

SUPPLEMENTAL TABLE 1. Genes Involved in Chemotactic Signaling in <i>Dictyostelium</i>								
Dd protein	Gene/Aliases	DDB # (hyperlinked to Dictybase)	Mammalian Homologs	Localization	Putative Role in Signaling	Growth or Developmental Phenotype ^a	Chemotaxis Phenotype ^a	Reference(s) ^b
ACA	<i>acaA, ACA</i>	DDB_G0281545	Adenylyl cyclases	Plasma membrane	Essential for cAMP production	No aggregation Expresses early genes	No defect	(69)
AleA (see RasGEFs)								
Arp2/3: Arp2 Arp3	<i>arpB</i> <i>arpC, aclA</i>	DDB_G0272106 DDB_G0283755	Arp2/3	Cortex and cytosol	Branching and nucleation of actin filaments in lamellipodia	ND ^c - possibly lethal	ND ^c	(33)
Actins	<i>act1, etc^d</i>	~30 genes ^d	Actin	Cortex and cytosol	Pseudopodial force generation	ND ^c - possibly lethal	ND ^c	(22)
cAMP Receptors: cAR1 cAR2 cAR3 cAR4	<i>carA-1, carA, carA1</i> <i>carA-2, carA, carA2</i> <i>carC, cAR3</i> <i>carD, cAR4</i>	DDB_G0273397 DDB_G0288179 DDB_G0277829 DDB_G0277831	G-protein-coupled receptors	Plasma membrane	Receptors for cAMP	<i>car1⁻/car3⁻</i> : No aggregation or early gene expression	<i>car1⁻/car3⁻</i> : No chemotaxis to cAMP	(38; 40; 52; 77)
Crac (see PH-domain Proteins)								
DockD (see RacGEFs)								
Dynein Heavy Chain	<i>dhcA</i>	DDB_G0276355	Dynein	Cytosol	Microtubule motor	Motor domain OE causes cytokinesis defect	Motor domain OE causes loss of polarity	(41)
ElmoA	<i>elmoA</i>	DDB_G0278051	Elmo family proteins	Cytosol	Dock associated protein	Wild-type like	Partial defect	(35)
Erk Proteins: Erk1 Erk2	<i>erkA, erk1</i> <i>erkB, erk2, dagC</i>	DDB_G0286353 DDB_G0283903	MAP kinases	Cytosol and nucleus	Erk1: MAP kinase Erk2: Important for cAMP production	<i>erk1⁻</i> : Abberant multicellular morphology <i>erk2⁻</i> : No aggregation, expresses early genes	<i>erk1⁻</i> : Enhanced chemotaxis to folic acid <i>erk2⁻</i> : Partial defect	(25; 64; 78)
G-protein α Subunits: Ga1 Ga2 Ga4 Ga5 Ga9 7 others ^d	<i>gpa, Ga1, gpa1</i> <i>gpaB, Ga2, gpa2</i> <i>gpaD, Ga4, gpa4</i> <i>gpaE, Ga5, gpa5</i> <i>gpaI, Ga9, gpa9</i>	DDB_G0283349 DDB_G0276267 DDB_G0285425 DDB_G0286185 DDB_G0283419	G-protein α subunits	Gα1 and Gα2: Plasma membrane and cytosol Gα4, Gα5 and Gα9: Plasma membrane	Gα1: Inhibits PLC Gα2: Links to cAR1 Gα4 and Gα5: Link to putative nutrient receptors (NRs) Gα9: Negative regulator of development	<i>ga1⁻</i> : Wild-type like <i>ga2⁻</i> : No aggregation, no early gene expression <i>ga4⁻</i> : Small plaques <i>ga4⁻</i> or <i>ga5⁻</i> : Abberant multicellular morphology <i>ga9⁻</i> : Many small aggregation territories	<i>ga1⁻</i> : No defect <i>ga2⁻</i> : No chemotaxis to cAMP <i>ga4⁻</i> : No chemotaxis to folic acid <i>ga5⁻</i> : Enhanced chemotaxis to folic acid <i>ga9⁻</i> : Enhanced chemotaxis to cAMP	(6; 7; 30; 43; 70)
G-protein βγ Subunits: Gβ Gγ	<i>gpbA, Gbeta, Gb</i> <i>gpgA, Ggamma, gg</i>	DDB_G0277143 DDB_G0274125	G-protein βγ subunits	Plasma membrane and cytosol	Link to all Ga subunits	<i>gβ⁻</i> or <i>gγ⁻</i> : No aggregation or early gene expression, small plaques	<i>gβ⁻</i> or <i>gγ⁻</i> : No chemotaxis to cAMP or folic acid	(49; 93; 94)
GbpC	<i>gbpC, gefT</i>	DDB_G0291079	Roco family	Cytosol	Required for cGMP regulation of myosin	Small aggregation territories and fruiting bodies Expresses early genes	Partial defect	(27)
GbpD (see RasGEFs)								
Guanylyl Cyclases: GCA sGC	<i>gcA, GC</i> <i>sgcA, sGC</i>	DDB_G0275009 DDB_G0276269	GCA: Guanylyl cyclases sGC: Soluble adenylyl cyclases	GCA: Membrane sGC: Cytosol, translocates to membrane or cortex	Produce cGMP after exposure to chemoattractant	<i>gcA⁻/sgc⁻</i> : Aberrant aggregation	<i>gcA⁻/sgc⁻</i> : Partial defect	(75)
ICMA	<i>icmA</i>	DDB_G0272799	Isoprenylcysteine carboxyl methyltransferase	Cytosol	Methylates prenylated proteins	Loose aggregates	Partial defect	(11)
Inositol 5-phosphatases: PI5P1 PI5P2 PI5P3 PI5P4	<i>Dd5P1</i> <i>Dd5P2</i> <i>Dd5P3</i> <i>Dd5P4, RacGAP</i>	DDB_G0279927 DDB_G0284187 DDB_G0292392 DDB_G0267462	Inositol 5-phosphatases (SHIPs) 5P4: OCRL	ND ^c	Degrade PI(3,4,5)P3	<i>5p1/2⁻, 5p1/3⁻, or 5p2/3⁻</i> : Wild-type like <i>5p4⁻</i> : Aberrant multicellular morphology, defect in phagocytosis	<i>5p1/2⁻, 5p1/3⁻, 5p2/3⁻, or 5p4⁻</i> : No defect	(51)
IplA	<i>iplA</i>	DDB_G0292564	InsP3 receptors	Membrane	Calcium influx	Wild-type like	No defect	(85)
KRS1	<i>krsA</i>	DDB_G0284181	Mammalian Sterile 20-like kinase (MST)1/2	Cortex and cytosol	Ste20-like kinase	Small aggregates	Partial defect	(1; 62)
Lis1	<i>lis1</i>	DDB_G0288375	LIS1	Cytosol	Microtubule-associated protein	OE causes cytokinesis defect	OE causes loss of polarity	(71)
Lst8	<i>lst8</i>	DDB_G0292592	TorC1 and TorC2 subunit LST8	ND ^c	Important for activation of PKBs and adenylyl cyclase	No aggregation	Partial defect	(45)

Mek1	<i>mekA, DdMEK1, mek1</i>	DDB_G0269152	MAP kinase kinase (MEK)	Cytosol, translocates to membrane or cortex	Coordinates acquisition of polarity with cell-cell signaling	Small aggregation territories and fruiting bodies Expresses early genes	Partial defect	(54)
MLCK	<i>mlkA, MLCK, MLCK-A</i>	DDB_G0279925	Myosin light chain kinases (MLCKs)	Cytosol	Phosphorylates myosin II regulatory light chain	Cytokinesis defect	ND ^c	(29)
Myosin II	<i>mhcA</i>	DDB_G0286355	Myosin II heavy chains	Cortex and cytosol	Role in polarity and motility Suppresses lateral pseudopods	Mound arrest Cytokinesis defect	Partial defect	(20)
Myosin Heavy Chain Kinases: MHCK-A MHCK-B MHCK-C One other ^d	<i>mhkA, MHCK-A</i> <i>mhkB, MHCK-B</i> <i>mhkC, MHCK-C</i>	DDB_G0291231 DDB_G0289115 DDB_G0290687	Myosin II heavy chain kinases (MHCKs)	MHCK-A: Cortex and cytosol; translocates to cortex MHCK-B: Cytosol MHCK-C: Cortex and cytosol	Phosphorylate myosin II, resulting in disassembly of myosin thick filaments	OE of MHCK-A: Mound arrest and cytokinesis defect <i>mhkA⁻/B⁻/C⁻</i> : Cytokinesis defect	ND ^c	(14; 15; 63)
Myosin Light Chains: Myosin ELC (Essential LC) Myosin RLC (Regulatory LC)	<i>mlcE, EMLC</i> <i>mlcR, RMLC</i>	DDB_G0277859 DDB_G0276077	Myosin II light chains	Cortex and cytosol	Bind to myosin II heavy chain	<i>mlcE⁻ or mlcR⁻</i> : Cytokinesis defect, mound arrest	<i>mlcE⁻ or mlcR⁻</i> : Partial defect	(12; 83)
Na-H exchanger	<i>nhe1</i>	DDB_G0275711	Sodium/hydrogen exchangers (NHEs)	Plasma membrane	Intracellular pH homeostasis	Aberrant aggregation	Polarity defect	(68)
NF1 (see RasGAPs)								
Pak Proteins: PakA PakB PakC 6 others ^d	<i>pakA, dpak1</i> <i>mihck, Ddpak</i> <i>pakC</i>	DDB_G0269166 DDB_G0276459 DDB_G0267450	p21-activated serine/threonine protein kinases	PakA: Membrane or cortex PakB: Cortex and cytosol PakC: Cytosol, translocates to membrane or cortex	p21-activated kinases	<i>pakA⁻</i> : Delayed development, cytokinesis defect <i>pakB⁻</i> : Wild-type like; OE of active protein causes cytokinesis defect <i>pakC⁻</i> : ND ^c	<i>pakA⁻ or pakC⁻</i> : Partial defect <i>pakB⁻</i> : No defect	(13; 19; 47; 48)
PDI	<i>pdiA</i>	DDB_G0277863	None identified	Secreted	Phosphodiesterase inhibitor	No aggregation	ND ^c	(92)
PDKs: PDKA PDKB	<i>pdkA</i> <i>pdkB</i>	DDB_G0281471 DDB_G0284489	PI-dependent kinases (PDKs)	PDKA: Plasma membrane and cytosol PDKB: cytosol	Phosphorylate PKBs	<i>pdkA⁻/pdkB⁻</i> : Mound arrest	<i>pdkA⁻/pdkB⁻</i> : Partial defect	(28)
PdsA (see Phosphodiesterases)								
PH-domain Proteins: Crac PhdA PKBA ~130 others ^d	<i>dagA, CRAC, synag7</i> <i>phdA, DG1093</i> <i>pkbA, Akt, PKB, pkfC, DK1</i>	DDB_G0285161 DDB_G0285845 DDB_G0268620	Crac and PhdA: None identified PKBA: AKT/Protein kinase B (PKB)	Crac, PhdA, and PKBA: Cytosol, translocate to membrane	Crac: Essential for activation of adenyl cyclase PhdA: Unknown PKBA: Phosphorylates six known substrates	<i>crac⁻</i> : No aggregation, expresses early genes <i>phdA⁻</i> : Small territories <i>pkbA⁻</i> : Wild-type like	<i>crac⁻</i> : Partial defect <i>phdA⁻</i> : Partial defect <i>pkbA⁻</i> : No defect alone, suppresses defects in <i>pten⁻</i> cells	(24; 32; 50; 58)
Phg2	<i>phg2</i>	DDB_G0283699	None identified	Membrane or cortex and cytosol, translocates to cortex	Serine/threonine kinase	Aberrant aggregation	Partial defect	(26)
Phosphodiesterases: Pde1 (PdsA) Pde2 (RegA) Pde3 Pde4 Pde5 (PdeD) Pde6 (PdeE) Pde7	<i>pde1, pdsA, pdeA, DdPDE1</i> <i>pde2, regA, DG1030, DdPDE2</i> <i>pde3, DdPDE3</i> <i>pde4, DdPDE4</i> <i>pde5, pdeD, gbpA, DdPDE5</i> <i>pde6, pdeE, gbpB, DdPDE6</i> <i>pde7, DdPDE7</i>	DDB_G0285995 DDB_G0284331 DDB_G0268634 DDB_G0289121 DDB_G0274383 DDB_G0276027 DDB_G0289145	Phosphodiesterases (PDEs) Pde5: cGMP PDEs Pde6: cAMP PDEs	Pde1 and Pde7: Membrane and secreted Pde2, Pde3, Pde5, and Pde6: cytosol Pde4: Membrane (extracellular catalytic domain)	Pde1, Pde4, and Pde7: Degrade extracellular cAMP Pde2 and Pde6: Degrade intracellular cAMP Pde3: Degrades cGMP Pde5: Degrades cGMP, required for polarization	<i>pde1⁻ or pde2⁻</i> : No aggregation <i>pde4⁻</i> : Aberrant multicellular morphology <i>pde5⁻</i> : Large streams <i>pde6⁻</i> : Wild-type like	<i>pde1⁻, pde4⁻, or pde6⁻</i> : No defect <i>pde2⁻ or pde5⁻</i> : Partial defect	(2-4; 27; 44; 65; 79)
PI 3-kinases: PI3K1 PI3K2 PI3K3 PI3K4 PI3K5	<i>pikA</i> <i>pikB</i> <i>pikC</i> <i>pikF</i> <i>pikG</i>	DDB_G0278727 DDB_G0283081 DDB_G0275011 DDB_G0268548 DDB_G0282625	Class I PI 3-kinases (PI3Ks)	PI3K1 and PI3K2: Cytosol, each translocates to membrane or cortex	PI3K1 and PI3K2: Produce PI(3,4,5)P3, amplification of signal	<i>pi3k1-5⁻</i> : Poor aggregation, expresses early genes, small plaques	<i>pi3k1-5⁻</i> : Partial defect	(23; 24)
PI5K	<i>DDB_G0267588</i>	DDB_G0267588	PI4P 5-kinase (PIP5K)	Membrane or cortex	PKBA/PKBR1 substrate	ND ^c - possibly lethal	ND ^c	(39)
PiaA	<i>piaA, DG1117, amiA, pia</i>	DDB_G0277399	TorC2 subunit Rictor	Cytosol	Important for activation of PKBs and adenyl cyclase	No aggregation Expresses early genes	Partial defect	(10)

PKA-C	<i>pkaC, PKA, pkacat, DdPK3, DdPK2, PKA-C, PK2, PK3</i>	DDB_G0283907	Protein kinase A catalytic subunit	Cytosol	Serine/threonine kinase	No early gene expression	ND ^c	(56)
PKA-R	<i>pkaR, PKA, rdeC</i>	DDB_G0279413	Protein kinase A regulatory subunit	Cytosol	Regulates PKA-C	Rapid development	Partial defect	(18)
PKBA (see PH-domain Proteins)								
PKBR1	<i>pkbB, PK2, PKBR1, pkiA, DK2</i>	DDB_G0290157	Protein kinase B (PKB), but lacks PH domain and is myristoylated	Plasma membrane	Phosphorylates six known substrates	Arrests at mound stage	Partial defect	(57)
PLA2	<i>plaA</i>	DDB_G0278525	Calcium-independent phospholipase A2 (iPLA2)	Cytosol	PI3K-independent pathway for chemotaxis	Wild-type like	Partial defect in <i>pi3k1⁻/pi3k2⁻</i> cells	(9; 89)
PLC	<i>plc, pipA</i>	DDB_G0292736	Phospholipase C delta (PLCd)	Cytosol	Degrades PI(4,5)P2	Wild-type like	No defect	(21)
PTEN	<i>pten, ptenA</i>	DDB_G0286557	Phosphatase and tensin homolog on chromosome 10 (PTEN)	Membrane or cortex, translocates to cytosol	Degrades PI(3,4,5)P3	No aggregation Expresses early genes Small plaques Cytokinesis defect	Partial defect	(31)
Rac Proteins: Rac1a Rac1b Rac1c RacB RacC RacE RacG ~14 others ^d	<i>rac1A rac1B rac1C racB racC racE racG</i>	DDB_G0277869 DDB_G0268622 DDB_G0282365 DDB_G0279605 DDB_G0293526 DDB_G0280975 DDB_G0269178	Rho GTPases	Cortex and cytosol	Involved in lamellipodia and filopodia formation	Rac1a, Rac1b, and Rac1c: OE of active or DN proteins causes cytokinesis defect RacB: OE causes growth defect RacE ⁻ : Cytokinesis defect	<i>racB⁻, racC⁻ or racE⁻</i> : Partial defect RacG: OE of active or DN proteins causes partial defect	(8)
RacGAPs: GacQ XacA ~40 others ^d	<i>gacQ, RacGAP xacA, RacGEF, RacGAP, DRG</i>	DDB_G0282395 DDB_G0291978	Rac GTPase activating proteins (GAPs) XacA also has RacGEF activity	GacQ: Cytosol XacA: Membrane or cortex and cytosol	GacQ: PKBA/PKBR1 substrate XacA: Regulates Rac1b activity and actin dynamics	<i>gacQ⁻</i> : Wild-type like <i>xacA⁻</i> : Small aggregates	<i>gacQ⁻</i> : No defect <i>xacA⁻</i> : Partial defect	(39; 53)
RacGEFs: DockD GxcA GxcB GxcDD ~35 others ^d	<i>docd gxcA, RacGEF, RacGEF1 gxcB, TRIX, RacGEF gxcDD, RacGEF</i>	DDB_G0284725 DDB_G0277987 DDB_G0269424 DDB_G0279733	Rac guanine nucleotide exchange factors (GEFs) DockD: Dock180 family proteins	DockD: Cytosol, translocates to membrane or cortex GxcA: Cortex and cytosol, translocates to cortex GxcB: Cortex and endosomes GxcDD: Membrane, cortex, cytosol and phagosomes	DockD: Regulates Rac activity GxcA: Activator of RacB GxcB: Regulates actin dynamics and the endocytic pathway GxcDD: Regulates Rac activity	<i>dockD⁻</i> : Wild-type like <i>gxcA⁻</i> : Delayed development; OE causes partial mound arrest <i>gxcB⁻ or gxcDD⁻</i> : Delayed development	<i>dockD⁻</i> : Partial defect GxcA: OE causes partial defect GxcB: ND ^c <i>gxcDD⁻</i> : No defect	(60; 66; 67; 81)
Ras Proteins: Rap1 RasB RasC RasD RasG ~13 others ^d	<i>rapA, rap1 rasB rasC rasD, ras, Ddras, rasA rasG, ddRASG</i>	DDB_G0291237 DDB_G0292998 DDB_G0281385 DDB_G0292996 DDB_G0293434	Ras GTPases	Rap1: Intracellular and plasma membranes RasB, RasC, RasD, and RasG: Plasma membrane and cytosol	Rap1 and RasB: Regulate myosin II RasC: Activates TorC2 RasD: Expression level increases in <i>rasG⁻</i> RasG: Activates PI3K	Rap1 and RasB: ND ^c - possibly lethal <i>rasC⁻</i> : No aggregation, expresses early genes <i>rasD⁻</i> : Wild-type like <i>rasG⁻</i> : Cytokinesis defect	Rap1: Constitutively active form causes partial defect RasB: OE causes partial defect <i>rasC⁻</i> : Partial defect <i>rasD⁻</i> : No defect <i>rasG⁻</i> : Partial defect	(16; 17; 72-74)
RasGAPs: NF1 RapGAP1 RapGAP3 ~20 others ^d	<i>nfaA rapgap1 DDB_G0271806</i>	DDB_G0271750 DDB_G0271734 DDB_G0271806	GTPase activating proteins (GAPs)	NF1: Cytosol RapGAP1 and RapGAP3: Cytosol, translocate to membrane	NF1: Regulates RasG RapGAP1 and RapGAP3: Regulate Rap1	<i>nfi⁻ or rapgap3⁻</i> : Delayed development <i>rapgap1⁻</i> : Wild-type like	<i>nfi⁻, rapgap1⁻ or rapgap3⁻</i> : Partial defect	(36; 37; 95)
RasGEFs: AleA GbpD GefN GefQ GefR GefS ~23 others ^d	<i>gefA, aimless, aleA, RasGEFA gbpD, gefU, RapGEF gefN, RasGEFN gefQ, RasGEFQ gefR, RasGEFR gefS, RasGEFS</i>	DDB_G0284329 DDB_G0282373 DDB_G0275703 DDB_G0289665 DDB_G0274605 DDB_G0271868	Ras guanine nucleotide exchange factors (GEFs)	Cytosol	AleA: Activates RasC, important for activation of TorC2 GbpD: Activates Rap1 GefN and GefS: PKBA/PKBR1 substrates GefQ: Activates RasB GefR: Activates RasG	<i>aleA⁻</i> : No aggregation, expresses early genes <i>gbpD⁻, gefN⁻, gefR⁻, or gefS⁻</i> : Wild-type like <i>gefQ⁻</i> : Aberrant multicellular morphology	<i>aleA⁻</i> : Partial defect <i>gbpD⁻</i> : Enhanced chemotaxis to cAMP; OE causes loss of polarity <i>gefN⁻, gefR⁻, or gefS⁻</i> : No defect <i>gefQ⁻</i> : Partial defect; OE causes loss of polarity	(27; 34; 91)

RegA (see Phosphodiesterases)									
RGS Proteins: Rck1 ~6 others ^d	<i>rckA</i> , <i>rck1</i>	DDB_G0278737	Regulators of G-protein signaling (RGS)	Rck1: Cytosol, translocates to membrane or cortex	Negative regulators of development	<i>rck1</i> ⁻ : Rapid development, delayed fruiting bodies	<i>rck1</i> ⁻ : Partial defect	(82)	
Rip3	<i>ripA</i>	DDB_G0284611	TorC2 subunit Sin1	Cytosol	Important for activation of PKBs and adenylyl cyclase	No aggregation	Partial defect	(46)	
SCAR	<i>scrA</i>	DDB_G0285253	SCAR/WAVE	Cytosol, translocates to membrane or cortex	Activates Arp2/3	Aberrant multicellular morphology Expresses early genes	No defect	(5)	
Shk1	<i>shkA</i> , <i>SHK1</i>	DDB_G0283267	SH2-containing kinase (Shk1)	Cortex	Negative regulator of PIP3 signaling	No aggregation Expresses early genes	Partial defect	(61)	
SMEK	<i>smkA</i>	DDB_G0289067	Suppressors of MEKs (SMEKs)	Nuclei	Regulates protein phosphatases	Wild-type like	No defect Suppresses <i>mek1</i> ⁻	(59)	
SodC	<i>sodC</i>	DDB_G0282993	Superoxide dismutase	Plasma membrane	Removes superoxides	Aberrant aggregation	Partial defect	(86; 90)	
SVKA	<i>svkA</i>	DDB_G0286359	Mammalian Sterile 20-like kinase (MST)1/2	Cytosol and centrosome	Ste20-like kinase	Delayed development Aberrant multicellular morphology Cytokinesis defect	Partial defect	(76)	
Talins: TalA TalB	<i>talA</i> <i>talB</i>	DDB_G0290481 DDB_G0287505	Talin	Cortex	Adhesion TalB: PKBA/PKBR1 substrate	<i>talA</i> ⁻ / <i>talB</i> ⁻ : Loose mounds	<i>talA</i> ⁻ / <i>talB</i> ⁻ : Partial defect	(42; 87)	
Tor	<i>tor</i>	DDB_G0281569	TorC1 and TorC2 subunit	Cytosol	Important for activation of PKBs and adenylyl cyclase	ND ^c - possibly lethal	ND ^c		
TorA	<i>torA</i> , <i>Tortoise</i>	DDB_G0276353	None identified	Sphere in one end of mitochondria	Coordinates acquisition of polarity with cell-cell signaling	Small aggregation territories and fruiting bodies Expresses early genes	Partial defect	(88)	
TsuA	<i>tsuA</i> , <i>Tsunami</i>	DDB_G0267962	Fused kinases	Irregular patches on microtubules and cell periphery	Coordinates acquisition of polarity with cell-cell signaling	Small aggregation territories and fruiting bodies Expresses early genes	Partial defect	(84)	
WASP	<i>wasA</i>	DDB_G0293834	WASP	Cortex and cytosol	Activates Arp2/3	ND ^c - possibly lethal	Hypomorph: Partial defect	(55)	
YakA	<i>yakA</i> , <i>dagB</i>	DDB_G0283605	Dyrk-related kinases	Cytosol	Serine/threonine and tyrosine kinase	No aggregation No early gene expression Small plaques OE blocks growth	No chemotaxis to cAMP or folic acid	(80)	

^a Phenotypes refer to null mutants unless otherwise specified.

^b Reference listed generally refers to the original identification of that protein/gene. A comprehensive list of references for each protein/gene can be found by searching the indicated Dictybase ID (DDB #) online at Dictybase (<http://www.dictybase.org/>).

^c ND means that the indicated information has not been determined to the best of our knowledge.

^d There are multiple members of this gene family in *Dictyostelium*. Listed are some that have been most extensively studied with respect to chemotaxis and signaling. Information on other genes can be found on Dictybase (<http://www.dictybase.org/>).

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