

Gene Symbol	Description	Score	Rank	siRNA sequence 1	siRNA sequence 2	siRNA sequence 3	siRNA sequence 4
ACP1	acid phosphatase 1, soluble	25	42	CCCATAGTGACACTTGTATA	TCCGTAGGAGCTCACAGTCTA	TCCGTGTGTAATCACGTTCCA	ATGGATGAAAGCAATCTGAGA
ACP2	acid phosphatase 2, lysosomal	-17	185	CAGCCTGAAGTCTTCGGCAAA	CTGGATGCTACAATGGTGAA	ACCAGTGAAGACATATCCCAA	CAGCGCTATCACGGCTTCCTA
ACP5	acid phosphatase 5, tartrate resistant	25	43	CTCGGGCAAGTCCCTCTTTAA	CTGGTACGTGCTAGCCGGAAA	ACGGCGTGTCTCATCTGCAA	CACTGGTGTGCAAGACATCAA
ACP6	acid phosphatase 6, lysophosphatidic	-8	176	CCATGTCAGTTTATACCTTAA	CCCCTGGACATGTTCTTGAA	GTGCCCTTATACAATGCCAAA	GAGGCCAAACTTGAATACAA
ACPP	acid phosphatase, prostate	+2	20	ACAGATGGCGCTAGATGTTTA	CCGGACTTTGATGAGTGCTAT	CTCTATTACCATTATGGATAA	ATGAACAGGTTTATATTCGAA
ACPT	acid phosphatase, testicular	0	128	CCCGCAAAGATGGAGGGAAT	CTGGTGTTCGTGGCTCTGGTA	CTGCTGAATGCTATCCTTGCA	CAGGGCATGGAAGGTTCTGGA
ALPI	alkaline phosphatase, intestinal	58	9	CACGTCCATCTGTACGGCAA	TCCATTCTCCTAGGAGACAAA	CCAGACAATAAAGGGACCAA	CCGGCTACGTGTCAACTCA
ALPL	alkaline phosphatase, liver/bone/kidney	25	44	CAGGATTGGAACATCAGTTAA	CCGGGACTGGTACTCAGACAA	CAGACTGCAGACATTCCTCAA	CACCATGATTTACCATTCTT
ALPPL2	alkaline phosphatase, placental-like 2	17	70	CTGGGAAACACAAAGCAATAA	TTGCTTTATCTTGTCTCTGAA	ATCGACCATTGGTCATCATGAA	CACGGTCTCTTATACGGAAA
CDC25A	cell division cycle 25A	17	71	AAGGCGCTATTTGGCGCTTCA	AAGGGTTATCTCTTTCATACA	CAGCTTAGCTAGCATTAATAA	CTGGCCAAATAGCAAAGACAA
CDC25B	cell division cycle 25B	50	13	CAGGAGGCTGAGGAACCTAAA	CCCAGTCTGTTGAGTTAGTTA	CGCCGAGAGCTTCTACTGAA	TTGGGTTAATACCAGCTTAAA
CDC25C	cell division cycle 25C	17	72	CAGGAAGGGCTTATGTTTAAA	CCAGAGCTATATATCTTAAA	CCAGGGAGCCTTAAACTTATA	GAGCTGCAATCTAGTTAACTA
CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	25	45	CACAATCAAGATCTGTATCAA	TCCGGACAAATTAGCTGCACA	CACCAGTGTATCAACTTGAA	CTAGCATAAATTTGATTTGAAA
CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	0	129	CCGGCTGTACGCACACACCAT	CTCCATGGTTTGCATTATTGA	CCCACAAACTTCCCGATAGA	CCGAATATTATCAAGGGATGA
CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	8	94	CCCGGAAACAGCGGGAAGTAA	TACGATCAGCGTGACAGAGTA	CCACCTAGCCATAGTCTCAAA	CTGCGTATAAGGAGGAAGCAA
CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	8	95	CCAGTGCACAGCTCAGCTTAAA	TACGCCAACTCTTTAGCCAA	TAGGAAATGCTACATCGCGAA	TTCGTTTAAAGCTATTAGTAA
DKFZP566K0524	DKFZP566K0524 protein	17	73	CCCACCCTAACACTTAAACATA	CTGGTGACAAGCTATACCTAA	TTGAATTTGGTTGAATAATTAA	TCACCTCTGTTGAAACATTTA
DOLPP1	dolichyl pyrophosphate phosphatase 1	0	130	AAGAATGCACCAAACAACAA	CAGGGTCTACCTGCTGTACCA	GAGGTGGTTTGAATTTAAGAAA	CAGGATGGACAGGATGACAGA
DUSP10	dual specificity phosphatase 10	8	96	ATGAGAATACAGGCTCTCTAA	CAGGTTTATAGACCCGAAGATA	CAGGGCAGCTTAAGTGGTCTA	CCGAAGATACTACACACTTTA
DUSP11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	8	97	CAGAACTGTCTCTTACTTAA	CCCTTATGTATTCAAGCTTAA	CACAATAAGCCTGTAAACAA	ATGATGCAATTTGAATATTCA
DUSP12	dual specificity phosphatase 12	0	131	ATGCTTTACATGGCAATCAAA	TACCGTTTCAACAAGGATTGAA	CTCAATGTACATCTTATTTCA	CAAGCTCAATGTACATCTTAT
DUSP13	dual specificity phosphatase 13	+2	21	ACCCTGAGATGTAACAGCAA	TCAGTCCATCTCTATAATAAA	ACCCAATTCAGAGATTCCTTA	CAGGTGGACACAGGTGCCAAA
DUSP14	dual specificity phosphatase 14	8	98	AAGGGAATGCATACATTTGCTA	ACCCTTATTATTTAGCTGTTA	CCCAGGATTATATTAGCATTA	TAGCTGTTAAGTAACTATAAT
DUSP15	dual specificity phosphatase-like 15	-42	208	ACGGCCTGGAGGGTATTAAA	CACCACGATTTGTACAGCGTA	CTGGAGGTTATTAAGAGACA	CCGAAATAAGATCACACACAT
DUSP16	dual specificity phosphatase 16	0	132	AAGTTGTAGTTTACGATCAA	CCGCCATTTGTGGAATACAA	CAGGACAAAGTGTAAATACA	AACCCAGTTGTTACTCTCTTA
DUSP18	dual specificity phosphatase 18	33	29	ACGGTCTCTCTCCGAAGAA	CCAGATCACCATTGGTCATCAA	CAGGAATGAATCTGCTACAA	CAAGCTATGCTGTCTAGCAA
DUSP19	dual specificity phosphatase 19	-8	177	ATGGTCAGTATCACTGGATAA	CAGAGTTAACCTAATGAGTCA	TACGGTCTCTTTCTCACATA	AAGGTCATATATACTATACAA
DUSP2	dual specificity phosphatase 2	33	30	CAGCCTGAGAGCTCCAAGGAA	CTGGTCCACCACCATTGTGAA	AAACTTAGCACTTTATATTTA	CGCGGAAAGACCCGAAAGGAA
DUSP21	dual specificity phosphatase 21	0	133	AACGTAGTAAGCCTTACCTTA	TCCGTGGAAGTGGTCAACGTA	ACCGGATGGTGCCTTGTAAA	ACGTACGATGATATCAATGTA
DUSP22	dual specificity phosphatase 22	0	134	CATGTTTATGTTGAGAATAA	GGGCAACTTAGCCAAGTTTAA	AAGCAACATAGAGTTTAAGTA	AAGCATGAGTCCATCAGTAT
DUSP23	dual specificity phosphatase 23	0	135	CAGTTCTACCAGCGAACGAAA	GAAGTGGACTAAAGTATTAAA	TTGGCTGAAGCACTGAAGTA	CAGGAGATGCCATTTGCTGAAA
DUSP24	dual specificity phosphatase 24 (putative dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related))	-33	203	AAGCTTCTGCACATCCGGATA	CAAGATTCAGAAGGACTTGAA	CACCCTGGAGATACTCTTAAA	CTGCCTGAAAGTCTCATGTTA
DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	-33	204	CCCGGGATCTACGTGGGCAA	CCGTATTTACTTAAACAGATT	AACAGATTCGTTGGAAGCTTA	TACGTTATTGTTATTATGGAA
DUSP6	dual specificity phosphatase 6	25	46	CTGCATTGCAGAGACCAATCTA	TACGGACACTATTTACTACTAA	TGCGGAAATGGTTAATACTAA	TCAGCTGTGCTAAACAGTATA
DUSP7	dual specificity phosphatase 7	33	31	CAAGGTGGTTTCAACAAGTTT	CGGCGCGAGTTCCACTACAA	TACGACTTTGTCAAGAGGAAA	GAAGATGAACCTGTCACTCAA
DUSP8	dual specificity phosphatase 8	+2	22	CCGCTCCTTCGTGGAGTACAA	TCCATCGAGTTCATCGATAAA	CAGGCCGTTTATAAATGTATA	GCGGGTGGTCTCGAGCTCTA
DUT	dUTP pyrophosphatase	+2	23	AAGCCTTGGATGACACCGAAA	TCCCTTCTCTTCACTAGTCTA	AAGCCTGTATTTAACTCATAT	AAAGCCTGTATTTAACTCATAT
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	8	126	CACCGGCTCCTAATAACGGAA	CAGATAAATACTATTCAATTTA	TGGCAAAACAGTAGACTTATA	AAGCATGAAACTTTACCTTAT
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	-33	205	ATGGATCATATTGCTCGGAA	CGGACTAGATATGATATCTTA	AAGCCTTATAAACCAACTTTA	CAGATATATTTAAGCCTTATA

ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	0	136	AACCTAATGTGTGATCTTCTA	CTGGCTGTTAGGAGTAAATCA	TAGCAATTTGGTACCTATGTA	ATGGTTATAACAATGAGTTTA
FBP1	fructose-1,6-bisphosphatase 1	0	137	CTCGCTCTGCACAGCAGTCAA	TTCTTAGAGAGCAGAAATAAA	CCTGGTTATGAACATGTTAAA	CTCCAACGACCTGGTTATGAA
FBP2	fructose-1,6-bisphosphatase 2	0	138	AGGACCCTAAATGAACGATAA	CAGGTTATGCGCTGTACGGTA	TCCACTTAATCACATACAGAA	CTCAATGCTGACGCCATCAA
FLJ32332	likely ortholog of mouse protein phosphatase 2C eta	-17	186	CAGAGTGACTTTACAACCTTAA	CCCAGAGACTCGGATTATCAA	CAGGATCTTGAACAGCCCAA	TCGGATTATCAATGCAGAGAA
G6PC	glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)	0	139	CAGCAGGTGTATACTACGTGA	TGGGATCCAGTCAACACATTA	CTGGCTTATTTCCCATGTGTGA	TAGCAGAGCAATCACCACCAA
G6PC2	glucose-6-phosphatase, catalytic, 2	50	14	CAGAGTATTATAGCAACACA	CTGGTGGGTCCAAGAACTCA	TGGTTAAACTTTATATTTAAA	TTGGTTAAACTTTATATTTAA
G6PC3	glucose 6 phosphatase, catalytic, 3	0	140	CAGGTGCTGGCTGGCCTAATA	GTGGCTCAACCTCATCTTCAA	CACATGTTCAAGTCCCAGGAA	CTGGGAAATGGCCAGAAGATA
ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	0	141	ATGGAGGAATTCGAGCCTCAA	CCCCTAGCAGTGGCGATTCA	TCGGGCAATCTTGTGTCGTTA	TTCGGTGATCTTTGGTCTGAA
IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	-17	187	ACGAAGAGTAATTCGTGCAAA	CCGGAAGAGACGAGTGC GGTA	TAGAAAGTTAACTGTTTGGAA	CCAGATTTGGTGACTCATCAA
INPP1	inositol polyphosphate-1-phosphatase	50	15	CCGTAATTAGTACAAGTGAAA	TAGATTTCAACTTATCAGTATA	CTGATGGGAGTCATCAATCAA	CACCAGCAGCTGCAACTGAAA
INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	8	99	AACGATTTGCGCCAAACTGAA	CCCGGAAAGTGTGAGCGGAAA	ATCGATGTCAGTGACACTTGA	CTCCATAGATTTGAAACAGAA
INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	8	100	CGGAAGGTTATGCTCCAGTTA	TCGAGTGATGCGATGAAAGAA	AACAATAATATCATGGGAGAA	CGAGTGCAAAATGGTCAAGAAA
INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	33	32	TTGCGGGAACATACAATGTAA	AAGAAGAGGATTACACCTATA	GAGGGCAATACAGGCATTTAA	CTGCGAGATACAATTTGTGAAA
INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	0	142	CAGGTGCTATGCCACATGAA	TCCCATCAACATGGTGTCCAA	CCCGGGACTGTTGACAGCCAA	TCGGAATTCGCTTTACTCTTA
INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	-23	197	ACGCATCGTGTCTCAGATCAA	ACGGATTTTCGAAGGAGATTCA	CACGTACGACAGCACCTCCAA	CAGAAATGTCCCAGACCCAA
INPP5F	inositol polyphosphate-5-phosphatase F	50	16	AAGACCTTTACGCATATTTAA	CAGATCTTCCATGGTGGCTTA	CTGAAATAATGTGTTTCTGAA	TACCATCTCTGATGACTCAA
ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	8	101	CTGGAGAAGTTAAAGCCTGAA	CTGGATGAGACTTGTTCCTCAA	GAGGAGGTCGTTTCAGATTTCTA	CAGGAGGCAGTTCCAGGTA
LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase similar to protein tyrosine phosphatase, receptor type, Q isoform 1 precursor; glomerular mesangial cell receptor protein-tyrosine phosphatase; glomerular mesangial cell receptor protein-tyrosine phosphatase precursor	8	102	CAGGAGGAACTAACAGTTCA	CCCAGTCACCTTTCAGACAA	CCCGGTGTGTGCAGGAGGAAA	ACCACTCACCATGGGCCTTTA
LOC387870	similar to Osteotesticular phosphatase; protein tyrosine phosphatase receptor type V; protein tyrosine phosphatase receptor type W; protein tyrosine phosphatase, receptor type, V	19	67	TAGCAGAAAGAGGAACCTTAA	CACGATATGTTTGTCTTGAA	CCAGGTGGTATTGTTAAAGTA	CAGGATCGTGTTCACAAGGAT
LOC389772	similar to SET-binding factor 1 (Sbf1) (Myotubularin-related protein 5)	0	143	TACATTCTAGTAAGCATCTTA	TAGTTTAAATATATACAATAA	AAAGCAATATGTAATCTTAA	AACATTATGTTGTATAGTTTA
LOC390997	similar to protein tyrosine phosphatase, receptor type, U isoform 2 precursor; protein tyrosine phosphatase J; protein tyrosine phosphatase receptor omicron; pi R-PTP-Psi	0	144	CAACCGCATGTTGACCACCAA	GAGGACGCCCATGTTCTACAA		
LOC391025	similar to TPTE and PTEN homologous inositol lipid phosphatase isoform alpha; TPTE and PTEN homologous inositol lipid phosphatase	56	12	CTCATTAATTATGATTATTGA	CAAAGGATTCGGAACAGAAA	CAGGAGGGTCTGTTGGCTCA	CAGATGAGTCTCAGCACAAAT
LOC400927	similar to fructose-1,6-bisphosphatase 2; fructose-1,6-bisphosphatase isozyme 2; D-fructose-1,6-bisphosphate 1-phosphohydrolase; FBPase; muscle fructose-bisphosphatase; hexosediphosphatase	17	74	TCCAGGTGATCTGAACCTGAA	ATGGATGTTCTTCTTCGAGTA	TCCACAGACAACGAATTTAA	CTGGTGTCCACCTATCAGTAAA
LOC442428	similar to SUMO1 pseudogene 3	25	47	CAACATTTGTGACCATAGTTTA	CAAGATTAGTAAGAAAGGAAA	CAGCCTTATGGACTCTCTCAA	CACCTGGATGCTACCAGGCTA
LOC474338	SUMO1 pseudogene 3	-8	178	CAGGCTTGTGGTGATAAATAA	AAGGAAGGTGAATATATTTAA	CTCATTAATTCATTAATGTTTA	CAGAGAATTGCTGATAATCAT
LOC642940	similar to myotubularin related protein 9 lipid phosphate phosphatase-related protein type 2	-6	175	CCGTGCGGTGATCGTGCCATA	CTCGGAGCAAAGCATGGACAA		
LPPR2	multiple inositol polyphosphate histidine	0	145	CCCGTGTCTAAGCATGTGCAA	CCGGGACAACCTCAGCCCTTA	CTGCGTTGTGCATAACTTTCA	CCCGTGGCCGAGTACCAGAAA
MINPP1	multiple inositol polyphosphate histidine	-42	209	CACGGTCAAAACAGATCCGCAA	CCGAGTGCAGATGTTATTTAA	AAGTCGGAAAAGTACAATGAAA	ATGAAATCTTCTACTTATA

	phosphatase, 1						
M-RIP	myosin phosphatase-Rho interacting protein	25	48	AAGCGGGACTTCACCAATGAA	CCGGACCAACAAGCAGAATCA	CGGGAGCTAGAGAACTTCGA	GCGACGGTTCTTCATCCTTTA
MTM1	myotubularin 1	25	49	CGAATAGGTCATGGTGATAAA not disclosed - validated	TCCGGTATGAGTGGGAAACGAA not disclosed - validated	GACATTGTTTATCCTAATGTA	CGGTATGAGTGGGAAACGAAA
MTMR1	myotubularin related protein 1	25	50				
MTMR2	myotubularin related protein 2	25	51	AACGATATGAACTTTGTGATA	CTGAGGGAGTCTAACAGTTA	ACCACTGCAATTCACATTATA	TAGGATGAGTTTAGAACTGTA
MTMR3	myotubularin related protein 3	0	146	GACCCTTATTACCGAACCATA	TTGCCTTTAGCCGAATGTAAA	CAGCCTTAAATCAAGAATATT	AGCATGTAACTTCAAGTTTA
MTMR4	myotubularin related protein 4	17	75	TCCGGCACTGGAGAGTACCAA	TTGCCATAGATGTAACCTAAA	AAGAGTGGCTCTCACGGCTAA	CCGGCTGCATATCAAATCAA
MTMR5	myotubularin related protein 5; SET binding factor 1	0	147	CAGCGCCGAGCTCTCCGTAA	CCGCGTGGTGTGGCCCTGTTA	TCCGGTCGTTACCGACCACTA	GACGCCTGTGTCCACAATTA
MTMR6	myotubularin related protein 6	33	33	CCCGGATAGCAAGCAAACCAA	CCCGTAAATGATGCTCTTCGA	TACAAAGTTACTGTTAACAA	AAGGGAAGTACAGATAGTTA
MTMR7	myotubularin related protein 7	17	69	CACCGATATGGCAATCTAGAT	CACGCGGATGGGCTCCCTAA		
MTMR8	myotubularin related protein 8	8	103	CAGCCCAAGCAGAGTATGCTA	CGGGAAGATCTAAGAGTCTAT	GGGAATTACTTTACTGATTAA	TGCCATGAGGTTTATATTTCA
MTMR9	myotubularin related protein 9	8	104	CAGACCTAGTATTCTAAGTTA	CAGGTCTAAGGATTAACATA	ATGCCTGAACCTGTTATCTAA	TACGTTGGAATAGATCCTCTA
MTMR10	myotubularin related protein 10	0	148	CTCGATGGTTAGAATATGTAA	CAACCAGAACTGAAATTTAA		
MTMR11	myotubularin related protein 11	0	149	CAGGGTCCCTGCATAAAATTTA	CACCCTTACTTCTCTGAGAAA		
MTMR12	myotubularin related protein 12	6	127	CAGATAGCCCTGTATATACCTA	CTGTGAGAGATTGCCAGCATA		
MTMR13	myotubularin related protein 13	0	150	CCAGATTATATTATCCAGAAA	AAGGGTAACCGTGGACCTTAA		
MTMR14	myotubularin related protein 14; hJUMPY	0	151	AAGGAATATAAAGATCGGGAT	GACGGTTTGTCTGCCAGTAA		
MTMR15	myotubularin related protein 15	13	93	CTGGTCAGAAGTTATATGTAA	CAGGTTGGCTTAATAAAATCA		
PDP2	pyruvate dehydrogenase phosphatase isoenzyme 2	8	105	CAGGACGATCATCATGGAGGA	TAGACAGGACAGGTTAATTTA	CAGGAATTAGACCATATTTAG	CCCATCCTATTGTCAAGGTTA
PDP2	pyruvate dehydrogenase phosphatase regulatory subunit	58	10	ACCACATAGCCCAGTGATTAA	ATCTCTTATCTCCTTGATATA	TAGCTACAAGATTACAGCTTTA	TTGGAGCAAGTATGTACTTAA
PDPR PHOSPH O1	phosphatase, orphan 1	-8	179	CGCCAACATGTGCAAGCACAA	TCCGGTCCGGACAGCCAGTAA	TACAACATAAAGGAGGTGAA	CCGTCCCTATCTATTCAAGTTA
PHPT1	phosphohistidine phosphatase 1	17	76	CACGCCATTTCAACTGAGAAA	TCCGGCGACATGCAGAAGCAA	CCGATTCCACGTTTCTTTAA	TAGCCTGGCCACAGAATAAA
PIB5PA	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	25	52	CAGGTAACATTTCAGTGAGGAA	CTGGGACTGGATCGGCTTATA	CTGGAGGTCATCCATTAGGAA	ATGGGAATACCTACCAGGTAA
PIP3AP	phosphatidylinositol-3-phosphate associated protein	0	152	CAGGGTCATGGCATAACCAATA	TGGGATGTGGATTATGCTTAA	CCGGCACTCCGTTAGAATAAA	CCCGGCACTCCGTTAGAATAA
PLIP	PTEN-like phosphatase	17	77	CAGCTCGCGCTCAGCACAGTA	CACCTTGGACAACCTCCAGAA	AACCTCCAGAAGGGAGTCCAA	CAGGAGTGGAAAGAGACTAGGA
PME-1	protein phosphatase methylesterase-1	33	34	AACATCGAGCTCTGTGTGAAA	AGGCGATACATCTGAGTTCAA	AGGAAGGAAGTGAAGTCTATA	ACGGCAGCGATTATTAGTAGA
PNKP	polynucleotide kinase 3'-phosphatase	17	78	CACGTGAACAGGGACACGCTA	CACGTGTGAGACAGCCCTGAA	CGGGAAGTCCACCTTTCTCAA	CAAGCTGGTGATCTTCAACAA
PPAP2A	phosphatidic acid phosphatase type 2A	8	106	AACCCGTCTGTCTTACTGTAA	CTGACATTTGCCAAGTATTTAA	CATGCTGTTTGTGGCACTTTA	CCGGGCAGAGACCATGTTTGA
PPAP2B	phosphatidic acid phosphatase type 2B	8	107	AGCGATCGTCCCGGAGAGCAA	CAGCACAAATTTCAGAAGAAAT	CCGGATCTATTACCTGAAGAA	CCGGGCACCTTGCATACTTTA
PPAP2C	phosphatidic acid phosphatase type 2C	8	108	CCGGGTCAACTGCTCGGTCTA	TCGCTCGGACTTCAACAACCTA	ACCCCGTGTCTGATTACAAA	CATGGTGTCTTGGCGCTGTA
PPEF1	protein phosphatase, EF hand calcium-binding domain 1	17	79	CAGCATTAGTACCTACATATT	CCCAATCGGTACAATCGTTGA	ATCGAATATGCTGATGAACAA	CTGGGAAACCCCTCTTCAATAA
PPEF2	protein phosphatase, EF hand calcium-binding domain 2	8	109	CACATGAATATCGACATTACA	CTGCAGGAGCATTGGCGTTAA	CCCACAAGCTACAAATGCTAA	CGGAGCATTGATTTCACAAAA
PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	0	153	AACGGCCTATTTAATATGTTA	CACGAGGTTGGTCTGAAAGA	CTGGTGTTTCCGAGACGGATA	TTCCAAGGTACAAACTTTAA
PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	0	154	AACGTTTGGGTGACTCATGAA	TACCAGCTGGATTAGGTTAA	TCCAATGAACGCTTACAACCTA	ACCGATGAAACTAGTCAATAA
PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	25	53	ACGGCTCAACTATGACCCGAA	CACGGGTAAAGAGAAGTGTTT	TCGAATGTTAGATCACCTTAA	CTGGTGGACGCTCGAATGTTA
PPFIA4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	25	54	CAGGATAGCTGGGTCCATTCA	TGGGTGTGTACTGTTACCAATAA	CAGGGACTCAGTCCAGATTAT	TCCCTGGGTAATGGATGGTAA
PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	-58	214	AAGCGTGATTTCAAACCATAA	TTCCATGAGTATTGCAGGTAA	CAAACCATAATTCGTGTTGTA	TAAGCGTGATTTCAAACCATA
PPM1B	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	17	80	CACCTAAGCATATCTACTTTA	CGAGATAACATGAGTATTGTA	CAACCAAGTGTTTAGAATGAA	TAGCCTAACTACACACATCAA
PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	8	110	ACGGGTCTTCCCTAGCACATCA	CTCGCGTCTGTCGAAGATAAA	ATGGCCAAGGGTGAATTTCTAA	TACATGGAGGACGTTACTCAA

PPM1E	protein phosphatase 1E (PP2C domain containing)	0	155	CCCATTTAGTCTGTACTAAA	GAGGCGGTTTATAGTCAGAAA	TTGGTTCATAAACTAGATAA	CCGCCTAATCATGTGTTTATA
PPM1F	protein phosphatase 1F (PP2C domain containing)	0	156	ATGGTTGGCCACAACAATGA	CACCTGGTGGTCTGATTCATA	ACCAAGTATTGCTTGGCTTAA	CAGGTGGTGTTAATAAGCCAT
PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	8	111	CAGGACCTGAGGACTCAACTA	CCAGAGGATGAAGTAGAACTA	TACTCTGTGAACTTTATTTAA	GAAGTTGTAGATTTTCATTCAA
PPM1L	protein phosphatase 1 (formerly 2C)-like	8	112	CAGGACTACGAGAAAGACAAA	CTGGTGGTCTTAGTCTATAA	AAGCGTGAACCCATATTGATA	CTGTAGAGTCACATATATGAA
PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	8	113	ACCGATTAAGGCCACAGGATA	CAAGATAGTAGTATTATTACA	CAGAATATCATATAATGTTTA	ATCGTACTTCTTATTTAGTAA
PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	17	81	AAGAGACGCTACAACATCAAA	CCGCAATTCGCCAAAGCCAA	CTGCCCTGCTGCTGCCCTATAA	CAGCGAGAAGCTCAACCTGGA
PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	-17	188	TACGAGGATGTCGTCCAGGAA	TAGGAATATGGTCGGCTGAA	AAGTATGTTGGTTAATAGGAA	CACTATTGGATGTGATTTCTAA
PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	17	82	AACATCGACAGCATTATCCAA	CTGGTTATAACAGCAAAATGAA	CTGCGGTGAAGTTGAGGCTTA	GAGGAGTAAGTGTACAATTGA
PPP1R1 0	protein phosphatase 1, regulatory subunit 10	-75	215	CCCAGCCTGCTGAGAAAGATA	CCGAAGGACCGTCACTACATA	CACAGGATCAGCTGCACCTTAA	CAGCAACATCTAAGCCCTTGA
PPP1R1 1	protein phosphatase 1, regulatory (inhibitor) subunit 11	0	157	AACATGAGTAGCGAACACTTA	CGCCCTAACTTTGCTTGCTAA	CAGAGATCAGTCAAATCCATA	TGGCTTGAGATTGGTCACTTA
PPP1R1 2A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	0	158	ATAGTACTCAACCATAAATTAA	CAGAAATTAACCCGTGAGTTAA	CAGGCAGGCTATGATGTTAAT	AACGAAGAGCTCTAGAAAGAA
PPP1R1 2B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	17	83	CAGGGTGTTCCTCTAAAGAA	CGGGAGGTAGTAATCTACAA	CTGGTTGTTGTTATATAGTTT	TAGGAAGATCAGCATATTTAT
PPP1R1 2C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	-8	180	CAGCGGGACCTCAACCAGAA	CAGGAGGACCTTCGGAACCAA	CAGGCGCTTTGGCTCCTGAA	TTGGAGGAACTGGCCCCGAAA
PPP1R1 3B	protein phosphatase 1, regulatory (inhibitor) subunit 13B	50	17	CGCGATGATGCCGATGATATT	CGGGCTGAGAGTCCGGTTTAA	CGCCTTAAATAAGTCAGTTAA	ACCAGCGGGGGTGGAGTTAAA
PPP1R1 4A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	-17	189	CCCAGTACGATCAACATTTGAT	TTGTATTTAATGGTTCTGTAA	TAATGGTTCGTACAATAAAA	GCCAGCTTGCTTGTGTATAA
PPP1R1 4C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	0	159	AAGAGCTGCTTTCTCGGATAA	TAAAGTTGTATGAACCTTAA	AACCTTAAATTTGAAGAACTA	CCGCAGAAGAAGAGTGTATGA
PPP1R1 4D	protein phosphatase 1, regulatory (inhibitor) subunit 14D	-25	198	CAGGAGCTCTTCCAGGATCAA	CCGCCGTGACAGTGAAGTATGA	CAGGCCTGCCCTGAAACTCCA	GAGCCTGAGATTGACCTGGAA
PPP1R1 5A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0	160	CCAGTTGTTGATCTTATGCAA	TGGGTTTATATAAGGAATAAA	GTGGGTTTATATAAGGAATAA	CAGGATCAGCCGAGGATGAAA
PPP1R1 5B	protein phosphatase 1, regulatory (inhibitor) subunit 15B	-25	199	AAGGTGCTAATTTGAGGCCAA	CAGGGTTACTACCTCAGTTTA	AAGGCTTGTACAGACAGGTA	CAGGTTTATTGTGTCTACTA
PPP1R1 6B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	-100	216	ACGGGGCAGAGTAGCAGTGAA	TCGCAGATCTTTGATATCGTA	CAGGCAATTTCTGTTCTGGAA	ATGGAGCTAGTCTCAGTGCAA
PPP1R1 A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	17	84	AAGGATCACACCACAATGAA	TTGCCAGATACATACCTAAA	CAGGGAAGAGTTCTTCCCTTA	GAGGAGGTATCTTGGGATCAA
PPP1R1 B	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	33	35	ATAAATCTTTGTAAATAACAA	CAGCTTGTGTTGAGCCCTTGA	CAGGGATTTGCCCTTCCAAAT	CTGAGTCTCACCTGCAGTCTA
PPP1R1 C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	67	7	CTCGATCTGGAAATTACAGCTA	TTGGAAGTGGTTAGTACCTAA	TAGGATTTATGTTATAGATAA	AATGAGTTTAAATGACTTCAA
PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	92	2	CACTACACGACTGTAATAAAA	TACCAC TGATTTAGAAACAAA	ATGAGATATATAATCAAAGTA	TTGAATGAGATATATAATCAA
PPP1R2 P9	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9	17	85	ACGTACAGAGATTACGATTTA	CTGGAGGGCGGTGGACGGCTA	AACGAAGAATTTGAACATCAAA	CAAGATGTGAAGAGAAAGAAA
PPP1R3 A	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle)	0	161	CACATCAGTATAGGCCATCAA	TCAGGTGGGATTAATCTGAA	TAGGCCATCAATATCACAATA	CAGAGGAAACTACTTCAAATA
PPP1R3 B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	17	86	CACCCAAGTTCTTATACGTTA	CCCGCTAGATATGCCATTCAA	CAGACAGTACTTTAAATGTTA	CTAGGATGACATGATGTTATA
PPP1R3 C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	0	162	TACGATGAATTTCAACGACGA	TCCGGAGAATCAAGATCTTAA	TGGCCTTTATCGATGAATTA	AGCCTTCAACCGATTACTTAA
PPP1R3 D	protein phosphatase 1, regulatory subunit 3D	-50	210	CAGGTACCCACCAACTTTATA	CTGAGTTAGGCAACTACTTAA	AAGGATAGCTTTCTTCGGTAT	TCAGGTGACTAGAGAATTTCA
PPP1R3 F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	-17	190	CGGGTTGGTACCGCTGTGAA	AACATGGATGATAACACCTTT	ACCGAAGACCTGTATGAGAA	CACAAATAGACTCTATGAGAA
PPP1R7	protein phosphatase 1, regulatory subunit 7	-25	200	CACAAACCCAATGGCAATAAA	TCAGATGCCGTTGCAATTA	TTCAGATGCCGTTGCAATTA	CCAGATCAAGAAGATTGAGAA
PPP1R8	protein phosphatase 1, regulatory (inhibitor) subunit 8	0	163	CAGGCCAGGAACTGAAGAAA	TACAAATAAAGATGCCCTAAA	CTGCTGAAGTTTCTTATTTAA	AACCTTGAAGCTGTAATGAA
PPP1R9 A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	-33	206	CTCCAATGTCAACAGAATTAA	GAGGGTAATATTTATCTCTTA	AAGGATGATATCTTAAGTTA	CTGCAGTTGGATGGAAATAAA

PPP1R9 B	protein phosphatase 1, regulatory subunit 9B, spinophilin	0	164	CAACTCGAAGCTGGTCAGCAA	CCCGGGAGGTGCGCAAGATTA	CACTGAGGAATTTCCAATTCTA	CCGGGAGGTGCGCAAGATTAA
PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	31	40	ATGGAAGCTTGACGACTACTCTA	CAAACAATCATTTGGAGCTTAA	ACACCTCGTGAATACAATTTA	CAGATACAAATTTACTTGTTTA
PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	19	68	CCGACAAATATCCCAAGTATA	TGGGATCTGTCTTGGCATTAA	ATGGAATTAGATGACACTTTA	CACCGGATACAAACTACTTAT
PPP2R1 A	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	25	55	ACGGCTGAACATCATCTCTAA	CTGGTGTCCGATGCCAACCAA	CAGAGAAAATAAAGGTCTAGAA	TCCCATCTTGGGCAAAGACAA
PPP2R1 B	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 65), beta isoform	92	3	CAGAAGTTAGGTCAAGATGAA	CAGGAAATAACTACTAAGCAA	CTGACGTTCTGTTTGAATATCA	TGGACCAATTTCTAGATACCAA
PPP2R2 A	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	-8	181	ATGGAAGGTATAGAGATCCCTA	CTGCAGATGATTTGCGGATTA	CTGCCGTGTCTGGCACTGAA	AAGCGAGACATAACCCCTAGAA
PPP2R2 B	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	25	56	CAGGAAATGATTGGAATAGAA	CAGGGACTACTTGACCCGTCAA	CCGGAAGATCCAAGCAACAGA	CGGCTACAAATAACCTTATATA
PPP2R2 C	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	33	36	ACCGCTCATTTCTTCGGAAA	CCGGGACTACCTTACAGTCAA	TACTGTACATCATAGATTTA	GAGGTTATTCTCAGTGGATTA
PPP2R2 D	protein phosphatase 2 (formerly 2A), regulatory subunit B, delta isoform	0	165	CAGAGACTACCTGTCCGGTGAA	TAGGTGGTTACCACAACAGAA	TTCATCCATATCCGATGTAAA	CCGCTCCATTAAGAACAGTGA
PPP2R3 A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	8	114	ACCTGTAGTAAATCATGAACAA	CAGGAGGATTTTCATCCCTCTA	ACCAAGGTAATCAAACATAA	TAGCATAACATTACCAAGGTA
PPP2R4	protein phosphatase 2A, regulatory subunit B' (PR 53)	33	37	CTCCGGGTGGATGACCAAAATA	CTGAGGTGGCTGTTTACCTAA	CCGCTCCCTAAGGGTAACCTA	CGGATTCATCCTTACCCCTCAA
PPP2R5 A	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	29	41	CAGCGTATTCTGATATAGTAA	CTGTATCATGGCCATAGTATA	CATGGCCATAGTATATTGTAA	CATCAGTATAATATAATTTAA
PPP2R5 B	protein phosphatase 2, regulatory subunit B (B56), beta isoform	-50	211	CCGCATGATCTCAGTGAATAT	CCGGTTCATCTATGAATTCGA	CCGGGAGCGTGAGTACCTCAA	AAGCCAGGGTGGGAACCCCTAA
PPP2R5 C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	17	87	AACGAGCTGCTTTAAGTGAAA	CCCATTGGAACAAGTAAGAAA	CTGCTACTTCAGTAAGAATAA	CTGAAAATATTGGGAAGTATA
PPP2R5 E	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-17	191	CACCGGGATTGCAAATCTAAT	CCGGTGATATTGACAATAGGA	CTCGTTCTATATCTCATCACA	AAGGACTTCAATCCAAAGTTT
PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	-25	201	TAGCGATATAGCATACCCAAA	TCGGCCTGTATGGGACTGTAA	CACGCTTCAGTACTATCTAA	CTGACATATACTGGAATGTAA
PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)	-17	192	AAGGGTTTGGATAGGATCAAT	TAGGAGATTAGATAGATTCAA	TAGTTTATTGTGAGTACTCAA	CAGCCCCGAAAGAAATCATAA
PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	25	57	CAGGCTTTCATCACTTATTA	CCGAGGGTGTCTTATTTCTA	CTGGACCGAATTAATGAGCGA	CAGGAATAAGATCAGAGCCAT
PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I)	-17	193	ATCCTTTTAGTACAGCGAGTAA	GCCCATATAAATGGTAATGGA	TCCCTTTATAGTTTCTCTATA	GAGCCTCATGAAGCCAACTAA
PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	-17	194	CGGACAATCGACCGAAAGCAA	TCGCCAGATCACGAGGTCTA	CTGGACGAGCATCTCCAGAAA	CCAACTGGTGATGGAAGGTTA
PPP4R1	protein phosphatase 4, regulatory subunit 1	0	166	CAGGCGTTGTTAGATCAGTAT	TGGGAGTGCCTGAGTCTTTAA	AACTGGTAACTACAAATCTA	CAGCTAGTAAATGAGAATGATA
PPP5C	protein phosphatase 5, catalytic subunit	+2	24	CCCGTTGGCCCACTGCATCAA	CTCGTGGAAAACCACACTCAA	CAAGGCCCTTCTGGAAAGAGAA	CACGGAGGCCCTGTTCACTGAA
PPP6C	protein phosphatase 6, catalytic subunit	-8	182	CACAAATGAGTTTGTTCATAT	CAGCAGCAAAGTTGTTATTCA	CACCCCTGGACTCATTGAGAA	CTGGTTTGGTCAGATCCTGAA
PR48	protein phosphatase 2A 48 kDa regulatory subunit	-50	212	CACGTGTCTCTGTACAGTGAA	CTGGCCTGAGTGAGCAGTAA	TGCGTTTGTACGGAATGATAA	CACCTTCTTCAACATCGAGAA
PSPH	phosphoserine phosphatase	+2	25	CCGGCATAAAGGAGCTGGTAA	TGCCAATAGGCTGAAATCTA	TAGGCTGAAATTTACTTTAA	CAGAGACTCATAGCAGAGCAA
PSTPIP1	proline-serine-threonine phosphatase interacting protein 1	-8	183	ACCGGGCGCTCTACGATTATA	CCGGCTGACCATTCTCCGCAA	CAGCATAGACGCCGACATCGA	CAAGAAGGCCATGGAGTCCAA
PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	8	115	CCACGTTTATGTCAGCAATGAA	CCGGCTAGTGCTTCTGTGATA	CTCAGTGGTGCAAGATTTAAA	ACGAATAAACTTCTTCCGGAA
PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-17	195	AAGATTTATGATGCACTTATT	CAATTTGAGATTTCTACAGTAA	ACGGGAAGACAAGTTTATGTA	TCCGGCTTCTCTGAAAGGGAA
PTP4A1	protein tyrosine phosphatase type IVA, member 1	8	116	ACGCCTTAAACACAGCTCTATA	CCCTTTGATCACGTTAATCTA	CCGACCCGTTGCCATGATTTAA	CACGTTAATCTAAATCTAGAT
PTP4A2	protein tyrosine phosphatase type IVA, member 2	8	117	AACAGCATACCTGCTAAGCTA	CAGAGAATGCTGGTAGCTTAA	ATGCAACAATAGATTTCCATTA	AGGGACTGTGTTGCTTGTGAA
PTP4A3	protein tyrosine phosphatase type IVA, member 3	23	66	CACCCAAGTATTTGCACAATA	CCGCGGAGCCATCAACAGCAA	CACCTTCAATTGAGGACCTGAA	CCGGTGGAGGTGAGCTACAAA
PTPDC1	protein tyrosine phosphatase domain containing 1	17	88	CGGAATGTTGAGTGCCCTCAA	TACGTAGATACCAGAGGCCAA	AGGCTATACATAAGTATTGTA	AACAGAGGGTTTCAAAGCATA

PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	17	89	ACCACTTGCCATACTTCATTA	CACTGTTTAATTGGAATTGTA	CTGGTGAACFTCTTACAATAT	AAGTGAGTTCAAGAATCTTTA
PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	8	118	CACGGCGTACCTGGTCATCTA	CAGCCAAGAAATAGTTTGGTA	TACGCTTAACFTTCTATGCAT	TCCTATGTTAATTTCCACCAA
PTPN1	protein tyrosine phosphatase, non-receptor type 1	25	58	CACGTGGGTATTTAATAAGAA	CAGGCATGCCCGGTAGGTAA	CAGGAATAGGCATTTGCCTAA	ACGGACGTTGGTTCTGCACTA
PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	75	5	CAGAAGCACAGTACCGATTTA	CCGCTCATGACTATACGCTAA	GCGGTCCAGCATTATATGAA	GCCGCTCATGACTATACGCTA
PTPN12	protein tyrosine phosphatase, non-receptor type 12	50	18	AAGCTTAATGAGAAATATCA	TTGCAGGTTATCAGAGATCAA	CTGCTGTAGACATGTTAATA	GTGGATCATGATAACACTTCA
PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	83	4	CGGTCTATTCTTACTAAGAAA	TCCAGGTACATTAAGATGAA	TCGATGGATAAGTATCATATA	AACCTTTGGATCAGTGTCTAA
PTPN14	protein tyrosine phosphatase, non-receptor type 14	58	11	AAGGGCGATTACGATGTACAT	CGGTGTGGCATTTACAATATA	CTGGCCAAACTAGGTFCAAA	TCGGTGGAAAGCACAGGGCAA
PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	69	6	CAGGCAGACATCAGTCCACAT	CCCAATGACTGTAGCATTCAA	GTGGCCCTGGATCAAAGTTAA	CCGGGTGTAAGTCTAACGCCA
PTPN2	protein tyrosine phosphatase, non-receptor type 2	0	167	AACTGTATTACATACATGTCAA	CCGCTGTACTTGGAAATTCGA	TCGATTGAATTGTTACTGGATA	CACAAAGGAGTTACATCTTAA
PTPN21	protein tyrosine phosphatase, non-receptor type 21	8	119	GAGGAGACCATTCAA'TTCAA	GTGCATAGATTTCTATCTTAA	AAGCACCTCCTTACC GGCAA	CCCACCGCAGTTGCACATATA
PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	8	120	CCGGGTAGAACTATCCCTGAT	TGGGATGTACGTTGTTACCAA	CCCAGGTCCTTTTATCTACAA	TACGTAATGCCTCTAATGTAA
PTPN23	protein tyrosine phosphatase, non-receptor type 23	-25	202	AACCTTGTACAGTCCATGCAA	CCGCCAGATCCTTACGCTCAA	CTGCGTGAGCTTATCCAGAAA	CCGGCCCGACACTGTCCAGGAA
PTPN3	protein tyrosine phosphatase, non-receptor type 3	8	121	CAGGTTATTTCAGCGATAGTTA	CCGGGTATTATTG CAGGAAA	CCGAGAAATGCTGGTCACAAA	CCGCTCATTTGCTGACTTCAA
PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	67	8	CTCCGAACAAATAGTAAATA	TCCGTCATCAACACAAGCTAA	CTCCGTATCAACACAAGCTA	AGCACGTACCTTAGAACTCTA
PTPN5	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	0	168	ATCGAGGAGATGAACGAGAAA	CACCAACATCGAGGAGATGAA	CAGCTGAGGGAGAGTTCTCTA	CCCTCTGAGTTCTCATACATA
PTPN6	protein tyrosine phosphatase, non-receptor type 6	25	59	CCGGAACAAATGCGTCCCATATA	TAGGCCCTGATGAGAACGCTA	CCGCACCTCGTCCAACACAA	CCAGTTCATTGAAACCACTAA
PTPN7	protein tyrosine phosphatase, non-receptor type 7	-50	213	CAGGTCTACCTCAGGACTGAA	CTGGCATTTATGACAGACAAA	AAGCTCCAGAACAGTAACCAA	CACCCATGTGTCATAAGAGTA
PTPN9	protein tyrosine phosphatase, non-receptor type 9	0	169	ACCAAAC TAGAGTAAGCTAA	AGGAACGGAGCGAATAATATA	CCAGTAGCAATGTGTCTTAA	CAAGTGGACAGTTTCACTACAA
PTPNS1	protein tyrosine phosphatase, non-receptor type substrate 1	15	92	CGCCTGTAAATTACTGAGAAA	CTCGCTGTGGACGCTGTAAA	ACGCCGTAAATTTACTGAGAA	CCCGAGAAGATGCCAGAGAA
PTPNS1 L2	protein tyrosine phosphatase, non-receptor type substrate 1-like 2	0	170	CAGGGCCAAACCGAAATTTAA	CCGGAAATTAATCTACAATTT	AAGGTAACFTTCCAGAGTAA	AAGCTCCAGGTTTCCACCACAA
PTPRA	protein tyrosine phosphatase, receptor type, A	42	26	CAGAGTGATCATTTCCAGTTAA	CCGGAGAAATGGCAGACGACAA	CAGGTGTAGGGCGTACAGGTA	AGGCATTTACAATTTCCACAAA
PTPRB	protein tyrosine phosphatase, receptor type, B	8	122	CCCGGAGATGTGGATAACTAT	CCGGTCGACTTTATCAAGTTA	TCGGGTGTATCAGACTAATTA	CCAGTATTAGTGGAGACTTAA
PTPRC	protein tyrosine phosphatase, receptor type, C	8	123	AACCGTTATGTGACATTTCTT	AAGAA'TGCGATTTCCGTGTA	TCGATTATTTCCCTGTACAATA	CAACTTCTTTGTAATCGTTAT
PTPRD	protein tyrosine phosphatase, receptor type, D	-17	196	ACGGCCAGTCCCGAACAGTAA	CTGGGTGTCATTGAAGCAATA	CGCCTTGTTAATATTTATGCCA	ATGGCATTATCACCAAGTATA
PTPRE	protein tyrosine phosphatase, receptor type, E	25	60	ACCACGGGCAATTTAACTTTA	CCGAGTGATCCTTTCCATGAA	CAGTGAATTCACAACCTGAA	GACCATCGTCATGTTAACAAA
PTPRF	protein tyrosine phosphatase, receptor type, F	0	171	CAGCGCTATCTAGATAGGTAA	CATCGTGT'TTGC AAAGTTAA	CCGAGGACTATGAAACCACTA	CAGGAGCGGATCATCATGTAT
PTPRG	protein tyrosine phosphatase, receptor type, G	25	61	AGGGTGAAGTTAAGACCTTTA	TCGGTGAGCTCTATTCTAATA	TAGGCACTGTTCAATACTGTA	CAGACTCTAGGTTATACAATA
PTPRH	protein tyrosine phosphatase, receptor type, H	0	172	CCGGGACGTTGTACAATTTCA	CCGGGTCAATGTATACGTGTT	CAGGTACTGACATCACCTTAA	TCGAAGCACAGCACACACTAA
PTPRJ	protein tyrosine phosphatase, receptor type, J	33	38	TCCGAGTATGTC'TACCATTTA	TCGGGTAGAAATAACCACCAA	ACGAGTCGTATCTAACTATA	ACCCGTATCTTCTACAATCAA
PTPRK	protein tyrosine phosphatase, receptor type, K	25	62	CCGGGTTAAATGCTATAAATA	CTGGAGATTAGTGTATGATTA	CCGGCGAGTCAAGTTATCAAAA	CAGGATTTGTATCGCTGTGTA
PTPRM	protein tyrosine phosphatase, receptor type, M	8	124	AAGGGTCAAATGCTGCAATA	CACATCCGTAGTTATGCTAAA	CAGGATATTTCCGATTTACAA	CACCTTTGAATCAAACCTGACA
PTPRN	protein tyrosine phosphatase, receptor type, N	8	125	CACCC'TTCACTGAGTTACGAA	CAGGTCTGGCTTGGCACCCAA	CAGGAAGGTGAACAAGTGCTA	CTGGTGAAGTCTGAACTGGAA
PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	25	63	AAGGTGCTAAAGAGATTGATA	CAGCGCAGTTTAGCAGTTAAA	AGCGGACAGAATGATGCCAAA	ACGGATGTTGTGAGGAATCAT

PTPRR	protein tyrosine phosphatase, receptor type, R	17	90	CGCCACCAGATTGTCAATTCA	TCGCCCTCATTGGAAAGAAGAA	TAGGTTTATCACACAGCCTAA	AACCCCTTGTGTCTATACCAA
PTPRS	protein tyrosine phosphatase, receptor type, S	100	1	CACGGCATCAGGCGTGCACAA	CGCGTCTACTACACCATGGAA	CAGGACATTCTCTCTGCACAA	AAGAACAACCCGACAGTAAA
PTPRV	protein tyrosine phosphatase, receptor type, V	50	19	AACGCTGAAGCAGTATATCTA	AAGGTGGGCAGTCATGTCCAA	ATCCCTTTCATGGGCATAAA	ATGCCACAGAGTGGACCTATA
PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	42	27	ACGCTGGAATTTGGTAGTGAA	TAGCCATATACCAATACCTAA	CCGCCAAATTTATATCATTTAA	CAGACTAATTACACTGAGATA
RNGTT	RNA guanylyltransferase and 5'-phosphatase	33	39	CAGGGTTGTTAAGTTGTACTA	CGGGATTTCTATATGGACATA	TACCATCTGCAGTATTATAAA	ATGGATTTAAAGGCGGCTAA
SGPP1	sphingosine-1-phosphate phosphatase 1 skeletal muscle and kidney enriched inositol phosphatase	0	173	AGAGATTAACCTTCCATATAA	ATCGGTATATTACCTATGGAA	CTGCCATTACCTTTCATGTTA	TGCGTAATTACTAGACCAGAA
SKIP	phosphatase	-33	207	CAGCCAAGTGTCTGCCACATA	CTGGAATTAGCCGCTTAAATA	CACGTTGACTTGGAGCTGAA	ACGGTCGGAGTCCGGAAGAAA
SNAP23	synaptosomal-associated protein, 23kDa SH2 domain containing phosphatase	0	174	CTGGCAAGGCTTATAAGACAA	CAGGCCATTAAACATCATACA	TACCACATGAATTCAGATTTA	AAGAGGTTGTTACCTCAGTAA
SPAP1	anchor protein 1	42	28	TCAGAAGATGGCTTACCATAA	TTCAAATATAGTAAAGATAAA	CAGGACCTGATGGCTATAGAA	ATGCCGGCAAATATTACTGTA
TA-PP2C	T-cell activation protein phosphatase 2C	17	91	AAAGGGATGGTACAAGTCTAA	CACAAATTGTACGTAATGATA	CCCTCAAAGCCTAGAAATTTA	CTCAATTCTCAGGGACTTTAA
TENC1	tensin like C1 domain containing phosphatase	-8	184	ACAGCACGTGGTCGTACTATA	CAAGGTGGCGACGCACAGAAA	ACGGCCATCCTAGATGACGAA	CTCGGTCTCTGTGACTACAA
TPTE	transmembrane phosphatase with tensin homology	25	64	CAGATTGGCAACCAAGACTAA	CTGAAATATGTTCAACTGCAA	TCGGTACTTGATAACATTACA	CAGACTTGTGTTATTCTAGCA
TPTE2	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	25	65	ACCTGGAGAACTGATAATAAA	CTGATAATAAATTTGTGGTTTA	ACAGGCAAATTTCAGAAACAA	AATGATTGAAATAGAGCTATA