

RNA binding	DNA binding		DNA replication origin binding	single-stranded DNA binding
	translation initiation factor activity	poly(U) RNA binding	snRNA binding	four-way junction DNA binding
	E-box binding	mRNA 3'-UTR binding	cAMP response element binding	translation elongation factor activity
	mRNA binding	sequence-specific mRNA binding	mRNA 5'-UTR binding	U1 snRNA binding

ubiquitin conjugating enzyme activity	nucleoside diphosphate kinase activity	cyclin-dependent protein serine/threonine kinase activity	tau-protein kinase activity	threonine-type endopeptidase activity	flap endonuclease activity
NADH dehydrogenase (ubiquinone) activity	histone methyltransferase activity (H3-K4 specific)	ATP hydrolysis activity	NADH dehydrogenase activity	DNA-directed 5'-3' RNA polymerase activity	
peptidyl-prolyl cis-trans isomerase activity	ubiquitin-ubiquitin ligase activity	polyoma-specific nucleuclease activity	histone methyltransferase activity	protein serine/threonine kinase activity	
	GTPase activity	5'-flap endonuclease activity	protein-disulfide reductase activity	histone demethylase activity	phospholipase D activity
			endopeptidase activity	protein serine/threonine phosphatase activity	RNA polymerase II CTD heptapeptide repeat phosphatase activity

A treemap visualization showing the distribution of protein binding categories. The central and largest category is 'unfolded protein binding', which is highlighted in a darker blue. Other categories include 'chaperone binding', 'ubiquitin binding', 'protein heterodimerization activity', 'calmodulin binding', 'cadherin binding', 'syntaxin binding', and 'hold a protein binding'. The size of each rectangle corresponds to the relative frequency or importance of that category.

Category	Relative Frequency (Estimated)
unfolded protein binding	35%
chaperone binding	15%
ubiquitin binding	15%
protein heterodimerization activity	15%
calmodulin binding	10%
cadherin binding	10%
syntaxin binding	10%
hold a protein binding	10%

A treemap visualization showing the hierarchical structure of microtubule binding. The central and largest area is labeled "microtubule binding" in white text on a dark blue background. This area is divided into several sub-categories, each represented by a different shade of blue and containing text in white or dark blue. The sub-categories include: "actin filament binding" (top right), "microtubule binding" (top left), "tubulin binding" (middle right), "alpha-tubulin binding" (bottom right), "actin binding" (bottom left), "microtubule minus-end binding" (bottom center), and "actin monomer binding" (bottom right).

Category	Sub-category
microtubule binding	actin filament binding
microtubule binding	microtubule binding
microtubule binding	tubulin binding
microtubule binding	alpha-tubulin binding
microtubule binding	actin binding
microtubule binding	microtubule minus-end binding
microtubule binding	actin monomer binding

A word cloud visualization of the text "GTPase activator activity". The words are arranged in a grid-like pattern, with the central text "GTPase activator activity" being the largest and most prominent. Other words include "protein", "phosphatase", "guanyl-nucleotide", "exchange factor", "activity", "serine/threonine", "kinase", "regulator", "inhibitor", and "activator". The words are in various shades of green and blue, and are of different sizes, creating a dynamic and visually appealing composition.

histone binding		K63–linked polyubiquitin modification-dependent binding
lysine–acetylated histone binding	methylated histone binding	
protein kinase binding	ubiquitin protein ligase binding	
protein kinase binding		ubiquitin–specific protease binding
nuclear		

nuclear androgen receptor binding	transcription factor binding	
<b>nuclear androgen receptor binding</b>		
aryl hydrocarbon receptor binding	TBP-class protein binding	nuclear receptor binding

phosphatidylinositol-4,5-bisphosphate binding	phosphatidylinositol-3,4,5-trisphosphate binding
phosphatidylinositol-4,5-bisphosphate binding	
phosphatidylinositol-3-phosphate binding	phosphatidylinositol binding
protein-containing	ribosome

protein-containing complex binding	ribosome binding
<b>protein-containing complex binding</b>	
MutLalpha complex binding	ribonucleoprotein complex binding
G-protein beta/gamma-subunit complex binding	

cytoskeletal motor activity	plus-end-directed microtubule motor activity
microtubule motor activity	microfilament motor activity

**cytoskeletal motor activity**

manganese ion binding	magnesium ion binding
<b>manganese ion binding</b>	Al <sup>3+</sup> binding
metal ion binding	

chromatin binding

**chromatin**

**binding**

nucleosome binding

cytochrome-c	proton-transporting	he
oxidase	ATP synthase	prote
activity	activity,	hea
cytochrome-c	rotational	prote
oxidase activity	mechanism	
phospholipid	ATP	Hsp
scramblase	transmembrane	b
activity	transporter	
	activity	

Diagram illustrating the Clathrin adaptor complex (AP-2). The complex is composed of several subunits: **clathrin adaptor activity** (orange box), **clathrin light chain binding** (yellow box), **protein folding chaperone** (blue box), and **clathrin** (green box). The clathrin adaptor activity subunit is shown interacting with the clathrin light chain binding subunit and the protein folding chaperone subunit. The clathrin subunit is shown interacting with the clathrin adaptor activity subunit.

structural constituent of ribosome

structural molecule activity	molecular adaptor activity
MHC class I protein binding	

protein binding	translation
<b>protein binding</b>	<b>initiation</b>
ribosome binding	<b>factor binding</b>

transcription coactivator activity	transcription coregulator activity
transcription coactivator activity	
transcription corepressor activity	DNA-binding transcription factor activity

<p>at shock</p> <p>tein binding</p> <p>at shock</p> <p>in binding</p>	<p><b>disordered</b></p> <p><b>domain</b></p> <p><b>specific</b></p> <p><b>binding</b></p> <p>RS domain</p> <p>binding</p>
<p>70 protein</p> <p>binding</p>	

4 iron, 4 sulfur cluster binding	misfolded protein binding
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e	cyclin binding	cyclosporin A binding
g		

dystroglycan binding	dynein intermediate chain binding
	Rho GDP-dissociation inhibitor

g	dynein light intermediate chain binding	ubiquitin binding
		proteasome-activating activity