BIOCARTA AKAPCENTROSOME PATHWAY—14	₁											T					•					T		Τ		Τ		
KEGG GAP JUNCTION—89	\vdash	+	+		\Box	\top	+		\forall	\Box	\top	+	\Box	\top	+	T		††	\top	++		\top	\top	•	9	•		\top
KEGG HEDGEHOG SIGNALING PATHWAY—56	5																											
KEGG PATHOGENIC ESCHERICHIA COLI INFECTION—55		\perp	\perp				\perp																	<u>•</u>	2.5	•		
NABA CORE MATRISOME—272	\vdash	•	•			\perp	\perp	\bot	•		\perp	_		\dashv	\perp	\sqcup		\sqcup		++	\perp		•	1		\bot	•	
NABA ECM GLYCOPROTEINS—193	\vdash					_	+	+	•	\vdash	+	_	\vdash	_	\perp	\vdash	-	\vdash	+	++	+	\perp	-	_		+		
NABA MATRISOME—1015 PID LKB1 PATHWAY—47	\vdash	╀	-		\vdash		+	+	╇	\vdash	+	+	\vdash	+	-	$\vdash \vdash$		$\vdash \vdash$	+	++		+	┩	+		+	+++	
REACTOME ACTIVATION OF AMPK DOWNSTREAM OF NMDARS—28	\vdash	+	+		\vdash	+	+	+	\vdash	\vdash	+	+	\vdash	+	+	+		++	+	++		-	+	-	•		,+-+-	+
REACTOME ACTIVATION OF NMDA RECEPTORS AND POSTSYNAPTIC EVENTS—92	\vdash	+	+			\top	+	+	H	\Box	\top	+		\top	+	\Box				++	•		\top	•				\top
REACTOME ACTIVATION OF SMO—18	3	T	\top		\Box	•		\top	П	\Box	\top	\top	\Box	•	\top	П							\top				\top	\top
REACTOME ADAPTIVE IMMUNE SYSTEM—781											• •											•	•	•		•		
REACTOME ASPARAGINE N LINKED GLYCOSYLATION—302		\perp	\perp				\perp	\perp						\perp	\perp	Ш		Ш							<u>.</u>	•		
REACTOME ASSEMBLY AND CELL SURFACE PRESENTATION OF NMDA RECEPTORS—42	\vdash	\perp	╄			\perp	_	_	Ш		\perp	_		\dashv	\perp	\sqcup		\sqcup		$\perp \perp$	$\perp \perp$			2	<u>.</u>	•	$\bot\bot$	\perp
REACTOME AXON GUIDANCE—548	\vdash	+	+		\square	\perp	•	•	\sqcup		+	_	$\vdash \vdash$	+	+	\sqcup		$\vdash \vdash$		++	++	4		•			++	+
REACTOME CARBOXYTERMINAL POST TRANSLATIONAL MODIFICATIONS OF TUBULIN—42 REACTOME CELLULAR RESPONSES TO EXTERNAL STIMULI—525	\vdash	+	+			_	+	+	+		_	_		+	+	\vdash		++		++				-			++	+
REACTOME CELLULAR RESPONSES TO EXTERNAL STIMULI—525 REACTOME CILIUM ASSEMBLY—199	\vdash	+	+		\vdash	+	+	+	\vdash	\vdash	+	+	\vdash	+	+	$\vdash \vdash$	+	$\vdash \vdash$	+	++		+	+	-			,+-+-	+
REACTOME CLASS B 2 SECRETIN FAMILY RECEPTORS—94	\vdash	+	+	0	\vdash			+	+	$\vdash \vdash$	+	+	+	+	+	+	+	++	+	++	++	+	+				++	
REACTOME COOPERATION OF PREFOLDIN AND TRIC CCT IN ACTIN AND TUBULIN FOLDING—33	\vdash	\dagger	\top					\top	$\dagger \dagger$	$ \uparrow $	\top	\top	\sqcap	\top	\top			$\dagger \dagger$		++	$\dagger \dagger$	\top	\top		9.5		11	
REACTOME COPI DEPENDENT GOLGI TO ER RETROGRADE TRAFFIC—99																										•		
REACTOME COPI INDEPENDENT GOLGI TO ER RETROGRADE TRAFFIC—52																									9	•		
REACTOME COPI MEDIATED ANTEROGRADE TRANSPORT—101		\prod					\perp		\Box					\int		\coprod		\prod						<u>•</u>	<u>.</u>	•	\prod	
REACTOME CRMPS IN SEMA3A SIGNALING—16	\vdash	_	_			\perp	•	•	\sqcup		\perp	_		\perp		\sqcup		\coprod			$\perp \perp$	\perp	\perp	1_		1	++	\perp
REACTOME DEVELOPMENTAL BIOLOGY—1095	\vdash	+	+		\square	_	-	•	+		+	+	\vdash	+	•	H		\vdash	•		+			•			++	+
REACTOME ER TO GOLGI ANTEROGRADE TRANSPORT—154 REACTOME FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION—167	\vdash	+	+		\square	+	+	+	+		+	+	+	+	+	++		++			<u>'</u>	+	+					+-
REACTOME FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION—167 REACTOME FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT TRIC—26	\vdash	+	+		\vdash	+	+	+	++	\vdash	+	+	+	\perp	+	++		++		++	+	+	+				,+-+	+
REACTOME GAP JUNCTION ASSEMBLY—37	\vdash	+	+	\vdash		+	+	+	+		+	+		\dashv	+	\forall		\vdash	+	++	+		+	•			++	+
REACTOME GAP JUNCTION TRAFFICKING AND REGULATION—50	\vdash	+	+				+	+	H					\top	+	\Box		H		++				•	9		+	+
REACTOME GOLGI TO ER RETROGRADE TRANSPORT—133		T	\top		\Box	\top	\top	\top	П	\Box	\top	\top	\Box	寸	\top	П		\Box			\top		\top	•		•		\top
REACTOME GPCR LIGAND BINDING—453				0																								0
REACTOME HEDGEHOG OFF STATE—111	L	\perp					\perp															•	•		2 9	•		
REACTOME HEDGEHOG ON STATE—84	\vdash	\perp	\bot					\bot	Ш	\sqcup	\perp	_	\sqcup	•	\perp	\sqcup		\sqcup	\perp	$\perp \perp$	\sqcup	4					++	\perp
REACTOME HSP90 CHAPERONE CYCLE FOR STEROID HORMONE RECEPTORS SHR—53	\vdash	+	+			\perp	+	+	\vdash	\vdash	+	_	\vdash	+	+	$\vdash \vdash$	_	\vdash	\perp	++	++	_	\perp	-		210	++	+
REACTOME INTRAFLAGELLAR TRANSPORT—54 REACTOME INTRA GOLGI AND RETROGRADE GOLGI TO ER TRAFFIC—202	\vdash	+	+		\vdash	+	+	+	\vdash	\vdash	+	+	\vdash	+	+	$\vdash \vdash$	+	$\vdash \vdash$		++	++	+	+	-				+
REACTOME INTICA GOLGI AND RETROGRADE GOLGI TO ER TRAFFIC—202 REACTOME KINESINS—60	\vdash	+	+		\vdash	+	+	+	++	\vdash	+	+	\vdash	+	+	\vdash	+	\vdash			++	-	+	—			,+-+-	+
REACTOME L1CAM INTERACTIONS—118	\vdash	+	+			\top	•		†	\vdash	+	+	\vdash	\top	+	\Box	+	\vdash		++	+		+				++	+
REACTOME MHC CLASS II ANTIGEN PRESENTATION—110		\top	T				\top	\top	T					\top		\Box		T		\top				•		•		\top
REACTOME MITOTIC G2 G2 M PHASES—195																						•	•	<u>•</u>	9	•		
REACTOME MITOTIC METAPHASE AND ANAPHASE—199		\perp						\perp	Ш					\perp		Ш		Ш				•			9	•		\perp
REACTOME MITOTIC PROMETAPHASE—196	5 <u> </u>	\perp	_			\perp	\perp	\bot	Ш		\perp		Ш	\perp	\perp	Ш	\perp	\sqcup		\sqcup	\perp		\perp	2	2.5	•	$\bot \bot$	\perp
REACTOME NEURONAL SYSTEM—409	\vdash	\bot	_				+	+	\sqcup					+	_	\sqcup		\Box		++	2			2		•	++	+
REACTOME NEUROTRANSMITTER RECEPTORS AND POSTSYNAPTIC SIGNAL TRANSMISSION—204	\vdash	+	+			+	+	+	\vdash		+	_	\vdash	+	+	\vdash				+-	-	\perp	+	-			++	+
REACTOME ORGANELLE BIOGENESIS AND MAINTENANCE—291 REACTOME POST CHAPERONIN TUBULIN FOLDING PATHWAY—23	\vdash	+	+		\vdash	+	+	+	++	\vdash	+	+	\vdash	+	+	$\vdash \vdash$	+	$\vdash \vdash$	+	++	_	+	+	-				+
REACTOME POST TRANSLATIONAL PROTEIN MODIFICATION—1417	\vdash	+	+		\vdash	+	+	+	++		•			+	+		+	\vdash	•		+			•			,+	+
REACTOME PREFOLDIN MEDIATED TRANSFER OF SUBSTRATE TO CCT TRIC—28	\vdash	+	+		\vdash	+	+	+	+	$\vdash \vdash$	+	+		+	+	 		+			+	+	+				++	+
REACTOME PROTEIN FOLDING—100																								•		•		
REACTOME RECRUITMENT OF NUMA TO MITOTIC CENTROSOMES—93																П									2	•	\Box	
REACTOME RECYCLING PATHWAY OF L1—48	\vdash						•																	<u>•</u>	<u>.</u>	•	\prod	
REACTOME RESOLUTION OF SISTER CHROMATID COHESION—125	\vdash	_	_			\perp	_	_	\coprod		\perp	-		\perp	\perp	\sqcup		\sqcup		+	+	\perp	\perp	2	2.5	•	++	
REACTOME RHO GTPASES ACTIVATE FORMINS—139	\vdash	+	+			+	+	+	+		+	-	\vdash	+	+	+		++	_	++	+	\perp	+	-			++	+
REACTOME RHO GTPASES ACTIVATE IQGAPS—31 REACTOME RHO GTPASE EFFECTORS—320	\vdash	+	+			+	+	+	+	\vdash	+		+	+	+	++		++	_	++	++	+	+				,+-+	+
REACTOME KIIO GITASE EFFECTORS—320 REACTOME SIGNALING BY HEDGEHOG—148	\vdash	+	+	\vdash			+	+	+	\vdash	+			•	+	++		++		++	+			•			++	+
REACTOME SIGNALING BY RHO GTPASES—449	\vdash	+	+		•				$\dagger \dagger$	\vdash	+		$\dagger \dagger$	\top	+	${\dagger}$		${\dagger}$	\top	++	$\dagger \dagger$	+	\top	•			++	+
REACTOME SIGNALING BY WNT—322					•	•									•													•
REACTOME THE ROLE OF GTSE1 IN G2 M PROGRESSION AFTER G2 CHECKPOINT—75																						•			9	•	$\perp \perp$	
REACTOME TRANSLOCATION OF SLC2A4 GLUT4 TO THE PLASMA MEMBRANE—71	\vdash	1																			<u>•</u>			•	<u>•</u>	•	\prod	
REACTOME TRANSMISSION ACROSS CHEMICAL SYNAPSES—269	\vdash	+	+			\perp	+	_	+	\square	+	_	\sqcup	_	+	\sqcup	<u> </u>	+		+-	2	\perp	+				+	
REACTOME TRANSPORT OF CONNEXONS TO THE PLASMA MEMBRANE—20	\vdash	+	+		$\vdash \vdash$	+	+	+	+	\vdash	+	+	\vdash	+	+	++		++			+	+	+	-			++	+
REACTOME TRANSPORT TO THE GOLGI AND SUBSEQUENT MODIFICATION—185 REACTOME VESICLE MEDIATED TRANSPORT—722	\vdash	+	+		H	+	+	+	+	\vdash	+	+	+	+	+	++		++				+	+				++	+
WNT SIGNALING—89	\vdash	+	+	\vdash	•	+	+	+	+	\vdash	+	+	+	+	+	+		++				+	+	1			++,	
	ಒ	A1	\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	\mathbb{R}_1	\prod	ACT1	, Tr	,T2	- <u></u>	[A3])311	1L3	[112]	458	LH5	1990 1990	AP2 PT	11R	EIS1 NSF	FUT2 PREB		P1	3S1	1A	(1B)	UBB3	VIT	
	AGBL	COL15A	COL18A	CRHR	DAAMI	DACT	DPYSL.	DPYSL	EMILIN	EPHA	FBXO11 FBXO31	FMNL3	ALNT12	GAS	ITIH5 KMT2D	LYPD6E	MAP2 MAPT	MC1R	MEIS1 NSI	POFUT!	PRKAG	RASGRP1	THBS	TUBA1A	TUBA1B	TUB	TIV	WISF1 WNT3
		Ŏ	Ŏ		-		П	. H	闰		, #4	•	d			Ι				Н	Д	\mathbf{R}_{ℓ}		L	I	4		