

WT_dpgA	1	ATGTCGATCCTTAACGACTACAAACGTAAGACAGAAGGCTCAGTATTGTGGGCACAACGC
OPT_dpgA	1	ATGTCATCCTGAACGACTACAAAGAAAGACTGAGGGTCTGTCTTCGGGGTCAACGCT
		M S I L N D Y K R K T E G S V F W A Q R
WT_dpgA	61	GCTCGGTCCGGTCATGCCCGACGGCGTAACCGCAGACACCCGAGTATTGACCACACACGGC
OPT_dpgA	61	GCTCGTCTGTGTCATGCCGTGATGGAGTTACTGCCGATACAGAGTCTTCGATCCACACGGT
		A R S V M P D G V T A D T R V F D P H G
WT_dpgA	121	CTTTTCATTAGTGACGCCCAAGGCGTTTCAAGACCGATGTAGACGGCAATGTGTACCTA
OPT_dpgA	121	TTGTTTCATCTCTGACGCTCAAGGAGTTTCAAGACGACGTCGATGGTAACTTTTACTTG
		L F I S D A Q G V H K T D V D G N V Y L
WT_dpgA	181	GACTTTTTCGGGGCACGGAGCCCTCGTACTAGGTCATGCCCATCCTCCGGTTAACGCA
OPT_dpgA	181	GACTTCTTCGGTGGTCACGGTGTCTGCTTGGGTCATGGTTCATCCTCCGTGTCAACGCC
		D F F G G H G A L V L G H G H P R V N A
WT_dpgA	241	GCATCGCCGAAGCTCTTAGCCATGGCGTCCAGTACCGGCCAGCCACCAGCTGGAAGTG
OPT_dpgA	241	GCTATTCGTCGAGCTCTGTCACCGGTGTCAGTACCGTGCCTTCTCATCCTCTGGAAGGT
		A I A E A L S H G V Q Y A A S H P L E V
WT_dpgA	301	CGATGGGCAAGACGCATCGTGCCGCAATTCCCTCAATTCGTAAACGCTTCACCGGA
OPT_dpgA	301	AGATGGGCGAGAGAAATCGTTGCTGCTTTCCCTTCCATCCGTAAGTTGAGATTCACTGGA
		R W A E R I V A A F P S I R K L R F T G
WT_dpgA	361	AGCGGCACCGAAACTACGCTGCTGGCTTTGCGGTAGCTCGTGCCTTCACGGGCCCGCC
OPT_dpgA	361	TCTGGTACTGAGACTACCCTGTTGGCCCTTGAAGTGTCTAGAGCTTTCACCTGGTAGACGT
		S G T E T T L L A L R V A R A F T G R R
WT_dpgA	421	ATGATACTGCGCATCGCCACTCATTATCATGGCTGGCACGATTTTCCCGAFTCGTTAT
OPT_dpgA	421	ATGATTTTGAATAATCGCTACTCATTACCACGGTGGCACGATTTTCCCGCCTCGTTAC
		M I L R I A T H Y H G W H D F S A S G Y
WT_dpgA	481	AACAGCCATTTCGATGGCCAGCCGGCCGGGGCTGCTACCTGAAATTCGAAGAACTACT
OPT_dpgA	481	AACCTCCACTTCGACGGTCAGCCTGCTCCAGGTGTCTTGCAGAAATCGCCAGAACTACT
		N S H F D G Q P A P G V L P E I A K N T
WT_dpgA	541	TTGCTGATTCCGCTCTGATGATATGAAGGCATGCGAGAAAGTTTTCGGCAGCATGGCAGC
OPT_dpgA	541	CTGTTGATTCCGCTCTGACGATCGAGGGTATGAGAGAGTTTTCGGTCAACATGGATCT
		L L I R P D D I E G M R E V F A Q H G S
WT_dpgA	601	GACATTCGAGCATTTCATGTCGAACCTGTGGGTTCGCACCTTGGCGTCACTCCAGTGAGC
OPT_dpgA	601	GACATCGCTGCCCTTCATCGCTGAACCAAGTTGGATTCACCTTCGGTGTACTCCAGTCTCT
		D I A A F I A E P V G S H F G V T P V S
WT_dpgA	661	GATAGCTTCTACCGAAGGCGAGAATTGGCTCGGCAATACGGTGCCTGTTCATCCTA
OPT_dpgA	661	GACTCCTTCTGAGAGAGGGTGTGAATTGGCTAGACAGTACGGTGTCTGTTCATCCTT
		D S F L R E G A E L A R Q Y G A L F I L
WT_dpgA	721	GACGAAAGTAATTTCTGGTTTCCGGTCCGGAAATCAGGAATGCAGGGCTCCTTGATGTT
OPT_dpgA	721	GACGAGGTATCTCCGGAATCCGTTGTCCGTTAACTATGGTATGCAGGGCTTGTCTGAGC
		D E V I S G F R V G N H G M Q A L L D V
WT_dpgA	781	CAGCCGGATCTCACCTGCTGGCTAAGGCCAGCGCAGGCGGGCTTCCCGCTGGCATCTTG
OPT_dpgA	781	CAGCCAGATTTGACTTGTGGCTAAGGCCCTCTGCCGAGGAACTTCCAGGAGGTATCTTG
		Q P D L T C L A K A S A G G L P G G I L

WT_dpgA	841	GGCGGGCGCGGAAGATGTCATGGGAGTTCCTCAGCCGAGGCAGTGA	TCCCAAGGTACTACAT
OPT_dpgA	841	GGAGGTAGAGAAGATGTCATGGGAGTCTTGTC	CCGTGGTTCCGACCGTAAAGTCTTGCAT
		G G R E D V M G V L S R G S D R K V L H	
WT_dpgA	901	CAGGGTACTTTTACC	CGCAACCCGATTACTTGC
OPT_dpgA	901	CAAGGTACTTTTACC	CGGAAATCCTATCACCGCCGCTGCTGCCATCGTGC
		Q G T F T G N P I T A A A A I A A I D T	
WT_dpgA	961	ATCCTTGAAGACGATGTTTTCGCGAAGATCAATGACCTTGGTCAATTCGCCAGGAGGCG	
OPT_dpgA	961	ATCTTGGAGGATGACGTTTTCGCTAAGATTAACGACTTGGTCAATTCGCCAGAGAAGCT	
		I L E D D V C A K I N D L G Q F A R E A	
WT_dpgA	1021	ATGAATCACTAATTGTC	CCGAAGGGA
OPT_dpgA	1021	ATGAATCACTTGTTCGCTAGAAAGGGTCTGA	ACTGGTTGGCTTACGGTACATTCTCCGGA
		M N H L F A R K G L N W L A Y G R F S G	
WT_dpgA	1081	TTCCACCTGATGCCGGGCTGCCACCTAA	TACAACCGACACCGGCTCCATAACCCGAGCT
OPT_dpgA	1081	TTCCATCTGATGCCTGGTTTGCCACCTAACACCAC	TGATACCGGTTCCATCACCTCGTGC
		F H L M P G L P P N T T D T G S I T R A	
WT_dpgA	1141	GAAGTCGCAACGCCCGATGTGAAGATGATCGCAGCAATGCCCATGGCA	TTGATATTGGAA
OPT_dpgA	1141	GAAGTCGCTAGACCTGACGTTAAGATGATCGCCGCTATGAGAA	TGGCCTTGATCCTGGAG
		E V A R P D V K M I A A M R M A L I L E	
WT_dpgA	1201	GGTGTGGATATCGGCGGGCGGGTCAAGTTTTCCTGTCAGCACGCA	TGAACCCGAACAT
OPT_dpgA	1201	GGTGTGATCATTGGTGGTAGAGGTTCCGTCTTCCTGTCCGCC	CAACACGAACCGTGA
		G V D I G G R G S V F L S A Q H E R E H	
WT_dpgA	1261	GTGAGCATCTGGTGACAACCTTTGATCGCGTATTAGACCGCC	TGGCGGACGAAACCTG
OPT_dpgA	1261	GTGGAACACCTTGTCAACACTTTTCGATAGAGTCTGGATCGTT	TGGCCGATGAGAACCTG
		V E H L V T T F D R V L D R L A D E N L	
WT_dpgA	1321	TTGTCTTGGCAACCAACTAATTTGTCTGGAAACCAATCATGA	-----
OPT_dpgA	1321	CTGTCTTGGCAACCAACTAACTTTGTCTGGTAACCAATCCAT	CACCATCACCATCACTGC
		L S W Q P T N L S G N Q S H H H H H H C	
WT_dpgA	1362	---	
OPT_dpgA	1381	TAA	
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