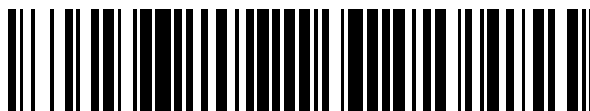


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ES 2 623 545 T3

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DESCRIPCIÓN

Empleo de polipéptidos/ácidos nucleicos de arroz para mejora de la planta

Antecedentes de la invención

5 Es de gran interés identificar polipéptidos de plantas que contribuyen a propiedades deseadas, p. ej. altos rendimientos o mayor tolerancia a agresiones ambientales. Cuando se introducen sus genes codificantes en una planta anfitriona, dichos polipéptidos imparten los rasgos deseados a la planta anfitriona.

10 El nº de entrada Q2R3X6 de la base de datos UniProt es una proteína presente en el genoma del arroz para la cual se conocen plantas transgénicas. Las solicitudes de patente de EE.UU. 2007/020621, 2007/118921 y 2007/039076 describen la producción de plantas transgénicas con secuencias nucleotídicas que codifican una proteína que es idéntica a la SEQ. ID. nº 103. La solicitud de patente de EE.UU. 2004/123343 describe unas secuencias de proteína y su correspondiente ácido nucleico, cuya proteína es 94% idéntica a la SEQ. ID. nº 103. Se han producido plantas transgénicas.

Compendio

15 Esta invención se basa en el descubrimiento de un número de polipéptidos del arroz que contribuyen a diversas propiedades importantes en el arroz, p. ej., peso/tamaño de la semilla y tamaño/densidad de la panícula, así como sus polinucleótidos codificantes.

20 En la presente memoria se describe un método de producción de una planta transgénica mediante la transformación de una planta anfitriona con un montaje de ADN recombinado que expresa en una célula vegetal un polipéptido que contiene una secuencia de aminoácidos al menos 80% idéntica (p. ej., 85%, 90%, 95 %, 98%, 99% o 100%) a una secuencia de aminoácidos seleccionada de las SEQ ID nºs: 1-49, 99-114 y 149. El montaje de ADN recombinado puede incluir una secuencia de nucleótidos seleccionada de las SEQ ID nºs: 50 -98, 115-148, 150 y 151, y una secuencia activadora funcional en una célula vegetal. La secuencia activadora está operativamente unida a la secuencia nucleotídica.

25 La planta transgénica resultante presenta una o más de las siguientes propiedades relativas a la planta anfitriona: (a) mejor tolerancia a una agresión ambiental, p. ej., sequía, frío, calor, sal, baja intensidad de fertilizantes, enfermedad vegetal, un herbicida, un estado osmótico extremo, un patógeno o plaga, (b) elevado crecimiento de las células vegetales, (c) aumento o disminución de la producción de galactomanano, lignina, celulosa, flavonoides o un regulador de crecimiento de las plantas, (d) aumento de los rendimientos por modificación de la fotosíntesis, utilización y/o fijación de hidratos de carbono, utilización y/o fijación de nitrógeno, utilización y/o fijación de fósforo, utilización y/o fijación de minerales, (e) aumento de los rendimientos de aceite de semillas, almidón y/o proteínas, y (f) aumento de la tasa de recombinación homóloga, (g) aumento del tamaño o peso de las semillas, (h) aumento de la longitud o densidad de la panícula, (i) aumento de la eficiencia de la floración, polinización o fertilización y (j) elevada tasa de desarrollo y maduración de las semillas.

35 La presente invención se refiere a un procedimiento para aumentar el tamaño el tamaño de la semilla en una planta, transformando una planta anfitriona o células de la planta anfitriona con un montaje de ADN recombinado que contiene una secuencia activadora operativamente unida a un polinucleótido que codifica un polipéptido que tiene una secuencia de aminoácidos al menos 80% idéntica con la secuencia SEQ. ID. nº: 103, siendo funcional la secuencia activadora en una célula de la planta anfitriona o en las células de la planta anfitriona.

40 Una planta transgénica es una planta cuyo genoma ha sido alterado por incorporación de material genético extraño o copias adicionales de material genético natural, p. ej., por transformación o recombinación.

Los detalles de uno o más aspectos se exponen en la siguiente descripción.

Descripción detallada

45 Se describen en esta memoria 66 polipéptidos aislados de arroz (SEQ ID nºs: 1-49, 99-114 y 149), y sus variantes funcionales, es decir, un polipéptido que tiene una identidad de secuencia de al menos 65% (p. ej., 70%, 75% , 80%, 85%, 90%, 95%, 98% o 99%) con una de las SEQ ID nºs: 1-49, 99-114 y 149 y que poseen la misma función que ese polipéptido.

50 La expresión "polipéptido aislado" se emplea en esta memoria se refiere a un polipéptido sustancialmente exento de moléculas asociadas de forma natural, es decir, las moléculas asociadas de forma natural que constituyen al menos el 20% en peso seco de un preparado que contiene el polipéptido. La pureza puede medirse por cualquier método apropiado, p. ej., cromatografía en columna, electroforesis en gel de poliácridamida y HPLC.

La identidad de secuencias de dos secuencias de aminoácidos puede determinarse usando el algoritmo descrito en Karlin y Altschul, *Proc. Natl. Acad. Sci. USA* 87: 2264-2268, 1990, modificado como se describe en Karlin y Altschul, *Proc. Natl. Acad. Sci. USA* 5873-5877, 1993. Dicho algoritmo está incorporado en los programas NBLAST y

XBLAST de Altschul *et al.*, *J. Mol. Biol.* 215:403-410, 1990. Se realizan búsquedas de nucleótidos BLAST con el programa NBLAST, puntuación = 100, longitud de palabra = 12, para obtener secuencias de nucleótidos homólogas a una molécula de ácido nucleico de la invención. Se realizan búsquedas de proteínas BLAST con el programa XBLAST, puntuación = 50, longitud de palabra = 3, para obtener secuencias de aminoácidos homólogas a un polipéptido de referencia. Para obtener alineaciones con huecos para comparación, se utiliza Gapped BLAST como se describe en Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402, 1997. Cuando se utilizan los programas BLAST y Gapped BLAST, se emplean los parámetros por defecto de los respectivos programas (p. ej., XBLAST y NBLAST). Véase www.ncbi.nlm.nih.gov.

Las Tablas 1 y 2 a continuación se da una lista de los números de entrada a GenBank, secuencias de aminoácidos y secuencias de nucleótidos codificantes de los 49 polipéptidos del arroz mencionados anteriormente. También se da una lista en la Tabla 1 con las funciones de estos polipéptidos.

Tabla 1. Polipéptidos de arroz que intervienen en el rendimiento de las semilla o la formación de panículas

Proteínas	Fenotipo	Linea de corte	Locus del gen	GOI	Proteína	ADNc	nº de entrada en GenBank
1	alto rendimiento de semillas	M0015163	LOC_Os03g572 90	cullina	SEQ ID nº: 1	SEQ ID nº: 50	AAT75245
2	alto rendimiento de semillas; tolerante a la sequía	M0019261	LOC_OS_01g61 420	proteína 5 del dedo anular	SEQ ID nº: 2	SEQ ID nº: 51	BAD73632
3	alto rendimiento de semillas; tolerante a la sequía		LOC_Os01g614 30	dedo de cinc unk HIT	SEQ ID nº: 3	SEQ ID nº: 52	NP_19461 1.2
4	rendimiento de semillas	M0025978	LOC_Os01g527 90	citocromo P450	SEQ ID nº: 4	SEQ ID nº: 53	NP_91675 4
5			LOC_0s01g5280 0	citocromo P450	SEQ ID nº: 5	SEQ ID nº: 54	BAD86930
6			LOC_Os01g528 10	PP2C	SEQ ID nº: 6	SEQ ID nº: 55	NP_56714 5 (ara)
7			LOC_Os01g528 30	unk	SEQ ID nº: 7	SEQ ID nº: 56	NP_91675 7 (ara)
8	panícula larga	M0038751	LOC_Os03g641 50	familia de salida MatE	SEQ ID nº: 8	SEQ ID nº: 57	XP_47049 7
9	panícula larga, semilla grande	M0046723	LOC_Os04g581 80	Gbeta con dominio WD	SEQ ID nº: 9	SEQ ID nº: 58	XP_47435 8
10			LOC_Os04g581 90	dof28	SEQ ID nº: 10	SEQ ID nº: 59	XP_47435 9
11	semilla grande	M0022658	LOC_Os02g289 70		SEQ ID nº: 11	SEQ ID nº: 60	NP_00104 6872.1
12	semilla grande	M0024255	LOC_Os07g101 10		SEQ ID nº: 12	SEQ ID nº: 61	NP_00104 4695.1
13	semilla grande	M0034189	LOC_Os04g394 30 ??	p450, dwarf4	SEQ ID nº: 13	SEQ ID nº: 62	NP_00105 3047.1

ES 2 623 545 T3

Proteínas	Fenotipo	Línea de corte	Locus del gen	GOI	Proteína	ADNc	nº de entrada en GenBank
14	semilla grande	M0034642-1	LOC_Os10g428 20	DUF221/ERD	SEQ ID nº: 14	SEQ ID nº: 63	NP_001065504.1
15	semilla grande	M0039539	LOC_Os04g556 90	unk	SEQ ID nº: 15	SEQ ID nº: 64	NP_001054091.1
16	semilla grande	M0040296	LOC_Os07g148 90	unk	SEQ ID nº: 16	SEQ ID nº: 65	NP_001059304.1
17			LOC_Os07g149 10	unk	SEQ ID nº: 17	SEQ ID nº: 66	NP_001059305.1
18	panícula densa	M0033394	LOC_Os02g562 50	GATA supuesta	SEQ ID nº: 18	SEQ ID nº: 67	CT828966, no predicho, NP_001048448.1
19	panícula densa	M0038155	LOC_Os02g325 04	unk	SEQ ID nº: 19	SEQ ID nº: 68	NP_001046996.1
20	panícula densa	M0039100	LOC_Os06g508 18	unk	SEQ ID nº: 20	SEQ ID nº: 69	NP_001058607.1
21			LOC_Os06g508 30	TF bzip supuesta	SEQ ID nº: 21	SEQ ID nº: 70	NP_001058608.1
22	panícula densa	M0039314	LOC_Os08g419 50	MADS, MADS7, MADS45	SEQ ID nº: 22	SEQ ID nº: 71	NP_001062335.1
23			LOC_Os08g419 60	Mads AGL72 imprevista	SEQ ID nº: 23	SEQ ID nº: 72	NP_001062336.1
24	panícula densa	M0039419	LOC_Os02g474 30	unk imprevista, peptidasa M20,	SEQ ID nº: 24	SEQ ID nº: 73	NP_001058304.1
25			LOC_Os02g474 40	sintaxina supuesta	SEQ ID nº: 25	SEQ ID nº: 74	NP_001047853.1
26	panícula densa	M0039485	LOC_Os12g152 22	unk	SEQ ID nº: 26	SEQ ID nº: 75	NP_001066501.1
27	panícula densa	M0043153	LOC_Os06g462 40	repetición de ARM	SEQ ID nº: 27	SEQ ID nº: 76	
28			LOC_Os06g462 50	unk, precursor proteophosphoglycan	SEQ ID nº: 28	SEQ ID nº: 77	NP_001058344.1

Proteínas	Fenotipo	Línea de corte	Locus del gen	GOI	Proteína	ADNc	nº de entrada en GenBank
29	panícula densa	M0050559	LOC_Os12g437 20	supuesto RXW8, DUF221, ERD	SEQ ID nº: 29	SEQ ID nº: 78	NP_001067352.1
30			LOC_Os12g437 30	Fbox imprevista, similar a ciclina	SEQ ID nº: 30	SEQ ID nº: 79	NP_001052038.1
31			LOC_Os12g437 40	deshidrogenasa de cadena corta	SEQ ID nº: 31	SEQ ID nº: 80	BAF30371.1
32	grano grande	M0027918	LOC_Os10g017 00	HSR201 unk expresada	SEQ ID nº: 32	SEQ ID nº: 81	
33	grano grande	M0028590-1	LOC_Os03g554 30	2 proteínas en 2 marcos?	SEQ ID nº: 33	SEQ ID nº: 82	
34				2 proteínas en 2 marcos	SEQ ID nº: 34	SEQ ID nº: 83	NP_001051361.1
35			LOC_Os03g554 50	unk	SEQ ID nº: 35	SEQ ID nº: 84	NP_001051362.1
36	grano grande	M0063563	LOC_Os08g329 30	unk	SEQ ID nº: 36	SEQ ID nº: 85	NP_001061837.1
37	grano grande	M0063736	LOC_Os08g311 30	unk integral mb prot DUF6 familia MtN21 ara similar	SEQ ID nº: 37	SEQ ID nº: 86	NP_001061761.1
38			LOC_Os08g311 20	unk parcial	SEQ ID nº: 38	SEQ ID nº: 87	NP_001066824.1
39	grano grande	M0063992	LOC_Os04g478 90	clase SHAQKYF, región de unión a ADN, similar a MYB	SEQ ID nº: 39	SEQ ID nº: 88	NP_001053582.1
40			LOC_Os04g479 00		SEQ ID nº: 40	SEQ ID nº: 89	
41	grano grande	M0064512	LOC_Os12g019 16	enlace DS ARN	SEQ ID nº: 41	SEQ ID nº: 90	NP_001065960.1

Proteínas	Fenotipo	Línea de corte	Locus del gen	GOI	Proteína	ADNc	nº de entrada en GenBank
42			LOC_Os12g019 22	Similar a WD, similar a raptor	SEQ ID nº: 42	SEQ ID nº: 91	NP_00106 5961.1
43	panícula larga	M0066298-1	LOC_Os10g401 40	proteína asociada a VAMP, proteína de esperma	SEQ ID nº: 43	SEQ ID nº: 92	NP_00106 5309.1
44	grano grande	M0067806	LOC_Os08g015 80	proteína de la familia de proteínas con resistencia a enfermedades	SEQ ID nº: 44	SEQ ID nº: 93	NP_00106 0.794,1
45			LOC_Os08g015 90	unk	SEQ ID nº: 45	SEQ ID nº: 94	NP_00106 0795.1
46	grano grande	M0068164	LOC_Os03g526 40	familia de proteína 95 unk	SEQ ID nº: 46	SEQ ID nº: 95	NP_00105 1193.1
47			LOC_Os03g526 50	Similar a syntaxina 111	SEQ ID nº: 47	SEQ ID nº: 96	NP_00105 1194.1
48	grano grande	M0068730	LOC_Os03g083 30	proteínas que contienen dominio ZIM	SEQ ID nº: 48	SEQ ID nº: 97	NP_00104 9168.1
49	grano grande	M0069991	LOC_Os03g149 80	CTLH, terminal C para proteínas que contienen el dominio con motivo Lish, TOPLESS	SEQ ID nº: 49	SEQ ID nº: 98	NP_00104 9587.1
50	grandes granos; tolerante a la sequía	BASF 163 (M0028590 - 2)	LOC_Os03g554 60		SEQ ID nº: 99	SEQ ID nº: 115	
51	granos grandes	BASF 162-1 (M0066298 - 2)	LOC_Os03g180 00	fosfolipasa C específica sitide fosfoíno	SEQ ID nº: 100	SEQ ID nº: 116	

Proteínas	Fenotipo	Línea de corte	Locus del gen	GOI	Proteína	ADNc	nº de entrada en GenBank
52	granos grandes	BASF 162-2 (M0066298 - 3)	LOC_Os03g180 10	fosfolipasa C específica sitide fosfoino	SEQ ID nº: 101	SEQ ID nº: 117	
53	granos grandes	BASF 162-3 (M0066298 - 4)	LOC_Os03g180 20	proteína similar a rodanese	SEQ ID nº: 102	SEQ ID nº: 118	
54	granos grandes	BASF 148-1 (M0037341 - 1)	LOC_Os03g304 30		SEQ ID nº: 103	SEQ ID nº: 119	
55	granos grandes	BASF 148-2 (M0037341 - 2)	LOC_Os03g304 84	proteína con dedos de zinc ZOS11-03-C2H2	SEQ ID nº: 104	SEQ ID nº: 120	
56	granos grandes	BASF 148-3 (M0037341 - 3)	LOC_Os03g304 10	proteínas que contienen el dominio de la familia ThiF	SEQ ID nº: 105	SEQ ID nº: 121	
57	granos grandes; planta más alta; panículas largas	BASF 7-1 (M0034642 - 2)	LOC_Os03g488 20		SEQ ID nº: 106	SEQ ID nº: 122	
58	granos grandes; planta más alta; panículas largas	BASF 7-2 (M0037341 - 3)	LOC_Os03g488 30		SEQ ID nº: 107	SEQ ID nº: 123	
59	granos grandes	BASF142	LOC_Os03g129 30		SEQ ID nº: 108	SEQ ID nº: 124	
60	granos grandes	BASF 143	LOC_Os03g129 40	proteínas que contienen el dominio de unión a hélice-bucle-hélice de ADN	SEQ ID nº: 109	SEQ ID nº: 125	
61	alto rendimiento de semillas; tolerante a la sequía	BASF 10-1	LOC_Os08g036 00	transportador de iones metálicos	SEQ ID nº: 110	SEQ ID nº: 126	
62	alto rendimiento de semillas; tolerante a la sequía	BASF 10-2	LOC_Os08g036 10	LSD1	SEQ ID nº: 111	SEQ ID nº: 127	

Proteínas	Fenotipo	Línea de corte	Locus del gen	GOI	Proteína	ADNc	nº de entrada en GenBank
63	granos grandes	BASF 12	LOC_Os04g394 20	6-fosfofructonasa 2	SEQ ID nº: 112	SEQ ID nº: 128	
64	alto rendimiento de semillas	BASF 165-1	LOC_Os10g335 40	alcohol oxidasa	SEQ ID nº: 113	SEQ ID nº: 129	
65	alto rendimiento de semillas	BASF 165-2	LOC_Os10g335 50	oxidoreductasa	SEQ ID nº: 114	SEQ ID nº: 130	
66	alto rendimiento de semillas, granos grandes		LOC_Os08g419 40	estructura 1 supuesta de glume (SPL16)	SEQ ID nº: 149	SEQ ID nº: 150	

unk: desconocida

Tabla 2. Secuencias de aminoácidos y nucleótidos de polipéptidos del arroz

SEQ ID NO:1	MKKAKFPSSSSSSSSAAAPGVTEKNGLHVDPTAAAARTGGRNTEEDAEMVLADQEELAAPSASAPAGVAANLFRKKAT LPQPSAARKPLRIKIGQPKLPNTFEEDTWAALKDAITAI FLKQKLSCDVEKLYQAAGDLCLHKLGANLYERIKKECEVH ISAKISALVGQSPDLVVFLSLVQRTWQDFCDQMLIIRGIALLLDVKYVKNVANICSVWDMGLKLFKHLKLSPEIEHKT VTGLRLIESERLGEAIDRTLSSHLLKMFTALGMYSESFEKPFLECTSEFYATEGVKYLQOSDIPDYLKHVETRLQEEH ERCILYLEANTRKPLITATEKQLLRHTSAILEKGFMTLMLEANRVKDLRMYTLFQRVDAIELLKQALSSYIRGTGGGI IMDEEKDKELVPFLLEFKASLDRIEESFAKNEAFSNTIKESFEHLINLRQISSPFFQQRNPAELIAKFLDEKLRAGN KGTSEEELEGILDKVLVLFRIQKDVFEAFYKDLAKRLLLGKSASIDAEKSMITKLKTECGSQFTNKLEGMFKDIEL SKEINESFKQSSQARTKLPSGIEMSVHVLTTGYWPTYPPMDVKLPHELVNYQDIFKEFYLSKYSGRRLMWQNSLGHCVL KAEPKGGKELAVSLFQSVVLMFLNDAQKLSFLDIKESTGIEDKELRRTLQSLACGKVRVLQKMPKGRDVEDKDEFEVFN EEFSAPLYRIKVNAIQMKETVEENTSTTERVFQDRQYQVDAIVRIMKTRKTLSTHTLLITELFQQLKFPKPSDIKKRI ESLIDREYLERDRSNPQIYNLA
SEQ ID NO:2	MDADEAAGSSRRMDNLNLYLGLPRAPRRRDLGSDLALSTPMPSSPSSSAASVDAPPPPELSPHPYSPSHADLSPPLQ EVSGLYNPDDPPASETHLPPYAPPPAPVVELPDDLEFGLHPPPLVRASELLGWEDRPSSSTASSSFLPDTAARYWRL LEQTGSRWLRARRFRSDLPPLSSEAYPAGRDAAVPVLQHEPMNDTVEHNKVAADGAEVGASEESEEQGRSAATFECNI CFDMASEPVTSCGHLFCWPCLYQWLVNYSNHKECPVCKGEVTEANITPIYGRGNSCLDAEKAVEGGKQTGPTIIPRPH GNRLSEFRQQPHHLRPISRRLGEAGLLSSWRRLLDQQIMNTASRFEGPPESAVQEMVDTAHAQHTSRLSRLASRMAR RLLREADNPNPPDGGSTSPDSGLIRNNASDPSRNGPSSLLPDGIDWLRGLTLLGYEDTERFASAMSDFRITGSPQYGA SASSNPNPNLESTFDRTHVVAAPSADQASNSSTA AVIQGDAGISESAGEPSNAGSSRSLRRRRGRSSALGSLDADGGGLQ RNKRRRIN
SEQ ID NO:3	MCPRATQTCEICEKVSKYKCPSCLVFPCSLGCFKIHKETPCAKPSDPSSTEEKPAASPAKEVPVKRPEEANDVVEKTQ QKASAAAPAKEIPVARPIIVEEEKYILEKTQFEAIASSSEIREALKDEPLQKLIYSIDSSSNPLQELDEAMGIEAFREF TDKILSNISKSNDQ
SEQ ID NO:4	MLGEAASPSWLAGAGAAVALLWLCAWTLQWAWWTPRRRLERALLRAQGLRGTRYRLFIGDVAENGRNLNREASRPLPLGSH DVVPRVMPFFCNVLKEHGKLSFVWTGPKPFVIRDPDLAREILSNKSGNFAKQTTAGIAKFFVGGVVTYEGEKWAKHRR ILNPAFHQEKIKRMLPVFLACCTKMITRWVNSMSSEGISLQVWDEFQNLTDGDISRTAFGSSYQEGWRIFQLQEEQAK RVLKAFQRI FIPGYWYLPDENRRRIEIDQEI RTILRGIIVKRDKA VRN GEGSNDLLGLLVESNMRSNEKEDVGM SI EDMIEECKLFYAAGSETTSMMLTWTLLLSMHPEWQEQA REEVMHFGRTTPDHGDL SRLKIVTMI LHEVLR LYPVVF LQRTTHKEIELGGIKYPEGVNFTLPVLSIHHDPSIWGQDAIKFNPERFANGVSKATKFQTAFSSFAWGPRI CLGQSFAI LEAKMALATILQSFSELSPSYTHAPHTVLTLPQPYGSPKLLKL
SEQ ID NO:5	MAKDHVKIVLKAYILGPIKYLISLESYHNCGLVVTMILHEVIRLYPSGIFLQRTTRKEIELGGIKYPEGANFTLPVP SIHHDPSIWGGDASEFNLERFANGVSKATKFRTAFFMFGWGSFLPWTELCNAGSQD GARHHPPELLL
SEQ ID NO:6	MCCSAVAVMKWEALLPNDTFLIVASSDGVFEKVTMQDVCMLMYVKLGVKQELGSFALTQQNLADYVVDLSL
SEQ ID NO:7	MSSSDQNPSPTPASGTGTSVPPPGRATTVSSQLLDMGAQAVQALKPVRQMKQHACS FALYAHDL SRQVEVHHFVSR LNQ DVLQCAVYDSKPSARLIGVEYIVSDAIFESLPPEEQKLWHSHAYEVKAGLWTDVGVPPELQSSSEMARMKTYGKLWCT WQVDRGDALPLGAPALMVSPQAVEPGRVRAELVHGRDERYKIDSSAQGLK GARVEMDEPEWINPNADYWR LHGKGFAID VTATEMKRHAPFP*
SEQ ID NO:8	MTPPPPPSPHERKTWAESEVASEFRAQRGIAFPLIAMNLTFWFAKLVTTAFLGRGLDLQLAAGTLGFSFANVTGFAVL TG LCAAMDPI CGAHGASNGKLLRKTLMATILLGASIPIAFLWLHVDVLLRFGQQADMSSNARSYVVCLLPDLAVTSF VNPLKSYLSAQGVTLPTLFASALALALHVPLTMWMARTRGIQGVATAVWVSDLAVAVMLAGYVLVSEERRKAGGGGGWV EQTRGEWVRLRLAVPSCINTCLEWWCYEILVLLTGRLPDARRTVAVMAVTLNFDYLLFAGMLSLSVSASVRVSNELGA GEAWAARRAGMVSIVGGAVGGVGGVAMVAARRAWSIYSSDAGVREGVGRAMEVMAVLEVNVNPLNVCGGIVRG TAR P AVGMYAVVAGFYVLALPLGVALAFKARLGIQGLLGLFVGAAASLAVLLTFIARMDWPAAEQKARTRTTATVAQFHQHD EVVQP

SEQ ID NO:9	MPEAAAAAAGHMDPVGDEAAERREMEKEEEEEEEDEEFYESLDRILSSSSCSSTASDDDDQQRHRRRRHHPQPQQL SSSATFSAYEWISEPTSVERRRVLRLRLGLANDSEPLPHPSPRVSSSSSPRPTSPSPSSSPRPAPVVAEEPRSS GHGKPLARNPSGGAEQCRI RNLDGTEFEVGEVHDEVVREVGTGRQLTFEEFELCIGRSPIVQELMRRATTAASSSTS DHAAPASKPRRKPGGWLGRIRHLAGSVAYGRSSSTDERDKEKEKEKEREARRLSATDDSLDNGSRNAGRVRVRQYK ACKELTGLFMTQELAAHSGSIWCINFSLDGRYLASAGEDRVHVVVESEGERKGELLGEGTVARENGGGCSPFLAAVGN GSPELATLSLSCADGGFVEKKRRPRMQSSRSKSVGSDHLVVECVFGFRDKPVCSSLGHAADVLDLSWSKSQYLLSSSMD KTVKLDWITTSTCLKTFSTDYVTCIQFNPVDDNFFISGSLDEKVRINWVHDKIEDWNDLHEMVTAAACYS PDGQVALV GSHKGSCHLFDTTTEKKLQYKSQIELRIRKKKSGQKITGFQFAPGSSSEVLITSADSRIRVNGDELVHKFKGFRNTSS QISASVAPNGKYVVCASEDSHVYVWRHNDTSHPSRSRSADVNTNSYEHFCHDVTVAITWPGAESRGSFGRSSRSNSDS DDAVMNTGRDAPVENSEHDLNGTVNRCTKRPVCEGVASTSNPPADGVSTSWPDEKQSSAKSSPGHCSSDLICIGALDVQR RSAWGLVIVTAGRGGEIRVFQNFQFGFPVQV
SEQ ID NO:10	MAPAVASSPSLVLSAAAATASNKRPADSDASPPHQGDRTGQOEKKQQLCEPCRSTNTKFCYNNYSTSQPRHFCRAC RRYWTHGGTLRDVPVGGASRRGGGKRRRVSADADPSSASPPPTTTSTTDAYADLPAGFPFLSDGAFLPQFGLAGVAPA AFSWASAVPDLYNCGIAPWDDGTAVTGAAWNDFADIAGLDLSWPPPGN
SEQ ID NO:11	MALLFRISLLLLVPLIPTAAASHHSPAGGGGAAPVLPRRRHRSVANTATALFYAPSMHQNHEAEEGQLLHVLA PFAAAPAAAEAPSGETAIAAVGAAAEATPTLIDDSPPQAAAASPPPPPPPPPPPLFAKPDLDSTAPPQKEGV YGSTTATATVTAAPLDEPAAATATTTTTTTTTLPLPRYSHVASPPPPVHAGVAGLGDEQRLEQLARVLSLGYNEMA SAALLLANSALLAAWPGSITVFAAPDVLASCPMCSRHHVLEHIALGYFPYTELAAASTAKLPSASGLCLNLASDH GPFaiHHVRLYVDGVEVSHPELYNDGRYVHGLHGLPPLSHGSCSHGSHNRHHYHYQYHHHHHHI IASSAASSATAA SVVRIMIREAIARLSDSGYFVALAMRVKFAELERLANMTVFALDDQAI FVGGGHYVSAVRFHVVPGRHLTHADLQRL HPGTMLPTLAGEQNLVVTQGSAGSGSGPRDVRINYIPIKDPDVVINSRIALHGVYVTFPRLHLANLAAVALASSNQ INATCGVFGDCASAAATSTTVPAAHRYGEGQ
SEQ ID NO:12	MDADEAAGSSRRMDNLNLYLGLPRAPRRSDLGSDALSTPMPSSPSSSAASVDAPPPPELSHPYSPSHADLSPPLO EVYSLYNPDDPPASETHLPPYAPPPAPVSELDDLEFGLHPPPLPVTGGFSSRLEADGSRGGLGRTFRHSVLKLTQ LGVMLPQSQNGPSSLLPDGIDWLRGLTLGYEDTERFASAMSDFRITGPSQYGASASSNPNLESTFDRTHVVAAPS ADQASNSSTA AVIQGDAGISESAGEPSNAGSSRSLRRGRSSALGSLDADGGGLQRNRRRIN
SEQ ID NO:13	MVGELVLAALVILLALLTLVLSHFLPLLLNPKAPKGSFGWPLLGETLRFSLPHASNTLGSFLEDHCSRYGRVFKSHL FCTPTIVSCDQELNHFILQNEERLFQCSYPRPIHGILGKSSMLVVLGEDHKRLNLALALVTSTKLKPSYLGDIKIAL HIVGSHGKSKDKGMVNVI AFCEEARKFAFSVIVKQVLGLSPEEPVTAMILEDFLAFMKGILISFPLYIPGTPYAKAVQA RARISSTVKGIIERRNAGSSNKGDFLDVLLSSNELSDEEKVSFVLDLGGYETTSLLISMVVYFLGQSAQDLELVKR EHGIRSKKEKDEFLSSDYKKMEYTHQVINEALRCGNIVKFVHRKALKDVRYKEYLIPSGWKVLPVFSVHLNPLH NAQQFQPCRWEGASQGTSSKFTFPFGGPRCLCPGSELAKVEAAFFLHHLVNLNRYWRIDGDDIPMAYPYVEFORGLPIEIE PLCSES
SEQ ID NO:14	MATLPDLGVSAFINILGAFVFLLI FAALRLQPINDRVYFPKLYLTGQRRHHPHGHGVNLDLCSYLRLFLAWVPGALRMS QPDLIHHAGLDSAVYLRIYTLGLKIFLPIMTVALLVLI PVNVSGGTLNLNRKEIVFSDIDKLSISNVNPGSNRFFIHL MAYVTFEWTCFMLYKEYSNVAFMRLHFLASQKRCADQFTVIVRNI PHVSSHSTSETVDEFERNHPDHYLGQQA VYNNAN RYAKLVKKKERLQNWLDYQKFERHFGKRPIGRTGCLGFCGREVDQIDYRARI SELDKKLASERQVRLNDPKAVMPV AFVTFDSRWGA AVCAQTQSKNPTQWLTOWAPEPRDVYQNLAI PFFSLSIRKFLISIAVFALVFFYMIPIAFVQSLAN LEGIEKVAPFLRPVIDTPVVKSFLLQGLPGLALKIFLYILPTVLMIMSKVEGYVSLSSLEERRAASKYFVFLVNVFLGS IIAGTAFEQLNAFFHQPPSIPTIGVAIPMKATFFMTYIMVDGWAGIANEILRVKPLVIYHLKNMFIVKTERDRERA MDPGSIGLAENLPSLQLYFLLGLVYAVVTPILLPFIIIFFAFAFLVYRHQIINVYNQEYESAAAFWPQVHSRIIASLLI SHVTLFGLMSTMKAAYSTPLLI FLPLLTIFWHKYCKSRFEPAFRKYPLEEAMEKDNLERTSEPNLNLKSYLQNAYLHPI FHMFEQQQQEQEQREEKVEVRIDKAQQHHHRQVEEEEEESKSSQATTHYHHHHEQTTHHHYHHEHMSHYHMG PSDTADSPSPPHFVYHYGVDF
SEQ ID NO:15	MEMTRSLTLVPLPATLRPASAAARRRRRRRLPFGALFSPSPSNQQQQEMHIRALQPRQDWVGEWVRSDTLVRGLPI LGGGASILLAVLLNRAVSGIAAVADASSQSRADILTLALSVDILAGLVWLSIRPKSISPVVPRGVECKRVGTGVLD LRELLWTWDSLTTATCCKSLVVVYGGNCVLQIGVAAGSPEDGNAMVMDAQKFMQGSLYRSAMESKKQSYLANLALY TELPLPANTQALILQPIGDKGIAVIGGDTIRGFTNLDQAWIAMIAADKLATLSKS
SEQ ID NO:16	MASSVAGSVTRRPPPVLLACRSRPNNRRLIRLLPLLFAVVVLLALLPPCVHGARALNDAKEAKVAEASDQTTTTTHAA AAVARWSVTVREGGGGGHSGHAGAGHGHSGHGRPEAEHHTGRRSAAAGSVRPPMAASCAALLVA VVALLRF
SEQ ID NO:17	MESAKRSCLAISLILLLLVP SIHGARHVAAIKGTGADSEMVTERTAGGGGGHGRGYTSRSHNPNNPNDGGSGTPV VDPHNVATRGHHHGAATRTAAGGDPRLAACMLRLGATFFLLVLG

SEQ ID NO:18	MAGVGFVEDMLREQSLLEATCGDLFDHIDDLDFPKEESAADVLLLDAPAPGSPSSRIIGGHATMAAAPPPPPQMMAL PPPPAPAKDDASALFDAAGALGAEEVDFRDKAHIGPCDELDMDMAQLEWLSGLFDDGTIPHEPSFPGVNCAPPIKASALT ANAGVVLDPKAEALFRSSSPISVLEHSGFNATNGGSSSSSSSSSSSPSPWTWTAV
SEQ ID NO:19	MIIVDDAGAFPLPALNHSPWDGVTIADFVMPFFLFMVGISLTLAYKRPDKLEATKKAVLRALKLFLCLGLVLQGGFFHGV RSLTFGVDITKIRLMGILQRIAIAYLLAAICEIWLKGGDDVDCGLDVIRRYRYQLVVALLLSTMYTVILNGVYVPDWEY QISGPGSTEKSFVRCGVGRDTPACNAVGMLDRTILGIDHLYRRPVYARTKQCSINYQNGPLPPDAPSWCQAPFDPE GLLSSVMAIVTCLIGLQFGHIIHFEEKHGRIINWLIPFSFMLALAFSMDFIGIRMNKPLYTISYALATSGAAGLLFAG IYTLVDVYGFRKLTIPMEWMGKHALMIYVLVACNILPIFIHGFYWREPKNLLKFIGVGA
SEQ ID NO:20	MAATGGAAGEKTASSLLGVGRYTSTLKNASTASCRLSAGHPIEVTLWEASPPALSHFSVHCPDLPSFNGNLLGAPKAI AAAVDDADGQLLLLLRVPIDQLGAPHNDYLVYHPDPPSPKLDLLENPPPTLGDHQLAILSCGDDRYVVAALHVVSEF TSTIRLYRSSCSSSGSWTSEEVSVEEPVRDRLCPIPSAKRQLYHVTTKTITLGGAKGTGVGVDLWRGILLCDVLDEMSP RKLDRMPLPWPAGKNWRMYLNGDVSFCRDIAISQHKDSIKYLEMEIVSPRTVTTTPTSTADPTSYLEWVRRSREPQP TRRRSVFHPGWSRITWSPPIPVTSWDDWRDCTAESREVHLDNPNSHHYELLHSLMLSNGSDEHREEAQGGATSSLS LGRRLCYPALSCIDDDVYLLGNAAGRGAKTGGMMVAVDVRNKELRGVAKLDPEKNTLYSMRCYLATGISKRLNTTDD TRVGRPEEDAEAAE
SEQ ID NO:21	MANYHHQEYYQMAAAAVAWPREPDSQLSIMSGCSSLFSISTLRDDDDGGGVRLAGAALPATPVSLAGIAGGASTPGG DEVDMEVRRQSGSGGDDRTIRMMNRRESALRSRARKRAYVEELEKEVRRRLVDDNLNLKKQCKELKQEVAAALVMPTKSS LRRTSSTQF
SEQ ID NO:22	MAEKKKKKKKKKQSLVLVTSWRSIGMGRGVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGK LYEFCSTQSMTKTLEKYQKCSYAGPETAVQNRESEQLKASRNEYLKLRARVENLQRTQRQYYKSKHRLCLVRSKVWNLV KIRDDVTEKLCMYERNLLGEDLDSLGIKELESLEKQLDSSLKHVRTTRTKHLVDQLTELQRKEQMVSEANRCLRRKLEE SNHVRGQQVWEQGCNLIGYERQPEVQQLHGGNGFFHPLDAAEPTLQIGYPAEHHEAMNSACMNTYMPWPWF
SEQ ID NO:23	MEGGGRRRRRGKVELRRIEDRTSRQVRFSSKRRSGLFKKAYELSVLCDAQVALLVFSAPGRLYEFASSTS
SEQ ID NO:24	MALLLSYPRRHPSIHLILSAYALFLPLDGLLELGGDGLYREILRDETVLRLKELGKISDGEGYLERTFLSPASIRAS AVIISWMKDAGLTTWIDQMGNIHGRFEPTNSTKEALLIGSHMDTVIDAGMYDGLGIIISAIKLVKVTGRLQRLTRP VEVIAFSDEEGVRFTTFLGSAVAGTLPESILQVSDKSGTTVQDVLKLSLEGTANALGEVRYSPESVGSYVEVHIEQ GPVLEALRYPLGVVKIAGQTRKVIINGSQGHAGTVPMKLRRDPMVAAELVLTLETLCKEPNKFLTYDEECGCFTTE SLAGLVCTVGELLTPSASNVIPGQVNFVDIRAMDDKVRETIIVTSFSRLVLQRCDDRLVDCAVEQKHAATAATPCDAEL TSRLERATRSTISSMAAGVRRAGGETPVLMSGAGHDAMAMARLTKVGMFLVRCRGGVSHSPEESVMDDDVWAAGLALVN FIDQNAVDAAAATAAES
SEQ ID NO:25	MSFADLEAGAVRAPRRARGPDATRALVFQITTAVASYRRLLNSLGTPKDTPALRDQLQKTSNIIQLAKDAKEKLRRRA EADKNADTSADKRVADMKLAKDFATTMEYGLQNLAIQREMAYPVVPQTSQPNYTTGGIEARDSGKIPEQHALLAES KRQEVQLDNEIVFNEAIIEREQAIQDIQQIGEVHEAFKDLATLVHIQGVTTIEIDTNIENSAAATKEAKTELAKAS KTQKSNSSLLCILLVIFGVVLLIVIIVLAT
SEQ ID NO:26	MQLYMTYQACPMGDLQMGDSVVSTIDIRALYCNKSPGKSSSSSSMYGASSSSSKRKACELNHGDGGSAAHDDVRDYGVDHVD DNGEYYGDDHDDVMHG
SEQ ID NO:27	MRAAAAASKAAGKEKSRRKGGGGGAGGGGGEQLLTDQVLSLRARLHLALGLAKSDGGPKKWQSTDAGIQSHVLKAA SAFLGCLTNEMLRLPPIKESIDILIALEGILQSKNVSVLIQATDVSLKLVSSVGNLARQYPVLEIVTCLASQLSANQ ITIAVSSASTLNCILNTLATARSSIHAEIWEALEKTDAVTSVIGALQNYSPDVHPLNYLMEMMSLLRIILWIWPSRY HVWSNCLNMGKLAQYCVASEMDVAVRVLKLYAALALCGNGAMVLLNEDLMKVGALLGKSNPSIARIEALKFYQILL RSSKGCDDLMAAHYQHIIIEGTINAMSRDDELLTIEGRTALLVLYAGDHHRLFWSHAIDVLYKILTGCTSSHKA NQILCHDKLFNMVSENFMDIHSYVWDILGNLAVHCKNEYLSVRKQDSALQALIHICISLAADAMQKSNMTKLSKDVH EPALRAVLMMLLSPSGYILSEASSKLLHVLPGLDDCLNILFTSLESNTTSITASFNVKIMSNLMSLAGMSINFVCI HCKRNLVDVIGVNCDCRDHYSEGLIRVLQNASQNLSPGPKLYISRLSLFGLCGFPKLGKMMRRALDDNELADLELL LSNGESLKAHTAIISVRCPKLLPSAKSLGSDGKITDEWGRSFYHVRMSDRVDSGLKKILEYTYTNSVMVDDDNIPKPR TLAKYCHLKSLOEMLQKEQPRWNSDCPRYDLTAALPEVKCSFSFSEVINVPLGWALNKLHWFYSGLPKIDPDCRW RNLNSEEQLSLRPYAELESSLSEFWFLEGVKEESLSVVTSCLSSTSTAASVEFVFAAQQLQWEMVEAAVGSVAHLYP KLKRDGQLEQLDDDLNMLRTEYVVRTQRTGVGSAAAQAGARVVTAVYRRGQRADYQSGGFGDNWNFMVILNASEE HCRESKFDITGVCKARFLYGVSRGFRRLTSGINKEGGPRGTVIYSRSSGLPPWCGAGSHDALAAVRWPSLPGLS HQTAQVIRRGAGRRGEGRDVNVTKQSNAPMRPETMQREQPOSRRARANGRWPPRRWRSGIREEQGVPSAKANQEKR KRTQQQRCAAPAAIASRLQL

SEQ ID NO:28	MASAVASNLPAAPAAVMPFGGWHGPRVSFSRDAAGAEAAAVVVCSSPLAAAAAVATTTTPEPAISKDFIDFEFSLGG SATMLPADELFAHGKLLPLRKAAPVEMDAAAPRPPQPEAMPAPSEPMKPLRAATAAVDAADPYVFSKAPSCSSRWRE LLGLKRAAAQSPKPSAPARTPGRAMNSTAARSLKLLQNNRSGSGASASELASAPLLRDSSDSEASLSLASRFS LSSSSSSSGHDDIPRLSLDAAADPNPPRIRLVRSSHRHSTSSSSSSRAGSPARRRPPPPPPRCLSVDSPRMNSSG KIVFQGLERSSSSPCTLHAAAKPRRAVDRSYSSGVRVAPVVLNVPVCSRPFVGFKKDKDAADAMAARTSSSLGRK TTAAPQG WSGELGRSCG
SEQ ID NO:29	MKISGLLTSGINIALSVLFISLYSLRKQANVRVYFGRRIAEHNRLREAFILERFVPSTGWIVKALQCTEEELAA AGLDAVFNRLVFSRLIFSLAAILCVFGLPLNYFGQDIHHVRI PSESLDIFTIGNVKVRSRWLVVHCVALYIISGVA CILLYLEYKHIA RLRLRHLTCAMPNPSHFTVLRGIPKETKESCSNAIDFFTKYHGSSYLHQVYVYKGVQKIMTGA KKAYRKFKHFTDSTIDQRCRAISYRCLCGASSNSFQLLATGLEQNGKSDLDQSSSLKDDQCEAAAFVYFRTRYAALV ASEILQTSNPMKWVTDLAPEDDVYWSNLWLPYKQLWIRRIATLLGSIVFMLFFLIPTVFIQGLSQLEQLQORLPFLKG ILEKKYMSQLVTGYLPSVILQIFLYAVAPIMILFSTLEGPIHSEKRSACCKVLYFTVWNIFFGNVLSGTVISQLNVL SSPKDIPVQLARAI PVQATFFITYVLTSGWASLSSELMQLFGLIWNFVRKYILRMPEDTEFVPSFPYHTEVPKVLFLGL LGFTCSVLAPLILPFLLVYFFLGVIYVRNQLNVRTRYDTGGLYWPIAHNAVIFSLVLTQIICLGVFGLKESPVAAAGF TIPLIILTLLFNQYCRNRLPLFRTPAQDLIDMDREDERSGRMDEIHHRLHSAYCQFHDTEIDPLEKIQTGVSDEEQG CSSDKSNGKESFEEPRAELSHPTLNLPLVSRRLRHAVK SITFLVRLQKRG LSE
SEQ ID NO:30	MAILREFGTIEGMENLLPEDVLSNIIHRLAPRYLAISRCVCKTWTCTIEAHNLLHVDLLPRPLCGIFINFNELSMSEFF SRPSKGPTVSGNFDYLPCCSSCIIDHCNGLLLFHKYVVPNATRQSAPLPCCPYMVVEHIFHREYLVFDPTLSPHFVFM PEIRRNWVWYMNLSDDKLDPAIEELEWPPSPCILHVFSSRTKVWEERSFVREGEAAGNVSDMRDLHPYVPTSVYVPD TSVYCRGVLYVYQNKYVMRISLSNGKYQVIKPPSDCEGMAYTNLYLGKSMKGVYCAVRHLASRFLIYILDESSDRMEW VCKDSCSIQPCQIIDGPGPWTLDQINNQERGFEYEDGNEAVVEDRFEWDSNDNVIETNSRSGGGYINFLVDTTRGR YNSGGYIDFLGFHPYKEVIFLSDSLRRLGAYHLNSSKIQLDGLSLRPTNYGTEVGIQPFIQKFFPYSPWMGRFPEDN
SEQ ID NO:31	MKISGLLTSGINIALSVLFISLYSLRKQANVRVYFGRRIAEHNRLREAFILERFVPSTGWIVKALQCTEEELAA AGLDAVFNRLVFSRLIFSLAAILCVFGLPLNYFGQDIHHVRI PSESLDIFTIGNVKVRSRWLVVHCVALYIISGVA CILLYLEYKHIA RLRLRHLTCAMPNPSHFTVLRGIPKETKESCSNAIDFFTKYHGSSYLHQVYVYKGVQKIMTGA KKAYRKFKHFTDSTIDQRCRAISYRCLCGASSNSFQLLATGLEQNGKSDLDQSSSLKDDQCEAAAFVYFRTRYAALV ASEILQTSNPMKWVTDLAPEDDVYWSNLWLPYKQLWIRRIATLLGSIVFMLFFLIPTVFIQGLSQLEQLQORLPFLKG ILEKKYMSQLVTGYLPSVILQIFLYAVAPIMILFSTLEGPIHSEKRSACCKVLYFTVWNIFFGNVLSGTVISQLNVL SSPKDIPVQLARAI PVQATFFITYVLTSGWASLSSELMQLFGLIWNFVRKYILRMPEDTEFVPSFPYHTEVPKVLFLGL LGFTCSVLAPLILPFLLVYFFLGVIYVRNQLNVRTRYDTGGLYWPIAHNAVIFSLVLTQIICLGVFGLKESPVAAAGF TIPLIILTLLFNQYCRNRLPLFRTPAQDLIDMDREDERSGRMDEIHHRLHSAYCQFHDTEIDPLEKIQTGVSDEEQG CSSDKSNGKESFEEPRAELSHPTLNLPLVSRRLRHAVKSITFLVRLQKRG LSE
SEQ ID NO:32	MVELSIADASASDLGGT LGQMVELVCEARLRVREEYVRSTVDLMALLRGRGMVFDGVYVVSNNLRLFAELDFGRGEWV VSGMAQPM LATFLVTCRNGDDEDAVAASMLPPPVKLRFAEELAGLMMSPHGGAAALCPAPASTYLP LMRGRRLHIP EGYGNALAYSITDASASDLGATLAQMMELVCEARLRVTEEYGRSTVDLMASLRGHDTVFDGVYVVS DLGAGSGWSAA WPSRCWRRSW
SEQ ID NO:33	MNQHQRSIEHCSIGCF LASPPRFFFPARTRSAPGELRMKLVVFLIRGCPGEVLLRPIVPAKEGLRTRTKWHILQRFC LEIISITETMITISSRSIIKSRCKSKNKILVFFLSMSVKFLITTRSLSVQKRSSTFSQLLH
SEQ ID NO:34	MCMDRAAVPVKRVWLGLAARLGLRRTSGLGKLKKEVRTCEYHDVHIMWEMLRKTDAVPMAEKEAAAAA VAAAAGARR RKAARWRFLYCCAF
SEQ ID NO:35	MATSRKLARVDIAELKQRLVKRLGRQAGQYFAHLTRLLNKLTKVEFDKLCYATIGRENIALHNALIRGIISNALSGV PPPSRQAVTGSGTTTAPSGQCVGIALQSARNVGAVVDSGDGFARERAVAGKVLVSDGEVEQVRSAPCVQSRSPIT APLGISTTPTYGARTWRLLDDPMVSCYDSHLLDTGSLFKGLQRRLSDGIGVSVQGVVNLNRLDEFLRLRIKPCMELS RSRSSGRRVTKGNAMFAARMNGLQANHGHC TTLQDFAVAMESDPHLLGTNWP TQLEKIQTATSGE
SEQ ID NO:36	MASPRCAAVALLHPAGVAAGGARRRVL LLDQERPLWGTEVRRRRRRRFSLETTPRCCKMYVPGFGEKSPKKAARNL QHFFNYIAVRVVLTLQESYNREAYGELMDVFNRLNSLNDADTFCKKLIRESPRHKQLAMRILEVRSAYVKHDFEWDNLKR LSFKMVDEANTKLMDYVLETS HIEDDN*
SEQ ID NO:37	MDITGAGAMGGGSTAATAAAAGAGWKT PVSMLVQLFITGQILLSKVSI GGGMLIFVLLAYNSFFAVVFLPFLALIFE RGKWRDMDWGAFGWIFLNAFIGYSVPMSLYYGLKDTTSSYSVIFLNTPLFTFILSLMFRLEAFKLRSIPGVKLIASI LLSIGGTM LLSLYKGKSLHLWDSIIQHNEHKSATNQLRG TILLVGSSFTFACWFLIQSKILKVYPKYWSSMVTCLVG VFQ TALVGIILRRDKSAWELGWNLNLTIVYTGALATAGKYILNSWAIKRGPTYPTMFSPLSVVFTTVVLDVSLGNDI TIGSLGTALVIVGLYLFLWAKAREIPKKST*

SEQ ID NO:38	MARRAAEKEAALRQGLTAGDGEARRTGALWRTDAWRQRAAASAAASVVRTWPSSAPWLFELDPWRRVCGEQDLQTAA CGGGDGAUGLSFETHHGGSVAPSPEFAACAASSCSAELMVLVLQRGELLVRHDPSPHHRRRFPPTPQPAEAAAIVEVG WGFQNRPRDAMTCLCKGL*
SEQ ID NO:39	MGSGGGGCGRNGAVRQYIRSKVPRLRWTGELHCSFVQAIEFLGGQDKATPKLILQLMGVKGLTISHVKSHLQMYRCSRL GSHGTGRRSEMQLQQRKHSCGADEQVPREFLCPPLKRTRMGTETATYKMGQSGQISEMRTTGTQYCIDDDYMQAMAMER RIKEEGLRWQRDAAAAAADGGAASNLQTVGCSVQESDPFKIIPKPEVHHLGPVLKLQCSKVENSGFISSTGTAAARDQ PEPPPLEKCSLSLSLGPDPKCMPIASSPSESSCILSSSSRSFSDCSGNSGCLVAPGVNLELSMSICGS*
SEQ ID NO:40	MAAADQPAYGDRRPSRRTYKPDQPEGLTISFRELYDLPTSPEFLFHEEALRSRRTCGEDLTFTYTGCGYLVGRAAGAAAG LKRAEEAERGESMKLRGQPRPQPVRLPRARVRQPARRRRAALRGDRHRGGFPRRRRRLGQHRRRRDRYRRALPRGCRP AGGDRRQLRRGAHGRRGGRGEASADEIRA*
SEQ ID NO:41	MDMPPTPLPPETANTSAPNGATAGIRVENCYVFKSRQLQEYAQKTGLQTPEYHTFKEGSPHEPVFKSTVVINNTSYDSL PGFFNRKAAEQSAAEVALMEIVKSI PANANI PAVQETGLCKNLLQEYAQKMNIAIPSYICTKSASGLAFFICTVEIGGI QYIGAAARTKKDAEIKAAARTALLAIQGGSEGSANGATKYIIVPGKRVGKEVEKRPIETPKPLKVKGGFKKKWNRKRFM KKDQGAQVDVEKDEARVAGDAHSDSVLMQPTVITQEASCGTLFLQPCEEAKRVEAEPPRDIEMVQPDKENQHSDAALVQP DDEARVEQEPSRDISVQPNEEAISGKQEPSIDAILQPKKEEASSVKQEPFIDTAMLQACKEAGSVELGPARDTVISQL NEQDRAVKQEPAGDIVVPQPDVHARVVE*
SEQ ID NO:42	MALGDLMASRLVHSSSSSAAPSAALPNHHTNHLVDDHLPVENGPDPRRDVPDEEPPPPPPQVALLPQVVVLCEQRHEG FDEAAAAAGPSTSGPVSKWRPKDRMKTGCVALVCLNISVDPPDVIKISPCARKECWIDPFMSAPPALETIGKTLHS QYERWQPKARYKLQLDPTLEEVKKLCNTRKFAFATERVLFHYNGHGVKPTANGEIWFNKSYTQYIPLPITDLDLWSLK TPSIYVFDCAAGMIVKAFLERLDWSSSSSASSSKDCILLAACEAHQTLQSAEFPAADVFTACLTTPIKMALHWFNCRS LLRDSMEHNLDIQIPGRQNDKRTLLGELNWIIFTAITDTIAWNVLPDHLFQRLFRQDLLVASLFRNFLAERIMRSANCS PISYPLLPPTHQHMMWDAWDMAAEICLSKLPQLIADPNAEFQSPFFTEQLTAFEVWLDHGSSEDKKPEQLPIVLQVLL SQSHREFRALVLLGRFLDMGPWAVDLALSVGIFPYVLKLLQTSAMELRQILVFIWTKILSLDKSCQVDLVKDGGHAYFIR FLDSDLAYPEQRAMAAFLAVIVDGHRIQGEACANAGLIDVCLRHLPENPNDQAQTEPLLQWLCLCLGKLWEDFPEAQ LLGLQSNAPAEIVICLLSEPQPEVRASAVFALGNLVDIGSPSLNGADDDSDDEKVRAEINVVRSLQISSDGSPLVRSE VAVALTRFAMGHNKHIKSVAEYWKQTNLSLLKSLPSLANINSSNVYSPSSLIQSSGLASHIGPVLRVGSDNSATARD GRISTSSPIATNSIMHGPSQSDSSQHSDSGILLRENASNGGLNYSRSPIDNGIYSQFIATMCNVAKDPYPRIASIGK RALSLIGVEQVSMRNSRLSNGGAHPGETSVPPSSNFGMARSSSWFDMNSGNFSVAFRTPPVSPQHDYLTGLRRVCSME FRPHVLNSPDGLADPLLSSSAAPSNGMGLYILPQSLIYRWSCGHFSRPLITGSDDNEEANARREERERIAMDCIACQRS SCKMTSQIASWDTRFELGTASLPLFPSPIVVAADENEQIRVWNYDDALPVNTFENHKLSDRGLSKLLINELDDSLLL VGSSDGNVRIWRNYTQKGGQKLVTAFSSVQGYRSAGRSIVFDWQQSGYLYASGDMSSILVWDLDEKQVNTIQSTADSG ISALSASQVRCCQFAAGFLDASVRIFDVRTPDRLVYTPHAPRSEKVVGIGFQPGFDPYKIVSASQAGDIQFLDVRRRA SEPYLTIEAHRGSLTALAVHRHAPVIASGSQAKMIKVFSLGEQQLTIIRYQPSFMGQIRIGSVNCLSFHRYKSLAAGAG DNALVSIYAEDNYQVR*
SEQ ID NO:43	MGASGRLISIIYPEDLTFLFELDKPCYCNLKVNNSEHHVAFKVKTTSPRKYFVRPNASIIQPWDSCITITITLQAKKEYP PDMQCKDKFLIQSTKVAASTDMDEIPMPTFNKEVDKVEEMKLKVVTYVPSGSSDDSGITSLGSRSFKLGSDDLTMKLN ASIEKIQTIQRLKDERDTLQONQMQRELDVIRRRRSRKSADAGFSLTFAAFAGLIGVLIGLLMSLIFPRPQAAA*
SEQ ID NO:44	MGVMNPLMAKLTTLMGDEYKLLKGLRKQVSFLKDELTMTSAFLEKLALMDDDDGELDPLAKDWRNHVREMAEDMEDI DDYFTSHLDHRYSSSDAGLIRKIARRLRALVRHRIASQINELKARVVEANERRVRYRLDDCENKHGVSANPAIDPRIT SLYQNAAGSLVIGDPSQELIQLLSLDRDTRDQRLKVSVVGFGLGKTTLAKYVYDKIGHQFDCATFVSVSHKPDITRI LSSIQSKLDIGGTSQACDDVQQLIDDIRAYLEHERYIIIVDDLWKQEAWVISCAPFNNGKGSRVIVTTRVKDVARLAC GKDGGYIKIQLPNNKDSRKLFFDRVFRPEDSCVLQYEEISTEILKKCSGLPLAIVTVGSLACRPTMEEWKSIKRSGLG APFDKNKSLEGMRNINLSYKNLPLHLKTCLLYIGKYPEDYEIGRDELVTEWIAEGIMGNPHGENLEATGNGYFSELIN RGLIQPESTGYGGEVLSCVHDMMLDLILIKCAEDNFVSVVAHSCKDYMRMAMHHERSCNKVRRLSLQCKAARSDCAIEG SVISTSMARARSVSVFGECSRGLPFLMLSIRVWHIELEGHGGQVLDLTAISHVLQRLRYLRVETPGCEIDLPSKICGLV HLETISFISHKAVSRPLPSDISSLPRLSVLSLVVPWATRLPNKLNKLKGSLSLTIILFNPPDALGMEAIKELKNLRDLNI SVNRWRDDEILSLYALGSSIGKLDLRLSLQIHVPATLGDVLDLGLSLPIFPQSIERLILHGWCFSKVPWRWINGTLRNLQ HVLLEVSETSSSEVDLLGELPSLADLEBRVGLKTRDVIAFGGTRASLFPALLKLKLRVGEHVASRLQFQAGVMPKQLSL HLWFRNCESGIHVTPEGMQHLLSLQISICVEIYLRDEELKATYPWDAMERAFREITGANPNRPSFKFVKQV*
SEQ ID NO:45	MECEPEELQFLGMVGIYREAAASILRAHRPLFARIAAAAFVLPLSLFLHIAISHALFSDHSDSDSALDSAPGTPAQRRL LLHRLADDWLALLLFAAYLLALLLFLSLSTAAAFVSASVSAKHDALSPRVLSVPRVVRRLAATFLAALLLFAFAY HLLFVAVFVALLVAADSGSGLAALLAFLALAYIAGLVYLSVVVHLASVSVLEDYKGFAMRKSALIQGKLWTASAI FFVLNVVVFIVVEVAFRAWVRGATHGIGAGSRLLGLAMLALCAVVMLALVVQTVVYLVCKSYHHSIDKSNLSHLE VYLGEYVPLKASDVQMEQFNL*

SEQ ID NO:46	MASSSALASSPFLPPLSTPNPRALSLRLPARRLPVASSAAPSGAAAAASARERRRFLERYGLNPDDFEDDAEAEPREER RRDRNRNRSGRGEADAPAKAAAEPRETHKMLQVLGGKVRRLKLLSPKDRNVPRMMEVVRGAADFILQSGAGFPASLRP GRWLDLYSGTGSVGIEMSRGCSEAHFVEMDPWVSEVLKPNLECTGFLDVSHIHMIRVENFLANAEEKSSGKYPSPFDYI SVTPPYLEVNYSTLLDQLARSPLVGEDCFILVEYPLKTDMAESCGSLIKVADRRFRGRTNLLIYGPTWAEKKRRS*
SEQ ID NO:47	MNDLMTKSFMSYVDLKKAAKMDLEAGGDGVELPEVGVTDERLKGFFQETEAVEEEEMAAIRDALARLNAANEKGSLHQ DALRALRGRVNADIIAIVLRARDIRARLEAMDRANAAQRRLSAGCREGTPLDRTRTALTAALRKKLKDLMLDFQALRQR IMSEYKDTVERRYYTLTGEVPEEEVIERIIISEGRSEELLCAAAVAEHGKGAFLATVHEIQDRHDAAREVERSLLELHQVF LDMAVVVESQGEQLDDIERHVNSATTYVQGGNKELRKAREHQRRSRKWLICIGIIILLVLLVIVPIATSEFKRS*
SEQ ID NO:48	MAMEGKSRRFAVACGVLSQYVRAEQKMAAAGAAPARAVTTLSLMPGAEEVVVEEERREVGEAEAGPATAPAAPLTIFY GGRMVVFEDFPADKAAEVMRMASSGMAAAPAQREGAALADMPIMRKASLQRFFAKRKDRLAATTPYARPSPAETKASEP EEKTPTSWDLAASASAAARRDSLTIAL*
SEQ ID NO:49	MSLSRELVLFLILQFLDEEKFKETVHKLEQESGFYFNMKYFEDEVINGNWDEVERYLGGFTKVDDNRYSMKIFFEIRKQ KYLEALDKHDRSKAVEILVKDLKFASFNEELFKEITQLLTLENFRENEQLSKYGDTKSARAIMLVELKKLIEANPLFR DKLQFPNLKSSRLRTLINQSLNWQHQLCKNPRPNPDIKTLFVDHSCGQPNGARAPSPANNPLGSIKPKPGFPPPLGAHA PFQFAPTVPVPLAGWMSNPPAVTHPAVSGGAIGFGTPTNPAAILKHPRTPTTANPSMDYPSGSDSHVSKRTRPVMGSEE VNLFPVNMLPVTPYQSHSYQDDDFHKNVARTLSQGSTPMSMDFHVPVQQTLLLVGTNVGDIGLNDVGTKERLVLRNFKVWD LTKCSMALQASLVKDPTVSVNRIIWSPDGTLFGVAYSRIHVQIYSYHGGDDIRQHLEIDAHVGGVNDIAFAHPNKQLCI ITCGDDKTIKWEATSGAKQFTFEGHEAPVYSVCPHYKENIQFIFSTALDGKIKAWLYDNLGSRVDYDAPGHWCCTMAY SADGSRLFCGTSKDGESHLVEWNESEGAVKRTYQGFRRKSMGVVQFDTTRNRFLAAGDEFILIKIWMONTSLITTIIDA DGGLEPASPRVRFNKEGTLLAVSTHENGIKILANADGVRLRLTLENRSFDASRSASETVTKPLMNPLTAAAAAASAAAA GTSSGNAAPPATITALNGDSRLVDVKPRIADEPLDKSKVWKLMEITESQCRSLKLTDMNRTSKISRLIYTNISGVAILA LASNAVHLLWKWPRNDRNSSGKATASVSPQLWQPPSGILMTNDITDNPEEAVHCFALSKNDSYVMSASGCKISLFNMMT FKTMTTFMPPPPAATFLAFHPQDNNIIAIGMDDSTIQIYNVRIDEVSKSLRGHSKKITGLAFSNVLNLVSSGADAQIC VWSTDGWDKLRMLQIPSSRPSSIILDRVQFHQDQLHPLVHVHETQIAIYETTKLEPVKQWVPVRENSSPITHAMFSCD SQLIYASFLDATVCI FNASSRLQCRILPASYLEQNISSNVYPVVVAAHPSEANQFALGLTDGGVYVLEPLESERKWGN PPPAENGSTALSSTPPNGASSSDQPER*
SEQ ID NO:50	ATGTCTCACCCCCACGCCACCGCCCCCAAGCGCCCCCGGCCACTTCTCCTCCTCCTCCGCCGCCGCCCTCCTCCCCGACC TCCCCCGCAGCCGCACATGAAGAAGGCCAAGTTCCTCCCGCTCCTCCTCCTCCTCCTCCTCCGCCGCCGCCCGCCCGG GTCACCGAGAAGAACGGGCTCCACGTCGATCCACGCGCCGCGCGCGCCGCGGACCGGTGGGCGCACCAACGGCAGGAG GATGCGGAGATGGTGCTCGCCGACCAGGAGGAGCTCGCCGCTCCGAGCGCATCGGCCCGCGCGGGGTGCGCCGCAAC CTCTTCCGGAAGAAGGCCACACTCCCCAGCCATCCGCCGCCCGCAAGCCCCCTCCGAATCAAAATAGGTCAGCCAAAA TTGCAACAAACTTTGAGGAGGATACATGGGCTATTTTGAAGATGCTATTACAGCTATATTCTAAAACAGAACTT TCGTGCGATGTTGAAAACTTTACCAGGCTGCAGGTGACCTTTGTCTACACAAGCTAGGCGCAATCTATACGAACGC ATAAAGAAAGAAATGTGAAGTACACATATCGGCAAAAATATCAGCATTAGTGGGTCAAAGTCCAGATTTAGTAGTATTT TTGTCTCTGGTGCAAAGAACATGGCAAGATTTTGGCATCAGATGTTGATTATTCGTGGTATTGCTTTACTTCTTGAT TGAAATATGTCAAGAATGTTGCAACATTTGTTCAGTGGGACATGGGGTTGAAGCTATTCCGCAAGCATCTTTCTCA CTGTCTCCGGAGATTGAACACAAAAGTGTACTGGTCTTCTAAGATTAATTGAGAGTGAGAGGCTTGGTGAAGCAATA GACAGGACATTACTTAGTCATCTTCTGAAGATGTTACTGCTCTTGGATGTATTCTGAGAGTTTGAAGGCCCTTT CTGGAGTGATCTGAAATTTATGCTACTGAAGGTGTTAAATATTTGCAGCAGTCTGATATTCAGACTATCTCAAG CATGTGGAGACAAAGGTTGCAAGAAGACATGAAAGGTGTATCTATATTGGAAGCTAACACTAGGAAGCCGCTTATA ACAGCTACAGAAAAGCAATTATTGCAGCGGCACACATCTGCAATTCTTGAGAAGGGATTACAAATGCTTATGGAAGCA AATCGTGTAAGAACCTCTCGAGGATGTACACACTCTCCAGAGGGTTGATGCCATTGAGTTGCTAAAGCAAGCACTT AGTTTCATATATTCCGGGCAAGGCCAGGGCATTATCATGGATGAAGAAAAGGACAAAGAACTGGTGCCCTTTCTCTG GAATTTAAGGCATCGCTTGATAGAATATTGGAGGAAAGTTTGGCAAAAATGAGGCTTTCTCCAATACAATAAAAGAG TCATTGCAACATCTTATCAATTTACGCCAGAATCGACCTGCTGAATTGATTGCGAAGTTTCTTGATGAGAACTTCGA GCTGGAATAAAGGTACCTCCGAAGAAGAGCTGGAGGGAATATTGGATAAAGTTTGGTCTGTCTCCGATTTATACAA GGAAAAGATGTATTTGAGGCATTCTACAAGAAGGATCTGGCTAAGAGGTTGCTGCTGGGGAAGAGTGATCGATAGAT GCTGAAAAATCAATGATAACAAAGCTCAAAACTGAGTGTGGAAGTCAATTTACCAACAAGCTGGAGGGAATGTTCAAG GACATTGAATTATCCAAAGAAATAAATGAGTCTTTCAAGCAATCATCTCAAGCAAGGACAAAGCTTCCATCTGGCATT GAAATGAGTGTTACAGTGCTTACAACAGGCTATTGGCCCAACATATCCACCAATGGATGTGAAACTCCCCCATGAACCT AATGCTCTATCAGGATATATTTAAAGAATTCTATTTGAGCAAGTATAGTGAAGGCGTTTGATGTGGCAAACTCATTTG GGTCACTGTGTATTTAAAGCAGAGTTCCCAAAAGGTAAAAAGGAACCTTGGGTGTCACTATTTTCAGAGTGTGGTTTTG ATGTTGTTCAATGATGCACAAAACTAAGCTTCTCGATATCAAGGAATCGACTGGTATTGAGGATAAAGAATTGCGA AGAAGCTGCAATCACTTGATGCGGTAAAGTTCCGGGTTCTCCAAAAGATGCCAAAAGGGCGAGACGTAGAAGATAAG GACGAATTTGTATTTAATGAAGAATTTAGTGCCCTCTCTATCGCATAAAGGTGAATGCTATTACAGATGAAGGAGACG GTTGAAGAAAAACAAGCACAACCTGAGAGAGTATCCAGGACAGACAGTATCAGGTGGATGCTGCCATAGTTCCGAATA ATGAAGACAGTAAACCTCAGCCACAGCTTCTAATAACTGAGCTTTTTCAGCAGCTCAAGTTCCCAATCAAGCCA TCGGATATCAAGAAAAGAAATAGAGAGCTAATCGACAGGGAGTACCTGGAGAGAGACAGGAGTAACCCCATGATCTAC AATTACCTGGCTTGA

SEQ ID NO:51	ATGGACGCCGATGAGGCCGCGGGAGTAGCAGGAGGATGGATCTGAACCTCTACCTTGGCCTCCACGCGCCCCGC GCCCCGCGCGCTCCGACCTCGGCTCCGACCTCGCCCTCAGCACCCCGATGCCCTCCTCCCGCTCCTCCTCCGCAGC CTCCGTCGACGCGCGCGCCACGCCCCGAGCTGTGCGATCCCCGCTACTCCCCCTCTCACGCCGACCTTTCCCCCT CCGCTGCAGGAGGTCTACTCCCTGTACAAACCCGACGACCCGCTGCTTCCGAGACGCACCTGCCGCGGTATGCGC CGCTCCGGCTCCGGTGGTCTCGGAGCTCCCTGACGACCTCGAGTTTGGCCTCCACCCCCCGCGCGCGTGGTGGC TGCCAGCGAACTGCTAGGTTGGGAGGACCGGCCGCTTCGTCGACGGCATCGTCTCTTTCCCTCCCTGACACCGCA GCCCCGTACTGGCGGCTTCTCGAGCAGACTGGAAGCAGATGGCTCCGTGCGAGGCGGTTTAGGTGCGACCTTCCGC CACTCAGTTCTGAAGCTTACCAGCTGGGCGTGATGCTGCCGAGTCCCAGTGTGACGATGAACCGATGAATGA TACTGTTGAACATAATAAGGTAGCTGCCGATGGCGCGGAAGTAGGCGCTCCGAGGAATCGGAGGAGCAGGGCAGG AGCGCTGCCACATTGAGTGTAAATATATGCTTCGATATGGCCAGCGAGCCGGTGGTCACCTCTTGTGGCCATCTCT TCTGTGCGCCTTGCTTGTACCAATGGCTCAATGTTTATTCGAATCACAAGGAATGCCAGTCTGCAAAGGCGAGGT GACTGAGGCGAATATTACTCCGATCTATGGGAGAGGGAATTCATGTTTGGATGCCGAGAAGGCTGTGGAAGGTGGG AAACAAACAGGTCTTACTATCCACCAAGACCACATGGAAATCGGCTCGAAAGCTTCAGGCAGCAGTTTACCATT TGCGACCGATCTCAAGAAGGCTGGTGAGGCTCATGGGTTATTGTCATCATGGAGGCGCCTTCTGGACCAACAGAT TATGAATACTGCGAGTAGGTTTGAAGGTCGCGCTGAATGCTGCGCAGTCCCAGTGTGACGATGAACCGATGAATGA CACACCAGTCGCGCTAAGTAGATTGGCGTCAAGGATGAGAGCAAGACGGTTGCTGAGAGAAGCAGACAACCCTAACC CTCCCGATGGCGGATCCACTTCCCTGACAGTGGTTTGTATCAGAAACAATGCATCGGATCCATCCAGAAATGGTCC GAGCTCATTATTACCAGATGGAATTGACTGGTTGCGTGACTTACCCTTCTTGGGTATGAAGACACGGAAGATTT GCATCTGCCATGAGTGATTTTAGAAGGATAACTGGACCAAGCCAATATGGTGCATCGGCTTATCATCGAATCCTC CAAATCTCGAGTCAACATTTGACAGAACTCATGTTGTTGACGACCTTCTGACAGCAAGCATCTAACTCAAGCAC TGCTGCGAGTGATACAGGGGATGCTGGTATCTCTGAGAGTGCAGGAGAACCAAGTAACGCGGGGTATCAAGATCC CTGAGGAGGAGAGGAGGAGCAGTGCCTGGGTTCTTTGGATGCTGATGGCGGGGCTCCCAACGGAACAAGAGGC GAAGGATAAACTGA
SEQ ID NO:52	ATGGCTGGTGGGAGCTGCGACGTGTGCAAGGAGGCGCGCTCCAAGTACAAGTGTCTCGCTTGCCGCACGCCATATTG CTCGTGGCATGCTTTAAAAATCACAAGATAAATTTTGCCAGAAGACAATACCTCTGGAAGAAGTTAGCAAGTCAT CTCTTCAGGAGGAAATTTCAAGGAACCTTAGGTCACTGGAAGAAGCAACAATTTGTCTTAATGACAAGGATCAAACC CCGCTCTTTATTATCGGACACGACTTGTCCACACAATATCCAAACACATTGCACTCTGCAAAATCTCTTGAAGTTGA GGATCCAAGCTGGCTTGTGACAAGAATGGATTAAGATCTTTAGCGGAATCTAATGAGATCCGAGATGCTCTGAAAG ATTGTAAGCTTCAGCAAATGCTACTTAAGATTGATGGCTCTGACAGGCCAGAAAAGGAATTAGAGAAATTGATGGAA GGACAAGTTTTTCAACAGTTCACCAATAAGATTCTTGACATTGTTAGCCCAACAACATGA
SEQ ID NO:53	ATGCTGGGAGAGGCCCGCTCACCGTGGAGCCTGGCCGGCGCGGGCGCGGCGCTGGCGCTGCTGTGGCTGTGCGCCT GGACGCTGCAGTGGGCGTGGTGACGCCGCGCGGCTGGAGCGGGCCCTGCGGGCGCAGGGCCTCCGGGGCACCAG GTACCGCTCTTCATCGGCGACGTGGCCGAGAACGGCCGGCTCAACAGAGAGGCCGCGTCAAGGCCGCTGCCGCTC GGCTCGCACGACGTCGTCCCGCGCGTCAATGCCCTTCTTCTGCAACGTCCTGAAAGAGCACGGGAAACTGCGTTG TTTGGACTGGCCCCAAAGCCATTGCTGATTATCAGAGACCCCTGACTTAGCGAGGGAGATTTTGTCCAACAAGCTG CAATTCGCCAAGCAAACGACCGCGGTATTGCTAAGTTCGTAGTTGGCGGAGTTGTAACGTATGAAGGTGAGAAA TGGGCAAAACATCGGAGAATTCTCAACCTGCTTCCACCAGGAGAAAATAAAGCGGATGCTGCCAGTGTTTTAG CATGTTGCACCAAAATGATCACTAGATGGGTGAATTCATGTCTTCAGAAGGAATATCTGAGTTAGACGTTTGGGA TGAATTTCAAAATCTTACTGGAGATGTCTCTCAAGAACGGCATTGGGAGCAGCTACCAGGAGGGGTGGAGAATT TTTCAGTTACAAGAAGAGCAAGCTAAACGCGTACTTAAAGCTTTTCAGAGAATCTTTATCCAGGCTACTGGTACT TACCAATCGAAAACAACAGAAGGATCAGGGAATTGATCAAGAAAATCCGCACAAATCTGCGAGGAATAATAGTAAA AAGAGACAAGGCAGTTAGAAATGGTGAAGGTAGCAATGATGATTTGTTGGGATTATTGGTGAATCGAATATGAGG CAATCAAATGAAAAAGAAGATGTGGGAATGAGTATAGAAGATATGATTGAGGAATGCAAGTTATTTTACGCTGCTG GTTGCGAGACAACATCAATGTTGCTCACTTGGACTTAAATCTGCTAAGCATGCACCTGAAATGGCAAGAGCAGGC AAGAGAGGAAGTGATGCACCATTTTGAAGAACCACACCAGATCATGATGGCTTGAGTCGTCTAAAGATTGTAACG ATGATTCTCCACGAGGTTCTTAGGTTGTACCCACCGGTGGTATTCTCCAAAGAACAACACACAAGGAATAGAGC TTGGTGGCATCAAATACCCTGAAGGAGTGAACCTCACATTGCCTGTTCTATCCATTACCACGATCCTAGCATCTG GGGACAAGATGCAATCAAATCAACCCGGAAAGGTTCCGCAACGGAGTCTCCAAGGCAACGAAGTTTACAGCCGCG TTCTTTTCGTTTGCATGGGGTCTCGGATCTGCCTTGGCCAGAGCTTTGCAATTCGGAAGCCAAGATGGCGCTCG CCACCATCTCCAGAGCTTCTCCTTCGAGCTCTCGCCGTCATACACCCACGCACCACACACCGTGCTAACTCTCCA ACCACAGTACGGTCTCCAATTAAATTGAAGAAGCTCTAG

SEQ ID NO:54	ATGGCTAAAGATCACGTGAAGATTGTGTTAAAGCTTACATTTTAGGACCTATAAAGTATATTTTAAGTTTAGAAT CTTTGTACCATAATTGTGGTGGACTGGTGGTAACAATGATTCTCCACGAAATTATAGGTTATACCCATCGGGGAT CTTCTCCAAAGAACAACACGCAAGGAAATAGAGCTTGGTGGCATCAAATACCCGTAAGGAGCAAACTTCACATTG CCCGTTCCATCTATCCACCATGATCCCAGCATCTGGGGAGGAGATGCAACCGAGTTCAACCTGGAGAGGTTTGCCA ACGGAGTCTCCAAGGCAACGAAGTTTAAGACCGCATTTCTTATGTTTGGATGGGGTTCTCGGATCTGCCTTGGAC AGAATTTGCAATGCTGGAAGCCAAGATGGCGCTCGCCACCATCTCCAGAGCTTCTCCTTTGA
SEQ ID NO:55	ATGTGCTGTTACAGTGTGTCTGTTATGAAGTGGGAAGCTCTATTACCAAATGATACCTTTCTTATGTTGCCTCCT CTGATGGCGTATTTGAGAAAGTGACTATGCAGGATGTCTGTGATCTGATGTTGTACGTGAAACTTGGTGTAAAGCA AGAATTAGGATCCTTTGCATTAACACAACAAGAAATTTGGCAGATTATGTGTTGATCTTTCTTTATAG
SEQ ID NO:56	ATGTCCTCTAGCGATCAGAACCACATCGCCAACACCGGCTCCGGCACCGGCACGTCCGTGCGCGCCAGGCAGGG CGACGACGGTATCCTCGCAGCTCCTGGACATGGGCGCGCAAGCGGTGCAGGCGCTGAAGCCCGTGCAGATGAA GCAGCACGCGTGCAGCTTCGCGCTGTACGCTCACGACCTGAGCCGCGCAGGTGAGGTCCACCCTTCGTCTCCCGC CTCAACCAGGACGTCTCCAGTGCAGCGCTCTACGACTCCGACAAGCCCTCGGCGCGCTCATCGGCGTGGAGTACA TCGTGTGCGGACGCCATCTTCGAGAGCTGCTTCCGAGGAGCAGAAGCTGTGGCACTCGCACGCGTACGAGGTGAA GGCCGGGCTGTGGACCGACGTGCGCGTGCAGGAGCCGCTGCAGAGCTCGGAGATGGCGAGGATGCCAAGACGTAC GGCAAGCTCTGGTGCACCTGGCAGGTGGACCGCGCGACGCGCTGCCCTGGGCGCGCGCGCTCATGGTCTCGC CGCAGGCGTGGAGCCCGGCGGGTGCAGCGCGAGCTCGTGCACGGCGCGACGAGAGGTACAAGATCGACAGCTC GGCGCAGGGGCTGAAGGGGGCCAGGGTTGAGATGGACGAGCCGAGTGGATCAACCCGAACGCCGACTACTGGCGC CTACACGGCAAGGGGTTCCGCTCGACGTACCGCCACCGAGATGAAGCGCCACGCGCCCTTCCCGTGA
SEQ ID NO:57	ATGACGCCTCCACCGCGTTCGCGCGCGCACGAGAGGAAAACGTGGGCGGAGTCCGTGGCCAGCGAGTTTCGGGCGC AGCGCGCATCGCGTTCCTCTCATCGCCATGAACCTCACCTGGTTCGCCAAGCTGGCCGTACACACCGCCTTCCT CGGCCGCTCGGCGACCTCCAGCTCGCGCGCGCACCTCGGCTTCAGCTTCGCCAATGTACCGGCTTCGCGCTC CTCACCGGCTCTGCGCGCGCATGGACCCCATCTGCGGCGAGCGCACGCGCGCCAGCAACGGGAAGCTCCTCCGCA AGACGCTGGTGATGGCCACCATCCTGTCTGCTGGGCGGTCCATCCCATCGCCTTCCTGTGGTGCACGTGGACGC CGTCTCTCTCGGTTCGGACAGCAGGCGGACATGAGCAGCAACGCACGCAGCTACGTGGTGTGCTCTCTCCGGAC CTCGCGTACCTCTCTCGTCAACCCGCTCAAGTCGTACCTGAGCGCGCAGGGGTGACGCTCCACACGCTGTTCG CCTCCGCGCTGGCCTGGCGCTCCACGTCCCGCTCACCATGTGGATGGCCAGGACAGGGGATCCAGGGCGTTCGC CACCGCGGTGTGGGTGACGACCTGGCCGTGGCCGTCTGCTCGCCGCTACGTGCTCTCGGAGCGACGACGG AAGGCGGAGGGGGCGCGGATGGGTGGAGCAGACGAGGGGTGAGTGGGTCCGGCTCCTCCGGCTGGCCGTTCCTCA GCTGCCCTCAACACCTGCTGAGTGGTGGTGTCTACGAGATACTGGTGCTCTGACGGGACGCTCCCGGACGCGCG GCGCACGGTGGCGGTGATGGCGGTGACGCTCAACTTCGACTACCTGCTGTTTCGCGGGGATGCTGTCTGTGCGGTG AGCGCGTGGTGGCGGTGTCGAACGAGCTGGGCGCGGGGAGGCGTGGGCGCGGAGGCGCGCGGCGCATGGTGTGCA TCGTGGGCGGCGGCTGGGCGGGGTGGGCGCGGGGTGGCGATGGTGGCGCGCGGCGGGGCTGGGGAGCATATA CAGCTCAGACGCGCGGGTGGCGGAGGGGTGGGAGGGCGATGGAGGTGATGGCGGTGCTGGAGGTGGTGAACCTC CCGCTGAACGTGTGCGGGGGATAGTGCAGGGGACGGCGAGGCGGGGTGGGATGTACGCGGTGGTGGCGGGCT TCTACGTGTGGCGCTGCGGCTCGGGGTGCGGCTCGCCTTCAAGGCCAGACTTGGGATCCAGGGCTCCTCCTGGG CTTCTGGTGGGCGCGCGGCCAGCTTGGCGGTGCTCTCACCTTCATCGCGCGCATGGATTGGCCCGCGAGGGCC CAAAAGCGCGGACTAGAACCACAGCAACCGTGGCCCAATTCCACCAACACGACGAGGTCTGCCAGCCTTGA
SEQ ID NO:58	ATGCCGAGGCTGCGCGCGCGCGCGGGCCACATGGATCCGGTTGGCGACGAGGCGCGGAGAGGAGGAGATGG AGGAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGATGAGGAGTTCTACGAGTCGTGGATCGGATCCTGTCTGTC GTCGTGCTCGTCCAGTCCGCTCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG CAGCAGCTGTCTGTCGTCGCGACGTTCTCCGCTACGAGGTCTGGATCTCCGAGCCGACATCCGTGAGGAGCGCC GCCGCTGTCTGCTGCTGCGCTCGGCTCGGCTCGCCACGACTCCGAGCCCTGCGCACCCGTCCTCCACGCGTATCATC CTCTCCCTCGTTGCGCGACCCCTTCCCCCGCTCTCTGTCGCGCTCGGCGGCTCCCGTGGTGGCGCGCGCG GAGGAGCCAGATCCAGCGGCCACGGGAAGCCGCGCTTGGCAGGAACCCGAGCGCGCGCGGAGCAATGCCGGA TCCGGAACCTGGACGACGTTACGGAGTTCGAGGTCCGGGAGGTTACGATGAGGTGGTCCGGGAGGTGCGCACTGG CCGGCAGCTCACCTTCGAGGAGTTCGAGCTCTGCATTGGCGCTCCCGATCGTCCAAGAGCTCATGCGCCGGGCC ACCACAGCCGATCATCTCCACCTCCGACCACGCGCGCCAGCATCAAGCCACGGAGGAAGCCTGGAGGCTGGC TGCGTGGCATCCGGACCTGGCGGGAAGCGTTGCATACGGGCGCAGCAGCACCAGATGAGAGGGACAAGGAGAAGGA GAAGGAGAAGAAGGAGAGGGAAGCGCGCGCTGAGCTCCGCCACCGATGACAGCTTGACGGCAACGGCTCGCGC AATGCAGGAGGGTACGGTGCAGGAGTATGGGAAGCGGTGCAAGGAGCTCACCGGCTGTTTATGACACAAGAAT TGGCTGCCCATTCGGGCTCAATCTGGTGTATCAACTTCAGCTTGGATGGACGATACCTTGCAAGCGCTGGCGAGGA CCGTGTCATCCATGTGTGGAGGTATCAGAGGGAGAAAGAAAGGAGAATTGCTCGGGGAAGGTACGGTGGCAAGG GAGAACCGGTGGTGGCTGCGAGCCGTTTCTGACGCTGTTGGGAATGGATCGCGGAGCTGGCAACATTGTCTATTGA GCTGTGCTGACGGGGTTTGTGGAAGAAGAGGAGGCCAAGGATGCAAAGCAGCCGGAAGTCTGTTGGCTCTGA TCATCTAGTTGTGCTGAATGTGTGTTGGGTTACAGAGATAAACCAGTATGCTCTCTATTGGGTACGCGCGCGAT

	GTTCTTGATCTATCATGGTCCAAATCTCAGTACTTGCTTTTCATCCTCAATGGACAAAACCTGTTAAACTATGGGACA TTACTACTAGTACCTGTCTGAAAACATTTTCACACACAGACTATGTGACTTGCATCCAGTTCAATCCCGTGGATGA TAACTTCTTCATTAGTGGATCACTGGATGAAAAAGTACGCATTTGGAATGTACATGATCGTAAGATTGAGGATTGG AATGATCTTCATGAGATGGTCACTGCTGCGTGTACTCCCTGATGGACAGGTTGCACTGGTGGGATCACACAAGG GAAGCTGTCATTTATTTGATACAACCTGAAAAGAAGCTTCAGTACAAAAGTCAGATAGAATAAGAATCAGGAAGAA GAAGTCTGGCCAGAAGAAGATAACTGGCTTCCAGTTTGTCTCTGGAAGCTCGTCGGAAGTCCGTGATTACCTCTGCA GATTCAAGAATCCGTGTTGTTAATGGTGATGAACTCGTTCACAAATTTAAAGGGTTCGGAATACAAGTAGCCAAA TATCCGCTTCTGTAGCTCCAAACGGGAAATATGTGGTCTGTGCCAGTGAGGACTCCACAGTGTATGTCTGGAGGCA TGACAATACTTCCCATCCGAGCAGAAGCAGGAGTGCAGTTGATGTAACCAACTCATATGAGCATTTCCATTGCCAT GATGTCACTGTGGCTATCACATGGCCCGCGCTGAATCCCGTGGCTCATTCGGGTCCCGTAGCAGCAGAAACAGTG ATTGAGACGATGCAGTGTGAACACGGGTGCGGATGCCCTGTAGAGAACAGTGCAGCATGATCTGAATGGCATGT CAATAGATGCACCAAGCGCCAGTTTGTGAAGGTGTTGCAAGCACAAGCAATCCTCCAGCGGATGGAGTATCAACG TCCTGGCCTGACGAGAAACAATCGTCTGCCAAGAGCAGTCTGGTCACTGCTCATCCGACCTTTGCATTGGAGCTT TGGATGTTACAGCGCCGCTCAGCTTGGGGATTGGTGATTGTCACTGCAGGAAGGGGTGGTGAATTAGGGTGTCCA GAATTTCCGGCTTCCCGGTTCAAGTGTA
SEQ ID NO:59	ATGGCTCCTGCGGTTGCCCTCCTCCCGTCACTCGTGCTCTCCGCGCGCGCCACCGCTCCAAACAGCGCCCG CCGATTCCGACGCTCGCCGCGCACCAGGGAGATCGCACGGGCGAGCAGGAGAAGAAGCAGCAGCAGCTGGAGTG CCCGCGCTGCCGATCCACCAACACCAAGTTCTGCTACTACAACAACCTACAGCACGTCGCAGCCGCGCCACTTCTGC CGCGCTTCCGCGCTACTGGACGACGGGGGACGCTCCGCGACGTCGCGGTGGGCGGCGCTCTCGCCGCGGCG GCGCGCGCAAGCGCCGAGGGTCTCCGCGACCGCCGACCTTCTCGCGCTCGCGCGCGCCACCCACGACTTCCAC CACGGACGCTACGCCGACCTCCAGCCGGCTTCCCGTCTCTCAGTGACGGCGCTTCTGCGCGAGTTCGGCTC GCCGGCGTTGCGCGCGCGCTTCTCTGGGCATCGGCTGTCCCTGACTTGTACAACCTGCGGGATCGCGCGGTGGG ACGATGGAACGGCGGTACCGGCGCGCGGTGGGACAACCTCGCCGACATCGCCGCGCTTGTCTCAGCTGCGCGCC GCCGGTAACGTA
SEQ ID NO:60	ATGTCTCACCCCCACGCCACCGCCCCCAAGCGCCCCGGCCACTTCTCCTCCTCCTCCGCGCGCGCTCCTCCCCGAC CTCCCCCGCGCAGCCGCACATGAAGAAGGCCAAGTTCCCGGCTCCTCCTCCTCCTCCTCCGCGCGCGCCCCCG GGGTACCCGAGAAGAAGCGGCTCCACGTGATCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG GAGGATGCGGAGATGGTGCTCGCCGACCAGGAGGAGCTCGCGCTCCGAGCGCATCGGCCCCGGCGGGGGTGCGCCG CAACCTCTTCCGGAAGAAGGCCACACTCCCCAGCCATCCCGCGCGCAAGCCCCCTCCGAATCAAAATAGGTGAGC CAAAATTGCCAACAACTTTGAGGAGGATACATGGGCTATTTTGAAGATGCTATTACAGCTATATTTCTAAACAG AACTTTCTGTCGATGTTGAAAACTTTACCAGGCTGCAGGTGACCTTTGTCTACACAAGCTAGGCGCAATCTATA CGAACGCATAAAGAAAGAAATGTGAAGTACACATATCGGCAAAAATATCAGCATTAGTGGGTCAAAGTCCAGATTTAG TAGTATTTTTGTCTCTGGTGCAAAGAATGGCAAGATTTTGGCATCAGATGTTGATTATTCTGTTGTTGCTTTA CTTCTTGATGTAATAATGTCAAGAAATGTTGCAACATTTGTTCAAGTGTGGGACATGGGGTTGAAGCTATTCCGCAA GCATCTTTCACTGTCTCGGAGATTGAACACAAAACCTGTTACTGGTCTTCTAAGATTAATGAGAGTGAGAGGCTTG GTGAAGCAATAGACAGGACATTACTAGTCTCTCTGAAGATGTTTACTGCTCTTGAATGTATTCTGAGAGTTTT GAAAAGCCCTTTCTGGAGTGTACATCTGAATTTATGCTACTGAAGGTGTTAAATATTTGCAGCAGTCTGATATTCC AGACTATCTCAAGCATGTGGAGACAAGGTTGCAAGAAGACATGAAGGTGTATTCTATATTTGGAAGCTAACACTA GGAAGCCGCTTATAACAGCTACAGAAAAGCAATTTATGCGAGCGGCACACATCTGCAATTTCTGAGAAGGGATTACA ATGCTTATGGAAGCAAACTCGTGTAAGACCTCTCGAGGATGTACACACTCTTCCAGAGGGTGTATGCCATTGAGTT GCTAAAGCAAGCACTTAGTTTATATATTCCGGGCGACAGGCCAGGGCATTATCATGGATGAAGAAAAGGACAAAGAAC TGGTGCCCTTTCTTCTGGAATTTAAGGCATCGCTTGATAGAATATTTGAGGAAAGTTTTGCAAAAATGAGGCTTTC TCCAATACATAAAAGAGTCATTGAAACATCTTATCAATTTACGCCAGAATCGACCTGCTGAATTGATTGCGAAGTT TCTTGATGAGAACTTCGAGCTGGAAATAAAGGTACCTCCGAAGAAGAGCTGGAGGGAATATTGGATAAAGTTTTGG TTCTGTTCCGATTTATACAAGGAAAAGATGTATTTGAGGCATTCTACAAGAAGGATCTGGCTAAGAGGTTGCTGCTG GGGAAGAGTGCATCGATAGATGCTGAAAAATCAATGATACAAAAGCTCAAAACTGAGTGTGGAGTCAATTTACCAA CAAGCTGGAGGGAATGTTCAAGGACATTGAATTTATCCAAAGAAATAAATGAGTCTTTCAAGCAATCATCTCAAGCAA GGACAAAGCTTCCATCTGGCATTGAAATGAGTGTTACGCTGCTTACAACAGGCTATTGGCCACATATCCACCAATG GATGTGAACTCCCCATGAACCTAATGTCTATCAGGATATATTTAAAGAATTTCTATTTGAGCAAGTATAGTGGAG GCGTTTGATGTGGCAAACTCATTTGGGTCACTGTGTATTTAAAGCAGAGTTCCTCAAAAGGTAAAAAGGAACTTCCGG TGTCATATTTTCAGAGTGTGGTTTTGATGTTGTTCAATGATGCACAAAACTAAGCTTCTCTGATATCAAGGAATCG ACTGGTATTGAGGATAAAGAATTGCGAAGAACGCTGCAATCACTTGCATGCGGTAAAGTTCCGGTTCTCCAAAGAT GCCAAAAGGGCGAGACGTAGAAGATAAGGACGAATTTGTATTTAATGAAGAATTTAGTGCCCTCTCTATCGCATAA AGGTGAATGCTATTGATGAAGGAGACGGTTGAAGAAAACACAAGCACAACCTGAGAGAGTATTCCAGGACAGACAG TATCAGGTGGATGCTGCCATAGTTTCAATAATGAAGACACGTAAAACCTCAGCCACACGCTTCTAATAACTGAGCT TTTTCAGCAGCTCAAGTTCCCAATCAAGCCATCGGATATCAAGAAAAGAATAGAGAGCCTAATCGACAGGGAGTACC TGGAGAGAGACAGGAGTAACCCCGATCTACAATTACCTGGCTTGA

SEQ ID NO: 61	ATGGACGCCGATGAGGCCGCGGGGAGTAGCAGGAGGATGGATCTGAACCTCTACCTTGGCCTCCCACGCGCCCCGG CCGCGCGCGCTCCGACCTCGGCTCCGACCTCGCCCTCAGCACCCCGATGCCCTCCTCCCGTCTCTCCGACGCT CCGTCGACGCGCCGCGCCACCGCCCGAGCTGTCGCATCCCCGTACTCCCCCTCTCACGCCGACCTTTCCCTCCG CTGCAGGAGGTCTACTCCCTGTACAACCCCGACGACCCGCTGCTTCCGAGACGCACTGCCGCGGTATGCGCCGCC TCCGCTCCGCTGGTCTCGGAGCTCCCTGACGACCTCGAGTTTGGCTCCACCCCCCGCGCGCTGGTGGCTGCCA GCGAACTGCTAGGTTGGGAGGACCGCGCTTTCGTGCGCGCATCGTCTCTTTCTCCCTGACACCGCAGCCGT TACTGGCGGCTTCTCGAGCAGACTGGAAGCAGATGGCTCCGTGCGAGGCGGTTTAGGTGCGACCTTCCGCCACTCAG TTCTGAAGCTTACCCAGCTGGGCGTGATGCTGCCGAGTCCAGTGTGCGAGCATGAACCGATGAATGATACTGTTG AACATAATAAGGTAGCTGCCGATGGCGCGGAAGTAGGCGCTCCGAGGAATCGGAGGAGCAGGCGAGGCGCTGCC ACATTTGAGTGTAATATATGCTTCGATATGGCCAGCGAGCCGCTGGTCACCTCTTGTGGCCATCTCTTCTGCTGGCC TTGCTTTGACCAATGGCTCAATGTTTATTCCAATCACAAGGAATGCCAGTCTGCAAAGGCGAGGTGACTGAGGCGA ATATTACTCCGATCTATGGGAGAGGGAATTCATGTTTGGATGCCGAGAAGGCTGTGGAAGGTGGGAAACAAACAGGT CCTACTATCCCACCAAGACCACATGGAATCGGCTCGAAAGCTTCAGGCAGCAGTTTACCATTTCGACCCGATCTC AAGAAGGCTTGGTGAGGCTCATGGGTTATTGTCATCATGGAGGCGCCTTCTGGACCAACAGATTATGAATCTGCGA GTAGGTTTGAAGGTCCGCTGAATCAGCTGTGCGAGGAATGGTTGACACTGCTCAGCTCAGCACACCAGTCGCCTA AGTAGATTGGCGTCAAGGATGAGAGCAAGACGGTTGCTGAGAGAAGCAGACAACCTTAACCTCCCGATGGCGGATC CACTTCCCTGACAGTGGTTTGTATCAGAAACAATGCATCGGATCCATCCAGAAATGGTCCGAGCTCATTATTACAG ATGGAATTGACTGGTTGGTGGACTTACCCTTCTTGGGTATGAAGACACGGAAAGATTGTCATCTGCCATGAGTGAT TTTAGAAGGATAACTGACCAAGCCAATATGGTGCATCGGCTTCATCATCGAATCCTCCAAATCTCGAGTCAACATT TGACAGAACTCATGTTGTTGCGAGCCTTCTGCGAGCAAGCATCTAATCAAGCACTGCTGCGATGATACAGGGGG ATGCTGGTATCTCTGAGAGTGCAGGAGAACCAAGTAACGCGGGGTCTCAAGATCCTGAGGAGGAGAGGAGGAGC AGTCCCTGGGTTCTTTGGATGCTGATGGCGGGGCTCCACGGAACAAGAGGCGAAGGATAAATCTGA
SEQ ID NO: 62	ATGGTGGGAGGAGAGCTTGTGCTGGCTGCTCTGGTGATCTGCTTGTCTTGTCTGCTGACCTGGTGTGAGCCACTT CCTGCCTTTTGTCTCTGAATCCCAAGGCTCCCAAGGGAAGCTTTGGGTGGCTCTCCTTGGTGAGACGCTGAGGTTCC TCAGTCTCTATGCTAGCAACACCTGGGCGAGTCTCTGGAGGATCAGTGTCTCCAGGTATGGGAGGGTGTTTAAGTCC CATCTGTTCTGCACCCCCACCATAGTGTCTGTGACAGGAGCTGAACCACTTCATCCTTCAGAATGAGGAGAGGCT GTTTCAGTGCAGCTACCCAGGCCAATTTCATGGCATTCTGGGCAAGTCTCCATGTTAGTGGTCTAGGGGAGGACC ACAAGAGGCTCAGGAACCTTGTCTAGCACTGGTCACTCCACAAAGCTCAAGCCAGCTACCTTGGCGACATTGAG AAGATTGCACTGCATATAGTTGGGTGATGGCATGGCAAGAGCAAGGACAAGGGGATGGTCAATGTCTATCGCTTCTG CGAGGAGGCAAGAAAGTTTGCATTGAGTGTAAAGTGAAGCAGGTGCTGGGCTATCACCAGAGGAGCCGGTCACTG CCATGATACTTGAAGATTTCTCGCTTCATGAAGGCTCTCATCTCTTCCCTCTCTACATCCAGGGACGCCCTAT GCCAAAGCTGTGCGAGCCAGAGCGAGGATATCAAGCACTGTGAAGGGTATTATTGAGGAGAGGAGGAATGCTGGCTC CAGCAACAAGGGTGATTTCCTTGATGTGCTGCTTTCAAGCAATGAGCTCTCTGATGAGGAGAAAGTGAAGTCTTGTG TGGATTCTTACTGGGAGGATATGAGACCACCTCACTCTTGTATCTCCATGGTTGTGATTTCTTGGCGAGTCAAGCT CAAGATCTGGAAGTGTGAAGAGGAGCATGAAGGCATAAGATCGAAGAAAGAGAAGGACGAGTTCTTGAGCTCTGA AGACTATAAAGAGATGGAATATACCAACATGTTATCAATGAGGCAGTGAAGTGTGGCAACATTGTCAAGTTTGTCC ACAGGAAGGCTCTCAAAGATGTGAGATACAAAGAGTATCTGATTCTTCTGTTTGAAGGTCCTACCTGTTTTAGT GCTGTTTCAATTGAACCCCTTACTTCATGGAATGCCCAACAATTTAGCCCTGCAGATGGGAGGGTGAAGCCAAGG GACAAGCAAGAAGTTTACGCGGTTCCGCGGTGGCCCGGCTCTGCCCTGGATCAGAGCTTGCAAAAGTAGAGGCTG CTTTCTTCTCCATCACCTTGTGCTCAATTATAGATGGAGAATCGATGGCGATGACATTCGATGGCATACCCGTAC GTGGAGTTCCAGAGAGGTCTGCCCATAGAAATCGAGCCACTTTGCTCTGAATCTCTGA
SEQ ID NO: 63	ATGGCGACGCTGCCGACCTGGGTGTGTCGCTCTCATCAACATCTTGGGCGCCTTCGTCTTCTCTCTCATCTTCGC CGCCTCCGCTCCAGCCCATCAAGCAGCGCTCTACTTCCCAAGCTCTACCTCACTGGCCAGCGACGCCACCACC CTCACCTCATGGCTTCGTCAACCTCGACCTCTGCTCTCACTCCGCTTCTCGCTCCGCTCCGCGCGCTCCGCG ATGTCACGCGCGACCTCATCCACCACGCGCGCTCGACTCCGCGCTCTACCTCCGAATCTACACGCTCGGCCTCAA GATATTTTGGCCATCATGACTGTGCGCTTGTGGTTCTTATTCCAGTTAATGTCTCTGGTGGCAGCTTACTTAATT TACGAAAAGAAATTGTCTTTAGTGATATTGATAAGCTTTCCATATCAAATGTCAACCTGGATCCAACAGGTTCTTT ATCCATCTATTAAATGGCATATGTGTTCACTTTTGGAGTGTCTTATGCTATACAAAGAGTATAGCAATGTGGCAT TATGAGATTGCACTTCTGGCTTCTCAGAAGCGTTGTGCTGATCAGTTCAGTGTGATTGAGAAACATACCTCATG TTTCAAGCCATTCAACATCTGAAACAGTGGATGAATCTTCCGTAGGAATCATCCAGACCCTATCTTGGTCAGCAG GCTGTTTATAACGCAACAGGTATGCTAACTTGTGAAGAAAAAGAGAGGCTTCAAACCTGGTTGGATTACTACCA GCTGAAGTTTGAAGGCATCTGGAAAAAGACCAATTGGAAGGACAGGGTGCCTTGGTTTCTGCGGTAGAGAAGTGG ATCAAATCGACTATTACCGTGCTAGAATCAGCGAGCTTGATAAGAAGCTTGATCTGAGCGTCAAAGAGTTCTCAAT GACCCAAAAGCTGTTATGCCAGTTGCTTTTGTGACATTTGACTCGAGATGGGAGCTGCTGTATGTGCACAGACACA ACAGTCAAAGATCTACCCAATGGCTAACTGATTGGGCTCTGAACCGCGGATGTATATTGGCAGAACTTGTCCA TTCCATTTTTCTCTCTCAGTATCCGCAAGTTCTGATATCCATTGCAGTTTTTGTCTGGTGTCTTCTACATGATA CCTATAGCTTTTGTGCAATCACTTCCAATCTTGGAGGATTTGAAAAAGTTGCACCTTTCTTAAGGCCTGTGATAGA CACACCAGTGGTGAAATCTTCTGCGAGGTTTCTTCCGGGTTTGGCTTTGAAGATTTTTCTGTATATCTTCCCAA CGGTTTTGATGATTATGTCAAAGTTGAAGTTATGTCTTTATCATCTCTGGAAGGAGGGCTGCTTCAAATAT TACTACTTCATGCTGGTGAATGTATTTCTTGAAGCATAAATCGCTGGCAGAGCTTTGAACAGCTAAATGCATTTTT CCATCAGCCACCTTCACAAATACCAAGGACCATTTGGAGTAGCTATACCAATGAAAGCTACATTTTTTATGACATACA TAATGGTTGACGGGTGGCTGGCATCGCAACGAGATTCTTCGAGTGAAGCCGCTGGTGATATACCACCTGAAGAAC

	ATGTTTATTGTGAAGACGGAGCGGGACAGGGAGAGGGCAATGGATCCGGGCAGCATTGGGCTTGACAGAGAACCCTCC ATCACTGCAGCTGTATTTCTTCTTGGGCTGTGTATGCTGTGGTCACCCCATTTCTCCTCCCTTTCATTATCATCT TCTTTGCCCTTCGCTTTCTCCTCGTGTACAGACACCAGATCATCAACGTGTACAACCAAGAATACGAGAGTGCTGCTGCG TTTTGGCCTCAGGTGCACTCTCGCATAATAGCGAGCTTGCTGATCTCGCATGTAACCTCTGTTTGGGCTGATGAGCAC CATGAAGGCTGCCTACTCCACCCGCTGCTTATCTTTCTGCCACTCCTCACCATATGGTTCACAAAGTACTGCAAGA GCCGTTTTCGAGCCTGCTTTCCGCAAGTACCCTCTAGAGGAAGCGATGGAGAAGGACAATCTGGAGCGCAGCTCGGAG CCAAACCTGAACCTCAAATCGTACCTGCAGAACGCTTACCTGCACCCCATTTTCCACATGTTTGAGCAGCAGCAGCA GCAGGAGCAGGAGCAGCAACGGAGGAGAGGTAGAGGTGCGAATCGACAAGGCGCAGCAACATCATCATCGGCAGG TAGAGGAGGAGAGGAGGAGGAGCAAGAGCAGCCAGGCTACAACACACTACTACCACCATCACCATGAGCAGACCACA ACGACGACACACCACCATTACCATCAGCATGAGCATATGAGCCACTACCACATGGGCCCTCCGACACAGCTGACTC ACCCTCGCCGCGCACTTTGTCTACCATTATGGCGTCGACCCTTGA
SEQ ID NO: 64	ATGGAGATGACCAGAAGCCTTACGCTCGTGCCGCTCCCGCGCAGCTCCGGCCGGCATCCGCGGCCCTGTGCGCCGGC GGCGGAGGCGGCGAGGGCTTCCCTTCCGGTGCACCTCTTCTCACCATCGCCTCCTTCGAACCAGCAGCAGCAGGAAAT GCACATCAGGGCGCTGCAGCCGCGGCGAGGATTGGGTGGGGGAGTGGGTCCGGAGCAACGACACGCTAGTCCGCGGC CTGCCATCCTCGGCGGCGGCGCCTCCCTGCTCGCCGCTCCTCTCAACCGTGCGGTTTTCCGGCATTCGAGCTGTG CCGAGCGCTCCAGTTCGAGTCAAGGGCTGACATACTGACTCTTGCTCTCTCCGTAACATGATATTTCTGCTGGCCT TGTTTGGTGTGCTATCCGCGCGAAATCCATTTCTCCTGTTGTTCTCGAGGTGTCGAGTGCAAAACGGGTAGGAACG GGTGTATTGGACTCGGCTCTTCTGTAACCTTTGGACATGGGATTCCCTTACAACCTGCAACTTGTGCAAACTCCT TGGTTGTTGTGTATGGAGGTAATTGTGTTCTTCAAAATGGGGTTGCTGCTGGCTCTCCAGAGGATGGTAATGCAGT TATGGTGGATGCACAGAAGTTCATGCAAGGTTCCCTTTATAGAAGTGCCATGGAATCCAAGAAGCAATCTTACCTA GCAAACTCTGCTTATATCCTGGAAGGACTGAACCTACCATTCTTGCCAGCTAACACGCGAGGCCCTAATATTGCAAC CAATTGGTGATAAAGGAATTGCACTTATGGTGGTGACACTATAAGGGGTTCACTAATCTTGATCAGGCATGGAT TGCAATGATAGCAGATAAACTGGATGCTACATTGTCAAAGTCGTAA
SEQ ID NO: 65	ATGGCATCATCAGTTGACAGGCTCAGTGACTCGTCTCCTCCTCCGCTGCTGCTGGCTTGCCGATCGCGACCAATAA TCGTCGCCCTCATCAGATTGTTACCGCTCCTCTTCGCCGCTCGTCTGCTTGCTCTTCTTCCACCATGCGTTCATG GAGCTCGTCTCTGATGATGCCAAAGAAGCCAAAGTTGACAGAGCCAGCGACCAGACGACGACGACGACGACGCC CGGCGCGGCGGCGGTGGCTCGGTGGTCTGTACCGTGAGGGAAGGAGGAGGTGGTGGTGGTTCACGGCAGCGGCCATGC CGGCGCGGCCACGGCCACGGCAGCGGCCACGGCAGCGCGGAGCCGAGCAGCCAGCAGCCACGCGGCGAGCGCGCG CGGCCGGATCCGTGCGCCCTCCCATGGCGGCCCTCTGCGCCGCCCTCCTTGTCGCCGCCGTCGTCGCTCTGCTTCGC TTCTGA
SEQ ID NO: 66	ATGGAGAGTGCAAAGAGATCTTGCCCTTGCTATCTCCCTCATCCTACTCCTACTCCTTGTTCGAAGTATCCATGGAGC AAGGCATGTTGCTGCAGCTATCAAGGGTACAGGCGCCGACAGCGAGATGGTGGTGACGGAGAGGACGGCCGGCGGCG GCGGCGGACATGGACGCGGTTACACAAGCCACCGGTGCGACAACCCCAACAATCCCAACGACGCGGTGGCTCCGGCAGC CCGGTGGTGACCCGACAAATGTCGCCACAGGGGCCACCAACCGCGCGCGGCGAGGACGCGCGCGCGCGCGCG CGACCCCGCCTGGCAGCCTGCATGCTTCTGCTGAGGAGCAGCTTCTTCTGCTGTTCTTGGCTGA
SEQ ID NO: 67	ATGGCGGGCGTTGGATTCTGTTGGAGGACATGCTGCGGGAGCAGAGCCTCCTGGAGGCGACCTGCGGCGACCTCTTCGAC CACATCGACGACCTGCTCGACTTCCCAAGGAGGAGTCCGGCCGCGACGTGCTCCTGCTCGACGCGCGGCGGCCAGGG AGCCCGCTGTCTCGCGCATCATCGGCGGCCACGCCACCATGGCGGCGGCGCGCCACCGCCGCGCAGATGATGGCG CTCCCCCGCGCGGCCCGCCGGAAGGACGACGCGTGGCGGTGTTTCGACGCGGCGCGCGCGCTCGGCGCGCGAGGTG TTGACCGCAAGGACGCGCCACATTGGCCCGTGTGATGAGCTGGACATGGACATGGCGCAGCTGGAGTGGCTGTGCGGG CTGTTTCGACGATGGAACCATCCGCGACGAGCCGAGTTTTCGGGCGTCAACTGCGCGCGCGCGATCAAGGCGTGGCG CTGACGCGCAACGCGCGCGTCTGCTGCGGACAAGCGGAGGAGGCGCTGTTCCGCGAGCTCCAGCCCCATCTCCGTG CTGGAGCACAGCGGCTTCAACGTGGCAACCAATGGGGGCTCCTCCTGCTGCTCCTCCTGTCGGCGTCTCCTGCTCG GAGTCTGTTCTCCGGCAGCGGCCGCGCTGCTGCGCGCCGCTGTCGCCGCGCGCGGAGCGCGCGCTGCTGCTCATCCCG GCGCGCGCGCGCAGCAACGGTCTAGGCCGTCCGCGTTCGGGCTGTCGCCGCGCGCGCGCGCGCGCGCGCGCGCG ATCCTGGTGCCGACGCAATGTACTCGTCCACCTCGTGCACCTCGGATCCGAGAGCATTGCCAGTCCAACCCGCAC CCGCGCGCGATGAAGAAGAAGAAGGCCAAGAAGCCGCGCGCTCCGGCCGCGCGCTGACGCGGAGGCGCGACGCC GACGCGCGGACGCGGACTACGAGGAAGGCGCGCGCTCGCGCTCCGCGCGGCGACCGTGCGGCGGTGCACGCATTGC CAGATCGAGAAGACGCGCAGTGGCGCGCGGCCCGCTCGGCCCAAGACGCTCTGCAACGCGTGGCGCGTCCGCTAC AAGTCCGCGCGCTCTTCCCGGAGTACCGCCCGCGCGGCGAGCCACCTTCATGCCGTCCATCCATTCCAACCTCCAC AAGAAGTGGTGGAGATGCGCCAGAAGGCAACCGGACCGCGCGCGCGCTGCGACCTCCTGCGAGTACATCCGCGCG CGGGATTAA

SEQ ID NO: 68	ATGGGCGGGTACGAGCTCGTCAGGAGCGACGACGCCGCGCGCGCGCGCCGCGCAGATCTCGAGCTCGGCGGCGAGCGGC AGCTGCAACGGCGGCGGCGTCTCGGCCAAGTCCCGGCTCCGTCATCGCCGCGTCCGAGGGCGGCGCGCGGACGCGG CTCGTCTCCCTCGACGTCTTCCGCGGGATCACCGTGCTGCTTATGATCATTGTGATGATGCTGGAGCTTTTCTCCCA GCACTGAACCACTCTCCATGGGACGCGGTAACCATTCGAGATTCGTGATGCCATTCTTCTTTTCATGGTTGGGATC TCTCTAACGCTCGCGTACAAGAGGGTGCCGACAAATTGGAGGCTACTAAGAAGGCTGTACTACGTGCCCTCAAGTTG TTCTGCCTTGGCCTTGTTCTCCAAGGCGGTTTTTCCATGGTGTCGCGAGTCTCACTTTGGTGTGATATTACAAAA ATACGGTTGATGGGTATACTTCAGAGAATTGCTATAGCTTATCTTTGGCTGCAATCTGTGAAATTTGGCTCAAGGGA GATGATGATGTAGATTGTGGACTCGATGTGATACGGAGATACCGTTACCAATTGGTTGTAGCATTGCTCCTGTCAACC ATGTATACTGTTATTTAAACGGTGTCTACGTTCCAGACTGGGAATACCAGATATCAGGTCCTGGTCCACAGAGAAA TCATTCTCTGTGAGATGTGGAGTAAGAGGAGACACTGGTCCAGCTTGCAATGCCGTTGGAATGCTTGACCGTACAATC TTGGGGATCGATCATCTCTACAGACGACCGGTTTATGCGCGTACAAAGCAATGTAGTATAAACTATCCGCAAAATGGG CCCCCTCCACCTGATGCTCCATCATGGTGTGAGGCTCCATTTGATCCTGAAGGCTCCTCAGCTCTGTTATGGCAATT GTCACATGCTTGATTGGGCTGCAGTTTGGACATATAATTATACATTTTGAAGAACACAAGGGAAGGATAATAAATTGG CTAATTCCTTCTTCCATGATGTTAGCACTGGCCTTCTCAATGGACTTCATTTGGGATTCGTATGAACAAGCCGCTGTAC ACGATAAGTTACGCCCTTGGCTACCTCTGGTGTGTCAGGGCTTCTTTTGTGGGATCTACACACTGGTGGACGTGTAT GGATTTCAGGAAACTTACCATCCCATGGAGTGGATGGGTAAGCACGCGCTGATGATCTACGTGCTAGTGGCATGCAAC ATCCTGCCCATTTTCATCCATGGTTTCTATTGGAGGGAGCCCAAGAACACCTTTTGAGTTTATCGGAGTTGGGGCA TGA
SEQ ID NO: 69	ATGGCCGCGACTGGCGGCGCCGCCGGGGAGAACGCGCCAGCAGCCTCCTGCTCGGCGTCCGGGGCTACACGTCCA CCCTCAAGAAGCCCTCCACCGCCAGCTGCAGGTTGAGCGCCGGCCATCCCATCGAGGTGACTTTGTGGGAGGCGTC CCCGCTGCCCCCTCTCCACTTCTCCGTCCTGCCCCGATCTCCCATCCTTCAATGGCAATCTGCTTGGCGCGCCT AAAGCCATCGCCCGCGCGCTCGACGACGCCGACGGCCAGCTCCTCCTCCTCCGAGTCCCATCGATCAGCTTG GTGCCCCGATGACAACGACTACTTGGTCTACCATCCGGATCCCCGCTCTCCGAACTGGATCTGCTCCCCAACCC GCCTCCCCCTACCTCGGTGACCACAGCTCGCCATACTCAGCTGCGGCGACGACCGCTACGTCGTGGCCGCCCTC CACGTCTGGAGTGAGTTCACTTCCACGCTGCGCCTGTACAGATCTTCTTGTTCGTCTGGGAGTTGGACATCGGAGG AGGTGTCCGTGGAGGAGCCGCTGAGGGACAGGCTGTGCCGATCCCGGACTCAGCCAAGAGGCGAGCTGTACCACGT CACCACCAAGACCATCACGCTCGGAGGTGCGAAGGGACCGTGGGCTGGGTTGATCTCTGGCGCGGCATCCTCCTC TGCGACGTGCTCGACGAAATGTCTCCAAGGAAGCTCCGCGACATGCCGCTGCCGCGGCCAAGGGCAATTGGA GGATGTACCTCAATGGAGATGTGTCTTTTGTGCGGACATCGCCATCAGCCAACACAAGGATTCCATCAAGTATCT GGAGATGGAGATCGTTTACCAGAAGCGGTGACCACACCATACCCACCTCCACCTCTGCAGATCCTACTTCATAC CTTGAATGGGTTCCGCCGAGCAGAGAACCTCAGCCGACACGGCGACGCTCCGTGTTCCACCCTGGTTCTGTGGAGAA TCACTACATGGAGCATGCCTATCCCGGTCACTTTCATGGGACGACTGGCGCGCTGACTGCACTGCTGAATCGCGTGA AGTCCATTTGACACCAACCCCAAGTCAACATTACGAGTTGCTTCATAGCCTCATGCTCAGCAACAGCGGTGATGAA CACAGGGAGGAGGCTCAAGGTCAAGGGGCAACCTCTTCTTGTCCCTAGGTCGCTGCGTTTGTGTTACCCGGCCT TGAGTTGATCGATGATGATGTTGTTTACCTCTTGGGCAACGCTGCTGGCAGGGGTGCTAAGACGGGAGGAATGAT GGTCCGTGTTGACGTCAGGAACAAGGAGCTGCGAGGAGTGGCCAAGCTTGACCCCGAAAGAACACCTCTACTCC ATGCGATGCTACCTTGCAACTGGGATCTCCAAACGCTCAACACTACCACAGACACAAGAGTTGGACGACCTGAGG AGGATGCAGAAGCCGCCGAGTAG
SEQ ID NO: 70	ATGGCGAATACCACCACCAGGAGTACTACCAGATGGCGGCGGCGGCGAGCGGTGGCGTGGCCGAGGGAGCCGGACAG CCCGCAGCTGAGCATCATGAGCGGCTGCAGCTCCCTCTTCTCCATCTCCACCCTGAGGACGACGACGCGCGCG GCGTCCGCTCGCCGGCGCCGCGCTGCCGCCACGCGGCTGTCGCTCGCCGGGATCGCCGGCGGCGCCAGTACCCCC GGCGGCGACGAGGTGGACATGGAGGTGCGGCGAGCAGAGCGGCGGCGAGCGGCGACGACCGGAGGACCATCCGGATGAT GAGGAACCGGGAGTCCGCGCTTCGCTCCAGGGCGCGCAAGAGGCGGTACGTTGAAGAGCTAGAGAAAGAGGTTCCGC GGCTGGTGGATGACAACCTGAATCTCAAGAAGCAGTGCAAGAGCTGAAACAGGAGGTTGCTGCAGTGGTGATGCCCT ACAAAGAGCTCACTGCGACGAACCTCATCAACTCAATTCTGA
SEQ ID NO: 71	ATGGCAGAGAAAAAGAAGAAGAAGAAGAAGAAGCCGAATCACTCCTAGTCTTTACAAGCTGGAGATCGATCGGG ATGGGGAGGGSTCGGGTGGAGCTGAAGAGGATCGAGAAACAGATCAACCGGCAGGTGACGTTTCGCCAAGCGCAGGAAT GGCCTGCTCAAGAAGGCGTACGAGCTCTCCGCTCTGCGACGCGGAGGTGCGCCTCATCATCTTCTCCAACCGCGGC AAGCTCTACGAGTTCTGCAGCACCAGAGCATGACTAAAACGCTTGAGAAGTATCAGAAATGCAGTTACGCAGGACCC GAAACAGCTGTCCAAAATAGAGAAAGTGAAGCAATTGAAAGCTAGCCGCAATGAATACCTCAAACCTGAAGGCAAGGGTT GAAAATTTACAACGGAATCAAAGGCAATACTACAAATCTAAACATAGGCTGTGTTTAGTTTCGGTCCAAAGTTTGAAT TTGGTTAAAATTAGAGACGATGTGACTGAAAAGTTGTGTATGTATGAAAGAAATTTGCTGGGTGAAGATCTTGATTCA TTAGGCATAAAAGAGCTCGAGAGCCTAGAGAAGCAGCTTGATTTCATCCCTGAAGCACGTGAGAACTACAAGGACAAAA CATCTGGTTGACCAACTGACGAGCTTCAGAGAAAGGAACAAATGGTTTCTGAAGCAATAGATGCCTTAGGAGAAAA CTGGAGGAAAGCAACCATGTTTCGCGGGCAGCAAGTGTGGGAGCAGGGCTGCAACTTAATTGGCTATGAACGTCAGCCT GAAGTGCAGCAGCTCTTACGCGCGCAATGGGTTCTTCCATCCACTTGATGCTGCTGGTGAACCCACCTTCAGATT GGGTACCCTGCAGAGCATCATGAGGCGATGAACAGTGCCTGATGAACACCTACATGCCCCATGGCTACCATGA

	AGGACACTTGCGAAGTATTGTCACTTGAAATCATTAACAAGAGATGCTTCAAAAAGAGCAGCCTAGGTGGAACCTCTGAT TGTCTAGATATGATCTTACTGCAGCACTTGAACCAGTTAAATGTTTCTTCTCTCAGAAAGTTATCAATGTTTCCA CTGGGGTGGCAAGCGCTGAACAACTGATCCACTGGTTCTACTCAGGCGAGCTACCCAAGATCGACCCCGATTGCCGA TGGCGAAACCTGAACAGCGAGGAGCAGCTTTCTCAGCTGCGGCCCTACGCCGAGCTGTCATCCCTGTCTGAATTCTGG TTCCTGGAGGGAGTGAAGGAGGAGAGCCTGTCACTGGTCACTCTCTGCTGAGTTCCACCAGCAGCGGCCCGCTCCGTC GAGTTCGTCTCTTCCGCGCGCAGCTGGGTCACTGGGAGATGGTGGAGGCCCGCTCGGCAGCGTCCGCCATCTGTAC CCCAAGCTGCGGACTCCGCTCAGCTGGAGCAGCTTGATGATGATGTGCTCAACATGCTGCGGACAGAGTATGTGAGA CGCACGCAAAAGAACGGAGTTGGCTCGCGCGCGCGCAGGCCGGGGCCAGAGTGGTGACGCGGTGTACAGGCGGGGG CAGAGGGCAGATTATTGGCAAAGTGGTGGTTTTGGAGATAATTGGAATTTTCAAATGGTGATTCTTAATGCCTCGGAA GAGCATTGCCGGGAGTCCAAATTTGATACAATTGAGTTTGTAAAGCTCGTTCTTGTACGGGAAGGTTTCTAGGGGA TTTAGATTGCGTACCTCGGTATAAACAAAGAGGGAGGCCCAAGAGGGGTACAGTAATTTATAGCAGGTCGTACAGGA GGGCTGCCTCCCTGGTGTGGTGCAGGAAGTACAGCAGCATTTGGCAGCCGTACAGATGGCCGTACTTCCAGGCTTGGAG TCGCATCAGACGGCGCAGGTGATAAGGCGAGGCGCAGGGCGCAGAGGCGAGGGGAGAGACGTAACCGTAACCAAGCAA AGCAAGCGCCCATGCGGCGCGCCGAGACGATGCAACGCGAGCAGCCGAGAGCAGAGCAAGAGCCAGCGTAGGAAA TGGCCACCACCAGCAGATGGAGATCCGAATTCCEAGGAGCAGGGGTGCCAAGTGCAAAGCGGTGCGAGGAGAAG AGGAAGAGGACACAGCAACAGCGTTGCGCACTGCTGCTGCCATTGCTGCCTCGCGTTTACAGCTATAG
SEQ ID NO:77	ATGGCCTCCGCCGTGCGAGTAACCTTGCTGCACTGCGCCCGCGGCTGTCATGCCGTTCCGTTGGATGGCATGGTC CGCGTGTCTCGTTACGCCGCGACGCCGCGCGGGGCTGAGGAGGCTGCCGCGGTGGTGTGTCTTCCGCCCTGGC CGCGCGCGCGCGGTTGGCAGCAGCAGCGCCGAGCGCGCGATATCAAGGACTTCATCGACTTCGAGTTTCAGC CTCGGGGCTCCGCCACCATGCTCCCGCGGACGAGCTCTTTGCGGACGGGAAGCTGCTCCCGCTTCGGAAGCGCG CGGCTGTGCCGAGATGGATGCGCGCGCGCCACGGCCGCGCAGCCTGAGGCAATGCCGGCGCTTCGGAGCCGAT GAAGCCACTACGGCGGCTACCGCCGCGGTTGACGCGCGCCGACCCGTACGTTTTCTCTCTTAAGGCGCCAGCTGC TCGAGCCGTTGGCGGAGTTGCTCGGCTGAAGAGAGCGCGCAGCGCAGAGCCGAGCCATCGCCGTCTGTGCGC CCGCGAGAACCCCGGGAGAGCGATGAACCTGACGCGCGCGAGGTGCTGAAGCTGCTGCTCCAACGGAACAACGG CCGCTGCTCCGGGCTCCGCGTCCGAGCTCGCCTCTGCGCGCTCTCCGCGACAGCTCCGACTCGGAGGCGTCT CTCTCCCTCGCTCTCCCGCTCTCTCTCTCTGCTGCTGCTCTCTCTCCGCGCACGACACGACATCCCGC GCCTCTCCCTCGACTCCGCGCTGACCCCAACCGCCCGCATCCGCTCTGCTCCGTTCTCTCCACCGCCACTCCAC CTCCTCATCCTCTCATCCGCGCGCGCGCAAGCCCGCGCGCGCGCCCTCCCGCGCGCGCGCGCGCTGC CTCTCCGTCGACTCCCGCGCATGAACCTCTCCGCAAGATCGTGTTCAGGGCTTGGAGCGCAGCTCCAGCTCAC CGTGACCCCTCCACGCGCGCGCAAGCCACGCTCCCGCGCGCTGACCGGTCTACTCTCTCCGGCGTCCGCGTGGC GCGGTGGTGTGAACGTCGCCGTGTGCTCGCGCGCGGTGTTCGGGTCTTCAAGGACAAGAGGACGCGCGCGCG AAGGACGCCATGGCGCGAGGACGAGGTGCTGCTGGGCGGAAGACGAGCGCGCGCGCGCAAGGGTGGAGCGCG AGCTGGGAGATCTTGTGGTAA
SEQ ID NO:78	ATGAAATCAGCGGACTTCTGACCTCTGCTGGCATCAATATCGCTCTTTCTGTGCTGTTTATATCGCTCTATTCTGT TCTGAGGAAGCAGCCAGCCAATGTCAGGCTCTACTTTGGGAGGAGGATTGCCGAGGAGCATAATCGGCTCCGAGAAG CTTTTATCTTGGAGAGATTGTACCATCTACTGCTGGATAGTAAAGCCCTGCAGTGTACCGAGGAAGAGATCTTG GCTGCTGCTGGGCTAGATGCTGTTGTTTTCAATAGAATTCTAGTATTCAGCTTACGCATCTTCTCTCTAGCTGCCAT TCTGTGTGTGTTGGAATCTACCACTGAACCTCTTGGGCAAGATATACATCATGTTCCGATTCTTCCAGATCAT TGGATATCTTTACAATTGGGAATGTGAAAGTGAGATCAAGATGGCTTTGGGTCCATTGTGTAGCCTTGTACATAATA TCAGGAGTAGCTGCATTCTCTATATCTTGAGTACAAGCACATTGCTAGGCTGAGGCTCCGTCATCTTACTTGTGC AATGCCCAATCAAGCCATTTTACTGTCCTTGTGCTGGAATACCAAGGAACCAAGAAATCATGCAATAGCTA TTGATGATTTCTTACCAAGTACCATGGATCAAGCTACCTGTTCCATCAAGTTGTTTACAAGTTGGAAGGTTTCAG AAGATAATGACTGGTGCTAAGAAGGCATACAGGAAATTCAAACATTTTACAGACAGCACTATTGATCAGAGGTGTCG AGCAATTTATACCGGTGCTGTCTGTGCGGAGCCTCATCTAATCTTCCAGCTGTTGGCACTGGGCTTGAGCAGA ATCAGGGGAAATCTGACCTCAAGATTCCAGCTGAACTAGATGATCAGGAATGTGCAGCTGCTTTTGTATATTT AGAACTCGGTATGCTGCTCTTGTGCTCAGAAATCTCCAACATCTAACCTATGAAATGGGTTACTGATCTAGC TCCAGAACCAGATGATGTGATTTGGTCAAATCTTGGCTACCTTATAAGCAGCTTTGGATTGCGCGAATAGCTACGC TCCTTGGTTCAATTGTTTTATGTTATCTTTCTGATACCACTGACATTTATACAAGGACTATCTCAGCTAGAGCAG TTGCAGCAGAGGCTTCTTCTGAGAGGGGATACTGGAGAAGAAATACATGAGCCAGCTTGTAACTGGGTACCTTCC CAGTGTACATCTGCAAAATATTTTATATGCCGTTGCACCGATAATGATATATTTTCTACATTAGAGGGGCTATAT CTCACAGTGAAGGAAGAGGAGTGTGCTGTAAAGTGCTGACTTCACTGTTTGAACATATCTTTGGAATGTA CTATCTGGTACTGTATAAGCCAATTGAATGTGTTATCAAGCCCAAGGACATCCCTGTCAGGCTTGCTAGAGCTAT ACCTGTCCAGGCTACCTTCTTATACCTATGTTCTGACATCAGGATGGGCCAGTTTATCATCTGAACCTTATGCAAT TATTTGGTTTTAATATGGAATTTGCTGAGGAAATATATTCTACGTATGCCAGAAGACACAGAGTTTGTTCCTCATTC CCATATCACACAGAAGTCCAAAAGTTTGTGCTTCCGACTACTGGGCTTCACATGCTCTGTACTGGCACCTTTGAT CTTACCTTTTCTGTAGTGTACTTCTTCTTGGTTACATCGTGTACCGCAATCAGTTGCTCAATGTTTACCGCACAA GATATGACACAGGGGGTTTGTACTGGCCAATCGCACACAACGAGTATATTCTCTCTGCTGCTCACACAGATTATC TGCCCTTGGTGTATTTGGCCTGAAAGAATCACCAGTAGCTGCAGGCTTACCATACTCTTATCATCTCTACTCTGTT ATTCAATCAGTATTGCAAAATCGACTTCTCCATTATTGCAACTACCCAGCACAGGATTAATTGACATGGACA GGGAAGACGAACGGTCAGGAAGAATGGATGAAATTCACCACCGGCTTCACTCTGCTATTGTGAGTTCCACGACACT

	AGCACCGGCACGGCTGCAAGGGATCAACCGAGCCGCCCGCTGGAGAAATGTTTCGCTGTCACTCTCCCTCGGTC CAGACCCCAAATGCATGCCGGCGATCGCCTCGTCGCCGAGCGAAAGCAGCTGCATCCTCTCGTCGTCCTCCAGGAG CTTCAGCGACTGCTCCGGGAACCTCAGGTTGTCTTGTGCCCCGGGTGTGAACCTTGAACCTCTCCATGTCCATCTGT GGATCTTAG
SEQ ID NO: 89	ATGGCTGCCGCCGACCGCCCTACGGCGATCGCCGGCCGTCCCGGCCACGTACAAGCCGGACCGCCGGAGG GCCTCACCATCTCGTTCGCGAGCTCTACGACCTGCCGACCTCGCCGGAGTTCTGTTCCACGAGGAGGCGCTCCG CAGCCGCCGACCTGTGGCGAGGACCTCAGCTTCTACACCGGCTGCGGCTACCTCGTCGGCCGGGCGCGGGGGCG GCCCGGGGCTGAAGCGCGCGGGGAGGAGGCGGAGCGCGCGAGTGCATGAAGCTGCGGGGGCAGCCGCTCTC AACCAGTGCGGCTCCTCGGGCGCGCTACGGCAACCGGCTCGGCGTCTGCGGCTGCTCTTCTGTTGGGATCGAGA GCACCGTGGGGGGCTCCGCGACGCGCGAGGCTGGGCCAACCCGTGCGCGCCGGGATCGGTACCGGCGCGCTCTA CCGCGGGCTGCCGGCCCGGGGCGGCGATCGTCGGCAGCTCCGTGCGGGGGCTCATGGCCGGCGCGGTGGTCTGTG GGGAGCAAGCGCTGACGAGATACGCGCTAA
SEQ ID NO: 90	ATGGACATGCCGCCACGCCCTTCCGCCGAGACCGCAACACCTCGCCCGCTCCCAACGGCGCCACCGCCGGAA TCCGGTTGAGAACTGCTACGTCTTCAAGAGCCGGCTGCAAGAGTATGCACAGAAAACCGCCCTCCAGACTCCAGA GTATCATACCTTCAAGGAGGAGCTTCCACGAGCCTGTCTTCAAGTCCACAGTGGTGATTAATAATACCAGCTAT GACTCCTGCCCCGATTCTTCAACAGAAAGGCTGCAGAACAGTCTGCTGCTGAAGTTGCCCTCATGGAAATTTGTCA AGTCCATTACCAGCAACGCAATATCCAGCTGTTCAAGAGACTGGGCTGTGCAAGATCTTCTTCAGGAGTATGC ACAGAGATGAATTATGCCATTCCATCTTATATTGACCAAAATCAGCCTCAGGCTTAGCTCCTTTCATATGCACT GTAGAGATTGGTGAATACATATATTGGTGTGTCAGCCAGGACAAAGAAAGATGCAGAGATAAAAGCTGCCCGAA CTGCTCTTCTGGCAATCCAGGTCAATCAGAGGGTTCGGCAATGGTGCAACAAATATATTGTAGTTCCTGGTAA AAGGTAGGTAAAGAGGTAGAGAAAAGGCCAATTGAAACACCGAAACCACTTAAAGTAAAGAAAGGTGGTTTCAAG AAGAAATGGAACAAGAGGAAATTCATGAAGAAGGATGGTCAAGCTGTTGATGTGAAAAGGATGAAGCTAGAGTGG CTGGAGATGCTCACGATTCTGATGTCTAATGCAGCAACAGTAATAACACAGGAGGCATCTTGTGGCACTCTGTT CCTGCAACCTTGTGAGGAAGCTAAAAGAGTAGAAGCTGAGCCACCTAGAGATATTGAAATGGTACAGCCTGATAAG GAGAACCAACACAGTACGCTGCATTGGTGAACCTGATGATGAAGCTAGAGTAGAACAGGAGCCATCCAGAGATA TTTCAGTGGTGCAACCTAATGAGGAAGCTATAAGTGGTAAGCAGGAACCATCCATCGATGCTGCAATTCTGCAACC TAAAGAGGAAGCTTCAAGTGTAAAGCAGGAGCCATTTCATCGATACTGCAATGCTGCAAGCTTGTAAAGGAAGCTGGA AGTGTAGAACCTTGGGCCAGCCAGAGATACTGTAATTTCCCAACTTAATGAGCAAGATAGGGCTGTAAAGCAGGAGC CAGCTGGTGACATTGTAGTGCCACAACCTGACGTGCACGCTAGGGTCTGTAAAGGAGTAG
SEQ ID NO: 91	ATGGCATTGGGGGATCTCATGGCCTCCAGGCTCGTCCACTCCTCCTCCTCCGCCGCGCCATCCGCGCGCCTGCG CCAATCACCATAACCAACCACCTCGTCGATGACCACCTCCCCGTGGAGAATGGACCGGACCCAGGAGGGACGTGCC CGACGAGGAGCCCGCCCGCCGCGCGCGAGGTGCGCTTGTGCTGCCAGGTGGTCTGCTGTGCGAGCAGCGCG CACGAGGGGTTTCGACGAGGCGCGCGCTGCGCGCGCGCGGCCCTCCACCAGCGGGCCCTCTCCAAATGGCGCCCA AAGACCGGATGAAAACCTGGCTGTGTGGCACTTGTGTTGTGTTAAACATTAGTGTGATCCGCCGGATGTGATCAA AATCTCCCCTTGTGCAAGAAAGGAGTGTGGATAGATCCATTTCTATGGCACCTCCAAAAGCCCTTGAACTATT GGGAAAACATTACACTCACAAATATGAGCGCTGGCAGCCAAAGGCTCGTTACAAGCTTCAGCTGGATCCGACATTAG AGGAAGTTAAGAAGCTATGTAATACTTGCCGTAATTTGCTAGAACAGAGAGAGTCTTTTTCATTACAATGGTCA TGGTGTACCAAGCCCTACAGCTAATGGGGAGATTGGGTATTAAACAAGAGTTACACACAGATATTTCCGCTTCTC ATTACTGATCTTGATTTCATGGCTGAAAACACCCCTCTATATATGTTTTTACTGCTCAGCAGCTGGAATGATCGTGA AAGCTTTTCTGGAGCGCTAGACTGGAGTCTAGCTCGTCTGCATCTTCATCGAAGGACTGCATTCTCCTTGGCGC CTGTGAGGCACATCAAACTCTCCACAGAGCGCAGAATTTCTGCTGATGTGTTACAGCTTGCCTCACCACACCC ATCAAAATGGCACTGCATGGTTTTGTAACCGATCGTTACTCCGTGATTCATGGAACACAATCTTATCGACCAAA TTCTTGGAAAGGCAAAATGACCGCAAACTCTTCTAGGGAGTTGAACCTGGATTTTCACTGCTATCACAGACACTAT TGATGGAATGTTCTTCTCATGATCTATTCCAAAGACTTTTCAGGAGGATCTTTGGTTGCTAGTCTCTTTCGCG AACTTCTTACTTGCTGAGAGAATCATGCGGTCCGCAAAATGTTCCCAATTTTCATACCCCTTTGTTGCCACCAACTC ATCAGCACCATATGTGGATGCTATGGGACATGGCTGCAGAGATCTGCCTTCTAAGCTTCTCAATTAATTGCTGA TCCTAATGCAGAGTTTCAGCCGAGTCCATTTTTCAGGAGCAATTGACAGCATTGGAAGTTTGGCTTGATCATGGC TCTGAAGACAAGAAACCCCAAGAGCTACCTATTGTTCTTCAAGTTTTGCTTAGTCAGTCACACAGATTTAGAG CACTGTTCTGCTTGGAAAGATTCTTGACATGGGACCTTGGGAGTTGATTTGGCTTTGTCGGTTGGCATCTTCCC TTATGTACTTAACTGCTTCAACAAGTGCAATGGAGTTGCGCCAAATTTCTGTGTTTCATATGGACAAAAATCTC TCTCTTGATAAGTCATGCCAGGTTGACTTGGTGAAGATGGAGGCGATGCATACTTTATCAGGTTTCTTGACAGTT TGGATGCTTACCAGAGCAGCGTGCATGGCTGCTTTCTGTTTAGCCGTTATTGTGGATGGGATAGGATTTGGTCA AGAGGCTTGTGCTAATGCAGGGCTTATAGATGTCTGCGCTGAGACATCTGCAACCTGAAAATCCGAATGATGCTCAG ACAGAGCCTTTGCTCTTGCAATGGCTTGTGTTATGCTTGGCAAACTTTGGGAAGATTCCCTGAGGCTCAGTTAC TTGGTCTGCAATCAACGCAACCGGAAATTTGTTATATGCTTATTGTGAGGCTCAACCTGAAGTCAGAGCTTCTGC TGTTTTTGCATTTGGAATCTTGTGGATATTGGATCTCCATCACTGAATGGAGCTGACGACGATTCTGATGATGAT GAAAAGGTGAGAGCTGAAATAAATGTTGTCCGAAGCCTTCTGCAGATCTCTTCAGATGGTAGCCCTCTTGTGATGAT CTGAGGTTGCCGTAGCGCTTACCCGCTTTGCAATGGGGCACATAAACAATATCAAACTCTGTTGCCGCCGAGTACTG GAAACCTCAAAACAATTCATGCTCAAGTCATTACCATCGTTGGCTAATATTAATTCAGGAATGTTTACAGTCCC AGCAGCTTAATAACAAGGTAGCAGTGGCTTGCCTCAGATATTGGTCTGTTTAAAGGTTGGCAGTGATAACAGTG CCACTGCTCGTGATGGAAGAATCTCTACGAGCAGCCGATTGCAACAAATAGCATCATGATGGTTCTCCACAGTC

	AGATGATTCTTCCCAACACTCTGATTGAGGATATTACTGAGAGAGAATGCAAGTAATGGTGGTCTCAACTACTCA AGATCGAGGCCTATTGATAATGGGATCTATTCCCAATTTATAGCAACTATGTGCAATGTTGCTAAAGATCCTTACC CAAGAATTGCAAGTATTGGGAAAAGGCATTGTCCCTCATAGGTGTTGAGCAAGTAAGCATGAGAAACAGTAGACT TAGCAATGGAGGTGCACACCCAGGAGAGACATCTGTGCCCCCTTCATCAAACCTTGAATGGCAGCGCTCCTCTTCC TGGTTTGATATGAACTCTGAAAATTTCTCGGTGGCCTTTAGGACTCCTCCTGTAGTCCCCCTCAGCATGACTACC TCACAGGATTGCGCCGAGTGTGCTCGATGGAGTTCAGACCACATGTTTTGAACACACATGATGGCTTAGCTGATCC GCTTTTAAGCTCCAGTGCAGCCCCCAGCAACATGGGGCTCTATATACTTCCCAATCATTAATTTACAGATGGAGT TGTGGTCACTTTTCTAGGCCACTTCTAACTGGTCTGATGATAACGAGGAAGCAAAATGCTAGAAGAGAGAGCGAG AACGAATTGCAATGGATTGCATTGCTAAATGCCAACGATCATCTTGCAAGATGACCAGCCAAATTTGCTAGCTGGGA TACGAGGTTTGAGTTGGGTACAAAAGCATCATTGTTGTTGCCATTTTCTCCTATTGTTGCTGCGGATGAAAAAT GAGCAAAATACGAGTATGGAATATGACGATGCGCTGCCAGTGAATACTTTTGAAAACACCAAGTTATCTGACAGAG GCCTATCTAAACTTTTGTGATCAATGAGCTTGATGATAGCTTGTGTTAGTTGGCTCAAGTATGGAATGTCCG CATATGGAGAACTATACCTCAAAGGGAGGACAAAACCTTGTAAGTCTTTTTCATCAGTTCAAGGCTATCGAAGT GCTGGTCCGAGTATTGTATTTGATTGGCAGCAACAGTCCGGTTATCTGTATGCATCTGGTGACATGTCTCTATCC TTGTATGGGATCTTGACAAGGAACAAGTCAACACCATCCAGTCAACTGCTGATAGCGGGATTTCAGCTCTTTCTGC ATCTCAGGTTTCGATGTGGCCAATTGCTGCTGTTTCTTGATGCATCTGTTAGGATATTGACGTGCGTACACCT GATAGGCTAGTATATACAGCAAGACCACATGCCCAAGATCAGAAAAGGTTGTTGGTATAGGATTTTTCAGCCTGGGT TTGATCCCTACAAGATTGTAAGTGCATCTCAAGCTGGAGACATTCAGTTCTTGTGATGTTAGAAGGGCATCTGAACC CTACCTCACTATTGAAGCACATAGGGGTTTCAATTAACGGCATTAGCTGTTTCATCGGCATGCCCGAGTTATTGCAAGC GGCTCAGCCCAAGCAGATGATCAAAGTGTGTTAGTCTTGAAGGAGAACAGTTGACAATAATTGCTACCGCCATCTT TTATGGGTCAACGAATAGGCAGCGTAACTGCCTTTCTTTCCACCGATACAAATCACTCCTTGGCGCTGGTGCTGG TGATAATGCTCTTGTCTTCTATCTACGCGGAGGACAATTACCAAGTACGATGA
SEQ ID NO:92	ATGGGTGCCAGCGGAAGGCTGATCTCCATTTACCCAGAGGATCTCACTTTCTTATTTGAGCTAGATAAGCCATGCT ATTGCAATCTCAAGGTGGTGAACAACAGCGAGCATCATGTTGCATTTAAGGTCAAGACGACATCACCGAGGAAGTA TTTTGTCCGGCCGAACCGGAGCATCATCCAGCCATGGGATTTCTGCACAATAACAATTACGCTCCAGGCGCAGAAA GAGTACCCACCAGATATGCAATGCAAGGATAAATTTCTTGATCCAGAGCACCAAGGTAGCTGCCAGTACTGACATGG ACGAGATCCCCCTAACACGTTCAACAAGGAAGTCGATAAGGTGATTGAGGAATGAAGCTTAAGCTTGTGTTATAC AGTTCCAGTGGAGATTCTGACGACTCTGGTATTACATCTTTAGGCAGCAGGAGCTTCAAATTTGGGGTCTGACGAT CTCAGGATGCTGAAGAATGCAAGCATTGAAAAGATACAGACAATACAACGCCATAAAGACGAACGAGACACCACCC TGCAGCAAAATCAGCAAAATGCAACGTGAATTGGATGTGATCAGGAGCGTAGAAGCCGCAAAAGCGATGCGGGTTT CTCCTTAACGTTTGTGCTTTTGTGCTGGGCTCATAGGTGTCTGATGGGCTCTTGATGAGCCTCATCTTCCCTCGC CCACAGGCTGCTGCTTAA
SEQ ID NO:93	ATGGGGGTGATGAACCCGCTGATGGCAAAGCTCACCACGCTCATGGGCGACGAGTACAAGAAGCTCAAGGGGCTCA GGAAGCAGGTCTCCTTCTCAAGGATGAGCTCACCACCATGAGCGCTTCTCGAGAAGCTCGCGCTCATGGATGA TGATGATGATGGTGAGCTCGATCCTTGGCCAAAGGACTGGAGGAACACGTCAGGGAGATGGCCTATGACATGGAA GACTGCATTGATGATTACTTCACAAGTCATCTTGATCATCGTTACTCTTCTCAGATGCAGGGTTAATCCGCAAGA TAGCTCGCCGCTCAGGGCATTGCGGGTGCCTCATCGCATAGCCAGCCAGATCAATGAGCTCAAGGCTCGTGTGGT CGAGGCAAAATGAGCGTCCGCTGAGATACAGGCTTGATGACTGTAACAACAACATGAGTGTCTGCAATCCTGCT ATAGATCCACGGATAACATCGCTCTACCAAAATGCCGGGAGTCTTGTGGGTATGATGGCCCAAGCCAAAGACTAA TCCAGCTGTTGTGCTTAGATCGTGATACCGATCAACGACAACTCAAAGTGGTGTCCGTCGTGGGATTGGAGGCT CGGTAACAACACTCTTGCAAAATATGTGTACGACAAGATCGGGCATCAATTCGATTGCACGGCATTCTGCTCAGTA TCCCACAAACCTGACATAACAAGGATCCTCAGTAGCATCCAATCCAAGCTTGACATAGGGGGCAGCTCAAGCTT GCGACGACGTGCAACAACCTCATCGACGACATACGAGCCTATCTGGAGCATGAAAGGTATATTATTATAGTCGATGA CCTGTGGAACAAGAAGCATGGGTATTATTAGTTGTGCCCTTCCAAACAATGGCAAAGGTAGCAGAGTGATAGTA ACCACAGGAGTGAAAGATGTGGCCAGGTTGGCATGTGGCAAGGATGGACAAATTTACAAAATACAGCCTCTGAACA ATAAGGACTCAAGAAAGTTATTCTTCGATAGAGTATTTAGGCCTGAAGATAGTTGTGTCTGCAGTATGAAGAAAT TTCAACTGAAATCTTAAAGAAGTGTAGTGGCTTGCCACTTGCAATTGTTACTGTAGGGAGCCTCTTAGCCTGTGCA CCAAGAACATGGAAGAATGGAAGAGCATACGGGATCTTCTTGGGTGCCCCGTTTGACAAAAACAAGAGCTTGGAG GCATGAGGAATATTTAAACCTGAGTTACAAGAATCTTCTCTCATCTCAAAACATGCCCTCTATATATTGGTAA ATATCCAGAGGACTATGAGATCGGGAGGGATGAACTAGTTACGAGTGGATAGCTGAAGGTATTATGGGTAAACCT CATGGGGAAAACCTTGGAGGCTACTGGTAATGGCTACTTCAGTGAGCTTATCAACAGGGGCTTGATTCAACCAGAGA GCACCGCTATGGTGGGGAGGTGTTGAGTTGCAAGGTGCATGATATGATGCTTGATCTGATCCTCATCAAGTGTGC AGAAGATAATTTGTGAGCGTTGCACACAGTTGTAAGACTACATGCGCATGGCTATGCACCATGAGCGGAGTTGC AATAAGGTCCGTCGGCTATCCCTGCAGTGCAAGGCTGCAAGATCAGATTGCGCAATTGAGGGCAGGCTCATTTCTA CAAGCATGGCTCGTCTCGATCAGTTTCAGTGTGTTGGTGAGTGTTCAGGTGGGCTCCCATTTCTGATGCTATCCAA GTATATACGGGTGGTGCACATCGAATTGGAAGGCCATGGCGGTCAAGTCGACCTCACTGCCATTAGCCATGTGCTT CAATTGAGGTATTGAGAGTGGAGACGCTGGTGTGAGATAGATCTCCCCAGCAAAATATGTGGGCTCGTGCATT TGGAGACATTGTCAATATTTTCCATAAAGCTGTAAGTCGGCTCCCTTCAGATATTAGCAGTCTTCCCCGCTTGTG AGTCTGTCCCTGGTGGTCCATGGGCTACAAGGCTACCAACAAGTTAAACAAGCTAAAAGGGTCACTACGCACT CTCACCATATTCAATCCCCCGATGCGTTAGGCATGGAGGCCATTGGTGAGCTGAAAAATCTAAGGGACCTTAA ACATCTCTGTTAACAGGTGGCGGGACGATGAGATCCTTAGCCTTTATGCTCTGGGGTCTTCCATTGGAATACTGGA

NO: 98	TGAGGTTGAGCGCTACCTCGGTGGCTTTACCAAGGTTGATGACAACCGCTACTCGATGAAGATATTCTTTGAGATC CGCAAACAGAAGTATCTTGAGGCCCTTGATAAGCATGATCGTTTGAAGGCGGTTGAAATCTTGGTCAAGGACCTGA AGGTCTTCGCGTCCTTTAACGAGGAGTTGTTTAAAGGAGATCACACAGCTTTTGACGTTGGAAAACCTTTAGGGAAAA TGAGCAACTCTCCAAATACGGTGATACAAAATCTGCCAGAGCAATAATGCTTGTGAACTAAAGAAGCTGATTGAA GCTAATCCCTTGTTCGGTGACAAGCTTCAGTTTCCAAATCTGAAGAGCTCCAGATTGCGGACACTTATAAACCAGA GCTTAAACTGGCAGCACCAGCTTTGCAAAAATCCTAGACCTAACCCCTGATATCAAGACTCTGTTTGTGATCATTC TTGTGGACAACCAAATGGTGCTCGTGCTCCATCGCCAGCAAAACAATCCATTACTTGGATCTATACCAAACCTGGA GGTTTCCCCCATTGGGTGCTCACGCGCCATTCAACCTGCACCTACACCTGTCCCACCTCTGGCTGGCTGGATGT CAAACCTCCAGCAGTAACACATCCTGCTGTCTGCTGGAGCTATTGGATTGGTACTCTACAAATCCTGCTGC TATATTAACATCCTAGAACACCAACAACCTGCCAATCCTTCTATGGATTATCCATCAGGAGATTCTGATCACGTC TCCAAGAGAACGAGACCAGTTGGGATGTCTGAGGAGGTGAATCTTCCAGTGAATATGTTACCTGTGACATATCCAC AGAGTCATAGTTACCCGCAAGATGATTTTCAAAAAATGTGACACGACATTGAGCCAAGGATCAACTCCAATGAG CATGGACTTCCATCCAGTTCAGCAAACTCTCCTTCTTGTGGTACCAATGTTGGTGACATTGGATTATGGGATGTC GGTACCAAGGAACGACTTGTTTTAAAGAACTCAAGGTTTGGGATCTACAAAATGCTCAATGGCCCTCCAGGCAT CACTTGTCAAAGACCTTACTGTCTCAGTTAACCGCATAATATGGAGTCTCTGATGGAACCTTGTGGTGTGCTTA TTCAAGGCATATTGTACAGATCTATTCATACCATGGCGGTGATGATATCAGGCAGCACTTGGAGATTGATGCGCAT GTCCGTGGTGTAAATGACATTGCAATTTGCCCATCCAAATAAGCAGCTATGTATAATAACCTGCGGAGATGACAAGA CAATTAAGGTCTGGGAGGCCACTAGTGGAGCAAAGCAATTTACATTTGAAGGTCATGAAGCTCCTGTTTACTCTGT TTGTCCACATTATAAGGAAAATATTCAGTTCATCTTCTCAACTGCTTGGATGGAAAGATAAAGGCTTGGCTATAT GATAATTTGGGATCCAGAGTTGACTATGATGCGCCAGGACATTGGTGCAACAATGGCATATAGTGCAGATGGTT CAAGGTTATTTCTTGTGGGACTAGCAAGGATGGCGAATCACATCTAGTGAATGGAATGAAAGTGAAGGAGCTGT CAAGAGAACCTTACCAGGATTTCCGAAGCGATCGATGGGTGTTGTCCAATTTGATACACACGGAACAGCTTTTGT GCTGTGGAGATGAATCTTGATTAAAGATATGGGACATGGACAACACAAGTCTTCTGACTACCATTGATGCCGATG GTGGTCTTCTGCAAGTCCACGGTCCGATTCAACAAGGAAGGTACTCTGCTGGCTGTTTCTACCCATGAAAATGG TATCAAGATCTTAGCAATGCTGATGGAGTACGGTTGCTGCGCACATTGGAAAATCGTTTCAATTTGATGCTTCTCGG AGTGCGTCTGAGACTGTAACAAAGCCCCTAATGAATCCATTGACTGCTGCTGCTGCTGCGGCGGCGTCAGCTGCTG CTGCCGGGACTAGTTCAGGAAATGCTGCTCCACCGCAATAACTGCATGAATGGGGATAGCCGAAGCTTGGTTGA TGTAAGCCCTAGAATAGCTGATGAGCCATTGGATAAATCAAAAGTCTGGAACTTATGGAGATAACCGACTCAAGT CAGTGCAGATCATTGAAATTAACAGATAAATAGAGGACAAGCAAGATTTCAAGACTTATTTACACAAATCTGGTG TCGCTATCTTGGCTTTAGCTTCAAATGCTGTTCATCTGCTCTGGAATGGCCTCGCAATGACCGAACTCAAGTGG AAAGGCTACTGCAAGTGTCTCTCTCAATTATGGCAACCTCCAAGCGGCATCCTCATGACTAATGACATAACTGAC AACCTGAAGAAGCTGTCCATTGCTTTGCTTGTCAAAGAATGATTCATATGTCATGTCTGCATCTGGAGGAAAA TATCTCTGTTTCAACATGATGACTTTAAGACGATGACAACTTTTATGCCCTCCGCGCGGCGCAACGTTTCTTGC TTTCCATCCTCAAGATAACAACATTATAGCAATTGGAATGGATGACTCAACCATCCAAATCTACAATGTTTGAATT GATGAGGTCAAAGCAAACCTTCGAGGGCACTTAAGAAAATTACTGGACTTGTCTTTTCAAATGTATTAAATGTGT TAGTCTCTTCTGGAGCTGATGCGCAGATATGTTGTGAGGACACAGATGGGTGGGATAAATTAAGAGCAGAATGTT ACAGATACCATCAAGTCGTCATCATCTATAATCTTAGACACAGTGTTCAGTTCCATCAGGATCAATTGCATTT CTTGTGTGCTATGAGACCCAGATTGCCATATATGAACTACAAAATTAGAACCCTGAAGCAGTGGCCTGTCCGGG AGAATCTTCTCCAATAACGCATGCCATGTTCTCTGCGATAGTCAATTGATTTATGCAAGCTTTCTGGATGCCAC TGTTTGCATATTTAATGCATCGAGTTTGAAGTCCAATGTGAATCTTCCAGCATCCTATCTTCTCAGAATATC AGTCAAATGTTTATCCTGTGCTTGTGGCGGCACATCCTCGGAAGCAAATCAGTTTGTCTAGGCCTGACTGATG GTGGTGTATTATGATTGAACCTTGAATCTGAGAGAAAATGGGAAAATCCTCCACCAGCAGAGAATGGATCAAC CAGCGCTTTGTCCACACCTCCTAATGGAGCATCAAGTTCTGATCAACCAGAAAGATAA
SEQ ID NO: 99	MPRHACLLQSDRIFFIATEECRRRRRQGGADAGAGGRGGRRCWAEAAEAHMAAAAHRAAAVHRAACGSSTVAVGLR ELHRRRLCSTCTGDGDGRMLMQRNDSSNSKWLMSRRASFPHVSAKFAWEVQESLLDGGSTWFLGSSAYFVAVKYDW *
SEQ ID NO: 100	MGTYKCCIFFTRRFALSDASTPGDVRMLFTRHAGGAPYMGIDELRRYLAASGEAHVDADTAERI I DRVLQERSRTPRFG KPSLTIDDFQYFLFSEDLNPPICHSKEESFDAMEKLEV*
SEQ ID NO: 101	MQVHDMNAPLSHYFIYTGHNSTLTGNQLSSDCSDIPIIKALQIGVRVIELDMWPNSKDDVDILHGRTLTPVSLIK LKSIEYAFVASPYPIITLEDHLTSDLOAKVAKMVLEVFGDTLYYPESKHLQEFPSPEALRGVILSTKPPKEYLESK GGTMKDRDIEPQFSKGQNEEAVWGTEVPDIQDEMOTADKQHEINDILYTRDVEEDEKMKCQHHPLEYKHLITIKAGKP KGAVVDALKGDPDKVRRLSLSEQLAKVAHHGRNIVSFTHKNLLRIYPKGTFRNSSNYPFLGWVHGAQMVAFNMQGY GRSLWLMHGFYKANGGCGYVKKPDEFMMQTCPDGNVDFPKADLPVKKTLKVVMGEGWQSDFKQTYFDYSPPDFYAKV GIAGVPSDSVMQKTKAVEDSWVPWEEEFVFLPTVPEIALLRVEVHEYDVSEDDFGQTALPVSELPGIRTVPFLFDHK GLKFKSVKLLMRFEFV*
SEQ ID NO: 102	MAMGAAAAPWYGAIGGGGSRARVRAQAAAPWAGGAEEELVRSGAVRAVRAREAAAGAMS AEGFRLLDVRPEWERARA AVR GSAHAPLFVGGDDTGPTLLKKWVHFGYI GLWTGQSFTKMNDRLDDVAAAAGEGKDAKLLVACGEGLRSLIAVRMLYD DGYKNLAWLAGGFSKVDGDFADVEGESKLQYATVGGVSYIFLQIILLRLRVK*

SEQ ID NO:103	MAAAQRRRSSASPEFRFWPLDADPAASPCADELFGGVLPLQPLPYPRRDADLSMSLAVADDDDDDEEEEEVQP GAAVASRAPPTAAVAASGGGGGSKRWTDIFAKKQQQPAEEKEKDQPTRRRRPAGGGGGSELNINIWPFSSRSAGGG GVGSSKPRPPRKASSAPCSRSNSRGEAAVASSLPPPPRRWAASPGRAGGGVPVGRSSPVWQIRPFPSPAAKHAAADR RPPHHKDKPTGGAKKPHTTSATGGGGIRGINLSINSCIGYRHQVSCRRADAGVARASAGGGGGGGLFGIKGFFSKKVH*
SEQ ID NO:104	MQQKPAEEAMEELKGEAVGPRRPLGLGLWLAARRRLAPDDPFFAAGDMERELLAKQVALDLSEDERYQLERMEVASANA LLCPIISGCGAHLDCLENFEDHYRTRHTASCVCWRVYPTSRLLSIHISEAHSFFQAKVARGFPMYECLEVEGCGVKLKS YKSRQQHLLDKHQFPKSEFFFKARPSQRQRNKNQKQRTVHKGDETSETLMDVDGKSSRYMNSRYRPKQHDGKESKE NEHSSCKEAKNNEMEVDKQVDELASAVSRLSTADSTPSSISFGHRRSRGLAFVPRSRQNKQVSQTEPK*
SEQ ID NO:105	MGGGGGAEELTAQETALYDRQIRVWGVDAQKRLSKAHVLVCGMNGTTTEFCNKIVLAGVGSLSLMDHLVTEDDLNNAN FLIPHDESIYGRSRAEVCCESLKDFFNMVRAVEKGDPSLIDGFEFLDKFDIIVVSCAPIKTKLLINDNCRKRSKHIAF YAIECKDSCGEIFVDLQNHSHYVQKVGGEKPKELAYPSLQEAISVPWKNLPRKTTKLYFAMRVLENYESSEGRNACEAS LSDRPAVLALRKDMCDKMSLESQIPTALLERLLAAGKKQHPVFCAILGGILGQEVKISISGKGDPKKNFFYYDAADGK GIAEDIPPLSSD*
SEQ ID NO:106	MAMPLPPPPPPRPLGRGLVGVGPAPAPATASQSNRPVPLQLPRCCHRSEGPWRTAAANGRRRWSDEDEMEEDD EEGYGYDDGGAPGSSAQELFGEFWFSKLFRAYGYVPLLLASMLVATGPRAFLMAMALPLAQSAISWVVSFFTRSRRO QEEESYGYDYDDDPAFQRREDDDDGDYDAGAWQWRSRSHQOSTESGSGFGGWDLLYDDEEKKEQESSGKKRTPPE PDTAASAAAADLGLGLRARRGPRRSNGGMSRGRSSSSMRYNQAPLLTRLLVALFPFLGWSFRIL*
SEQ ID NO:107	MRSLEVHAIGRHAASPCALRLKALPALDMMRYQRLSPDCLPLANGGGGSGSVTRKPARSRCKDDGGMAVAADSSRL SSYLPSQLDSKPLRARAPQSSSSAAAWSPARDHAHAHHHHHHHPDSSDSTASPSNGAGTGGDVLQWGHNRKR CRRDASSANAAPSSSQRRQTASAAGKILRRSSAPAEKLMPPPPSTTGSYTRGSNLRSSASSFTRSAAAAAGVDAHH HRSVEERSGGGYKRSKPKAHKSALDAALHMDSKNNHHHHHHHDSVTTANGCAGAGEKIGSERFELPRIYISLSRKEKE DFLIMKGTLPQRPKKRAKNVDKTLQYVFFGMWLSDLTRGRYEVREKKCVKKVYSTLHLAFSVHAFVFLQTRRGKLP FRASVTQIGWV*
SEQ ID NO:108	MATTASLLPPLLPAPSSSPRHLHPSRHLRPLPPIRLRAARRRHDPDAVVVPDARPWVGDLSGAAASYRDGREEDDD AGEEDDENDDDDEDRLDLLVRFLHSVFRKVSRRARRAARSVLPPSPVPAELVKFSVNGVLVLTFLWLKGLLEVVCTFG SMVFVTILLVRGIWGSVTYIENRYSYIRQIDNDDNRWSRVQTAG*
SEQ ID NO:109	MKLRLRSMQDQGGAGGAAETHRVQLPDTATLSDVKAFLATKLSAAQVPAESVRLTLNRSEELLTPDPSATLPALGLAS GDLLYFTLSPLSPSPPPQPPQAQLPRNPNDVPSIAGAADPTKSPVESGSSSSMPQALCTNPGLPVASDPHHPPPD VMAEAFVAVIKSSSLVVGDTREMNVGADGTVICRLVVALHAALLDAGFLYANPVGSCLQLPQNWASGSFVPVSMKY TLPELVEALPVVEGMAVLNYSLMGNFMVYGHVPGATSGVRRCLCLELPELAPLLYLDSEVSTAEEREIHLELWRLK DEMCLPLMISLCQLNNSLPPCLMALPGDVAKVLEFVPGVDLARVQCTCKELRDIAADDNLWKKKCEMFNTQDTCGC MMCKCIYSQDKDIVLADKYTCGNMQKPVTPQGRWLIILVYHSLLCQYITIGLSLLWYHLVDLVQDAPAGIHEDCII PLPINPYQLPPSAGACCSTTQASASAKDGGNMYSPPCSAAASSQGHCFAVGANQLASLDLAMDDEPILFPVHNASLQ GIQFYNTGDTQLSRNMSIDKCLGSKRKSGEGSSSLHSEETGEMPQRELSMEHAGEKAGDADASREYVHVRAKRG QATNSHSLAERFRREKINERMKLLQDLVPGCNKITGKAMLMDEIINYVQSLQRQVEFLSMKLSTISPELNSDLQDIL CSQDARSFLGCSPLSNAPNLVRAAQCLSPGLYGSVCVNPADVHLARAGHLASFPQQRGLIWNEELRNIA PAGF ASDAAGTSSLENSDSMKVE*
SEQ ID NO:110	MAAAGAGEPSPYAEAAGDLANARAPSPVVGKHLPSGAVPRHAYVFDGEGGFADAAWDVAAAAPGAFTWHHIELPRQ PGGAAAKPLHHAQALIELLCPPLTLQEILAFVATGPHCGVVDGGGGGGAGALLRVSSPGPVGSAFALRLAARVTDSSV VTVSVGGVPRLAFTTQASLLSEVPLGVTASLSDEGHGGGRAVEGGVVEERLLESLLAMNHADGAHTDNPVPTVSNL LVHVLGTHVDHVDIVTRLEMELDSIELHLDKGGHFMKRLLLDGRFPKMHLDLQRLQLQVSHGDQVFPRVKEKCAKSKS WFASEDIVALEDLIGRLRLKENLGFITNRVTTLQASLDSWQSEQINKSLYYLSFLSIIIFLPLSIVTGVFGMNVGGVPW TEQKNPANLDGFFNVMLICVILLILLCLFLPSLYSHVSAWRTRRALARSSSQNRHLKLFKGHKDGYMRL*
SEQ ID NO:111	MQDQLICSGCRRVVQYRRGVAGVCCPGCNTLTAVNPSAVADMSELICSGCPTLLFYNRGASNIRCPSCNRLNSTRSANQ IAHLTCGQCRTTLMHPGASTVQCATCRYVNHVRDARPQTVLVENPKTLDKGLKLVSNVVVGVTSWKR*
SEQ ID NO:112	MRGAVAI FNEFKRRGLNISITGIPKTVNDIGIIDRSFGFQTAVEIAQQAIDAAHVEAVSAVNGIGLVKLMGRSTGHIA LHATLSSRDVDCCLIPEDVFYLEGKGGLFEFLYERIKQKHAVVVVAEGAGQELIPRTDDQKREQDESIGNIVFLDVGPW LKSELGKWKREHPSSELTFTVKYIDPTYMIRAVPANATDNLYCTLLAHSIAHIGIMAGYTGFPVGPINGNYSIIPLEDVAV AKNPVDVNDHKWAWVRSVTNQPDFMKPKY*
SEQ ID NO:113	MVESASMVNENSENPYKAI GYRVEEPRRDRAESMPSPSPSPVSRRLDNGVVEETRALTDTTLLRS LAAGLAVRPGAS DEHHTVRCDIAVIGSGCGGVA AVLASAGYKVVVVEKGDYFTKEDYSSIEGFSMERLFRGGVFCTSNVTMTI FTGAT VGGGS AVNWSASIRT PAGVMQEW SREHGLAVFASPGYARAMDAVCERLGVTDACREEGFQNKVVRGCDALGLRADAVP RNSSEGHFCGSCNFGCPTGDKKGTDTTWLVDAVERGAVILTGCKAEHFIVESNGGGGGRSKRCVGLVATCMSNGITKKL

	TACGCGGCATCAACCTGAGCATCAACTCCTGCATCGGGTACCGCCACCAGGTGAGCTGCCCGCGCGACCGCGGAGT CGCCCGCGCTCCGCCGCGCGCGCGCGCGCGCGGCTCTTCGGCATCAAGGGTCTCTTCTCCAAGAAGGTGCATTGA
SEQ ID NO:120	ATGCAGCAGAAGCCCGCGCGGAGGCCATGGAGGAGGAGTTGAAGGGGAGGCCGTGGGGCCCCCGCGCCCGGGCTAG GGTTATGGTTGGCGCGCGCGCGCGGCTGGCCCCCGACGACCCCTTCTTCGCCCGCGGGGACATGGAGCGCGAGCTCTCT CGCCAAAGTATGGCTTGGCTTGGATCTCTCCGAAGATGAACGCTACAGCTTGAGAGGATGGAAGTGGCGAGTGGCAATGCC CTTTTATGCCCAATTTCTGGCTGTGGTGTCTATCTAGATTGCTGGAGAACTTTGAGGACCACTATCGCACCCGTCATA CTGCTTCATGCTCTGTATGTTGGAGAGTGTATCCAACCTCAAGGCTGTGAGTATTCATATTTCTGAGGCACATGATTC CTTTTTTCAAGCAAAAGTTGCCCGTGGTTTTCCAATGTATGAGTGTGGTGGAGGGTTGTGGGGTGAAGTTGAAGAGC TACAAAAGTCGGCAGCAGCATCTCTTGATAAGCACCAGTTTCCCAAGTCATTGGAATCTCTCAAAAAAGCACGCCCT CGCAACGCCAGCGGAACAAGAACCAGAAGCAACGGCAACAGATTCAAGGGAGACGAGACAAGCGAAACACTAATGGA TGTTGATGGGAAGAAGAGCTCAAGGTACATGAATTCAGATATCGGCCAAAGCAACATGATGAGCAAGAGTCAAAAGAA AATGAGCATAGTAGCTGTAAAGGAGGCCAAGAACAAAGAAATGGAGGTTGACAAGCAGGTTGATGAGCTTGTCTCGGCCG TATCAAGACTGAGCACAGCGGATTCAACTCCTCTAGCATAAGCTTGGTTCATCGTCTCGCTCTCGCGGTCTGTCTTTGT CCCTAGGTCGATTTCGGCAAAACAGCAGGTTTCTCAGACAGAACCAAAATGA
SEQ ID NO:121	ATGGGCGCGCGCGCGCGCGGAGGAGGAGCTGACGGCGCAGGAGACGGCGCTCTACGACCGCCAGATCCGCGTCTGGG GCGTTGACGCCCAGAAGAGGCTAAGTAAAGCTCATGTGCTCGTGTGCGGCATGAATGGTACTACTACTAGTTCTGCAA GAATATTGTTCTAGCAGGAGTTGGCAGTTTATCCTTGATGGATGATCATTTAGTCACAGAGGATGATCTCAATGCAAA TTCTTAATTCCTCATGATGAGAGCATATATGTTGGTAGATCACGAGCTGAGGTTTGTGTGAGTCCCTGAAAGATTTC ATCCAATGGTCCGAGTTGCAGTCGAAAAGGGTGATCCATCATTAATTGATGGAGAATTCCTTGACAAGTTTGACATAAT TGATGTTAGCTGTGCGCTATTAACAAAGTTGTTAATTAACGACAACCTGCCGGAAGAGAAGCAAGCATATTGCATTC TAGCCATTGAGTGTGGGAGATTCTGTGGTGAATATTTGTGATTTCAGAACCATATGTTTCAAGAGTTGGAG GTGAACCCAAACAAAGGAGTTGGCATATCCAAGTCTCCAGGAAGCTATCTCCGTACCCTGGAAGAATTTACCAAGAAA AACAACTAACTGTACTTTGCCATGAGAGTACTGGAGAATTATGAGTCATCTGAAGGCCGCAATGCTTGTGAGGCATCA CTTTCTGATCGACCTGCAGTTTTGGCTCTGAGGAAGGACATGTCTGATAAAATGTCTTTAAGTGAGTCTCAAATTCCTA CTGCTCTCCTGGAACGGCTTTTAGCAGCTGGAAGAAGCAACATCCTCCTGTATGTGCAATCCTTGGCGGCATTCTTGG TCAGGAGGTGATTAAGTCAATATCTGGTAAGGGTGATCCGATCAAGAATTTCTTCTATTACGACGCCGTGATGGTAA GGGATCGCTGAAGACATTCTCCCTTTCTTCAGACTGA
SEQ ID NO:122	ATGGCTATGCGCTGCCGCGCGCGCGCGCTCGTCTCTCTTGGACGGGACGGCTCGTCCGAGTAGGACCAGCTC CAGCACCAGCAACGGCTCCCAATPCAACCGCCAGTGCCCCCTGTCAGCTGCTCGCTGCCGCTGCCATCGCTCGGA GGGACCCCTGGAGGACGACGGCGCGCGCGCAACGGGAGGAGGCGGTGGTGGTCCGACGAGGACATGGAGGAAGAGGACGAC GAGGAGGATACGGATACGACGACGCGCGCGCGGACGCGGCTCAGCGGCTCAGCGCAGGAGCTGTTCCGCGAGCCATGGTTTTCCA AGCTCTTCCGTGCGTACGGCTACGTGCTGCCGCTGCTGCTGGCTCCATGCTGGTGGCCAGGCGCCAGGAGCTTTCTCT CATGGCCATGGCGCTGCCGCTCGCCAGTCCGCCATCTCTGGGTGCTCTCTTCTTACCACCAGGAGTCTGTCGGCAG CAGGAGGAGGAGGAGTCTGACGATACGACTACGATACGATCCCGCTTCCAACGCGGAGAGGAAGACGACGACGACG GCCACTACTATGATGCCGGGGCATGGCAATGGCGGAGCAGGAGCCACCAGCAATCGACCGGAATCCGGCTCCGGTTTGG AGGATGGGATGACCTCTCTACGACGATGAGGAGAAGAGGAGCAGGAGAGCTCAGGGAAGAAGAGGACGCCACCGGAG CCCGACAGCGCGCGCTGCTGCCGCTCCGATCTGGGATGGGATTGCGGGCAGGAGAGGTTCCACGACGACGCAATG GCGGCATGTGCGGAGGAAGACGACGACGATGAGGTATAACCAGGCGCCACTGCTGACGCGCTTCTCGTGGCACT CTTCCCTTCTCTCGGCTCATGGTTCAAGATACTCTAA
SEQ ID NO:123	ATGCGTGGCTCCCTGGAGGTCACGCGATTGGCAGACACGCGCGCTCGCGCTCGCGCTGAGACTGAAAGCCCTCCCGG CATTGGACATGATGAGGTACCAAGGCTTAGCCCGGACTGCTCCCGTATGCCAACGCGCGCGGAGGAAGCGGTAG CTGACACAGACCGCGCTCGAGATCCTGCAAGACGACGATGGCGCATGGCCGTCCGCGCGGACGATCCCGCTC TCGTGCTACCTCCCGTCTGTCACAGCTCGATTCCAAGCCGCTGCGCGCTCGGGCGCGCAGCCGTCTGCTCGTCCGCGG CGCCTGGAGCCCGCGCGGACACGCGCAGCGCCACCACAACCACCACCACCACCACCCGCTCCGACTCTCTCCGA CAGCGCTCGCGAGCTCCAACGCGCGCGGACCGGTTGCGCAGCTGCTGCTGAGTGGGGGACAAACAGCGGTCCCGC TGCGCGCGCAGCGCTCTCTCGGCCAACGCGGCTCCTCTCTCGCAGCGCGCCGACAGCCGCTCCGCGCGCGGCA AGATCCTGCGCGCTCTCGCGCGCGCGGGAAGCTCATGCGCGCGCGCCCATCCACACCACCGGTCGTACAC GCGCGGGTCCAACCTGAGGTCGCTTCTGCTCTCCGACGCGGTCGCGCGCGCGCGCGCGCTCGGAGACGACACAC CACAGGTCGCGCTGGAGGAGGATCAGGCGCGGGTACAAGCGGTGCGCGGACAAGGCGCACAAAGTCCGCCCTGGACG CGCGCTGCATGATGATTCCAAGAACAAACCACATCACACCACCACGACTCTGCTGAGTACGCAAAACGCGCGCGCGG CGCGCGGAGAGAAGATCGGCTCCGAGCGGTTTGAAGTGCCTCCGCTATCATCTCGCTGTCGCGCAAGGAGAAGGAGGAC GACTTCTTATGATCAAGGCGCCCAAGAGTGCCTCAGAGGCCCCAAGAGGGCCAAAGAGTGGACAAGACCTCCAA ATGTTATTCCTGGATGTGGCTTTAGACTTGACGAGGACGTTAGAGGTGAGAGAGAAAGTCTGTAAGAAGGT ATACTCCACTCTGCACCTGGCATTTCAGTTTCATGCATTCTGTGTATTTTTACAGACAAGAAGAGGAAAATTACCTAGA TTTAGGGCATCAGTGACCCAGATTGGTTGGGTCTAA
SEQ ID NO:124	ATGGCGACCACCGCTCCCTCCTCCTCCTCCTCCTCCCGGCCCTTCTCCTCCCGCGCCACCTCCACCCCTCCCTC GCCACTCCGCGCTTGGCCACGATCCGCTCCTCCGCGCGCGCGCGCGCCACCCGACGCGCTGCTGCTGCTCC GGACGCCCGCCCTGGGTGCGGACCTCTCGGGCGCGCGCGCTCTACCGGACGCGCAGGAAGAGGACGACGACGAC

	CGGGGGGAGGAGGATGACGAAAACGACGACGACGACGAGGACCGCAGCCTGGACCTCCTGGTCCGCTTCTGCACTCGG TGTTCAGGAAGGTCTCCCGCGCGCGCGCGCGCGCCAGGTCCGTGCTGCCGCCCTCCGTCCCGCTGAGCTGGTGAA GTTCTCGGTCAACGGCGTCTTGTTCACGTTTCTATGGGTCTAAAGGGGCTACTTGAGGTGGTGTGCACATTTGGA AGTATGGTGTTCGTGACCATCCTTCTTGTTCGTGGAATATGGTCTGGAGTGACTTACATAAGAGAAAACCGATATAGCT ATATTGCCAGATTGATAATGATGACAACCGATGGAGCAGAGTACAGACTGCTGGCTAA
SEQ ID NO:125	ATGAAGCTTCGGTTGCGATCCATGGACCAGCGCGCGCGCGCGCGCGCGAGACCCACCGCGTGCAGCTGCCGG ACACGGCCACGCTCTCCGACGTCAAGGCCTTCCCTCGCCACCAAGCTGTCCGCGCGCAGCCCGTGCCCGCGAGTCCGGT GCGCCTCACCCCTCAACCGCTCCGAGGAGCTCCTCACCCCCGACCCCTCCGCTACCCCTCCCGGCCCTCGGGCTCGCGTCC GGTGATCTCCTCTACTTCACGCTCTCCCCCTCCGTCGCCCTCGCCTCCGCGCGCAGCCGAGCCACAGGCCCAACCCCT GCCCCGTAACCCCTAACCCCTGATGTCCCTCGATCGCGGGAGCTGCTGACCCGACCAATCTCCTGTGGAGTCTGGTAGT CCTCGTCGATGCCGCAAGCTTTGTGCACGAATCCTGGCTTACCTGTGCGATCCGATCCGCATCATCTCCACCGGATGT GGTGATGGCGGAGGCCCTTCGCCGTGATCAAGAGCAAGTCGAGTCTCGTCGTCCGGGATACGAGAGAGAGATGGAGAAT GTCGGTGGTGCGGATGGAACCGTCATCTGTGCGCTTGTGCTGGCGCTGCATGCGGCCCTTGCTCGATGCCGGCTTCTCT ATGCAAACCCGGTGGGGTCTTGCCCTCAGCTGCCACAGAATTGGCGTCAGGTTCTTTGTCCCCGTATCGATGAAGTA CACCCCTGCCAGAGCTTGTAGAAGCGTTACCTGTGTTGAGGAGGGATGGTGGCAGTCTGAACCTACTCCTTGTATGGGG AATTTTATGATGGTGTATGGGCATGTGCTGGGCAACATCGGGGGTGCAGAGGTTGTGCTTGGAGCTGCCGAGCTTG CGCCTTGTGTGACTTGGATAGTGTGAGGTGAGCACAGCAGAGGAGAGGGAAATTCATGAGCTGTGGAGGGTCTTGAA GGATGAGATGTGCTTGCCTCTGATGATATCGTTGTGTCAACTGAACAATTTGAGCTTGCCACCGTGTCTGATGGCGCTG CCAGGTGATGTCAAGCAAGGTCTTGAGTTTGTCTGGGGTGGATCTTGCAAGGGTCAATGCACGTGCAAGGAAT TGAGGGATCTTGCTGCAGATGATAATCTTTGGAAGAAGAAGTGTGAGATGGAGTTCAATACCTCAAGATACATGCCGTTG TATGATGTGTAATGCATTTACTCTGACCAAAGGAAGGATATCGTACTAGCTGATAAGTATACCTGTGGTAATTATATG CAGAAGCCCGTACACAACCTGGTAGGTGGCTTATTATATTAGTCTACCATTCCCTACTTTGCCAGTACATCACTATTG GGTTGAGTTTGTGTGTTATCATTTGGTTGATTGGTTTCAGGATGCTCCTGCAGCAGGCATTCACCTTTGACTGTATTAT TCCACTGCCAATCAATCCTTACCAGCTTCCCCATCTGCTGGTGCCTGCTGCTCAACAACCTCAAGCTTCAGCATCAGCA AAAGATGGTGGCAATATGTATTCCCCCTCCCTGCAGTGTCTGCTGCAAGCAGCCAAGGGCATTGTTTTCGCGGTCCGAGCTA ACCAGCTTGCTTCGCTTGACCTTGCCATGGACTTCGACGAGCCTATCCTTTTTCTGTGCATAATGCAAGTTTGGCAAGA GGGGATTCAGTTTACAACTCTACCGCGGATCTCAGCTAAGTAGAAACATGAGCATTGACAAGTGTTTGAAGGGCAGT AAAAGGAAGGGCTCAGGCGAGGGCAGTTTCATCGCTACATTCCTCAAGAGGAAACCGGTGAATGCCTCAGAGAGAACTCA GCATGGAGCATGCCGAGAGAAGCGGGTGTGCTGACGCTAGCAGGGAGGAGTACGTGCATGTCCGGGCAAAACCGCGG CCAGGCGACCAACAGCCACAGCCTTGACAGAAAGATTTGAAAGGGAGAGATAAACCAAGGATGAAGCTTCTGCAGGAC CTCGTCCCAGGATGCAACAAGATTACAGGGAAGGCCATGATGCTCGACGAGATCATAAATACGTCCAGTCTCTGCAGC GACAGGTGGAGTTCTCTCGATGAAGCTCTCGACAATCAGTCTGAGTTGAACCTCTGACCTCGACCTGCAAGATATCCT TTGTTTCAAGATGCTCGCTCCGCATTTCTGGGATGCAGCCCGCAATTGAGCAATGCCATCCTAACCTTTACAGGGCG GCTCAGCAATGCCTCTCACCTCCTGGCTTGTACGGGAGTGTGTGTGCCAAATCCCGCAGATGTTTCAATTTGGCAAGGG CCGGTCACTTGGCTTCTGTTTCTCAGCAGAGAGGCCTCATCTGGAACGAGGAATTCGCAACATTTGCTCCGCCCGGTTT CGCTTCAGACGCGCTGGCACCAGTCTTAGAGAACTCTGATTTCATGAAAGTGAGTAG
SEQ ID NO:126	ATGGCGCGCGCGCGCGCGCGCGCGCGGAGCGCGCGGGATCCGACCTCGCGAATGCGCGGGCGC CGTCTCCCGTGGTGGCAAGCACCTCCCGTCCGGCGCGGTGCCGCGCCACGCGTACGTGTTTCGACGGCGAGGGGGGTT CGCCGACGCGCGGTGGGACGTCCGCGCGCGCGCGCGCGGGGGCGTTTACGTGGCACCACATCGAGCTCCCGCGCAGCAG CCCGGGGGCGCCCGCGAAGCCGCTCCACACGCGCAGGCGCTGATCGAGTCTGCTGCCGCGCTCAGCTCGCAGG AGATCCTCGCGTTCTGTCGCCACGGGCGCGCACTGCGGCGTCTGAGCGCGCGCGCGCGCGGGGGCGGGCGCGCTCCT TCTCCGCGTGTGCTCGCGGGGCGGTGGGGAGCGGTTCCGCGCTCCGCTCGCGCGCGCGCTCACGGACAGCTCCGTG GTGACCGTGTCCGTGGGCGCGGTCCCGCGCTCGCGTTCGGGACCACGACAGGCGTCTGCTCCTCTCCGAGGTGCCGCTCG GGGTGACCGCTCGCTCTCCGACGAGGGCCACGGCGCGGGCGCGCGCTCGAGGGCGGGGTGGTGATCGAGGAGCGGCT GCTCGAGTCTGCTCGCATGAACCACGCGCGCGCGCGCACACCGACAACCCGTCGCCGCGGACCGTGTCCAACCTC CTCGTGACGCTCTGGGAACGCACGTAGACCACGTCCACGACATCGTCACGCGCTCGAGATGGAGCTCGACAGCATCG AGCTGCATCTCGACAAGGGTGGTCACTTTATGAGGAACTTTTGTGGATGGAAGGAGATTCCCCAAAATGCATCTTGA TCTACAGCGCTGCTTCAGGTTGTTTCTCATGGTGACCAAGTATTCCCCCGTGTAAAGGAAAAATGTGCGAGCAAGAGT TGGTTTTCGAGTGAAGATATTGTGCTCTTGAAGATCTGATAGGCCGCTTAGGAGGCTGAAGGAAAAATCTTGGATTGA TAACGAATAGGGTGACTACACTTCAAGCTAGTCTAGATAGTGGCAATCTGAGCAGATAAACAAAAGCTTGTACTATCT TTCATTTTTGTCCATAATATTCCTTCTCTATCCATTGCTACTGGAGTTTTTGGGATGAATGTTGGTGGTGTGCCATGG ACTGAGCAGAAAAACCTGCAAACTAGATGGCTTCTTCAATGTGATGTTAATATGCGTCTGATCTTGTGATCCTGC TGCTTTGTTTCTTATTTCCTTCATTGTATTACACGTGTGCGCATGGAGAACCCGCGTGCCTGGCCCGGAGCAGTTT TCAGAACAGAGACATCTGAACTCTTTAAGGGTCACAAAGATGGTTACATGCGCTCTGA
SEQ ID NO:127	ATGCAGGACAGCTGATCTGCAGCGGCTGCAGGCGCGTCTCCAGTACAGGAGAGGGGTCCGCGCGCTGCTGCCCGG GCTGCAACACGCTCACCGCGTCAACCCGTGAGCGGTGGCCGACATGTCGGAGCTCATCTGCAGCGGCTGCCCCACGCT GCTGTTCTACAACCGCGCGCGCTCCAACATCCGCTGCCCGAGCTGCAACAGGCTCAACTCCACAGATCAGCCAACAG ATTGCACACCTGACATGCGGGCAGTGCCGGACGACTCTGATGCACCCACCTGGAGCCTCAACTGTGAGTGTGCACCT GCAGATATGTTAACCATGTGAGGGATGCTCGGCCTCAAATGTCTTGTAGAGAATCCTAAGACACTGGATGATAAGGG CAAGCTGGTGAGCAATGTGGTTGTTGGTGTACCTCATGAAAAGATGA

[illegible]

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3	TCGCATATCCCGTTACCTTTGCCGCGCGCGCGCGCGCGCTCTCCGCTCGCCGCGCGCGAGGGCGCCCGTCGCGCGCGC GTGGAGCGAGCCTAGCCGCACGAGCTGAAAGCACCTAAAAGGTCAGCGCGTCCCTCCCTCTCTCTCTCGCGCGCT CCCGCAGCAGCCACAGGACACCTGAGACGGGTCTGGGGGTGCAGGTGCGCGCTGGAGGAATCCCTAGGGGCTAGGGGAGGT GGCTGGAGATGGCTGGTGGGAGCTGCGACGTGTGCAAGGAGGCGCGCTCCAAGTACAAGTGTCCGCTTGCCGACGCCAT AGTAAGTCCAGCCACCGGATATCTCCACCCTTCTGTGCTTACAGCTTCCATGGGTAGCGTCGTCGCATACCACTGTCTTA AAATTTGGGAAATCGCTTCGATCATGGTGCTCAGTAATGGCCTACTAGCTAGCATAACAATTGAATTGAAGAACAATTGTT ACGGTTTTAGTGCAATGTCCTACTTGTGTGTTACATCGATTACTTCACTGCTTACTGCTTGAAAGAGAGTACGGGTTT GCTAGGTCAATAGAGTAGATTGATGATTAATGGTTGGAAGCATTAGCTTCTTTTGAATATAGCCCTACATCAGAATTAG CTTGATATATTTTGGGTTTGAAGTGGTAGCTTGTGCTGGAGTGGTTTTGCATGAGTAAAAAAGGAGGAGCAGCAA AACAAGACATGTAAACCTTTCTCTCATATCTGGTGTCAGTGTGGTTTTGGTACTAAGCTGTATTGAATTAGTATTCAGA GGCAAACGTCCATCATTAATAATCTGTAATACTTTGCTTATTTTTCTTGAATACGCAAGAGAATTACATATCATACTTT ATGACTTCTCTTGCACAATTGTTTCAAGGATGTAACCTTAGGATTGCCAAATATGATTATCTAAACAAACTGTTTTCAAG ATTCCCTGAAACTAAATGGACTACTGAACTAACATACTGTTTCCAGCGATGCAATCACGGTTGGACATCTTCTATGTGCTCCT GTAGATTGTTTTGGTAAATGCTCTTTTCCCTAAAGTTGAATGGCATTGGCTCATTGGCCACAGTCCGGTGTATGACAA CTGGGGCCAGGGCTACATGTTATACACATATGTGGCAAAAGAGCAGCATGTCATATGTAGACCAATTAAGAGCATGGTC GTTTCAATTTCTGCTGCTCTTTTCTCTATGTGTGTAAGTGGCCTTACAAACGGTTTCAATATCCCTTGCAGTTG CTCGGTGGCATGCTTTAAAAATCACAAAGTACTCAGTGCTATCTTGGTAGTTTCTAAATATAGCTCTAGTGTGCTG CTGAAAGTAGCTCAAGTAGCGGAGGGGGCTGTAGCAAACTGCCGTGTTCCCTCTGTGCTTCTAGTTGTGTATTTAAA TCAACAGCTTCCCTGTACTGCTTTTCTCTCTTTGGCCAGCGTCTTTGGCAGCCGATTTTTAAACATAGCTCAATAAA CCAAACCTTTAAAAAATATAGCAAGTGATAAATGCTTATCACACTCCAAGTGTCCAAGTCTGCGGGGACCTTTTGT TTGAAATTTTGGCAATTTTACTATTGTAATTTGGTTTGGAGTATGGGAAAGGCTGAACAGTCAACACAGCAAAATAT AACTATCATTTATGCAATGCTTTTATGCAACAAAATGGCCACCAAAATATCTTATCTCCCTTTTTAGAGGAATATATT TATTATCTGTAGCCAGTATTTGTGCTAAATATCGTTTTGCCAACAGATAAATTTTGGCAGAGACAATACCTCTGGAA GAAGTTAGCAAGTCACTCTTTCAGGAGGAAATTTGTAAGTGCTCTAGCTTTTGGTGAAGTCAATACAGTTGTTTGAACAGCT ATATAGTCTCTATATATGGAATTTGAGTTGAAACCATGATCAATAAAATAGAGGGCTCTACATATAAATAGATAT ACTGTAATAGAGCATTGACTGTGTACACCTAAAAGTCTGCGAGGCGATGACTTGGCCATATATAAGGGCTGAATATCT TATCATATAGTCATTCAATTAATTTGTCAATTTGTTCTGTCTACTAATATGTTTCTAAATAATCTACTGGAATTTACAGTTG TGCTTCTTATTTGTTTTAGCAAGGAACTCTAGGTCACTGGAAGAAGCAAAATTTGCTCTAATGACAAGGATCAAAACCCGCT CTTTTCAAAAATGCACCATACTTATCTCTGTTGTAATCTCCATTTCTCTATTTGGTTTTCATTAATTTGATTGAA CTCAAACTTTATAGATCATGACTACCTTCAGTTGTAACAATGTAACCATATGCTATCTCTGCAAAAAAAGAGAAGAGT AACCATATGCTATGCTTTTTAATCAATAATTTAAATTTAGTTTCTCTAGAATTTATTATAAGGGCTATAATATTATTCATTGT GAATCTTGAAGGCAAGAAAATTTATGTTAAGTCAATTTTTTGTCTGTAGTATCGGACACGACTTGTCCACACAATATCC AAACACATTTGCACTCTGCAAAATCTCTGAAGTTGAGGATCCAAGCTGGCTTGTGACAAGAAATGGATTAAAGATCTTAGGT ATTGCCATGTTTGAATTTTATACCATGATTTGTGTTTTTAAAAAGGAATCCTTTGCTTTTACTTGATTCTGGCTTTA TTTGTAGCTGAAACAAATGTCTCCATGTTAGTATAGTCCAGCATTTCAACCAAGAAATATCGACTTCAATTTCAATAATTAT CTGAACCTAATCCCAATCCTACAGACCTACAGTATAGGAGTAAAATATTGGCATGCATTTAGTAATGGGGAATTTAACTA TTTGCCACTTTTATAAATGGCTACTCTCGTTTGCCATTTCTACATTTCTCTACGGATTGGCCACAGAGAGAAGTTTCTT AATCATTTGCCACTTTTACCTATTAAGCATGCTAGTGAGGACAGCCAAATGTGGACAAGAGACACAAAAGTCCATTTTACCC ATGGCCCTTCCCTTGTGTTCCCCCTCTCTCCCTTTCTTTTTCAGATTTGAGCTCACCTCCGCGCTGTTTCTCGTCCATCT TCTGCACTGCTGTGTAGTGACAAGCCATTAGGTAGCAGTAACACTTAGGTGCGTGATGGATGTTCTTTGGCTGCTATTGAT TGCGGATGTACCTTCTCTTGTGGCTGTGATGACAACCTTCAACCTTGCGGATGTACCTTCTCTTGTACCTCAACGTGCT CCTCACTTGCCGCGCTTGCATCAATGAACCGCATGACGACTGACACCGGGGTGCTCCGCTGCTCCAGTGGTTTGGG GCCTCGCGTTATCTGGCTTCCGAAGAAGATGATGCAGATGCAGTGCACAACCTTCTTGGCGCTGACACATGATTGACGAG GCTTGATGAGACAGCGTGGCTGGTGTGGCGCGGATGGTCTCAATGAGGAGGTGACCCCGCAAGCAGGAGGCCAGAGCATA CGTGACCCGCTGTGGATGATCTCAATGAGATGAAGGGAGTGGCAGGGGCAAAAAGGACATTCACGCTCCTCAGTCCATGCTG GTATGCCACATCGGTGAAAGGGGCAAAATGTTAAGAAAATTTCTCTCCGTTGGCAAAAATGTAAGGACAATCGTAAGTGGCA TTTGGAGAGTGGTTATTCGTAAGAGTTGACAAATAGTTAGTAAGGATAGTACTGTAAGCAGAAATATGGGCTTCATGCTAGTC AATTTTGTATATTGGTTCCACATCCCTCCCTGTACAAATTTTATAACCTGCTAGCATTCTACCTTATTTAATTAATCATAG TAATACTCATCGTCTTGTCTCGCAAAAAGAAATAACATCATCAATTAACCTGCTGATTTTGTATCCATGCCAGCGG AATCTAATGAGATCCGAGATGCTCTGAAAGATTGTAAGCTTCAAGCAATGCTACTTAAGATTGATGGCTCTGAGAGCCAGA AAAGGTAATTTCTACTCTTGTGATAACTGCAAGTTTATTTAACAAGTTAATGATGTTTGAATTTCTGTCCGGCTGCTCAA ATAACATGCACATAATATGCCAATACCTATTGAGGACAATGGTTTGCAGTAATGAACATTGTCACTGTATAGTACAACACT TCTGTTTCTTATTTCCACCATCATGACTTCATTTTCTACCAGTAGTTGAGAAGCTTCAATGGGACAGCTTCGATGAATTAAT TCCTTTTACTATAGTCTGCTGAATACTGATACGAATATAACTTTTCTCACTTACATTTATTTTTTCTCTCTCTACCACT TTATTTTATGATGCCCACTCCCTCATTAATTCATCTCAGGAATTAGAGAAATTTGATGGAAGGACAAGTTTTTCAACAGTTT ACCAATAAGGTTTCTCTTTCCGTTGCATTTGCTCTTCTATCCACAAGATATTCCTTGTAACTCTAAGTTAATTAACAGAC ACTTGCACGTTTTTGTCTCTGTGTTTGCAGATTCTTGACATTGTTAGCCCAACAATGAACACCAACTTTCTGTGTGA GCTATTGAGCAGAAGAGTGCACGATCGGGGCAATGACAACATGTAGAGCAACTTACCTCAGATGCTGTTTCTTACCATG ATGAGATTGCCTATACCCGTGACATTTCTCTTACTACTTTGAGAAAGTTTTGTGCTCCAATATGGTGCTAGTATTTTACCA TGGCATCTTGGCTCAATCAACAAGTGTCAATTTGTCTACATCCGTGACATCTTCTTGGCTAATGGCTACTGTGAGAGTT TTGTTGTCCATTTATGTTTTTTTTGTGGTATACTCCCTCCAGTTTTAGGTTTTGTGTTGCTGTTTTGTGTTTACCAAGTCA AACTACTTTAAGTTTGACTAACGTTATAGACAAATACAATAATATTCACATTACCAAA (SEQ ID NO:132)
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50	ATGCCAGGCACGCATGTCTGCTGCAGGTAGCCAAAACCTGAAACTTAGAAATCCGTGTACGCGTCGCTTAAAGTGCCTTCGG CTTAAGGATGGGCATTTCGGTTCAGGCTGAAAAATTCGGTCTCGGTTTTTAGTTTTTGGTTAGTTTCGGTTTTTGAACCTC AGGACCGAATTTTCATCACAAAAATCTCATAACTGATAAATTCGGTCTCGGTTTTCGGTTCTCAGTCTGACCGAATTTTTTTC ATAGCCACTGAAGAGTGCAGACGGAGGCGACGCCAAGGAGGTGCCGACGCCGCGCTGGAGGCGAGAGGGCGGAGGCGCCG GTGCTGGGCGGAGGCGGCGGAGGCGGCACATGGCGGCGGCGGCGCATAGGCGGCGGCGGTGCACAGGGCGGCCCT GCGGTAGCTCCACCGTCGCGCTCGGGCTGCGGGAGCTCCACCGGCGTCTCTGTCAGACCTGCACGGGGATGGGGAT GGGGATAGGGTATGGATGGAGAGATGCTTGTGGTGGTGGGTGGATAAGGTTTTTCTTTTGTCTGTGGTCTGTGGAGGTATT GGGCCTAATGGGCCAATGCAATATTTTCGGTTTTTGTCAATTCGGTTAACCGAGCCAAAAACCGAATTGACCGAACTAA ATTTGGTTAGCTGAACTGCTGACCGAATTTGTGACCGAATTTTCAGTCTCGGTTAGTTCGGTTTTCGGTTCTCGGTTATT TTGGTTTCGGTTTTTTCGGTTTCGGCCTTTTTTCCACCCCTACTCGGAGAAATGCAGCGCGATGGGCCTCCAATCTTTGTCC TGCTTAGCTCGCGGCGGATGTGTAGTTGCATGATCCGAGCAGATTTGTCGTGGCGGCTGCGGTCAATATCGGGATCAGC GCAGTGGCGCGGCGGCGGACACCGGCAGACGTAGCGGCCAGCGGTTTCGGGTTGATCAACCGGCTGGGGGTGCCCGG TCCACGTCTCTTTGACGGTATACGTACATATTCATAATATCATATATTTTCATTGATATTTTCCCTCTGTTTCATATTA TAATTTCTATTTGACTCTTTTTTAAAGTCATTTTTTCTAAATTTGATTAAGTTTATGTAAAAATTTAGTAACATTTTACA ACACGAAATTAATTTTCATTTAACTAACATTTAATATATTTGATAATATTTATGTTTTATGTCAAAAAATTTGTCAAATTT TTTTCTATAAATTTAATCGTTCTTAAAAAAATTAATTAGAAAAAAATCAAAACAACCTTAAACCGAAGTTTGAACCTGAG GAAGTACATATCATATTTTAAAGACGTAATAGTTACTACGAAAGAGCAGCCGATTAAACGGAAGCAATAGAGAAGA ACGTACGAACGTGCGGTGCGCGAAAGGAGGACAGAAAGAAAGATCGATCGATCGATGGATCGGCCAACGCGAGCGAAAC GTCGTACACATGTACACACAGATCACGAGTTTACGGCTCATGGGTGTGCGGCCCTTCTTTGTGCAAAAGAAAAATTTGTT CGGTGACTGAATGGAGATTTTCAGATTTCTGCGTGCTCGGTTAGTTGATTACAAGTACTAGTTACTAGTATACGCAACAG AGACGTACGTCGTCTGCTGCGATCTCAATATCTCATGCTCACGTTTGGTGGTGGTTGCTGTTTCGATCGTCCAGGTATTA ATTGTCGAGCCATGCAATCCACGTGCACAGGGTATCATGTTTAAATTCGTGACTTACATGTCCTTTATGGTTGATGTCCTCA TTGGATTGATCATTTTTCTGGGAGATAATTAATTACTTACTCTACTCCCTCGGTCGAGAAAGAGACGATTTCTGGAG GGGAGGATTTGTCCAAAAAAGCAATTCCTCTACAGAAATCAAGAAACTTCAAGTATATCGTATCATTATGGGCCCA AGTGATAGCGAATTCCTTTCTCTCGTTTACATTTACCCCAACAAGATCTTATCGCCTGCGGCTCTCTCGCAGTCTCG CATTTCTCTCTTTTTCTCTCACGTTTCTCTCCGTTTCCCAATTCGATTGTCATCGATGTCGCGGCGGCGGAGGCGACGG GAGACGCGGCTTCGTGCGGCGGCGGAGACGCGGAGGCCACGAGGAGACGTGGCGTCTGTCGAGGCGGAGGCAACAAA TGGATGCTGCTTCGTGCGGCGGCGGCGGCTTGTATGCTTAACGTCTTATCATCCCCGGAAGAAGATCTGATGCGGTTGCC TGATGCACGAGCTGCGTTGTTCTTGTGTTTCAATGTTGTTTCACTGACTGCATTTCTTTTTCTTTGGGTTCTTGCCATGTTT ATGCGTGCGTCAGATGCTTATGCAGAGAAATGACAGTAGCAATAGCAATGGATGTTGTCACGGAGGGCATTTTTCGCTT TTTCACGTGAGTGCTAAATTTGCATGGGAGGTACAGGAATCGCTTCTGGATGGAGGGAGTACCTGGTTCTGTTTAGGAT CTAGTGCCTACTTTGTGCGAGTCAAAACGATTGGTGA (SEQ ID NO:133)
51	ATGGGGACGTACAAGTGCTGCATCTTCTTACCCCGCAGGTTTCGCGCTGAGCGACGCGTCCACGCGGGCGACGTGCGCA TGCTGTTTACCCCGCCACGCGCGGCGCGCCCTACATGGGCATCGACGAGCTCCGCGCTACCTCGCCGCCAGCGGGGA GGCCACGTCGACGCGACACGGCGGAGCGGATCATCGACCGGTCCTGCAGGAGCGCAGCCGACCCCGCGCTTCGGG AAGCGTCGCTCACCATCGACGATTTCCAGTACTTCTCTTCTCCGAGGACCTCAACCGGCCATCTGCCATTTCAAGG AAGTAAGCAAACTACCCGCTCGATCCCCAATTTCCCAATGCTGTTAGATTTCATCGTCAATCCGTCGATAATCTGCGGT TGCACAATGCGGTGAAATGGCGTAATTTGCTAGGATTACAGAGGGGATTCTTGGGGTTGTTTGTGTTTCAATTAATTT AAAAGTTTGGTTAAAATTTGAATGATGTGACGAAAAGTTAGAAGTTTGTGTGTCAGGAAAGTTTGTATGCGATGGAAA AGTTGGAAGTTTGA (SEQ ID NO:134)
52	ATGCAGGTAATGAATTGAATTTCCATACAACATTCTGCTCTCCTAAGAAATTACGCTTACAAGTTCATTGGATATTGC TAACTCCATTTTGATATTACTTAGTGTGACTGAATGATCTAAGATGTGAGTTGATGGTAGATCTCGTGCTCTCAGGT CCATCAGCATGAATGCACCATTTATCGCACTACTTCATATACACTGGACACAACCTCGTATCTGACGGCAATCAACTT AGCAGTGACTGCAGTGATATCCCATCATTAAGGCACTGCAATAGGCGTCCGTGTAATTTGAAGTGGACATGTGGCCAA ATTCTTCTAAGATGATGTTGATATTCTCCATGGAAGGTATGCATGAGAATTGCTCACTTGAAGACATTTTGTCTGTC ACTGGAGGCCATTCGATATGCTATGACCTTATTCAACTATTTGCTTCTTTGGTAGGACACTGACTGCCCAATGATCA CTTATCAAATGCTTGAATCCATCAAAGAATATGCCCTTTGTTGCGTCTCCCTACCCTGTTATTTATAACATTAGAAGACC ACCTTACATCTGATCTTCAGGCGAAAGTAGCTAAGGTAATTCATTTTCTCGTATGATCAATAATTTGGTGCAGTTGA TTCTGTTGTAGCTAGTTATGAAATTTTCTTTAGATGGTTCTTGAAGTATTTGGAGATACCCCTATATTATCCCGAGTCAA AACATCTTCAAGAATTTCTTACCCGAAGCACTGAGGGGACGTGTCATCCTCTCAACAAAAACCCCAAGGAGTACCT TGAATCAAAGGTGGTACTATGAAAGACAGAGACATTGAGCCTCAGTTTAGCAAAGGACAAAAAGAGCTGTCTGG GGAACAGAAAGTCCCAGATATTCAGGATGAGATGCAAAACCGCGACAAGGTTCTACTGGTTTTAACATTTGTTGTTCTT GTTTCTTAGCATATGGTGTATGTCCATCACTGTTGTATTGGCTTTATTTCCCTAGCAGCATGAGAATGATATACTATACA CCCAAGAGATGTGGAAGAAGATGATGAGAAGAAATGTGCCAGCATCACCCACTAGAGTATAAACACCTTATTACTAT TAAGGCAGGAAAGCCAAAGGGTGTGTGATTTGATGCTTAAAGGGTATCCAGATAAAGTTAGACGCTCAGTTTGTAGT GAGCAGGAACCTTGCAAAAGTGGCAGCGCATCATGGTGAACATCGTGAGGTTTCGTTTAGCAAATATACTGAATTTCTG AGCAAAGTATTTCTATCATTTGCACAGAGCTCTCTATGTCCATTGACCTTAACTTCAATCTGTTTATCAAAGCAGCT TTACACATAAAAAATCTTCTGAGAATATACCCAAAGGCACTCGCTTCAATTTCTCGAATAATCCGTTTCTTGGTTG GGTGCATGGTGCACAAATGGTGGCATTTAATATGCAGGTACATTTCTAACATGACACTCCTCTGCTACATCATATTGGC CTGAATGCCTGATACATTTTTCTTCGAGGGGTATGGAAGATCTCTTTGGCTAATGCACGATTCTACAAGGCCAACGG

	TGGCTGCGGTTATGTGAAGAACCCAGATTTTCATGATGCAAACCTGTCCAGATGGAAATGTTTTGACCCGAAAGCAGATTTACCTGTGAAGAAAACACTCAAGGTAGGTTTGTGGCATATGTTCTTCCTTTTCATTTTCATCTCTGAAATTCAGGAATCGAGCTACTTACAGCTTGCCGTGTTTGTCTACCAGGTCAAAGTATACATGGGCGAAGGTTGGCAGAGCGACTTCAAGCAGACATACTTCGACACGTATTCCCTCCAGACTTCTACGCAAGGTACATCGAATTTTACGCTGATGCCAAACGCCAACAAATTTGCAAATGCAAAACGGAGCTTTGAAAAACATGTATATATGTATAACTTTTACATATGGAGTGAGATGAAGACAAACTTTATATCAAAATTTAGAGCTCCATGAGTTCTACGACGTTCTTATTGACTAGTCCATCGTTCCATCATATAACAGGTGGGCATTGCCGGGTTCCGTCCGACTCGGTGATGCAGAAGACGAAAGCCGTGGAGGACAGCTGGGTTCCCGTGTGGGAGGAGGAGTTCCGTGCCGTGACCGTCCCGGAGATCGCGCTGCTCCGCGTGAGGTGCACGAGTACGACGTGAGCGAGGACGACTTCGCGGGGAGACGGCGCTCCCGGTGTCGGAGCTGCGGCCGGGGATCCGCACCGTGCCGCTCTTCGACCACAAGGGCTCAAGTTCAAGAGCGTCAAGCTCCTCATGCGGTTTCGAGTTTCGTCTAGCAAATTCAGTAGGCATATCACTCGCTCATGTGTGTTGATACTTAGCATGATGATCTATTTCTCTAGTAGCAAGATTAGATTTTACTTATGTGTGTTGTATACGTAGTATGATGATATTTCTAGCAAGATCAGAATTTTGGACTACCTGTTTTCTAGGAAAAACAGATTATTTGGACATGGTGACCAGAATTTTGGACTAGCAAGATAGATTTGGACTGCTTTGATCTGCAGATCGGTGGACATTTTCTAGCAAGATTAGAATATTAGATTATGGTTTGTATTAGATTTAAGAACCTTGTTTTGGTCTCTATGTAGATCGGAGAATCAGTTCCATC (SEQ ID NO:135)
53	ATGGCGATGGGAGCCGCGGGCGCCATGGTACGGCGCCATCGGCGGCGGTGGCTCGCGGCGCGCGGGTGAGGGCGCAGGGCGGCGCGCTGGGCGAGGCGCGGAGGAGCTGGTGCGGTTCGGGCGCGGTGCGGGCGGTGCGGGCGAGGGAGGC GGCGGGGGCGATGTCCGCGGAGGGTTCCGGCTGCTGGACGTCCGGCGGAGTGGGAGCGCGCGCGCGCGCGCTGCGG GGCTCGGCGCACGCGCGCTGTTTCGGGGGACGACGACGCGGCGCGCTCACGCTGCTCAAGAAGTGGGTCCACTTCG GCTACATCGGCTCTGGACCGCCAGTCCCTTACCAAGATGAACGACCGCTTCTCGACGAGTTCGCGCGCGCGCGG CGAAGGCAAGGACGCCAAGCTGCTCGTCCGCTGCGGCGAAGGCTCCGGTAATTAATCTAATCACACTGAAGCTACTGA GAATTTTATCTGTTTAGTGTGTAATACAACGTGGCAATTAAGCTTTCGGATCGGTTGCATGCATCCGAAGTAGGGCTG CTTTCCGAAGTACTAAACGGTGTGTTTTTGTAAAAAATTTCTATAGGAAAGTTGTTTTAAAGAAATCATATTAATCCAT TTTTAAAGTTTAAAAATTAATTAATCTCAATTAATCATGTACTAATGGCTCACCTCGTTTAAAGATCTTCCCAATCTCC TCTATCTCCTCCTCCTCAACACAGGTGCTTGATCGCGGTGAGGATGCTGTACGACGACGGGTACAAGAACCTGGCGTG GCTCGCGGAGGGTTTCAGCAAGTGCCTCGACGGCGACTTCGCGCAGCTGGAGGGGAGAGCAAGCTGCAGTATGCCACC GTGGGTGGGGTGTCTACATCTTCTCCAGATCCTGCTTCTGCTGCGGGTAGTCAAGTGATGATCATGTAACATCAGGA CATGCATCCGAGTATCCGACCAATGTTGAGTGGAATATGCTGCCAAGTCCCAATATTCTCCC (SEQ ID NO:136)
54	ATCTCCAAGAAGCAGTCTCCACGCCGATCCGAGATGGCCGCGACGCGCAGAGGCGGCGGAGCAGCAGCGCTCCCCGG AGTTCCGCTTCTGGCCCTCGACGCGGACCCCGCGCATCCCCCTCCTGCGCCGACGAGCTCTTCTCCGGCGCGCTCCT CCTCCCCCTCCAACCCCTCCCTACCCCGCGCGAGCGCGACCTCTCCATGTCCCTCGCCGTCGCGGATGATGATGAT GATGAGGACGAGGAGGAGGAGGTGCAGCCTGGTGCGCCGTGCGCTCCAGGGCGCGCCCACTGCTGCGGTGGCGG CGTCGGGTGGTGGTGGTGGTGGTTCGAAGAGGTGGACGGATATATTGCGCAAGAAGCAGCAGCAGCGCGCGCGGAGGA GAAGGAGAAGGATCAGCCGACGAGGCGGCGGAGACCGGCGGAGGCGGAGGCGGATCGGAGCTGAACATTAACATCTGG CCGTTCTCCGAGCCGCTCCGCGCGGGGCGCGGTGGGGTCTGCGAAGCCCGCCCGCGCGCGGGAAGGCGAGTA GCGCCCCGTGCTCCCGCAGCAACTCCCGCGGCGAGGCGGCGCGGTGGCGTCTGCTCCTTCTCCTCCTCCTCGCGCTG GGCGCCGAGCCCGCGCGCGCAGGCGGCGCGTGCCTGGGCGGCTTAGCCCGGTCTGGCAGATCAGGCGCCGCCCA TCGCGCGGCGGGAAGCAGCGCGCGCGGACAGGAGGCGCGCACCAAGGACAAGCAACCGGCGGCGGCAAGAAAC CCCACACACCTCCGCCACCGCGGCGGCGGATACGCGGCATCAACCTGAGCATCAACTCTGCATCGGGTACGCCCA CCAGGTGAGCTGCGCGCGCGCGGACGCGGAGTGCCTCGCGCGCTCCGCGGCGGCGGCGGCGGCGGCTCTTCGGC ATCAAGGGGTCTTCTCCAAGAAGGTGCATTGAGCCATGGAAGCCTTCTTTTACCTTAGCTAGAGATCCAAATAACTT TTAATTTTCTCCTCTCTTTTTTACCCTCCTTTTTTACTTTTCTTTTTTTTTTACCTTTTGTAACTTTTTTGTAACT CTTTGGGGTGCTTGTGATCATGATGATGATGATGGCTGTAATTACATGTAATTAAGCCAATAACCTGTTTTTGTAA (SEQ ID NO:137)
55	AAAAACGAAAAAAAAAATCAAAATCCTTCCCCCTTCAAATTCGAATTTTGAATCAAAACGCGCAGCTCCTCTCT CCTCTCCCCCTCTCGATCGAGGCACGCTTCTCCGCGGCGGCGCGCGCGACCGGATCAGGCGGCGGGGAGGGAGGGG AGGGGAGGATGCAGCAGAAGCCCGCGCGGAGGCGCATGGAGGAGGAGTTGAAGGGGGAGGCCGTGGGGGCCCGCGCCC CGGGCTAGGGTTATGGTTGGCGGCGGCGGCGGCTGGCCCCGACGACCCCTTCTTCGCGCGCGGGGACATGGAGCGC GAGCTCCTCGCCAAGCAAGTGCCTTCTTCCCCCTTCACTCCCTCCTTCTGCTCGCTTAATTTGGGCGCTTAGCT TCTTCGATTTTACGGGGATTTTTTTTGTAGCTGTATTGAGCTGGAACCCGTGGAAGAGATGAATAGAGATAGTAAAA TCAGCCATGATAACCTTTGATTTTGAGAAATTCAGCTGTACTGTACATAAGAGGAAAAGCTTTGCGCTTCTTTGAAA AAAAAAGAGAGAAGAAATTCAGCTGCACTTAGCATCAGTTAGGTGGGAATTCCTTAATGCTCTGCAATACTTGTCTT TTGATTTCTTGAACGGATCATGGCCGATTAGCTCAGATACCTGCCCTGATGTGAAAAGTGTAGATGAAGTGTGCTTTT ACTCAACAAGTCCCTATACCTCACTGTTTTTTAGGTGTCTGATGTTTTCTTGTTTAGGTTGCTCTGGATCTCTCCGA AGATGAACCGTACCAGCTTGAGAGGATGGAAGTGGCGAGTGCCAAGTAAGAGATTGATCTTTACTTTTACTCTTCTT GGATTGATGATTATTTATCCTTTCCGTTTACGCGGAATTAGGGGGGGGGGGGGTGTAGTCCCTGTACATCAGATGTT TGGACACTAATTTGAAGTATTAACGTAGACTATTGACAAAACCCACTCCATAACCTTGGACTAATTCGCGAGACGAAT CTATTGAGCCAAATTAATCCATGATTAGCCTATGTGATGCTACAGTCAACATGTGCTAATTATGGATTAAATAGGCTTA AAAAAATTTACGTGAATTAGCTCTCATTTATGTAATTAGTTTTGTAAAGTAGTCTATGTTTAACTCTAAGGGCCCC

[illegible]

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	TAGATTCTCCACAAGAATTAGGCTCAGCACATGCACCTAATCACCTAGTAGTATCTCCATCCATCAAGGTTTCTGCTTA ATCTCGGGCACTAACCGAAAACCTCTGTTTCTGACTATGCAGAGGCGTAGAGGGCTGAAAGGGATGGAGAGCATGGACA GTGACTCGGAGTGACGGCAGCTGGAGGTCAAGCGAGGCACCCAAAGCGAAAGGAGCAATAAGATTGGAGTGGATGGAGA TTGGGCCATTGCAATCAAAGTGGATGGGGGGAGAAGAAGTAAGGGCAAGCCAAAGGGAAGGCCAAGGCGAAGAGTGT TTTGTGTAAATGGAGAGGAAAAAGAAGAGGAGGATGTGCCGAGGGCAGGAGGTGCACGCGTAACGCGTTTGCCTCACAC ACCCTCCTCGAGGCGCCCGGCCAGCGGAAGTGGTGGCTTGAGACGACGACGACGACTATGCCCGGGGTGAATTTTTT TCGTTTCTTCGGGTTTTGTGTCAGAGCCGGCCACCTGCTCGCAGCTCGTCGAGCGGCGCACAACTTGGTGGCGGTTTT TCTCCCCCGAGAGGCCATTTTGTGGTGAATTTTTTGGGTGGGCTCCGTTGGCCCGGCGGCTCGCTTCTGTGAG CTTTTGGGGTTTGGTTGGTTGGTAATGGTTACCCGGTGACTCTTGTGCATAGTTCTTACTATAGTACTAGTACCATT TTTTTCTTCTTCTTCTCCCATTCATTACGTTGGGCAAGTCTTCGGAACACCAAAAGTATTCTGAAAAGGTTAAAAA AAAAAGAAAGAAATCATTGTGCAGTCGCAATGAGGCAGGAGATTCTGAATGGATTACGATATGGGCCAGGGCCAGGGCTGA TGGAGGCTGCTTCGATGGGCTGGCGCGTCGCGGTACCTGCAAGTGGGTTAGTCCCTTGTGACGAGCTGACAAACGT TCGGACGCGGACGGACGGGGCTGAGATATCTAACGAGGATCTTCTACGTCATATGATGGAAAGAACTCTGTACAG AAGTTTGGCATGGCTCGTCTATCAGCCGTGCGATTACACCGAATATTGGACACGTGTGCGCATCTCGCGTGATCAACTT GACCACIATTTCTTTGGCTTCTCCTTCGTCCATCAGTTGTGTGTACAGTACTGTTGTGGAGAGGGCGATGATTAAAC TCTCAATCATGTATTCTATGTGCTGATGCGTATATGTATGTGCACGTACATGTGGGCGAGTATGGGAGGGCCGTGAGG TCGAGGAAAGCGTGGTTGAAAAACGCCAGCGACCCAGATTTCCTACGCAACGCGGCGCATTTGCTGGTGAAGTAGCTC TTTTTCCCTTTTCTTTGAAAACCTGTACTACTCTTTACCCAGTTTGCATATTTTAGGGTGGAGGAGTACTCCGT ATTTAGTTTAGGGGCGGAGAATTTGAGGCTTTGTTGTTCCGACATGGTACGAGTGGCGAAGTGGCGGCGATGGCAGCCA TAAACAGGAACACAATTTGTCTGTCTGTCTGTATGTTTACTACAGACTGTTTACGGTCTCATGTCCAGCTGTTTGAATTT TGTACCTGAATGTTTTTTCTTTGGACAAAAGATGGAGTATTTGAATA (SEQ ID NO:141)
59	ACACCTGCTTTCCAAATCGCAGCTGCCTCCCATGGCGACCACCGCCTCCCTCCTCCTCCTCCTCCTCCCGGCCCTTCTCT CCTCCCCCGCCACCTCCACCCCTCCCTCGCCACCTCCGCCCCCTGCCACCGATCCGCGCTCCTCCGCGCCGCCCGCGCG CCGCCACCCCGACGCGCGTCTGTCGTCTCCGACGCGCCCGCCCTGGGTCCGCGACCTCTCGGGCGCCCGCGCGCTCTAC CGGGACGCGCAGGGAAGAGGACGACGACGCGCGGGGAGGAGGATGACGAAAACGACGACGACGACGAGGACCGCGAGCC TGGACCTCCTGGTCCGCTTCTGCACTCGGTGTTGAGGAAGGTCTCCCGCCGCGCGCGCGCGCGCGCGAGGTCCGTGCT GCCGCTTCCGCTCCCGCTGAGCTGGTCCGTTCAACCCCTTCGCTTCTCCCTTTGGTTTCAATCTTCTTCTGTTCAA ATTGAGCGGATCCTTCTCTGATTGTGTGATCTGGCCTTGATATGTTTAGTTTATGCTTGTGCGAGGTGAAGTTCTCGGT CAACGCGTGCTTGTCTCACGTTTCTATGGGTCTTAAAGGGCTACTTGAGGTGAGCAATTCATTTGTCTGAGGCTTG TTTCAAAATTTGAGCTGATTGTGATCATGCCCTTGATATGAACACTAAGTGTACACTGTGATACATATCCAGTGGAG GATTGAGGAATTTCTTGAGCCTGGTCAAACCTAGTGATGTATAACAAGTACATAAAAAATCAGTATAGCTCCATACTT CCATAGACCATATACTATGAACGCAAGCAAAACCGACAGCTGCCAAGTTGTGATTAGGAAGAGCAAAACAGTACGTA CGAGAGATTATATCGTTGAGATGATGGCTGTCTATTGCCAATGGGCTAGACTATGGGGCTATTATCATCCTGCACAAATG TGGTGATGAGTGCTAGCTTAGAGTTGTGTCGGTTTGACCTCGTGAGCAACATTCAAACCGGCATATCAAGTAGTTT GCTTGGTTGGTTTGGCTCCCATTCGAACAGCAGATCAAGTAGTAATTGATGGAGTGCTGTCTTGTCTCATGTGCTGATC GCAGAGCCTGGAGACCAGCCACAGTTGCTGGGGCTTGGCTCCTCCGCTGATATAACAGTGACATATATGGAATAACA TTATATGTCCAGAGAACAACATTTGTGCATGCTTCTGAATTTCTGATGTATGCCAGAGAACAATGGGTGTTCTACCTTC TTGTCTATTCTGCTTAGAGAGTGAAGAAGACAATCAGTGTCTGATTACATGCTGATGACACTTTTAAATGTTGATTT GAGTTTTTCCCTTCATTCTGATGTCTCGTAAATTTGGTTTTCAAATTTTGGTCAACCAAGTTTGATGAACATGGATGA GAACAGACAAGTGTATATGATACCAAAAAAGATTGTCCTTTTCTCTAACTGTCACGTGTAGATGAGAATCCTCACT TTGTTGAGTGTATGCCCTCTTTCCCTTGATAGATGCTTGGTCCAGTTTGGAGCATAAACAAAAACATGTTCTAG TACAGAGTATATAAATGTGCATATATACTCAGAGTAGGAATGGTGCACATCAGCACATGGTTCAATCATTCCTTAT TGATTGTCTACTCTTTGATTGGAGTCTGCTTATGATCAATAAACAGTTATGCTTTCAATTCAGAAAAATATAAAAAAA AATTGTGATGAAATAACAATACTCCACATGCATTACAAGTACAAGTTGTTTCTGGGAGACATACAAGTAGTTAGAA TCATGAGATTACTTAATGCTTATAATGGCGTTTTTCGATGGATGAATTCAGACCAATGAGAAATGAATCTGTATTCTTT TGCACTGACACTTTCAGCAAATTCATTCTTAGCATTCGGTAGTTTGGTCATGTGATTTACCTCTGGTGCTTTTGGGA ATACGAGTTTTTTATTCGTTGTAACATTTCTTATTGATAATAGATGGAATGGTTCGCTTTATTAAGATGATTCTCTTT AGTGAAATTTATGAATTTCTGTTTAGTAGAGAAAGAGCCTACTGCTACTGCTGTCAAGTTTGTATCCCATACCCACCCCAAC CCCCAGCGTCTGGCGGGCTTCCCTTCTGGATGAGCTCGTCCACGCTATCCTCCACAAGTCTGCCATTGTCTCC GTGCTTCCCTCCTCCACTCCTGTGCTTGCCTTCCCTTCCCTTCCGTCGATCTGAAGGCAGTGAGCAGAGAGGCCA AGGTGGTGGGCTCAAGGAGTAGATGGCGATGTGCGTGGATCCAAGAGAGAGAGAAGGGGTGAAGAGGAATATATGCTG GCAATGGGGACAGTCGGATTTTGTAAATTTATTTCTAATCTTGTGCTGAGTGGATTGCCATGTGACCAATTAACACCA TGATGATCAAAACCACTCCGTTTTTGGCAGGGGGTAAATTTGTCCAGATTCAATAGCTTGGAGGTGTCAATGTCCG GTATTGTAGTGTAGTTCCGCGAGGGCGGGTGGGTGTGGGGGTAAATCGTACGGTCCTAACCTTATAATTGCATACAA GCTTAACTACACCTGGTTCTCAAGCAGGGCTACTGAGTACTGACTGTTACTCTTCACTGACACCCCTACACACT GTCTTCTAGTGCCATGCCCTTCTTCACTAAGTGTATATTTGTTGTTGCTCAGGTGGTGTGCACATTGGGAAGTATGG TGTTCGTGACCATCCTTCTTGTTCGTGGAATATGGTCTGGAGTGACTTACATAAGAGAAAACCGATATAGCTATATTG CCAGATTGATAATGATGACAACCGATGGAGCAGATACAGACTGCTGGCTAATCATTGATTTCCTTACTACATACAT ACACTTTGCACCAAGGGATCATCAGTAAACCTTCTCTACTGTTAAGACAGCATGCTACCAGTTGACACCAACTGCC AACGCTGTTGCTATACAGCAGATTGAACAAGAACAAAAGGAATCCCATGTATTCGTCGAATAAGTGAATTTCTTC CTCTGCAAAATGCAGGAGGGATGGTTGAGCTGAACAAGATTAAACGCGGTGTAACCAATCCAGCAACTGATGAATG AGAGTGTGCTGTGATGCATTTCTGCTACTCTTTCTTGAAGAGATGTATCGTCTTATTAGTGTATGTATGTTT

	CATGCTGTTACAAC TAGCCGGTGTAGAAAACTCATGTTTGTGATTGAAAGGTGGTGCACGATACCTTTTGGTTAA AAAGTGAATATCATTTCCGATTCATTTGAA (SEQ ID NO:142)
60	GGTAGACACCGCTTCAGCCTCTGCCATCCAAC TCGCAAAATTTCCCCACGATTCCACGAAAGTAGGAACCATGAAGCT TCGGTTGCGATCCATGGACAGCGCGCGCGCGCGCGCGCGAGACCCACCGCTGCAGCTGCCGACACGGCC ACGCTCTCCGACGTCAAGGCCTTCTCGCCACCAAGCTGTCCGCGCGCAGCCCGTGCCTGCCGCTCA CCCTCAACCGCTCCGAGGAGCTCTCACCCCGACCCCTCCGCTACCTCCCGGCCCTCGGGCTCGCGTCCGGTGATCT CCTCTACTTCACGCTCTCCCCCTCCCGTCCGCTCGCTCCGCGCAGCCGACGACAGGCCCAACCCCTGCCCGCT AACCTAACCTGATGTCCCCTCGATCGCGGGAGCTGTGACCCGACCAATCTCCTGTGGAGTCTGGTAGCTCCTCGT CGATGCCGCAAGCTTTGTGCACGAATCCTGGCTTACCTGTGCGATCCGATCCGATCATCTCCACCGGATGTGGTGAT GGCGGAGGCCCTTCGCGGTGATCAAGAGCAAGTCGAGTCTCGTGTGCGGGATACGAAGAGAGAGATGGAGAATGTGGT GGTGGGATGGAACCGTCACTGTGCGCTTGTGTGGCGCTGCATGCGGCCTTGTCTCGATGCCGCTTCTCTATGCAA ACCCGGTGGGGTCTTGCCCTTCAGCTGCCACAGAATTGGGCGTCAGGTTCTTTTGTCCCCGTATCGATGAAGTACACCCCT GCCAGAGCTTGTAGAAGCGTTACCTGTGGTTGAGGAGGGGATGGTGGCAGTGTGAGTCACTCTTGTATGGGGAATTTT ATGATGGTGTATGGGCATGTGCTGGGGCAACATCGGGGTCGCAAGGTTGTGCTTGGAGCTGCCGAGCTTCCGCTT TGTGTACTTGGATAGTGTGAGGTGAGCACAGCAGAGGAGAGGGAAATTCATGAGCTGTGAGGGTCTGAAGGATGA GATGTGCTTGCCCTGTATGATATCGTTGTCAACTGAACAATTTGAGCTTGCCACCGTGTCTGATGGCGCTGCCAGGT GATGTCAAGGCAAGGTCTGGAGTTGTTCCTGGGTGAGTCTTGTGATGATGTTAAGAATATTTTCATCTGAAAAGCTACATATAAC ATCTGTGTCAGATGATAATCTTTGGAAGAAGAAGTGTGAGTGGAGTTCAATACTCAAGGTGAGAGTTCTCAGGTGGG CAGGAAGTGAAGGAAGGTTGGAGCAGCCTGGAAGGTTTCTAACAATAAGGGCCAGAAGAGGCCAGTCTTTTTTTT AATATGGCTGGGTAATCCTTATAGTCCACATGGCTTTCCGCTGATGGTGGGGATTGAGACATGCTCCGCTTTATCG GGCATCCCAATCTCCTTGGGCGCAGCTTTGGAATCAGCGCAGGAACATCTCACCAGCTGCAGTTTGGTGGACACCA TCGCAACTTTCTTGGTTAAGTCATTTCTGGTGGTTTGTCTAGTATGTTAAGAATATTTTCATCTGAAAAGCTACATATAAC ATATTGTACATATTTTATAGTTGGCACTTTATGCTATGTTAGTTGTTAACTGTATTACTGTACTCGTAATCTTTCTTT CTTTGTTGATATATCTATATTTCTTGTAGTACCAGTGTATGATGCCTTAATCATGGTAAAGTATCGTCTGTTTAA TTCTCTGTGCTACAATATGCATTTCAAACACTTGTAACTTGTAACTCTCATTTGTTGGATGCCTTTAGTCAATCTGATT ATTTCAATCCATCAACGGAGAAACAAGATACTGGTCATGTTATATACCATCATGATCTGCTGATGAGATTGAACTGTCA CTTGTCTTCTAAAGTTTGGTGAATAACTGGAAGCAGGTGGTGTCTTTCTTTGGTAAAAGAAAAGTATTGTCTTATCA TCTCTTGTCTTTTCTGTTTATATGCTATGAAAAGATATATTCATCCATATTTCCGATAATTTGGAATACTTGTCTGC CTTTTGTGCTATGGCACTTATGCTATATTTTGTATTTTATGTTTCTGGGGGGTGTAGCCTCACAGGTTGTAGC CTCCATCTGAATCGTGCAAACTGCTATCCTACAAAGAGGACAAACAACCTGATAGGCTGTACTCATTAAATCAATG TCTAAGCTAGTGGGATTAACCTTGGGCGAGCATATGGTCCGAAAACAAGAGGAAAAGTGAACATATATCAGGAACAGA TCAATAGACTTATCACGAGACTATAACCACTGGTGCCAAACGAATTAGCAACAGATAATACCTTAGAATTTTGTATT TGGCAATAAAATCTAGTAAGAATTTGTTGAGCTGCACTACAAACATGTATAGATAAGAAATAGCATCCAAGCGCAGGAT GATATGTTGTTAAGACATACTATCGAGCAATCCTGTGGCAGGTTTCTCTTACACCAGGTTTACCTATGGTTTGTAAAG TTTCTACCTGATTTTCAATGTATATATTTTGTGATTACAGCAATCAATTGTTTCTCTATATATTGCTGAAACCG AGCTGCCCTGTTTAAATGCATTAGTTAATGTTATACGTTATCTGTGTTGATAAAAAGCTTCTATGAACTATGACCAC TGTTTGCTTTTGTGTTGATCAAGCTTTCAGTGCAAGGACTTTTGGTGTGTCACAGTATGTGACATTTAGTGGATTTT TAAATCAAAATACATTATCAGTACTTGGGGCTGGAGCAATCTGTTCCTGGGGATACTTTTAGCAGGAACATGACTGAA ACATTATCAGTTTAAACAATATGACTGATGTCTTCTTATTTGTAATTGTAATTAGCAGGAACATGATTTCTGA AACTTGTGCTTGTATGATCAGATACATGCGGTTGTATGATGTGTAATGCATTTACTGTACCAAGGAAGGATATCGT ACTAGCTGATAAGTATACCTGTGGTAATTATATGCAAGCCCGTACACAACTGGTAGGTGAGTAATATATATAAGC ACTCTGGGGAACATTTATTTCTTTCTAGAAATATTTCTGAATAGTTGTTATGTTACCTGCATGCCTAAGTTAATTTCTT ATTCCTTTGTGTCCTTTTGTGTTTGTCTGTTTACTTTATTTTGTACAATGTTTCGCAGATCGTCAATATTTCTCGTGGC TTGCATCTCAATTTGATTTTCTCAACTGATGCTTCCCTCAACATATCCATTTTGGTGTGCGCTACTTGTGTTATGAT AAAGGAGAATAAAGGAGTCATCCTTTTTTTTTTCACTTCGACTACGAATATGGTTTATTTTCTTGGTGTGATGCAC CACTTTATGAATCTGACTGTAGTATTGCTTTTACTTTTATTTTCTTCGCAATAGGTGGCTTATTATATTAGTCTAC CATTCCTACTTTGCCAGTACATCACTATTTGGGTTGAGTTTGTCTGTGGTATCATTTGGTTGATTTGGTTGAGGTATAAT TTTTTAAGAGATTTTAGTCTTTTGTCTAAGTGAATATGGGTTGAGGATCTATATGACAATAAAGTTCTTGATTTTAT ACAGAAGCTTACATTTTACACTGCAGTCACTACTGAATTATCAACATTTCTCACTATACATATATAATCAGCTGAACG CCTGAACCTTTTGAATATTTGAGTTATGACTAGAGGCAAAATGGATAGTTTCTTTGTAACGATATATAACATCA ATAATGGTTTTTCTGAGCTTCTGAAGCAACTCGACATTTGATGTTCCCATACCATATTTTCTTGAGGCTATGATGGTT GAGTGAACCATATAGCTCTTCTCTCTCCATAGTCCATTGGAGTCTTAGACCTGGGGGGCCAAAGATTGCTCCATTTCTT TAAAGTGGGCTTTATATTGACCGCAGGGAGAAATATCACTTTTGGTGTAGGCGTGCATCTACTTTGCTTACAC ATGTTCTATTGACTATTGGACTCATCTGTCTTTATGTTGCATAATTAACCATGAAATATCTTTTATGAGATTTAACTT TTTGATCACTTCTCTTTGGACTGAGACTGAACCACCGTTACGATACTCAAATGGGAGCTGTACGGAGTGTACGGAGTC CAAGAAAAGCTACAACCTTCAGTAAGGGGAGTACTTTGCTTGTGGCTTGGTGCAGTGAAGAGATTGTGGGGGAAGGA GTATGGGAAGAAAGAGTTTATAAATCCAAATGGGTAAGAATTTGAGTGTCTTACTGCCAGGATATCTCAATGCTATGAT TGGTGATCTAAATATGTTTAAACGTTTACTCTGTGGTTCCATGAACCTTGGCTGCTCTATGAAAAGTATTTAGTTTCAG TTCCGTGCCAAATACAGCAATTTGAGTTTCACTTATGTGGCACTACCGTTTACACGAGCCTTATATATTTTCTCATT GTTCTTTTACCAATAGTCTGTAAACCCGAATCTTCTGTTTACATTTCACTTTGTCTGCTATACAGTATGTTTAC GTTCTCAGCTGTCTATTTTGAAGGCTATTGCAATGCACTGGAGGACCTGAAGCGATCTGCATCCGACGACCCCA GCTCAATTCACGCATCCAGTTCTGTAGCTCGGAACAATAGTACTCTACAGATAGCTGGCTGATCTGCACAAGCTA

	CAGGCAGCCTCAGCGGAGTAAGTACAAGAATCCAATTTCGCTGCCAACACACGCTCTGCCTGCCGCTGGCAGGATGCTCCT GCAGCAGGCATTCACTTTGACTGTATTATTCCTACTGCCAATCAATCCTTACCAGCTTCCCCATCTGCTGGTGCCTGCT GCTCAACAACCTCAAGCTTCAGCATCAGCAAAAGATGGTGGCAATGTACTCCAGATTCCAAAGCCTCTTGAAGTGAACA GCACAGTGATGAACCTCTATGATTGACACTTGGGCACCCTGCTTTGAGCTTTGCCCTTTTGCTCTCTCATCTGCTACTAG TAGCATGCTGGACCTTATCCTTATGCAACACAAGTAAATATATACTAACAGGTATTGCTTGTGGAGAAGGCCTAACCCGGA CCGATTTTTAAGCCAAGGTGGATAGGATAATCTTGTGGCAATTGAAATCTGCAAAATGTGCAACTAGTCTTCTTCATGAA GGGAAGTTGTACTTCTGCTATGCTTACACCGAGGTGTAATCAAATAAAGACACTGGGAAGCTGGTGAAGCAGCAGTGG TGGCCTTCTAGTATCTTTTATTTACCCCTCCTGTCCTAGCCACATGTCTCTGCATGCAGCCACTACATGGTGAACACT ATTGCTTCTACCATAGGCTGGTGAAGTAACTAACACCTCTGATCAAGAGAGGTGGAGCAGAGAAAGTGGCAGCAGCCCTC ACCCCGACTGGTAATAAGAAGTCTCCCTTCCATCCTAAATATATATCTTGTTCATATTTTCTACATCAATTTTATG CATTTTGGCAGATAGTTTCTTTGTAGACAGTGCATTGTTTTTCCCTTGATGAAACTACAGCACAGAACATTATTAG CTGTTTGCCTCATTAAGTGCCAACAGCCTTTTACTGAACGGTTTCTGTGCTCCATCCAAGTCCCTTTGCTCTCCTCAA TCTACACATTAAGAAAAGGGGAGAAGTTTCAACGTTGTACTAACCTTGTCTTGATGCAAGTCAATCAATTTCTCC CTTCTGAATTTGAGATAGCCCTTAACTGTGATGGTAGAAGCTCTGAATTGGTGGTGTAGTACGAAGTGTGAGAGCCT GTGTAATAATCGGGCAGTCAATGTGCTGCTGACAGATCATTTACAGTGCCAGCACCAAATTCGGATGATGGTATGTACG ATACTCACTGTTGAGAGCCGAAGAATCCCTCTGCTTGTCTACTGATAACAAATCAGCTCTCTTTTAACTTTTATCGATC ATAGAACCTAATCACTTCCCTGGTTTCTCTGATGATTCTGAAAGCTTTCACATTTCTAGCTGTTGCTGTCTTGTGTT GTTCTGTGGATCTGATTCTACAGAACGAAGTCTGACATTTCCATTGAGATTTACAGAGCAGAGTTTGAAGTGTGTAAC AAGTAACCTTCTGCTCTTGTACCTCTAGCCTCAGATCCACCCCACTGAATACGCAATCTGAGTCTTTGTGTGGAGAT TTCGTTTAAATTACAAATTAAGAGAGAGGAGTAAAGTTTGTCTGTAACATTAATTACACACTTGAAGCAGCAGCCTTA CATCTAGGCAGTCCACTGAAAGGTGGGTTCCTTTTCTCTCTTATGCAAGAATTGTTGAACATGTTAAGAAATAAGAC TTTGAAACTAAAACTTGAAGTTGGGTATTATGAGAAAAAATGGTGAAGAAGGTATTAACTCAGTAGTCAAGAAATTT AAGAGGGTTAAGGCTTTAAGCAAGATGGATCTGGTTTCAATTAATCAATTAACCTTATTTCTGGGCTGGCCATACA GTGGATGCAATAGCATCTGTTCTTTGGTTTGGTCTTCATTTTACAGTACCACCTGCAATTTATCTTAATTGAGAGAT TTTATTTCTGATTCATGGATGTGATCCAGCTGGTGCATGGTGTGTTAGCAGTACCGACAATTTCTATTTCCAGGACTGTGGTT TCCACCTTTGCCCTTGGCTTGTCTATTTGCTATTTGCTTAACTTTTCACTTTGGACAATCTTTATGTAAGGCTGTC AAGGGTTAGTTGTTCTTGTGAGCCTTGAAGAAATGACTGCCACAGCTCCCGATCTACCCTACCCTTTAAGTAAAG CCCATTCACTTGTCAAAGCTGACAATTTAGAAGGCCATCAGCATTTCTTAAATGATTGCAATATCACCTCGAGATCA AGTATCAGGCACAAGGTTGGTGGCTTGTAAATTTCTCATATGTATGTTCTTGGGAGTTGGGAAGTACATCTATCTA ATCTAGTACACACTAGATGACTTATCTCAGAGAGTTGTGATATAATGGTATCATGTGATCTGTTCTCTCTGTC AGATGTATTTCCCTCCCTGCAGTGTCTGCTGCAAGCAGCCAAGGGCATTGTTTCGGGTCGGAGCTAACAGCTTGTCTC GCTTGACCTTGCCATGGACTTCGACGAGCCTATCCTTTTTCTGTCATATGCAAGTTTGAAGAGGGGATTAGTTT TACAATCTTACCGCGGTATGTCTCTCTCGTTACCTATGTTCTATTTTCAAGGATAACCACAGTATCCTCCTCTCTTTT TTTTTTTTCAATTAGATAACCACAGTTTCTTAATTTGTGAAGTTTCTTAATTTACAGTTTCCGCTGTTCCAACCTCCCAAG ATACTCAGCTAAGTAGAAACATGAGCATTGACAAAGTGTGTAAGGGCAGTAAAGGAAGGGCTCAGGCGAGGGCAGTTT ATCGCTACATTTCCAAGTAACAAGTTAATTAGAAGCTCTCTTTGCTTAGCTTATCGGGTGGGAGCAGTTTTCATCGTG AAATCTGTACTACTGACGAGGAAACCGGTGAATGCCTCAGAGAGAATCAGCATGAGAGATGCCGAGAGAGAGGGCGG GTGATGCTGACGCTAGCAGGGAGGAGTACGTGCATGTCGGGGCAAAACCGGGCCAGGCGACCAACAGCCACAGCCTTGC AGAAAGATTAATTGATCTCTCAACATTAATGGAAGATCTTTCTGTGTATAGATTTTCTGTCTACACAGCTTCAACAT CTGAATGCAGTTTGAAGGGAGAAGATAAAGCAAGAGTGAAGCTTCTGCAGGACCTCGTCCCAGGATGCAACAAGGTA GCAACGAATCAATAACTCTTTGAGTCTGTGATGGTGTGGTGTGCTCTAACCTGTGTGAACATGTTGCTCTTGACAAAG CAGATTACAGGGAAGGCCATGATGCTCGACGAGATCATAAACTACGTCCAGTCTCTGCAGCGACAGGTGGAGGTAAGTG TCCGAAATTAACATCTTGTCAACAAGAAATTTACATTTCTCAATGCCAATCACTGAGTGAATCCATGAGAGTGTCTT ATCCGTGCCGGGTTTTGAGTTCCTCTCGATGAAGCTCTCGACAATCAGTCTGAGTTGAAGTCTGACCTCGACCTGCA AGATGTAAGATGAAAAACTCCAACCTCTGAAGAACAAATAACTCATCTATCACCATTGCTACACCTTGATCCTTTCTTT TTCACTGCCATACAGATCCTTTGTTCAAGATGCTCGCTCCGCAATTTCTGGGATGCAGCCCGCAATTTGAGCAATGCCC ATCCTAACCTTTTACAGGGCGGCTCAGCAATGCCCTCACCTCTGCTTGTACGGGAGTGTGTGTGTTCCCAATCCCGC AGATGTTCAATTTGGCAAGGGCCGGTCACTTGGCTTCGTTTCTCAGGTCTACATCTAACTCCAGTGAATACAGTAGTTC AAATCCTTCAGAACAGCCGAGAGTTATTATGTTTTCTTGTGCTGACGAGAGGGCTCATCTGGAACGAGGAACCTCG CAACATTGCTCCGGCCGGTTTCGCTTCAGACGCCGCTGGCACCAGTAGCTTAGAGAACTCTGGTATTTTTAGAGCTCC ACTGCCCTACTTGTCTTTTTTAAATACATTTCTTCTGAGCTGAAATCTGCGGATCGTGATGCTGCAGATTTCATGAA AGTGGAGTAGTACTGACAGCTGGTGTGATGAACAATTGACACGCCGTGAAGTCTGAAATGATCGCGCTTGAGACTGCT AATGGAGGGATGCACTCTTTAGGTTTGAAGGCTGCACACAGGTTTCCATTGGGGTGAGCGAATTTGGTGGTCTGTCG AAGTTCTCGAGGAAACTCTGTAGCCTAATCATTTGTACAGTTTGAATAATCGAAAAGATGAAAGTTTGAGA (SEQ ID NO:143)
61	ATGGCGGCGCGCGCGCGCGCGGAGCGCTCGCGGTACGCGGAGGCGGCGGGATCCGACCTCGCGAATGCGCGGGCGC CGTCTCCCGTGGTGGCAAGCACCTCCCGTCCGGCGCCGTGCCGCGCCACGCGTACGTGTTGACGCGCAGGGGGGGGTT CGCCGACGCGCGGTGGGACGTCGCGCGCGCGCGCGCGGGGGCGTTTACGTTGGCACCACATCCGAGCTCCCGCGGCAGCAG CCCGGGGGCGCGCGCGGAAGCGCTCCACCACGCGCAGGCGCTGATCGAGCTGCTCTGCCCGCTCACGCTCCAGG AGATCCTCGCGTTCTGTCGCCACGGGCGGCACTGCGGCGTCTGGACGCGCGCGCGCGGGGGCGGGCGCGCTCCT TCTCCGCTGAGCTCGCGGGGGCGGTGGGGAGCGGTTCCGCTCCGCTCGCGCGCGGTCAGGACAGCTCCGCTG GTGACCGTGTCCGTGGGCGGCGTCCCGCGCTCGGTTCCGGACACGCAAGCGCTCGCTCCTCTCCGAGGTGCCGCTCG

	GGGTGACCCGCTCGCTCTCCGACGAGGGCCACGCGCGCGGGCGCGCCGTCGAGGCGGGGTGGTGATCGAGGAGCGGCT GCTCGAGTGCCTGCTCGCCATGAACACGCGCGACGGCGCGCACACCGACAACCCCGTCCCGCGGACCGTGTCCAACCTC CTCGTGACGCTCCTGGGAACGCGATGACACCGTCCACGACATCGTCACGCGCCTCGAGATGGAGCTCGACAGCATCG AGCTGCATCTCGACAAGGGTAGGTGGAGTGTCTTCTGACTAGTAATCGCATATAAACATAAAATCAAATTTATTAGGG TTCTAAGAACATCTCCATTCGTTAGACAAAGTTGGTGCCCTTTTTCCTTTCTGGTGATGTTGTTAGGTAGGACGA ACTAGCTTCTTCGTTACGTCCTGTTGTTTCATGATTATGCACGAGAGAAATTTATTGTGCTTTGCTTTGTTCTATGGGCTC ATTGGATTACACTAACTGGAAGTCTAAAAATTTGGGAATTTGTGCGAAATTTATCGATTCTGTTGTGATTGTCCATCCGC ATTGGGCGCGCACTTGATGAAAAAATCCTATGATTGGAAGGAGGTGTCTGATGCTATTGAATTTGATTGTTATGTTA CTGTTCCATGGAGAAGTTCAAATTTCCATATTCGTGCTTAAATTTGATTCTGAAGCGGTGATTCTTTTCTAGGTGATT TCGGGTGTGTTTAGTTCACCAAAATTTGGAAGTTTGGTTGAAATTTGGAACGATGTGACGGAAGAAAGTTGGAAGTTTGT TGTGTAGGAAAGTTTGTGATGTGATGGAAAAGATGGAAGTTTGAGAAAACCTTTGGAACCTAAACCCAGCCAATAAATTA TAAATTTGGGGTGAAGTAAGGTCAGAGAAGAAGGAAGGTCATCAATTTATAGTTTGTGTTATGTATGGTGGAAATGAAAT TCTGAATGTCTAGTTTGGCAGCAACCGTATTTCTGAAATGCCATGATTATTTGCTAGCTGTGATTTCCAGATGGGATTC ATTTCCACATGATCAGTATGTGCAACAGAAATATTTTCTGAGATGGATTCTCAGCTAGTCTATGGATATCTGTTCTACTT CTACATAGGTTAATGTCAATGGAAGTCAATGTGAAGTCTAGTTTATTTACTACTAGCCAACTTATGCTCAAATTTGTT ATAGCAATTCGCAGATGTTATTCTTCTTAAATGGGCTTTGAAGGTATTTATGATATTTCTGTGAATCTTGCTTGCAG GTGGTCACTTTATGAGGAACTTTTGTGTGATGGAAGAGATTTCCCAAAATGCATCTTGATCTACAGCGCTGCTTCA GGTATTTTCTGAGATTATCTCAAATTTGCTAAATTTGAGGTTCAATGATAGTATGTTATTTGTTCACTGGATCGGGAAC GCATAATAGAAGTCATGGGCTTAAATGATTTCTTGCTAGGTTGTTTCTCATGGTGACCAAGTATTTCCCGCGTGAAG GAAAAATGTGCGAGCAAGAGTTGGTTTGGCAGTGAAGATATTGTTGCTCTTGAAGATCTGATAGGCCGCTTTAGGAGGC TGAAGGAAAAATCTTGGATTTATAACGAATAGGGTGACTACACTTCAAGCTAGCTAGATAGCTGGCAATCTGAGCAGAT AAACAAAAGCTTGTACTATCTTTCATTTTGTCCATAATATTCTTCTCTATCCATTTGCTAGTGGAGTATGTTTCCCA TGCGTATTTCTGATGCCATTTATTGCTTAAAGTCTCCAAATTTACATGATCTGCTGCAATGTTTGTGCAAGTTTTGGGAT GAATGTTTGGTGGTGTGCCATGGACTGAGCAGAAAAACCTGCAAATCTAGATGGCTTCTCAATGTCTGTTAATATGC GTCGTGATCTTGTGATCCTGCTGCTTTGTTTCTTATTTCTTCAATGATTACACGCTGTCGGCATGGAGAACCCGCC GTGCACTGGCCCGGACGTTCTCAGAACAGAGACATCTGAAACTCTTTAAGGGTCACAAAGATGTTTACATGCGCCT CTGA (SEQ ID NO:144)
62	ACCGTGGAGCACTCGATCTCCAAGCTCATCTAGCTCTTCTTGCTTCAGCTTCTTCTCTCTCTCACAGTTTCATCACACTGG CTTTTGGAGTCAGGTGCTTGTCTTCTCTGCTGTTCTTGCTTGGTAATGCTCTTGATCTCTTCTTAGATGTAATCTTGGGT AGCTAGCATGCAGTCTTGGGGTTTATCTCATCTTCTGTAGTTTAGTGTGTCAGGTTTAGTAGTAATGTTTGGTTCGAGAAA ACAAAATGATATATGGTTGGATGAATGGAGAAGATGTGGTTTCAGTTCAGTGTGATCATCTTCTGTTGTGGCTCTGAATC GAATGAGCTGTGAATTTGGTGAATTTGACGGCATATCGAGGACCGATGATCTGCAGCGGCTCGAGCGCGCTCGTCCAGTAC AGGAGAGGGGTGCGCGGGCTGCTGCTGCGGGCTGCAACACGCTCACCGCGTCAACCCGTCAGCGGTGGCCGACATGTCCG AGCTCATCTGCAGCGGCTGCCCCACGCTGCTGTTCTACAACCGCGCGCTCCAACTCCCGTCCCGTCCAGCTGCAACAGGCT CAACTCCACCAGATCAGGTGAATGATCATATTTTGCACATACTATATCTTTCTCTGAAAAGATCATATTTGCAGCTGATTC AGAGCTGCAAAATTTGGATGAAATTAATCTACTGAAATCTGAGCTGAATGATGATGTTTATTGTTGGTGGTTCAGCCAAACGAG ATTGCACACCTGACATGCGGCGAGTCCGCGACGACTGATGCACCCACCTGGAGCCTCAACTGTGTCAGTGTGCAACCTGCA GATATGTTAAACCATGTCAAGGTATGTTCTCATCTGTAATGTTTCTACCTCTATATTTCTGCGATTCGCGCATTCGCTCTCC GGTTTCGCTCTCTGTTAGTAATCATCGTGGGCTCATCGGCTCGGTGATAACCAAGGTTGGAATTTCCGAAACGAAATTTCCG AAATTTCCGACATTTTAGACCTCTCGATATGATATTTTTCGCGCAAAATTTTATTTTTTAAATTTTTTCGTGAACCTTT GGTAATATTGTTCAAATCTCAACTAAATTTTATCAAAATTTCCGAAATTTTCAGACCGAAATTTCAAAAAATTTGGCATTTC CATGAGGACCGGATCAATCGCTGCAACCGGAAAGGTTTAAACCTGAGTGATAAATAGTTAGTGTCTTCTGAATGATCTTTCCA CAACTGAACAGCAACCTGAGTTGATCAACTGGAAAGATGGAATAACCTTTTAACTTTGCCTAGAATATCAGTAGTCGGCACA GGTTTTCTGAGGCTGAAAAATATGGAATTTTCAATTAGATTTTCTCATTTCTGTGAACAAAAATTCATGGGACCATTGACTG AACAAACACGACGACTTGCTTTTATCTTAAATTTTGCATCAACTAGGGGATGCATATGTTTCTCTCTTTAAAAAAGATGAC AACTTTGGTAGGTTTCAGCTTGTCTTCTACTATCTACTTCTTAAAAGACGTCAGTCTCCATGCCATGATGATGCTAGCCAGCAG AACTCGATGCCTCGGCCAAGATTTTATCTTCCAATTCGGTTATCAGGACAAATGAACTAAATGATGATGGTCCATTGGGAC AAATGAAACAATCTGAATCTTATGTGATGTCAAATGTTCCATGATGACGATGCTAGCTTTGTTCTGTAATTTCTTTTCTT TCTCTACTTTGCAGGATGCTCGGCCCTCAAACTGTCTCTTGTAGAGAACTCAAGACATGGATGATAGGGCAAGCTGGTAAG CCTCATCTCTAGGCTATATATCTCTACTATCTACTTCTTAAAAGACGTCAGTCTCCATGCCATGATGATGCTAGCCAGCAGC GAGAAAAATCTGTAATAAACCGAACCGGCCACCCACCGCACCTCTTCCGCGACCGCGTGAGAGAAAAAAGAGTCAGCAG TCCGACTTCCATGTCGCTCTTCTCGTAGAAAAACCGAGTTTCAGTATCAGACAAAAATATGATAGTTGTTTTTATGGGTCCA TTGCAACGCCCTAGACATTTAATAGTAGTACCTTAAACCCAAATTTCTTCTGAAATTTTTTCTTGGAAATAGCAGAAAGTT TCACTTCTGAAATGATAGCTGAAGATACATGATTTTCACTCTGAAATGCTCAAGTCTGATTGACTGTTCTGTTTTGTTATGG TATAGGTGAGCAATGTGGTTGTGGTGTGCTCATGGAAGAAGATGATGAACAGGGGCTCATCTAGGTTTAAATCCCAAGGG TCTATGGATGATTGATACCTTGGTGGATTGTATCATTACTACAAAGCTATTGTTAAATCAAGTGTGTTTTGAAGCTTGAT ATAACAAGAGAAAAACAATAGGGCAAAAAATGAAGAAAAAATATATCCGAAATGTGCCATGTTGTGCTCTTTTGTGAG AAAAAAAATGTAATATGCTGGCTATGGTGTGCTAGCTATGTGCTTTTTAGCAAAAAGGAATGGAATGAGATGAGCAGCAT TGTGCTCTGGAATTTTTAT (SEQ ID NO:145)

63	CCCCTTCATTTTCTCGAAGCGCTTCCCTTCCCTTCGCTTCCCCGCACAATCTGCAAAACGGCCACCCCGTCGCTCATAAA CCCTCTCCCTCTCTCTGCGCCGACACATGGACCCACCGCTCCCAACTCCGCGGACGCCAACGGCGCGCGCGCC GACGCCACCGCCCGTCCAACACCACCGTCACCTCCCGCGCTCACCTCCGAGACGTGCCCTGCTCCCGTCGCGCG CGCGCGGACCGACACGATCCCCAACCCGATCTCCGCGCACCCCTACTTCCACCCGCGCGCCACCTTCTACATCTCCCC GGGTGACGTCTCCCTCCGCCACGCTTCTTGCACCTCGCTCCGCGTCGCGCTCCCGCTCGTCGCTACCGCCCGCG GGGCCGCGCGCGGGGGTCCGCGTGGACCCCGCGCGCGCGCGCGCGCTCGTCACCTCGCGGGGGCTCTGCCCGGGC CTCAACACCGTCTCAGGGAGCTCGTCGTCGCGCTCCGGGAGCTCTACGGCGTCCGCGACGTCTTCGCGCTCGCCCGC GCTACCGCGGGTCTACGGCCCGGACGCGGACCGCCCGCTGGACCTGGCCGCGCTCGACGACTGGCACAAGAAGGG CGGCACCGTGCTCAAGACCACCCGTGGTGGCTTTGATCTCAACAAGATCGTTGACGGCATCGTCGCGCGGGTATACG CAGGTGAGAGCAAACCCCTACCGTTTTTAGAGTTTTAGGTTTTATGTATTTTTTGGCAAATAGCTAAAGTTTAACT GATCTCACAATCATGTGACGTGGAAACCCCTAAGCTTCTTTTACGCCAAGCTGGCAAATGAAGCTGGCCAATTTT GTTAAGATTAGAAGCACAAGAAACATGTTACAGTATTTGCAAGTGTACAATGTGTCTCATCTGAATTGGCAAGGATACTA TCTTGGTGCTACAAATTTGCTTTAGACATTTTAGTATGTTGGTGTACAATCATGGGGTTGTTCTGAATTGAGAGGAG TAGTACTTATTATGTTAGGTGTCTATTATGGAAGAATTATCTCAAAGAATTTGTCTGTCCAGAATTTTTCTTTGTCTAGTA GAGTTTCTTTTCCACCGGGCTCTTTGTGCGTTAGAGTGGTCAAGTACTCAAGTGGTGAAGTCTTACTGATTTGATCG GCTGTTCCAGCAAATGCGACTGACAATCTGTACTGTACATTTGTTGGCAGATTCGCGCATTCATGGCTGCTGGT TGACCTCAAACACTTTTTATCATGACTATATCTTGCTGAGGTTTATGCAATTGGAGGAAAGGGGGCTGTTTGAG TGTGGCCATCTTCAACGAGTTTAAAGCGCGTGGTTTGAACATTTCTATTACAGGGATCCCGAAAACGTGGGACAATGAT ATCGGCATCATAGACAGGTCAATTGGGTTCCAAACCGCAGTGGAGATTGCTCAGCAGGCAATCGACGACGACATGTCTG AGGCTGTGAGCGCGGTGAATGGCATTGGACTTGTCAAACCTTATGGGAGGAGCAGGCGCACATTTGCTCTTCATGCCAC CTTGAGCAGCGCGATGTTGACTGCTGTTGATTCCTGAGGTTTATGCAATTGGAGGAAAGGGGGCTGTTTGAG TTCTTGATGAAAGGATAAAACAGAAGGACATGCTGTTGTCTGTTGCTGAAGGTGCTGGTCAGGAATTGATTCCAA GGACTGACGATCAAAGCGGGAGCAGGACGAGTCCGCGCAACATTGTGTCTCTGATGTGGGTCCCTGGTTAAATCTGA GCTGGGTAAATGGTGAAGAGAGAACACCCAAGCGAGTTGTTCACTGTGAAGTATATCGATCCCCTTACATGATACGA AACTCGGAGAAATGCCACTGACAATCTGTACTGTACATTTGTTGGCAGATTCGCGCATTCATGGCTGCTGGTGGT ACCTGGCTTCGTCCTTGGCCGATTAAATGGAACATATAGCTACATACCGCTGGAAGATGTTGCTGTGGCGAAGAACCC GGTGGAATGTAATGATCACAATGGGCATGGGTAGATCAGTCACAAACCAACGAGATTCATGAAGCCAAATACTAA GACCAAAGTGCTGTTACTGGACATGGTTGTATGACTTTTTCTCCCTGGAGCCTTGACAGCTTAAAGCTTGATTTCTTTC TATCCAGTTTCTTCTCTTGTATGCGCATCTATCTATAAGATGTTAGGTATTCTGATCTCCCTGGTTTGTGTTGTGTG CACTTGAAATCGTGTAGCAGGTATTGCTGTAAATCTGTAGTACATAAATAAATGAAGTGGCAGGAAATGTTGTTCTC ATTGGCG (SEQ ID NO:146)
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[illegible]

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AACATGATGGTGCCAAGTGAGAACTGCAGTATTGTGCAGTTTTTCAGTTTTGAGTCTAAGTTGTATAAACTTGACAG
(SEQ ID NO:151)

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Los polipéptidos descritos anteriormente participan en una o más propiedades biológicas importantes en las plantas, p. ej., en los rendimientos de las semillas de arroz, la formación de la panícula, y/o la tolerancia a agresiones ambientales. Dichos polipéptidos pueden producirse en plantas transgénicas para proporcionar plantas que tienen propiedades fenotípicas mejoradas o un mejor respuesta a las condiciones ambientales agresivas.

También se describe en esta memoria un ácido nucleico aislado que incluye un polinucleótido (p. ej., SEQ ID n^{os}: 50-98, 115-148, 150 y 151) que codifica cualquiera de los polipéptidos descritos anteriormente. Un ácido nucleico aislado se refiere a un ácido nucleico cuya estructura no es idéntica a la de cualquier ácido nucleico de origen natural o a la de cualquier fragmento de un ácido nucleico genómico de origen natural. Por tanto, la expresión abarca, por ejemplo, (a) un ADN que tiene la secuencia de parte de una molécula de ADN genómico de origen natural pero no está flanqueado por ambas secuencias codificadoras que flanquean esa parte de la molécula en el genoma del organismo en el que se produce de forma natural; (b) un ácido nucleico incorporado en un vector o en el ADN genómico de un procariota o eucariota de una manera tal que la molécula resultante no es idéntica a cualquier vector de origen natural o ADN genómico; (c) una molécula independiente tal como un ADNc, un fragmento genómico, un fragmento producido por reacción en cadena de la polimerasa (PCR), o un fragmento de restricción; y (d) una secuencia de nucleótidos recombinados que es parte de un gen híbrido, es decir, un gen que codifica una proteína de fusión. En un ejemplo, el ácido nucleico aislado que se acaba de describir es una porción de un montaje de ADN recombinado, que preferiblemente es un vector de expresión que contiene una región activadora operativamente unida al ácido nucleico que se acaba de mencionar. Tras la introducción en una célula vegetal, este montaje de ADN expresa un polipéptido codificado por el polinucleótido.

El vector de expresión descrito anteriormente puede utilizarse para generar plantas transgénicas para proporcionar aumento de la expresión de los polipéptidos también descritos anteriormente. Como resultado de dichas aplicaciones biotecnológicas, se obtienen plantas, particularmente plantas de cultivo, con propiedades mejoradas. Las plantas de cultivo de interés en la presente invención incluyen, pero no se limitan a soja, algodón, canola, maíz, trigo, girasol, sorgo, alfalfa, cebada, mijo, arroz, tabaco, cultivos de frutas y vegetales y césped.

Cualquiera de los montajes de ADN recombinado descritos anteriormente pueden usarse para transformar una célula anfitriona, p. ej., una *E. coli*, una levadura, un insecto, una planta o una célula de mamífero. El montaje de ADN y la célula anfitriona transformada pueden utilizarse para producir un polipéptido descrito en la presente memoria.

El montaje de ADN que se acaba de describir y una célula vegetal anfitriona transformada con el montaje de ADN también se pueden utilizar para generar una planta transgénica que contiene el montaje de ADN recombinado descrito anteriormente para proporcionar la expresión aumentada o disminuida de los polipéptidos descritos en la presente memoria. Para generar una planta transgénica, se puede (1) introducir en una célula vegetal un ácido nucleico recombinado que codifica un polipéptido heterólogo que se acaba de describir; (2) expresar el polipéptido en la célula, y (3) cultivar la célula para generar una planta. Como resultado de dichas aplicaciones biotecnológicas, se obtienen plantas, en particular, plantas de cultivo que tienen una o más de las propiedades mejoradas descritas a continuación. Las plantas de cultivo ilustrativas incluyen, pero no se limitan a, soja, algodón, canola, maíz, trigo, girasol, sorgo, alfalfa, cebada, mijo, arroz, tabaco, cultivos de frutas y vegetales y césped. Las plantas de cultivo, cuando se transforman con cualquiera de los montajes de ADN descritos en la presente memoria tienen mejores rendimientos resultantes de uno o más de los siguientes mecanismos:

(1) Mejorar la utilización de compuestos bioquímicos clave, tales como nitrógeno, fósforo, minerales e hidratos de carbono. Por ejemplo, un polipéptido de interés puede mejorar la circulación del nitrógeno, la detección, la absorción, el almacenamiento y/o el transporte. Ejemplos de dicho polipéptido incluyen los que intervienen en la biosíntesis del aspartato y glutamato, en el transporte del aspartato y glutamato, asociado con la ruta de TOR (diana de rapamicina), transportadores de nitrato, transportadores de amonio, transportadores de clorato, o que intervienen en la biosíntesis de tetrapirrol. En otro ejemplo, un polipéptido de interés efectúa el metabolismo de los hidratos de carbono, por ejemplo, aumentando la producción y/o el transporte de sacarosa, p. ej., un polipéptido que interviene en el metabolismo de la sacarosa o del almidón, en la asimilación del carbono o el transporte de hidratos de carbono (p. ej., transportadores de sacarosa o transportadores de glucosa/hexosa). Dicho polipéptido puede ser también una enzima implicada en la glucólisis/gluconeogenia, el ciclo de las pentosas fosfato, o la biosíntesis de rafinosa, o el que está implicado en la señalización de la glucosa, tales como las proteínas del complejo SNF1. En otro ejemplo todavía, un polipéptido de interés, p. ej., una fosfatasa o transportador de fosfato, es capaz de aumentar la absorción, el transporte o la utilización del fósforo.

(2) Mejorar de las respuestas a agresiones ambientales, tales como frío, calor, sequía, sal, plagas/patógenos o herbicidas. Los polipéptidos útiles para mejorar la tolerancia a agresiones en una variedad de condiciones agresivas incluyen polipéptidos que intervienen en la regulación génica, tales como serina/treonina-proteína cinasas, MAP cinasas, MAP cinasa cinasas, y MAP cinasa cinasa cinasas; polipéptidos que actúan como receptores para la transducción y regulación de señales, tales como receptor proteína cinasas; proteínas de señalización intracelular, tales como proteína fosfatasas, proteínas de unión a GTP, y proteínas de señalización de fosfolípidos; polipéptidos que intervienen en la biosíntesis de arginina; polipéptidos que intervienen en el metabolismo de ATP, incluyendo por ejemplo ATPasa, transportadores de adenilato y polipéptidos que intervienen en la síntesis y el transporte de ATP; polipéptidos que intervienen en la biosíntesis de glicina betaína, ácido jasmónico, flavonoides o esteroides; y hemoglobina. La actividad mejorada o reducida de dichos polipéptidos en plantas transgénicas proporcionará cambios en la capacidad de una planta para responder a una variedad de agresiones ambientales, tales como las mencionadas anteriormente.

Por ejemplo, los polipéptidos que mejoran la tolerancia de las plantas a temperaturas frías o de congelación incluyen los que intervienen en la biosíntesis de trehalosa o rafinosa, los codificados por genes inducidos por el frío, acil graso desaturasas y otros involucrados en la biosíntesis de glicerolípido o de lípidos de la membrana, que encuentran utilización en la modificación composición de ácidos grasos de la membrana, oxidasa alternativa, proteínas cinasas dependientes del calcio, proteínas LEA y proteínas de desacoplamiento. Polipéptidos ejemplares capaces de mejorar la tolerancia de la planta al calor incluyen polipéptidos que intervienen en la biosíntesis de trehalosa, la biosíntesis de glicerolípidos o el metabolismo de los lípidos de la membrana (para alterar la composición de ácidos grasos de la membrana), p. ej., proteínas de choque térmico o NDK mitocondrial. Los polipéptidos que aumentan la tolerancia de las plantas a condiciones osmóticas extremas son las que intervienen en la biosíntesis de prolina, y polipéptidos que aumentan la tolerancia de las plantas a la sequía son los que participan en la biosíntesis de trehalosa, cera, proteínas LEA o invertasa, p. ej., acuaporinas. En cuanto a la tolerancia a plagas/patógenos, cualquiera de los siguientes polipéptidos contribuye a esta función: proteasas, un polipéptido que interviene en la biosíntesis de antocianina, un polipéptido que interviene en el metabolismo de la pared celular (p. ej., celulasas, glucosidasas, pectina metilesterasa, pectinasa, poligalacturonasa, quitinasa, quitosanasa, o celulosa sintasa), un polipéptido que interviene en la biosíntesis de terpenoides o indol para la producción de metabolitos bioactivos destinados a proporcionar defensas contra los insectos herbívoros. Los polipéptidos que contribuyen a la tolerancia a herbicidas vegetales incluyen los que intervienen en la ruta del shikimato, que son de interés por proporcionar plantas tolerantes a glifosato. Dichos polipéptidos incluyen polipéptidos que intervienen en la biosíntesis de corismato, fenilalanina, tirosina y triptófano.

(3) Modificar la tasa de crecimiento o el ciclo celular de las plantas. Dichos polipéptidos incluyen los que codifican las enzimas del ciclo celular y los reguladores de la ruta del ciclo celular, p. ej., las ciclinas y las proteínas de la ruta EIF5alpha, polipéptidos que intervienen en el metabolismo de poliaminas, polipéptidos que actúan como reguladores de la ruta del ciclo celular, incluidas las cinasas dependientes de ciclina (CDK), cinasas activadoras de CDK, inhibidores de CDK, Rb y proteínas de unión a Rb, y factores de transcripción que activan genes que intervienen en la proliferación y la división celular, tales como la familia E2F de factores de transcripción, proteínas que intervienen en la degradación de las ciclinas, tales como cullinas, y homólogos vegetales de polipéptidos supresores tumorales. También incluyen los que intervienen en la biosíntesis de las hormonas del crecimiento de plantas, tales como las giberelinas, citocininas, auxinas, etileno y ácido abscísico, y otras proteínas que participan en la actividad y/o el transporte de dichos polipéptidos, como por ejemplo, la oxidasa citocinina, citocinina/purina permeasas, proteínas de la secuencia F, proteínas G y fitosulfocinas. Estos polipéptidos son útiles para la manipulación de la tasa de crecimiento en las plantas para proporcionar vigor prematuro y maduración acelerada que conduce a mejor rendimiento. Las mejoras en las características de calidad, tales como el contenido de aceite de semilla, también pueden obtenerse mediante la expresión de las enzimas del ciclo celular y reguladores del ciclo celular.

(4) Modificación de ruta de la fotosíntesis. Los polipéptidos útiles para aumentar la tasa de fotosíntesis incluyen fitocromo, proteínas de los fotosistemas I y II, transportadores de electrones, ATP sintasa, NADH deshidrogenasa y citocromo oxidasa.

- (5) Regulación de la formación y tamaño/peso de la semilla/panícula. Dichos polipéptidos aumentan la cantidad/calidad proteínas en la semilla (p. ej., los polipéptidos que intervienen en el metabolismo de los aminoácidos en las plantas, y polipéptidos que intervienen en la biosíntesis de metionina/cisteína y lisina, de transportadores de aminoácidos, de portadores de la salida de aminoácidos, de proteínas de almacenamiento de semillas, de proteasas y de polipéptidos que intervienen en el metabolismo de ácido fítico), aumentan la cantidad y/o la calidad del aceite de las semillas (p. ej., los polipéptidos que intervienen en la biosíntesis de ácidos grasos y glicerolípidos, enzimas beta-oxidación, las enzimas que intervienen en la biosíntesis de compuestos nutritivos, tales como carotenoides y tocoferoles, y polipéptidos que aumentar el tamaño del embrión o el número o el grosor de la aleurona).
- (6) Regulación de la recombinación homóloga. El aumento de la tasa de recombinación homóloga en plantas es útil para acelerar la introgresión de transgenes en variedades de reproducción por retrocruzamiento, y para mejorar el proceso de reproducción convencional, permitiendo recombinados raros entre los genes estrechamente relacionados en fase de repulsión para ser identificados más fácilmente. Los polipéptidos útiles para la expresión en plantas para proporcionar un aumento de la recombinación homóloga comprenden polipéptidos que intervienen en la mitosis y/o meiosis, como por ejemplo, las resolvasas y miembros de polipéptidos del grupo de epistasia de RAD52. Los polipéptidos descritos en la presente memoria también pueden intervenir en impartir mayor resistencia a enfermedades mejorada o mayor reserva de polisacáridos para su uso en la industria alimentaria, farmacéutica, cosmética, papelería y de pintura mejorando la producción de galactomananos, a una planta transgénica que lleva genes que codifican tales. También pueden modificar el metabolismo de flavonoides/isoflavonoides en las plantas (p. ej., cinamato-4-hidroxilasa, chalcona sintasa), o afectar a la biosíntesis de lignina. El aumento o reducción de actividad de dichos polipéptidos en plantas transgénicas proporcionará cambios en la cantidad y/o la velocidad del metabolismo de los flavonoides en plantas, mejorará la resistencia a las enfermedades al estimular la síntesis de metabolitos secundarios de protección o al mejorar las rutas de señalización que regulan la resistencia a enfermedades, o aumentará la resistencia de las plantas al alojamiento y para aumentar la utilidad de los materiales vegetales como biocombustibles.
- Además de los mecanismos expuestos anteriormente, los polipéptidos descritos en la presente memoria también pueden afectar a la eficacia de la floración, de la polinización o la fertilización o mejorar el crecimiento de las plantas en condiciones no deseadas, p. ej., baja concentración de fertilizantes o agresiones ambientales. La Tabla 1 anterior muestra los fenotipos a los que contribuyen los polipéptidos descritos en la presente memoria. Otras funciones de estos polipéptidos pueden determinarse por comparación de la secuencia de aminoácidos de los nuevos polipéptidos con las secuencias de aminoácidos de polipéptidos conocidos. Una variedad de algoritmos de búsqueda basada en la homología están disponibles para comparar una secuencia de consulta con una base de datos de proteínas, como por ejemplo, BLAST, FASTA, y Smith-Waterman. En la presente solicitud, se utilizan los algoritmos BLASTX y BLASTP para proporcionar información de la función de las proteínas.
- También se describe una planta transgénica producida por el método descrito anteriormente.

LISTA DE SECUENCIAS

<110> Yu, Su-May
Ko, Swee-Suak
Hsing, Yue-le C.

5 <120> Empleo de polipéptidos/ácidos nucleicos de arroz para mejora de la planta

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ES 2 623 545 T3

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ES 2 623 545 T3

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 Gln Gly Lys Asp Val Phe Glu Ala Phe Tyr Lys Lys Asp Leu Ala Lys
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ES 2 623 545 T3

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ES 2 623 545 T3

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ES 2 623 545 T3

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Gly Ile Lys Tyr Pro Glu Gly Ala Asn Phe Thr Leu Pro Val Pro Ser
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Pro Leu Lys Ser Tyr Leu Ser Ala Gln Gly Val Thr Leu Pro Thr Leu
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ES 2 623 545 T3

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 Ala Val Val Ala Gly Phe Tyr Val Leu Ala Leu Pro Leu Gly Val Ala
 405 410 415
 Leu Ala Phe Lys Ala Arg Leu Gly Ile Gln Gly Leu Leu Leu Gly Phe
 420 425 430
 Leu Val Gly Ala Ala Ala Ser Leu Ala Val Leu Leu Thr Phe Ile Ala
 435 440 445
 Arg Met Asp Trp Pro Ala Glu Ala Gln Lys Ala Arg Thr Arg Thr Thr
 450 455 460
 Ala Thr Val Ala Gln Phe His Gln His Asp Glu Val Val Gln Pro
 465 470 475

<210> 9
 <211> 819
 <212> PRT
 <213> Oryza sativa

ES 2 623 545 T3

<400> 9

Met	Pro	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Gly	His	Met	Asp	Pro	Val	Gly
1				5					10					15	

Asp Glu Ala Ala Glu Arg Arg Glu Met Glu Glu Lys Glu Glu Glu Glu
20 25 30

Glu Glu Glu Glu Glu Asp Glu Glu Phe Tyr Glu Ser Leu Asp Arg Ile
35 40 45

Leu Ser Ser Ser Cys Ser Ser Thr Ser Ala Ser Asp Asp Asp Asp Gln
50 55 60

Gln His Arg Arg Arg Arg Arg His His Pro Gln Pro Gln Gln Leu Ser
65 70 75 80

Ser Ser Ala Thr Phe Ser Ala Tyr Glu Val Trp Ile Ser Glu Pro Thr
85 90 95

Ser Val Glu Glu Arg Arg Arg Val Leu Leu Arg Arg Leu Gly Leu Ala
100 105 110

His Asp Ser Glu Pro Leu Pro His Pro Ser Pro Arg Val Ser Ser Ser
115 120 125

Ser Pro Arg Ser Pro Thr Pro Ser Pro Pro Ser Ser Ser Pro Pro Arg
130 135 140

Pro Ala Pro Val Val Ala Ala Ala Glu Glu Pro Arg Ser Ser Gly His
145 150 155 160

Gly Lys Pro Pro Leu Ala Arg Asn Pro Ser Gly Gly Ala Glu Gln Cys
165 170 175

Arg Ile Arg Asn Leu Asp Asp Gly Thr Glu Phe Glu Val Gly Glu Val
180 185 190

His Asp Glu Val Val Arg Glu Val Gly Thr Gly Arg Gln Leu Thr Phe
195 200 205

Glu Glu Phe Glu Leu Cys Ile Gly Arg Ser Pro Ile Val Gln Glu Leu
210 215 220

Met Arg Arg Ala Thr Thr Ala Ala Ser Ser Ser Thr Ser Asp His Ala
225 230 235 240

Ala Pro Ala Ser Lys Pro Arg Arg Lys Pro Gly Gly Trp Leu Arg Gly
245 250 255

ES 2 623 545 T3

Ile Arg His Leu Ala Gly Ser Val Ala Tyr Gly Arg Ser Ser Thr Asp
 260 265 270
 Glu Arg Asp Lys Glu Lys Glu Lys Glu Lys Lys Glu Arg Glu Ala Arg
 275 280 285
 Arg Leu Ser Ser Ala Thr Asp Asp Ser Leu Asp Gly Asn Gly Ser Arg
 290 295 300
 Asn Ala Gly Arg Val Arg Val Arg Gln Tyr Gly Lys Ala Cys Lys Glu
 305 310 315 320
 Leu Thr Gly Leu Phe Met Thr Gln Glu Leu Ala Ala His Ser Gly Ser
 325 330 335
 Ile Trp Cys Ile Asn Phe Ser Leu Asp Gly Arg Tyr Leu Ala Ser Ala
 340 345 350
 Gly Glu Asp Arg Val Ile His Val Trp Glu Val Ser Glu Gly Glu Arg
 355 360 365
 Lys Gly Glu Leu Leu Gly Glu Gly Thr Val Ala Arg Glu Asn Gly Gly
 370 375 380
 Gly Cys Ser Pro Phe Leu Ala Ala Val Gly Asn Gly Ser Pro Glu Leu
 385 390 395 400
 Ala Thr Leu Ser Leu Ser Cys Ala Asp Gly Gly Phe Val Glu Lys Lys
 405 410 415
 Arg Arg Pro Arg Met Gln Ser Ser Arg Lys Ser Val Gly Ser Asp His
 420 425 430
 Leu Val Val Pro Glu Cys Val Phe Gly Phe Arg Asp Lys Pro Val Cys
 435 440 445
 Ser Leu Leu Gly His Ala Ala Asp Val Leu Asp Leu Ser Trp Ser Lys
 450 455 460
 Ser Gln Tyr Leu Leu Ser Ser Ser Met Asp Lys Thr Val Lys Leu Trp
 465 470 475 480
 Asp Ile Thr Thr Ser Thr Cys Leu Lys Thr Phe Ser His Thr Asp Tyr
 485 490 495
 Val Thr Cys Ile Gln Phe Asn Pro Val Asp Asp Asn Phe Phe Ile Ser
 500 505 510

ES 2 623 545 T3

Gly Ser Leu Asp Glu Lys Val Arg Ile Trp Asn Val His Asp Arg Lys
 515 520 525

Ile Glu Asp Trp Asn Asp Leu His Glu Met Val Thr Ala Ala Cys Tyr
 530 535 540

Ser Pro Asp Gly Gln Val Ala Leu Val Gly Ser His Lys Gly Ser Cys
 545 550 555 560

His Leu Phe Asp Thr Thr Glu Lys Lys Leu Gln Tyr Lys Ser Gln Ile
 565 570 575

Glu Leu Arg Ile Arg Lys Lys Lys Ser Gly Gln Lys Lys Ile Thr Gly
 580 585 590

Phe Gln Phe Ala Pro Gly Ser Ser Ser Glu Val Leu Ile Thr Ser Ala
 595 600 605

Asp Ser Arg Ile Arg Val Val Asn Gly Asp Glu Leu Val His Lys Phe
 610 615 620

Lys Gly Phe Arg Asn Thr Ser Ser Gln Ile Ser Ala Ser Val Ala Pro
 625 630 635 640

Asn Gly Lys Tyr Val Val Cys Ala Ser Glu Asp Ser His Val Tyr Val
 645 650 655

Trp Arg His Asp Asn Thr Ser His Pro Ser Arg Ser Arg Ser Ala Val
 660 665 670

Asp Val Thr Asn Ser Tyr Glu His Phe His Cys His Asp Val Thr Val
 675 680 685

Ala Ile Thr Trp Pro Gly Ala Glu Ser Arg Gly Ser Phe Gly Ser Arg
 690 695 700

Ser Ser Arg Asn Ser Asp Ser Asp Asp Ala Val Met Asn Thr Gly Arg
 705 710 715 720

Asp Ala Pro Val Glu Asn Ser Glu His Asp Leu Asn Gly Thr Val Asn
 725 730 735

Arg Cys Thr Lys Arg Pro Val Cys Glu Gly Val Ala Ser Thr Ser Asn
 740 745 750

Pro Pro Ala Asp Gly Val Ser Thr Ser Trp Pro Asp Glu Lys Gln Ser
 755 760 765

ES 2 623 545 T3

Ser Ala Lys Ser Ser Pro Gly His Cys Ser Ser Asp Leu Cys Ile Gly
770 775 780

Ala Leu Asp Val Gln Arg Arg Ser Ala Trp Gly Leu Val Ile Val Thr
785 790 795 800

Ala Gly Arg Gly Gly Glu Ile Arg Val Phe Gln Asn Phe Gly Phe Pro
805 810 815

Val Gln Val

<210> 10

<211> 206

5 <212> PRT

<213> Oryza sativa

<400> 10

Met Ala Pro Ala Val Ala Ser Ser Pro Ser Leu Val Leu Ser Ala Ala
1 5 10 15

Ala Ala Thr Ala Ser Asn Lys Arg Pro Ala Asp Ser Asp Ala Ser Pro
20 25 30

Pro His Gln Gly Asp Arg Thr Gly Gln Gln Glu Lys Lys Gln Gln Gln
35 40 45

Leu Glu Cys Pro Arg Cys Arg Ser Thr Asn Thr Lys Phe Cys Tyr Tyr
50 55 60

Asn Asn Tyr Ser Thr Ser Gln Pro Arg His Phe Cys Arg Ala Cys Arg
65 70 75 80

Arg Tyr Trp Thr His Gly Gly Thr Leu Arg Asp Val Pro Val Gly Gly
85 90 95

Ala Ser Arg Arg Gly Gly Gly Gly Lys Arg Arg Arg Val Ser Ala Asp
100 105 110

Ala Asp Pro Ser Ser Ala Ser Pro Pro Pro Pro Thr Thr Ser Thr Thr
115 120 125

Asp Ala Tyr Ala Asp Leu Pro Ala Gly Phe Pro Phe Leu Ser Asp Gly
130 135 140

Ala Phe Leu Pro Gln Phe Gly Leu Ala Gly Val Ala Pro Ala Ala Phe
145 150 155 160

Ser Trp Ala Ser Ala Val Pro Asp Leu Tyr Asn Cys Gly Ile Ala Pro
165 170 175

ES 2 623 545 T3

Trp Asp Asp Gly Thr Ala Val Thr Gly Ala Ala Trp Asp Asn Phe Ala
180 185 190

Asp Ile Ala Gly Leu Asp Leu Ser Trp Pro Pro Pro Gly Asn
195 200 205

<210> 11

<211> 583

<212> PRT

<213> Oryza sativa

<400> 11

Met Ala Leu Leu Phe Arg Ile Ser Leu Leu Leu Leu Leu Val Pro Leu
1 5 10 15

Ile Pro Thr Ala Ala Ala Ser His His His Ser Pro Ala Gly Gly Gly
20 25 30

Gly Ala Ala Val Pro Leu His Pro Arg Arg His His Arg Ser Val Ala
35 40 45

Asn Thr Ala Thr Ala Leu Phe Tyr Pro Ala Pro Ser Met His Gln Asn
50 55 60

His Ile Glu Ala Glu Glu Gly Gln Leu Leu His Val Leu Ala Asp Pro
65 70 75 80

Phe Ala Ala Ala Pro Ala Ala Ala Glu Ala Pro Ser Gly Glu Thr Ala
85 90 95

Ile Ala Ala Val Gly Ala Ala Ala Glu Glu Ala Thr Pro Thr Leu Ile
100 105 110

Asp Asp Ser Pro Gln Gln Ala Ala Ala Ala Ser Pro Pro Pro Pro Pro
115 120 125

Pro Pro Pro Pro Pro Pro Pro Pro Leu Phe Ala Lys Pro Asp Leu Asp
130 135 140

Ser Thr Ala Pro Pro Gln Pro Lys Glu Glu Gly Val Asp Gly Tyr Gly
145 150 155 160

Ser Thr Thr Ala Thr Ala Thr Val Thr Ala Ala Pro Pro Leu Asp Glu
165 170 175

Pro Ala Ala Ala Thr Ala Thr Thr Thr Thr Thr Thr Thr Thr Leu
180 185 190

ES 2 623 545 T3

Pro Leu Pro Arg Tyr Ser His Val Ala Ser Pro Pro Pro Pro Pro Val
 195 200 205
 His Ala Gly Val Ala Gly Leu Gly Asp Glu Gln Arg Leu Glu Gln Leu
 210 215 220
 Ala Arg Val Leu Ser Ser Leu Gly Tyr Asn Glu Met Ala Ser Ala Ala
 225 230 235 240
 Leu Leu Leu Ala Asn Ser Ala Leu Leu Ala Ala Trp Pro Gly Ser Ile
 245 250 255
 Thr Val Phe Ala Ala Pro Asp Val Phe Leu Arg Ala Ser Cys Pro Met
 260 265 270
 Cys Ser Arg Arg His Val Leu Leu Glu His Ile Ala Leu Gly Tyr Phe
 275 280 285
 Pro Tyr Thr Glu Leu Ala Ala Ala Ser Thr Ala Lys Leu Pro Ser Ala
 290 295 300
 Ser Pro Gly Leu Cys Leu Asn Leu Ala Ser Asp His Gly Pro Phe Ala
 305 310 315 320
 Ile His His Val Arg Leu Tyr Val Asp Gly Val Glu Val Ser His Pro
 325 330 335
 Glu Leu Tyr Asn Asp Gly Arg Tyr Val Val His Gly Leu His Gly Phe
 340 345 350
 Leu Pro Pro Leu Ser His Gly Ser Cys Ser His Gly Ser Asn His Arg
 355 360 365
 His His Tyr His Tyr Gln Tyr His His His His His His Ile Ile Ala
 370 375 380
 Ser Ser Ala Ala Ser Ser Ala Ala Thr Ala Ala Ser Val Val Arg Ile
 385 390 395 400
 Met Ile Arg Glu Ala Ile Ala Arg Leu Arg Asp Ser Gly Tyr Gly Phe
 405 410 415
 Val Ala Leu Ala Met Arg Val Lys Phe Ala Glu Leu Glu Arg Leu Ala
 420 425 430
 Asn Met Thr Val Phe Ala Leu Asp Asp Gln Ala Ile Phe Val Gly Gly
 435 440 445
 Gly His Asp Tyr Val Ser Ala Val Arg Phe His Val Val Pro Gly His

ES 2 623 545 T3

450

455

460

Arg Leu Thr His Ala Asp Leu Gln Arg Leu His Pro Gly Thr Met Leu
465 470 475 480

Pro Thr Leu Ala Gly Glu Gly Gln Asn Leu Val Val Thr Gln Gly Ala
485 490 495

Ser Gly Ser Gly Ser Gly Pro Arg Asp Val Arg Ile Asn Tyr Ile Pro
500 505 510

Ile Lys Asp Pro Asp Val Val Ile Asn Ser Arg Ile Ala Leu His Gly
515 520 525

Val Tyr Val Thr Phe Pro Arg Leu His Leu Ala Asn Leu Ala Ala Ala
530 535 540

Val Ala Leu Ala Ser Ser Asn Gln Ile Asn Ala Thr Cys Gly Val Phe
545 550 555 560

Gly Asp Cys Ala Ser Ala Ala Ala Thr Ser Thr Thr Val Pro Ala Ala
565 570 575

His Arg Tyr Gly Glu Gly Gln
580

<210> 12

<211> 300

<212> PRT

<213> Oryza sativa

<400> 12

Met Asp Ala Asp Glu Ala Ala Gly Ser Ser Arg Arg Met Asp Leu Asn
1 5 10 15

Leu Tyr Leu Gly Leu Pro Arg Ala Pro Arg Pro Arg Arg Ser Asp Leu
20 25 30

Gly Ser Asp Leu Ala Leu Ser Thr Pro Met Pro Ser Ser Pro Ser Ser
35 40 45

Ser Ala Ala Ser Val Asp Ala Pro Pro Pro Pro Glu Leu Ser His
50 55 60

Pro Pro Tyr Ser Pro Ser His Ala Asp Leu Ser Pro Pro Leu Gln Glu
65 70 75 80

Val Tyr Ser Leu Tyr Asn Pro Asp Asp Pro Pro Ala Ser Glu Thr His
85 90 95

ES 2 623 545 T3

Leu Pro Pro Tyr Ala Pro Pro Pro Ala Pro Val Val Ser Glu Leu Pro
100 105 110

Asp Asp Leu Glu Phe Gly Leu His Pro Pro Pro Pro Leu Pro Val Thr
115 120 125

Gly Gly Phe Ser Ser Arg Leu Glu Ala Asp Gly Ser Val Arg Gly Gly
130 135 140

Leu Gly Arg Thr Phe Arg His Ser Val Leu Lys Leu Thr Gln Leu Gly
145 150 155 160

Val Met Leu Pro Gln Ser Gln Asn Gly Pro Ser Ser Leu Leu Pro Asp
165 170 175

Gly Ile Asp Trp Leu Arg Gly Leu Thr Leu Leu Gly Tyr Glu Asp Thr
180 185 190

Glu Arg Phe Ala Ser Ala Met Ser Asp Phe Arg Arg Ile Thr Gly Pro
195 200 205

Ser Gln Tyr Gly Ala Ser Ala Ser Ser Ser Asn Pro Pro Asn Leu Glu
210 215 220

Ser Thr Phe Asp Arg Thr His Val Val Ala Ala Pro Ser Ala Asp Gln
225 230 235 240

Ala Ser Asn Ser Ser Thr Ala Ala Val Ile Gln Gly Asp Ala Gly Ile
245 250 255

Ser Glu Ser Ala Gly Glu Pro Ser Asn Ala Gly Ser Ser Arg Ser Leu
260 265 270

Arg Arg Arg Gly Arg Ser Ser Ala Leu Gly Ser Leu Asp Ala Asp Gly
275 280 285

Gly Gly Leu Gln Arg Asn Lys Arg Arg Arg Ile Asn
290 295 300

<210> 13
<211> 480
<212> PRT
<213> Oryza sativa

<400> 13

Met Val Gly Gly Glu Leu Val Leu Ala Ala Leu Val Ile Leu Leu Ala
1 5 10 15

Leu Leu Leu Thr Leu Val Leu Ser His Phe Leu Pro Leu Leu Leu Asn

ES 2 623 545 T3

20	25	30
Pro Lys Ala Pro Lys Gly Ser Phe Gly Trp Pro Leu Leu Gly Glu Thr		
35	40	45
Leu Arg Phe Leu Ser Pro His Ala Ser Asn Thr Leu Gly Ser Phe Leu		
50	55	60
Glu Asp His Cys Ser Arg Tyr Gly Arg Val Phe Lys Ser His Leu Phe		
65	70	75
Cys Thr Pro Thr Ile Val Ser Cys Asp Gln Glu Leu Asn His Phe Ile		
85	90	95
Leu Gln Asn Glu Glu Arg Leu Phe Gln Cys Ser Tyr Pro Arg Pro Ile		
100	105	110
His Gly Ile Leu Gly Lys Ser Ser Met Leu Val Val Leu Gly Glu Asp		
115	120	125
His Lys Arg Leu Arg Asn Leu Ala Leu Ala Leu Val Thr Ser Thr Lys		
130	135	140
Leu Lys Pro Ser Tyr Leu Gly Asp Ile Glu Lys Ile Ala Leu His Ile		
145	150	155
Val Gly Ser Trp His Gly Lys Ser Lys Asp Lys Gly Met Val Asn Val		
165	170	175
Ile Ala Phe Cys Glu Glu Ala Arg Lys Phe Ala Phe Ser Val Ile Val		
180	185	190
Lys Gln Val Leu Gly Leu Ser Pro Glu Glu Pro Val Thr Ala Met Ile		
195	200	205
Leu Glu Asp Phe Leu Ala Phe Met Lys Gly Leu Ile Ser Phe Pro Leu		
210	215	220
Tyr Ile Pro Gly Thr Pro Tyr Ala Lys Ala Val Gln Ala Arg Ala Arg		
225	230	235
Ile Ser Ser Thr Val Lys Gly Ile Ile Glu Glu Arg Arg Asn Ala Gly		
245	250	255
Ser Ser Asn Lys Gly Asp Phe Leu Asp Val Leu Leu Ser Ser Asn Glu		
260	265	270
Leu Ser Asp Glu Glu Lys Val Ser Phe Val Leu Asp Ser Leu Leu Gly		
275	280	285

ES 2 623 545 T3

Gly Tyr Glu Thr Thr Ser Leu Leu Ile Ser Met Val Val Tyr Phe Leu
290 295 300

Gly Gln Ser Ala Gln Asp Leu Glu Leu Val Lys Arg Glu His Glu Gly
305 310 315 320

Ile Arg Ser Lys Lys Glu Lys Asp Glu Phe Leu Ser Ser Glu Asp Tyr
325 330 335

Lys Lys Met Glu Tyr Thr Gln His Val Ile Asn Glu Ala Leu Arg Cys
340 345 350

Gly Asn Ile Val Lys Phe Val His Arg Lys Ala Leu Lys Asp Val Arg
355 360 365

Tyr Lys Glu Tyr Leu Ile Pro Ser Gly Trp Lys Val Leu Pro Val Phe
370 375 380

Ser Ala Val His Leu Asn Pro Leu Leu His Gly Asn Ala Gln Gln Phe
385 390 395 400

Gln Pro Cys Arg Trp Glu Gly Ala Ser Gln Gly Thr Ser Lys Lys Phe
405 410 415

Thr Pro Phe Gly Gly Gly Pro Arg Leu Cys Pro Gly Ser Glu Leu Ala
420 425 430

Lys Val Glu Ala Ala Phe Phe Leu His His Leu Val Leu Asn Tyr Arg
435 440 445

Trp Arg Ile Asp Gly Asp Asp Ile Pro Met Ala Tyr Pro Tyr Val Glu
450 455 460

Phe Gln Arg Gly Leu Pro Ile Glu Ile Glu Pro Leu Cys Ser Glu Ser
465 470 475 480

<210> 14
<211> 810
<212> PRT
<213> Oryza sativa

<400> 14
Met Ala Thr Leu Pro Asp Leu Gly Val Ser Ala Phe Ile Asn Ile Leu
1 5 10 15

Gly Ala Phe Val Phe Leu Leu Ile Phe Ala Ala Leu Arg Leu Gln Pro
20 25 30

ES 2 623 545 T3

Ile Asn Asp Arg Val Tyr Phe Pro Lys Leu Tyr Leu Thr Gly Gln Arg
 35 40 45
 Arg His His Pro His Pro His Gly Phe Val Asn Leu Asp Leu Cys Ser
 50 55 60
 Tyr Leu Arg Phe Leu Ala Trp Val Pro Gly Ala Leu Arg Met Ser Gln
 65 70 75 80
 Pro Asp Leu Ile His His Ala Gly Leu Asp Ser Ala Val Tyr Leu Arg
 85 90 95
 Ile Tyr Thr Leu Gly Leu Lys Ile Phe Leu Pro Ile Met Thr Val Ala
 100 105 110
 Leu Leu Val Leu Ile Pro Val Asn Val Ser Gly Gly Thr Leu Leu Asn
 115 120 125
 Leu Arg Lys Glu Ile Val Phe Ser Asp Ile Asp Lys Leu Ser Ile Ser
 130 135 140
 Asn Val Asn Pro Gly Ser Asn Arg Phe Phe Ile His Leu Leu Met Ala
 145 150 155 160
 Tyr Val Phe Thr Phe Trp Thr Cys Phe Met Leu Tyr Lys Glu Tyr Ser
 165 170 175
 Asn Val Ala Phe Met Arg Leu His Phe Leu Ala Ser Gln Lys Arg Cys
 180 185 190
 Ala Asp Gln Phe Thr Val Ile Val Arg Asn Ile Pro His Val Ser Ser
 195 200 205
 His Ser Thr Ser Glu Thr Val Asp Glu Phe Phe Arg Arg Asn His Pro
 210 215 220
 Asp His Tyr Leu Gly Gln Gln Ala Val Tyr Asn Ala Asn Arg Tyr Ala
 225 230 235 240
 Lys Leu Val Lys Lys Lys Glu Arg Leu Gln Asn Trp Leu Asp Tyr Tyr
 245 250 255
 Gln Leu Lys Phe Glu Arg His Pro Gly Lys Arg Pro Ile Gly Arg Thr
 260 265 270
 Gly Cys Leu Gly Phe Cys Gly Arg Glu Val Asp Gln Ile Asp Tyr Tyr
 275 280 285
 Arg Ala Arg Ile Ser Glu Leu Asp Lys Lys Leu Ala Ser Glu Arg Gln

ES 2 623 545 T3

290	295	300
Arg Val Leu Asn Asp 305	Pro Lys Ala Val Met 310	Pro Val Ala Phe Val Thr 315 320
Phe Asp Ser Arg Trp 325	Gly Ala Ala Val Cys 330	Ala Gln Thr Gln Gln Ser 335
Lys Asn Pro Thr Gln 340	Trp Leu Thr Asp Trp 345	Ala Pro Glu Pro Arg Asp 350
Val Tyr Trp Gln Asn 355	Leu Ala Ile Pro Phe 360	Phe Ser Leu Ser Ile Arg 365
Lys Phe Leu Ile Ser 370	Ile Ala Val Phe Ala 375	Leu Val Phe Phe Tyr Met 380
Ile Pro Ile Ala Phe 385	Val Gln Ser Leu Ala 390 395	Asn Leu Glu Gly Ile Glu 400
Lys Val Ala Pro Phe 405	Leu Arg Pro Val Ile 410	Asp Thr Pro Val Val Lys 415
Ser Phe Leu Gln Gly 420	Phe Leu Pro Gly Leu 425	Ala Leu Lys Ile Phe Leu 430
Tyr Ile Leu Pro Thr 435	Val Leu Met Ile Met 440	Ser Lys Val Glu Gly Tyr 445
Val Ser Leu Ser Ser 450	Leu Glu Arg Arg Ala 455	Ala Ser Lys Tyr Tyr Tyr 460
Phe Met Leu Val Asn 465	Val Phe Leu Gly Ser 470 475	Ile Ile Ala Gly Thr Ala 480
Phe Glu Gln Leu Asn 485	Ala Phe Phe His Gln 490	Pro Pro Ser Gln Ile Pro 495
Arg Thr Ile Gly Val 500	Ala Ile Pro Met Lys 505	Ala Thr Phe Phe Met Thr 510
Tyr Ile Met Val Asp 515	Gly Trp Ala Gly Ile 520	Ala Asn Glu Ile Leu Arg 525
Val Lys Pro Leu Val 530	Ile Tyr His Leu Lys 535	Asn Met Phe Ile Val Lys 540
Thr Glu Arg Asp Arg 545	Glu Arg Ala Met Asp 550	Pro Gly Ser Ile Gly Leu 555 560

ES 2 623 545 T3

Ala Glu Asn Leu Pro Ser Leu Gln Leu Tyr Phe Leu Leu Gly Leu Val
 565 570 575
 Tyr Ala Val Val Thr Pro Ile Leu Leu Pro Phe Ile Ile Ile Phe Phe
 580 585 590
 Ala Phe Ala Phe Leu Val Tyr Arg His Gln Ile Ile Asn Val Tyr Asn
 595 600 605
 Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp Pro Gln Val His Ser Arg
 610 615 620
 Ile Ile Ala Ser Leu Leu Ile Ser His Val Thr Leu Phe Gly Leu Met
 625 630 635 640
 Ser Thr Met Lys Ala Ala Tyr Ser Thr Pro Leu Leu Ile Phe Leu Pro
 645 650 655
 Leu Leu Thr Ile Trp Phe His Lys Tyr Cys Lys Ser Arg Phe Glu Pro
 660 665 670
 Ala Phe Arg Lys Tyr Pro Leu Glu Glu Ala Met Glu Lys Asp Asn Leu
 675 680 685
 Glu Arg Thr Ser Glu Pro Asn Leu Asn Leu Lys Ser Tyr Leu Gln Asn
 690 695 700
 Ala Tyr Leu His Pro Ile Phe His Met Phe Glu Gln Gln Gln Gln Gln
 705 710 715 720
 Glu Gln Glu Gln Gln Arg Glu Glu Lys Val Glu Val Arg Ile Asp Lys
 725 730 735
 Ala Gln Gln His His His Arg Gln Val Glu Glu Glu Glu Glu Glu Ser
 740 745 750
 Lys Ser Ser Gln Ala Thr Thr His Tyr Tyr His His His His Glu Gln
 755 760 765
 Thr Thr Thr Thr Thr His His His Tyr His Gln His Glu His Met Ser
 770 775 780
 His Tyr His Met Gly Pro Ser Asp Thr Ala Asp Ser Pro Ser Pro Pro
 785 790 795 800
 His Phe Val Tyr His Tyr Gly Val Asp Pro
 805 810

<210> 15
 <211> 293
 <212> PRT
 <213> Oryza sativa

ES 2 623 545 T3

<400> 15

Met	Glu	Met	Thr	Arg	Ser	Leu	Thr	Leu	Val	Pro	Leu	Pro	Ala	Thr	Leu
1				5					10					15	
Arg	Pro	Ala	Ser	Ala	Ala	Cys	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Gly	Leu
			20					25					30		
Pro	Phe	Gly	Ala	Leu	Phe	Ser	Pro	Ser	Pro	Pro	Ser	Asn	Gln	Gln	Gln
		35					40					45			
Gln	Glu	Met	His	Ile	Arg	Ala	Leu	Gln	Pro	Arg	Gln	Asp	Trp	Val	Gly
	50					55					60				
Glu	Trp	Val	Arg	Ser	Asn	Asp	Thr	Leu	Val	Arg	Gly	Leu	Pro	Ile	Leu
65					70					75					80
Gly	Gly	Gly	Ala	Ser	Leu	Leu	Ala	Val	Leu	Leu	Asn	Arg	Ala	Val	Ser
				85					90					95	
Gly	Ile	Ala	Ala	Val	Ala	Asp	Ala	Ser	Ser	Ser	Gln	Ser	Arg	Ala	Asp
			100					105					110		
Ile	Leu	Thr	Leu	Ala	Leu	Ser	Val	Thr	Asp	Ile	Leu	Ala	Gly	Leu	Val
		115					120					125			
Trp	Leu	Ser	Ile	Arg	Pro	Lys	Ser	Ile	Ser	Pro	Val	Val	Pro	Arg	Gly
	130					135					140				
Val	Glu	Cys	Lys	Arg	Val	Gly	Thr	Gly	Val	Leu	Asp	Ser	Ala	Leu	Arg
145					150					155					160
Glu	Leu	Leu	Trp	Thr	Trp	Asp	Ser	Leu	Thr	Thr	Ala	Thr	Cys	Cys	Lys
				165					170					175	
Ser	Leu	Val	Val	Val	Tyr	Gly	Gly	Asn	Cys	Val	Leu	Gln	Ile	Gly	Val
			180					185					190		
Ala	Ala	Gly	Ser	Pro	Glu	Asp	Gly	Asn	Ala	Val	Met	Val	Asp	Ala	Gln
		195					200					205			
Lys	Phe	Met	Gln	Gly	Ser	Leu	Tyr	Arg	Ser	Ala	Met	Glu	Ser	Lys	Lys
	210					215					220				
Gln	Ser	Tyr	Leu	Ala	Asn	Leu	Ala	Leu	Tyr	Pro	Gly	Arg	Thr	Glu	Leu

ES 2 623 545 T3

225 230 235 240

Pro Phe Leu Pro Ala Asn Thr Gln Ala Leu Ile Leu Gln Pro Ile Gly
245 250 255

Asp Lys Gly Ile Ala Val Ile Gly Gly Asp Thr Ile Arg Gly Phe Thr
260 265 270

Asn Leu Asp Gln Ala Trp Ile Ala Met Ile Ala Asp Lys Leu Asp Ala
275 280 285

Thr Leu Ser Lys Ser
290

<210> 16
<211> 155
<212> PRT
<213> Oryza sativa

<400> 16
Met Ala Ser Ser Val Ala Gly Ser Val Thr Arg Arg Pro Pro Pro Val
1 5 10 15

Leu Leu Ala Cys Arg Ser Arg Pro Asn Asn Arg Arg Leu Ile Arg Leu
20 25 30

Leu Pro Leu Leu Phe Ala Val Val Val Leu Leu Ala Leu Leu Pro Pro
35 40 45

Cys Val His Gly Ala Arg Ala Leu Asn Asp Ala Lys Glu Ala Lys Val
50 55 60

Ala Glu Ala Ser Asp Gln Thr Thr Thr Thr Thr His Ala Ala Ala Ala
65 70 75 80

Ala Val Ala Arg Trp Ser Val Thr Val Arg Glu Gly Gly Gly Gly Gly
85 90 95

Gly His Gly Ser Gly His Ala Gly Ala Gly His Gly His Gly Ser Gly
100 105 110

His Gly Arg Pro Glu Pro Ala Glu His His Thr Gly Arg Arg Ser Ala
115 120 125

Ala Ala Gly Ser Val Arg Pro Pro Met Ala Ala Ser Cys Ala Ala Leu
130 135 140

Leu Val Ala Ala Val Val Ala Leu Leu Arg Phe
145 150 155

<210> 17
<211> 124

ES 2 623 545 T3

<212> PRT
<213> Oryza sativa

<400> 17

Met Glu Ser Ala Lys Arg Ser Cys Leu Ala Ile Ser Leu Ile Leu Leu
1 5 10 15

Leu Leu Leu Val Pro Ser Ile His Gly Ala Arg His Val Ala Ala Ala
20 25 30

Ile Lys Gly Thr Gly Ala Asp Ser Glu Met Val Val Thr Glu Arg Thr
35 40 45

Ala Gly Gly Gly Gly Gly His Gly Arg Gly Tyr Thr Ser His Arg Ser
50 55 60

His Asn Pro Asn Asn Pro Asn Asp Gly Gly Ser Gly Thr Pro Val Val
65 70 75 80

Asp Pro His Asn Val Ala Thr Arg Gly His His His Arg Gly Ala Ala
85 90 95

Thr Arg Thr Ala Ala Gly Gly Asp Pro Arg Leu Ala Ala Cys Met Leu
100 105 110

Arg Leu Gly Ala Thr Phe Phe Leu Leu Val Leu Gly
115 120

<210> 18
<211> 215
<212> PRT
<213> Oryza sativa

<400> 18

Met Ala Gly Val Gly Phe Val Glu Asp Met Leu Arg Glu Gln Ser Leu
1 5 10 15

Leu Glu Ala Thr Cys Gly Asp Leu Phe Asp His Ile Asp Asp Leu Leu
20 25 30

Asp Phe Pro Lys Glu Glu Ser Ala Ala Asp Val Leu Leu Leu Asp Ala
35 40 45

Pro Ala Pro Gly Ser Pro Leu Ser Ser Arg Ile Ile Gly Gly His Ala
50 55 60

Thr Met Ala Ala Ala Pro Pro Pro Pro Pro Gln Met Met Ala Leu Pro
65 70 75 80

ES 2 623 545 T3

Pro Pro Pro Ala Pro Ala Lys Asp Asp Ala Ser Ala Leu Phe Asp Ala
85 90 95

Ala Gly Ala Leu Gly Ala Glu Val Phe Asp Arg Lys Asp Ala His Ile
100 105 110

Gly Pro Cys Asp Glu Leu Asp Met Asp Met Ala Gln Leu Glu Trp Leu
115 120 125

Ser Gly Leu Phe Asp Asp Gly Thr Ile Pro His Glu Pro Ser Phe Pro
130 135 140

Gly Val Asn Cys Ala Ala Pro Ile Lys Ala Ser Ala Leu Thr Ala Asn
145 150 155 160

Ala Gly Val Val Leu Pro Asp Lys Ala Glu Glu Ala Leu Phe Arg Ser
165 170 175

Ser Ser Pro Ile Ser Val Leu Glu His Ser Gly Phe Asn Val Ala Thr
180 185 190

Asn Gly Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Ser Pro Trp
195 200 205

Thr Trp Thr Trp Thr Ala Val
210 215

<210> 19
<211> 376
<212> PRT
<213> Oryza sativa

<400> 19
Met Ile Ile Val Asp Asp Ala Gly Ala Phe Leu Pro Ala Leu Asn His
1 5 10 15

Ser Pro Trp Asp Gly Val Thr Ile Ala Asp Phe Val Met Pro Phe Phe
20 25 30

Leu Phe Met Val Gly Ile Ser Leu Thr Leu Ala Tyr Lys Arg Val Pro
35 40 45

Asp Lys Leu Glu Ala Thr Lys Lys Ala Val Leu Arg Ala Leu Lys Leu
50 55 60

Phe Cys Leu Gly Leu Val Leu Gln Gly Gly Phe Phe His Gly Val Arg
65 70 75 80

ES 2 623 545 T3

Ser Leu Thr Phe Gly Val Asp Ile Thr Lys Ile Arg Leu Met Gly Ile
 85 90 95
 Leu Gln Arg Ile Ala Ile Ala Tyr Leu Leu Ala Ala Ile Cys Glu Ile
 100 105 110
 Trp Leu Lys Gly Asp Asp Asp Val Asp Cys Gly Leu Asp Val Ile Arg
 115 120 125
 Arg Tyr Arg Tyr Gln Leu Val Val Ala Leu Leu Leu Ser Thr Met Tyr
 130 135 140
 Thr Val Ile Leu Asn Gly Val Tyr Val Pro Asp Trp Glu Tyr Gln Ile
 145 150 155 160
 Ser Gly Pro Gly Ser Thr Glu Lys Ser Phe Ser Val Arg Cys Gly Val
 165 170 175
 Arg Gly Asp Thr Gly Pro Ala Cys Asn Ala Val Gly Met Leu Asp Arg
 180 185 190
 Thr Ile Leu Gly Ile Asp His Leu Tyr Arg Arg Pro Val Tyr Ala Arg
 195 200 205
 Thr Lys Gln Cys Ser Ile Asn Tyr Pro Gln Asn Gly Pro Leu Pro Pro
 210 215 220
 Asp Ala Pro Ser Trp Cys Gln Ala Pro Phe Asp Pro Glu Gly Leu Leu
 225 230 235 240
 Ser Ser Val Met Ala Ile Val Thr Cys Leu Ile Gly Leu Gln Phe Gly
 245 250 255
 His Ile Ile Ile His Phe Glu Lys His Lys Gly Arg Ile Ile Asn Trp
 260 265 270
 Leu Ile Pro Ser Phe Ser Met Leu Ala Leu Ala Phe Ser Met Asp Phe
 275 280 285
 Ile Gly Ile Arg Met Asn Lys Pro Leu Tyr Thr Ile Ser Tyr Ala Leu
 290 295 300
 Ala Thr Ser Gly Ala Ala Gly Leu Leu Phe Ala Gly Ile Tyr Thr Leu
 305 310 315 320
 Val Asp Val Tyr Gly Phe Arg Lys Leu Thr Ile Pro Met Glu Trp Met
 325 330 335
 Gly Lys His Ala Leu Met Ile Tyr Val Leu Val Ala Cys Asn Ile Leu

ES 2 623 545 T3

340 345 350

Pro Ile Phe Ile His Gly Phe Tyr Trp Arg Glu Pro Lys Asn Asn Leu
355 360 365

Leu Lys Phe Ile Gly Val Gly Ala
370 375

<210> 20
<211> 488
5 <212> PRT
<213> Oryza sativa

<400> 20
Met Ala Ala Thr Gly Gly Ala Ala Gly Glu Lys Thr Ala Ser Ser Leu
1 5 10 15

Leu Leu Gly Val Arg Gly Tyr Thr Ser Thr Leu Lys Asn Ala Ser Thr
20 25 30

Ala Ser Cys Arg Leu Ser Ala Gly His Pro Ile Glu Val Thr Leu Trp
35 40 45

Glu Ala Ser Pro Pro Ala Leu Ser His Phe Ser Val His Cys Pro Asp
50 55 60

Leu Pro Ser Phe Asn Gly Asn Leu Leu Gly Ala Pro Lys Ala Ile Ala
65 70 75 80

Ala Ala Val Asp Asp Ala Asp Gly Gln Leu Leu Leu Leu Leu Arg Val
85 90 95

Pro Ile Asp Gln Leu Gly Ala Pro His Asp Asn Asp Tyr Leu Val Tyr
100 105 110

His Pro Asp Pro Pro Ser Pro Lys Leu Asp Leu Leu Pro Asn Pro Pro
115 120 125

Pro Pro Thr Leu Gly Asp His Gln Leu Ala Ile Leu Ser Cys Gly Asp
130 135 140

Asp Arg Tyr Val Val Ala Ala Leu His Val Trp Ser Glu Phe Thr Ser
145 150 155 160

Thr Leu Arg Leu Tyr Arg Ser Ser Cys Ser Ser Gly Ser Trp Thr Ser
165 170 175

Glu Glu Val Ser Val Glu Glu Pro Val Arg Asp Arg Leu Cys Pro Ile
180 185 190

ES 2 623 545 T3

Pro Asp Ser Ala Lys Arg Gln Leu Tyr His Val Thr Thr Lys Thr Ile
 195 200 205
 Thr Leu Gly Gly Ala Lys Gly Thr Val Gly Trp Val Asp Leu Trp Arg
 210 215 220
 Gly Ile Leu Leu Cys Asp Val Leu Asp Glu Met Ser Pro Arg Lys Leu
 225 230 235 240
 Arg Asp Met Pro Leu Pro Trp Pro Ala Lys Gly Asn Trp Arg Met Tyr
 245 250 255
 Leu Asn Gly Asp Val Ser Phe Cys Arg Asp Ile Ala Ile Ser Gln His
 260 265 270
 Lys Asp Ser Ile Lys Tyr Leu Glu Met Glu Ile Val Ser Pro Arg Thr
 275 280 285
 Val Thr Thr Thr Ile Pro Thr Ser Thr Ser Ala Asp Pro Thr Ser Tyr
 290 295 300
 Leu Glu Trp Val Arg Arg Ser Arg Glu Pro Gln Pro Thr Arg Arg Arg
 305 310 315 320
 Ser Val Phe His Pro Gly Ser Trp Arg Ile Thr Thr Trp Ser Met Pro
 325 330 335
 Ile Pro Val Thr Ser Trp Asp Asp Trp Arg Arg Asp Cys Thr Ala Glu
 340 345 350
 Ser Arg Glu Val His Leu Asp Thr Asn Pro Ser His His Tyr Glu Leu
 355 360 365
 Leu His Ser Leu Met Leu Ser Asn Ser Gly Asp Glu His Arg Glu Glu
 370 375 380
 Ala Gln Gly Gln Gly Ala Thr Ser Ser Leu Ser Leu Gly Arg Leu Arg
 385 390 395 400
 Leu Cys Tyr Pro Ala Leu Ser Cys Ile Asp Asp Asp Val Val Tyr Leu
 405 410 415
 Leu Gly Asn Ala Ala Gly Arg Gly Ala Lys Thr Gly Gly Met Met Val
 420 425 430
 Ala Val Asp Val Arg Asn Lys Glu Leu Arg Gly Val Ala Lys Leu Asp
 435 440 445

ES 2 623 545 T3

Pro Glu Lys Asn Thr Leu Tyr Ser Met Arg Cys Tyr Leu Ala Thr Gly
450 455 460

Ile Ser Lys Arg Leu Asn Thr Thr Thr Asp Thr Arg Val Gly Arg Pro
465 470 475 480

Glu Glu Asp Ala Glu Ala Ala Glu
485

<210> 21
<211> 167
<212> PRT
<213> Oryza sativa

<400> 21
Met Ala Asn Tyr His His Gln Glu Tyr Tyr Gln Met Ala Ala Ala Ala
1 5 10 15

Ala Val Ala Trp Pro Arg Glu Pro Asp Ser Pro Gln Leu Ser Ile Met
20 25 30

Ser Gly Cys Ser Ser Leu Phe Ser Ile Ser Thr Leu Arg Asp Asp Asp
35 40 45

Asp Gly Gly Gly Val Arg Leu Ala Gly Ala Ala Leu Pro Ala Thr Pro
50 55 60

Val Ser Leu Ala Gly Ile Ala Gly Gly Ala Ser Thr Pro Gly Gly Asp
65 70 75 80

Glu Val Asp Met Glu Val Arg Gln Gln Ser Gly Gly Ser Gly Asp Asp
85 90 95

Arg Arg Thr Ile Arg Met Met Arg Asn Arg Glu Ser Ala Leu Arg Ser
100 105 110

Arg Ala Arg Lys Arg Ala Tyr Val Glu Glu Leu Glu Lys Glu Val Arg
115 120 125

Arg Leu Val Asp Asp Asn Leu Asn Leu Lys Lys Gln Cys Lys Glu Leu
130 135 140

Lys Gln Glu Val Ala Ala Leu Val Met Pro Thr Lys Ser Ser Leu Arg
145 150 155 160

Arg Thr Ser Ser Thr Gln Phe
165

<210> 22
<211> 310
<212> PRT
<213> Oryza sativa

ES 2 623 545 T3

<400> 22

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Met Ala Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Pro Gln Ser Leu
1      5      10      15

Leu Val Leu Thr Ser Trp Arg Ser Ile Gly Met Gly Arg Gly Arg Val
20      25      30

Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe Ala
35      40      45

Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu
50      55      60

Cys Asp Ala Glu Val Ala Leu Ile Ile Phe Ser Asn Arg Gly Lys Leu
65      70      75      80

Tyr Glu Phe Cys Ser Thr Gln Ser Met Thr Lys Thr Leu Glu Lys Tyr
85      90      95

Gln Lys Cys Ser Tyr Ala Gly Pro Glu Thr Ala Val Gln Asn Arg Glu
100     105     110

Ser Glu Gln Leu Lys Ala Ser Arg Asn Glu Tyr Leu Lys Leu Lys Ala
115     120     125

Arg Val Glu Asn Leu Gln Arg Thr Gln Arg Gln Tyr Tyr Lys Ser Lys
130     135     140

His Arg Leu Cys Leu Val Arg Ser Lys Val Trp Asn Leu Val Lys Ile
145     150     155     160

Arg Asp Asp Val Thr Glu Lys Leu Cys Met Tyr Glu Arg Asn Leu Leu
165     170     175

Gly Glu Asp Leu Asp Ser Leu Gly Ile Lys Glu Leu Glu Ser Leu Glu
180     185     190

Lys Gln Leu Asp Ser Ser Leu Lys His Val Arg Thr Thr Arg Thr Lys
195     200     205

His Leu Val Asp Gln Leu Thr Glu Leu Gln Arg Lys Glu Gln Met Val
210     215     220

Ser Glu Ala Asn Arg Cys Leu Arg Arg Lys Leu Glu Glu Ser Asn His
225     230     235     240

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ES 2 623 545 T3

Val Arg Gly Gln Gln Val Trp Glu Gln Gly Cys Asn Leu Ile Gly Tyr
245 250 255

Glu Arg Gln Pro Glu Val Gln Gln Pro Leu His Gly Gly Asn Gly Phe
260 265 270

Phe His Pro Leu Asp Ala Ala Gly Glu Pro Thr Leu Gln Ile Gly Tyr
275 280 285

Pro Ala Glu His His Glu Ala Met Asn Ser Ala Cys Met Asn Thr Tyr
290 295 300

Met Pro Pro Trp Leu Pro
305 310

5 <210> 23
<211> 69
<212> PRT
<213> Oryza sativa

<400> 23
Met Glu Gly Gly Gly Arg Arg Arg Lys Arg Gly Lys Val Glu Leu Arg
1 5 10 15

Arg Ile Glu Asp Arg Thr Ser Arg Gln Val Arg Phe Ser Lys Arg Arg
20 25 30

Ser Gly Leu Phe Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala
35 40 45

Gln Val Ala Leu Leu Val Phe Ser Pro Ala Gly Arg Leu Tyr Glu Phe
50 55 60

10 Ala Ser Ser Thr Ser
65

<210> 24
<211> 491
<212> PRT
15 <213> Oryza sativa

<400> 24
Met Ala Leu Leu Leu Ser Tyr Pro Arg Arg His Pro Ser Ile His Leu
1 5 10 15

Leu Ile Leu Ser Ala Tyr Ala Leu Phe Leu Leu Pro Ile Leu Asp Gly
20 25 30

Leu Glu Leu Gly Gly Asp Gly Leu Tyr Arg Glu Ile Leu Arg Asp Glu
35 40 45

ES 2 623 545 T3

Thr	Val	Leu	Arg	Leu	Lys	Glu	Leu	Gly	Lys	Ile	Ser	Asp	Gly	Glu	Gly	50	55	60	
Tyr	Leu	Glu	Arg	Thr	Phe	Leu	Ser	Pro	Ala	Ser	Ile	Arg	Ala	Ser	Ala	65	70	75	80
Val	Ile	Ile	Ser	Trp	Met	Lys	Asp	Ala	Gly	Leu	Thr	Thr	Trp	Ile	Asp	85	90	95	
Gln	Met	Gly	Asn	Ile	His	Gly	Arg	Phe	Glu	Pro	Thr	Asn	Ser	Thr	Lys	100	105	110	
Glu	Ala	Leu	Leu	Ile	Gly	Ser	His	Met	Asp	Thr	Val	Ile	Asp	Ala	Gly	115	120	125	
Met	Tyr	Asp	Gly	Ala	Leu	Gly	Ile	Ile	Ser	Ala	Ile	Ser	Ala	Leu	Lys	130	135	140	
Val	Leu	Lys	Val	Thr	Gly	Arg	Leu	Gln	Arg	Leu	Thr	Arg	Pro	Val	Glu	145	150	155	160
Val	Ile	Ala	Phe	Ser	Asp	Glu	Glu	Gly	Val	Arg	Phe	Gln	Thr	Thr	Phe	165	170	175	
Leu	Gly	Ser	Ala	Ala	Val	Ala	Gly	Thr	Leu	Pro	Glu	Ser	Ile	Leu	Gln	180	185	190	
Val	Ser	Asp	Lys	Ser	Gly	Thr	Thr	Val	Gln	Asp	Val	Leu	Lys	Leu	Asn	195	200	205	
Ser	Leu	Glu	Gly	Thr	Ala	Asn	Ala	Leu	Gly	Glu	Val	Arg	Tyr	Ser	Pro	210	215	220	
Glu	Ser	Val	Gly	Ser	Tyr	Val	Glu	Val	His	Ile	Glu	Gln	Gly	Pro	Val	225	230	235	240
Leu	Glu	Ala	Leu	Arg	Tyr	Pro	Leu	Gly	Val	Val	Lys	Gly	Ile	Ala	Gly	245	250	255	
Gln	Thr	Arg	Leu	Lys	Val	Ile	Ile	Asn	Gly	Ser	Gln	Gly	His	Ala	Gly	260	265	270	
Thr	Val	Pro	Met	Lys	Leu	Arg	Arg	Asp	Pro	Met	Val	Ala	Ala	Ala	Glu	275	280	285	
Leu	Val	Leu	Thr	Leu	Glu	Thr	Leu	Cys	Lys	Glu	Pro	Asn	Lys	Phe	Leu	290	295	300	

ES 2 623 545 T3

Thr Tyr Asp Glu Glu Cys Gly Cys Phe Thr Glu Glu Ser Leu Ala Gly
305 310 315 320

Leu Val Cys Thr Val Gly Glu Leu Leu Thr Trp Pro Ser Ala Ser Asn
325 330 335

Val Ile Pro Gly Gln Val Asn Phe Thr Val Asp Ile Arg Ala Met Asp
340 345 350

Asp Lys Val Arg Glu Thr Ile Val Thr Ser Phe Ser Arg Leu Val Leu
355 360 365

Gln Arg Cys Asp Asp Arg Leu Val Asp Cys Ala Val Glu Gln Lys His
370 375 380

Ala Ala Ala Ala Thr Pro Cys Asp Ala Glu Leu Thr Ser Arg Leu Glu
385 390 395 400

Arg Ala Thr Arg Ser Thr Ile Ser Ser Met Ala Ala Gly Val Arg Arg
405 410 415

Ala Gly Gly Glu Thr Pro Val Leu Met Ser Gly Ala Gly His Asp Ala
420 425 430

Met Ala Met Ala Arg Leu Thr Lys Val Gly Met Leu Phe Val Arg Cys
435 440 445

Arg Gly Gly Val Ser His Ser Pro Glu Glu Ser Val Met Asp Asp Asp
450 455 460

Val Trp Ala Ala Gly Leu Ala Leu Val Asn Phe Ile Asp Gln Asn Ala
465 470 475 480

Val Asp Ala Ala Ala Thr Ala Ala Glu Ser
485 490

<210> 25

<211> 267

5 <212> PRT

<213> Oryza sativa

<400> 25

Met Ser Phe Ala Asp Leu Glu Ala Gly Ala Val Arg Ala Pro Arg Arg
1 5 10 15

Ala Arg Gly Pro Asp Ala Thr Arg Ala Leu Val Phe Gln Ile Thr Thr
20 25 30

Ala Val Ala Ser Tyr Arg Arg Leu Leu Asn Ser Leu Gly Thr Pro Lys
35 40 45

ES 2 623 545 T3

Asp 50	Thr	Pro	Ala	Leu	Arg	Asp 55	Gln	Leu	Gln	Lys	Thr 60	Ser	His	Asn	Ile
Leu 65	Gln	Leu	Ala	Lys	Asp 70	Ala	Lys	Glu	Lys	Leu 75	Arg	Arg	Ala	Ala	Glu 80
Ala	Asp	Lys	Asn	Ala 85	Asp	Thr	Ser	Ala	Asp 90	Lys	Arg	Val	Ala	Asp 95	Met
Lys	Leu	Ala	Lys 100	Asp	Phe	Ala	Thr	Thr 105	Met	Glu	Glu	Tyr	Gly 110	Lys	Leu
Gln	Asn	Leu 115	Ala	Ile	Gln	Arg	Glu 120	Met	Ala	Tyr	Lys	Pro 125	Val	Val	Pro
Gln 130	Thr	Ser	Gln	Pro	Asn	Tyr 135	Thr	Thr	Gly	Gly	Ile 140	Glu	Ala	Arg	Asp
Ser 145	Gly	Lys	Ile	Pro	Glu 150	Gln	His	Ala	Leu 155	Leu	Ala	Glu	Ser	Lys	Arg 160
Gln	Glu	Val	Leu 165	Gln	Leu	Asp	Asn	Glu	Ile 170	Val	Phe	Asn	Glu	Ala	Ile
Ile	Glu	Glu	Arg 180	Glu	Gln	Ala	Ile	Gln 185	Asp	Ile	Gln	Gln	Gln 190	Ile	Gly
Glu	Val	His 195	Glu	Ala	Phe	Lys	Asp 200	Leu	Ala	Thr	Leu	Val 205	His	Ile	Gln
Gly 210	Val	Thr	Ile	Glu	Glu	Ile 215	Asp	Thr	Asn	Ile	Glu 220	Asn	Ser	Ala	Ala
Ala 225	Thr	Lys	Glu	Ala	Lys 230	Thr	Glu	Leu	Ala	Lys 235	Ala	Ser	Lys	Thr	Gln 240
Lys	Ser	Asn	Ser	Ser 245	Leu	Leu	Cys	Ile	Leu 250	Leu	Val	Ile	Phe	Gly 255	Val
Val	Leu	Leu	Ile 260	Val	Ile	Ile	Val	Leu 265	Ala	Thr					

<210> 26
<211> 95
<212> PRT
<213> *Oryza sativa*

ES 2 623 545 T3

<400> 26

Met Gln Leu Tyr Met Thr Tyr Gln Ala Cys Pro Met Gly Asp Leu Gln
1 5 10 15

Met Gly Asp Ser Val Val Ser Thr Ile Asp Ile Arg Ala Leu Tyr Cys
20 25 30

Asn Lys Ser Pro Gly Lys Ser Ser Ser Ser Ser Met Tyr Gly Ala Ser
35 40 45

Ser Ser Ser Lys Arg Lys Ala Cys Glu Leu Asn His Gly Asp Gly Gly
50 55 60

Ser Ala His Asp Asp Val Arg Asp Tyr Gly Val Asp His Val Asp Asp
65 70 75 80

Asn Gly Glu Tyr Tyr Gly Asp Asp His Asp Asp Val Met His Gly
85 90 95

<210> 27

<211> 1113

<212> PRT

<213> Oryza sativa

<400> 27

Met Arg Ala Ala Ala Ala Ala Ser Lys Ala Ala Gly Lys Glu Lys Ser
1 5 10 15

Arg Arg Lys Gly Gly Gly Gly Gly Ala Gly Gly Gly Gly Gly Glu Gln
20 25 30

Leu Leu Thr Asp Gln Val Leu Ser Leu Arg Ala Arg Leu His Leu Ala
35 40 45

Leu Ala Leu Gly Leu Ala Lys Ser Asp Gly Gly Pro Lys Lys Trp Gln
50 55 60

Ser Thr Asp Ala Gly Ile Gln Ser His Val Leu Lys Ala Ala Ser Ala
65 70 75 80

Phe Leu Gly Cys Leu Thr Asn Glu Met Leu Arg Leu Pro Pro Ile Lys
85 90 95

Glu Ser Ile Ser Asp Ile Leu Ile Ala Leu Glu Gly Ile Leu Gln Ser
100 105 110

Lys Asn Val Ser Val Leu Ile Gln Ala Thr Asp Val Ser Leu Lys Leu
115 120 125

Val Ser Ser Val Gly Asn Leu Ala Arg Gln Tyr Pro Val Leu Glu Ile
130 135 140

ES 2 623 545 T3

Val	Thr	Cys	Leu	Ala	Ser	Gln	Leu	Ser	Ala	Asn	Gln	Ile	Thr	Ile	Ala	145	150	155	160
Val	Ser	Ser	Ala	Ser	Thr	Leu	Asn	Cys	Ile	Leu	Asn	Thr	Leu	Ala	Thr	165	170	175	
Ala	Arg	Ser	Ser	Ile	His	Ala	Glu	Ile	Trp	Glu	Ala	Leu	Glu	Lys	Thr	180	185	190	
Asp	Ala	Val	Thr	Ser	Val	Ile	Gly	Ala	Leu	Gln	Asn	Tyr	Ser	Pro	Asp	195	200	205	
Val	His	Pro	Leu	Asn	Tyr	Leu	Met	Glu	Met	Met	Ser	Leu	Leu	Arg	Ile	210	215	220	
Ile	Leu	Trp	Ile	Trp	Pro	Ser	Ser	Arg	Tyr	His	Val	Trp	Ser	Asn	Cys	225	230	235	240
Asn	Leu	Met	Gly	Lys	Leu	Ala	Gln	Tyr	Cys	Val	Ala	Ser	Glu	Met	Asp	245	250	255	
Val	Ala	Val	Arg	Val	Leu	Lys	Leu	Tyr	Ala	Ala	Leu	Ala	Leu	Cys	Gly	260	265	270	
Asn	Gly	Ala	Met	Val	Leu	Leu	Asn	Asn	Glu	Asp	Leu	Met	Ala	Lys	Val	275	280	285	
Gly	Ala	Leu	Leu	Gly	Lys	Ser	Asn	Pro	Ser	Ile	Ala	Arg	Ile	Glu	Ala	290	295	300	
Leu	Lys	Phe	Tyr	Gln	Ile	Leu	Leu	Arg	Ser	Ser	Lys	Gly	Cys	Asp	Leu	305	310	315	320
Leu	Met	Ala	Ala	His	Tyr	Gln	His	Ile	Ile	Glu	Gly	Thr	Ile	Asn	Ala	325	330	335	
Met	Ser	Arg	Asp	Asp	Glu	Arg	Leu	Leu	Thr	Ile	Glu	Gly	Cys	Arg	Thr	340	345	350	
Ala	Leu	Leu	Val	Leu	Arg	Tyr	Ala	Gly	Asp	His	His	Arg	Leu	Phe	Trp	355	360	365	
Ser	His	Ala	Ile	Asp	Asp	Val	Leu	Tyr	Lys	Ile	Leu	Thr	Gly	Gly	Cys	370	375	380	
Thr	Ser	Ser	His	Lys	Ala	Asn	Gln	Ile	Leu	Cys	His	Asp	Lys	Leu	Phe	385	390	395	400

ES 2 623 545 T3

Asn Met Val Ser Glu Asn Phe Met Asp Ile His Ser Tyr Val Trp Asp
 405 410 415
 Ile Leu Gly Asn Leu Ala Val His Cys Lys Asn Glu Tyr Leu Ser Val
 420 425 430
 Arg Lys Gly Gln Asp Ser Ala Leu Gln Ala Leu Ile His Cys Ile Cys
 435 440 445
 Ser Leu Ala Ala Asp Ala Met Gln Lys Ser Asn Thr Met Lys Leu Ser
 450 455 460
 Lys Asp Val His Glu Pro Ala Leu Arg Ala Val Leu Met Met Leu Leu
 465 470 475 480
 Ser Pro Ser Gly Tyr Ile Leu Ser Glu Ala Ser Ser Lys Leu Leu His
 485 490 495
 Val Leu Pro Leu Gly Asp Asp Cys Leu Asn Ile Leu Phe Thr Ser Leu
 500 505 510
 Glu Ser Asn Thr Thr Arg Ser Ile Thr Ala Ser Phe Asp Asn Val Lys
 515 520 525
 Ile Met Ser Asn Leu Met Ser Leu Ala Gly Met Ser Ile Asn Phe Val
 530 535 540
 Cys Ile His Cys Lys Arg Asn Leu Asp Val Gly Ile Val Cys Asn Asp
 545 550 555 560
 Cys Arg Asp His Tyr Ser Glu Gly Leu Ile Arg Val Leu Gln Asn Ala
 565 570 575
 Ser Cys Gln Asn Leu Ser Pro Gly Pro Lys Leu Tyr Ile Ser Arg Ile
 580 585 590
 Leu Ser Leu Phe Gly Leu Cys Gly Phe Pro Ser Lys Leu Gly Gly Lys
 595 600 605
 Met Arg Arg Ala Leu Asp Asp Asn Glu Leu Ala Asp Leu Glu Leu Leu
 610 615 620
 Leu Ser Asn Gly Glu Ser Leu Lys Ala His Thr Ala Ile Ile Ser Val
 625 630 635 640
 Arg Cys Pro Lys Leu Leu Pro Ser Ala Lys Ser Leu Gly Ser Asp Gly
 645 650 655

ES 2 623 545 T3

Lys Ile Thr Asp Glu Trp Gly Arg Ser Phe Tyr His Val Arg Met Ser
 660 665 670
 Asp Arg Val Asp Ser Cys Gly Leu Lys Lys Ile Leu Glu Tyr Thr Tyr
 675 680 685
 Thr Asn Ser Val Met Val Asp Asp Asp Asn Ile Lys Pro Arg Thr Leu
 690 695 700
 Ala Lys Tyr Cys His Leu Lys Ser Leu Gln Glu Met Leu Gln Lys Glu
 705 710 715 720
 Gln Pro Arg Trp Asn Ser Asp Cys Pro Arg Tyr Asp Leu Thr Ala Ala
 725 730 735
 Leu Glu Pro Val Lys Cys Ser Phe Ser Phe Ser Glu Val Ile Asn Val
 740 745 750
 Pro Leu Gly Trp Gln Ala Leu Asn Lys Leu Ile His Trp Phe Tyr Ser
 755 760 765
 Gly Glu Leu Pro Lys Ile Asp Pro Asp Cys Arg Trp Arg Asn Leu Asn
 770 775 780
 Ser Glu Glu Gln Leu Ser Gln Leu Arg Pro Tyr Ala Glu Leu Ser Ser
 785 790 795 800
 Leu Ser Glu Phe Trp Phe Leu Glu Gly Val Lys Glu Glu Ser Leu Ser
 805 810 815
 Val Val Thr Ser Cys Leu Ser Ser Thr Ser Thr Ala Ala Ser Val Glu
 820 825 830
 Phe Val Val Phe Ala Ala Gln Leu Gly Gln Trp Glu Met Val Glu Ala
 835 840 845
 Ala Val Gly Ser Val Ala His Leu Tyr Pro Lys Leu Arg Asp Ser Gly
 850 855 860
 Gln Leu Glu Gln Leu Asp Asp Asp Val Leu Asn Met Leu Arg Thr Glu
 865 870 875 880
 Tyr Val Arg Arg Thr Gln Arg Thr Gly Val Gly Ser Ala Ala Ala Gln
 885 890 895
 Ala Gly Ala Arg Val Val Thr Ala Val Tyr Arg Arg Gly Gln Arg Ala
 900 905 910
 Asp Tyr Trp Gln Ser Gly Gly Phe Gly Asp Asn Trp Asn Phe Gln Met

ES 2 623 545 T3

915	920	925
Val Ile Leu Asn Ala Ser Glu Glu His Cys Arg Glu Ser Lys Phe Asp 930 935 940		
Thr Ile Gly Val Cys Lys Ala Arg Phe Leu Tyr Gly Lys Val Ser Arg 945 950 955 960		
Gly Phe Arg Leu Arg Thr Ser Gly Ile Asn Lys Glu Gly Gly Pro Arg 965 970 975		
Gly Gly Thr Val Ile Tyr Ser Arg Ser Ser Gly Gly Leu Pro Pro Trp 980 985 990		
Cys Gly Ala Gly Ser His Asp Ala Leu Ala Ala Val Arg Trp Pro Ser 995 1000 1005		
Leu Pro Gly Leu Glu Ser His Gln Thr Ala Gln Val Ile Arg Arg 1010 1015 1020		
Gly Ala Gly Arg Arg Gly Glu Gly Arg Asp Val Asn Val Thr Lys 1025 1030 1035		
Gln Ser Asn Ala Pro Met Arg Pro Pro Glu Thr Met Gln Arg Glu 1040 1045 1050		
Gln Pro Gln Ser Arg Ala Arg Ala Asn Gly Arg Lys Trp Pro Pro 1055 1060 1065		
Pro Arg Arg Trp Arg Ser Gly Ile Arg Glu Glu Gln Gly Val Pro 1070 1075 1080		
Ser Ala Lys Ala Trp Gln Glu Lys Arg Lys Arg Thr Gln Gln Gln 1085 1090 1095		
Arg Cys Ala Leu Pro Ala Ala Ile Ala Ala Ser Arg Leu Gln Leu 1100 1105 1110		
<210> 28		
<211> 412		
<212> PRT		
<213> Oryza sativa		
<400> 28		
Met Ala Ser Ala Val Ala Ser Asn Leu Pro Ala Ala Ala Pro Ala Ala 1 5 10 15		
Val Met Pro Phe Gly Gly Trp His Gly Pro Arg Val Ser Phe Ser Arg 20 25 30		

5

10

ES 2 623 545 T3

Asp Ala Ala Gly Ala Glu Glu Ala Ala Ala Val Val Val Cys Ser Ser
 35 40 45
 Pro Leu Ala Ala Ala Ala Ala Val Ala Thr Thr Thr Thr Pro Glu Pro
 50 55 60
 Ala Ile Ser Lys Asp Phe Ile Asp Phe Glu Phe Ser Leu Gly Gly Ser
 65 70 75 80
 Ala Thr Met Leu Pro Ala Asp Glu Leu Phe Ala Asp Gly Lys Leu Leu
 85 90 95
 Pro Leu Arg Lys Ala Ala Ala Val Pro Glu Met Asp Ala Ala Ala Pro
 100 105 110
 Arg Pro Pro Gln Pro Glu Ala Met Pro Ala Pro Ser Glu Pro Met Lys
 115 120 125
 Pro Leu Arg Ala Ala Thr Ala Ala Val Asp Ala Ala Asp Pro Tyr Val
 130 135 140
 Phe Ser Pro Lys Ala Pro Ser Cys Ser Ser Arg Trp Arg Glu Leu Leu
 145 150 155 160
 Gly Leu Lys Arg Ala Ala Ala Gln Ser Pro Lys Pro Ser Pro Ser Ser
 165 170 175
 Ala Pro Ala Arg Thr Pro Gly Arg Ala Met Asn Ser Thr Ala Ala Arg
 180 185 190
 Ser Leu Lys Leu Leu Leu Gln Arg Asn Asn Gly Arg Ser Ser Gly Ala
 195 200 205
 Ser Ala Ser Glu Leu Ala Ser Ala Pro Leu Leu Arg Asp Ser Ser Asp
 210 215 220
 Ser Glu Ala Ser Leu Ser Leu Ala Ser Ser Arg Phe Ser Leu Ser Ser
 225 230 235 240
 Ser Ser Ser Ser Ser Gly His Asp His Asp Asp Ile Pro Arg Leu Ser
 245 250 255
 Leu Asp Ser Ala Ala Asp Pro Asn Pro Pro Arg Ile Arg Leu Val Arg
 260 265 270
 Ser Ser His Arg His Ser Thr Ser Ser Ser Ser Ser Arg Ala Gly
 275 280 285

ES 2 623 545 T3

Arg Ser Pro Ala Arg Arg Arg Pro Ser Pro Pro Pro Pro Pro Arg Cys
290 295 300

Leu Ser Val Asp Ser Pro Arg Met Asn Ser Ser Gly Lys Ile Val Phe
305 310 315 320

Gln Gly Leu Glu Arg Ser Ser Ser Ser Pro Cys Thr Leu His Ala Ala
325 330 335

Ala Lys Pro Arg Ser Arg Ala Val Asp Arg Ser Tyr Ser Ser Gly Val
340 345 350

Arg Val Ala Pro Val Val Leu Asn Val Pro Val Cys Ser Arg Pro Val
355 360 365

Phe Gly Phe Phe Lys Asp Lys Lys Asp Ala Ala Ala Lys Asp Ala Met
370 375 380

Ala Ala Arg Thr Arg Ser Ser Leu Gly Arg Lys Thr Thr Ala Ala Pro
385 390 395 400

Gln Gly Trp Ser Gly Glu Leu Gly Arg Ser Cys Gly
405 410

<210> 29
<211> 763
<212> PRT
<213> Oryza sativa

<400> 29
Met Lys Ile Ser Gly Leu Leu Thr Ser Ala Gly Ile Asn Ile Ala Leu
1 5 10 15

Ser Val Leu Phe Ile Ser Leu Tyr Ser Val Leu Arg Lys Gln Pro Ala
20 25 30

Asn Val Arg Val Tyr Phe Gly Arg Arg Ile Ala Glu Glu His Asn Arg
35 40 45

Leu Arg Glu Ala Phe Ile Leu Glu Arg Phe Val Pro Ser Thr Gly Trp
50 55 60

Ile Val Lys Ala Leu Gln Cys Thr Glu Glu Glu Ile Leu Ala Ala Ala
65 70 75 80

Gly Leu Asp Ala Val Val Phe Asn Arg Ile Leu Val Phe Ser Leu Arg
85 90 95

Ile Phe Ser Leu Ala Ala Ile Leu Cys Val Phe Gly Ile Leu Pro Leu
100 105 110

5

10

ES 2 623 545 T3

Asn	Tyr	Phe	Gly	Gln	Asp	Ile	His	His	Val	Arg	Ile	Pro	Ser	Glu	Ser	115	120	125
Leu	Asp	Ile	Phe	Thr	Ile	Gly	Asn	Val	Lys	Val	Arg	Ser	Arg	Trp	Leu	130	135	140
Trp	Val	His	Cys	Val	Ala	Leu	Tyr	Ile	Ile	Ser	Gly	Val	Ala	Cys	Ile	145	150	155
Leu	Leu	Tyr	Leu	Glu	Tyr	Lys	His	Ile	Ala	Arg	Leu	Arg	Leu	Arg	His	165	170	175
Leu	Thr	Cys	Ala	Met	Pro	Asn	Pro	Ser	His	Phe	Thr	Val	Leu	Val	Arg	180	185	190
Gly	Ile	Pro	Lys	Glu	Thr	Lys	Glu	Ser	Cys	Ser	Asn	Ala	Ile	Asp	Asp	195	200	205
Phe	Phe	Thr	Lys	Tyr	His	Gly	Ser	Ser	Tyr	Leu	Phe	His	Gln	Val	Val	210	215	220
Tyr	Lys	Val	Gly	Lys	Val	Gln	Lys	Ile	Met	Thr	Gly	Ala	Lys	Lys	Ala	225	230	235
Tyr	Arg	Lys	Phe	Lys	His	Phe	Thr	Asp	Ser	Thr	Ile	Asp	Gln	Arg	Cys	245	250	255
Arg	Ala	Ile	Ser	Tyr	Arg	Cys	Cys	Leu	Cys	Gly	Ala	Ser	Ser	Asn	Ser	260	265	270
Phe	Gln	Leu	Leu	Ala	Thr	Gly	Leu	Glu	Gln	Asn	Gln	Gly	Lys	Ser	Asp	275	280	285
Leu	Gln	Asp	Ser	Ser	Leu	Lys	Leu	Asp	Asp	Gln	Glu	Cys	Ala	Ala	Ala	290	295	300
Phe	Val	Tyr	Phe	Arg	Thr	Arg	Tyr	Ala	Ala	Leu	Val	Ala	Ser	Glu	Ile	305	310	315
Leu	Gln	Thr	Ser	Asn	Pro	Met	Lys	Trp	Val	Thr	Asp	Leu	Ala	Pro	Glu	325	330	335
Pro	Asp	Asp	Val	Tyr	Trp	Ser	Asn	Leu	Trp	Leu	Pro	Tyr	Lys	Gln	Leu	340	345	350
Trp	Ile	Arg	Arg	Ile	Ala	Thr	Leu	Leu	Gly	Ser	Ile	Val	Phe	Met	Leu	355	360	365

ES 2 623 545 T3

Phe Phe Leu Ile Pro Val Thr Phe Ile Gln Gly Leu Ser Gln Leu Glu
 370 375 380
 Gln Leu Gln Gln Arg Leu Pro Phe Leu Lys Gly Ile Leu Glu Lys Lys
 385 390 395 400
 Tyr Met Ser Gln Leu Val Thr Gly Tyr Leu Pro Ser Val Ile Leu Gln
 405 410 415
 Ile Phe Leu Tyr Ala Val Ala Pro Ile Met Ile Leu Phe Ser Thr Leu
 420 425 430
 Glu Gly Pro Ile Ser His Ser Glu Arg Lys Arg Ser Ala Cys Cys Lys
 435 440 445
 Val Leu Tyr Phe Thr Val Trp Asn Ile Phe Phe Gly Asn Val Leu Ser
 450 455 460
 Gly Thr Val Ile Ser Gln Leu Asn Val Leu Ser Ser Pro Lys Asp Ile
 465 470 475 480
 Pro Val Gln Leu Ala Arg Ala Ile Pro Val Gln Ala Thr Phe Phe Ile
 485 490 495
 Thr Tyr Val Leu Thr Ser Gly Trp Ala Ser Leu Ser Ser Glu Leu Met
 500 505 510
 Gln Leu Phe Gly Leu Ile Trp Asn Phe Val Arg Lys Tyr Ile Leu Arg
 515 520 525
 Met Pro Glu Asp Thr Glu Phe Val Pro Ser Phe Pro Tyr His Thr Glu
 530 535 540
 Val Pro Lys Val Leu Leu Phe Gly Leu Leu Gly Phe Thr Cys Ser Val
 545 550 555 560
 Leu Ala Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Phe Phe Leu Gly
 565 570 575
 Tyr Ile Val Tyr Arg Asn Gln Leu Leu Asn Val Tyr Arg Thr Arg Tyr
 580 585 590
 Asp Thr Gly Gly Leu Tyr Trp Pro Ile Ala His Asn Ala Val Ile Phe
 595 600 605
 Ser Leu Val Leu Thr Gln Ile Ile Cys Leu Gly Val Phe Gly Leu Lys
 610 615 620

ES 2 623 545 T3

Glu Ser Pro Val Ala Ala Gly Phe Thr Ile Pro Leu Ile Ile Leu Thr
625 630 635 640

Leu Leu Phe Asn Gln Tyr Cys Arg Asn Arg Leu Leu Pro Leu Phe Arg
645 650 655

Thr Thr Pro Ala Gln Asp Leu Ile Asp Met Asp Arg Glu Asp Glu Arg
660 665 670

Ser Gly Arg Met Asp Glu Ile His His Arg Leu His Ser Ala Tyr Cys
675 680 685

Gln Phe His Asp Thr Glu Asp Ile Pro Leu Glu Lys Ile Gln Thr Val
690 695 700

Gly Ser Asp Glu Glu Gln Gly Cys Ser Ser Asp Lys Ser Asn Gly Lys
705 710 715 720

Glu Ser Phe Glu Glu Pro Arg Ala Glu Leu Ser His Pro Thr Leu Asn
725 730 735

Gly Leu Pro Val Ser Arg Leu Arg His Ala Val Lys Ser Ile Thr Phe
740 745 750

Leu Val Arg Leu Gln Lys Arg Gly Leu Ser Glu
755 760

<210> 30

<211> 471

<212> PRT

<213> Oryza sativa

<400> 30

Met Ala Ile Leu Arg Glu Phe Gly Thr Ile Glu Gly Met Glu Asn Leu
1 5 10 15

Leu Pro Glu Asp Val Leu Ser Asn Ile Ile His Arg Leu Ala Pro Arg
20 25 30

Tyr Leu Ala Ile Ser Arg Cys Val Cys Lys Thr Trp Cys Thr Ile Ile
35 40 45

Glu Ala His Asn Leu Leu His Val Asp Leu Leu Pro Arg Pro Leu Cys
50 55 60

Gly Ile Phe Ile Asn Phe Asn Glu Leu Ser Met Ser Glu Phe Phe Ser
65 70 75 80

Arg Pro Ser Lys Gly Pro Thr Val Ser Gly Asn Phe Asp Tyr Leu Pro
85 90 95

5

10

ES 2 623 545 T3

Cys Ser Ser Cys Ile Ile Asp His Cys Asn Gly Leu Leu Leu Phe His
 100 105 110
 Lys Tyr Val Val Asn Pro Ala Thr Arg Gln Ser Ala Pro Leu Pro Pro
 115 120 125
 Cys Pro Tyr Met Val Val Glu His Ile Phe His Arg Glu Tyr Leu Val
 130 135 140
 Phe Asp Pro Thr Leu Ser Pro His Phe Glu Val Phe Met Ile Pro Glu
 145 150 155 160
 Ile Arg Arg Ser Asn Val Trp Tyr Asn Met Leu Asn Ser Asp Asp Lys
 165 170 175
 Leu Asp Pro Ala Ile Glu Glu Leu Glu Trp Pro Pro Ser Pro Cys Ile
 180 185 190
 Leu His Val Phe Ser Ser Arg Thr Lys Val Trp Glu Glu Arg Ser Phe
 195 200 205
 Val Arg Glu Gly Glu Ala Ala Gly Asn Val Ser Asp Met Arg Leu Asp
 210 215 220
 His Pro Tyr Val Pro Asp Thr Ser Val Tyr Val Pro Asp Thr Ser Val
 225 230 235 240
 Tyr Cys Arg Gly Val Leu Tyr Val Tyr Cys Gln Asn Lys Tyr Val Met
 245 250 255
 Arg Ile Ser Leu Ser Asn Gly Lys Tyr Gln Val Ile Lys Pro Pro Ser
 260 265 270
 Asp Cys Glu Gly Met Ala Tyr Thr Asn Leu Tyr Leu Gly Lys Ser Met
 275 280 285
 Lys Gly Val Tyr Cys Ala Val Arg His Leu Ala Ser Arg Phe Leu Ile
 290 295 300
 Tyr Ile Leu Asp Glu Ser Ser Asp Arg Met Glu Trp Val Cys Lys Asp
 305 310 315 320
 Ser Cys Ser Ile Gln Pro Cys Gln Ile Ile Asp Gly Pro Gly Pro Trp
 325 330 335
 Thr Leu Gln Asp Ile Asn Asn Gln Glu Arg Gly Phe Glu Tyr Glu Asp
 340 345 350

ES 2 623 545 T3

Gly Asn Asn Glu Ala Val Val Glu Asp Arg Phe Glu Trp Asp Ser Asp
355 360 365

Asn Asp Asn Val Ile Glu Thr Asn Ser Arg Gly Ser Gly Gly Tyr Ile
370 375 380

Asn Phe Leu Val Asp Thr Thr Arg Arg Gly Arg Tyr Asn Ser Gly Gly
385 390 395 400

Tyr Ile Asp Phe Leu Gly Phe His Pro Tyr Lys Glu Val Ile Phe Leu
405 410 415

Ser Asp Ser Leu Arg Arg Gly Leu Ala Tyr His Leu Asn Ser Ser Lys
420 425 430

Ile Gln Asp Leu Gly Ser Leu Arg Pro Thr Asn Tyr Gly Thr Glu Val
435 440 445

Gly Ile Gln Pro Phe Ile Gln Lys Phe Phe Pro Tyr Ser Pro Trp Met
450 455 460

Gly Arg Phe Pro Glu Asp Asn
465 470

<210> 31
<211> 763
<212> PRT
<213> Oryza sativa

<400> 31
Met Lys Ile Ser Gly Leu Leu Thr Ser Ala Gly Ile Asn Ile Ala Leu
1 5 10 15

Ser Val Leu Phe Ile Ser Leu Tyr Ser Val Leu Arg Lys Gln Pro Ala
20 25 30

Asn Val Arg Val Tyr Phe Gly Arg Arg Ile Ala Glu Glu His Asn Arg
35 40 45

Leu Arg Glu Ala Phe Ile Leu Glu Arg Phe Val Pro Ser Thr Gly Trp
50 55 60

Ile Val Lys Ala Leu Gln Cys Thr Glu Glu Glu Ile Leu Ala Ala Ala
65 70 75 80

Gly Leu Asp Ala Val Val Phe Asn Arg Ile Leu Val Phe Ser Leu Arg
85 90 95

Ile Phe Ser Leu Ala Ala Ile Leu Cys Val Phe Gly Ile Leu Pro Leu

5

10

ES 2 623 545 T3

100	105	110
Asn Tyr Phe Gly Gln Asp Ile His His Val Arg Ile Pro Ser Glu Ser		
115	120	125
Leu Asp Ile Phe Thr Ile Gly Asn Val Lys Val Arg Ser Arg Trp Leu		
130	135	140
Trp Val His Cys Val Ala Leu Tyr Ile Ile Ser Gly Val Ala Cys Ile		
145	150	155
160		
Leu Leu Tyr Leu Glu Tyr Lys His Ile Ala Arg Leu Arg Leu Arg His		
165	170	175
Leu Thr Cys Ala Met Pro Asn Pro Ser His Phe Thr Val Leu Val Arg		
180	185	190
Gly Ile Pro Lys Glu Thr Lys Glu Ser Cys Ser Asn Ala Ile Asp Asp		
195	200	205
Phe Phe Thr Lys Tyr His Gly Ser Ser Tyr Leu Phe His Gln Val Val		
210	215	220
Tyr Lys Val Gly Lys Val Gln Lys Ile Met Thr Gly Ala Lys Lys Ala		
225	230	235
240		
Tyr Arg Lys Phe Lys His Phe Thr Asp Ser Thr Ile Asp Gln Arg Cys		
245	250	255
Arg Ala Ile Ser Tyr Arg Cys Cys Leu Cys Gly Ala Ser Ser Asn Ser		
260	265	270
Phe Gln Leu Leu Ala Thr Gly Leu Glu Gln Asn Gln Gly Lys Ser Asp		
275	280	285
Leu Gln Asp Ser Ser Leu Lys Leu Asp Asp Gln Glu Cys Ala Ala Ala		
290	295	300
Phe Val Tyr Phe Arg Thr Arg Tyr Ala Ala Leu Val Ala Ser Glu Ile		
305	310	315
320		
Leu Gln Thr Ser Asn Pro Met Lys Trp Val Thr Asp Leu Ala Pro Glu		
325	330	335
Pro Asp Asp Val Tyr Trp Ser Asn Leu Trp Leu Pro Tyr Lys Gln Leu		
340	345	350
Trp Ile Arg Arg Ile Ala Thr Leu Leu Gly Ser Ile Val Phe Met Leu		
355	360	365

ES 2 623 545 T3

Phe Phe Leu Ile Pro Val Thr Phe Ile Gln Gly Leu Ser Gln Leu Glu
 370 375 380
 Gln Leu Gln Gln Arg Leu Pro Phe Leu Lys Gly Ile Leu Glu Lys Lys
 385 390 395 400
 Tyr Met Ser Gln Leu Val Thr Gly Tyr Leu Pro Ser Val Ile Leu Gln
 405 410 415
 Ile Phe Leu Tyr Ala Val Ala Pro Ile Met Ile Leu Phe Ser Thr Leu
 420 425 430
 Glu Gly Pro Ile Ser His Ser Glu Arg Lys Arg Ser Ala Cys Cys Lys
 435 440 445
 Val Leu Tyr Phe Thr Val Trp Asn Ile Phe Phe Gly Asn Val Leu Ser
 450 455 460
 Gly Thr Val Ile Ser Gln Leu Asn Val Leu Ser Ser Pro Lys Asp Ile
 465 470 475 480
 Pro Val Gln Leu Ala Arg Ala Ile Pro Val Gln Ala Thr Phe Phe Ile
 485 490 495
 Thr Tyr Val Leu Thr Ser Gly Trp Ala Ser Leu Ser Ser Glu Leu Met
 500 505 510
 Gln Leu Phe Gly Leu Ile Trp Asn Phe Val Arg Lys Tyr Ile Leu Arg
 515 520 525
 Met Pro Glu Asp Thr Glu Phe Val Pro Ser Phe Pro Tyr His Thr Glu
 530 535 540
 Val Pro Lys Val Leu Leu Phe Gly Leu Leu Gly Phe Thr Cys Ser Val
 545 550 555 560
 Leu Ala Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Phe Phe Leu Gly
 565 570 575
 Tyr Ile Val Tyr Arg Asn Gln Leu Leu Asn Val Tyr Arg Thr Arg Tyr
 580 585 590
 Asp Thr Gly Gly Leu Tyr Trp Pro Ile Ala His Asn Ala Val Ile Phe
 595 600 605
 Ser Leu Val Leu Thr Gln Ile Ile Cys Leu Gly Val Phe Gly Leu Lys
 610 615 620

ES 2 623 545 T3

Glu Ser Pro Val Ala Ala Gly Phe Thr Ile Pro Leu Ile Ile Leu Thr
625 630 635 640

Leu Leu Phe Asn Gln Tyr Cys Arg Asn Arg Leu Leu Pro Leu Phe Arg
645 650 655

Thr Thr Pro Ala Gln Asp Leu Ile Asp Met Asp Arg Glu Asp Glu Arg
660 665 670

Ser Gly Arg Met Asp Glu Ile His His Arg Leu His Ser Ala Tyr Cys
675 680 685

Gln Phe His Asp Thr Glu Asp Ile Pro Leu Glu Lys Ile Gln Thr Val
690 695 700

Gly Ser Asp Glu Glu Gln Gly Cys Ser Ser Asp Lys Ser Asn Gly Lys
705 710 715 720

Glu Ser Phe Glu Glu Pro Arg Ala Glu Leu Ser His Pro Thr Leu Asn
725 730 735

Gly Leu Pro Val Ser Arg Leu Arg His Ala Val Lys Ser Ile Thr Phe
740 745 750

Leu Val Arg Leu Gln Lys Arg Gly Leu Ser Glu
755 760

<210> 32

<211> 247

<212> PRT

5 <213> Oryza sativa

<400> 32

Met Val Glu Leu Ser Ile Ala Asp Ala Ser Ala Ser Asp Leu Cys Gly
1 5 10 15

Gly Thr Leu Gly Gln Met Val Glu Leu Val Cys Glu Ala Arg Leu Arg
20 25 30

Val Arg Glu Glu Tyr Val Arg Ser Thr Val Asp Leu Met Ala Leu Leu
35 40 45

Arg Gly Arg Gly Met Val Phe Asp Gly Val Tyr Val Val Ser Asn Leu
50 55 60

Thr Arg Leu Phe Ala Glu Leu Asp Phe Gly Arg Gly Glu Trp Val Val
65 70 75 80

Ser Gly Met Ala Gln Pro Met Leu Ala Thr Phe Leu Val Thr Cys Arg

ES 2 623 545 T3

					85						90					95			
Asn	Gly	Asp	Asp	Glu	Asp	Ala	Val	Ala	Ala	Ser	Met	Leu	Leu	Pro	Pro				
			100					105					110						
Pro	Val	Lys	Leu	Arg	Phe	Ala	Glu	Glu	Leu	Ala	Gly	Leu	Met	Met	Ser				
		115					120					125							
Met	Pro	His	Gly	Gly	Ala	Ala	Leu	Cys	Pro	Ala	Pro	Ala	Ser	Thr	Tyr				
	130					135					140								
Leu	Pro	Leu	Ser	Met	Arg	Gly	Arg	Arg	Trp	Leu	His	Ile	Pro	Glu	Gly				
145					150				155						160				
Tyr	Tyr	Gly	Asn	Ala	Leu	Ala	Tyr	Ser	Ile	Thr	Asp	Ala	Ser	Ala	Ser				
			165						170					175					
Asp	Leu	Cys	Gly	Ala	Thr	Leu	Ala	Gln	Met	Met	Glu	Leu	Val	Cys	Glu				
			180					185					190						
Ala	Arg	Leu	Arg	Val	Thr	Glu	Glu	Tyr	Gly	Arg	Ser	Thr	Val	Asp	Leu				
		195					200					205							
Met	Ala	Ser	Leu	Arg	Gly	His	Asp	Thr	Val	Phe	Asp	Gly	Val	Tyr	Val				
	210					215					220								
Val	Ser	Asp	Leu	Gly	Ala	Gly	Ser	Gly	Trp	Ser	Ala	Ala	Trp	Pro	Ser				
225					230				235					240					
Arg	Cys	Trp	Arg	Arg	Ser	Trp													
					245														

5 <210> 33
 <211> 144
 <212> PRT
 <213> Oryza sativa

<400> 33
 Met Asn Gln Gln His Gln Arg Ser Ile Glu His Cys Ser Ile Gly Cys
 1 5 10 15

Phe Leu Ala Ser Pro Pro Pro Arg Phe Phe Pro Ala Arg Thr Arg Ser
 20 25 30

Ala Pro Gly Glu Leu Arg Met Lys Leu Val Val Phe Leu Ile Arg Gly
 35 40 45

Cys Pro Gly Glu Val Leu Leu Arg Pro Ile Val Pro Ala Lys Glu Gly
 50 55 60

ES 2 623 545 T3

Leu Arg Thr Arg Thr Lys Trp His Ile Leu Gln Arg Phe Cys Lys Leu
65 70 75 80

Glu Ile Ile Ser Ile Glu Thr Glu Thr Met Ile Thr Ile Ser Ser Arg
85 90 95

Ser Ile Ile Lys Ser Arg Cys Lys Lys Ser Asn Lys Lys Ile Leu Val
100 105 110

Phe Phe Leu Ser Met Ser Val Lys Phe Leu Leu Ile Thr Thr Arg Arg
115 120 125

Ser Leu Ser Val Gln Lys Arg Ser Ser Thr Phe Ser Gln Leu Leu His
130 135 140

<210> 34
<211> 94
<212> PRT
<213> Oryza sativa

<400> 34
Met Cys Met Asp Arg Ala Ala Val Pro Val Lys Arg Val Trp Leu Gly
1 5 10 15

Leu Ala Ala Arg Leu Gly Leu Arg Arg Thr Ser Gly Leu Gly Lys Leu
20 25 30

Lys Lys Glu Val Arg Thr Cys Glu Tyr His Asp Val His Ile Met Trp
35 40 45

Glu Met Leu Arg Lys Thr Asp Ala Pro Val Pro Met Ala Glu Lys Glu
50 55 60

Ala Ala Ala Ala Ala Val Ala Ala Ala Ala Gly Ala Arg Arg Arg
65 70 75 80

Lys Ala Ala Trp Arg Arg Phe Leu Tyr Tyr Cys Cys Ala Phe
85 90

<210> 35
<211> 303
<212> PRT
<213> Oryza sativa

<400> 35
Met Ala Thr Ser Arg Lys Leu Ala Arg Val Asp Ile Ala Glu Leu Lys
1 5 10 15

Gln Arg Leu Val Lys Arg Leu Gly Arg Gln Arg Ala Gly Gln Tyr Phe
20 25 30

ES 2 623 545 T3

Ala	His	Leu	Thr	Arg	Leu	Leu	Asn	Leu	Lys	Leu	Thr	Lys	Val	Glu	Phe	35	40	45
Asp	Lys	Leu	Cys	Tyr	Ala	Thr	Ile	Gly	Arg	Glu	Asn	Ile	Ala	Leu	His	50	55	60
Asn	Ala	Leu	Ile	Arg	Gly	Ile	Ile	Ser	Asn	Ala	Leu	Ser	Gly	Val	Pro	65	70	75
Pro	Pro	Ser	Arg	Gln	Ala	Val	Thr	Gly	Gln	Ser	Gly	Thr	Thr	Thr	Ala	85	90	95
Pro	Ser	Gly	Gln	Cys	Val	Gly	Ile	Ala	Leu	Gln	Ser	Ala	Arg	Asn	Val	100	105	110
Gly	Ala	Val	Val	Asp	Ser	Gly	Asp	Gly	Asp	Phe	Ala	Arg	Glu	Arg	Ala	115	120	125
Val	Ala	Gly	Lys	Val	Leu	Ser	Val	Glu	Asp	Gly	Glu	Glu	Val	Glu	Gln	130	135	140
Val	Arg	Ser	Ala	Pro	Cys	Val	Gln	Ser	Arg	Ser	Pro	Ile	Thr	Ala	Pro	145	150	155
Leu	Gly	Ile	Ser	Thr	Thr	Pro	Thr	Tyr	Gly	Ala	Arg	Thr	Trp	Arg	Leu	165	170	175
Asp	Asp	Pro	Met	Val	Ser	Cys	Tyr	Asp	Ser	His	His	Leu	Leu	Asp	Thr	180	185	190
Gly	Ser	Leu	Phe	Lys	Gly	Leu	Gln	Arg	Arg	Leu	Glu	Ser	Asp	Gly	Ile	195	200	205
Gly	Val	Ser	Val	Gln	Gly	Val	Glu	Val	Leu	Asn	Arg	Gly	Leu	Asp	Glu	210	215	220
Phe	Leu	Arg	Arg	Leu	Ile	Lys	Pro	Cys	Met	Glu	Leu	Ser	Arg	Ser	Arg	225	230	235
Ser	Ser	Gly	Arg	Arg	Val	Thr	Lys	Gly	Asn	Ala	Met	Phe	Ala	Ala	Arg	245	250	255
Met	Asn	Gly	Leu	Gln	Gln	Ala	Asn	His	Gly	His	Cys	Thr	Thr	Leu	Gln	260	265	270
Asp	Phe	Ala	Val	Ala	Met	Glu	Ser	Asp	Pro	His	Leu	Leu	Gly	Thr	Asn	275	280	285
Trp	Pro	Thr	Gln	Leu	Glu	Lys	Ile	Gln	Ala	Thr	Ser	Phe	Gly	Glu		290	295	300

ES 2 623 545 T3

<210> 36
 <211> 186
 <212> PRT
 <213> Oryza sativa

5

<400> 36
 Met Ala Ser Pro Arg Cys Ala Ala Val Ala Leu Leu His Pro Ala Gly
 1 5 10 15
 Val Ala Ala Gly Gly Gly Ala Arg Arg Arg Val Leu Leu Leu Asp Gln
 20 25 30
 Glu Arg Pro Leu Trp Gly Thr Glu Val Arg Arg Arg Arg Arg Arg Arg
 35 40 45
 Phe Ser Ser Leu Glu Thr Pro Pro Arg Cys Ser Lys Met Tyr Val Pro
 50 55 60
 Gly Phe Gly Glu Gly Ser Pro Glu Lys Lys Ala Ala Arg Asn Leu Gln
 65 70 75 80
 His Phe Phe Asn Tyr Ile Ala Val Arg Val Val Leu Thr Gln Leu Glu
 85 90 95
 Ser Tyr Asn Arg Glu Ala Tyr Gly Glu Leu Met Asp Phe Val Asn Arg
 100 105 110
 Asn Ser Leu Asn Asp Ala Asp Thr Phe Cys Lys Lys Leu Ile Arg Glu
 115 120 125
 Ser Pro Arg His Lys Gln Leu Ala Met Arg Ile Leu Glu Val Arg Ser
 130 135 140
 Ala Tyr Val Lys His Asp Phe Glu Trp Asp Asn Leu Lys Arg Leu Ser
 145 150 155 160
 Phe Lys Met Val Asp Glu Ala Asn Thr Lys Leu Met Arg Asp Tyr Val
 165 170 175
 Leu Glu Thr Ser His Ile Glu Asp Asp Asn
 180 185

10 <210> 37
 <211> 347
 <212> PRT
 <213> Oryza sativa

15

ES 2 623 545 T3

<400> 37

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Met Asp Ile Thr Gly Ala Gly Ala Met Gly Gly Gly Ser Thr Ala Ala
1      5      10      15

Thr Ala Ala Ala Ala Ala Gly Ala Gly Trp Lys Thr Pro Val Ser Met
      20      25      30

Val Leu Val Gln Leu Phe Ile Thr Gly Gln Ile Leu Leu Ser Lys Val
      35      40      45

Ser Ile Gly Gly Gly Met Leu Ile Phe Val Leu Leu Ala Tyr Asn Ser
50      55      60

Phe Phe Ala Val Val Phe Leu Leu Pro Phe Ala Leu Ile Phe Glu Arg
65      70      75      80

Gly Lys Trp Arg Asp Met Asp Trp Gly Ala Phe Gly Trp Ile Phe Leu
      85      90      95

Asn Ala Phe Ile Gly Tyr Ser Val Pro Met Ser Leu Tyr Tyr Tyr Gly
      100      105      110

Leu Lys Asp Thr Thr Ser Ser Tyr Ser Val Ile Phe Leu Asn Ile Thr
      115      120      125

Pro Leu Phe Thr Phe Ile Leu Ser Leu Met Phe Arg Leu Glu Ala Phe
      130      135      140

Lys Leu Arg Ser Ile Pro Gly Val Leu Lys Ile Ala Ser Ile Leu Leu
145      150      155      160

Ser Ile Gly Gly Thr Met Leu Ile Ser Leu Tyr Lys Gly Lys Ser Leu
      165      170      175

His Leu Trp Asp Ser Ile Ile Gln His Gln Asn Glu His Lys Ser Ala
      180      185      190

Thr Asn Gln Leu Arg Gly Thr Ile Leu Leu Val Gly Ser Ser Phe Thr
      195      200      205

Phe Ala Cys Trp Phe Leu Ile Gln Ser Lys Ile Leu Lys Val Tyr Pro
210      215      220

Tyr Lys Tyr Trp Ser Ser Met Val Thr Cys Leu Val Gly Val Phe Gln
225      230      235      240

Thr Ala Leu Val Gly Ile Ile Leu Arg Arg Asp Lys Ser Ala Trp Glu
      245      250      255

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Leu Gly Trp Asn Leu Asn Leu Val Thr Ile Val Tyr Thr Gly Ala Leu
260 265 270

Ala Thr Ala Gly Lys Tyr Ile Leu Asn Ser Trp Ala Ile Thr Lys Arg
275 280 285

Gly Pro Thr Tyr Pro Thr Met Phe Ser Pro Leu Ser Val Val Phe Thr
290 295 300

Val Val Leu Asp Ser Val Leu Leu Gly Asn Asp Ile Thr Ile Gly Ser
305 310 315 320

Leu Leu Gly Thr Ala Leu Val Ile Val Gly Leu Tyr Leu Phe Leu Trp
325 330 335

Ala Lys Ala Arg Glu Ile Pro Lys Lys Ser Thr
340 345

5 <210> 38
<211> 175
<212> PRT
<213> Oryza sativa

<400> 38
Met Ala Arg Arg Ala Ala Glu Lys Glu Ala Ala Leu Arg Gln Gly Leu
1 5 10 15

Thr Ala Gly Asp Gly Glu Ala Arg Arg Thr Gly Ala Leu Trp Arg Thr
20 25 30

Asp Ala Trp Arg Gln Arg Ala Ala Ala Ser Ala Ala Ala Ser Val
35 40 45

Val Arg Thr Trp Pro Ser Ser Ala Pro Trp Leu Arg Phe Glu Leu Asp
50 55 60

Pro Trp Arg Arg Val Cys Gly Glu Gln Asp Leu Gln Thr Ala Ala Cys
65 70 75 80

Gly Gly Gly Asp Gly Ala Val Gly Leu Ser Phe Glu Thr His His Gly
85 90 95

Gly Ser Val Ala Pro Ser Pro Glu Phe Ala Ala Cys Ala Ala Ser Ser
100 105 110

Cys Ser Ala Glu Leu Met Val Leu Leu Val Leu Gln Arg Gly Glu Leu
115 120 125

10 Leu Val Arg His Asp Arg Pro Ser His His His Arg Arg Arg Phe Pro

ES 2 623 545 T3

130

135

140

Thr Pro Gln Pro Ala Glu Ala Ala Ala Ala Val Glu Val Gly Trp Gly
145 150 155 160

Phe Gln Asn Pro Arg Asp Ala Met Thr Cys Leu Cys Lys Gly Leu
165 170 175

<210> 39

<211> 306

<212> PRT

<213> Oryza sativa

<400> 39

Met Gly Ser Gly Gly Gly Gly Cys Gly Arg Asn Gly Ala Val Arg Gln
1 5 10 15

Tyr Ile Arg Ser Lys Val Pro Arg Leu Arg Trp Thr Gly Glu Leu His
20 25 30

Cys Ser Phe Val Gln Ala Ile Glu Phe Leu Gly Gly Gln Asp Lys Ala
35 40 45

Thr Pro Lys Leu Ile Leu Gln Leu Met Gly Val Lys Gly Leu Thr Ile
50 55 60

Ser His Val Lys Ser His Leu Gln Met Tyr Arg Cys Ser Arg Leu Gly
65 70 75 80

Ser His Gly Thr Gly Arg Arg Ser Glu Met Gln Pro Gln Leu Gln Arg
85 90 95

Lys His Ser Cys Gly Ala Asp Glu Gln Val Pro Arg Glu Phe Leu Cys
100 105 110

Pro Pro Leu Lys Arg Thr Arg Met Gly Thr Glu Ala Thr Tyr Lys Gly
115 120 125

Met Gln Gly Ser Gln Gly Ile Ser Glu Met Arg Thr Thr Gly Thr Gln
130 135 140

Tyr Cys Ile Asp Asp Tyr Met Gln Ala Met Ala Met Glu Arg Arg Ile
145 150 155 160

Lys Glu Glu Gly Leu Arg Trp Gln Arg Asp Ala Ala Ala Ala Ala Ala
165 170 175

Ala Asp Gly Gly Ala Ala Ala Ser Asn Leu Gln Thr Val Gly Cys Ser
180 185 190

ES 2 623 545 T3

Val Gln Glu Ser Asp Pro Phe Lys Ile Ile Lys Pro Glu Val His His
195 200 205

Leu Gly Pro Val Leu Lys Leu Gln Cys Ser Lys Val Glu Asn Ser Gly
210 215 220

Phe Ile Ser Ser Ser Thr Gly Thr Ala Ala Arg Asp Gln Pro Glu Pro
225 230 235 240

Pro Pro Leu Glu Lys Cys Ser Leu Ser Leu Ser Leu Gly Pro Asp Pro
245 250 255

Lys Cys Met Pro Ala Ile Ala Ser Ser Pro Ser Glu Ser Ser Cys Ile
260 265 270

Leu Ser Ser Ser Ser Arg Ser Phe Ser Asp Cys Ser Gly Asn Ser Gly
275 280 285

Cys Leu Val Ala Pro Gly Val Asn Leu Glu Leu Ser Met Ser Ile Cys
290 295 300

Gly Ser
305

5 <210> 40
<211> 187
<212> PRT
<213> Oryza sativa

<400> 40
Met Ala Ala Ala Asp Gln Pro Ala Tyr Gly Asp Arg Arg Pro Ser Arg
1 5 10 15

Arg Thr Tyr Lys Pro Asp Gln Pro Glu Gly Leu Thr Ile Ser Phe Arg
20 25 30

Glu Leu Tyr Asp Leu Pro Thr Ser Pro Glu Phe Leu Phe His Glu Glu
35 40 45

Ala Leu Arg Ser Arg Arg Thr Cys Gly Glu Asp Leu Thr Phe Tyr Thr
50 55 60

Gly Cys Gly Tyr Leu Val Gly Arg Ala Ala Gly Ala Ala Ala Gly Leu
65 70 75 80

Lys Arg Ala Ala Glu Glu Ala Glu Arg Gly Glu Ser Met Lys Leu Arg
85 90 95

10 Gly Gln Pro Arg Pro Gln Pro Val Arg Leu Pro Arg Ala Arg Val Arg

ES 2 623 545 T3

100 105 110

Gln Pro Ala Arg Arg Arg Arg Ala Ala Leu Arg Gly Asp Arg Glu His
115 120 125

Arg Gly Gly Pro Pro Arg Arg Arg Arg Leu Gly Gln His Arg Arg Arg
130 135 140

Arg Asp Arg Tyr Arg Arg Ala Leu Pro Arg Gly Cys Arg Pro Ala Gly
145 150 155 160

Gly Asp Arg Arg Gln Leu Arg Arg Gly Ala His Gly Arg Arg Gly Gly
165 170 175

Arg Gly Glu Ala Ser Ala Asp Glu Ile Arg Ala
180 185

<210> 41
5 <211> 424
<212> PRT
<213> Oryza sativa

<400> 41
Met Asp Met Pro Pro Thr Pro Leu Pro Pro Glu Thr Ala Asn Thr Ser
1 5 10 15

Pro Ala Pro Asn Gly Ala Thr Ala Gly Ile Arg Val Glu Asn Cys Tyr
20 25 30

Val Phe Lys Ser Arg Leu Gln Glu Tyr Ala Gln Lys Thr Gly Leu Gln
35 40 45

Thr Pro Glu Tyr His Thr Phe Lys Glu Gly Pro Ser His Glu Pro Val
50 55 60

Phe Lys Ser Thr Val Val Ile Asn Asn Thr Ser Tyr Asp Ser Leu Pro
65 70 75 80

Gly Phe Phe Asn Arg Lys Ala Ala Glu Gln Ser Ala Ala Glu Val Ala
85 90 95

Leu Met Glu Ile Val Lys Ser Ile Pro Ala Asn Ala Asn Ile Pro Ala
100 105 110

Val Gln Glu Thr Gly Leu Cys Lys Asn Leu Leu Gln Glu Tyr Ala Gln
115 120 125

Lys Met Asn Tyr Ala Ile Pro Ser Tyr Ile Cys Thr Lys Ser Ala Ser
130 135 140

10

ES 2 623 545 T3

Gly	Leu	Ala	Pro	Phe	Ile	Cys	Thr	Val	Glu	Ile	Gly	Gly	Ile	Gln	Tyr	145	150	155	160
Ile	Gly	Ala	Ala	Ala	Arg	Thr	Lys	Lys	Asp	Ala	Glu	Ile	Lys	Ala	Ala	165	170	175	
Arg	Thr	Ala	Leu	Leu	Ala	Ile	Gln	Gly	Gln	Ser	Glu	Gly	Ser	Ala	Asn	180	185	190	
Gly	Ala	Thr	Lys	Tyr	Ile	Val	Val	Pro	Gly	Lys	Arg	Val	Gly	Lys	Glu	195	200	205	
Val	Glu	Lys	Arg	Pro	Ile	Glu	Thr	Pro	Lys	Pro	Leu	Lys	Val	Lys	Lys	210	215	220	
Gly	Gly	Phe	Lys	Lys	Lys	Trp	Asn	Lys	Arg	Lys	Phe	Met	Lys	Lys	Asp	225	230	235	240
Gly	Gln	Ala	Val	Asp	Val	Glu	Lys	Asp	Glu	Ala	Arg	Val	Ala	Gly	Asp	245	250	255	
Ala	His	Asp	Ser	Asp	Val	Leu	Met	Gln	Pro	Thr	Val	Ile	Thr	Gln	Glu	260	265	270	
Ala	Ser	Cys	Gly	Thr	Leu	Phe	Leu	Gln	Pro	Cys	Glu	Glu	Ala	Lys	Arg	275	280	285	
Val	Glu	Ala	Glu	Pro	Pro	Arg	Asp	Ile	Glu	Met	Val	Gln	Pro	Asp	Lys	290	295	300	
Glu	Asn	Gln	His	Ser	Asp	Ala	Ala	Leu	Val	Gln	Pro	Asp	Asp	Glu	Ala	305	310	315	320
Arg	Val	Glu	Gln	Glu	Pro	Ser	Arg	Asp	Ile	Ser	Val	Val	Gln	Pro	Asn	325	330	335	
Glu	Glu	Ala	Ile	Ser	Gly	Lys	Gln	Glu	Pro	Ser	Ile	Asp	Ala	Ala	Ile	340	345	350	
Leu	Gln	Pro	Lys	Glu	Glu	Ala	Ser	Ser	Val	Lys	Gln	Glu	Pro	Phe	Ile	355	360	365	
Asp	Thr	Ala	Met	Leu	Gln	Ala	Cys	Lys	Glu	Ala	Gly	Ser	Val	Glu	Leu	370	375	380	
Gly	Pro	Ala	Arg	Asp	Thr	Val	Ile	Ser	Gln	Leu	Asn	Glu	Gln	Asp	Arg	385	390	395	400

ES 2 623 545 T3

Ala Val Lys Gln Glu Pro Ala Gly Asp Ile Val Val Pro Gln Pro Asp
405 410 415

Val His Ala Arg Val Val Lys Glu
420

<210> 42

<211> 1359

<212> PRT

<213> Oryza sativa

<400> 42

Met Ala Leu Gly Asp Leu Met Ala Ser Arg Leu Val His Ser Ser Ser
1 5 10 15

Ser Ser Ala Ala Pro Ser Ala Ala Leu Pro Asn His His Thr Asn His
20 25 30

Leu Val Asp Asp His Leu Pro Val Glu Asn Gly Pro Asp Pro Arg Arg
35 40 45

Asp Val Pro Asp Glu Glu Pro Pro Pro Pro Pro Pro Gln Val Ala
50 55 60

Leu Leu Pro Gln Val Val Val Leu Cys Glu Gln Arg His Glu Gly Phe
65 70 75 80

Asp Glu Ala Ala Ala Ala Ala Ala Gly Pro Ser Thr Ser Gly Pro Val
85 90 95

Ser Lys Trp Arg Pro Lys Asp Arg Met Lys Thr Gly Cys Val Ala Leu
100 105 110

Val Leu Cys Leu Asn Ile Ser Val Asp Pro Pro Asp Val Ile Lys Ile
115 120 125

Ser Pro Cys Ala Arg Lys Glu Cys Trp Ile Asp Pro Phe Ser Met Ala
130 135 140

Pro Pro Lys Ala Leu Glu Thr Ile Gly Lys Thr Leu His Ser Gln Tyr
145 150 155 160

Glu Arg Trp Gln Pro Lys Ala Arg Tyr Lys Leu Gln Leu Asp Pro Thr
165 170 175

Leu Glu Glu Val Lys Lys Leu Cys Asn Thr Cys Arg Lys Phe Ala Arg
180 185 190

Thr Glu Arg Val Leu Phe His Tyr Asn Gly His Gly Val Pro Lys Pro
195 200 205

ES 2 623 545 T3

Thr	Ala	Asn	Gly	Glu	Ile	Trp	Val	Phe	Asn	Lys	Ser	Tyr	Thr	Gln	Tyr
210						215					220				
Ile	Pro	Leu	Pro	Ile	Thr	Asp	Leu	Asp	Ser	Trp	Leu	Lys	Thr	Pro	Ser
225					230					235					240
Ile	Tyr	Val	Phe	Asp	Cys	Ser	Ala	Ala	Gly	Met	Ile	Val	Lys	Ala	Phe
				245						250					255
Leu	Glu	Arg	Leu	Asp	Trp	Ser	Ser	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Lys
			260							265				270	
Asp	Cys	Ile	Leu	Leu	Ala	Ala	Cys	Glu	Ala	His	Gln	Thr	Leu	Pro	Gln
		275					280					285			
Ser	Ala	Glu	Phe	Pro	Ala	Asp	Val	Phe	Thr	Ala	Cys	Leu	Thr	Thr	Pro
	290					295					300				
Ile	Lys	Met	Ala	Leu	His	Trp	Phe	Cys	Asn	Arg	Ser	Leu	Leu	Arg	Asp
305					310					315					320
Ser	Met	Glu	His	Asn	Leu	Ile	Asp	Gln	Ile	Pro	Gly	Arg	Gln	Asn	Asp
				325					330					335	
Arg	Lys	Thr	Leu	Leu	Gly	Glu	Leu	Asn	Trp	Ile	Phe	Thr	Ala	Ile	Thr
			340					345					350		
Asp	Thr	Ile	Ala	Trp	Asn	Val	Leu	Pro	His	Asp	Leu	Phe	Gln	Arg	Leu
		355					360					365			
Phe	Arg	Gln	Asp	Leu	Leu	Val	Ala	Ser	Leu	Phe	Arg	Asn	Phe	Leu	Leu
	370					375					380				
Ala	Glu	Arg	Ile	Met	Arg	Ser	Ala	Asn	Cys	Ser	Pro	Ile	Ser	Tyr	Pro
385					390					395					400
Leu	Leu	Pro	Pro	Thr	His	Gln	His	His	Met	Trp	Asp	Ala	Trp	Asp	Met
				405					410					415	
Ala	Ala	Glu	Ile	Cys	Leu	Ser	Lys	Leu	Pro	Gln	Leu	Ile	Ala	Asp	Pro
			420					425					430		
Asn	Ala	Glu	Phe	Gln	Pro	Ser	Pro	Phe	Phe	Thr	Glu	Gln	Leu	Thr	Ala
		435					440					445			
Phe	Glu	Val	Trp	Leu	Asp	His	Gly	Ser	Glu	Asp	Lys	Lys	Pro	Pro	Glu
	450					455					460				

ES 2 623 545 T3

Gln Leu Pro Ile Val Leu Gln Val Leu Leu Ser Gln Ser His Arg Phe
465 470 475 480

Arg Ala Leu Val Leu Leu Gly Arg Phe Leu Asp Met Gly Pro Trp Ala
485 490 495

Val Asp Leu Ala Leu Ser Val Gly Ile Phe Pro Tyr Val Leu Lys Leu
500 505 510

Leu Gln Thr Ser Ala Met Glu Leu Arg Gln Ile Leu Val Phe Ile Trp
515 520 525

Thr Lys Ile Leu Ser Leu Asp Lys Ser Cys Gln Val Asp Leu Val Lys
530 535 540

Asp Gly Gly His Ala Tyr Phe Ile Arg Phe Leu Asp Ser Leu Asp Ala
545 550 555 560

Tyr Pro Glu Gln Arg Ala Met Ala Ala Phe Val Leu Ala Val Ile Val
565 570 575

Asp Gly His Arg Ile Gly Gln Glu Ala Cys Ala Asn Ala Gly Leu Ile
580 585 590

Asp Val Cys Leu Arg His Leu Gln Pro Glu Asn Pro Asn Asp Ala Gln
595 600 605

Thr Glu Pro Leu Leu Leu Gln Trp Leu Cys Leu Cys Leu Gly Lys Leu
610 615 620

Trp Glu Asp Phe Pro Glu Ala Gln Leu Leu Gly Leu Gln Ser Asn Ala
625 630 635 640

Pro Glu Ile Val Ile Cys Leu Leu Ser Glu Pro Gln Pro Glu Val Arg
645 650 655

Ala Ser Ala Val Phe Ala Leu Gly Asn Leu Val Asp Ile Gly Ser Pro
660 665 670

Ser Leu Asn Gly Ala Asp Asp Asp Ser Asp Asp Asp Glu Lys Val Arg
675 680 685

Ala Glu Ile Asn Val Val Arg Ser Leu Leu Gln Ile Ser Ser Asp Gly
690 695 700

Ser Pro Leu Val Arg Ser Glu Val Ala Val Ala Leu Thr Arg Phe Ala
705 710 715 720

ES 2 623 545 T3

Met Gly His Asn Lys His Ile Lys Ser Val Ala Ala Glu Tyr Trp Lys
725 730 735

Pro Gln Thr Asn Ser Leu Leu Lys Ser Leu Pro Ser Leu Ala Asn Ile
740 745 750

Asn Ser Ser Asn Val Tyr Ser Pro Ser Ser Leu Ile Gln Gly Ser Ser
755 760 765

Gly Leu Ala Ser His Ile Gly Pro Val Leu Arg Val Gly Ser Asp Asn
770 775 780

Ser Ala Thr Ala Arg Asp Gly Arg Ile Ser Thr Ser Ser Pro Ile Ala
785 790 795 800

Thr Asn Ser Ile Met His Gly Ser Pro Gln Ser Asp Asp Ser Ser Gln
805 810 815

His Ser Asp Ser Gly Ile Leu Leu Arg Glu Asn Ala Ser Asn Gly Gly
820 825 830

Leu Asn Tyr Ser Arg Ser Arg Pro Ile Asp Asn Gly Ile Tyr Ser Gln
835 840 845

Phe Ile Ala Thr Met Cys Asn Val Ala Lys Asp Pro Tyr Pro Arg Ile
850 855 860

Ala Ser Ile Gly Lys Arg Ala Leu Ser Leu Ile Gly Val Glu Gln Val
865 870 875 880

Ser Met Arg Asn Ser Arg Leu Ser Asn Gly Gly Ala His Pro Gly Glu
885 890 895

Thr Ser Val Pro Pro Ser Ser Asn Phe Gly Met Ala Arg Ser Ser Ser
900 905 910

Trp Phe Asp Met Asn Ser Gly Asn Phe Ser Val Ala Phe Arg Thr Pro
915 920 925

Pro Val Ser Pro Pro Gln His Asp Tyr Leu Thr Gly Leu Arg Arg Val
930 935 940

Cys Ser Met Glu Phe Arg Pro His Val Leu Asn Ser Pro Asp Gly Leu
945 950 955 960

Ala Asp Pro Leu Leu Ser Ser Ser Ala Ala Pro Ser Asn Met Gly Leu
965 970 975

Tyr Ile Leu Pro Gln Ser Leu Ile Tyr Arg Trp Ser Cys Gly His Phe

ES 2 623 545 T3

980					985					990					
Ser	Arg	Pro	Leu	Leu	Thr	Gly	Ser	Asp	Asp	Asn	Glu	Glu	Ala	Asn	Ala
		995					1000					1005			
Arg	Arg	Glu	Glu	Arg	Glu	Arg	Ile	Ala	Met	Asp	Cys	Ile	Ala	Lys	
	1010					1015					1020				
Cys	Gln	Arg	Ser	Ser	Cys	Lys	Met	Thr	Ser	Gln	Ile	Ala	Ser	Trp	
	1025					1030					1035				
Asp	Thr	Arg	Phe	Glu	Leu	Gly	Thr	Lys	Ala	Ser	Leu	Leu	Leu	Pro	
	1040					1045					1050				
Phe	Ser	Pro	Ile	Val	Val	Ala	Ala	Asp	Glu	Asn	Glu	Gln	Ile	Arg	
	1055					1060					1065				
Val	Trp	Asn	Tyr	Asp	Asp	Ala	Leu	Pro	Val	Asn	Thr	Phe	Glu	Asn	
	1070					1075					1080				
His	Lys	Leu	Ser	Asp	Arg	Gly	Leu	Ser	Lys	Leu	Leu	Leu	Ile	Asn	
	1085					1090					1095				
Glu	Leu	Asp	Asp	Ser	Leu	Leu	Leu	Val	Gly	Ser	Ser	Asp	Gly	Asn	
	1100					1105					1110				
Val	Arg	Ile	Trp	Arg	Asn	Tyr	Thr	Gln	Lys	Gly	Gly	Gln	Lys	Leu	
	1115					1120					1125				
Val	Thr	Ala	Phe	Ser	Ser	Val	Gln	Gly	Tyr	Arg	Ser	Ala	Gly	Arg	
	1130					1135					1140				
Ser	Ile	Val	Phe	Asp	Trp	Gln	Gln	Gln	Ser	Gly	Tyr	Leu	Tyr	Ala	
	1145					1150					1155				
Ser	Gly	Asp	Met	Ser	Ser	Ile	Leu	Val	Trp	Asp	Leu	Asp	Lys	Glu	
	1160					1165					1170				
Gln	Val	Asn	Thr	Ile	Gln	Ser	Thr	Ala	Asp	Ser	Gly	Ile	Ser	Ala	
	1175					1180					1185				
Leu	Ser	Ala	Ser	Gln	Val	Arg	Cys	Gly	Gln	Phe	Ala	Ala	Gly	Phe	
	1190					1195					1200				
Leu	Asp	Ala	Ser	Val	Arg	Ile	Phe	Asp	Val	Arg	Thr	Pro	Asp	Arg	
	1205					1210					1215				
Leu	Val	Tyr	Thr	Ala	Arg	Pro	His	Ala	Pro	Arg	Ser	Glu	Lys	Val	
	1220					1225					1230				

ES 2 623 545 T3

Val Gly Ile Gly Phe Gln Pro Gly Phe Asp Pro Tyr Lys Ile Val
1235 1240 1245

Ser Ala Ser Gln Ala Gly Asp Ile Gln Phe Leu Asp Val Arg Arg
1250 1255 1260

Ala Ser Glu Pro Tyr Leu Thr Ile Glu Ala His Arg Gly Ser Leu
1265 1270 1275

Thr Ala Leu Ala Val His Arg His Ala Pro Val Ile Ala Ser Gly
1280 1285 1290

Ser Ala Lys Gln Met Ile Lys Val Phe Ser Leu Glu Gly Glu Gln
1295 1300 1305

Leu Thr Ile Ile Arg Tyr Gln Pro Ser Phe Met Gly Gln Arg Ile
1310 1315 1320

Gly Ser Val Asn Cys Leu Ser Phe His Arg Tyr Lys Ser Leu Leu
1325 1330 1335

Ala Ala Gly Ala Gly Asp Asn Ala Leu Val Ser Ile Tyr Ala Glu
1340 1345 1350

Asp Asn Tyr Gln Val Arg
1355

<210> 43

<211> 233

5 <212> PRT

<213> Oryza sativa

<400> 43

Met Gly Ala Ser Gly Arg Leu Ile Ser Ile Tyr Pro Glu Asp Leu Thr
1 5 10 15

Phe Leu Phe Glu Leu Asp Lys Pro Cys Tyr Cys Asn Leu Lys Val Val
20 25 30

Asn Asn Ser Glu His His Val Ala Phe Lys Val Lys Thr Thr Ser Pro
35 40 45

Arg Lys Tyr Phe Val Arg Pro Asn Ala Ser Ile Ile Gln Pro Trp Asp
50 55 60

Ser Cys Thr Ile Thr Ile Thr Leu Gln Ala Gln Lys Glu Tyr Pro Pro
65 70 75 80

ES 2 623 545 T3

Asp Met Gln Cys Lys Asp Lys Phe Leu Ile Gln Ser Thr Lys Val Ala
85 90 95

Ala Ser Thr Asp Met Asp Glu Ile Pro Pro Asn Thr Phe Asn Lys Glu
100 105 110

Val Asp Lys Val Ile Glu Glu Met Lys Leu Lys Val Val Tyr Thr Val
115 120 125

Pro Ser Gly Ser Ser Asp Asp Ser Gly Ile Thr Ser Leu Gly Ser Arg
130 135 140

Ser Phe Lys Leu Gly Ser Asp Asp Leu Thr Met Leu Lys Asn Ala Ser
145 150 155 160

Ile Glu Lys Ile Gln Thr Ile Gln Arg Leu Lys Asp Glu Arg Asp Thr
165 170 175

Thr Leu Gln Gln Asn Gln Gln Met Gln Arg Glu Leu Asp Val Ile Arg
180 185 190

Arg Arg Arg Ser Arg Lys Ser Asp Ala Gly Phe Ser Leu Thr Phe Ala
195 200 205

Ala Phe Ala Gly Leu Ile Gly Val Leu Ile Gly Leu Leu Met Ser Leu
210 215 220

Ile Phe Pro Arg Pro Gln Ala Ala Ala
225 230

<210> 44

<211> 939

<212> PRT

<213> Oryza sativa

5

ES 2 623 545 T3

<400> 44

Met Gly Val Met Asn Pro Leu Met Ala Lys Leu Thr Thr Leu Met Gly
1 5 10 15

Asp Glu Tyr Lys Lys Leu Lys Gly Leu Arg Lys Gln Val Ser Phe Leu
20 25 30

Lys Asp Glu Leu Thr Thr Met Ser Ala Phe Leu Glu Lys Leu Ala Leu
35 40 45

Met Asp Asp Asp Asp Asp Gly Glu Leu Asp Pro Leu Ala Lys Asp Trp
50 55 60

Arg Asn His Val Arg Glu Met Ala Tyr Asp Met Glu Asp Cys Ile Asp
65 70 75 80

ES 2 623 545 T3

Asp Tyr Phe Thr Ser His Leu Asp His Arg Tyr Ser Ser Ser Asp Ala
 85 90 95
 Gly Leu Ile Arg Lys Ile Ala Arg Arg Leu Arg Ala Leu Arg Val Arg
 100 105 110
 His Arg Ile Ala Ser Gln Ile Asn Glu Leu Lys Ala Arg Val Val Glu
 115 120 125
 Ala Asn Glu Arg Arg Val Arg Tyr Arg Leu Asp Asp Cys Asn Asn Lys
 130 135 140
 His Gly Val Ser Ala Asn Pro Ala Ile Asp Pro Arg Ile Thr Ser Leu
 145 150 155 160
 Tyr Gln Asn Ala Gly Ser Leu Val Gly Ile Asp Gly Pro Ser Gln Glu
 165 170 175
 Leu Ile Gln Leu Leu Ser Leu Asp Arg Asp Thr Asp Gln Arg Gln Leu
 180 185 190
 Lys Val Val Ser Val Val Gly Phe Gly Gly Leu Gly Lys Thr Thr Leu
 195 200 205
 Ala Lys Tyr Val Tyr Asp Lys Ile Gly His Gln Phe Asp Cys Thr Ala
 210 215 220
 Phe Val Ser Val Ser His Lys Pro Asp Ile Thr Arg Ile Leu Ser Ser
 225 230 235 240
 Ile Gln Ser Lys Leu Asp Ile Gly Gly Thr Ser Gln Ala Cys Asp Asp
 245 250 255
 Val Gln Gln Leu Ile Asp Asp Ile Arg Ala Tyr Leu Glu His Glu Arg
 260 265 270
 Tyr Ile Ile Ile Val Asp Asp Leu Trp Lys Gln Glu Ala Trp Val Ile
 275 280 285
 Ile Ser Cys Ala Phe Pro Asn Asn Gly Lys Gly Ser Arg Val Ile Val
 290 295 300
 Thr Thr Arg Val Lys Asp Val Ala Arg Leu Ala Cys Gly Lys Asp Gly
 305 310 315 320
 Gln Ile Tyr Lys Ile Gln Pro Leu Asn Asn Lys Asp Ser Arg Lys Leu
 325 330 335

ES 2 623 545 T3

Phe Phe Asp Arg Val Phe Arg Pro Glu Asp Ser Cys Val Leu Gln Tyr
 340 345 350
 Glu Glu Ile Ser Thr Glu Ile Leu Lys Lys Cys Ser Gly Leu Pro Leu
 355 360 365
 Ala Ile Val Thr Val Gly Ser Leu Leu Ala Cys Arg Pro Arg Thr Met
 370 375 380
 Glu Glu Trp Lys Ser Ile Arg Asp Ser Leu Gly Ala Pro Phe Asp Lys
 385 390 395 400
 Asn Lys Ser Leu Glu Gly Met Arg Asn Ile Leu Asn Leu Ser Tyr Lys
 405 410 415
 Asn Leu Pro Leu His Leu Lys Thr Cys Leu Leu Tyr Ile Gly Lys Tyr
 420 425 430
 Pro Glu Asp Tyr Glu Ile Gly Arg Asp Glu Leu Val Thr Glu Trp Ile
 435 440 445
 Ala Glu Gly Ile Met Gly Asn Pro His Gly Glu Asn Leu Glu Ala Thr
 450 455 460
 Gly Asn Gly Tyr Phe Ser Glu Leu Ile Asn Arg Gly Leu Ile Gln Pro
 465 470 475 480
 Glu Ser Thr Gly Tyr Gly Gly Glu Val Leu Ser Cys Lys Val His Asp
 485 490 495
 Met Met Leu Asp Leu Ile Leu Ile Lys Cys Ala Glu Asp Asn Phe Val
 500 505 510
 Ser Val Ala His Ser Cys Lys Asp Tyr Met Arg Met Ala Met His His
 515 520 525
 Glu Arg Ser Cys Asn Lys Val Arg Arg Leu Ser Leu Gln Cys Lys Ala
 530 535 540
 Ala Arg Ser Asp Cys Ala Ile Glu Gly Ser Val Ile Ser Thr Ser Met
 545 550 555 560
 Ala Arg Ala Arg Ser Val Ser Val Phe Gly Glu Cys Ser Arg Gly Leu
 565 570 575
 Pro Phe Leu Met Leu Ser Lys Tyr Ile Arg Val Val His Ile Glu Leu
 580 585 590

ES 2 623 545 T3

Glu Gly His Gly Gly Gln Val Asp Leu Thr Ala Ile Ser His Val Leu
 595 600 605
 Gln Leu Arg Tyr Leu Arg Val Glu Thr Pro Gly Cys Glu Ile Asp Leu
 610 615 620
 Pro Ser Lys Ile Cys Gly Leu Val His Leu Glu Thr Leu Ser Ile Phe
 625 630 635 640
 Ser His Lys Ala Val Ser Arg Leu Pro Ser Asp Ile Ser Ser Leu Pro
 645 650 655
 Arg Leu Ser Val Leu Ser Leu Val Val Pro Trp Ala Thr Arg Leu Pro
 660 665 670
 Asn Lys Leu Asn Lys Leu Lys Gly Ser Leu Arg Ser Leu Thr Ile Leu
 675 680 685
 Phe Asn Pro Pro Asp Ala Leu Gly Met Glu Ala Ile Gly Glu Leu Lys
 690 695 700
 Asn Leu Arg Asp Leu Asn Ile Ser Val Asn Arg Trp Arg Asp Asp Glu
 705 710 715 720
 Ile Leu Ser Leu Tyr Ala Leu Gly Ser Ser Ile Gly Lys Leu Asp Glu
 725 730 735
 Leu Arg Ser Leu Gln Ile His Val Pro Pro Ala Thr Leu Gly Asp Val
 740 745 750
 Asp Leu Leu Gly Ser Leu Pro Ile Phe Pro Gln Ser Ile Glu Arg Leu
 755 760 765
 Ile Leu His Gly Trp Cys Phe Ser Lys Val Pro Arg Trp Ile Asn Gly
 770 775 780
 Thr Leu Arg Asn Leu Gln His Val Leu Leu Glu Val Ser Glu Thr Ser
 785 790 795 800
 Ser Ser Glu Val Asp Leu Leu Gly Glu Leu Pro Ser Leu Ala Asp Leu
 805 810 815
 Glu Leu Arg Val Gly Leu Lys Thr Arg Asp Val Ile Ala Phe Gly Gly
 820 825 830
 Thr Arg Ala Ser Leu Phe Pro Ala Leu Leu Lys Leu Lys Leu Arg Val
 835 840 845
 Gly Glu His Val Ala Ser Arg Leu Gln Phe Gln Ala Gly Val Met Pro

ES 2 623 545 T3

850

855

860

Lys Leu Gln Ser Leu His Leu Trp Phe Arg Asn Cys Glu Ser Gly Ile
865 870 875 880

His Val Thr Pro Glu Gly Met Gln His Leu Leu Ser Leu Gln Ser Ile
885 890 895

Cys Val Glu Ile Tyr Leu Arg Asp Glu Glu Leu Lys Ala Thr Tyr Pro
900 905 910

Trp Asp Ala Met Glu Arg Ala Phe Arg Glu Ile Thr Gly Ala Asn Pro
915 920 925

Asn Arg Pro Ser Phe Lys Phe Val Lys Gln Val
930 935

<210> 45

<211> 337

<212> PRT

<213> Oryza sativa

<400> 45

Met Glu Cys Glu Pro Glu Glu Leu Gln Phe Leu Gly Met Val Gly Ile
1 5 10 15

Tyr Arg Glu Ala Ala Ser Ile Leu Arg Ala His Arg Pro Leu Phe Ala
20 25 30

Arg Ile Ala Ala Ala Phe Val Leu Pro Leu Ser Leu Leu Phe Leu Leu
35 40 45

His Ile Ala Ile Ser His Ala Leu Phe Ser His Ile Asp Ser Asp Asp
50 55 60

Ser Ala Leu Asp Ser Ala Ala Pro Gly Thr Pro Ala Gln Arg Arg Leu
65 70 75 80

Leu His Arg Leu Ala Asp Asp Trp Leu Ala Leu Leu Leu Phe Lys Ala
85 90 95

Ala Tyr Leu Leu Ala Leu Leu Leu Phe Ser Leu Leu Ser Thr Ala Ala
100 105 110

Ala Val Phe Ser Val Ala Ser Val Tyr Ser Ala Lys His Asp Ala Leu
115 120 125

Ser Phe Pro Arg Val Leu Ser Val Val Pro Arg Val Trp Arg Arg Leu
130 135 140

ES 2 623 545 T3

Ala Ala Thr Phe Leu Ala Ala Phe Leu Leu Leu Phe Ala Tyr His Leu
145 150 155 160

Leu Phe Val Ala Val Phe Val Ala Leu Leu Val Ala Ala Asp Ser Gly
165 170 175

Ser Gly Leu Ala Ala Leu Leu Ala Phe Leu Leu Ala Leu Ala Tyr Ile
180 185 190

Ala Gly Leu Val Tyr Leu Ser Val Val Trp His Leu Ala Ser Val Val
195 200 205

Ser Val Leu Glu Asp Tyr Lys Gly Phe Glu Ala Met Arg Lys Ser Lys
210 215 220

Ala Leu Ile Gln Gly Lys Leu Trp Thr Ala Ser Ala Ile Phe Phe Val
225 230 235 240

Leu Asn Val Val Phe Ile Val Val Glu Val Ala Phe Arg Ala Trp Val
245 250 255

Val Arg Gly Ala Thr His Gly Leu Gly Ala Gly Ser Arg Leu Leu Leu
260 265 270

Gly Leu Ala Met Leu Ala Ala Leu Cys Ala Val Val Met Leu Ala Leu
275 280 285

Val Val Gln Thr Val Val Tyr Leu Val Cys Lys Ser Tyr His His Glu
290 295 300

Ser Ile Asp Lys Ser Asn Leu Ser Asp His Leu Glu Val Tyr Leu Gly
305 310 315 320

Glu Tyr Val Pro Leu Lys Ala Ser Asp Val Gln Met Glu Gln Phe Asn
325 330 335

Leu

<210> 46

5 <211> 311

<212> PRT

<213> Oryza sativa

<400> 46

Met Ala Ser Ser Ser Ala Leu Ala Ser Ser Pro Phe Leu Pro Pro Leu
1 5 10 15

10 Ser Thr Pro Asn Pro Arg Ala Leu Ser Leu Arg Leu Pro Ala Arg Arg

ES 2 623 545 T3

20										25					30				
Leu	Pro	Val	Ala	Ser	Ser	Ala	Ala	Pro	Ser	Gly	Ala	Ala	Ala	Ala	Ala				
		35					40					45							
Ser	Ala	Arg	Glu	Arg	Arg	Arg	Phe	Leu	Glu	Arg	Tyr	Gly	Leu	Asn	Pro				
	50					55					60								
Asp	Asp	Phe	Glu	Asp	Asp	Ala	Glu	Ala	Glu	Pro	Arg	Glu	Glu	Arg	Arg				
65					70					75					80				
Arg	Asp	Arg	Arg	Asn	Arg	Arg	Ser	Gly	Arg	Gly	Glu	Ala	Glu	Asp	Ala				
				85					90					95					
Pro	Ala	Lys	Ala	Ala	Ala	Glu	Pro	Arg	Glu	Thr	His	Lys	Met	Leu	Gln				
		100						105					110						
Val	Leu	Gly	Gly	Lys	Val	Arg	Arg	Arg	Lys	Leu	Leu	Ser	Pro	Lys	Asp				
		115					120					125							
Arg	Asn	Val	Arg	Pro	Met	Met	Glu	Val	Val	Arg	Gly	Ala	Ala	Phe	Asp				
	130					135					140								
Ile	Leu	Gln	Ser	Ala	Gly	Gly	Phe	Pro	Ala	Ser	Leu	Arg	Pro	Gly	Arg				
145					150					155					160				
Trp	Leu	Asp	Leu	Tyr	Ser	Gly	Thr	Gly	Ser	Val	Gly	Ile	Glu	Ala	Met				
				165					170					175					
Ser	Arg	Gly	Cys	Ser	Glu	Ala	His	Phe	Val	Glu	Met	Asp	Pro	Trp	Val				
			180					185					190						
Val	Ser	Glu	Val	Leu	Lys	Pro	Asn	Leu	Glu	Cys	Thr	Gly	Phe	Leu	Asp				
		195					200					205							
Val	Ser	His	Ile	His	Met	Ile	Arg	Val	Glu	Asn	Phe	Leu	Ala	Asn	Ala				
		210				215					220								
Glu	Lys	Ser	Ser	Gly	Lys	Tyr	Pro	Ser	Phe	Asp	Tyr	Ile	Ser	Val	Thr				
225					230					235					240				
Pro	Pro	Tyr	Leu	Glu	Val	Asn	Tyr	Ser	Thr	Leu	Leu	Asp	Gln	Leu	Ala				
				245					250					255					
Arg	Ser	Pro	Leu	Val	Gly	Glu	Asp	Cys	Phe	Ile	Leu	Val	Glu	Tyr	Pro				
			260					265					270						
Leu	Lys	Thr	Asp	Met	Ala	Glu	Ser	Cys	Gly	Ser	Leu	Ile	Lys	Val	Ala				
		275					280					285							

ES 2 623 545 T3

Asp Arg Arg Phe Gly Arg Thr Asn Leu Leu Ile Tyr Gly Pro Thr Trp
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Ala Glu Lys Lys Arg Arg Ser
305 310

<210> 47

<211> 311

<212> PRT

<213> Oryza sativa

<400> 47

Met Asn Asp Leu Met Thr Lys Ser Phe Met Ser Tyr Val Asp Leu Lys
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Lys Ala Ala Met Lys Asp Leu Glu Ala Gly Gly Asp Gly Val Glu Leu
20 25 30

Pro Glu Val Gly Val Thr Asp Glu Arg Leu Lys Gly Phe Phe Gln Glu
35 40 45

Thr Glu Ala Val Glu Glu Glu Met Ala Ala Ile Arg Asp Ala Leu Ala
50 55 60

Arg Leu Asn Ala Ala Asn Glu Glu Gly Lys Ser Leu His Gln Pro Asp
65 70 75 80

Ala Leu Arg Ala Leu Arg Gly Arg Val Asn Ala Asp Ile Ile Ala Val
85 90 95

Leu Arg Arg Ala Arg Asp Ile Arg Ala Arg Leu Glu Ala Met Asp Arg
100 105 110

Ala Asn Ala Ala Gln Arg Arg Leu Ser Ala Gly Cys Arg Glu Gly Thr
115 120 125

Pro Leu Asp Arg Thr Arg Thr Ala Leu Thr Ala Ala Leu Arg Lys Lys
130 135 140

Leu Lys Asp Leu Met Leu Asp Phe Gln Ala Leu Arg Gln Arg Ile Met
145 150 155 160

Ser Glu Tyr Lys Asp Thr Val Glu Arg Arg Tyr Tyr Thr Leu Thr Gly
165 170 175

Glu Val Pro Glu Glu Glu Val Ile Glu Arg Ile Ile Ser Glu Gly Arg
180 185 190

ES 2 623 545 T3

Ser Glu Glu Leu Leu Cys Ala Ala Val Ala Glu His Gly Lys Gly Ala
195 200 205

Val Leu Ala Thr Val His Glu Ile Gln Asp Arg His Asp Ala Ala Arg
210 215 220

Glu Val Glu Arg Ser Leu Leu Glu Leu His Gln Val Phe Leu Asp Met
225 230 235 240

Ala Val Val Val Glu Ser Gln Gly Glu Gln Leu Asp Asp Ile Glu Arg
245 250 255

His Val Asn Ser Ala Thr Thr Tyr Val Gln Gly Gly Asn Lys Glu Leu
260 265 270

Arg Lys Ala Arg Glu His Gln Arg Ser Ser Arg Lys Trp Leu Cys Ile
275 280 285

Gly Ile Ile Ile Leu Leu Leu Leu Val Leu Leu Val Ile Val Pro Ile
290 295 300

Ala Thr Ser Phe Lys Arg Ser
305 310

<210> 48
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<213> Oryza sativa

<400> 48
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Ala Ala Pro Ala Arg Ala Val Thr Thr Leu Ser Leu Met Pro Gly Ala
35 40 45

Glu Val Val Val Glu Glu Glu Glu Arg Arg Glu Val Gly Glu Glu Glu
50 55 60

Ala Gly Pro Ala Thr Ala Pro Ala Ala Pro Leu Thr Ile Phe Tyr Gly
65 70 75 80

Gly Arg Met Val Val Phe Glu Asp Phe Pro Ala Asp Lys Ala Ala Glu
85 90 95

Val Met Arg Met Ala Ser Ser Gly Met Ala Ala Ala Pro Ala Gln Arg
100 105 110

ES 2 623 545 T3

Glu Gly Ala Ala Leu Ala Asp Met Pro Ile Met Arg Lys Ala Ser Leu
115 120 125

Gln Arg Phe Phe Ala Lys Arg Lys Asp Arg Leu Ala Ala Thr Thr Pro
130 135 140

Tyr Ala Arg Pro Ser Pro Ala Glu Thr Lys Ala Ser Glu Pro Glu Glu
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Lys Lys Thr Pro Thr Ser Trp Leu Asp Leu Ala Ala Ser Ala Ser Ala
165 170 175

Ala Ala Arg Arg Asp Ser Leu Thr Ile Ala Leu
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<210> 49

<211> 1133

<212> PRT

<213> Oryza sativa

<400> 49

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Gly Phe Tyr Phe Asn Met Lys Tyr Phe Glu Asp Glu Val Ile Asn Gly
35 40 45

Asn Trp Asp Glu Val Glu Arg Tyr Leu Gly Gly Phe Thr Lys Val Asp
50 55 60

Asp Asn Arg Tyr Ser Met Lys Ile Phe Phe Glu Ile Arg Lys Gln Lys
65 70 75 80

Tyr Leu Glu Ala Leu Asp Lys His Asp Arg Ser Lys Ala Val Glu Ile
85 90 95

Leu Val Lys Asp Leu Lys Val Phe Ala Ser Phe Asn Glu Glu Leu Phe
100 105 110

Lys Glu Ile Thr Gln Leu Leu Thr Leu Glu Asn Phe Arg Glu Asn Glu
115 120 125

Gln Leu Ser Lys Tyr Gly Asp Thr Lys Ser Ala Arg Ala Ile Met Leu
130 135 140

ES 2 623 545 T3

Val	Glu	Leu	Lys	Lys	Leu	Ile	Glu	Ala	Asn	Pro	Leu	Phe	Arg	Asp	Lys	
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Gln	Ser	Leu	Asn	Trp	Gln	His	Gln	Leu	Cys	Lys	Asn	Pro	Arg	Pro	Asn	
			180					185					190			
Pro	Asp	Ile	Lys	Thr	Leu	Phe	Val	Asp	His	Ser	Cys	Gly	Gln	Pro	Asn	
		195					200					205				
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	210					215					220					
Pro	Lys	Pro	Gly	Gly	Phe	Pro	Pro	Leu	Gly	Ala	His	Ala	Pro	Phe	Gln	
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Pro	Ala	Pro	Thr	Pro	Val	Pro	Pro	Leu	Ala	Gly	Trp	Met	Ser	Asn	Pro	
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Pro	Ala	Val	Thr	His	Pro	Ala	Val	Ser	Gly	Gly	Ala	Ile	Gly	Phe	Gly	
			260					265					270			
Thr	Pro	Thr	Asn	Pro	Ala	Ala	Ile	Leu	Lys	His	Pro	Arg	Thr	Pro	Thr	
		275					280					285				
Thr	Ala	Asn	Pro	Ser	Met	Asp	Tyr	Pro	Ser	Gly	Asp	Ser	Asp	His	Val	
	290					295					300					
Ser	Lys	Arg	Thr	Arg	Pro	Val	Gly	Met	Ser	Glu	Glu	Val	Asn	Leu	Pro	
305					310					315				320		
Val	Asn	Met	Leu	Pro	Val	Thr	Tyr	Pro	Gln	Ser	His	Ser	Tyr	Pro	Gln	
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Arg	Leu	Val	Leu	Arg	Asn	Phe	Lys	Val	Trp	Asp	Leu	Thr	Lys	Cys	Ser	
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Met	Ala	Leu	Gln	Ala	Ser	Leu	Val	Lys	Asp	Pro	Thr	Val	Ser	Val	Asn	

ES 2 623 545 T3

405										410					415				
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Arg	His	Ile	Val	Gln	Ile	Tyr	Ser	Tyr	His	Gly	Gly	Asp	Asp	Ile	Arg				
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Gln	His	Leu	Glu	Ile	Asp	Ala	His	Val	Gly	Gly	Val	Asn	Asp	Ile	Ala				
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Phe	Ala	His	Pro	Asn	Lys	Gln	Leu	Cys	Ile	Ile	Thr	Cys	Gly	Asp	Asp				
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Phe	Glu	Gly	His	Glu	Ala	Pro	Val	Tyr	Ser	Val	Cys	Pro	His	Tyr	Lys				
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Glu	Asn	Ile	Gln	Phe	Ile	Phe	Ser	Thr	Ala	Leu	Asp	Gly	Lys	Ile	Lys				
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Ala	Trp	Leu	Tyr	Asp	Asn	Leu	Gly	Ser	Arg	Val	Asp	Tyr	Asp	Ala	Pro				
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Gly	His	Trp	Cys	Thr	Thr	Met	Ala	Tyr	Ser	Ala	Asp	Gly	Ser	Arg	Leu				
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Glu	Asn	Gly	Ile	Lys	Ile	Leu	Ala	Asn	Ala	Asp	Gly	Val	Arg	Leu	Leu				
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ES 2 623 545 T3

Arg Thr Leu Glu Asn Arg Ser Phe Asp Ala Ser Arg Ser Ala Ser Glu
 675 680 685
 Thr Val Thr Lys Pro Leu Met Asn Pro Leu Thr Ala Ala Ala Ala Ala
 690 695 700
 Ala Ala Ser Ala Ala Ala Ala Gly Thr Ser Ser Gly Asn Ala Ala Pro
 705 710 715 720
 Pro Ala Ile Thr Ala Leu Asn Gly Asp Ser Arg Ser Leu Val Asp Val
 725 730 735
 Lys Pro Arg Ile Ala Asp Glu Pro Leu Asp Lys Ser Lys Val Trp Lys
 740 745 750
 Leu Met Glu Ile Thr Glu Ser Ser Gln Cys Arg Ser Leu Lys Leu Thr
 755 760 765
 Asp Asn Met Arg Thr Ser Lys Ile Ser Arg Leu Ile Tyr Thr Asn Ser
 770 775 780
 Gly Val Ala Ile Leu Ala Leu Ala Ser Asn Ala Val His Leu Leu Trp
 785 790 795 800
 Lys Trp Pro Arg Asn Asp Arg Asn Ser Ser Gly Lys Ala Thr Ala Ser
 805 810 815
 Val Ser Pro Gln Leu Trp Gln Pro Pro Ser Gly Ile Leu Met Thr Asn
 820 825 830
 Asp Ile Thr Asp Asn Pro Glu Glu Ala Val His Cys Phe Ala Leu Ser
 835 840 845
 Lys Asn Asp Ser Tyr Val Met Ser Ala Ser Gly Gly Lys Ile Ser Leu
 850 855 860
 Phe Asn Met Met Thr Phe Lys Thr Met Thr Thr Phe Met Pro Pro Pro
 865 870 875 880
 Pro Ala Ala Thr Phe Leu Ala Phe His Pro Gln Asp Asn Asn Ile Ile
 885 890 895
 Ala Ile Gly Met Asp Asp Ser Thr Ile Gln Ile Tyr Asn Val Arg Ile
 900 905 910
 Asp Glu Val Lys Ser Lys Leu Arg Gly His Ser Lys Lys Ile Thr Gly
 915 920 925

ES 2 623 545 T3

Leu Ala Phe Ser Asn Val Leu Asn Val Leu Val Ser Ser Gly Ala Asp
930 935 940

Ala Gln Ile Cys Val Trp Ser Thr Asp Gly Trp Asp Lys Leu Lys Ser
945 950 955 960

Arg Met Leu Gln Ile Pro Ser Ser Arg Pro Ser Ser Ile Ile Leu Asp
965 970 975

Thr Arg Val Gln Phe His Gln Asp Gln Leu His Phe Leu Val Val His
980 985 990

Glu Thr Gln Ile Ala Ile Tyr Glu Thr Thr Lys Leu Glu Pro Val Lys
995 1000 1005

Gln Trp Pro Val Arg Glu Asn Ser Ser Pro Ile Thr His Ala Met
1010 1015 1020

Phe Ser Cys Asp Ser Gln Leu Ile Tyr Ala Ser Phe Leu Asp Ala
1025 1030 1035

Thr Val Cys Ile Phe Asn Ala Ser Ser Leu Arg Leu Gln Cys Arg
1040 1045 1050

Ile Leu Pro Ala Ser Tyr Leu Pro Gln Asn Ile Ser Ser Asn Val
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Tyr Pro Val Val Val Ala Ala His Pro Ser Glu Ala Asn Gln Phe
1070 1075 1080

Ala Leu Gly Leu Thr Asp Gly Gly Val Tyr Val Leu Glu Pro Leu
1085 1090 1095

Glu Ser Glu Arg Lys Trp Gly Asn Pro Pro Pro Ala Glu Asn Gly
1100 1105 1110

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<211> 2511

<212> DNA

<213> Oryza sativa

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<212> DNA

<213> Oryza sativa

5

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	attttgtcca acaagtctgg caatttcgcc aagcaaacga ccgcggtat tgctaagttc	420
	gtagttggcg gagttgtaac gtatgaaggT gagaatggg caaaacatcg gagaattctc	480

ES 2 623 545 T3

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ES 2 623 545 T3

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 <212> DNA
 <213> Oryza sativa

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<212> DNA
<213> Oryza sativa

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<212> DNA
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<212> DNA
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<212> DNA
<213> Oryza sativa

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 <211> 933

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10 <213> Oryza sativa

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20 <213> Oryza sativa

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<212> DNA
15 <213> Oryza sativa

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<210> 76
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 <212> DNA
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<213> Oryza sativa

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<213> Oryza sativa

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<210> 91
<211> 4080
<212> DNA
<213> Oryza sativa

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 <213> Oryza sativa

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<211> 1014
<212> DNA
<213> Oryza sativa

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 <213> Oryza sativa

<400> 99

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		20					25					30			
Gly	Ala	Gly	Gly	Arg	Gly	Gly	Gly	Arg	Arg	Cys	Trp	Ala	Glu	Ala	Ala
		35					40					45			
Glu	Ala	Ala	His	Met	Ala	Ala	Ala	Ala	Ala	His	Arg	Ala	Ala	Ala	Val
		50				55					60				
His	Arg	Ala	Ala	Cys	Gly	Ser	Ser	Thr	Val	Ala	Val	Gly	Leu	Arg	Glu
65					70					75					80
Leu	His	Arg	Arg	Arg	Leu	Cys	Ser	Thr	Cys	Thr	Gly	Asp	Gly	Asp	Gly
				85					90					95	
Asp	Arg	Met	Leu	Met	Gln	Arg	Asn	Asp	Ser	Ser	Asn	Ser	Lys	Trp	Met
			100					105					110		
Leu	Ser	Arg	Arg	Ala	Phe	Ser	Pro	Phe	His	Val	Ser	Ala	Lys	Phe	Ala
			115				120					125			
Trp	Glu	Val	Gln	Glu	Ser	Leu	Leu	Asp	Gly	Gly	Ser	Thr	Trp	Phe	Cys
	130					135					140				
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 <212> PRT
 <213> Oryza sativa

ES 2 623 545 T3

<400> 100

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20 25 30

Ala Gly Gly Ala Pro Tyr Met Gly Ile Asp Glu Leu Arg Arg Tyr Leu
35 40 45

Ala Ala Ser Gly Glu Ala His Val Asp Ala Asp Thr Ala Glu Arg Ile
50 55 60

Ile Asp Arg Val Leu Gln Glu Arg Ser Arg Thr Pro Arg Phe Gly Lys
65 70 75 80

Pro Ser Leu Thr Ile Asp Asp Phe Gln Tyr Phe Leu Phe Ser Glu Asp
85 90 95

Leu Asn Pro Pro Ile Cys His Ser Lys Glu Glu Ser Phe Asp Ala Met
100 105 110

Glu Lys Leu Glu Val
115

<210> 101

<211> 490

<212> PRT

<213> Oryza sativa

<400> 101

Met Gln Val His His Asp Met Asn Ala Pro Leu Ser His Tyr Phe Ile
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Tyr Thr Gly His Asn Ser Tyr Leu Thr Gly Asn Gln Leu Ser Ser Asp
20 25 30

Cys Ser Asp Ile Pro Ile Ile Lys Ala Leu Gln Ile Gly Val Arg Val
35 40 45

Ile Glu Leu Asp Met Trp Pro Asn Ser Ser Lys Asp Asp Val Asp Ile
50 55 60

Leu His Gly Arg Thr Leu Thr Ala Pro Val Ser Leu Ile Lys Cys Leu

ES 2 623 545 T3

65		70		75		80
Lys Ser Ile Lys Glu Tyr Ala Phe Val Ala Ser Pro Tyr Pro Val Ile	85	90	95			
Ile Thr Leu Glu Asp His Leu Thr Ser Asp Leu Gln Ala Lys Val Ala	100	105	110			
Lys Met Val Leu Glu Val Phe Gly Asp Thr Leu Tyr Tyr Pro Glu Ser	115	120	125			
Lys His Leu Gln Glu Phe Pro Ser Pro Glu Ala Leu Arg Gly Arg Val	130	135	140			
Ile Leu Ser Thr Lys Pro Pro Lys Glu Tyr Leu Glu Ser Lys Gly Gly	145	150	155	160		
Thr Met Lys Asp Arg Asp Ile Glu Pro Gln Phe Ser Lys Gly Gln Asn	165	170	175			
Glu Glu Ala Val Trp Gly Thr Glu Val Pro Asp Ile Gln Asp Glu Met	180	185	190			
Gln Thr Ala Asp Lys Gln His Glu Asn Asp Ile Leu Tyr Thr Gln Arg	195	200	205			
Asp Val Glu Glu Asp Asp Glu Lys Lys Met Cys Gln His His Pro Leu	210	215	220			
Glu Tyr Lys His Leu Ile Thr Ile Lys Ala Gly Lys Pro Lys Gly Ala	225	230	235	240		
Val Val Asp Ala Leu Lys Gly Asp Pro Asp Lys Val Arg Arg Leu Ser	245	250	255			
Leu Ser Glu Gln Glu Leu Ala Lys Val Ala Ala His His Gly Arg Asn	260	265	270			
Ile Val Ser Phe Thr His Lys Asn Leu Leu Arg Ile Tyr Pro Lys Gly	275	280	285			
Thr Arg Phe Asn Ser Ser Asn Tyr Asn Pro Phe Leu Gly Trp Val His	290	295	300			
Gly Ala Gln Met Val Ala Phe Asn Met Gln Gly Tyr Gly Arg Ser Leu	305	310	315	320		
Trp Leu Met His Gly Phe Tyr Lys Ala Asn Gly Gly Cys Gly Tyr Val	325	330	335			

ES 2 623 545 T3

Lys Lys Pro Asp Phe Met Met Gln Thr Cys Pro Asp Gly Asn Val Phe
340 345 350

Asp Pro Lys Ala Asp Leu Pro Val Lys Lys Thr Leu Lys Val Lys Val
355 360 365

Tyr Met Gly Glu Gly Trp Gln Ser Asp Phe Lys Gln Thr Tyr Phe Asp
370 375 380

Thr Tyr Ser Pro Pro Asp Phe Tyr Ala Lys Val Gly Ile Ala Gly Val
385 390 395 400

Pro Ser Asp Ser Val Met Gln Lys Thr Lys Ala Val Glu Asp Ser Trp
405 410 415

Val Pro Val Trp Glu Glu Glu Phe Val Phe Pro Leu Thr Val Pro Glu
420 425 430

Ile Ala Leu Leu Arg Val Glu Val His Glu Tyr Asp Val Ser Glu Asp
435 440 445

Asp Phe Gly Gly Gln Thr Ala Leu Pro Val Ser Glu Leu Arg Pro Gly
450 455 460

Ile Arg Thr Val Pro Leu Phe Asp His Lys Gly Leu Lys Phe Lys Ser
465 470 475 480

Val Lys Leu Leu Met Arg Phe Glu Phe Val
485 490

<210> 102

<211> 211

<212> PRT

<213> Oryza sativa

<400> 102

Met Ala Met Gly Ala Ala Ala Ala Pro Trp Tyr Gly Ala Ile Gly Gly
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Gly Gly Ser Arg Arg Ala Arg Val Arg Ala Gln Ala Ala Ala Pro Trp
20 25 30

Ala Gly Gly Ala Glu Glu Leu Val Arg Ser Gly Ala Val Arg Ala Val
35 40 45

Arg Ala Arg Glu Ala Ala Gly Ala Met Ser Ala Glu Gly Phe Arg Leu
50 55 60

ES 2 623 545 T3

Leu Asp Val Arg Pro Glu Trp Glu Arg Ala Arg Ala Ala Val Arg Gly
65 70 75 80

Ser Ala His Ala Pro Leu Phe Val Gly Asp Asp Asp Thr Gly Pro Val
85 90 95

Thr Leu Leu Lys Lys Trp Val His Phe Gly Tyr Ile Gly Leu Trp Thr
100 105 110

Gly Gln Ser Phe Thr Lys Met Asn Asp Arg Phe Leu Asp Asp Val Ala
115 120 125

Ala Ala Ala Gly Glu Gly Lys Asp Ala Lys Leu Leu Val Ala Cys Gly
130 135 140

Glu Gly Leu Arg Ser Leu Ile Ala Val Arg Met Leu Tyr Asp Asp Gly
145 150 155 160

Tyr Lys Asn Leu Ala Trp Leu Ala Gly Gly Phe Ser Lys Cys Val Asp
165 170 175

Gly Asp Phe Ala Asp Val Glu Gly Glu Ser Lys Leu Gln Tyr Ala Thr
180 185 190

Val Gly Gly Val Ser Tyr Ile Phe Leu Gln Ile Leu Leu Leu Leu Arg
195 200 205

Val Val Lys
210

<210> 103
<211> 315
<212> PRT
<213> Oryza sativa

<400> 103
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Phe Arg Phe Trp Pro Leu Asp Ala Asp Pro Ala Ala Ser Pro Ser Cys
20 25 30

Ala Asp Glu Leu Phe Ser Gly Gly Val Leu Leu Pro Leu Gln Pro Leu
35 40 45

Pro Tyr Pro Arg Arg Asp Ala Asp Leu Ser Met Ser Leu Ala Val Ala
50 55 60

Asp Asp Asp Asp Asp Glu Asp Glu Glu Glu Glu Glu Val Gln Pro Gly
65 70 75 80

ES 2 623 545 T3

Ala Ala Val Ala Ser Arg Ala Pro Pro Thr Ala Ala Val Ala Ala Ser
85 90 95

Gly Gly Gly Gly Gly Gly Ser Lys Arg Trp Thr Asp Ile Phe Ala Lys
100 105 110

Lys Gln Gln Gln Pro Ala Ala Glu Glu Lys Glu Lys Asp Gln Pro Thr
115 120 125

Arg Arg Arg Arg Pro Ala Gly Gly Gly Gly Ser Glu Leu Asn Ile
130 135 140

Asn Ile Trp Pro Phe Ser Arg Ser Arg Ser Ala Gly Gly Gly Gly Val
145 150 155 160

Gly Ser Ser Lys Pro Arg Pro Pro Pro Arg Lys Ala Ser Ser Ala Pro
165 170 175

Cys Ser Arg Ser Asn Ser Arg Gly Glu Ala Ala Ala Val Ala Ser Ser
180 185 190

Leu Pro Pro Pro Pro Arg Arg Trp Ala Ala Ser Pro Gly Arg Ala Gly
195 200 205

Gly Gly Val Pro Val Gly Arg Ser Ser Pro Val Trp Gln Ile Arg Arg
210 215 220

Pro Pro Ser Pro Ala Ala Lys His Ala Ala Ala Asp Arg Arg Pro Pro
225 230 235 240

His His Lys Asp Lys Pro Thr Gly Gly Ala Lys Lys Pro His Thr Thr
245 250 255

Ser Ala Thr Gly Gly Gly Gly Ile Arg Gly Ile Asn Leu Ser Ile Asn
260 265 270

Ser Cys Ile Gly Tyr Arg His Gln Val Ser Cys Arg Arg Ala Asp Ala
275 280 285

Gly Val Ala Arg Ala Ser Ala Gly Gly Gly Gly Gly Gly Gly Leu Phe
290 295 300

Gly Ile Lys Gly Phe Phe Ser Lys Lys Val His
305 310 315

<210> 104
<211> 306
<212> PRT
<213> Oryza sativa

ES 2 623 545 T3

<400> 104

Met Gln Gln Lys Pro Ala Ala Glu Ala Met Glu Glu Glu Leu Lys Gly
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Glu Ala Val Gly Pro Arg Arg Pro Gly Leu Gly Leu Trp Leu Ala Ala
20 25 30

Arg Arg Arg Leu Ala Pro Asp Asp Pro Phe Phe Ala Ala Gly Asp Met
35 40 45

Glu Arg Glu Leu Leu Ala Lys Gln Val Ala Leu Asp Leu Ser Glu Asp
50 55 60

Glu Arg Tyr Gln Leu Glu Arg Met Glu Val Ala Ser Ala Asn Ala Leu
65 70 75 80

Leu Cys Pro Ile Ser Gly Cys Gly Ala His Leu Asp Cys Leu Glu Asn
85 90 95

Phe Glu Asp His Tyr Arg Thr Arg His Thr Ala Ser Cys Ser Val Cys
100 105 110

Trp Arg Val Tyr Pro Thr Ser Arg Leu Leu Ser Ile His Ile Ser Glu
115 120 125

Ala His Asp Ser Phe Phe Gln Ala Lys Val Ala Arg Gly Phe Pro Met
130 135 140

Tyr Glu Cys Leu Val Glu Gly Cys Gly Val Lys Leu Lys Ser Tyr Lys
145 150 155 160

Ser Arg Gln Gln His Leu Leu Asp Lys His Gln Phe Pro Lys Ser Phe
165 170 175

Glu Phe Phe Lys Lys Ala Arg Pro Ser Gln Arg Gln Arg Asn Lys Asn
180 185 190

Gln Lys Gln Arg Gln Thr Val His Lys Gly Asp Glu Thr Ser Glu Thr
195 200 205

Leu Met Asp Val Asp Gly Lys Lys Ser Ser Arg Tyr Met Asn Ser Arg
210 215 220

Tyr Arg Pro Lys Gln His Asp Gly Lys Glu Ser Lys Glu Asn Glu His
225 230 235 240

Ser Ser Cys Lys Glu Ala Lys Asn Asn Glu Met Glu Val Asp Lys Gln

ES 2 623 545 T3

245 250 255
 Val Asp Glu Leu Ala Ser Ala Val Ser Arg Leu Ser Thr Ala Asp Ser
 260 265 270
 Thr Pro Ser Ser Ile Ser Phe Gly His Arg Arg Ser Arg Gly Leu Ala
 275 280 285
 Phe Val Pro Arg Ser Ile Arg Gln Asn Lys Gln Val Ser Gln Thr Glu
 290 295 300
 Pro Lys
 305
 5 <210> 105
 <211> 328
 <212> PRT
 <213> Oryza sativa
 <400> 105
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 1 5 10 15
 Ala Leu Tyr Asp Arg Gln Ile Arg Val Trp Gly Val Asp Ala Gln Lys
 20 25 30
 Arg Leu Ser Lys Ala His Val Leu Val Cys Gly Met Asn Gly Thr Thr
 35 40 45
 Thr Glu Phe Cys Lys Asn Ile Val Leu Ala Gly Val Gly Ser Leu Ser
 50 55 60
 Leu Met Asp Asp His Leu Val Thr Glu Asp Asp Leu Asn Ala Asn Phe
 65 70 75 80
 Leu Ile Pro His Asp Glu Ser Ile Tyr Gly Gly Arg Ser Arg Ala Glu
 85 90 95
 Val Cys Cys Glu Ser Leu Lys Asp Phe Asn Pro Met Val Arg Val Ala
 100 105 110
 Val Glu Lys Gly Asp Pro Ser Leu Ile Asp Gly Glu Phe Leu Asp Lys
 115 120 125
 Phe Asp Ile Ile Val Val Ser Cys Ala Pro Ile Lys Thr Lys Leu Leu
 130 135 140
 10 Ile Asn Asp Asn Cys Arg Lys Arg Ser Lys His Ile Ala Phe Tyr Ala
 145 150 155 160

ES 2 623 545 T3

Ile Glu Cys Lys Asp Ser Cys Gly Glu Ile Phe Val Asp Leu Gln Asn
165 170 175

His Ser Tyr Val Gln Lys Val Gly Gly Glu Pro Lys Pro Lys Glu Leu
180 185 190

Ala Tyr Pro Ser Leu Gln Glu Ala Ile Ser Val Pro Trp Lys Asn Leu
195 200 205

Pro Arg Lys Thr Thr Lys Leu Tyr Phe Ala Met Arg Val Leu Glu Asn
210 215 220

Tyr Glu Ser Ser Glu Gly Arg Asn Ala Cys Glu Ala Ser Leu Ser Asp
225 230 235 240

Arg Pro Ala Val Leu Ala Leu Arg Lys Asp Met Cys Asp Lys Met Ser
245 250 255

Leu Ser Glu Ser Gln Ile Pro Thr Ala Leu Leu Glu Arg Leu Leu Ala
260 265 270

Ala Gly Lys Lys Gln His Pro Pro Val Cys Ala Ile Leu Gly Gly Ile
275 280 285

Leu Gly Gln Glu Val Ile Lys Ser Ile Ser Gly Lys Gly Asp Pro Ile
290 295 300

Lys Asn Phe Phe Tyr Tyr Asp Ala Ala Asp Gly Lys Gly Ile Ala Glu
305 310 315 320

Asp Ile Pro Pro Leu Ser Ser Asp
325

<210> 106

<211> 301

<212> PRT

<213> Oryza sativa

<400> 106

Met Ala Met Pro Leu Pro Pro Pro Pro Pro Arg Pro Pro Leu Gly
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Arg Gly Arg Leu Val Gly Val Gly Pro Ala Pro Ala Pro Ala Thr Ala
20 25 30

Ser Gln Ser Asn Arg Pro Val Pro Pro Leu Gln Leu Pro Arg Cys Arg
35 40 45

Cys His Arg Ser Glu Gly Pro Trp Arg Thr Thr Ala Ala Ala Asn Gly

ES 2 623 545 T3

50		55		60
Arg Arg Arg Trp Trp Ser Asp Glu Asp Met Glu Glu Glu Asp Asp Glu				
65		70		75
				80
Glu Gly Tyr Gly Tyr Asp Asp Gly Gly Ala Pro Gly Gly Ser Ala Gln				
		85		90
				95
Glu Leu Phe Gly Glu Pro Trp Phe Ser Lys Leu Phe Arg Ala Tyr Gly				
		100		105
				110
Tyr Val Leu Pro Leu Leu Leu Ala Ser Met Leu Val Ala Thr Gly Pro				
		115		120
				125
Arg Ala Phe Leu Met Ala Met Ala Leu Pro Leu Ala Gln Ser Ala Ile				
		130		135
				140
Ser Trp Val Val Ser Phe Phe Thr Thr Arg Ser Arg Arg Gln Gln Glu				
		145		150
				155
Glu Glu Glu Ser Tyr Gly Tyr Asp Tyr Asp Asp Asp Pro Ala Phe Gln				
		165		170
				175
Arg Arg Glu Glu Asp Asp Asp Asp Gly Asp Tyr Tyr Asp Ala Gly Ala				
		180		185
				190
Trp Gln Trp Arg Ser Arg Ser His Gln Gln Ser Thr Glu Ser Gly Ser				
		195		200
				205
Gly Phe Gly Gly Trp Asp Asp Leu Leu Tyr Asp Asp Glu Glu Lys Lys				
		210		215
				220
Glu Gln Glu Ser Ser Gly Lys Lys Arg Thr Pro Pro Glu Pro Asp Thr				
		225		230
				235
Ala Ala Ala Ala Ala Ala Ser Asp Leu Gly Leu Gly Leu Arg Ala Arg				
		245		250
				255
Arg Gly Pro Arg Arg Ser Asn Gly Gly Met Ser Arg Gly Arg Ser Ser				
		260		265
				270
Ser Ser Met Arg Tyr Asn Gln Ala Pro Leu Leu Thr Arg Leu Leu Val				
		275		280
				285
Ala Leu Phe Pro Phe Leu Gly Ser Trp Phe Arg Ile Leu				
		290		295
				300

<210> 107

<211> 406

<212> PRT

<213> Oryza sativa

ES 2 623 545 T3

<400> 107

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Met Arg Gly Ser Leu Glu Val His Ala Ile Gly Arg His Ala Ala Ser
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Pro Cys Ala Leu Arg Leu Lys Ala Leu Pro Ala Leu Asp Met Met Arg
          20          25          30

Tyr Gln Arg Leu Ser Pro Asp Cys Leu Pro Leu Ala Asn Gly Gly Gly
          35          40          45

Gly Gly Ser Gly Ser Val Thr Arg Lys Pro Ala Ser Arg Ser Cys Lys
50          55          60

Asp Asp Asp Gly Gly Met Ala Val Ala Ala Asp Ser Ser Arg Leu Ser
65          70          75          80

Ser Tyr Leu Pro Ser Ser Gln Leu Asp Ser Lys Pro Leu Arg Ala Arg
          85          90          95

Ala Pro Gln Pro Ser Ser Ser Ser Ala Ala Ala Trp Ser Pro Ala Arg
          100          105          110

Asp His Ala His Ala His His Asn His His His His His His Pro Ser
          115          120          125

Asp Ser Ser Asp Thr Ala Ser Pro Ser Ser Asn Gly Ala Gly Thr Gly
130          135          140

Gly Asp Val Leu Leu Gln Trp Gly His Asn Lys Arg Ser Arg Cys Arg
145          150          155          160

Arg Asp Ala Ser Ser Ser Ala Asn Ala Ala Pro Ser Ser Ser Gln Arg
          165          170          175

Arg Gln Thr Ala Ser Ala Ala Gly Lys Ile Leu Arg Arg Ser Ser Ala
          180          185          190

Pro Ala Glu Lys Leu Met Pro Pro Pro Pro Pro Ser Thr Thr Thr Gly
195          200          205

Ser Tyr Thr Arg Gly Ser Asn Leu Arg Ser Ala Ser Ser Phe Pro Thr
210          215          220

Arg Ser Ala Ala Ala Ala Ala Val Gly Asp Ala His His His Arg Ser
225          230          235          240

```

Ala Val Glu Glu Arg Ser Gly Gly Gly Tyr Lys Arg Ser Pro Asp Lys
245 250 255

Ala His Lys Ser Ala Leu Asp Ala Ala Leu His Met Asp Ser Lys Asn
260 265 270

Asn His His His His His His Asp Ser Ser Val Thr Ala Asn Gly Gly
275 280 285

Ala Gly Ala Gly Glu Lys Ile Gly Ser Glu Arg Phe Glu Leu Pro Arg
290 295 300

Ile Tyr Ile Ser Leu Ser Arg Lys Glu Lys Glu Asp Asp Phe Leu Ile
305 310 315 320

Met Lys Gly Thr Lys Leu Pro Gln Arg Pro Lys Lys Arg Ala Lys Asn
325 330 335

Val Asp Lys Thr Leu Gln Tyr Val Phe Pro Gly Met Trp Leu Ser Asp
340 345 350

Leu Thr Arg Gly Arg Tyr Glu Val Arg Glu Lys Lys Cys Val Lys Lys
355 360 365

Val Tyr Ser Thr Leu His Leu Ala Phe Ser Val His Ala Phe Cys Val
370 375 380

Phe Leu Gln Thr Arg Arg Gly Lys Leu Pro Arg Phe Arg Ala Ser Val
385 390 395 400

Thr Gln Ile Gly Trp Val
405

<210> 108

<211> 203

<212> PRT

<213> Oryza sativa

<400> 108

Met Ala Thr Thr Ala Ser Leu Leu Pro Pro Leu Leu Pro Ala Pro Ser
1 5 10 15

Ser Ser Pro Arg His Leu His Pro Ser Pro Arg His Leu Arg Pro Leu
20 25 30

Pro Pro Ile Arg Leu Leu Arg Ala Ala Arg Arg Arg His Pro Asp Ala
35 40 45

Val Val Val Val Pro Asp Ala Arg Pro Trp Val Gly Asp Leu Ser Gly
50 55 60

ES 2 623 545 T3

Ala Ala Ala Ser Tyr Arg Asp Gly Arg Glu Glu Asp Asp Asp Ala
65 70 75 80

Gly Glu Glu Asp Asp Glu Asn Asp Asp Asp Glu Asp Arg Ser Leu
85 90 95

Asp Leu Leu Val Arg Phe Leu His Ser Val Phe Arg Lys Val Ser Arg
100 105 110

Arg Ala Arg Arg Ala Ala Arg Ser Val Leu Pro Pro Ser Val Pro Ala
115 120 125

Glu Leu Val Lys Phe Ser Val Asn Gly Val Leu Val Leu Thr Phe Leu
130 135 140

Trp Val Leu Lys Gly Leu Leu Glu Val Val Cys Thr Phe Gly Ser Met
145 150 155 160

Val Phe Val Thr Ile Leu Leu Val Arg Gly Ile Trp Ser Gly Val Thr
165 170 175

Tyr Ile Arg Glu Asn Arg Tyr Ser Tyr Ile Arg Gln Ile Asp Asn Asp
180 185 190

Asp Asn Arg Trp Ser Arg Val Gln Thr Ala Gly
195 200

<210> 109

<211> 809

<212> PRT

<213> Oryza sativa

<400> 109

Met Lys Leu Arg Leu Arg Ser Met Asp Gln Arg Gly Gly Ala Gly Gly
1 5 10 15

Ala Ala Glu Thr His Arg Val Gln Leu Pro Asp Thr Ala Thr Leu Ser
20 25 30

Asp Val Lys Ala Phe Leu Ala Thr Lys Leu Ser Ala Ala Gln Pro Val
35 40 45

Pro Ala Glu Ser Val Arg Leu Thr Leu Asn Arg Ser Glu Glu Leu Leu
50 55 60

Thr Pro Asp Pro Ser Ala Thr Leu Pro Ala Leu Gly Leu Ala Ser Gly
65 70 75 80

ES 2 623 545 T3

Asp Leu Leu Tyr Phe Thr Leu Ser Pro Leu Pro Ser Pro Ser Pro Pro
 85 90 95
 Pro Gln Pro Gln Pro Gln Ala Gln Pro Leu Pro Arg Asn Pro Asn Pro
 100 105 110
 Asp Val Pro Ser Ile Ala Gly Ala Ala Asp Pro Thr Lys Ser Pro Val
 115 120 125
 Glu Ser Gly Ser Ser Ser Ser Met Pro Gln Ala Leu Cys Thr Asn Pro
 130 135 140
 Gly Leu Pro Val Ala Ser Asp Pro His His Pro Pro Pro Asp Val Val
 145 150 155 160
 Met Ala Glu Ala Phe Ala Val Ile Lys Ser Lys Ser Ser Leu Val Val
 165 170 175
 Gly Asp Thr Arg Glu Met Glu Asn Val Gly Gly Ala Asp Gly Thr Val
 180 185 190
 Ile Cys Arg Leu Val Val Ala Leu His Ala Ala Leu Leu Asp Ala Gly
 195 200 205
 Phe Leu Tyr Ala Asn Pro Val Gly Ser Cys Leu Gln Leu Pro Gln Asn
 210 215 220
 Trp Ala Ser Gly Ser Phe Val Pro Val Ser Met Lys Tyr Thr Leu Pro
 225 230 235 240
 Glu Leu Val Glu Ala Leu Pro Val Val Glu Glu Gly Met Val Ala Val
 245 250 255
 Leu Asn Tyr Ser Leu Met Gly Asn Phe Met Met Val Tyr Gly His Val
 260 265 270
 Pro Gly Ala Thr Ser Gly Val Arg Arg Leu Cys Leu Glu Leu Pro Glu
 275 280 285
 Leu Ala Pro Leu Leu Tyr Leu Asp Ser Asp Glu Val Ser Thr Ala Glu
 290 295 300
 Glu Arg Glu Ile His Glu Leu Trp Arg Val Leu Lys Asp Glu Met Cys
 305 310 315 320
 Leu Pro Leu Met Ile Ser Leu Cys Gln Leu Asn Asn Leu Ser Leu Pro
 325 330 335
 Pro Cys Leu Met Ala Leu Pro Gly Asp Val Lys Ala Lys Val Leu Glu

ES 2 623 545 T3

340	345	350
Phe Val Pro Gly Val Asp Leu Ala Arg Val Gln Cys Thr Cys Lys Glu 355 360 365		
Leu Arg Asp Leu Ala Ala Asp Asp Asn Leu Trp Lys Lys Lys Cys Glu 370 375 380		
Met Glu Phe Asn Thr Gln Asp Thr Cys Gly Cys Met Met Cys Lys Cys 385 390 395 400		
Ile Tyr Ser Asp Gln Arg Lys Asp Ile Val Leu Ala Asp Lys Tyr Thr 405 410 415		
Cys Gly Asn Tyr Met Gln Lys Pro Val Thr Gln Pro Gly Arg Trp Leu 420 425 430		
Ile Ile Leu Val Tyr His Ser Leu Leu Cys Gln Tyr Ile Thr Ile Gly 435 440 445		
Leu Ser Leu Leu Trp Tyr His Leu Val Asp Leu Val Gln Asp Ala Pro 450 455 460		
Ala Ala Gly Ile His Phe Asp Cys Ile Ile Pro Leu Pro Ile Asn Pro 465 470 475 480		
Tyr Gln Leu Pro Pro Ser Ala Gly Ala Cys Cys Ser Thr Thr Gln Ala 485 490 495		
Ser Ala Ser Ala Lys Asp Gly Gly Asn Met Tyr Ser Pro Pro Cys Ser 500 505 510		
Ala Ala Ala Ser Ser Gln Gly His Cys Phe Ala Val Gly Ala Asn Gln 515 520 525		
Leu Ala Ser Leu Asp Leu Ala Met Asp Phe Asp Glu Pro Ile Leu Phe 530 535 540		
Pro Val His Asn Ala Ser Leu Gln Glu Gly Ile Gln Phe Tyr Asn Pro 545 550 555 560		
Thr Gly Asp Thr Gln Leu Ser Arg Asn Met Ser Ile Asp Lys Cys Leu 565 570 575		
Lys Gly Ser Lys Arg Lys Gly Ser Gly Glu Gly Ser Ser Ser Leu His 580 585 590		
Ser Gln Glu Glu Thr Gly Glu Met Pro Gln Arg Glu Leu Ser Met Glu 595 600 605		

ES 2 623 545 T3

His Ala Gly Glu Lys Ala Gly Asp Ala Asp Ala Ser Arg Glu Glu Tyr
610 615 620

Val His Val Arg Ala Lys Arg Gly Gln Ala Thr Asn Ser His Ser Leu
625 630 635 640

Ala Glu Arg Phe Arg Arg Glu Lys Ile Asn Glu Arg Met Lys Leu Leu
645 650 655

Gln Asp Leu Val Pro Gly Cys Asn Lys Ile Thr Gly Lys Ala Met Met
660 665 670

Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu Gln Arg Gln Val Glu
675 680 685

Phe Leu Ser Met Lys Leu Ser Thr Ile Ser Pro Glu Leu Asn Ser Asp
690 695 700

Leu Asp Leu Gln Asp Ile Leu Cys Ser Gln Asp Ala Arg Ser Ala Phe
705 710 715 720

Leu Gly Cys Ser Pro Gln Leu Ser Asn Ala His Pro Asn Leu Tyr Arg
725 730 735

Ala Ala Gln Gln Cys Leu Ser Pro Pro Gly Leu Tyr Gly Ser Val Cys
740 745 750

Val Pro Asn Pro Ala Asp Val His Leu Ala Arg Ala Gly His Leu Ala
755 760 765

Ser Phe Pro Gln Gln Arg Gly Leu Ile Trp Asn Glu Glu Leu Arg Asn
770 775 780

Ile Ala Pro Ala Gly Phe Ala Ser Asp Ala Ala Gly Thr Ser Ser Leu
785 790 795 800

Glu Asn Ser Asp Ser Met Lys Val Glu
805

<210> 110

<211> 467

5 <212> PRT

<213> Oryza sativa

<400> 110

Met Ala Ala Ala Ala Gly Ala Gly Glu Pro Ser Pro Tyr Ala Glu Ala
1 5 10 15

10

ES 2 623 545 T3

Ala	Gly	Ser	Asp	Leu	Ala	Asn	Ala	Arg	Ala	Pro	Ser	Pro	Val	Val	Gly			
			20					25					30					
Lys	His	Leu	Pro	Ser	Gly	Ala	Val	Pro	Arg	His	Ala	Tyr	Val	Phe	Asp			
		35					40					45						
Gly	Glu	Gly	Gly	Phe	Ala	Asp	Ala	Ala	Trp	Asp	Val	Ala	Ala	Ala	Ala			
	50					55					60							
Pro	Gly	Ala	Phe	Thr	Trp	His	His	Ile	Glu	Leu	Pro	Arg	Gln	Gln	Pro			
65					70					75					80			
Gly	Gly	Ala	Ala	Ala	Lys	Pro	Leu	His	His	Ala	Gln	Ala	Leu	Ile	Glu			
				85					90					95				
Leu	Leu	Cys	Pro	Pro	Leu	Thr	Leu	Gln	Glu	Ile	Leu	Ala	Phe	Val	Ala			
			100					105					110					
Thr	Gly	Pro	His	Cys	Gly	Val	Val	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Ala			
		115					120					125						
Gly	Ala	Leu	Leu	Leu	Arg	Val	Ser	Ser	Pro	Gly	Pro	Val	Gly	Ser	Ala			
	130					135					140							
Phe	Ala	Leu	Arg	Leu	Ala	Ala	Arg	Val	Thr	Asp	Ser	Ser	Val	Val	Thr			
145					150					155					160			
Val	Ser	Val	Gly	Gly	Val	Pro	Arg	Leu	Ala	Phe	Gly	Thr	Thr	Gln	Ala			
			165					170						175				
Ser	Leu	Leu	Ser	Glu	Val	Pro	Leu	Gly	Val	Thr	Ala	Ser	Leu	Ser	Asp			
			180					185					190					
Glu	Gly	His	Gly	Gly	Gly	Arg	Ala	Val	Glu	Gly	Gly	Val	Val	Ile	Glu			
		195					200					205						
Glu	Arg	Leu	Leu	Glu	Ser	Leu	Leu	Ala	Met	Asn	His	Ala	Asp	Gly	Ala			
	210					215					220							
His	Thr	Asp	Asn	Pro	Val	Pro	Arg	Thr	Val	Ser	Asn	Leu	Leu	Val	His			
225					230					235					240			
Val	Leu	Gly	Thr	His	Val	Asp	His	Val	His	Asp	Ile	Val	Thr	Arg	Leu			
				245					250					255				
Glu	Met	Glu	Leu	Asp	Ser	Ile	Glu	Leu	His	Leu	Asp	Lys	Gly	Gly	His			
			260					265					270					
Phe	Met	Arg	Lys	Leu	Leu	Leu	Asp	Gly	Arg	Arg	Phe	Pro	Lys	Met	His			

ES 2 623 545 T3

275	280	285
Leu Asp Leu Gln Arg Leu Leu Gln Val Val Ser His Gly Asp Gln Val 290 295 300		
Phe Pro Arg Val Lys Glu Lys Cys Ala Ser Lys Ser Trp Phe Ala Ser 305 310 315 320		
Glu Asp Ile Val Ala Leu Glu Asp Leu Ile Gly Arg Leu Arg Arg Leu 325 330 335		
Lys Glu Asn Leu Gly Phe Ile Thr Asn Arg Val Thr Thr Leu Gln Ala 340 345 350		
Ser Leu Asp Ser Trp Gln Ser Glu Gln Ile Asn Lys Ser Leu Tyr Tyr 355 360 365		
Leu Ser Phe Leu Ser Ile Ile Phe Leu Pro Leu Ser Ile Val Thr Gly 370 375 380		
Val Phe Gly Met Asn Val Gly Gly Val Pro Trp Thr Glu Gln Lys Asn 385 390 395 400		
Pro Ala Asn Leu Asp Gly Phe Phe Asn Val Met Leu Ile Cys Val Val 405 410 415		
Ile Leu Leu Ile Leu Leu Leu Cys Phe Leu Phe Pro Ser Leu Tyr Ser 420 425 430		
His Val Ser Ala Trp Arg Thr Arg Arg Ala Leu Ala Arg Ser Ser Ser 435 440 445		
Gln Asn Lys Arg His Leu Lys Leu Phe Lys Gly His Lys Asp Gly Tyr 450 455 460		
Met Arg Leu 465		
<210> 111		
<211> 147		
<212> PRT		
<213> Oryza sativa		
<400> 111		
Met Gln Asp Gln Leu Ile Cys Ser Gly Cys Arg Arg Val Val Gln Tyr 1 5 10 15		
Arg Arg Gly Val Ala Gly Val Cys Cys Pro Gly Cys Asn Thr Leu Thr 20 25 30		

ES 2 623 545 T3

Ala Val Asn Pro Ser Ala Val Ala Asp Met Ser Glu Leu Ile Cys Ser
35 40 45

Gly Cys Pro Thr Leu Leu Phe Tyr Asn Arg Gly Ala Ser Asn Ile Arg
50 55 60

Cys Pro Ser Cys Asn Arg Leu Asn Ser Thr Arg Ser Ala Asn Gln Ile
65 70 75 80

Ala His Leu Thr Cys Gly Gln Cys Arg Thr Thr Leu Met His Pro Pro
85 90 95

Gly Ala Ser Thr Val Gln Cys Ala Thr Cys Arg Tyr Val Asn His Val
100 105 110

Arg Asp Ala Arg Pro Gln Thr Val Leu Val Glu Asn Pro Lys Thr Leu
115 120 125

Asp Asp Lys Gly Lys Leu Val Ser Asn Val Val Val Gly Val Thr Ser
130 135 140

Trp Lys Arg
145

<210> 112
<211> 266
<212> PRT
<213> Oryza sativa

<400> 112
Met Arg Gly Ala Val Ala Ile Phe Asn Glu Phe Lys Arg Arg Gly Leu
1 5 10 15

Asn Ile Ser Ile Thr Gly Ile Pro Lys Thr Val Asp Asn Asp Ile Gly
20 25 30

Ile Ile Asp Arg Ser Phe Gly Phe Gln Thr Ala Val Glu Ile Ala Gln
35 40 45

Gln Ala Ile Asp Ala Ala His Val Glu Ala Val Ser Ala Val Asn Gly
50 55 60

Ile Gly Leu Val Lys Leu Met Gly Arg Ser Thr Gly His Ile Ala Leu
65 70 75 80

His Ala Thr Leu Ser Ser Arg Asp Val Asp Cys Cys Leu Ile Pro Glu
85 90 95

Val Asp Phe Tyr Leu Glu Gly Lys Gly Gly Leu Phe Glu Phe Leu Tyr

ES 2 623 545 T3

100				105				110							
Glu	Arg	Ile	Lys	Gln	Lys	Gly	His	Ala	Val	Val	Val	Val	Ala	Glu	Gly
115				120				125							
Ala	Gly	Gln	Glu	Leu	Ile	Pro	Arg	Thr	Asp	Asp	Gln	Lys	Arg	Glu	Gln
130				135				140							
Asp	Glu	Ser	Gly	Asn	Ile	Val	Phe	Leu	Asp	Val	Gly	Pro	Trp	Leu	Lys
145				150				155				160			
Ser	Glu	Leu	Gly	Lys	Trp	Trp	Lys	Arg	Glu	His	Pro	Ser	Glu	Leu	Phe
				165				170				175			
Thr	Val	Lys	Tyr	Ile	Asp	Pro	Thr	Tyr	Met	Ile	Arg	Ala	Val	Pro	Ala
				180				185				190			
Asn	Ala	Thr	Asp	Asn	Leu	Tyr	Cys	Thr	Leu	Leu	Ala	His	Ser	Ala	Ile
195				200				205							
His	Gly	Ile	Met	Ala	Gly	Tyr	Thr	Gly	Phe	Val	Pro	Gly	Pro	Ile	Asn
210				215				220							
Gly	Asn	Tyr	Ser	Tyr	Ile	Pro	Leu	Glu	Asp	Val	Ala	Val	Ala	Lys	Asn
225				230				235				240			
Pro	Val	Asp	Val	Asn	Asp	His	Lys	Trp	Ala	Trp	Val	Arg	Ser	Val	Thr
				245				250				255			
Asn	Gln	Pro	Asp	Phe	Met	Lys	Pro	Lys	Tyr						
260				265											

<210> 113
<211> 595
<212> PRT
<213> *Oryza sativa*

<400> 113
Met Val Glu Ser Ala Ser Met Val Asn Glu Asn Ser Glu Asn Pro Tyr
1 5 10 15

Trp Lys Ala Ile Gly Tyr Arg Val Glu Glu Pro Arg Arg Asp Arg Ala
20 25 30

Glu Ser Met Pro Ser Pro Ser Pro Ser Pro Val Ser Arg Arg Pro Leu
35 40 45

Asp Asn Gly Val Val Glu Thr Arg Ala Leu Thr Asp Thr Thr Leu Leu
50 55 60

ES 2 623 545 T3

Arg	Ser	Leu	Ala	Ala	Lys	Gly	Leu	Ala	Val	Arg	Pro	Gly	Ala	Ser	Asp	65	70	75	80
Glu	His	His	Thr	Val	Arg	Cys	Asp	Ala	Val	Ile	Val	Gly	Ser	Gly	Cys	85	90	95	
Gly	Gly	Gly	Val	Ala	Ala	Ala	Val	Leu	Ala	Ser	Ala	Gly	Tyr	Lys	Val	100	105	110	
Val	Val	Val	Glu	Lys	Gly	Asp	Tyr	Phe	Thr	Lys	Glu	Asp	Tyr	Ser	Ser	115	120	125	
Ile	Glu	Gly	Pro	Ser	Met	Glu	Arg	Leu	Phe	Glu	Arg	Gly	Gly	Val	Phe	130	135	140	
Cys	Thr	Ser	Asn	Val	Thr	Thr	Met	Ile	Phe	Thr	Gly	Ala	Thr	Val	Gly	145	150	155	160
Gly	Gly	Ser	Ala	Val	Asn	Trp	Ser	Ala	Ser	Ile	Arg	Thr	Pro	Ala	Gly	165	170	175	
Val	Met	Gln	Glu	Trp	Ser	Arg	Glu	His	Gly	Leu	Ala	Val	Phe	Ala	Ser	180	185	190	
Pro	Gly	Tyr	Ala	Arg	Ala	Met	Asp	Ala	Val	Cys	Glu	Arg	Leu	Gly	Val	195	200	205	
Thr	Asp	Ala	Cys	Arg	Glu	Glu	Gly	Phe	Gln	Asn	Lys	Val	Val	Arg	Arg	210	215	220	
Gly	Cys	Asp	Ala	Leu	Gly	Leu	Arg	Ala	Asp	Ala	Val	Pro	Arg	Asn	Ser	225	230	235	240
Ser	Glu	Gly	His	Phe	Cys	Gly	Ser	Cys	Asn	Phe	Gly	Cys	Pro	Thr	Gly	245	250	255	
Asp	Lys	Lys	Gly	Thr	Asp	Thr	Thr	Trp	Leu	Val	Asp	Ala	Val	Glu	Arg	260	265	270	
Gly	Ala	Val	Ile	Leu	Thr	Gly	Cys	Lys	Ala	Glu	His	Phe	Ile	Val	Glu	275	280	285	
Ser	Asn	Gly	Gly	Gly	Gly	Gly	Arg	Ser	Lys	Arg	Cys	Val	Gly	Leu	Val	290	295	300	
Ala	Thr	Cys	Met	Ser	Asn	Gly	Ile	Thr	Lys	Lys	Leu	Arg	Val	Glu	Ala	305	310	315	320

ES 2 623 545 T3

Lys Val Ser Ile Ser Ala Ser Gly Ala Leu Met Thr Pro Pro Leu Leu
 325 330 335
 Arg Asn Ser Gly Leu Lys Asn Arg His Ile Gly Arg Asn Leu His Leu
 340 345 350
 His Pro Val Ser Met Ala Trp Gly Tyr Phe Pro Asp Asn Thr Pro Glu
 355 360 365
 Pro His Ile Pro Gly Lys Cys Tyr Glu Gly Gly Ile Ile Thr Ser Met
 370 375 380
 His Arg Val Thr Glu Arg Thr Ile Ile Glu Thr Pro Ala Leu Gly Pro
 385 390 395 400
 Gly Ala Phe Ala Ala Leu Val Pro Trp Glu Ser Gly Arg Asp Met Lys
 405 410 415
 Glu Arg Met Arg Arg Tyr Ala Arg Thr Ala His Ala Phe Ala Leu Val
 420 425 430
 Arg Asp Arg Gly Ala Gly Ser Val Asp Gly Glu Gly Arg Val Arg Tyr
 435 440 445
 Ala Pro Ser Arg Asp Asp Ala Glu Glu Leu Arg Ala Gly Leu Arg Arg
 450 455 460
 Ala Leu Arg Ile Leu Val Ala Ala Gly Ala Ala Glu Val Gly Thr His
 465 470 475 480
 Arg Ser Asp Gly Ala Arg Leu Arg Cys Lys Gly Ala Arg Asp Ala Asp
 485 490 495
 Val Glu Ala Phe Leu Asp Glu Val Thr Val Glu Lys Gly Pro Met His
 500 505 510
 Ser Thr Thr Asp Lys Trp Ser Val Leu Cys Ser Ala His Gln Met Gly
 515 520 525
 Ser Cys Arg Met Gly Ala Ser Pro Arg Asp Gly Ala Val Asp Val Ala
 530 535 540
 Gly Glu Ser Trp Glu Ala Glu Gly Leu Tyr Val Cys Asp Gly Ser Leu
 545 550 555 560
 Leu Pro Thr Ala Val Gly Val Asn Pro Met Ile Thr Ile Gln Ser Ile
 565 570 575
 Ala Tyr Cys Val Ala Lys Gly Ile Ala Asp Ser Met Ala His Gly Lys
 580 585 590
 Glu Gln Arg
 595

ES 2 623 545 T3

<210> 114
 <211> 177
 <212> PRT
 <213> Oryza sativa

5

<400> 114
 Met Ala Pro His Pro Leu Leu Arg Gly Gly Ala Arg Arg Gly Arg Lys
 1 5 10 15
 Tyr Ala His Gly Met His Pro Ala Gln Met Glu Ala Leu Arg Ala Met
 20 25 30
 Cys Gly Ala Leu Ile Pro Ser Leu Pro Val Asp Ala Asp Gly Gly Asp
 35 40 45
 Gly Gly Arg Arg Pro Gly Asp Lys Asp Leu Glu Arg Phe Tyr Leu Ala
 50 55 60
 Ser Ala Ala Asp Ser Ser Ile Pro Asp Glu Val Ala Glu Leu Leu Val
 65 70 75 80
 Thr Arg Cys Ile Trp Glu Ala Val Ala Leu Thr Trp Val Val Leu Trp
 85 90 95
 Ala Leu Ser Thr Arg Ala Gly Thr Leu Leu Leu Cys Gly Arg Asp Ser
 100 105 110
 Val Ala Ala Val Asp Gly Gly Gly Phe Pro Phe Val Ser Val Arg Arg
 115 120 125
 Phe Ala Asp Met Pro Ala Ala Arg Arg Glu Ala Ala Leu Trp Arg Trp
 130 135 140
 Ser Gly Ala Arg Trp Leu Phe Phe Pro Leu Arg Ile Ala Phe Ala Ile
 145 150 155 160
 Ala Lys Ile Leu Cys His Tyr Val Phe Tyr Ser Met Ile Leu Val Ser
 165 170 175

Ala

<210> 115
 <211> 477
 <212> DNA
 <213> Oryza sativa

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	tgcagacgga ggcgacgcc aaggagtgcc gacgccggcg ctggaggcag aggcggaggg	120
	cgccggtgct gggcggaggc ggcggaggcg gcgcacatgg cggcggcggc ggcgcatagg	180
	gcggcggcgg tgcacagggc ggcctgcggt agctccaccg tcgccgtcgg gctgcgggag	240
	ctccaccggc gtcgtctctg cagcacctgc acgggggatg gggatgggga taggatgctt	300
	atgcagagaa atgacagtag caatagcaaa tggatgttgt cacggagggc attttcgcct	360
	tttcacgtga gtgctaaatt tgcattggag gtacaggaat cgcttctgga tggaggaggt	420
	acctggttct gtttaggac tagtgcttac tttgtgcag tcaaatacga ttggtga	477
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5	<211> 354	
	<212> DNA	
	<213> Oryza sativa	
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	acgccgggcg acgtgcgcat gctgttcacc cgccacgccg gcggcgcgcc ctacatgggc	120
	atcgacgagc tccggcgcta cctcgccgcc agcggggagg cccacgtcga cgccgacacg	180
	gcggagcgga tcacgacggc ggtcctgcag gacgcagcc gcaccccgcg cttcgggaag	240
	ccgtcgtca ccatcgacga tttccagtac ttctcttctt ccgaggacct caaccgccc	300
10	atctgccatt ccaaggaaga aagttttgat gcgatggaaa agttggaagt ttga	354
<210> 117		
	<211> 1473	
	<212> DNA	
15	<213> Oryza sativa	
<400> 117		
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	aactcgtatc tgacgggcaa tcaacttagc agtgactgca gtgatattcc catcattaag	120
	gcactgcaaa taggcgtccg tgtaattgaa ctggacatgt ggccaaattc ttctaaagat	180
	gatgttgata ttctccatgg aaggacactg actgccccag tatcacttat caaatgcttg	240
	aaatccatca aagaatatgc ctttgttgcg tctccctacc ctgttattat aacattagaa	300
	gaccacctta catctgatct tcaggcgaaa gtagctaaga tggttcttga agtatttgga	360
	gataccctat attatcccga gtcaaaacat cttcaagaat ttccttcacc cgaagcactg	420
	aggggacgtg tcatcctctc aacaaaaccc ccaaaggagt accttgaatc aaaagtggt	480
	actatgaaag acagagacat tgagcctcag tttagcaaag gacaaaatga agaagctgtc	540
	tggggaacag aagtcccaga tattcaggat gagatgcaaa ccgccgacaa gcagcatgag	600

aatgatatac tatacaccca aagagatgtg gaagaagatg atgagaagaa aatgtgccag 660
catcacccac tagagtataa acaccttatt actattaagg caggaaagcc aaaggggtgct 720
gtagttgatg ccttaaaggg tgatccagat aaagtttagac gcctcagttt gagtgcagcag 780
gaacttgcaa aagtggcagc gcatcatggg cgtaacatcg tgagctttac acataaaaat 840
cttctgagaa tataacccaaa gggcactcgc ttcaattctt cgaactataa tccgtttctt 900
ggttgggtgc atggtgcaca aatggtggca tttaatatgc aggggtatgg aagatctctt 960
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aagaaaacac tcaaggtcaa agtatacatg ggcgaagggt ggcagagcga cttcaagcag 1140
acatacttcg acacgtattc cctccagac ttctacgaa aggtgggcat tgccgggggtt 1200
ccgtcggact cggtgatgca gaagacgaaa gccgtggagg acagctgggt tcccgtgtgg 1260
gaggaggagt tcgtgttccc gctgaccgtc ccggagatcg cgctgctccg cgtggagggtg 1320
cacgagtacg acgtgagcga ggacgacttc ggccgggcaga cggcgctccc ggtgtcggag 1380
ctgcggccgg ggatccgcac cgtgccgctc ttccaccaca aggggctcaa gttcaagagc 1440
gtcaagctcc tcatgcgggt cgagttcgtc tag 1473

5 <210> 118
<211> 636
<212> DNA
<213> Oryza sativa

<400> 118
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cggtcggggc cggtcggggc ggtgcggggc agggagggcg cgggggcgat gtccgcggag 180
gggttccggc tgctggacgt ccggccggag tgggagcgcg cgcgcgccgc cgtgcggggc 240
tcggcgcacg cgccgctgtt cgtcggggac gacgacacgg gcccgcgtac gctgctcaag 300
aagtgggtcc acttcggcta catcggcctc tggaccggcc agtccttcac caagatgaac 360
gaccgcttcc tcgacgacgt cgccgccgcc gccggcgaag gcaaggacgc caagctgctc 420
gtcgctcgcg gcgaaggcct ccggctcgtt atcgcggtga ggatgctgta cgacgacggg 480
tacaagaacc tggcgtggct cgccggaggg ttccagcaagt gcgtcgacgg cgacttcgcc 540
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<210> 121
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<210> 122
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<212> DNA
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<210> 124
<211> 612
<212> DNA
<213> Oryza sativa

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<210> 125
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<212> DNA
<213> Oryza sativa

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 <211> 1404
 <212> DNA
 <213> Oryza sativa

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<211> 444
<212> DNA
<213> Oryza sativa

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<210> 128
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<212> DNA
<213> Oryza sativa

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<212> DNA
<213> Oryza sativa

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 <211> 534
 <212> DNA
 <213> Oryza sativa

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ES 2 623 545 T3

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<212> DNA
<213> Oryza sativa

5

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10

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ES 2 623 545 T3

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Arg Gln Glu Cys Ser Val Asp Leu Lys Leu Gly Gly Leu Gly Glu Phe
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Gly Gly Gly Gly Ala Gln Pro Arg Val Ala Val Ala Gly Glu Pro Ala
65      70      75      80

Lys Gly Lys Gly Pro Ala Ala Ala Ala Thr Gly Ala Ala Ala Ala Ala
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Ser Ser Ala Pro Ala Lys Arg Pro Arg Gly Ala Ala Ala Ala Gly Gln
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Gln Gln Cys Pro Ser Cys Ala Val Asp Gly Cys Lys Glu Asp Leu Ser
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Lys Cys Arg Asp Tyr His Arg Arg His Lys Val Cys Glu Ala His Ser
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Lys Thr Pro Leu Val Val Val Ser Gly Arg Glu Met Arg Phe Cys Gln
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Gln Cys Ser Arg Phe His Leu Leu Gln Glu Phe Asp Glu Ala Lys Arg
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Ser Cys Arg Lys Arg Leu Asp Gly His Asn Arg Arg Arg Arg Lys Pro
      180      185      190

Gln Pro Asp Pro Met Asn Ser Ala Ser Tyr Leu Ala Ser Gln Gln Gly
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Ala Arg Phe Ser Pro Phe Ala Thr Pro Arg Pro Glu Ala Ser Trp Thr
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Gly Met Ile Lys Thr Glu Glu Ser Pro Tyr Tyr Thr His His Gln Ile
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Pro Leu Gly Ile Ser Ser Arg Gln Gln His Phe Val Gly Ser Thr Ser

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ES 2 623 545 T3

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Ala Ala Ala Ala Ser Val Cys Gln Pro Leu Leu Lys Thr Val Ala Pro	290		295		300
Pro Pro Pro Pro His Gly Gly Gly Gly Ser Gly Gly Gly Lys Met Phe	305		310		315
Ser Asp Gly Gly Leu Thr Gln Val Leu Asp Ser Asp Cys Ala Leu Ser	325		330		335
Leu Leu Ser Ala Pro Ala Asn Ser Thr Ala Ile Asp Val Gly Gly Gly	340		345		350
Arg Val Val Val Gln Pro Thr Glu His Ile Pro Met Ala Gln Pro Leu	355		360		365
Ile Ser Gly Leu Gln Phe Gly Gly Gly Gly Gly Ser Ser Ala Trp Phe	370		375		380
Ala Ala Arg Pro His His Gln Ala Ala Thr Gly Ala Ala Ala Thr Ala	385		390		395
Val Val Val Ser Thr Ala Gly Phe Ser Cys Pro Val Val Glu Ser Glu	405		410		415
Gln Leu Asn Thr Val Leu Ser Ser Asn Asp Asn Glu Met Asn Tyr Asn	420		425		430
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ES 2 623 545 T3

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ES 2 623 545 T3

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REIVINDICACIONES

1. Un procedimiento para aumentar el tamaño el tamaño de la semilla en una planta al transformar una planta anfitriona o células de la planta anfitriona con un montaje de ADN recombinado que contiene una secuencia activadora operativamente unida a un polinucleótido que codifica un polipéptido que tiene una secuencia de aminoácidos al menos 80% idéntica a la secuencia SEQ. ID. nº: 103, siendo funcional la secuencia activadora en una célula de la planta anfitriona o en las células de la planta anfitriona.
2. El procedimiento de la reivindicación 1, en donde el polinucleótido codifica un polipéptido que tiene la secuencia de aminoácidos SEQ. ID. nº: 103.
3. El procedimiento de la reivindicación 1, en donde el polinucleótido tiene la secuencia de nucleótidos de SEQ. ID. nº: 119.
4. El procedimiento de la reivindicación 1, en donde en donde la planta anfitriona es una planta cultivada.