Supplement 4. Probe sets for genes related to axonal transport genes in serotonin neurons.All probe sets changed 2-fold or greater with E or E+P treatment compared to placebo

Search	**Mean Signal Intensity**					
	Ovx	**E**	**E+P**	**Gene Identifier**	**Other ID**	**Gene Name**
Axon carg	206.5	1948	741	NM_004181	MmugDNA.7056.1.S1_at	gDNA.g4759283 FEA=U133PSR GEN=UCHL1 DEF=Orthologous to 201387_s_at ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
	46.25	242.75	164.6	BG473130	MmugDNA.1261.1.S1_at	gDNA.Hs.259873.0.S1 FEA=U133PSR GEN=KIF1A DEF=Orthologous to 203849_s_at kinesin family member 1A
	458.2	2443.75	883.6	NM_000430	MmugDNA.30079.1.S1_at	gDNA.g6031206 FEA=U133PSR GEN=PAFAH1B1 DEF=Orthologous to 200816_s_at platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
	624.6	2499.05	1408	AL566528	MmugDNA.136.1.S1_at	gDNA.Hs.211584.0.A3 FEA=U133PSR GEN=NEFL DEF=Orthologous to 221801_x_at neurofilament, light polypeptide 68kDa
	716.5	2571.9	1775	NM_005382	MmugDNA.33139.1.S1_at	gDNA.g4885512 FEA=U133PSR GEN=NEF3 DEF=Orthologous to 205113_at neurofilament 3 (150kDa medium)
	210.9	930.55	310.6	AI819734	MmugDNA.10001.1.S1_at	gDNA.Hs.301206.0.A1 FEA=U133PSR GEN=KIF3B DEF=Orthologous to 225205_at kinesin family member 3B
	967.5	3314.35	1915	BF939474	MmugDNA.13708.1.S1_at	gDNA.Hs.129908.0.A2 FEA=U133PSR GEN=KIF1B DEF=Orthologous to 209234_at kinesin family member 1B
	172.5	580.45	330.5	NM_003119	MmugDNA.2782.1.S1_at	gDNA.g4507172 FEA=U133PSR GEN=SPG7 DEF=Orthologous to 202104_s_at spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
	440.4	1182.1	505.9	AL135264	MmugDNA.39479.1.S1_at	gDNA.Hs.14434.0.A1 FEA=U133PSR GEN=KIF1B DEF=Orthologous to 225878_at Kinesin family member 1B
	4088	8395.2	5754	AL566528	MmugDNA.136.1.S1_s_at	gDNA.Hs.211584.0.A3 FEA=U133PSR GEN=NEFL DEF=Orthologous to 221801_x_at neurofilament, light polypeptide 68kDa
	300.9	759.5	285.3	AB011139	MmugDNA.1866.1.S1_at	gDNA.Hs.147946.0.S2 FEA=U133PSR GEN=OPA1 DEF=Orthologous to 212213_x_at optic atrophy 1 (autosomal dominant)
	422.7	1043.1	409.4	BE256969	MmugDNA.24123.1.S1_at	gDNA.Hs.77318.0.A2 FEA=U133PSR GEN=PAFAH1B1 DEF=Orthologous to 200813_s_at platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
	422.1	965.55	406.1	NM_005200	MmugDNA.24516.1.S1_s_at	gDNA.Hs.272480.0.S1 FEA=U133PSR GEN=SPG7 DEF=Orthologous to 214494_s_at spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
	674.8	313.2	767.1	NM_022822	MmugDNA.26537.1.S1_at	gDNA.g12383061 FEA=U133PSR GEN=KLC2 DEF=Orthologous to 218906_x_at likely ortholog of kinesin light chain 2
	193.7	248.5	35.75	NM_004798	MmugDNA.29117.1.S1_s_at	gDNA.g4758645 FEA=U133PSR GEN=KIF3B DEF=Orthologous to 203943_at kinesin family member 3B
	15596	4570.5	8352	BC004369	MmugDNA.36988.1.S1_x_at	gDNA.g13325111 FEA=U133PSR GEN=APP DEF=Orthologous to 211277_x_at amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
cytoskeletal-dependent intracellular transport						
	37	508.45	225.1	AI805050	MmugDNA.35068.1.S1_at	gDNA.Hs.89981.3.A1 FEA=U133PSR GEN=RAB6B DEF=Orthologous to 225259_at RAB6B, member RAS oncogene family
	206.5	1948	741	NM_004181	MmugDNA.7056.1.S1_at	gDNA.g4759283 FEA=U133PSR GEN=UCHL1 DEF=Orthologous to 201387_s_at ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
	999.3	7049.35	4582	BF223224	MmugDNA.8525.1.S1_at	gDNA.Hs.149436.0.A1 FEA=U133PSR GEN=KIF5B DEF=Orthologous to 201991_s_at kinesin family member 5B
	46.25	242.75	164.6	BG473130	MmugDNA.1261.1.S1_at	gDNA.Hs.259873.0.S1 FEA=U133PSR GEN=KIF1A DEF=Orthologous to 203849_s_at kinesin family member 1A
	59.2	342.95	155.8	NM_020153	MmugDNA.16369.1.S1_at	gDNA.g9910357 FEA=U133PSR GEN=FLJ21827 DEF=Orthologous to 218483_s_at hypothetical protein FLJ21827
	154.8	760.85	414.2	NM_004182	MmugDNA.7088.1.S1_at	gDNA.g4759297 FEA=U133PSR GEN=UXT DEF=Orthologous to 218495_at ubiquitously-expressed transcript
	458.2	2443.75	883.6	NM_000430	MmugDNA.30079.1.S1_at	gDNA.g6031206 FEA=U133PSR GEN=PAFAH1B1 DEF=Orthologous to 200816_s_at platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
	126	644.6	145.6	AI653608	MmugDNA.39791.1.S1_at	gDNA.Hs.182490.0.S1 FEA=U133PSR GEN=LRPPRC DEF=Orthologous to 211971_s_at leucine-rich PPR-motif containing
	624.6	2499.05	1408	AL566528	MmugDNA.136.1.S1_at	gDNA.Hs.211584.0.A3 FEA=U133PSR GEN=NEFL DEF=Orthologous to 221801_x_at neurofilament, light polypeptide 68kDa
	716.5	2571.9	1775	NM_005382	MmugDNA.33139.1.S1_at	gDNA.g4885512 FEA=U133PSR GEN=NEF3 DEF=Orthologous to 205113_at neurofilament 3 (150kDa medium)
	577.9	2515.1	925.5	AW118072	MmugDNA.35069.1.S1_at	gDNA.Hs.89981.3.A2 FEA=U133PSR GEN=RAB6B DEF=Orthologous to 221792_at RAB6B, member RAS oncogene family
	210.9	930.55	310.6	AI819734	MmugDNA.10001.1.S1_at	gDNA.Hs.301206.0.A1 FEA=U133PSR GEN=KIF3B DEF=Orthologous to 225205_at kinesin family member 3B
	33.65	125.45	69.15	NM_004521	MmugDNA.29118.1.S1_at	gDNA.g4758647 FEA=U133PSR GEN=KIF5B DEF=Orthologous to 201992_s_at kinesin family member 5B
	118	360.8	295.9	BF688108	MmugDNA.20017.1.S1_at	gDNA.Hs.14202.2.S1 FEA=U133PSR GEN=RHOT1 DEF=Orthologous to 222148_s_at ras homolog gene family, member T1
	202.2	665.3	437.9	AI341076	MmugDNA.8919.1.S1_at	gDNA.Hs.54310.0.A1 FEA=U133PSR GEN=LRPPRC DEF=Orthologous to 230194_at Leucine-rich PPR-motif containing
	967.5	3314.35	1915	BF939474	MmugDNA.13708.1.S1_at	gDNA.Hs.129908.0.A2 FEA=U133PSR GEN=KIF1B DEF=Orthologous to 209234_at kinesin family member 1B
	172.5	580.45	330.5	NM_003119	MmugDNA.2782.1.S1_at	gDNA.g4507172 FEA=U133PSR GEN=SPG7 DEF=Orthologous to 202104_s_at spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
	402.9	1372.5	579.3	M92439	MmugDNA.34357.1.S1_s_at	gDNA.g177109 FEA=U133PSR GEN=LRPPRC DEF=Orthologous to 211615_s_at leucine-rich PPR-motif containing leucine-rich PPR-motif containing
	399	1145.7	711.7	NM_014970	MmugDNA.19383.1.S1_at	gDNA.g7657592 FEA=U133PSR GEN=KIFAP3 DEF=Orthologous to 203333_at kinesin-associated protein 3
	440.4	1182.1	505.9	AL135264	MmugDNA.39479.1.S1_at	gDNA.Hs.14434.0.A1 FEA=U133PSR GEN=KIF1B DEF=Orthologous to 225878_at Kinesin family member 1B
	1047	2508.5	1465	NM_018307	MmugDNA.8301.1.S1_at	gDNA.g8922837 FEA=U133PSR GEN=RHOT1 DEF=Orthologous to 218323_at ras homolog gene family, member T1
	313.2	689.35	409.5	CA777994	MmugDNA.17946.1.S1_s_at	gDNA.Hs2.164975.3.A1 FEA=U133PSR GEN=BICD1 DEF=Orthologous to 1556051_a_at bicaudal D homolog 1 (Drosophila)
	4088	8395.2	5754	AL566528	MmugDNA.136.1.S1_s_at	gDNA.Hs.211584.0.A3 FEA=U133PSR GEN=NEFL DEF=Orthologous to 221801_x_at neurofilament, light polypeptide 68kDa
	300.9	759.5	285.3	AB011139	MmugDNA.1866.1.S1_at	gDNA.Hs.147946.0.S2 FEA=U133PSR GEN=OPA1 DEF=Orthologous to 212213_x_at optic atrophy 1 (autosomal dominant)
	422.7	1043.1	409.4	BE256969	MmugDNA.24123.1.S1_at	gDNA.Hs.77318.0.A2 FEA=U133PSR GEN=PAFAH1B1 DEF=Orthologous to 200813_s_at platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
	422.1	965.55	406.1	NM_005200	MmugDNA.24516.1.S1_s_at	gDNA.Hs.272480.0.S1 FEA=U133PSR GEN=SPG7 DEF=Orthologous to 214494_s_at spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
	674.8	313.2	767.1	NM_022822	MmugDNA.26537.1.S1_at	gDNA.g12383061 FEA=U133PSR GEN=KLC2 DEF=Orthologous to 218906_x_at likely ortholog of kinesin light chain 2
	193.7	248.5	35.75	NM_004798	MmugDNA.29117.1.S1_s_at	gDNA.g4758645 FEA=U133PSR GEN=KIF3B DEF=Orthologous to 203943_at kinesin family member 3B
	455.1	143.7	317.6	BC012504	MmugDNA.35280.1.S1_at	gDNA.Hs2.383134.1.S1 FEA=U133PSR GEN=DNCI1 DEF=Orthologous to 1569843_at dynein, cytoplasmic, intermediate polypeptide 1
	15596	4570.5	8352	BC004369	MmugDNA.36988.1.S1_x_at	gDNA.g13325111 FEA=U133PSR GEN=APP DEF=Orthologous to 211277_x_at amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
dynactin						
	486.1	1835.8	1158	NM_006571	MmugDNA.34757.1.S1_s_at	gDNA.g5730115 FEA=U133PSR GEN=DCTN6 DEF=Orthologous to 203261_at dynactin 6
	269.2	1003.55	579.9	BE218028	MmugDNA.3795.1.S1_at	gDNA.Hs.180952.0.A2 FEA=U133PSR GEN=DCTN4 DEF=Orthologous to 222488_s_at dynactin 4 (p62)
	114.3	183.6	238.8	BC004191	MmugDNA.6161.1.S1_at	gDNA.g13278857 FEA=U133PSR GEN=MGC3248 DEF=Orthologous to 209232_s_at dynactin 4
	897.1	2077.15	1181	AI985890	MmugDNA.9774.1.S1_s_at	gDNA.Hs.180952.2.A1 FEA=U133PSR GEN=DCTN4 DEF=Orthologous to 233490_at Dynactin 4 (p62)
	499.1	1147.3	501.9	NM_007234	MmugDNA.14686.1.S1_s_at	gDNA.g13259516 FEA=U133PSR GEN=DCTN3 DEF=Orthologous to 204246_s_at dynactin 3 (p22)
	1116	2281.15	886.4	NM_006400	MmugDNA.14660.1.S1_at	gDNA.g13259506 FEA=U133PSR GEN=DCTN2 DEF=Orthologous to 200932_s_at dynactin 2 (p50)
dynein	142.1	2283.3	826.6	CK230640	Mmu.14082.1.S1_at	gb:CK230640 DB_XREF=gi:39636821 DB_XREF=ILLUMIGEN_MCQ_991 TID=Mmu.14082.1 CNT=5 FEA=EST TIER=ConsEnd STK=0
	31.65	338.8	128.6	BF000332	MmugDNA.23886.1.S1_at	gDNA.Hs.7720.0.A1 FEA=U133PSR GEN=DNCH1 DEF=Orthologous to 229115_at dynein, cytoplasmic, heavy polypeptide 1
	88.35	739.5	512.7	AK026653	MmugDNA.6787.1.S1_at	gDNA.Hs.7086.1.S1 FEA=U133PSR GEN=C14orf168 DEF=Orthologous to 226309_at chromosome 14 open reading frame 168
	199.2	1112	706.4	AK024863	MmugDNA.27200.1.S1_at	gDNA.Hs.325093.0.A1 FEA=U133PSR GEN=DNCLI2 DEF=Orthologous to 224614_at dynein, cytoplasmic, light intermediate polypeptide 2
	992.6	5689.8	3015	NM_014183	MmugDNA.33113.1.S1_at	gDNA.g7661821 FEA=U133PSR GEN=DNCL2A DEF=Orthologous to 217917_s_at dynein, cytoplasmic, light polypeptide 2A
	168.4	392.7	472.5	BF592008	MmugDNA.19684.1.S1_at	gDNA.Hs.87372.1.S1 FEA=U133PSR GEN=DNCI2 DEF=Orthologous to 242363_at Dynein, cytoplasmic, intermediate polypeptide 2
	150.9	447.3	282.9	CB311093	Mmu.3811.1.S1_at	gb:CB311093 DB_XREF=gi:28833807 DB_XREF=AGENCOURT_11837347 CLONE=IMAGE:6916605 TID=Mmu.3811.1 CNT=4 FEA=EST TIER=ConsEnd STK=0
	1479	4101.7	2584	BG110975	MmugDNA.27201.1.S1_at	gDNA.Hs.325093.0.A2 FEA=U133PSR GEN=DNCLI2 DEF=Orthologous to 224616_at dynein, cytoplasmic, light intermediate polypeptide 2
	433.2	1023.6	871.3	NM_006519	MmugDNA.34145.1.S1_at	gDNA.g5730084 FEA=U133PSR GEN=TCTEL1 DEF=Orthologous to 201999_s_at t-complex-associated-testis-expressed 1-like 1
	3079	7599.9	5676	NM_006141	MmugDNA.19273.1.S1_at	gDNA.g5453633 FEA=U133PSR GEN=DNCLI2 DEF=Orthologous to 203590_at dynein, cytoplasmic, light intermediate polypeptide 2
	797.5	2080	1181	AF250307	MmugDNA.41136.1.S1_at	gDNA.g13649464 FEA=U133PSR GEN=DNCI2 DEF=Orthologous to 211684_s_at dynein, cytoplasmic, intermediate polypeptide 2
	892.6	2091	1380	NM_006520	MmugDNA.34151.1.S1_at	gDNA.g5730086 FEA=U133PSR GEN=TCTE1L DEF=Orthologous to 203303_at t-complex-associated-testis-expressed 1-like
	4432	10043.3	7009	NM_003746	MmugDNA.2252.1.S1_at	gDNA.g4505812 FEA=U133PSR GEN=DNCL1 DEF=Orthologous to 200703_at dynein, cytoplasmic, light polypeptide 1
	205.6	285.2	428.6	NM_024606	MmugDNA.11626.1.S1_at	gDNA.g13375812 FEA=U133PSR GEN=DNCH2 DEF=Orthologous to 219469_at dynein, cytoplasmic, heavy polypeptide 2
	772.3	353.65	413.4	NM_012192	MmugDNA.14592.1.S1_at	gDNA.g6912381 FEA=U133PSR GEN=FXC1 DEF=Orthologous to 217981_s_at fracture callus 1 homolog (rat)
	359.7	114.9	329.8	AI986267	MmugDNA.7110.1.S1_at	gDNA.Hs2.376169.1.S1 FEA=U133PSR GEN=DNCH1 DEF=Orthologous to 1556831_at Dynein, cytoplasmic, heavy polypeptide 1
	455.1	143.7	317.6	BC012504	MmugDNA.35280.1.S1_at	gDNA.Hs2.383134.1.S1 FEA=U133PSR GEN=DNCI1 DEF=Orthologous to 1569843_at dynein, cytoplasmic, intermediate polypeptide 1
	263.4	76.15	205.6	AI005163	MmugDNA.24258.1.S1_at	gDNA.Hs.201378.0.A1 FEA=U133PSR GEN=FLJ40427 DEF=Orthologous to 243802_at hypothetical protein FLJ40427
	474	93.3	327.5	AI076810	MmugDNA.35712.1.S1_at	gDNA.Hs.133977.0.A1 FEA=U133PSR GEN=MGC27277 DEF=Orthologous to 242283_at hypothetical protein MGC27277
	378.7	56.4	361.1	AI821235	MmugDNA.10049.1.S1_at	gDNA.Hs.187802.0.A1 FEA=U133PSR GEN=DNAH11 DEF=Orthologous to 241246_at Dynein, axonemal, heavy polypeptide 11
	251.9	67.15	61.9	NM_003462	MmugDNA.22105.1.S1_at	gDNA.g13518030 FEA=U133PSR GEN=DNALI1 DEF=Orthologous to 205186_at dynein, axonemal, light intermediate polypeptide 1
	268.1	69.65	64.55	AI823600	MmugDNA.38210.1.S1_at	gDNA.Hs.87372.0.A1 FEA=U133PSR GEN=DNCI2 DEF=Orthologous to 236698_at Dynein, cytoplasmic, intermediate polypeptide 2
	228.9	20.2	85.95	AL512706	MmugDNA.33414.1.S1_at	gDNA.Hs.246306.0.S1 FEA=U133PSR GEN=FLJ23529 DEF=Orthologous to 234893_s_at hypothetical protein FLJ23529
kinesin						
	145.2	1651.7	798.1	AV705253	MmugDNA.16319.1.S1_at	gDNA.Hs.154248.0.S1 FEA=U133PSR GEN=ALS2CR3 DEF=Orthologous to 202124_s_at amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3
	999.3	7049.35	4582	BF223224	MmugDNA.8525.1.S1_at	gDNA.Hs.149436.0.A1 FEA=U133PSR GEN=KIF5B DEF=Orthologous to 201991_s_at kinesin family member 5B
	335.3	2362.25	783.3	AA284075	MmugDNA.39631.1.S1_at	gDNA.Hs.117977.1.A1 FEA=U133PSR GEN=KNS2 DEF=Orthologous to 212877_at kinesin 2 60 70kDa
	78.35	496.6	234.7	NM_014965	MmugDNA.11023.1.S1_at	gDNA.g7662457 FEA=U133PSR GEN=OIP106 DEF=Orthologous to 202080_s_at OGT(O-Glc-NAc transferase)-interacting protein 106 KDa
	46.25	242.75	164.6	BG473130	MmugDNA.1261.1.S1_at	gDNA.Hs.259873.0.S1 FEA=U133PSR GEN=KIF1A DEF=Orthologous to 203849_s_at kinesin family member 1A
	422.6	1656.05	1695	Z22551	MmugDNA.42843.1.S1_s_at	gDNA.Hs.211577.1.S1 FEA=U133PSR GEN=KTN1 TXNDC7 DEF=Orthologous to 214709_s_at kinectin 1 (kinesin receptor) thioredoxin domain containing 7
	715.4	2736.3	2117	BF589024	MmugDNA.18302.1.S1_at	gDNA.Hs.211577.0.S1 FEA=U133PSR GEN=KTN1 DEF=Orthologous to 200914_x_at kinectin 1 (kinesin receptor)
	51.2	258.15	67.15	BF197057	MmugDNA.3787.1.S1_at	gDNA.Hs.265317.0.A1 FEA=U133PSR GEN=C14orf153 DEF=Orthologous to 225948_at chromosome 14 open reading frame 153
	210.9	930.55	310.6	AI819734	MmugDNA.10001.1.S1_at	gDNA.Hs.301206.0.A1 FEA=U133PSR GEN=KIF3B DEF=Orthologous to 225205_at kinesin family member 3B
	33.65	125.45	69.15	NM_004521	MmugDNA.29118.1.S1_at	gDNA.g4758647 FEA=U133PSR GEN=KIF5B DEF=Orthologous to 201992_s_at kinesin family member 5B
	967.5	3314.35	1915	BF939474	MmugDNA.13708.1.S1_at	gDNA.Hs.129908.0.A2 FEA=U133PSR GEN=KIF1B DEF=Orthologous to 209234_at kinesin family member 1B

1090	3542.7	2303	BF059313	MmugDNA.11696.1.S1_at	gDNA.Hs.6641.0.S1 FEA=U133PSR GEN=KIF5C DEF=Orthologous to 203129_s_at kinesin family member 5C
84.7	215.15	208.8	NM_024704	MmugDNA.12624.1.S1_at	gDNA.g13375994 FEA=U133PSR GEN=C20orf23 DEF=Orthologous to 219570_at chromosome 20 open reading frame 23
784.6	2245.9	1598	AA630326	MmugDNA.33489.1.S1_at	gDNA.Hs.149436.1.A1 FEA=U133PSR GEN=KIF5B DEF=Orthologous to 224662_at kinesin family member 5B
399	1145.7	711.7	NM_014970	MmugDNA.19383.1.S1_at	gDNA.g7657592 FEA=U133PSR GEN=KIFAP3 DEF=Orthologous to 203333_at kinesin-associated protein 3
179.6	496.8	286.9	AI657069	MmugDNA.19156.1.S1_s_at	gDNA.Hs.105187.3.S1 FEA=U133PSR GEN=KIF9 DEF=Orthologous to 231319_x_at kinesin family member 9
2598	6859.25	3490	NM_004522	MmugDNA.29119.1.S1_at	gDNA.g4758649 FEA=U133PSR GEN=KIF5C DEF=Orthologous to 203130_s_at kinesin family member 5C
673.4	1811.25	843.1	NM_015049	MmugDNA.24148.1.S1_at	gDNA.g13027379 FEA=U133PSR GEN=ALS2CR3 DEF=Orthologous to 202125_s_at amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3
440.4	1182.1	505.9	AL135264	MmugDNA.39479.1.S1_at	gDNA.Hs.14434.0.A1 FEA=U133PSR GEN=KIF1B DEF=Orthologous to 225878_at Kinesin family member 1B
327.8	669.4	331.7	BF056095	MmugDNA.28049.1.S1_at	gDNA.Hs.30861.0.A1 FEA=U133PSR GEN=TMEM42 DEF=Orthologous to 226361_at transmembrane protein 42
674.8	313.2	767.1	NM_022822	MmugDNA.26537.1.S1_at	gDNA.g12383061 FEA=U133PSR GEN=KLC2 DEF=Orthologous to 218906_x_at likely ortholog of kinesin light chain 2
193.7	248.5	35.75	NM_004798	MmugDNA.29117.1.S1_s_at	gDNA.g4758645 FEA=U133PSR GEN=KIF3B DEF=Orthologous to 203943_at kinesin family member 3B
341.2	64.2	215.6	BC000712	MmugDNA.9497.1.S1_at	gDNA.g12653842 FEA=U133PSR GEN=KIFC1 DEF=Orthologous to 209680_s_at kinesin family member C1