interactions between protein pairs was expertly annotated and relevant PMID numbers stored with interactions (Supplementary tables). No high-throughput yeast 2 hybrid data was included unless confirmed by other techniques. A second curator re-checked all interactions used in our analysis.

Power-law analysis was performed as a linear regression fit of  $\ln p(k)$  to  $\ln k$ , where  $k$  is the number of interactions and  $p(k)$  the probability that a protein has  $k$  interactions.

Clustering was performed with the algorithm of Newman and Girvan (2004), using edge (rather than the shortest path) betweenness. The modularity score  $Q$  that they define was used to identify the best clustering of the network. Interaction data incorporated while this manuscript was in preparation was found to alter the clustering identified by the algorithm. With a modularity score of  $Q=0.56$  (calculated with updated interaction data), the original clustering of the network appeared to better reflect its structure than the altered clustering ( $Q=0.53$ ). To look at the variance in these scores, we calculated  $Q$  for all neighbouring clusterings that differ by moving a single protein into another cluster in which it has an interaction partner. For the neighbourhood containing the original clustering  $Q=0.5502 \pm 0.0074$  (mean  $\pm$  s.d.), while for the altered clustering  $Q=0.5233 \pm 0.0073$ . The original clustering seems to be a markedly better reflection of network structure, and is the version presented here. Note that the majority of the significant overlaps between

clusters and annotations discussed in the text were found to be valid for analogous clusters in the alternative network clustering.

The % change in 100 Hz LTP (as a percentage of baseline EPSP) was calculated as:  $100 \times (\text{mutant} - \text{wild type}) / (\text{wild type} - 100)$ , where wild type and mutant are the mean changes in amplitudes (% baseline) of excitatory postsynaptic potentials (evoked by test stimulus) caused by a 100 Hz stimulation protocol (see Supplementary Table 11). Where multiple sets of experimental data were available for a single protein, the absolute value of the mean change was used.

## Supplementary information

Supplementary information is available at the *Molecular Systems Biology* website ([www.nature.com/msb](http://www.nature.com/msb)).

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Glossary: annotations referenced in text

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*synaptic plasticity*—proteins identified as essential to normal synaptic plasticity by either pharmacological or mutation studies (Supplementary Tables 3 and 6)  
*drug*—proteins identified by pharmacological studies as essential to normal synaptic plasticity (Supplementary Table 3)  
*mutation*—proteins identified by mutation studies as essential to normal synaptic plasticity (Supplementary Table 3)  
*behavioural plasticity*—proteins whose mutation produces behavioural a learning phenotype in rodents (spatial learning or cue/contextual conditioning) phenotypes in rodents (Supplementary Table 3 and 6)  
*spatial learning*—proteins whose mutation affects spatial learning in rodents (Supplementary Table 3)  
*cue/contextual conditioning*—proteins whose mutation affects cue/contextual conditioning in rodents (Supplementary Table 3)  
*behavioural (other)*—proteins implicated in rodent behaviour by other studies (Supplementary Table 3)  
*cognitive*—proteins implicated in human psychiatric disorders with a major cognitive component (schizophrenia or mental retardation) (Supplementary Tables 3 and 6)  
*affective*—proteins implicated in human psychiatric disorders with a major affective component (bipolar or depressive) (Supplementary Tables 3 and 6)  
*schizophrenia*—proteins implicated in schizophrenia (Supplementary Table 3)  
*mental retardation*—proteins implicated in mental retardation (Supplementary Table 3)  
*bipolar*—proteins implicated in bipolar disorder (Supplementary Table 3)  
*depressive*—proteins implicated in depressive illness (Supplementary Table 3)  
*fly*—proteins with identified orthologues in *D. melanogaster* (Supplementary Table 4)  
*yeast*—proteins with identified orthologues in *S. cerevisiae* (Supplementary Table 4)  
*mammalian*—proteins with no identified orthologues in either *D. melanogaster* or *S. cerevisiae* (Supplementary Tables 4 and 6)  
*glutamate receptors*—proteins assigned to the 'Glutamate Receptor' functional sub-family (Supplementary Table 1)  
*cell adhesion and cytoskeletal*—proteins assigned to the 'Cell Adhesion and Cytoskeletal' functional family (Supplementary Table 1)  
*other enzymes*—proteins assigned to the 'Other Enzymes' functional sub-family (Supplementary Table 1)  
*phosphatases*—proteins assigned to the 'Protein Phosphatases' functional family (Supplementary Table 1)  
*ser/thr kinases*—proteins assigned to the 'Ser/Thr Kinases' functional sub-family (Supplementary Table 1)  
*G-proteins*—proteins assigned to the 'G-proteins' functional sub-family (Supplementary Table 1)  
*G- $\alpha$  proteins*—proteins with Interpro annotation IPR001019: Guanine nucleotide binding protein (G-protein), alpha subunit (Supplementary Table 2)  
*ionotropic glutamate receptor*—proteins with Interpro annotation IPR001320: Ionotropic glutamate receptor (Supplementary Table 2)  
*metabotropic glutamate receptor*—proteins with Interpro annotation IPR000162: Metabotropic glutamate receptor (Supplementary Table 2)  
*C2*—proteins with Interpro annotation IPR000008: C2 (Supplementary Table 2)  
*L27*—proteins with Interpro annotation IPR004172: L27 (Supplementary Table 2)  
*Ser/Thr-specific phosphatases*—proteins with Interpro annotation IPR006186: Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphate (Supplementary Table 2)  
*tyrosine kinases*—proteins with Interpro annotation IPR001245: Tyrosine protein kinase (Supplementary Table 2)  
*SH2 motif*—proteins with Interpro annotation IPR000980: SH2 motif (Supplementary Table 2)  
*PKC, phorbol ester/DAG binding*—proteins with Interpro annotation IPR002219: Protein kinase C, phorbol ester/diacylglycerol binding (Supplementary Table 2)  
*Erk1/2 MAP kinase*—proteins with Interpro annotation IPR008349: ERK1/2 MAP kinase (Supplementary Table 2)  
*tyrosine & dual specificity phosphatase*—proteins with Interpro annotation IPR000387: Tyrosine specific protein phosphatase and dual specificity protein phosphatase (Supplementary Table 2)

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