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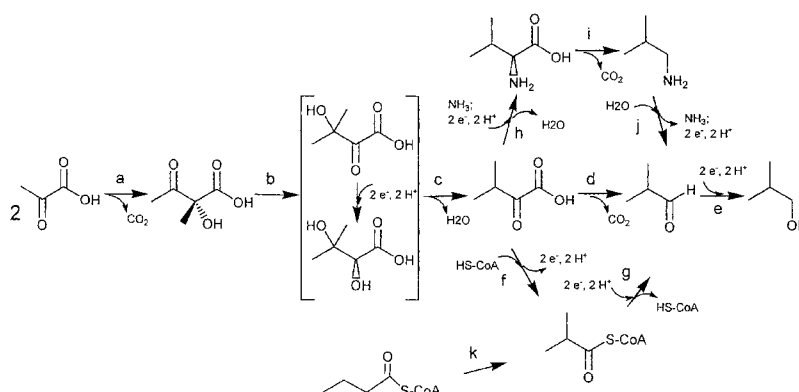


FIG. 1

(57) Abstract: Lactic acid bacterial (LAB) cells were modified such that they have a specific activity of dihydroxy-acid dehydratase enzyme activity that is increased to about 0.1 $\mu\text{mol min}^{-1} \text{mg}^{-1}$. LAB cells with even higher activities of 0.2 to 0.6 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ of DHAD activity were obtained. These modified cells may be used to produce isobutanol when additional isobutanol biosynthetic pathway enzymes are expressed.

TITLEENHANCED DIHYDROXY-ACID DEHYDRATASE ACTIVITY IN LACTIC
ACID BACTERIA5 CROSS-REFERENCE TO RELATED APPLICATIONS

This application is related to and claims the benefit of priority of U.S. Provisional Application No. 61/100,810, filed September 29, 2008, the entire contents of which is herein incorporated by reference.

FIELD OF THE INVENTION

10 The invention relates to the field of industrial microbiology and expression of dihydroxy-acid dehydratase activity. More specifically, increased levels of dihydroxy-acid dehydratase activity were achieved in lactic acid bacteria, allowing increased production of compounds from pathways including dihydroxy-acid dehydratase, such as isobutanol.

15 BACKGROUND OF THE INVENTION

Dihydroxy-acid dehydratase (DHAD), also called acetohydroxy acid dehydratase, catalyzes the conversion of 2,3-dihydroxyisovalerate to α -ketoisovalerate and of 2,3-dihydroxymethylvalerate to α -ketomethylvalerate. The DHAD enzyme requires binding of an iron-sulfur (Fe-S) cluster for activity, is classified as E.C. 4.2.1.9, and is part of naturally occurring biosynthetic pathways producing valine, isoleucine, leucine and pantothenic acid (vitamin B5). DHAD catalyzed conversion of 2,3-dihydroxyisovalerate to α -ketoisovalerate is also a common step in the multiple isobutanol biosynthetic pathways that are disclosed in commonly owned and co-pending US Patent Application Publication US 20070092957 A1. Disclosed therein is engineering of recombinant microorganisms for production of isobutanol. Isobutanol is useful as a fuel additive, whose availability may reduce the demand for petrochemical fuels.

30 High levels of DHAD activity are desired for increased production of products from biosynthetic pathways that include this enzyme activity,

including for enhanced microbial production of branched chain amino acids, pantothenic acid, and isobutanol.

There is a need therefore to increase DHAD activity in lactic acid bacterial (LAB) cells to allow increased production of isobutanol and other products whose biosynthetic pathways include DHAD.

SUMMARY OF THE INVENTION

Provided herein is a recombinant lactic acid bacterial cell comprising at least one gene encoding a heterologous polypeptide having dihydroxy-acid dehydratase activity and wherein the bacterial cell is substantially free of lactate dehydrogenase activity. In some embodiments, the heterologous polypeptide having dihydroxy-acid dehydratase activity has a specific activity of at least about $0.1 \mu\text{mol min}^{-1} \text{mg}^{-1}$ total soluble protein in a crude cell extract. In other embodiments, the heterologous polypeptide having dihydroxy-acid dehydratase activity has a specific activity of at least about $0.6 \mu\text{mol min}^{-1} \text{mg}^{-1}$ total soluble protein in a crude cell extract.

In some embodiments, the dihydroxy-acid dehydratase enzyme is expressed by a nucleic acid molecule that is heterologous to the bacteria, and in some embodiments, the dihydroxy-acid dehydratase is a [2Fe-2S] dihydroxy-acid dehydratase. In some embodiments, the dihydroxy-acid dehydratase polypeptide has an amino acid sequence that matches the Profile HMM of table 7 with an E value of $< 10^{-5}$ wherein the polypeptide additionally comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the *Streptococcus mutans* DHAD enzyme corresponding to SEQ ID NO:168.

In some embodiments, the dihydroxyacid dehydratase polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:310, SEQ ID NO:298, SEQ ID NO:168, SEQ ID No:164, SEQ ID NO:346, SEQ ID NO:344, SEQ ID NO:232, and SEQ ID NO:230.

Also provided herein is a recombinant lactic acid bacterial cell comprising at least one gene encoding a heterologous polypeptide having dihydroxy-acid dehydratase activity wherein the bacterial cell is

substantially free of lactate dehydrogenase activity and comprising a disruption in, or some other genetic modification that reduces expression of, at least one endogenous gene encoding a polypeptide having lactate dehydrogenase activity. In some embodiments, the gene encoding lactate dehydrogenase is selected from the group consisting of IdhL, IdhD, IdhL1, and IdhL2. In some embodiments, the lactic acid bacteria is selected from the group consisting of *Lactococcus*, *Lactobacillus*, *Leuconostoc*, *Oenococcus*, *Pediococcus*, and *Streptococcus*.

In some embodiments, the lactic acid host cell is *Lactobacillus plantarum* and the polypeptide having lactate dehydrogenase activity has an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 498, and 500. In other embodiments, the lactic acid host cell is *Lactococcus lactis* and the polypeptide having lactate dehydrogenase activity has an amino acid sequence as set forth in SEQ ID NO:502. In other embodiments, the lactic acid host cell is *Leuconostoc mesenteroides* and the polypeptide having lactate dehydrogenase activity has an amino acid sequence as set forth in SEQ ID NO:504. In other embodiments, the lactic acid host cell is *Streptococcus thermophilus* and the polypeptide having lactate dehydrogenase activity has an amino acid sequence as set forth in SEQ ID NO:506. In other embodiments, the lactic acid host cell is *Pediococcus pentosaceus* and the polypeptide having lactate dehydrogenase activity has an amino acid sequence selected from the group consisting of SEQ ID NO:508 and 510. In other embodiments, the lactic acid host cell is *Lactobacillus acidophilus* and the polypeptide having lactate dehydrogenase activity has an amino acid sequence selected from the group consisting of SEQ ID NO:512, 514 and 516.

Also provided is a recombinant lactic acid bacterial cell comprising at least one gene encoding a heterologous polypeptide having dihydroxy-acid dehydratase activity wherein the bacterial cell is substantially free of lactate dehydrogenase activity and wherein the bacteria produces isobutanol. In some embodiments, the bacteria comprises an isobutanol biosynthetic pathway, and in some embodiments, the isobutanol

biosynthetic pathway comprises genes encoding acetolactate synthase, acetohydroxy acid isomeroreductase, dihydroxy-acid dehydratase, branched-chain α -keto acid decarboxylase, and branched-chain alcohol dehydrogenase.

5 Also provided herein is a method of making isobutanol comprising providing the recombinant lactic acid bacteria described herein and growing the lactic acid bacteria under conditions wherein isobutanol is produced.

BRIEF DESCRIPTION OF THE FIGURES AND SEQUENCE DESCRIPTIONS

The various embodiments of the invention can be more fully understood from the following detailed description, the figures, and the accompanying sequence descriptions, which form a part of this application.

15 Figure 1 shows biosynthetic pathways for biosynthesis of
isobutanol.

Table 7 is a table of the Profile HMM for dihydroxy-acid dehydratases based on enzymes with assayed function. Table 7 is submitted herewith electronically and is incorporated herein by reference.

20 The following sequences conform with 37 C.F.R. 1.821-1.825
("Requirements for Patent Applications Containing Nucleotide Sequences
and/or Amino Acid Sequence Disclosures - the Sequence Rules") and are
consistent with World Intellectual Property Organization (WIPO) Standard
ST.25 (1998) and the sequence listing requirements of the EPO and PCT
25 (Rules 5.2 and 49.5(a-bis), and Section 208 and Annex C of the
Administrative Instructions). The symbols and format used for nucleotide
and amino acid sequence data comply with the rules set forth in
37 C.F.R. §1.822.

30 Table 1. SEQ ID NOs of representative bacterial [2Fe-2S] DHAD proteins
and encoding sequences

Organism of derivation	SEQ ID NO : Nucleic acid	SEQ ID NO : Peptide
Mycobacterium sp. MCS	1	2
Mycobacterium gilvum PYR-GCK	3	4
Mycobacterium smegmatis str. MC2 155	5	6
Mycobacterium vanbaalenii PYR-1	7	8
Nocardia farcinica IFM 10152	9	10
Rhodococcus sp. RHA1	11	12
Mycobacterium ulcerans Agy99	13	14
Mycobacterium avium subsp. paratuberculosis K-10	15	16
Mycobacterium tuberculosis H37Ra	17	18
Mycobacterium leprae TN *	19	20
Kineococcus radiotolerans SRS30216	21	22
Janibacter sp. HTCC2649	23	24
Nocardioides sp. JS614	25	26
Renibacterium salmoninarum ATCC 33209	27	28
Arthrobacter aurescens TC1	29	30
Leifsonia xyli subsp. xyli str. CTCB07	31	32
marine actinobacterium PHSC20C1	33	34
Clavibacter michiganensis subsp. michiganensis NCPPB 382	35	36
Saccharopolyspora erythraea NRRL 2338	37	38
Acidothermus cellulolyticus 11B	39	40
Corynebacterium efficiens YS-314	41	42
Brevibacterium linens BL2	43	44
Tropheryma whipplei TW08/27	45	46
Methylobacterium extorquens PA1	47	48
Methylobacterium nodulans ORS 2060	49	50

Rhodopseudomonas palustris BisB5	51	52
Rhodopseudomonas palustris BisB18	53	54
Bradyrhizobium sp. ORS278	55	56
Bradyrhizobium japonicum USDA 110	57	58
Fulvimarina pelagi HTCC2506	59	60
Aurantimonas sp. SI85-9A1	61	62
Hoeflea phototrophica DFL-43	63	64
Mesorhizobium loti MAFF303099	65	66
Mesorhizobium sp. BNC1	67	68
Parvibaculum lavamentivorans DS-1	69	70
Loktanelia vestfoldensis SKA53	71	72
Roseobacter sp. CCS2	73	74
Dinoroseobacter shibae DFL 12	75	76
Roseovarius nubinhibens ISM	77	78
Sagittula stellata E-37	79	80
Roseobacter sp. AzwK-3b	81	82
Roseovarius sp. TM1035	83	84
Oceanicola batsensis HTCC2597	85	86
Oceanicola granulosus HTCC2516	87	88
Rhodobacterales bacterium HTCC2150	89	90
Paracoccus denitrificans PD1222	91	92
Oceanibulbus indolifex HEL-45	93	94
Sulfitobacter sp. EE-36	95	96
Roseobacter denitrificans OCh 114	97	98
Jannaschia sp. CCS1	99	100
Caulobacter sp. K31	101	102
Candidatus Pelagibacter ubique HTCC1062	103	104
Erythrobacter litoralis HTCC2594	105	106
Erythrobacter sp. NAP1	107	108
Comamonas testosterone KF-1	109	110

Sphingomonas wittichii RW1	111	112
Burkholderia xenovorans LB400	113	114
Burkholderia phytofirmans PsJN	115	116
Bordetella petrii DSM 12804	117	118
Bordetella bronchiseptica RB50	119	120
Bradyrhizobium sp. ORS278	121	122
Bradyrhizobium sp. BTAi1	123	124
Bradyrhizobium japonicum	125	126
Sphingomonas wittichii RW1	127	128
Rhodobacterales bacterium HTCC2654	129	130
Solibacter usitatus Ellin6076	131	132
Roseiflexus sp. RS-1	133	134
Rubrobacter xylanophilus DSM 9941	135	136
Salinispora tropica CNB-440	137	138
Acidobacteria bacterium Ellin345	139	140
Thermus thermophilus HB27	141	142
Maricaulis maris MCS10	143	144
Parvularcula bermudensis HTCC2503	145	146
Oceanicaulis alexandrii HTCC2633	147	148
Plesiocystis pacifica SIR-1	149	150
Bacillus sp. NRRL B-14911	151	152
Oceanobacillus iheyensis HTE831	153	154
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	155	156
Bacillus selenitireducens MLS10	157	158
Streptococcus pneumoniae SP6-BS73	159	160
Streptococcus sanguinis SK36	161	162
Streptococcus thermophilus LMG 18311	163	164
Streptococcus suis 89/1591	165	166
Streptococcus mutans UA159	167	168
Leptospira borgpetersenii serovar	169	170

Hardjo-bovis L550		
Candidatus Vesicomysocius okutanii HA	171	172
Candidatus Ruthia magnifica str. Cm (Calypotgena magnifica)	173	174
Methylococcus capsulatus str. Bath	175	176
uncultured marine bacterium EB80_02D08	177	178
uncultured marine gamma proteobacterium EBAC31A08	179	180
uncultured marine gamma proteobacterium EBAC20E09	181	182
uncultured gamma proteobacterium eBACHOT4E07	183	184
Alcanivorax borkumensis SK2	185	186
Chromohalobacter salexigens DSM 3043	187	188
Marinobacter algicola DG893	189	190
Marinobacter aquaeolei VT8	191	192
Marinobacter sp. ELB17	193	194
Pseudoalteromonas haloplanktis TAC125	195	196
Acinetobacter sp. ADP1	197	198
Opitutaceae bacterium TAV2	199	200
Flavobacterium sp. MED217	201	202
Cellulophaga sp. MED134	203	204
Kordia algicida OT-1	205	206
Flavobacteriales bacterium ALC-1	207	208
Psychroflexus torquis ATCC 700755	209	210
Flavobacteriales bacterium HTCC2170	211	212
unidentified eubacterium SCB49	213	214

Gramella forsetii KT0803	215	216
Robiginitalea biformata HTCC2501	217	218
Tenacibaculum sp. MED152	219	220
Polaribacter irgensii 23-P	221	222
Pedobacter sp. BAL39	223	224
Flavobacteria bacterium BAL38	225	226
Flavobacterium psychrophilum JIP02/86	227	228
Flavobacterium johnsoniae UW101	229	230
Lactococcus lactis subsp. cremoris SK11	231	232
Psychromonas ingrahamii 37	233	234
Microscilla marina ATCC 23134	235	236
Cytophaga hutchinsonii ATCC 33406	237	238
Rhodopirellula baltica SH 1	239	240
Blastopirellula marina DSM 3645	241	242
Planctomyces maris DSM 8797	243	244
Algoriphagus sp. PR1	245	246
Candidatus Sulcia muelleri str. Hc (Homalodisca coagulata)	247	248
Candidatus Carsonella ruddii PV	249	250
Synechococcus sp. RS9916	251	252
Synechococcus sp. WH 7803	253	254
Synechococcus sp. CC9311	255	256
Synechococcus sp. CC9605	257	258
Synechococcus sp. WH 8102	259	260
Synechococcus sp. BL107	261	262
Synechococcus sp. RCC307	263	264
Synechococcus sp. RS9917	265	266
Synechococcus sp. WH 5701	267	268
Prochlorococcus marinus str. MIT 9313	269	270
Prochlorococcus marinus str. NATL2A	271	272
Prochlorococcus marinus str. MIT 9215	273	274

Prochlorococcus marinus str. AS9601	275	276
Prochlorococcus marinus str. MIT 9515	277	278
Prochlorococcus marinus subsp. pastoris str. CCMP1986	279	280
Prochlorococcus marinus str. MIT 9211	281	282
Prochlorococcus marinus subsp. marinus str. CCMP1375	283	284
Nodularia spumigena CCY9414	285	286
Nostoc punctiforme PCC 73102	287	288
Nostoc sp. PCC 7120	289	290
Trichodesmium erythraeum IMS101	291	292
Acaryochloris marina MBIC11017	293	294
Lyngbya sp. PCC 8106	295	296
Synechocystis sp. PCC 6803	297	298
Cyanothece sp. CCY0110	299	300
Thermosynechococcus elongatus BP-1	301	302
Synechococcus sp. JA-2-3B'a(2-13)	303	304
Gloeobacter violaceus PCC 7421	305	306
Nitrosomonas eutropha C91	307	308
Nitrosomonas europaea ATCC 19718	309	310
Nitrospira multiformis ATCC 25196	311	312
Chloroflexus aggregans DSM 9485	313	314
Leptospirillum sp. Group II UBA	315	316
Leptospirillum sp. Group II UBA	317	318
Halorhodospira halophila SL1	319	320
Nitrococcus mobilis Nb-231	321	322
Alkalilimnicola ehrlichei MLHE-1	323	324
Deinococcus geothermalis DSM 11300	325	326
Polynucleobacter sp. QLW-P1DMWA-1	327	328
Polynucleobacter necessarius STIR1	329	330
Azoarcus sp. EbN1	331	332

Burkholderia phymatum STM815	333	334
Burkholderia xenovorans LB400	335	336
Burkholderia multivorans ATCC 17616	337	338
Burkholderia cenocepacia PC184	339	340
Burkholderia mallei GB8 horse 4	341	342
Ralstonia eutropha JMP134	343	344
Ralstonia metallidurans CH34	345	346
Ralstonia solanacearum UW551	347	348
Ralstonia pickettii 12J	349	350
Limnobacter sp. MED105	351	352
Herminiimonas arsenicoxydans	353	354
Bordetella parapertussis	355	356
Bordetella petrii DSM 12804	357	358
Polaromonas sp. JS666	359	360
Polaromonas naphthalenivorans CJ2	361	362
Rhodoferax ferrireducens T118	363	364
Verminephrobacter eiseniae EF01-2	365	366
Acidovorax sp. JS42	367	368
Delftia acidovorans SPH-1	369	370
Methylobium petroleiphilum PM1	371	372
gamma proteobacterium KT 71	373	374
Tremblaya princeps	375	376
Blastopirellula marina DSM 3645	377	378
Planctomyces maris DSM 8797	379	380
Microcystis aeruginosa PCC 7806	381	382
Salinibacter ruber DSM 13855	383	384
Methylobacterium chloromethanicum	385	386

Table 2. SEQ ID NOs of representative fungal and plant [2Fe-2S] DHAD proteins and encoding sequences

Description	SEQ ID NO:	SEQ ID NO:
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	Nucleic acid	Peptide
<i>Schizosaccharomyces pombe</i> ILV3	387	388
<i>Saccharomyces cerevisiae</i> ILV3	389	390
<i>Kluyveromyces lactis</i> ILV3	391	392
<i>Candida albicans</i> SC5314 ILV3	393	394
<i>Pichia stipitis</i> CBS 6054 ILV3	395	396
<i>Yarrowia lipolytica</i> ILV3	397	398
<i>Candida glabrata</i> CBS 138 ILV3	399	400
<i>Chlamydomonas reinhardtii</i>	401	402
<i>Ostreococcus lucimarinus</i> CCE9901	403	404
<i>Vitis vinifera</i> (Unnamed protein product: CAO71581.1)	405	406
<i>Vitis vinifera</i> (Hypothetical protein: CAN67446.1)	407	408
<i>Arabidopsis thaliana</i>	409	410
<i>Oryza sativa</i> (indica cultivar-group)	411	412
<i>Physcomitrella patens</i> subsp. Patens	413	414
<i>Chaetomium globosum</i> CBS 148.51	415	416
<i>Neurospora crassa</i> OR74A	417	418
<i>Magnaporthe grisea</i> 70-15	419	420
<i>Gibberella zeae</i> PH-1	421	422
<i>Aspergillus niger</i>	423	424
<i>Neosartorya fischeri</i> NRRL 181 (XP_001266525.1)	425	426
<i>Neosartorya fischeri</i> NRRL 181 (XP_001262996.1)	427	428
<i>Aspergillus niger</i> (hypothetical protein An03g04520)	429	430
<i>Aspergillus niger</i> (Hypothetical protein An14g03280)	431	432

<i>Aspergillus terreus</i> NIH2624	433	434
<i>Aspergillus clavatus</i> NRRL 1	435	436
<i>Aspergillus nidulans</i> FGSC A4	437	438
<i>Aspergillus oryzae</i>	439	440
<i>Ajellomyces capsulatus</i> NAm1	441	442
<i>Coccidioides immitis</i> RS	443	444
<i>Botryotinia fuckeliana</i> B05.10	445	446
<i>Phaeosphaeria nodorum</i> SN15	447	448
<i>Pichia guilliermondii</i> ATCC 6260	449	450
<i>Debaryomyces hansenii</i> CBS767	451	452
<i>Lodderomyces elongisporus</i> NRRL YB-4239	453	454
<i>Vanderwaltozyma polyspora</i> DSM 70294	455	456
<i>Ashbya gossypii</i> ATCC 10895	457	458
<i>Laccaria bicolor</i> S238N-H82	459	460
<i>Coprinosia cinerea okayama7#130</i>	461	462
<i>Cryptococcus neoformans</i> var. <i>neoformans</i> JEC21	463	464
<i>Ustilago maydis</i> 521	465	466
<i>Malassezia globosa</i> CBS 7966	467	468
<i>Aspergillus clavatus</i> NRRL 1	469	470
<i>Neosartorya fischeri</i> NRRL 181 (Putative)	471	472
<i>Aspergillus oryzae</i>	473	474
<i>Aspergillus niger</i> (hypothetical protein An18g04160)	475	476
<i>Aspergillus terreus</i> NIH2624	477	478
<i>Coccidioides immitis</i> RS (hypothetical protein CIMG_04591)	479	480
<i>Paracoccidioides brasiliensis</i>	481	482

<i>Phaeosphaeria nodorum</i> SN15	483	484
<i>Gibberella zeae</i> PH-1	485	486
<i>Neurospora crassa</i> OR74A	487	488
<i>Coprinopsis cinerea</i> okayama 7#130	489	490
<i>Laccaria bicolor</i> S238N-H82	491	492
<i>Ustilago maydis</i> 521	493	494

Table 3. SEQ ID NOs of representative [4Fe-4S] 2+ DHAD proteins and encoding sequences

Organism	SEQ ID NO: Nucleic Acid	SEQ ID NO: Peptide
<i>Escherichia coli</i> str. K-12 substr. MG1655	525	526
<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	527	528
<i>Agrobacterium tumefaciens</i> str. C58	529	530
<i>Burkholderia cenocepacia</i> MC0-3	531	532
<i>Psychrobacter cryohalolentis</i> K5	533	534
<i>Psychromonas</i> sp. CNPT3	535	536
<i>Deinococcus radiodurans</i> R1	537	538
<i>Wolinella succinogenes</i> DSM 1740	539	540
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ZM4	541	542
<i>Clostridium acetobutylicum</i> ATCC 824	543	544
<i>Clostridium beijerinckii</i> NCIMB 8052	545	546
<i>Pseudomonas fluorescens</i> Pf-5	547	548
<i>Methanococcus maripaludis</i> C7	549	550
<i>Methanococcus aeolicus</i> Nankai-3	551	552
<i>Vibrio fischeri</i> ATCC 700601	553	554

(ES114)		
<i>Shewanella oneidensis</i> MR-1 ATCC 700550	555	556

Table 4. SEQ ID NOs of representative lactate dehydrogenase proteins and encoding sequences

Organism and gene name	SEQ ID NO: nucleic acid	SEQ ID NO: amino acid
<i>Lactobacillus plantarum</i> ldhD	495	496
<i>Lactobacillus plantarum</i> ldhL1	497	498
<i>Lactobacillus plantarum</i> ldhL2	499	500
<i>Lactococcus lactis</i> ldhL	501	502
<i>Leuconostoc mesenteroides</i> ldhD	503	504
<i>Streptococcus thermophilus</i> ldhL	505	506
<i>Pediococcus pentosaceus</i> ldhD	507	508
<i>Pediococcus pentosaceus</i> ldhL	509	510
<i>Lactobacillus acidophilus</i> ldhL1	511	512
<i>Lactobacillus acidophilus</i> ldhL2	513	514
<i>Lactobacillus acidophilus</i> ldhD	515	516

5 Table 5. SEQ ID NOs of additional proteins and encoding sequences

Description	SEQ ID NO: Encoding seq	SEQ ID NO: Protein
<i>Vibrio cholerae</i> KARI	517	518
<i>Pseudomonas aeruginosa</i> PAO1 KARI	523	524
<i>Pseudomonas fluorescens</i> PF5 KARI	519	520
<i>Achromobacter xylosoxidans</i> butanol dehydrogenase sadB	521	522
<i>Lactobacillus plantarum</i> orotidine-	571	-

5'-phosphate decarboxylase, pyrF		
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Table 6. SEQ ID NOs of primers and vectors

Name	Description	SEQ ID NO:
3T-ilvDLI(BamHI)	ilvD(<i>L. lactis</i>) forward primer	557
5B-ilvDLI(NotI)	ilvD(<i>L. lactis</i>) reverse primer	558
F-primer	ilvD(<i>S. mutans</i>) forward primer	559
R-primer	ilvD(<i>S. mutans</i>) reverse primer	560
pET28a-F(NotI)	pET28a forward primer	561
pET28a-R(NheI)	pET28a reverse primer	562
pDM1 vector	Vector	563
pFP996	Vector	565
oBP120	Primer	567
oBP182	Primer	568
oBP190	Primer	569
oBP192	Primer	570
Top D F1	Primer	572
Top D R1	Primer	573
Bot D F2	Primer	574
Bot D R2	Primer	575
ldhD Seq F1	Primer	576
D check R	Primer	577
D check F3	Primer	578
oBP31	Primer	579
oBP32	Primer	580
oBP33	Primer	581
oBP34	Primer	582

oBP42	Primer	584
oBP49	Primer	583
oBP56	Primer	585
oBP57	Primer	586

SEQ ID NO:564 is the nucleotide sequence of the *Lactococcus lactis subsp lactis* NCDO2118 *ilvD* coding region.

5 SEQ ID NO:566 is the nucleotide sequence of a ribosome binding site.

DETAILED DESCRIPTION OF THE INVENTION

Provided herein is a recombinant lactic acid bacterial cell comprising at least one gene encoding a heterologous polypeptide having dihydroxy-acid dehydratase activity and wherein the bacterial cell is substantially free of lactate dehydrogenase activity. Further disclosed herein is the discovery that the specific activity of Fe-S requiring DHAD is increased in lactic acid bacterial hosts that are substantially free of lactate dehydrogenase activity.

15 The recombinant lactic acid bacterial (LAB) cells described herein have been engineered to have increased dihydroxy-acid dehydratase (DHAD) activity. In one embodiment, the engineered LAB cells have at least about 0.1 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ of DHAD activity as measured for specific activity. LAB cells with this level of DHAD activity are useful for production of compounds in biochemical pathways including DHAD, such as valine, isoleucine, leucine, pantothenic acid (vitamin B5), and isobutanol. In addition, the present invention relates to a method for producing isobutanol using the present engineered LAB cells with increased DHAD activity. Production of isobutanol in lactic acid bacteria will reduce the need for petrochemicals through use of isobutanol as a fuel additive.

25 The following abbreviations and definitions will be used for the interpretation of the specification and the claims.

As used herein, the terms “comprises,” “comprising,” “includes,” “including,” “has,” “having,” “contains” or “containing,” or any other

variation thereof, are intended to cover a non-exclusive inclusion. For example, a composition, a mixture, process, method, article, or apparatus that comprises a list of elements is not necessarily limited to only those elements but may include other elements not expressly listed or inherent to such composition, mixture, process, method, article, or apparatus. Further, unless expressly stated to the contrary, "or" refers to an inclusive or and not to an exclusive or. For example, a condition A or B is satisfied by any one of the following: A is true (or present) and B is false (or not present), A is false (or not present) and B is true (or present), and both A and B are true (or present).

Also, the indefinite articles "a" and "an" preceding an element or component of the invention are intended to be nonrestrictive regarding the number of instances (i.e. occurrences) of the element or component. Therefore "a" or "an" should be read to include one or at least one, and the singular word form of the element or component also includes the plural unless the number is obviously meant to be singular.

The term "invention" or "present invention" as used herein is a non-limiting term and is not intended to refer to any single embodiment of the particular invention but encompasses all possible embodiments as described in the specification and the claims.

As used herein, the term "about" modifying the quantity of an ingredient or reactant of the invention employed refers to variation in the numerical quantity that can occur, for example, through typical measuring and liquid handling procedures used for making concentrates or use solutions in the real world; through inadvertent error in these procedures; through differences in the manufacture, source, or purity of the ingredients employed to make the compositions or carry out the methods; and the like. The term "about" also encompasses amounts that differ due to different equilibrium conditions for a composition resulting from a particular initial mixture. Whether or not modified by the term "about", the claims include equivalents to the quantities. In one embodiment, the term "about"

means within 10% of the reported numerical value, preferably within 5% of the reported numerical value.

The term "isobutanol biosynthetic pathway" refers to an enzyme pathway to produce isobutanol from pyruvate.

5 The term "lactate dehydrogenase" refers to a polypeptide (or polypeptides) having an enzyme activity that catalyzes the conversion of pyruvate to lactate. Lactate dehydrogenases are known as EC 1.1.1.27 (L-lactate dehydrogenase) or EC 1.1.1.28 (D-lactate dehydrogenase), and are further characterized herein.

10 The term "substantially free" when used in reference to the presence or absence of lactate dehydrogenase enzyme activity means that the level of the enzyme activity is substantially less than that of the same enzyme in the wild-type host, where less than 50% of the wild-type level is preferred and less than about 90% of the wild-type level is most
15 preferred. The reduced level of enzyme activity may be attributable to genetic modification genes encoding this enzyme such that expression levels of the enzyme are reduced.

The term "a facultative anaerobe" refers to a microorganism that can grow in both aerobic and anaerobic environments.

20 The term "carbon substrate" or "fermentable carbon substrate" refers to a carbon source capable of being metabolized by host organisms of the present invention and particularly carbon sources selected from the group consisting of monosaccharides, oligosaccharides, polysaccharides, and one-carbon substrates or mixtures thereof.

25 The term "gene" refers to a nucleic acid fragment that is capable of being expressed as a specific protein, optionally including regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence. "Native gene" refers to a gene as found in nature with its own regulatory sequences. "Chimeric gene"
30 refers to any gene that is not a native gene, comprising regulatory and coding sequences that are not found together in nature. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences

that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that found in nature. "Endogenous gene" refers to a native gene in its natural location in the genome of an organism. A

5 "foreign gene" or "heterologous gene" refers to a gene not normally found in the host organism, but that is introduced into the host organism by gene transfer. "Heterologous gene" includes a native coding region, or portion thereof, that is reintroduced into the source organism in a form that is different from the corresponding native gene. For example, a heterologous
10 gene may include a native coding region that is a portion of a chimeric gene including non-native regulatory regions that is reintroduced into the native host. Also a foreign gene can comprise native genes inserted into a non-native organism, or chimeric genes. A "transgene" is a gene that has been introduced into the genome by a transformation procedure.

15 As used herein the term "coding region" refers to a DNA sequence that codes for a specific amino acid sequence. "Suitable regulatory sequences" refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing
20 or stability, or translation of the associated coding sequence. Regulatory sequences may include promoters, translation leader sequences, introns, polyadenylation recognition sequences, RNA processing site, effector binding site and stem-loop structure.

The term "promoter" refers to a DNA sequence capable of
25 controlling the expression of a coding sequence or functional RNA. In general, a coding sequence is located 3' to a promoter sequence. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic DNA segments. It is understood by
30 those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental or physiological

conditions. Promoters which cause a gene to be expressed in most cell types at most times are commonly referred to as "constitutive promoters". It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments
5 of different lengths may have identical promoter activity.

The term "operably linked" refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one is affected by the other. For example, a promoter is operably linked with a coding sequence when it is capable of effecting the expression of that
10 coding sequence (i.e., that the coding sequence is under the transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation.

The term "expression", as used herein, refers to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from
15 the nucleic acid fragment of the invention. Expression may also refer to translation of mRNA into a polypeptide.

As used herein the term "transformation" refers to the transfer of a nucleic acid fragment into a host organism, resulting in genetically stable inheritance. Host organisms containing the transformed nucleic acid
20 fragments are referred to as "transgenic" or "recombinant" or "transformed" organisms.

The terms "plasmid" and "vector" as used herein, refer to an extra chromosomal element often carrying genes which are not part of the central metabolism of the cell, and usually in the form of circular double-
25 stranded DNA molecules. Such elements may be autonomously replicating sequences, genome integrating sequences, phage or nucleotide sequences, linear or circular, of a single- or double-stranded DNA or RNA, derived from any source, in which a number of nucleotide sequences have been joined or recombined into a unique construction
30 which is capable of introducing a promoter fragment and DNA sequence for a selected gene product along with appropriate 3' untranslated sequence into a cell.

As used herein the term “codon degeneracy” refers to the nature in the genetic code permitting variation of the nucleotide sequence without effecting the amino acid sequence of an encoded polypeptide. The skilled artisan is well aware of the “codon-bias” exhibited by a specific host cell in
5 usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a gene for improved expression in a host cell, it is desirable to design the gene such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

The term “codon-optimized” as it refers to genes or coding regions
10 of nucleic acid molecules for transformation of various hosts, refers to the alteration of codons in the gene or coding regions of the nucleic acid molecules to reflect the typical codon usage of the host organism without altering the polypeptide encoded by the DNA.

As used herein, an “isolated nucleic acid fragment” or “isolated
15 nucleic acid molecule” will be used interchangeably and will mean a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. An isolated nucleic acid fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

20 A nucleic acid fragment is “hybridizable” to another nucleic acid fragment, such as a cDNA, genomic DNA, or RNA molecule, when a single-stranded form of the nucleic acid fragment can anneal to the other nucleic acid fragment under the appropriate conditions of temperature and solution ionic strength. Hybridization and washing conditions are well
25 known and exemplified in Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory: Cold Spring Harbor, NY (1989), particularly Chapter 11 and Table 11.1 therein (entirely incorporated herein by reference). The conditions of temperature and ionic strength determine the “stringency” of
30 the hybridization. Stringency conditions can be adjusted to screen for moderately similar fragments (such as homologous sequences from distantly related organisms), to highly similar fragments (such as genes

that duplicate functional enzymes from closely related organisms).

Post-hybridization washes determine stringency conditions. One set of preferred conditions uses a series of washes starting with 6X SSC, 0.5% SDS at room temperature for 15 min, then repeated with 2X SSC, 0.5% SDS at 45 °C for 30 min, and then repeated twice with 0.2X SSC, 0.5% SDS at 50 °C for 30 min. A more preferred set of stringent conditions uses higher temperatures in which the washes are identical to those above except for the temperature of the final two 30 min washes in 0.2X SSC, 0.5% SDS was increased to 60 °C. Another preferred set of highly stringent conditions uses two final washes in 0.1X SSC, 0.1% SDS at 65 °C. An additional set of stringent conditions include hybridization at 0.1X SSC, 0.1% SDS, 65 °C and washes with 2X SSC, 0.1% SDS followed by 0.1X SSC, 0.1% SDS, for example.

Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (see Sambrook et al., *supra*, 9.50-9.51). For hybridizations with shorter nucleic acids, i.e., oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (see Sambrook et al., *supra*, 11.7-11.8). In one embodiment the length for a hybridizable nucleic acid is at least about 10 nucleotides. Preferably a minimum length for a hybridizable nucleic acid is at least about 15 nucleotides; more preferably at least about 20 nucleotides; and most preferably the length is at least

about 30 nucleotides. Furthermore, the skilled artisan will recognize that the temperature and wash solution salt concentration may be adjusted as necessary according to factors such as length of the probe.

A “substantial portion” of an amino acid or nucleotide sequence is
5 that portion comprising enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to putatively identify that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Altschul, S. F., et al.,
10 *J. Mol. Biol.*, 215:403-410 (1993)). In general, a sequence of ten or more contiguous amino acids or thirty or more nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene specific oligonucleotide probes comprising
15 20-30 contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12-15 bases may be used as amplification primers in PCR in order to obtain a particular nucleic acid
20 fragment comprising the primers. Accordingly, a “substantial portion” of a nucleotide sequence comprises enough of the sequence to specifically identify and/or isolate a nucleic acid fragment comprising the sequence. The instant specification teaches the complete amino acid and nucleotide sequence encoding particular proteins. The skilled artisan, having the
25 benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.
30 The term “complementary” is used to describe the relationship between nucleotide bases that are capable of hybridizing to one another.

For example, with respect to DNA, adenosine is complementary to thymine and cytosine is complementary to guanine.

The term “percent identity”, as known in the art, is a relationship between two or more polypeptide sequences or two or more
5 polynucleotide sequences, as determined by comparing the sequences. In the art, “identity” also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. “Identity” and “similarity” can be readily calculated by known methods, including but
10 not limited to those described in: 1.) Computational Molecular Biology (Lesk, A. M., Ed.) Oxford University: NY (1988); 2.) Biocomputing: Informatics and Genome Projects (Smith, D. W., Ed.) Academic: NY (1993); 3.) Computer Analysis of Sequence Data, Part I (Griffin, A. M., and Griffin, H. G., Eds.) Humana: NJ (1994); 4.) Sequence Analysis in
15 Molecular Biology (von Heinje, G., Ed.) Academic (1987); and 5.) Sequence Analysis Primer (Gribskov, M. and Devereux, J., Eds.) Stockton: NY (1991).

Preferred methods to determine identity are designed to give the best match between the sequences tested. Methods to determine identity
20 and similarity are codified in publicly available computer programs. Sequence alignments and percent identity calculations may be performed using the MegAlign™ program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences is performed using the “Clustal method of alignment” which
25 encompasses several varieties of the algorithm including the “Clustal V method of alignment” corresponding to the alignment method labeled Clustal V (described by Higgins and Sharp, *CABIOS*. 5:151-153 (1989); Higgins, D.G. et al., *Comput. Appl. Biosci.*, 8:189-191 (1992)) and found in the MegAlign™ program of the LASERGENE bioinformatics computing
30 suite (DNASTAR Inc.). For multiple alignments, the default values correspond to GAP PENALTY=10 and GAP LENGTH PENALTY=10. Default parameters for pairwise alignments and calculation of percent

identity of protein sequences using the Clustal method are KTUPLE=1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. For nucleic acids these parameters are KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4. After alignment of the sequences using the

5 Clustal V program, it is possible to obtain a “percent identity” by viewing the “sequence distances” table in the same program. Additionally the “Clustal W method of alignment” is available and corresponds to the alignment method labeled Clustal W (described by Higgins and Sharp, *CABIOS*. 5:151-153 (1989); Higgins, D.G. et al., *Comput. Appl. Biosci.* 8:189-191(1992), Thompson, J. D., Higgins, D. G., and Gibson T. J. (1994) *Nuc. Acid Res.* 22: 4673 4680) and found in the MegAlign™ v6.1 program of the LASERGENE bioinformatics computing suite (DNASTAR Inc.). Default parameters for multiple alignment (GAP PENALTY=10, GAP LENGTH PENALTY=0.2, Delay Divergen Seqs(%)=30, DNA Transition

10 Weight=0.5, Protein Weight Matrix=Gonnet Series, DNA Weight Matrix=IUB). After alignment of the sequences using the Clustal W program, it is possible to obtain a “percent identity” by viewing the “sequence distances” table in the same program.

It is well understood by one skilled in the art that many levels of

20 sequence identity are useful in identifying polypeptides, from other species, wherein such polypeptides have the same or similar function or activity. Useful examples of percent identities include, but are not limited to: 24%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%, or any integer percentage from 24% to 100% may be

25 useful in describing the present invention, such as 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%,

30 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%. Suitable nucleic acid fragments not only have the above homologies but typically encode a polypeptide having

at least 50 amino acids, preferably at least 100 amino acids, more preferably at least 150 amino acids, still more preferably at least 200 amino acids, and most preferably at least 250 amino acids.

The term "sequence analysis software" refers to any computer
5 algorithm or software program that is useful for the analysis of nucleotide or amino acid sequences. "Sequence analysis software" may be commercially available or independently developed. Typical sequence analysis software will include, but is not limited to: 1.) the GCG suite of
10 programs (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, WI); 2.) BLASTP, BLASTN, BLASTX (Altschul et al., *J. Mol. Biol.*, 215:403-410 (1990)); 3.) DNASTAR (DNASTAR, Inc. Madison, WI); 4.) Sequencher (Gene Codes Corporation, Ann Arbor, MI); and 5.) the FASTA program incorporating the Smith-Waterman algorithm (W. R. Pearson, *Comput. Methods Genome Res.*, [Proc. Int. Symp.]
15 (1994), Meeting Date 1992, 111-20. Editor(s): Suhai, Sandor. Plenum: New York, NY). Within the context of this application it will be understood that where sequence analysis software is used for analysis, that the results of the analysis will be based on the "default values" of the program referenced, unless otherwise specified. As used herein "default values"
20 will mean any set of values or parameters that originally load with the software when first initialized.

Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by Sambrook, J., Fritsch, E. F. and Maniatis, T., *Molecular Cloning: A Laboratory Manual*, Second
25 Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) (hereinafter "Maniatis"); and by Silhavy, T. J., Bennis, M. L. and Enquist, L. W., *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1984); and by Ausubel, F. M. et al., *Current Protocols in Molecular Biology*, published by Greene
30 Publishing Assoc. and Wiley-Interscience (1987).

The invention relates to the engineering of a lactic acid bacterial cell such that the cell is substantially free of lactic acid dehydrogenase

(LDH) activity and has DHAD activity. Surprisingly, it was found that expression of the Fe-S cluster requiring DHAD enzyme in a host cell substantially lacking LDH activity resulted in increased specific activity as compared to the activity of the same DHAD enzyme when expressed in a host containing LDH activity.

DHAD activity

Lactic acid bacteria cells substantially free of lactic acid dehydrogenase and expressing DHAD enzymes having a specific activity level of at least about $0.1 \mu\text{mol min}^{-1} \text{mg}^{-1}$ where mg is the amount of total soluble protein in a crude cell extract. In addition, DHAD specific activities of at least about $0.2 \mu\text{mol min}^{-1} \text{mg}^{-1}$, and of at least about $0.4 \mu\text{mol min}^{-1} \text{mg}^{-1}$ may be achieved in LAB cells, where specific activities of at least about $0.6 \mu\text{mol min}^{-1} \text{mg}^{-1}$ are reasonably expected. Disclosed herein are LAB cells having these levels of DHAD activity.

In the disclosed LAB cells, any gene encoding a DHAD enzyme may be used to provide expression of DHAD activity in a LAB cell. DHAD, also called acetohydroxy acid dehydratase, catalyzes the conversion of 2,3-dihydroxyisovalerate to α -ketoisovalerate and of 2,3-dihydroxymethylvalerate to α -ketomethylvalerate and is classified as E.C. 4.2.1.9. Coding sequences for DHADs that may be used herein may be derived from bacterial, fungal, or plant sources. DHADs that may be used may have a [4Fe-4S] cluster or a [2Fe-2S] cluster bound by the apoprotein. Tables 1, 2, and 3 list SEQ ID NOs for coding regions and proteins of representative DHADs that may be used in the present invention. Proteins with at least about 95% identity to those listed sequences have been omitted for simplification, but it is understood that the omitted proteins with at least about 95% sequence identity to any of the proteins listed in Tables 1, 2, and 3 and having DHAD activity may be used as disclosed herein. Additional DHAD proteins and their encoding sequences may be identified by BLAST searching of public databases, as well known to one skilled in the art. Typically BLAST (described above) searching of publicly available databases with known DHAD sequences,

such as those provided herein, is used to identify DHADs and their encoding sequences that may be expressed in the present cells. For example, DHAD proteins having amino acid sequence identities of at least about 80-85%, 85%- 90%, 90%- 95% or 98% sequence identity to any of the DHAD proteins of Table 1 may be expressed in the present cells. Identities are based on the Clustal W method of alignment using the default parameters of GAP PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix over the full length of the protein sequence.

Additional [2Fe-2S] DHADs may be identified using the analysis described in co-pending US Patent Application 61/100792, which is herein incorporated by reference. The analysis is as follows: A Profile Hidden Markov Model (HMM) was prepared based on amino acid sequences of eight functionally verified DHADs. These DHADs are from *Nitrosomonas europaea* (DNA SEQ ID NO:309; protein SEQ ID NO:310), *Synechocystis* sp. PCC6803 (DNA SEQ ID:297; protein SEQ ID NO:298), *Streptococcus mutans* (DNA SEQ ID NO:167; protein SEQ ID NO:168), *Streptococcus thermophilus* (DNA SEQ ID NO:163; SEQ ID No:164), *Ralstonia metallidurans* (DNA SEQ ID NO:345; protein SEQ ID NO:346), *Ralstonia eutropha* (DNA SEQ ID NO:343; protein SEQ ID NO:344), and *Lactococcus lactis* (DNA SEQ ID NO:231; protein SEQ ID NO:232). In addition the DHAD from *Flavobacterium johnsoniae* (DNA SEQ ID NO:229; protein SEQ ID NO:230) was found to have dihydroxy-acid dehydratase activity when expressed in *E. coli* and was used in making the Profile. The Profile HMM is prepared using the HMMER software package (The theory behind profile HMMs is described in R. Durbin, S. Eddy, A. Krogh, and G. Mitchison, Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press, 1998; Krogh et al., 1994; J. Mol. Biol. 235:1501–1531), following the user guide which is available from HMMER (Janelia Farm Research Campus, Ashburn, VA). The output of the HMMER software program is a Profile Hidden Markov Model (HMM) that characterizes the input

sequences. The Profile HMM prepared for the eight DHAD proteins is given in Table 7. Any protein that matches the Profile HMM with an E value of $< 10^{-5}$ is a DHAD related protein, which includes [4Fe-4S] DHADs, [2Fe-2S] DHADs, aldonic acid dehydratases, and phosphogluconate dehydratases. Sequences matching the Profile HMM are then analyzed for the presence of the three conserved cysteines, corresponding to positions 56, 129, and 201 in the *Streptococcus mutans* DHAD. The presence of all three conserved cysteines is characteristic of proteins having a [2Fe-2S] cluster. Proteins having the three conserved cysteines include arabinonate dehydratases and [2Fe-2S] DHADs and are members of a [2Fe-2S] DHAD/aldonic acid dehydratase group. The [2Fe-2S] DHADs may be distinguished from the aldonic acid dehydratases by analyzing for signature conserved amino acids found to be present in the [2Fe-2S] DHADs or in the aldonic acid dehydratases at positions corresponding to the following positions in the *Streptococcus mutans* DHAD amino acid sequence. These signature amino acids are in [2Fe-2S] DHADs or in aldonic acid dehydratases, respectively, at the following positions (with greater than 90% occurrence): 88 asparagine vs glutamic acid; 113 not conserved vs glutamic acid; 142 arginine or asparagine vs not conserved; 165: not conserved vs glycine; 208 asparagine vs not conserved; 454 leucine vs not conserved; 477 phenylalanine or tyrosine vs not conserved; and 487 glycine vs not conserved.

Additionally, the sequences of DHAD coding regions provided herein may be used to identify other homologs in nature. For example each of the DHAD encoding nucleic acid fragments described herein may be used to isolate genes encoding homologous proteins. Isolation of homologous genes using sequence-dependent protocols is well known in the art. Examples of sequence-dependent protocols include, but are not limited to: 1.) methods of nucleic acid hybridization; 2.) methods of DNA and RNA amplification, as exemplified by various uses of nucleic acid amplification technologies [e.g., polymerase chain reaction (PCR), Mullis et al., U.S. Patent 4,683,202; ligase chain reaction (LCR), Tabor, S. et al.,

Proc. Acad. Sci. USA 82:1074 (1985); or strand displacement amplification (SDA), Walker, et al., *Proc. Natl. Acad. Sci. U.S.A.*, 89:392 (1992)]; and 3.) methods of library construction and screening by complementation.

5 For example, genes encoding similar proteins or polypeptides to the DHAD encoding genes provided herein could be isolated directly by using all or a portion of the instant nucleic acid fragments as DNA hybridization probes to screen libraries from any desired organism using methodology well known to those skilled in the art. Specific
10 oligonucleotide probes based upon the disclosed nucleic acid sequences can be designed and synthesized by methods known in the art (Maniatis, *supra*). Moreover, the entire sequences can be used directly to synthesize DNA probes by methods known to the skilled artisan (e.g., random primers DNA labeling, nick translation or end-labeling techniques),
15 or RNA probes using available *in vitro* transcription systems. In addition, specific primers can be designed and used to amplify a part of (or full-length of) the instant sequences. The resulting amplification products can be labeled directly during amplification reactions or labeled after amplification reactions, and used as probes to isolate full-length DNA
20 fragments by hybridization under conditions of appropriate stringency.

 Typically, in PCR-type amplification techniques, the primers have different sequences and are not complementary to each other. Depending on the desired test conditions, the sequences of the primers should be designed to provide for both efficient and faithful replication of the target
25 nucleic acid. Methods of PCR primer design are common and well known in the art (Thein and Wallace, "The use of oligonucleotides as specific hybridization probes in the Diagnosis of Genetic Disorders", in *Human Genetic Diseases: A Practical Approach*, K. E. Davis Ed., (1986) pp 33-50, IRL: Herndon, VA; and Rychlik, W., In Methods in Molecular Biology,
30 White, B. A. Ed., (1993) Vol. 15, pp 31-39, PCR Protocols: Current Methods and Applications. Humana: Totowa, NJ).

Generally two short segments of the described sequences may be used in polymerase chain reaction protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. The polymerase chain reaction may also be performed on a library of cloned
5 nucleic acid fragments wherein the sequence of one primer is derived from the described nucleic acid fragments, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding microbial genes.

Alternatively, the second primer sequence may be based upon
10 sequences derived from the cloning vector. For example, the skilled artisan can follow the RACE protocol (Frohman et al., *PNAS USA* 85:8998 (1988)) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the instant
15 sequences. Using commercially available 3' RACE or 5' RACE systems (e.g., BRL, Gaithersburg, MD), specific 3' or 5' cDNA fragments can be isolated (Ohara et al., *PNAS USA* 86:5673 (1989); Loh et al., *Science* 243:217 (1989)).

Alternatively, the provided DHAD encoding sequences may be
20 employed as hybridization reagents for the identification of homologs. The basic components of a nucleic acid hybridization test include a probe, a sample suspected of containing the gene or gene fragment of interest, and a specific hybridization method. Probes are typically single-stranded nucleic acid sequences that are complementary to the nucleic acid
25 sequences to be detected. Probes are "hybridizable" to the nucleic acid sequence to be detected. The probe length can vary from 5 bases to tens of thousands of bases, and will depend upon the specific test to be done. Typically a probe length of about 15 bases to about 30 bases is suitable. Only part of the probe molecule need be complementary to the nucleic
30 acid sequence to be detected. In addition, the complementarity between the probe and the target sequence need not be perfect. Hybridization does occur between imperfectly complementary molecules with the result

that a certain fraction of the bases in the hybridized region are not paired with the proper complementary base.

Hybridization methods are well defined. Typically the probe and sample must be mixed under conditions that will permit nucleic acid hybridization. This involves contacting the probe and sample in the presence of an inorganic or organic salt under the proper concentration and temperature conditions. The probe and sample nucleic acids must be in contact for a long enough time that any possible hybridization between the probe and sample nucleic acid may occur. The concentration of probe or target in the mixture will determine the time necessary for hybridization to occur. The higher the probe or target concentration, the shorter the hybridization incubation time needed. Optionally, a chaotropic agent may be added. The chaotropic agent stabilizes nucleic acids by inhibiting nuclease activity. Furthermore, the chaotropic agent allows sensitive and stringent hybridization of short oligonucleotide probes at room temperature (Van Ness and Chen, *Nucl. Acids Res.* 19:5143-5151 (1991)). Suitable chaotropic agents include guanidinium chloride, guanidinium thiocyanate, sodium thiocyanate, lithium tetrachloroacetate, sodium perchlorate, rubidium tetrachloroacetate, potassium iodide and cesium trifluoroacetate, among others. Typically, the chaotropic agent will be present at a final concentration of about 3 M. If desired, one can add formamide to the hybridization mixture, typically 30-50% (v/v).

Various hybridization solutions can be employed. Typically, these comprise from about 20 to 60% volume, preferably 30%, of a polar organic solvent. A common hybridization solution employs about 30-50% v/v formamide, about 0.15 to 1 M sodium chloride, about 0.05 to 0.1 M buffers (e.g., sodium citrate, Tris-HCl, PIPES or HEPES (pH range about 6-9)), about 0.05 to 0.2% detergent (e.g., sodium dodecylsulfate), or between 0.5-20 mM EDTA, FICOLL (Pharmacia Inc.) (about 300-500 kdal), polyvinylpyrrolidone (about 250-500 kdal) and serum albumin. Also included in the typical hybridization solution will be unlabeled carrier nucleic acids from about 0.1 to 5 mg/mL, fragmented nucleic DNA (e.g.,

calf thymus or salmon sperm DNA, or yeast RNA), and optionally from about 0.5 to 2% wt/vol glycine. Other additives may also be included, such as volume exclusion agents that include a variety of polar water-soluble or swellable agents (e.g., polyethylene glycol), anionic polymers
5 (e.g., polyacrylate or polymethylacrylate) and anionic saccharidic polymers (e.g., dextran sulfate).

Nucleic acid hybridization is adaptable to a variety of assay formats. One of the most suitable is the sandwich assay format. The sandwich assay is particularly adaptable to hybridization under non-
10 denaturing conditions. A primary component of a sandwich-type assay is a solid support. The solid support has adsorbed to it or covalently coupled to it immobilized nucleic acid probe that is unlabeled and complementary to one portion of the sequence.

Genetic modification for expression of DHAD activity

15 LAB cells that may be engineered to create cells of the present invention include, but are not limited to, *Lactococcus*, *Lactobacillus*, *Leuconostoc*, *Oenococcus*, *Pediococcus*, and *Streptococcus*.

LAB cells are genetically modified for expression of DHAD activity using methods well known to one skilled in the art. Expression of DHAD is
20 generally achieved by transforming suitable LAB host cells with a sequence encoding a DHAD protein. Typically the coding sequence is part of a chimeric gene used for transformation, which includes a promoter operably linked to the coding sequence as well as a ribosome binding site and a termination control region. The coding region may be from the host
25 cell for transformation and combined with regulatory sequences that are not native to the natural gene encoding DHAD. Alternatively, the coding region may be from another host cell.

Codons may be optimized for expression based on codon usage in the selected host, as is known to one skilled in the art. Vectors useful for
30 the transformation of a variety of host cells are common and described in the literature. Typically the vector contains a selectable marker and sequences allowing autonomous replication or chromosomal integration in

the desired host. In addition, suitable vectors may comprise a promoter region which harbors transcriptional initiation controls and a transcriptional termination control region, between which a coding region DNA fragment may be inserted, to provide expression of the inserted coding region. Both
5 control regions may be derived from genes homologous to the transformed host cell, although it is to be understood that such control regions may also be derived from genes that are not native to the specific species chosen as a production host.

Initiation control regions or promoters, which are useful to drive
10 expression of a DHAD coding region in LAB are familiar to those skilled in the art. Some examples include the *amy*, *apr*, and *npr* promoters; *nisA* promoter (useful for expression Gram-positive bacteria (Eichenbaum et al. *Appl. Environ. Microbiol.* 64(8):2763-2769 (1998)); and the synthetic P11 promoter (useful for expression in *Lactobacillus plantarum*, Rud et al.,
15 *Microbiology* 152:1011-1019 (2006)). In addition, the *ldhL1* and *fabZ1* promoters of *L. plantarum* are useful for expression of chimeric genes in LAB. The *fabZ1* promoter directs transcription of an operon with the first gene, *fabZ1*, encoding (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase.

20 Termination control regions may also be derived from various genes, typically from genes native to the preferred hosts. Optionally, a termination site may be unnecessary, however, it is most preferred if included.

Vectors useful in LAB include vectors having two origins of
25 replication and one or two selectable markers which allow for replication and selection in both *Escherichia coli* and LAB. Examples are pFP996 (SEQ ID NO:565) and pDM1 (SEQ ID NO:563), which are useful in *L. plantarum* and other LAB. Many plasmids and vectors used in the transformation of *Bacillus subtilis* and *Streptococcus* may be used
30 generally for LAB. Non-limiting examples of suitable vectors include pAM β 1 and derivatives thereof (Renault et al., *Gene* 183:175-182 (1996); and O'Sullivan et al., *Gene* 137:227-231 (1993)); pMBB1 and pHW800, a

- derivative of pMBB1 (Wyckoff et al. *Appl. Environ. Microbiol.* 62:1481-1486 (1996)); pMG1, a conjugative plasmid (Tanimoto et al., *J. Bacteriol.* 184:5800-5804 (2002)); pNZ9520 (Kleerebezem et al., *Appl. Environ. Microbiol.* 63:4581-4584 (1997)); pAM401 (Fujimoto et al., *Appl. Environ. Microbiol.* 67:1262-1267 (2001)); and pAT392 (Arthur et al., *Antimicrob. Agents Chemother.* 38:1899-1903 (1994)). Several plasmids from *Lactobacillus plantarum* have also been reported (e.g., van Kranenburg R, Golic N, Bongers R, Leer RJ, de Vos WM, Siezen RJ, Kleerebezem M. *Appl. Environ. Microbiol.* 2005 Mar; 71(3): 1223-1230).
- 10 Vectors may be introduced into a host cell using methods known in the art, such as electroporation (Cruz-Rodz et al. *Molecular Genetics and Genomics* 224:1252-154 (1990), Bringel, et al. *Appl. Microbiol. Biotechnol.* 33: 664-670 (1990), Alegre et al., *FEMS Microbiology letters* 241:73-77 (2004)), and conjugation (Shrago et al., *Appl. Environ. Microbiol.* 52:574-15 576 (1986)). A chimeric DHAD gene can also be integrated into the chromosome of LAB using integration vectors (Hols et al., *Appl. Environ. Microbiol.* 60:1401-1403 (1990), Jang et al., *Micro. Lett.* 24:191-195 (2003)).

Reduced lactate dehydrogenase activity

- 20 DHAD activity of at least about 0.1, 0.2, 0.4 or 0.6 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ may be achieved in a LAB cell by modifying the cell such that it is substantially free of lactate dehydrogenase enzyme activity. Lactate dehydrogenases are known as EC 1.1.1.27 (L-lactate dehydrogenase) or EC 1.1.1.28 (D-lactate dehydrogenase). At least one genetic modification 25 is made in a LAB cell to render it substantially free of lactate dehydrogenase activity. DHAD is expressed as described above in the so modified LAB cell.

- Endogenous lactate dehydrogenase activity in lactic acid bacteria (LAB) converts pyruvate to lactate. LAB may have one or more genes, 30 typically one, two or three genes, encoding lactate dehydrogenase. For example, *Lactobacillus plantarum* has three genes encoding lactate dehydrogenase which are named *ldhL2* (protein SEQ ID NO: 500, coding

region SEQ ID NO: 499), IdhD (protein SEQ ID NO: 496, coding region SEQ ID NO: 495), and IdhL1 (protein SEQ ID NO: 498, coding region SEQ ID NO: 497). *Lactococcus lactis* has one gene encoding lactate dehydrogenase which is named IdhL (protein SEQ ID NO: 502, coding region SEQ ID NO: 501), and *Pediococcus pentosaceus* has two genes named IdhD (protein SEQ ID NO: 508, coding region SEQ ID NO: 507) and IdhL (protein SEQ ID NO: 510, coding region SEQ ID NO: 509).

In the present LAB strains, lactate dehydrogenase activity is reduced so that the cells are substantially free of lactate dehydrogenase activity. Genetic modification is made in at least one gene encoding lactate dehydrogenase to reduce activity. When more than one lactate dehydrogenase gene is active under the growth conditions to be used, each of these active genes may be modified to reduce expression. For example, in *L. plantarum* IdhL1 and IdhD genes are modified. It is not necessary to modify the third gene, IdhL2, for growth in typical conditions as this gene appears to be inactive in these conditions. Typically, expression of one or more genes encoding lactate dehydrogenase is disrupted to reduce expressed enzyme activity. Examples of LAB lactate dehydrogenase genes that may be targeted for disruption are represented by the coding regions of SEQ ID NOs: 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, and 515 listed in Table 4. Other target genes, such as those encoding lactate dehydrogenase proteins having at least about 80-85%, 85%-90%, 90%-95%, or 98% sequence identity to the lactate dehydrogenases of SEQ ID NOs: 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, and 516 listed in Table 4 may be identified in the literature and using bioinformatics approaches, as is well known to the skilled person, since lactate dehydrogenases are well known. Typically BLAST (described above) searching of publicly available databases with known lactate dehydrogenase amino acid sequences, such as those provided herein, is used to identify lactate dehydrogenases, and their encoding sequences, that may be targets for disruption to reduce lactate dehydrogenase activity. Identities are based on the Clustal W method of alignment using

the default parameters of GAP PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix.

Additionally, the sequences described herein or those recited in the art may be used to identify other homologs in nature in other LAB strains
5 as described above for DHAD homolog analysis.

In the present LAB strains, at least one modification is engineered that results in cells substantially free of lactate dehydrogenase activity. This may be accomplished by eliminating expression of at least one endogenous gene encoding lactate dehydrogenase. Any genetic
10 modification method known by one skilled in the art for reducing the expression of a protein may be used to alter lactate dehydrogenase expression. Methods include, but are not limited to, deletion of the entire or a portion of the lactate dehydrogenase encoding gene, inserting a DNA fragment into the lactate dehydrogenase encoding gene (in either the
15 promoter or coding region) so that the encoded protein cannot be expressed, introducing a mutation into the lactate dehydrogenase coding region which adds a stop codon or frame shift such that a functional protein is not expressed, and introducing one or more mutations into the lactate dehydrogenase coding region to alter amino acids so that a non-
20 functional protein is expressed. In addition lactate dehydrogenase expression may be blocked by expression of an antisense RNA or an interfering RNA, and constructs may be introduced that result in cosuppression. All of these methods may be readily practiced by one skilled in the art making use of the known lactate dehydrogenase
25 encoding sequences such as those of SEQ ID NOs: 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, and 515.

For some methods genomic DNA sequences that surround a lactate dehydrogenase encoding sequence are useful, such as for homologous recombination-based methods. These sequences may be
30 available from genome sequencing projects such as for *Lactobacillus plantarum*, which is available through the National Center for Biotechnology Information (NCBI) database, with Genbank TM

identification gi|28376974|ref|NC_004567.1|[28376974]. Adjacent genomic DNA sequences may also be obtained by sequencing outward from a lactate dehydrogenase coding sequence using primers within the coding sequence, as well known to one skilled in the art.

- 5 A particularly suitable method for creating a genetically modified LAB strain with substantially no lactate dehydrogenase activity, as exemplified herein in Example 1, is using homologous recombination mediated by lactate dehydrogenase coding region flanking DNA sequences to delete the entire gene. The flanking sequences are cloned
10 adjacent to each other so that a double crossover event using these flanking sequences deletes the lactate dehydrogenase coding region.

Isobutanol and other products

- Isobutanol and any other product made from a biosynthetic pathway including DHAD activity may be produced with greater
15 effectiveness in a LAB cell disclosed herein having at least about 0.1, 0.2, or 0.4 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ of DHAD activity. Such products include, but are not limited to valine, isoleucine, leucine, pantothenic acid (vitamin B5), 2-methyl-1-butanol, 3-methyl-1-butanol, and isobutanol.

- For example, biosynthesis of valine includes steps of acetolactate
20 conversion to 2,3-dihydroxy-isovalerate by acetohydroxyacid reductoisomerase (ilvC), conversion of 2,3-dihydroxy-isovalerate to α -ketoisovalerate (also called 2-keto-isovalerate) by dihydroxy-acid dehydratase (ilvD), and conversion of α -ketoisovalerate to valine by branched-chain amino acid aminotransferase (ilvE). Biosynthesis of
25 leucine includes the same steps to α -ketoisovalerate, followed by conversion of α -ketoisovalerate to leucine by enzymes encoded by leuA (2-isopropylmalate synthase), leuCD (isopropylmalate isomerase), leuB (3-isopropylmalate dehydrogenase), and tyrB/ ilvE (aromatic amino acid transaminase). Biosynthesis of pantothenate includes the same steps to
30 α -ketoisovalerate, followed by conversion of α -ketoisovalerate to pantothenate by enzymes encoded by panB (3-methyl-2-oxobutanoate hydroxymethyltransferase), panE (2-dehydropantoate reductase), and

panC (pantoate-beta-alanine ligase). Engineering expression of enzymes for enhanced production of pantothenic acid in microorganisms is described in US 6177264.

- Increased conversion of 2,3-dihydroxy-isovalerate to α -ketoisovalerate will increase flow in these pathways, particularly if one or more additional enzymes of a pathway is overexpressed. Thus it is desired for production of, for example, valine, leucine, or pantothenate to use an engineered LAB cell disclosed herein.

- The α -ketoisovalerate product of DHAD is an intermediate in isobutanol biosynthetic pathways disclosed in commonly owned and co-pending US Patent Pub No. 20070092957 A1, which is herein incorporated by reference. A diagram of the disclosed isobutanol biosynthetic pathways is provided in Figure 1. Production of isobutanol in a strain disclosed herein benefits from increased DHAD activity. As described in US Patent Pub No. US20070092957 A1, steps in an example isobutanol biosynthetic pathway include conversion of:
- pyruvate to acetolactate (Fig. 1 pathway step a), as catalyzed for example by acetolactate synthase,
 - acetolactate to 2,3-dihydroxyisovalerate (Fig. 1 pathway step b) as catalyzed for example by acetohydroxy acid isomeroreductase;
 - 2,3-dihydroxyisovalerate to α -ketoisovalerate (Fig. 1 pathway step c) as catalyzed for example by acetohydroxy acid dehydratase, also called dihydroxy-acid dehydratase (DHAD);
 - α -ketoisovalerate to isobutyraldehyde (Fig. 1 pathway step d) as catalyzed for example by branched-chain α -keto acid decarboxylase ;and
 - isobutyraldehyde to isobutanol (Fig. 1 pathway step e) as catalyzed for example by branched-chain alcohol dehydrogenase.

- The substrate to product conversions, and enzymes involved in these reactions, for steps f, g, h, i, j, and k of alternative pathways are described in US Patent Pub No. US20070092957 A1.

Genes that may be used for expression of the pathway step enzymes named above other than the DHADs disclosed herein, as well as

those for two additional isobutanol pathways, are described in US Patent Pub No. 20070092957 A1, and additional genes that may be used can be identified by one skilled in the art through bioinformatics or experimentally as described above. The preferred use in all three pathways of ketol-acid

- 5 reductoisomerase (KARI) enzymes with particularly high activities is disclosed in co-pending US Patent Pub No. US20080261230 A1. Examples of high activity KARIs disclosed therein are those from *Vibrio cholerae* (DNA: SEQ ID NO:517; protein SEQ ID NO:518), *Pseudomonas aeruginosa* PAO1, (DNA: SEQ ID NO:523; protein SEQ ID NO:524), and
10 *Pseudomonas fluorescens* PF5 (DNA: SEQ ID NO:519; protein SEQ ID NO:520).

Additionally described in US Patent Pub No. 20070092957 A1 are construction of chimeric genes and genetic engineering of bacteria for isobutanol production using the disclosed biosynthetic pathways.

- 15 Expression of these enzymes in LAB is as described above for expression of DHADs.

Growth for production

- Recombinant LAB cells disclosed herein may be used for fermentation production of isobutanol and other products as follows. The
20 recombinant cells are grown in fermentation media which contains suitable carbon substrates. Suitable substrates may include but are not limited to monosaccharides such as glucose and fructose, or mixtures of monosaccharides that include C5 sugars such as xylose and arabinose, oligosaccharides such as lactose or sucrose, polysaccharides such as
25 starch or cellulose or mixtures thereof and unpurified mixtures from renewable feedstocks such as cheese whey permeate, cornsteep liquor, sugar beet molasses, and barley malt.

- Although it is contemplated that all of the above mentioned carbon substrates and mixtures thereof are suitable in the present invention,
30 preferred carbon substrates are glucose, fructose, and sucrose. Sucrose may be derived from renewable sugar sources such as sugar cane, sugar beets, cassava, sweet sorghum, and mixtures thereof. Glucose and

dextrose may be derived from renewable grain sources through saccharification of starch based feedstocks including grains such as corn, wheat, rye, barley, oats, and mixtures thereof. In addition, fermentable sugars may be derived from renewable cellulosic or lignocellulosic biomass through processes of pretreatment and saccharification, as described, for example, in co-owned and co-pending US Patent Pub No. US20070031918A1, which is herein incorporated by reference. Biomass refers to any cellulosic or lignocellulosic material and includes materials comprising cellulose, and optionally further comprising hemicellulose, lignin, starch, oligosaccharides and/or monosaccharides. Biomass may also comprise additional components, such as protein and/or lipid. Biomass may be derived from a single source, or biomass can comprise a mixture derived from more than one source; for example, biomass may comprise a mixture of corn cobs and corn stover, or a mixture of grass and leaves. Biomass includes, but is not limited to, bioenergy crops, agricultural residues, municipal solid waste, industrial solid waste, sludge from paper manufacture, yard waste, wood and forestry waste. Examples of biomass include, but are not limited to, corn grain, corn cobs, crop residues such as corn husks, corn stover, grasses, wheat, wheat straw, barley, barley straw, hay, rice straw, switchgrass, waste paper, sugar cane bagasse, sorghum, soy, components obtained from milling of grains, trees, branches, roots, leaves, wood chips, sawdust, shrubs and bushes, vegetables, fruits, flowers, animal manure, and mixtures thereof.

In addition to an appropriate carbon source, fermentation media must contain suitable minerals, salts, cofactors, buffers and other components, known to those skilled in the art, suitable for the growth of the cultures and promotion of the enzymatic pathway necessary for isobutanol production.

Typically cells are grown at a temperature in the range of about 25 °C to about 40 °C in an appropriate medium. Suitable growth media are common commercially prepared media such as Bacto Lactobacilli MRS broth or Agar (Difco), Luria Bertani (LB) broth, Sabouraud Dextrose (SD)

broth or Yeast Medium (YM) broth. Other defined or synthetic growth media may also be used, and the appropriate medium for growth of the particular bacterial strain will be known by one skilled in the art of microbiology or fermentation science. The use of agents known to
5 modulate catabolite repression directly or indirectly, e.g., cyclic adenosine 2':3'-monophosphate, may also be incorporated into the fermentation medium.

Suitable pH ranges for the fermentation are between pH 5.0 to pH 9.0, where pH 6.0 to pH 8.0 is preferred as the initial condition.

10 Fermentations may be performed under aerobic or anaerobic conditions, where anaerobic or microaerobic conditions are preferred.

Isobutanol, or other product, may be produced using a batch method of fermentation. A classical batch fermentation is a closed system where the composition of the medium is set at the beginning of the
15 fermentation and not subject to artificial alterations during the fermentation. A variation on the standard batch system is the fed-batch system. Fed-batch fermentation processes are also suitable in the present invention and comprise a typical batch system with the exception that the substrate is added in increments as the fermentation progresses.
20 Fed-batch systems are useful when catabolite repression is apt to inhibit the metabolism of the cells and where it is desirable to have limited amounts of substrate in the media. Batch and fed-batch fermentations are common and well known in the art and examples may be found in Thomas D. Brock in *Biotechnology: A Textbook of Industrial Microbiology*, Second
25 Edition (1989) Sinauer Associates, Inc., Sunderland, MA., or Deshpande, Mukund V., *Appl. Biochem. Biotechnol.*, 36:227, (1992), herein incorporated by reference.

Isobutanol, or other product, may also be produced using continuous fermentation methods. Continuous fermentation is an open
30 system where a defined fermentation medium is added continuously to a bioreactor and an equal amount of conditioned media is removed simultaneously for processing. Continuous fermentation generally

maintains the cultures at a constant high density where cells are primarily in log phase growth. Continuous fermentation allows for the modulation of one factor or any number of factors that affect cell growth or end product concentration. Methods of modulating nutrients and growth factors for continuous fermentation processes as well as techniques for maximizing the rate of product formation are well known in the art of industrial microbiology and a variety of methods are detailed by Brock, *supra*.

It is contemplated that the production of isobutanol, or other product, may be practiced using batch, fed-batch or continuous processes and that any known mode of fermentation would be suitable. Additionally, it is contemplated that cells may be immobilized on a substrate as whole cell catalysts and subjected to fermentation conditions for isobutanol production.

Methods for Isobutanol Isolation from the Fermentation Medium

Bioproducted isobutanol may be isolated from the fermentation medium using methods known in the art for ABE fermentations (see for example, Durre, *Appl. Microbiol. Biotechnol.* 49:639-648 (1998), Groot et al., *Process. Biochem.* 27:61-75 (1992), and references therein). For example, solids may be removed from the fermentation medium by centrifugation, filtration, decantation, or the like. Then, the isobutanol may be isolated from the fermentation medium using methods such as distillation, azeotropic distillation, liquid-liquid extraction, adsorption, gas stripping, membrane evaporation, or pervaporation.

EXAMPLES

The present invention is further defined in the following Examples. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various uses and conditions.

The meaning of abbreviations used is as follows: “min” means minute(s), “h” means hour(s), “sec” means second(s), “ μ l” means microliter(s), “ml” means milliliter(s), “L” means liter(s), “nm” means nanometer(s), “mm” means millimeter(s), “cm” means centimeter(s), “ μ m” means micrometer(s), “mM” means millimolar, “M” means molar, “mmol” means millimole(s), “ μ mole” means micromole(s), “g” means gram(s), “ μ g” means microgram(s), “mg” means milligram(s), “rpm” means revolutions per minute, “w/v” means weight/volume, “OD” means optical density, and “OD600” means optical density measured at a wavelength of 600 nm.

10 GENERAL METHODS:

Standard recombinant DNA and molecular cloning techniques used in the Examples are well known in the art and are described by Sambrook, J., Fritsch, E. F. and Maniatis, T., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989, by T. J. Silhavy, M. L. Bannan, and L. W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1984, and by Ausubel, F. M. et al., *Current Protocols in Molecular Biology*, Greene Publishing Assoc. and Wiley-Interscience, N.Y., 1987. Additional methods used in the Examples are described in manuals including

20 Advanced Bacterial Genetics (Davis, Roth and Botstein, Cold Spring Harbor Laboratory, 1980), Experiments with Gene Fusions (Silhavy, Berman and Enquist, Cold Spring Harbor Laboratory, 1984), Experiments in Molecular Genetics (Miller, Cold Spring Harbor Laboratory, 1972) Experimental Techniques in Bacterial Genetics (Maloy, in Jones and

25 Bartlett, 1990), and A Short Course in Bacterial Genetics (Miller, Cold Spring Harbor Laboratory 1992).

Example 1

Construction of dihydroxy-acid dehydratase (DHAD) expression cassettes

The purpose of this example is to describe how to clone and

30 express a gene encoding dihydroxy-acid dehydratase (*ilvD*) from different bacterial sources in *Lactobacillus plantarum* PN0512 (ATCC PTA-7727)

and *Lactobacillus plantarum* PN0512 carrying a double lactate dehydrogenase deletion, $\Delta ldhD \Delta ldhL1$.

A *Lactobacillus plantarum* PN0512 strain that is deleted for the two genes that encode the major lactate dehydrogenases was prepared as follows. The major end product of fermentation in *Lactobacillus plantarum* is lactic acid. Pyruvate is converted to lactate by the action of two lactate dehydrogenases encoded by the *ldhD* and *ldhL1* genes. A double deletion of *ldhD* and *ldhL1* was made in *Lactobacillus plantarum* PN0512 (ATCC strain # PTA-7727).

Gene knockouts were constructed using a process based on a two-step homologous recombination procedure to yield unmarked gene deletions (Ferain et al., 1994, *J. Bact.* 176:596). The procedure utilized a shuttle vector, pFP996 (SEQ ID NO:565). pFP996 is a shuttle vector for gram-positive bacteria. It can replicate in both *E. coli* and gram-positive bacteria. It contains the origins of replication from pBR322 (nucleotides #2628 to 5323) and pE194 (nucleotides #43 to 2627). pE194 is a small plasmid isolated originally from a gram positive bacterium, *Staphylococcus aureus* (Horinouchi and Weisblum *J. Bacteriol.* (1982) 150(2):804-814). In pFP996, the multiple cloning sites (nucleotides #1 to 50) contain restriction sites for EcoRI, BglII, XhoI, SmaI, ClaI, KpnI, and HindIII. There are two antibiotic resistance markers; one is for resistance to ampicillin and the other for resistance to erythromycin. For selection purposes, ampicillin was used for transformation in *E. coli* and erythromycin was used for selection in *L. plantarum*.

Two segments of DNA, each containing 900 to 1200 bp of sequence either upstream or downstream of the intended deletion, were cloned into the plasmid to provide the regions of homology for the two genetic cross-overs. Cells were grown for an extended number of generations (30-50) to allow for the cross-over events to occur. The initial cross-over (single cross-over) integrated the plasmid into the chromosome by homologous recombination through one of the two homology regions on the plasmid. The second cross-over (double cross-over) event yielded

either the wild-type sequence or the intended gene deletion. A cross-over between the sequences that led to the initial integration event would yield the wild-type sequence, while a cross-over between the other regions of homology would yield the desired deletion. The second cross-over event
5 was screened for by antibiotic sensitivity. Single and double cross-over events were analyzed by PCR and DNA sequencing.

All restriction enzymes, DNA modifying enzymes and Phusion High-Fidelity PCR Master Mix were purchased from NEB Inc. (Ipswich, Ma). PCR SuperMix and Platinum PCR SuperMix High Fidelity were
10 purchased from Invitrogen Corp (Carlsbad, CA). DNA fragments were gel purified using Zymoclean™ Gel DNA Recovery Kit (Zymo Research Corp, Orange, CA) or Qiaquick PCR Purification Kit (Qiagen Inc., Valencia, CA). Plasmid DNA was prepared with QIAprep Spin Miniprep Kit (Qiagen Inc., Valencia, CA). Oligonucleotides were synthesized by Sigma-Genosys
15 (Woodlands, TX) or Invitrogen Corp (Carlsbad, CA). *L. plantarum* PN0512 genomic DNA was prepared with MasterPure DNA Purification Kit (Epicentre, Madison, WI).

Lactobacillus plantarum PN0512 was transformed by the following procedure: 5 ml of Lactobacilli MRS medium (Accumedia, Neogen
20 Corporation, Lansing, MI) containing 1% glycine (Sigma-Aldrich, St. Louis, MO) was inoculated with PN0512 cells and grown overnight at 30°C. 100 ml MRS medium with 1% glycine was inoculated with overnight culture to an OD600 of 0.1 and grown to an OD600 of 0.7 at 30°C. Cells were harvested at 3700xg for 8 min at 4 °C, washed with 100 ml cold 1 mM
25 MgCl₂ (Sigma-Aldrich, St. Louis, MO), centrifuged at 3700xg for 8 min at 4 °C, washed with 100 ml cold 30% PEG-1000 (Sigma-Aldrich, St. Louis, MO), recentrifuged at 3700xg for 20 min at 4 °C, then resuspended in 1 ml cold 30% PEG-1000. 60 µl cells were mixed with ~100 ng plasmid DNA in a cold 1 mm gap electroporation cuvette and electroporated in a BioRad
30 Gene Pulser (Hercules, CA) at 1.7 kV, 25 µF, and 400 Ω. Cells were resuspended in 1 ml MRS medium containing 500 mM sucrose (Sigma-Aldrich, St. Louis, MO) and 100 mM MgCl₂, incubated at 30°C for 2 hrs,

plated on MRS medium plates containing 1 or 2 µg/ml of erythromycin (Sigma-Aldrich, St. Louis, MO), then placed in an anaerobic box containing a Pack-Anaero sachet (Mitsubishi Gas Chemical Co., Tokyo, Japan) and incubated at 30°C.

5

ΔldhD

The knockout cassette to delete the *ldhD* gene was created by amplifying from PN0512 genomic DNA an upstream flanking region with primers Top D F1 (SEQ ID NO:572) containing an EcoRI site and Top D R1 (SEQ ID NO:573). The downstream homology region including part of the coding sequence of *ldhD* was amplified with primers Bot D F2 (SEQ ID NO:574) and Bot D R2 (SEQ ID NO:575) containing an XhoI site. The two homology regions were joined by PCR SOE as follows. The 0.9 kbp upstream and downstream PCR products were gel-purified. The PCR products were mixed in equal amounts in a PCR reaction and re-amplified with primers Top D F1 and Bot D R2. The final 1.8 kbp PCR product was gel-purified and TOPO cloned into pCR4BluntII-TOPO (Invitrogen) to create vector pCRBluntII::ldhD. To create the integration vector carrying the internal deletion of the *ldhD* gene, pFP996 was digested with EcoRI and XhoI and the 5311-bp fragment gel-purified. Vector pCRBluntII::ldhD was digested with EcoRI and XhoI and the 1.8 kbp fragment gel-purified. The *ldhD* knockout cassette and vector were ligated using T4 DNA ligase, resulting in vector pFP996::ldhD ko.

Electrocompetent *Lactobacillus plantarum* PN0512 cells were prepared, transformed with pFP996::ldhD ko, and plated on MRS containing 1 µg/ml of erythromycin. To obtain the single-crossover event (sco), transformants were passaged for approximately 50 generations in MRS medium at 37 °C. After growth, aliquots were plated for single colonies on MRS containing 1 µg/ml of erythromycin. The erythromycin-resistant colonies were screened by PCR amplification with primers ldhD Seq F1 (SEQ ID NO:576) and D check R (SEQ ID NO:577) to distinguish between wild-type and clones carrying the sco event. To obtain clones

with a double crossover, the sco strains were passaged for approximately 30 generations in MRS medium with 20 mM D, L-lactate (Sigma, St. Louis, MO) at 37 °C and then plated for single colonies on MRS with lactate.

- Colonies were picked and patched onto MRS with lactate and MRS with
 5 lactate containing 1 µg/ml of erythromycin to find colonies sensitive to erythromycin. Sensitive colonies were screened by PCR amplification using primer D check R (SEQ ID NO:577) and D check F3 (SEQ ID NO:578). Wild-type colonies gave a 3.2 kbp product and deletion clones, called PN0512 Δ *ldhD*, gave a 2.3 kbp PCR product.

10

Δ ldhD Δ ldhL1

- A deletion of the *ldhL1* gene was made in the PN0512 Δ *ldhD* strain background in order to make a double *Δ ldhL1 Δ ldhD* deletion strain. The knockout cassette to delete the *ldhL1* gene was amplified from PN0512
 15 genomic DNA. The *ldhL1* left homologous arm was amplified using primers oBP31 (SEQ ID NO:579) containing a BglII restriction site and oBP32 (SEQ ID NO:580) containing an XhoI restriction site. The *ldhL1* right homologous arm was amplified using primers oBP33 (SEQ ID NO:581) containing an XhoI restriction site and oBP34 (SEQ ID NO:582)
 20 containing an XmaI restriction site. The *ldhL1* left homologous arm was cloned into the BglII/XhoI sites and the *ldhL1* right homologous arm was cloned into the XhoI/XmaI sites of pFP996pyrF Δ erm, a derivative of pFP996. pFP996pyrF Δ erm contains the *pyrF* sequence (SEQ ID NO:571) encoding orotidine-5'-phosphate decarboxylase from *Lactobacillus*
 25 *plantarum* PN0512 in place of the erythromycin coding region in pFP996. The plasmid-borne *pyrF* gene, in conjunction with the chemical 5-fluoroorotic acid in a Δ *pyrF* strain, can be used as an effective counter-selection method in order to isolate the second homologous crossover. The XmaI fragment containing the *ldhL1* homologous arms was isolated
 30 following XmaI digestion and cloned into the XmaI restriction site of pFP996, yielding a 900 bp left homologous region and a 1200 bp right homologous region resulting in vector pFP996-*ldhL1*-arms.

PN0512 Δ *ldhD* was transformed with pFP996-*ldhL1*-arms and grown at 30°C in Lactobacilli MRS medium with lactate (20 mM) and erythromycin (1 µg/ml) for approximately 10 generations. Transformants were then grown under non-selective conditions at 37°C for about 50
5 generations by serial inoculations in MRS + lactate before cultures were plated on MRS containing lactate and erythromycin (1 µg/ml). Isolates were screened by colony PCR for a single crossover using chromosomal specific primer oBP49 (SEQ ID NO:583) and plasmid specific primer oBP42 (SEQ ID NO:584). Single crossover integrants were grown at 37°C
10 for approximately 40 generations by serial inoculations under non-selective conditions in MRS with lactate before cultures were plated on MRS medium with lactate. Isolates were patched to MRS with lactate plates, grown at 37°C, and then patched onto MRS plates with lactate and erythromycin (1 µg/ml). Erythromycin sensitive isolates were screened by
15 colony PCR for the presence of a wild-type or deletion second crossover using chromosomal specific primers oBP49 (SEQ ID NO:583) and oBP56 (SEQ ID NO:585). A wild-type sequence yielded a 3505 bp product and a deletion sequence yielded a 2545 bp product. The deletions were confirmed by sequencing the PCR product and absence of plasmid was
20 tested by colony PCR with primers oBP42 (SEQ ID NO:584) and oBP57 (SEQ ID NO:586).

The *Lactobacillus plantarum* PN0512 double *ldhDldhL1* deletion strain was designated PNP0001. The Δ *ldhD* deletion included 83 bp upstream of where the *ldhD* start codon was through amino acid 279 of
25 332. The Δ *ldhL1* deletion included the fMet through the final amino acid.

ilvD expression

The *E. coli*-*L. plantarum* shuttle vector pDM1 (SEQ ID NO:563) was used for cloning and expression of *ilvD* coding regions from *Lactococcus*
30 *lactis* subsp *lactis* NCDO2118 (NCIMB #702118) [Godon et al., J. Bacteriol. (1992) 174:6580-6589] and *Streptococcus mutans* ATCC #700610 in *L. plantarum* PN0512. Plasmid pDM1 contains a minimal pLF1

replicon (~0.7 Kbp) and pemK-pemI toxin-antitoxin(TA) from *Lactobacillus plantarum* ATCC14917 plasmid pLF1, a P15A replicon from pACYC184, chloramphenicol marker for selection in both *E. coli* and *L. plantarum*, and P30 synthetic promoter [Rud et al, *Microbiology* (2006) 152:1011-1019].

- 5 Plasmid pLF1 (C.-F. Lin et al., GenBank accession no. AF508808) is closely related to plasmid p256 [Sørvig et al., *Microbiology* (2005) 151:421-431], whose copy number was estimated to be ~5-10 copies per chromosome for *L. plantarum* NC7. A P30 synthetic promoter was derived from *L. plantarum* rRNA promoters that are known to be among the
10 strongest promoters in lactic acid bacteria (LAB) [Rud et al. *Microbiology* (2005) 152:1011-1019].

- The *Lactococcus lactis ilvD* coding region (SEQ ID NO:564) was PCR-amplified from *Lactococcus lactis subsp lactis* NCDO2118 genomic DNA with primers 3T-ilvDLI(BamHI) (SEQ ID NO:557) and 5B-ilvDLI(NotI)
15 (SEQ ID NO:558). *L. lactis subsp lactis* NCDO2118 genomic DNA was prepared with a Puregene Gentra Kit (QIAGEN; Valencia,CA). The 1.7 Kbp *L. lactis ilvD* PCR product (ilvDLI) was digested with NotI and treated with the Klenow fragment of DNA polymerase to make blunt ends. The resulting *L. lactis ilvD* coding region fragment was digested with BamHI
20 and gel-purified using a QIAGEN gel extraction kit (QIAGEN). Plasmid pDM1 was digested with ApaLI, treated with the Klenow fragment of DNA polymerase to make blunt ends, and then digested with BamHI. The gel purified *L. lactis ilvD* coding region fragment was ligated into the BamHI and ApaLI(blunt) sites of the plasmid pDM1. The ligation mixture was
25 transformed into *E. coli* Top10 cells (Invitrogen; Carlsbad, CA). Transformants were plated for selection on LB chloramphenicol plates. Positive clones were screened by Sall digestion, giving one fragment with an expected size of 5.3 Kbp. The positive clones were further confirmed by DNA sequencing. The correct clone was named pDM1-ilvD(*L. lactis*),
30 which has the *L. lactis ilvD* coding region expressed from P30.

The *S. mutans* ATCC 700610 *ilvD* coding region was PCR-amplified with a specific forward primer with an NheI restriction site (SEQ

ID NO:559) and a specific reverse primer with a NotI restriction site (SEQ ID NO:560). The genomic DNA of *Streptococcus mutans* ATCC 700610 was used as a template. Genomic DNA was prepared using a MasterPure DNA Purification Kit (Epicentre, Madison, WI). The plasmid vector

5 pET28a (Novagen, Germany) was amplified with primers pET28a-F(NotI) (SEQ ID NO:561) and pET28a-R(NheI) (SEQ ID NO:562). Both coding region and plasmid fragments were digested with NheI and NotI, and ligated. The ligation mixture was transformed into *E. coli* (Top 10) competent cells (Invitrogen). Transformants were grown on LB agar plates

10 supplemented with 50 µg/ml of kanamycin. Positive clones were confirmed by DNA sequencing. The *S. mutans ilvD* coding region from the plasmid pET28a was then sub-cloned into the *E.coli-L. plantarum* shuttle vector pDM1. The plasmid pET28a containing the *S. mutans ilvD* was digested with XbaI and NotI, treated with the Klenow fragment of DNA

15 polymerase to make blunt ends, and a 1,759 bp fragment containing the *S. mutans ilvD* coding region was gel-purified. Plasmid pDM1 was digested with BamHI, treated with the Klenow fragment of DNA polymerase to make blunt ends, and then digested with PvuII. The gel

20 purified fragment containing *S. mutans ilvD* coding region was ligated into the BamHI(blunt) and PvuII sites of the plasmid pDM1. The ligation mixture was transformed into *E. coli* Top10 cells (Invitrogen, Carlsbad, CA). Transformants were plated for selection on LB chloramphenicol plates. Positive clones were screened by ClaI digestion, giving one

25 fragment with an expected size of 5.5 Kbp. The correct clone was named pDM1-ilvD(*S. mutans*), which has the *S. mutans ilvD* coding region expressed from P30.

Example 2

Measurement of expressed DHAD activity

L. plantarum PN0512 and *L. plantarum* PN0512 Δ ldhD Δ ldhL1 were

30 transformed with plasmid pDM1-ilvD(*L. lactis*) or pDM1-ilvD(*S. mutans*) by electroporation. Electro-competent cells were prepared by the following procedure. 5 ml of Lactobacilli MRS medium was inoculated with PN0512

colonies from a freshly grown MRS plate and grown overnight at 30°C.

100 ml MRS medium was inoculated with the overnight culture to an OD600 = 0.1 and grown to an OD600 = 0.7 at 30°C. Cells were harvested at 3700xg for 8 min at 4 °C, washed with 100 ml cold 1 mM MgCl₂,

- 5 centrifuged at 3700xg for 8 min at 4 °C, washed with 100 ml cold 30% PEG-1000 (81188, Sigma-Aldrich, St. Louis, MO), recentrifuged at 3700xg for 20 min at 4 °C, then resuspended in 1 ml cold 30% PEG-1000. 60 µl of electro-competent cells were mixed with ~100 ng plasmid DNA in a cold 1 mm gap electroporation cuvette and electroporated in a BioRad Gene
10 Pulser (Hercules, CA) at 1.7 kV, 25 µF, and 400 Ω. Cells were resuspended in 1 ml MRS medium containing 500 mM sucrose and 100 mM MgCl₂, incubated at 30°C for 2 hrs, and then plated on MRS medium plates containing 10 µg/ml of chloramphenicol.

- L. plantarum* PN0512 and *L. plantarum* PN0512 Δ ldhD Δ ldhL1,
15 which carried pDM1-ilvD(*L. lactis*) or pDM1-ilvD(*S. mutans*), as well as control transformants with the pDM1 vector alone, were grown overnight in Lactobacilli MRS medium at 30°C. 120 ml of MRS medium supplemented with 100 mM MOPS (pH7.5), 40 µM ferric citrate, 0.5 mM L-cysteine, and 10 µg/ml chloramphenicol was inoculated with overnight culture to an
20 OD600 = 0.1 in a 125 ml screw cap flask, for each overnight sample. The cultures were anaerobically incubated at 37 °C until reaching an OD600 of 1-2. Cultures were centrifuged at 3700xg for 10 min at 4 °C. Pellets were washed with 50 mM potassium phosphate buffer pH 6.2 (6.2 g/L KH₂PO₄ and 1.2 g/L K₂HPO₄) and re-centrifuged. Pellets were frozen and stored at
25 -80 °C until assayed for DHAD activity.

- Enzymatic activity of the crude extract was assayed at 37 °C as follows. Cells to be assayed for DHAD were suspended in 2-5 volumes of 50 mM Tris, 10 mM MgSO₄, pH 8.0 (TM8) buffer, then broken by sonication at 0 °C. The crude extract from the broken cells was centrifuged
30 to pellet the cell debris. The supernatants were removed and stored on ice until assayed (initial assay was within 2 hrs of breaking the cells). It was found that the DHADs assayed herein were stable in crude extracts kept

on ice for a few hours. The activity was also preserved when small samples were frozen in liquid N₂ and stored at -80 °C.

The supernatants were assayed using the reagent 2,4-dinitrophenyl hydrazine as described in Flint and Emptage (J. Biol. Chem. (1988) 263:

5 3558-64). When the activity was so high that it became necessary to dilute the crude extract to obtain an accurate assay, the dilution was done in 5 mg/ml BSA in TM8. Protein assays were performed using the Pierce Better Bradford reagent (cat # 23238) using BSA as a standard. Dilutions for protein assays were made in TM8 buffer when necessary.

10 The DHAD activity results are given in Table 8. Specific activity of *L. lactis* DHAD and *S. mutans* DHAD in *L. plantarum* PN0512 showed 0.014 and 0.067 $\mu\text{mol min}^{-1} \text{mg}^{-1}$, respectively, while the vector control sample exhibited no detectable activity. Specific activity of *L. lactis* DHAD and *S. mutans* DHAD in *L. plantarum* PN0512 $\Delta\text{ldhD}\Delta\text{ldhL1}$ showed 0.052
15 and 0.106 $\mu\text{mol min}^{-1} \text{mg}^{-1}$, respectively, which increased 3.7 fold and 1.6 fold in the specific activity as compared to the activity in PN0512.

Table 8. DHAD activity in *L. plantarum* PN0512 and *L. plantarum* PN0512 $\Delta\text{ldhD}\Delta\text{ldhL1}$.

Source of DHAD	Plasmid	Specific Activity ($\mu\text{mol min}^{-1} \text{mg}^{-1}$)	
		PN0512	PN0512 $\Delta\text{ldhD}\Delta\text{ldhL1}$
Vector control	pDM1	0.000	0.000
<i>Lactococcus lactis</i> subsp <i>lactis</i> NCDO2118	pDM1-ilvD(<i>L. lactis</i>)	0.014	0.052
<i>Streptococcus mutans</i> ATCC 700610	pDM1-ilvD(<i>S. mutans</i>)	0.067	0.106

20

Example 3

Construction of plasmid for expression of *Lactococcus lactis* ilvD

The purpose of this example is to describe the construction of another plasmid used for the expression of *Lactococcus lactis* ilvD (SEQ
25 ID NO:564). The shuttle vector pDM1 (SEQ ID NO:563), described in

Example 1, was used for construction of the plasmid for expression of the *ilvD* gene from *Lactococcus lactis subsp lactis* NCDO2118 (NCIMB 702118) [Godon et al., J. Bacteriol. (1992) 174:6580-6589]. The plasmid was constructed using standard molecular biology methods known in the art. All restriction and modifying enzymes and Phusion High-Fidelity PCR Master Mix were purchased from New England Biolabs (Ipswich, MA). DNA fragments were purified with Qiaquick PCR Purification Kit (Qiagen Inc., Valencia, CA). Plasmid DNA was prepared with QIAprep Spin Miniprep Kit (Qiagen Inc., Valencia, CA). Oligonucleotides were synthesized by Sigma-Genosys (Woodlands, TX). All vector constructs were confirmed by DNA sequencing.

Vector pDM1 was modified by deleting nucleotides 3281-3646 spanning the *lacZ* region and replacing with a multi cloning site. Primers oBP120 (SEQ ID NO:567), containing an XhoI site, and oBP182 (SEQ ID NO:568), containing DrdI, PstI, HindIII, and BamHI sites, were used to amplify the P30 promoter from pDM1 with Phusion High-Fidelity PCR Master Mix. The resulting PCR product and vector pDM1 were digested with XhoI and DrdI. This digestion cuts out the *lacZ* region and P30. The PCR product and the large fragment of the pDM1 digestion were ligated to yield vector pDM20, which has P30 restored along with addition of the multi cloning site.

The *ilvD* coding region (SEQ ID NO:564) from *Lactococcus lactis subsp lactis* and a ribosome binding sequence (SEQ ID NO:566) were cloned into pDM20 to create vector pDM20-*ilvD*(LI). Primers oBP190 (SEQ ID NO:569), containing a BamHI site and ribosome binding sequence, and oBP192 (SEQ ID NO:570), containing a PstI site, were used to amplify the *ilvD* coding region from vector pDM1-*ilvD*(*L. lactis*), which was described in Example 1, with Phusion High-Fidelity PCR Master Mix. The resulting PCR product and pDM20 were ligated after digestion with BamHI and PstI to yield vector pDM20-*ilvD*(LI), with the *ilvD* coding region downstream of the P30 promoter.

Example 4

Increased DHAD activity with expression of *Lactococcus lactis* *ilvD* in a Δ *ldhD* Δ *ldhL1* *Lactobacillus plantarum* strain background

The purpose of this example is to demonstrate the effect on DHAD activity, from expression of *L. lactis* *ilvD*, of the *L. plantarum* Δ *ldhD* Δ *ldhL1* background as compared to the wild-type background.

Lactobacillus plantarum PN0512 and *Lactobacillus plantarum* PN0512 Δ *ldhD* Δ *ldhL1* were transformed with vector pDM20-*ilvD*(LI). Cells were transformed as in Example 1, except transformants were selected for on MRS medium plates containing 10 µg/ml of chloramphenicol and strain PN0512 Δ *ldhD* Δ *ldhL1* was grown in the absence of glycine. The transformed strains were called PN0512/pDM20-*ilvD*(LI) and PN0512 Δ *ldhD* Δ *ldhL1*/pDM20-*ilvD*(LI). These two strains were grown in 50 ml of Lactobacilli MRS medium supplemented with 100 mM MOPS (Sigma-Aldrich, St. Louis, MO), 40 µM ferric citrate (Sigma-Aldrich, St. Louis, MO), 0.5 mM L-cysteine (Sigma-Aldrich, St. Louis, MO), and 10 µg/ml chloramphenicol adjusted to pH 7 with KOH, which had been deoxygenated in an anaerobic chamber (Coy Laboratories Inc., Grass Lake, MI), in 50 ml conical tubes at 37°C in the anaerobic chamber until reaching an OD600 of approximately 1.5-2.8. Cultures were centrifuged at 3700xg for 10 min at 4°C. Pellets were washed with 50 mM potassium phosphate buffer pH 6.2 (6.2 g/L KH₂PO₄ (Sigma-Aldrich, St. Louis, MO) and 1.2 g/L K₂HPO₄ (Sigma-Aldrich, St. Louis, MO)) and re-centrifuged. Pellets were frozen and stored at -80 °C until assayed for DHAD activity. Samples were assayed for DHAD activity using a dinitrophenylhydrazine based method as described in Example 2, except cells were broken using a bead beater with Lysing Matrix B (MP Biomedicals, Solon, OH).

The two strains were grown and assayed using the same conditions three separate times. The DHAD activity results for each experiment, as well as the average, are given in Table 9. Expression of the *L. lactis* DHAD in the *L. plantarum* Δ *ldhD* Δ *ldhL1* background led on

average to approximately a 10-fold increase in DHAD activity compared to expression in the wild-type background.

- Table 9. Expression of *L. lactis* DHAD in wild-type *Lactobacillus plantarum* PN0512 and *Lactobacillus plantarum* PN0512 Δ *dhD* Δ *dhL1*. DHAD activity is in μ moles KIVA/min/mg total protein.

<u>Expt.</u>	<u>Strain</u>	<u>DHAD Activity</u>
1	PN0512/pDM20-ilvD(LI)	0.021
1	PN0512 Δ <i>dhD</i> Δ <i>dhL1</i> /pDM20-ilvD(LI)	0.575
2	PN0512/pDM20-ilvD(LI)	0.042
2	PN0512 Δ <i>dhD</i> Δ <i>dhL1</i> /pDM20-ilvD(LI)	0.643
3	PN0512/pDM20-ilvD(LI)	0.052
3	PN0512 Δ <i>dhD</i> Δ <i>dhL1</i> /pDM20-ilvD(LI)	0.223
Avg	PN0512/pDM20-ilvD(LI)	0.038
Avg	PN0512 Δ <i>dhD</i> Δ <i>dhL1</i> /pDM20-ilvD(LI)	0.480

Table 7

HMMER2.0 [2.2g]
 NAME dhad_for_hmm
 LENG 564
 ALPH Amino
 MAP yes
 COM /app/public/hmmer/current/bin/hmmbuild -F dhad-exp_hmm dhad_for_hmm.ain
 COM /app/public/hmmer/current/bin/hmmcalibrate dhad-exp_hmm
 NSEQ 8
 DATE Tue Jun 3 10:48:24 2008
 XT -8455 -4 -1000 -8455 -4 -8455 -4
 NULT -4 -8455

Program name and version
 Name of the input sequence alignment file
 Length of the alignment: include indels
 Type of residues
 Map of the match states to the columns of the alignment
 Commands used to generate the file: this one means that hmmbuild (default parameters) was applied to the alignment file
 Commands used to generate the file: this one means that hmmcalibrate (default parameters) was applied to the hmm profile
 Number of sequences in the alignment file
 When was the file generated

The transition probability distribution for the null model (single G state).

The symbol emission probability distribution for the null model (G state); consists of K (e.g. 4 or 20) integers. The null probability values are set when the model is calibrated with hmmbcalibrate.

The extreme value distribution parameters μ and λ used to convert these back to model probabilities is $1/K$. Lambda is positive and nonzero. These values are set when the model is calibrated with hmmbcalibrate.

EVD -499.650970 0.086142

HMM	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	Position in alignment
	m->m	m->i	m->d	i->m	i->i	d->m	d->d	b->m	m->b												
1(M)	-233	-1296	99	1223	-1477	-1132	89	-1122	420	-1248	1757	1553	-1296	464	-24	-190	-188	-838	-1578	-985	6
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378	-538	*												
2(E)	-220	-1288	232	1356	-1807	1016	-70	-1474	190	-1584	-775	132	-1298	300	-282	-193	1140	-1092	-1872	-1262	7
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378	*	*												
3(K)	-448	-1932	1558	658	-2220	-1048	40	-1993	1569	-1938	-1091	1558	-1319	450	-193	-278	-419	-1552	-2121	-1397	8
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378	*	*												
4(V)	-404	-498	-1497	-939	-588	-1810	-640	1591	914	-127	335	-982	-1866	-562	-767	-888	-357	1720	-1169	-763	9
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378	*	*												
5(E)	-265	-1340	-52	1376	-1572	-1189	113	-1125	1345	-1287	-496	99	-1321	505	198	-218	-205	597	-1598	-1032	10
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378	*	*												
6(S)	256	-397	-1014	-830	-1841	-646	-862	-1443	-767	-1740	-963	-568	-1249	-651	-1007	2267	1566	-862	-2080	-1672	11
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378	*	*												
7(M)	-990	-889	-2630	157	-513	-2514	-1346	1309	-1767	820	3683	-1898	-2491	-1496	-1799	-1589	-925	150	-1336	-1041	12
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
8(E)	588	-1875	-194	1536	-2188	-1373	-59	-1931	957	-1890	-977	904	292	393	-162	483	-372	-1495	-2070	-1391	13
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 7

-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
9(N)	-514	-1116	1207	-315	447	-1650	-304	-778	-224	825	-277	1457	-1738	-123	-618	-454	-603	-1186	763	14	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
10(N)	-815	-1190	-1360	-922	-904	-1967	-797	-442	-670	381	1700	3009	-2099	-654	-934	-1051	-791	-445	-1490	-979	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
11(K)	-1530	-2498	-1722	-855	-3141	-2246	-428	-2627	2828	-2404	-1656	-927	662	-2	2047	-1421	-1337	-2324	-2357	-2081	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
12(Y)	-872	-1887	-861	-290	-1369	-1801	1662	-1797	325	-1793	-1031	893	-1876	56	2219	-812	-780	-1514	-1565	2287	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
13(S)	-830	-1586	-1471	-1099	-2717	-1642	-1010	-2479	-266	-2518	-1746	-1065	-2069	-676	1822	2748	-1000	-1850	-2597	-2189	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
14(Q)	-851	-2131	-775	-153	-2554	-1735	-211	-2205	1908	-2094	-1244	-386	-1802	2254	974	1001	-747	-1819	-2181	-1667	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
15(T)	-405	-1258	-618	-100	-1490	-1466	1156	-1121	1	-1299	-514	578	-1607	65	-433	960	1849	343	-1677	-1143	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
16(I)	-1772	-1325	-4307	-387	-1405	-3993	-3383	2935	-3705	820	-217	-3632	-3761	-3400	-3692	-3260	-1742	2033	-2838	-2525	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
17(T)	-1018	-1329	-2004	-1771	-409	-1993	-1000	-1256	-1512	-1464	-966	-1543	-2367	-1428	-1638	-1257	3050	-1090	-1012	2448	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
18(Q)	-1509	-3056	1970	44	-3310	-1666	-886	-3242	-877	-3158	-2439	-322	-2123	3562	-1493	-1259	-1550	-2779	-3260	-2446	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
19(D)	-1006	-2199	2178	-88	-3159	1997	-936	-2974	-948	-2977	-2174	-382	-1960	-589	-1571	1295	-1157	-2369	-3178	-2430	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
20(M)	445	-796	-1082	-521	-841	-1643	-412	-403	-370	-692	2213	-646	536	1166	-698	-630	660	831	-1204	-767	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

21(O)	741	-990	-1025	-507	-1249	-1551	-519	-720	-357	-1082	-345	-835	-1739	1770	-713	-589	1576	1129	-1559	-1097	26
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
22(R)	-1753	-2648	-2072	-1047	-3365	-2405	-452	-2782	1989	-2495	-1773	-1062	-2379	2402	2643	-1829	-1506	-2504	-2397	-2190	27
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
23(S)	-330	-1010	-1820	-1828	-2778	-1228	-1652	-2481	-1592	-2691	-1841	-1273	2130	-1426	-1834	2449	1034	-1716	-2961	-2594	28
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
24(P)	1882	-1119	-2231	-2302	-3062	-1360	-2209	-2710	-2339	-3013	-2243	-1876	3304	-2117	-2409	-742	-918	-1916	-3263	-3022	29
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
25(N)	969	-1230	-1066	-915	-2593	-1313	-1196	-2242	-1033	-2447	-1628	3197	-1850	-898	-1392	-582	1155	-1644	-2736	-2256	30
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
26(R)	-1847	-2840	-2014	-1161	-3282	-2428	-579	-2818	-2242	-2553	-1889	-1165	-2462	2447	3181	-1746	-1630	-2555	-2447	-2228	31
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
27(A)	3048	-932	-2480	-2533	-3075	-1200	-2274	-2765	-2501	-3071	-2221	-1858	-1948	-2205	-2512	1225	-739	-1842	-3322	-3078	32
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
28(M)	-2406	-2266	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-598	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	33
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
29(Y)	-1674	-1506	-2863	-2464	596	-2872	2251	-972	-2024	2197	-552	-1986	-2876	-1739	-1998	-1987	-1801	-1002	-95	2332	34
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
30(Y)	-2013	-2305	-2428	-1781	-328	-2709	-654	-2240	-258	-2084	-1826	-1831	-2788	-899	2789	-2017	-1896	-2130	-857	3434	35
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
31(A)	2822	-1031	-2418	-2539	-3226	1898	-2364	-2941	-2626	-3229	-2379	-1722	-2026	-2302	-2634	-654	-848	-1983	-3415	-3226	36
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
32(I)	-1247	-941	-3569	-3039	-1082	-3101	-2195	2227	-2763	766	-78	-2700	-3050	-2469	-2697	-2253	1322	1974	-1988	-1633	37
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
33(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	38
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
334(F)	-1511	-1236	-3511	-3017	-2747	-2982	-1089	-260	-2651	992	2737	-2407	-2904	-2088	-2418	-2099	-1434	-489	-537	2056	39
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
335(Q)	-576	-1869	-401	92	-2232	831	-173	-1930	1505	-1913	-1042	-186	-1620	1653	-51	-482	1346	-1534	-2098	-1490	40
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
336(D)	-1352	-3066	3028	1349	-3303	-1566	-724	-3141	1155	-3043	-2267	-165	-1991	-354	-1350	-1086	-1368	-2659	-3221	-2356	41
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
337(E)	-1507	-3288	2042	2762	-3520	515	-853	-3401	-981	-3296	-2566	-182	-2064	-503	-1753	-1209	-1553	-2895	-3486	-2547	42
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
338(D)	-1445	-2778	3529	-53	-3524	-1590	-1129	-3476	-1367	-3459	-2774	-396	-2156	-825	-2122	554	-1609	-2880	-3582	-2717	43
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
339(F)	-2658	-2176	-4213	-4000	3815	-3933	-1352	-531	-3638	1121	-19	-3184	-3709	-2820	-3296	-3219	-2579	-1037	-601	403	44
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
40(D)	-684	-2193	1738	1460	-2494	-1437	-249	-2257	1694	-2199	-1308	-62	-1637	185	-450	-531	633	-1808	-2374	-1657	45
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
41(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2968	46
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
42(P)	1882	-1118	-2231	-2302	-3062	-1360	-2209	-2710	-2339	-3013	-2243	-1876	3304	-2117	-2409	-742	-918	-1916	-3263	-3022	47
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
43(I)	-1006	-992	-2347	-1784	-650	-2452	-1256	-2372	-1386	77	2213	-1720	-2455	2030	-1490	-1528	-946	106	-1441	-1111	48
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
44(V)	-1771	-1603	-3750	-3889	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2628	-1917	3536	-3074	-2677	49
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
45(G)	-2594	-2690	-3304	-3623	-4328	-3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	50
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

46(I)	-1759	-1303	-4330	-3968	-1751	-4051	-3743	3027	-3837	-597	-528	-3729	-3875	-3688	-3910	-3369	-1751	2438	-3259	-2819	51
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
47(V)	1736	-1012	-3546	-3078	-1377	-3073	-2434	2052	-2843	-608	-331	-2754	-3122	-2619	-2855	-2270	-1277	2193	-2333	-1941	52
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
48(N)	-686	-1511	-702	-806	-2927	-1386	-1339	-2841	-1264	-2950	-2137	2702	-1979	-1062	-1648	2444	-971	-2105	-3054	-2475	53
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
49(M)	-411	-857	-1800	-1434	-1528	1914	-1202	-1029	-1247	-1347	2989	-1217	-1912	-1119	-1444	-676	1550	-767	-1922	-1539	54
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
50(W)	-782	-1258	793	-683	1193	346	2051	-932	-556	-1092	-441	-798	-1893	-426	-909	-904	-720	-779	3163	1546	55
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
51(W)	1009	-798	-1470	-935	-463	-1773	-545	-460	-751	-736	-66	-943	-1904	-606	-1002	1604	-507	-322	2535	1521	56
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
52(D)	-1137	-2711	2125	1847	-2995	-1523	-617	-2786	-528	-2743	-1833	-150	-1897	-234	-1165	-924	2117	-2331	-2948	-2141	57
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
53(I)	-599	-1102	-1031	-829	-1522	1429	-927	2119	-880	-1369	-699	1692	-1938	-759	-1188	-799	-698	-689	-1887	-1419	58
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
54(T)	-666	-1412	-954	-984	-2702	-1428	-1357	-2418	-1208	-2650	-1866	2293	-2000	-1101	-1519	-787	2967	-1835	-2866	-2360	59
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
55(P)	-632	-1230	-2074	-2144	-2896	-1453	-2116	-2631	-2128	-2928	-2213	-1658	3610	-2006	-2221	-852	1302	-1931	-3185	-2917	60
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
56(C)	-2476	5735	-4102	-4358	-3712	-2763	-3545	-3518	-4167	-3859	-3569	-3631	-3363	-4030	-3832	-2793	-2860	-3158	-3464	-3718	61
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
57(N)	-2171	-2655	-1458	-1748	-3334	-2384	-2287	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2808	-2224	-2439	-3392	-3253	-2909	62
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
58(M)	672	-918	-3119	-2578	-742	-2668	-1734	1807	-2283	16	3713	-2271	-2704	-1960	-2216	-1806	-1058	493	-1612	-1306	63
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

[illegible]

Table 7

71(V)	-1760	-1333	-4244	-3788	-1262	-3902	-3190	1495	-3588	1270	-96	-3536	-3677	-3238	-3534	-3148	-1725	2865	-2654	-2373	76
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
72(W)	-1054	-2172	-1112	-403	-2566	-1917	-286	-2196	2516	-2095	-1292	1183	-1958	140	1333	-959	-922	-1867	2531	-1720	77
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
73(D)	611	-1995	1525	937	-2295	-1400	-148	-2043	211	-2006	-1106	-37	-1553	1420	-312	-408	1235	-1609	-2193	-1499	78
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
74(A)	2716	-902	-2380	-2205	-2799	-1197	-1975	-2459	-2081	-2736	-1895	-1520	-1895	-1844	-2201	1191	1299	-1669	-3045	-2758	79
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
75(G)	-1709	-2833	2424	-409	-3781	2819	-1457	-3777	-1728	-3733	-3076	-739	-2389	-1180	-2441	-1557	-1893	-3158	-3660	-3038	80
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-212	-2809	-8150	-273	-2534	-701	-1378*	*													
76(A)	2529	-1119	-2814	-2330	-1245	-1983	-1829	-377	-2042	1435	-341	-1937	-2411	-1873	-2088	-1266	-1059	-397	-2083	-1713	82
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
77(W)	-472	-361	-2421	-1812	-298	-1979	-826	1164	-1486	-143	2485	873	-2028	-1185	-1428	-1048	-412	1116	2999	-454	83
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
78(P)	-1198	-1737	-2187	-2394	-3665	2006	-2550	-3630	-2743	-3756	-3008	-2052	3474	-2495	-2835	-1401	-1593	-2736	-3511	-3519	84
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
79(Q)	-899	-1075	-2108	-1568	-726	-2370	-1175	83	-1185	1373	218	-1566	-2400	2445	-1340	-1445	-846	1441	-1501	-1146	85
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
80(Q)	-885	-779	-2609	-2018	-481	-2414	-1253	1645	-1736	799	1924	-1827	-2405	2262	-1752	-1484	-821	802	-1240	-935	86
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
81(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	87
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
82(G)	-998	-2100	-120	-175	-2567	2528	2174	-2558	-587	-2583	-1806	1422	-1966	-461	-1038	-925	-1088	-2095	-2657	-1948	88
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
83(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	89
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*														
84(I)	-1286	-1279	-2907	-2883	-1446	-2549	-2198	-3290	-2407	-726	-534	-2386	1172	-2299	-2437	-1895	-1392	283	-2302	283	-2302	-1913	90
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
85(T)	-493	-1105	-2189	-2267	-3101	1880	-2196	-2791	-2334	-3081	-2269	-1649	-2058	-2099	-2410	-719	3135	-1948	-3282	-3046	-3046	-249	91
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
86(V)	-1750	-1296	-4319	-3957	-1765	-4038	-3733	2364	-3826	-619	-543	-3716	-3869	-3685	-3902	-3354	-1743	3012	-3265	-2817	-2817	-249	92
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
87(S)	923	-962	-2348	-2422	-3132	-1207	-2248	-2850	-2440	-3140	-2285	-1624	-1954	-2158	-2471	3171	-758	-1896	-3362	-3103	-3103	-249	93
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
88(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	-3552	-249	94
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
89(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	-4222	-249	95
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
90(I)	-1880	-1493	-4193	-3724	-953	-3837	-2980	3251	-3420	257	2372	-3485	-3608	-3005	-3310	-3087	-1840	617	-2373	-2155	-2155	-249	96
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
91(S)	2150	-939	-2407	-2415	-3075	-1197	-2205	-2781	-2384	-3065	-2205	-1613	-1936	-2105	-2436	2652	-729	-1850	-3306	-3049	-3049	-249	97
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-294	-249	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
92(M)	-979	-1455	-1242	-1122	-1434	-1860	-1131	-1171	-974	-1285	4091	2176	-2226	-1017	-1187	-1166	-1086	-1063	-1929	-1345	-1345	-249	98
-	-149	-500	233																				

Table 7

96(G)	-2594	-2680	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2838	-2981	-4004	-3688	-4222	102
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
97(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2811	-2552	-1398	-2513	-2207	103
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
98(R)	-2097	-2786	-2688	-1415	-3622	-2625	-555	-2964	2585	-2627	-1957	-1318	-2577	-137	3015	-1978	-1791	-2732	-2489	-2363	104
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
99(Y)	-3615	-2706	-4169	-4413	2626	-4044	-396	-2535	-3993	-1939	-1985	-2747	-3930	-2852	-3446	-3296	-3494	-2686	347	4252	105
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
100(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2886	-3497	-2780	-1973	-2360	-2483	-2703	3485	-1316	-2413	-3310	-3025	106
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
101(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3185	-541	-3734	3130	-31	-3935	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	107
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
102(V)	-1381	-1065	-3714	-3252	-1453	-3300	-2646	1872	-3023	-615	-373	-2949	-3287	-2816	-3039	-2506	1346	2750	-2489	-2087	108
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
103(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2886	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	108
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
104(R)	-2857	-3022	-3318	-2735	-3796	-2998	-1988	-3912	-846	-3631	-3157	-2611	-3280	-1724	4056	-3026	-2913	-3650	-3096	-3185	110
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
105(E)	-1719	-3572	2596	2779	-3767	-1632	-993	-3700	-1241	-3578	-2920	-234	-2167	-666	-2090	-1380	-1789	-3182	-3742	-2756	111
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
106(V)	-1746	-1296	-4308	-3946	-1757	-4020	-3712	2190	-3811	-614	-539	-3702	-3858	-3667	-3884	-3338	-1740	3098	-3250	-2803	112
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
107(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	113
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
108(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	114
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
109(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	115
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
110(S)	-352	2942	-2955	-2957	-2876	-1254	-2382	-2573	-2692	-2827	-2128	-1827	-2001	-2405	-2607	3103	-778	-1757	-3171	-2911	116
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
111(U)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	117
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
112(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3365	118
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
113(T)	1556	-936	-2493	-2457	-2805	-1256	-2159	-2210	-2319	-2681	-1932	-1656	-1974	-2089	-2352	-598	3235	-1547	-3111	-2847	119
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
114(C)	1784	2119	-2013	-1532	-1093	-1580	-1089	-436	-1322	-937	-273	1093	-1932	-1127	-1472	-748	-515	1585	-1536	-1163	120
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
115(M)	1831	2019	-2596	-2038	-605	-1979	-1126	244	-1727	-359	2501	-1655	-2145	-1435	-1683	-1106	-557	1087	-1153	-804	121
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
116(Q)	-987	-2211	-43	-62	-2833	2229	-691	-2616	-407	-2604	-1797	1197	-1917	2260	-858	-880	-1045	-2139	-2772	-2099	122
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
117(G)	2313	-1042	-2391	-2528	-3250	2601	-2372	-2972	-2637	-3257	-2407	-1721	-2032	-2310	-2646	-662	-859	-2003	-3434	-3247	123
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
118(O)	-914	-2350	-48	1661	-2621	-1571	2504	-2400	68	-2331	-1486	-201	-1786	2646	-351	-754	-865	-1984	-2463	-1767	124
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
119(W)	-517	-1294	-733	-183	-1062	-1605	-234	-1037	19	-1207	-456	1435	-1690	33	756	411	-454	-819	3340	1286	125
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
120(M)	410	-469	-2417	-1828	-341	-2041	-897	195	-1513	-156	3130	-1634	-2102	-1230	-1484	-1117	-507	954	-894	2253	126
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												

Table 7

121(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2821	-4385	-3958	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	127
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
122(G)	2142	-930	-2334	-2298	-3100	2237	-2139	-2842	-2302	-3074	-2187	-1557	-1809	-2010	-2397	1136	-701	-1871	-3308	-3053	128
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
123(V)	-1514	-1144	-3950	-3459	1821	-3487	-2577	2274	-3208	-209	-87	-3112	-3362	-2864	-3118	-2680	-1476	2426	-2194	-1786	129
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
124(V)	-1743	-1294	-4292	-3873	-1511	-3988	-3433	2287	-3712	598	-319	-3626	-3774	-3456	-3716	-3260	-1717	2790	-2931	-2577	130
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
125(A)	2911	-954	-2808	-2665	-2115	-1577	-2196	-575	-2445	-1646	-1202	-1906	-2208	-2218	-2451	-901	-876	1294	-2727	-2394	131
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
126(I)	-1784	-1323	-4298	-3936	-1668	-3994	-3655	3337	-3783	-508	-482	-3889	-3838	-3808	-3835	-3311	-1759	1847	-3184	-2747	132
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
127(G)	-1157	-1705	-2169	-2375	-3654	3021	-2534	-3611	-2730	-3741	-2994	-2024	-2418	-2475	-2826	-1361	-1555	-2705	-3513	-3509	133
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
128(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	134
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
128(C)	-2476	5735	-4102	-4358	-3712	-2763	-3545	-3518	-4167	-3859	-3569	-3631	-3363	-4030	-3832	-2793	-2860	-3158	-3484	-3718	135
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
130(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2821	-4385	-3958	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	136
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
131(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	137
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
132(N)	-2171	-2655	-1456	-1748	-3334	-2364	-2287	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	138
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
133(M)	-2408	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	139
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
134(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4821	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	140
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
135(G)	-2594	-2690	-3304	-3623	-4328	-3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	141
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
136(A)	2180	-935	-2286	-2196	-3057	1098	-2058	-2796	-2174	-3021	-2134	-1516	-1898	-1906	-2302	2146	-689	-1849	-3256	-2983	142
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
137(M)	-1799	-1433	-4142	-3579	-669	-3668	-2608	1558	-3293	1235	3799	-3296	-3401	-2717	-3088	-2843	-1726	1156	-2002	-1868	143
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
138(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	144
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
139(A)	3103	-1036	-2445	-2572	-3222	1051	-2380	-2930	-2650	-3226	-2381	-1739	-2034	-2327	-2648	-664	-857	-1981	-3412	-3228	145
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
140(M)	-2325	-1891	-4598	-4012	-498	-4222	-3013	1242	-3722	1864	3929	-3855	-3711	-2910	-3414	-3439	-2215	-299	-2076	-2098	146
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
141(A)	3103	-1036	-2445	-2572	-3222	1051	-2380	-2930	-2650	-3226	-2381	-1739	-2034	-2327	-2648	-664	-857	-1981	-3412	-3228	147
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
142(R)	-1588	-2442	-1399	-953	-3069	-2171	-708	-2795	373	-2625	-1916	1858	-2357	-324	3294	-1520	-1505	-2453	-2523	-2186	148
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
143(M)	-1448	-1256	-3396	-2819	-474	-3024	-1923	175	-2473	2225	2756	-2574	-2922	-2063	-2375	-2153	952	-151	-1599	-1410	149
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
144(N)	-1662	-3306	2055	78	-3621	-1643	-1040	-3622	-1272	-3531	-2870	3477	-2182	-724	-2071	-1371	-1757	-3092	-3633	-2700	150
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
145(I)	-1066	-921	-2828	-2339	-1041	-2675	-1601	2235	-1668	-455	-92	-2067	-2692	-1688	1701	-1795	-1024	1960	-1771	-1396	151
-	-149	-500	-233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

146(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4821	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	152
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
147(S)	1568	-940	-2267	-2192	-3082	1101	-2068	-2826	-2185	-3049	-2159	-1515	-1801	-1915	-2313	2603	-694	-1866	-3279	-3006	153
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
148(I)	-1880	-1492	-4195	-3728	-963	-3841	-2991	3272	-3425	246	2277	-3490	-3613	-3014	-3317	-3092	-1841	628	-2385	-2163	154
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
149(F)	-2204	-1797	-3724	-3473	3206	-3383	-628	-1077	-3092	-746	3167	-2502	-3309	-2372	-2792	-2535	-2120	-1245	28	2460	155
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
150(V)	1265	-1028	-3200	-2994	-1833	-2150	-2480	417	-2771	-1122	-818	-2349	-2640	-2559	-2766	-1464	-1118	3028	-2700	-2325	156
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
151(Y)	-3482	-2868	-3701	-3919	238	-3552	-1112	-3000	-3638	-2516	-2528	-3027	-3772	-3101	-3341	-3418	-3527	-3071	-441	4711	157
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
152(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	158
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
153(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	159
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
154(T)	-359	-976	-2225	-2228	-2800	-1242	-2074	-2560	-2170	-2875	-2064	-1561	-1958	-1969	-2247	1110	3375	-1760	-3152	-2850	160
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
155(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	161
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
156(H)	861	-1924	-394	1010	-2260	-1477	1787	-1974	1769	-1918	-1022	-120	-1566	362	697	-417	-459	-1557	-2073	-1446	162
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
157(P)	-655	-1502	-711	-557	-2204	-1463	2143	-2122	-586	-2233	-1445	-888	2841	-560	-941	855	-805	-1657	-2368	-1763	163
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
158(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	164
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
1559(H)	-744	-2193	-114	1118	-2513	-1512	2486	-2252	1178	-2183	-1308	2230	-1689	180	-233	-598	-887	-1823	-2335	-1670	165
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
160(W)	-2872	-2139	-3850	-3748	941	-3611	-489	-1891	-3306	1047	-1217	-2551	-3534	-2514	-2980	-2788	-2577	-1799	4205	3466	166
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
161(K)	386	-1981	779	279	-2295	-1403	-114	-2043	2059	-1991	-1082	941	-1536	1263	-211	-384	-457	-1602	-2161	-1476	167
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
162(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	168
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
163(K)	-1144	-2365	-912	2048	-2856	-1912	-326	-2459	2267	-2295	-1482	-556	-1989	108	1334	-1013	-1014	-2093	-2324	-1881	169
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
164(D)	-1091	-2610	2941	174	-2957	-1527	-595	-2750	1084	-2696	-1877	-176	-1885	-206	-1006	740	-1098	-2288	-2880	-2105	170
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
165(L)	-2387	-1922	-4674	-4155	-617	-4366	-3250	1889	-3865	2650	558	-4023	-3847	-3098	-3586	-3647	-2296	-38	-2247	-2224	171
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
166(N)	-1021	-2427	1806	133	-2870	-1499	-635	-2647	-521	-2640	-1825	2171	-1874	-255	-1124	-860	2122	-2184	-2853	-2090	172
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
167(I)	-1830	-1390	-4327	-3873	-1210	-3994	-3274	2987	-3678	1259	-30	-3633	-3730	-3283	-3604	-3249	-1791	1570	-2661	-2417	173
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
168(V)	-1771	-1603	-3750	-3689	-2037	-3050	-32														

Table 7

171(F)	-3342	-2776	-4026	-4232	4354	-3645	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	177
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
172(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2859	-1842	-2560	-2479	-2750	-3722	-3563	-3385	178
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
173(A)	2966	-1031	-2429	-2551	-3222	1544	-2368	-2934	-2633	-3225	-2377	-1727	-2028	-2309	-2637	-656	-850	-1900	-3412	-3224	179
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
174(V)	-1769	-1342	-4255	-3793	-1216	-3901	-3162	1633	-3589	1486	-51	-3537	-3667	-3214	-3518	-3143	-1731	2892	-2609	-2345	180
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
175(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	181
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
176(Q)	-729	-2116	-413	1086	-2484	-1587	1599	-2186	1695	-2094	-1219	-223	-1698	2418	90	-599	-649	-1770	-2213	-1815	182
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
177(W)	-1652	-1707	-2340	-1879	1896	-2733	2013	-1398	1758	-1386	-938	-1641	-2751	-1364	-1762	-1780	-1577	-1325	3577	2136	183
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
178(T)	-421	-753	-1251	-704	-846	-1670	-535	894	-548	-690	-1	1376	-1791	-421	-846	373	1461	858	-1236	-812	184
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
179(H)	1498	-1593	-504	15	-1895	-1494	2279	-1559	1119	-1640	-810	-242	-1611	194	-171	-462	815	-1231	-1914	-1340	185
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
180(G)	-1515	-2130	-1298	-1450	-2658	3285	2212	-3276	-1691	-3291	-2638	-1524	-2582	-1662	-1925	-1600	-1764	-2713	-2804	-2234	186
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
181(K)	-528	-2010	1346	1082	-2329	-1408	-118	-2080	1475	-2018	-1108	1161	-1543	331	1052	-394	-471	-1632	-2181	-1494	187
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
182(M)	-1894	-1521	-4170	-3679	-840	-3793	-2868	2827	-3360	375	3445	-3437	-3555	-2902	-3223	-3028	-1846	470	-2249	-2059	188
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
183(T)	-670	-1758	1731	-141	-2591	-1399	-691	-2319	-499	-2384	-1543	-387	-1786	-316	-1016	1676	2044	-1811	-2624	-1981	189
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
188A(E)	345	-2074	925	1994	-2378	-1408	-177	-2135	922	-2084	-1183	-38	641	264	-356	-444	-536	-1690	-2261	-1556	190
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
185(E)	-1493	-2900	93	3174	-2903	-1743	1987	-3042	-646	-2957	-2238	-411	-2146	-506	-1121	-1272	-1503	-2629	-2905	-2134	191
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
188(D)	-1293	-2959	2673	2121	-3219	-1546	-713	-3043	-707	-2974	-2191	-158	-1967	-342	-1394	-1043	701	-2567	-3172	-2311	192
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
187(F)	-1137	-905	-3250	-2707	2365	-2647	-1016	-34	-2336	1239	267	-2150	-2626	-1861	-2133	-1752	-1069	1461	-599	1844	193
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
188(K)	-479	-1713	-409	1031	-1925	-1467	1755	-1650	1844	-349	-827	-140	-1556	319	-75	-403	-411	-1301	-1900	843	194
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
189(G)	433	-2144	52	1047	-2717	2303	-615	-2467	-442	-2482	-1655	1123	-1828	-233	-995	-763	-923	-2000	-2710	-2005	195
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
190(V)	-1752	-1320	-4254	-3806	-1311	-3916	-3232	1701	-3614	1188	-140	-3551	-3693	-3280	-3568	-3166	-1718	2833	-2703	-2409	196
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
191(E)	-1199	-1750	-734	2668	-1820	-2038	-1068	1892	-867	-1273	-897	-922	-2285	-797	-1238	-1340	-1197	-426	-2325	-1769	197
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
192(C)	-1182	3528	-1398	-620	-2541	-2038	-358	-2093	1181	-2037	-1272	-747	-2070	1553	2213	-1123	-1038	-1817	-2142	-1774	198
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
193(N)	-1478	-2527	-261	-403	-2011	-1837	2032	-2925	-735	-2845	-2195	3635	-2259	-721	-1085	-1352	-1546	-2522	-2307	-1431	199
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
194(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	200
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
195(C)	-1220	4911	-3609	-3314	-1440	-2525	-2482	1565	-2922	-706	-544	-2678	-2896	-2710	-2836	-1869	-1375	379	-2371	-1957	201
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

196(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4821	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	202
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
197(G)	-477	-1115	-1983	-2189	-3315	3154	-2272	-3172	-2506	-3387	-2522	-1599	-2042	-2177	-2583	1217	-805	-2130	-3477	-3225	203
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
198(A)	1653	-1347	-705	-249	-1969	-1385	-477	-1629	-159	-1759	-935	-434	1285	1404	-586	-450	1019	-1243	-2070	-1522	204
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
199(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	205
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
200(S)	1870	-838	-2270	-2183	-3068	1488	-2056	-2810	-2168	-3032	-2144	-1511	-1898	-1901	-2300	2236	-690	-1857	-3285	-2990	208
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
201(C)	-2476	5735	-4102	-4358	-3712	-2763	-3545	-3518	-4167	-3859	-3569	-3631	-3363	-4030	-3832	-2793	-2860	-3158	-3484	-3718	207
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
202(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	208
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
203(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	209
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
204(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	210
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
205(Y)	-3590	-2700	-4146	-4378	2092	-4028	-404	-2517	-3963	-1928	-1973	-2744	-3921	-2845	-3431	-3284	-3474	-2669	336	4423	211
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
206(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2800	-2708	-2753	-1463	3819	-2197	-3286	-3156	212
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
207(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	213
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
208(N)	-2171	-2655	-1458	-1748	-3334	-2384	-2287	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	214
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 7

-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	
20209(T)	-1213	-1674	-2755	-2806	-3163	-1922	-2659	-2698	215
-	-149	-500	233	43	-381	399	106	-626	-3156
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21210(M)	-2355	-1988	-4343	-3834	-504	-4051	-2868	105	216
-	-149	-500	233	43	-381	399	106	-626	-1925
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21211(S)	2150	-939	-2407	-2415	-3075	-1197	-2205	-2781	217
-	-149	-500	233	43	-381	399	106	-626	-3049
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21212(S)	-344	-979	-2190	-2162	-2959	-1227	-2042	-2651	218
-	-149	-500	233	43	-381	399	106	-626	-2882
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21213(A)	3048	-932	-2480	-2533	-3075	-1200	-2274	-2765	219
-	-149	-500	233	43	-381	399	106	-626	-3078
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21214(I)	-1924	-1546	-4067	-3658	-2312	-3663	-2081	3030	220
-	-149	-500	233	43	-381	399	106	-626	-692
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21215(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	221
-	-149	-500	233	43	-381	399	106	-626	-3363
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21216(A)	2389	-814	-2506	-2162	-1696	-1545	-1698	-499	222
-	-149	-500	233	43	-381	399	106	-626	-1856
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21217(M)	-2576	-2118	-4725	-4165	-461	-4430	-3185	99	223
-	-149	-500	233	43	-381	399	106	-626	-2145
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21218(G)	-2594	-2690	-3304	-3623	-4328	-3747	-3462	-4761	224
-	-149	-500	233	43	-381	399	106	-626	-4222
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21219(M)	-2313	-1968	-4258	-3765	-518	-3966	-2808	98	225
-	-149	-500	233	43	-381	399	106	-626	-1874
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249
21220(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	226
-	-149	-500	233	43	-381	399	106	-626	-3025
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	-249

Table 7

221(L)	-2631	-2159	-4766	-4228	-462	-4506	-3231	96	-3878	2828	2482	-4157	-3880	-3016	-3541	-3793	-2509	-608	-2134	-2182	227
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
222(P)	-1501	-1778	-2473	-2371	-1710	-2311	-2045	-1321	-2060	827	-1068	-2173	3594	-2082	-2130	-1798	-1698	-1373	-2373	-1942	228
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
223(V)	-1068	-1670	-865	-836	-631	1198	-767	-1828	-1059	-1914	-1304	692	-2203	-806	-1387	-1136	-1163	-1566	-1195	3670	229
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
224(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	230
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
225(S)	1172	-954	-2387	-2422	-3120	-1204	-2237	-2835	-2426	-3122	-2265	-1821	-1948	-2145	-2487	3107	-749	-1884	-3349	-3092	231
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
226(S)	-342	-975	-2176	-2124	-2912	-1229	-2003	-2594	-2087	-2878	-2048	-1510	-1936	-1868	-2184	2553	2492	-1773	-3143	-2833	232
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
227(M)	-720	-1440	-710	-343	-1228	-1693	2436	-1209	-132	-1364	3099	1904	-1852	-183	-458	-776	-680	-1004	-1540	-890	233
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
228(P)	2240	-1100	-2241	-2293	-3037	-1346	-2188	-2683	-2317	-2986	-2210	-1863	3041	-2093	-2391	-722	-895	-1893	-3243	-2998	234
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
229(A)	2958	-1235	-1299	-1377	-2868	-1345	-1673	-2580	-1661	-2843	-2054	1555	-1995	-1468	-1921	-715	-888	-1871	-3084	-2630	235
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
230(E)	-509	-1046	-884	1664	-1116	-1669	-441	-485	-283	250	-208	-577	689	-200	-656	-870	-459	1290	-1487	-995	236
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
231(D)	-1203	-2412	2595	-117	-3286	-1536	-1057	-3178	-1165	-3186	-2436	-428	-2088	-736	-1824	2377	-1366	-2578	-3334	-2552	237
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
232(C)	954	-1983	-100	971	-2337	177	-267	-2087	81	-2060	-1189	-125	-1637	2600	-418	-514	-597	-1649	-2268	-1597	238
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
233(E)	-2641	-3308	-866	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3365	239
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 7

-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-2620	-2861	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	240	
-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-2325(R)	377	-1802	-415	988	-2095	-1474	-95	-1786	1452	-1785	-911	-135	-1560	343	1555	-409	-431	376	-1986	-1375	241
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-236(D)	1083	-1565	2662	-244	-1941	-1573	-679	612	-527	-1651	-980	-490	-1869	-358	-1003	-771	-766	-903	-2208	-1633	242
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-248	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-237(E)	-1225	-2868	1894	1948	-3149	-1532	-671	-2975	-630	-2902	-2101	-150	-1935	-293	-1299	1884	-1241	-2496	-3093	-2248	243
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-238(C)	1375	3262	-2620	-2108	-827	-1866	-1267	1631	-1811	-599	-10	-1674	-2137	-1531	-1786	-1034	790	249	-1361	-1010	244
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-239(E)	635	-1798	1055	1761	-2018	-1464	-263	1191	28	-1767	-946	-148	-1637	135	-481	-520	-553	-1300	-2077	-1441	245
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-240(E)	593	-2044	-252	2548	-2437	-1542	-328	-2133	151	-2120	-1274	-244	-1738	89	946	-646	-717	-1734	-2305	-1686	246
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-241(S)	1884	-835	-1962	-1576	-1634	-1436	-1320	1041	-1409	-1453	-781	-1293	-1922	-1241	-1606	1973	-597	-669	-2036	-1656	247
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-242(G)	2267	-1043	-2398	-2526	-3253	2642	-2373	-2975	-2639	-3260	-2410	-1722	-2033	-2311	-2648	-663	-860	-2005	-3436	-3250	248
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-243(R)	-876	-2087	-829	1490	-2474	-1766	-229	-2106	1269	-44	-1198	-424	-1829	205	2225	-775	-768	-1753	-2143	-1647	249
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-244(V)	2339	-967	-2970	-2766	-1878	-1847	-2252	32	-2541	-1299	-918	-2087	-2399	-2316	-2545	-1157	-971	2345	-2605	-2251	250
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
-245(I)	-1827	-1398	-4307	-3331	-1099	-3939	-3142	2286	-3619	1835	69	-3579	-3671	-3177	-3511	-3178	-1781	1918	-2524	-2310	251
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

246(V)	-1178	-1448	-1943	-1452	-1776	-2261	-1140	-227	1866	-1260	-816	-1444	-2448	-902	-540	-1496	-1176	2697	-2161	-1764	252
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
247(E)	-508	-1976	840	1547	-2280	-1393	-117	-2029	1400	-1984	-1077	1158	-1531	330	-253	-378	-454	262	-2163	-1471	253
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
248(M)	1703	-991	-2901	-2342	-528	-2567	-1550	166	-2031	1544	2668	-2104	-2591	-1715	-2010	-1685	-1052	-12	-1442	-1177	254
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
249(I)	-1947	-1516	-4385	-3885	-916	-4013	-3118	2193	-3658	2186	257	-3656	-3687	-3109	-3494	-3250	-1889	1383	-2397	-2258	255
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
250(E)	-1322	-2647	-272	2491	-3071	-1811	-576	-2759	2306	-2633	-1854	-464	-2066	-175	-177	-1144	-1256	-2368	-2692	-2140	256
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
251(K)	-1395	-2059	-1711	-1014	-2215	-2218	-641	-1709	3021	-1652	2578	-1075	-2303	-282	287	-1423	-1283	-1603	-2159	-1803	257
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
252(D)	-1285	-2888	2677	176	-3210	1189	-737	-3047	-715	-2977	-2195	-190	-1978	2106	-1378	-1050	-1315	-2564	-3181	-2320	258
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
253(I)	-2073	-1632	-4434	-3975	-911	-4130	-3238	3164	-3706	1451	244	-3778	-3785	-3187	-3557	-3413	-2021	546	-2449	-2273	259
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
254(K)	-1570	-2144	-1897	-1191	-2098	-2363	-750	-1603	3034	938	-1112	-1231	-2436	-408	215	-1616	-1443	-1580	-2166	-1804	260
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
255(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4185	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4084	261
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
256(R)	-928	-1705	-1507	-1055	-2761	-1730	-866	-2490	-44	-2489	-1723	-1042	-2102	-543	2614	2258	-1053	-1998	-2546	-2158	262
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
257(D)	-1280	-2865	3154	175	-3194	-1547	-743	-3034	-728	-2971	-2184	-190	-1979	1342	-1391	553	-1316	-2552	-3161	-2317	263
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
258(I)	-1997	-1562	-4355	-3927	-1042	-4066	-3261	3343	-3654	937	87	-3718	-3783	-3239	-3555	-3364	-1959	702	-2549	-2295	264
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
2559(M)	-2252	-1821	-4572	-3991	-530	-4164	-2990	2068	-3709	1993	3197	-3808	-3685	-2916	-3406	-3378	-2149	-172	-2084	-2031	265
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
260(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3619	-2197	-3286	-3156	266
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
261(R)	-2131	-2786	-2704	-1460	-3618	-2638	-587	-2976	1735	-2645	-1985	-1353	-2603	-173	3492	-2020	-1828	-2748	-2484	-2394	267
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
262(K)	-1349	-2635	-381	2083	-3083	-1857	-565	-2750	2690	-2612	-1837	-514	-2090	-161	-61	-1178	-1271	-2369	-2655	-2138	268
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
263(A)	2821	-932	-2451	-2472	-3065	-1198	-2233	-2763	-2434	-3056	-2201	-1633	-1940	-2147	-2468	1831	-730	-1840	-3305	-3055	269
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
264(F)	-2063	-1686	-4037	-3677	3437	-3644	-1706	2063	-3359	135	67	-3095	-3486	-2739	-3127	-2876	-2012	-83	-1038	-158	270
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
265(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2580	-2479	-2750	-3722	-3563	-3385	271
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
266(N)	-1662	-3306	2055	78	-3621	-1643	-1040	-3822	-1272	-3531	-2870	3477	-2182	-724	-2071	-1371	-1757	-3092	-3633	-2700	272
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
267(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	273
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
268(I)	-1760	-1307	-4325	-3962	-1735	-4042	-3726	3135	-3828	-579	-515	-3722	-3869	-3673	-3896	-3359	-1752	2276	-3240	-2806	274
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
269(T)	1428	-904	-2334	-2158	-2747	-1206	-1940	-2392	-2037	-2678	-1846	-1504	-1896	-1809	-2163	902	3001	-1635	-2999	-2705	275
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
270(V)	-1745	-1300	-4266	-3558	-1446	-3967	-3370	2358	-3688	852	-261	-3606	-3749	-3403	-3673	-3232	-1717	2643	-2856	-2524	276
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

271(V)	-1404	-1072	-3766	-3305	-1464	-3356	-2696	2276	-3080	-616	-379	-3001	-3325	-2870	-3091	-2563	1344	2521	-2516	-2113	277
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
272(M)	866	-1113	-2656	-2412	-1322	-1920	-1883	-487	-2061	-587	4451	-1950	-2387	-1928	-2078	-1220	-1053	-498	-2134	-1803	278
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
273(A)	2601	-957	-2898	-2711	-1943	-1740	-2211	-165	-2487	-1406	-1001	-2008	-2320	-2260	-2494	-1053	-929	1890	-2626	-2279	279
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
274(L)	-1171	-983	-3266	-2733	-786	-2795	-1888	590	-2418	2001	188	-2418	-2816	-2106	-2362	-1844	965	1777	-1724	-1426	280
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
275(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	281
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
276(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	282
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
277(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2886	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	283
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
278(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	284
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
279(N)	-2171	-2655	-1458	-1748	-3334	-2364	-2267	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	285
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
280(A)	3134	-934	-2491	-2567	-3083	-1203	-2300	-2766	-2540	-3082	-2237	-1672	-1954	-2240	-2537	874	-747	-1844	-3333	-3093	286
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
281(V)	-984	-1045	-3169	-2909	-1709	-2304	-2404	531	-2643	-988	-697	-2378	-2722	-2480	-2661	-1601	1504	3014	-2588	-2201	287
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
282(L)	-2631	-2159	-4786	-4228	-462	-4506	-3231	96	-3878	2828	2482	-4157	-3880	-3016	-3541	-3793	-2509	-608	-2134	-2182	288
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
283(H)	-3205	-3079	-2723	-2890	-2110	-3046	5295	-4135	-2617	-3813	-3561	-2886	-3482	-2833	-2620	-3291	-3356	-3895	-2397	-1681	289
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
284(L)	-1623	-1338	-3726	-3164	-251	-3255	-1820	1373	-2808	2371	514	-2785	-3086	-2281	-2613	-2389	-1543	-161	-1311	1782	280
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
285(L)	-2333	-1873	-4640	-4127	-650	-4326	-3241	2176	-3843	2519	523	-3892	-3833	-3105	-3579	-3604	-2247	56	-2288	-2230	281
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
286(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	292
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
287(M)	-1886	-1507	-4178	-3693	-877	-3806	-2901	3008	-3380	335	3109	-3451	-3570	-2934	-3251	-3044	-1840	524	-2288	-2089	293
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
288(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	294
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
289(H)	-1490	-2484	-362	-476	-1816	-1880	4320	-2854	-684	-2770	-2133	2185	-2285	-728	-1000	-1377	-1550	-2475	-2146	-1255	295
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
290(A)	2439	-911	-2326	-2131	-2811	-1197	-1934	-2480	-2011	-2745	-1898	-1490	-1888	-1785	-2153	1898	1073	-1682	-3044	-2749	296
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
291(I)	2038	-985	-3398	-2919	-1320	-2893	-2277	2155	-2877	-587	-297	-2593	-2992	-2450	-2697	-2087	-1208	1681	-2229	-1846	297
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
292(G)	-1243	-2769	311	1902	-3172	1980	-744	-2892	-697	-2936	-2152	1923	-1974	-377	-1331	-1030	-1284	-2506	-3125	-2308	298
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
293(V)	-1738																				

Table 7

296(T)	-350	-973	-2204	-2178	-2893	-1236	-2035	-2561	-2117	-2862	-2043	-1536	-1846	-1916	-2214	1618	3198	-1758	-3137	-2831	302
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
297(L)	-1443	-1268	-3144	-2576	-528	-3014	-1816	1945	-2155	2102	508	-2422	-2899	1193	-2133	-2129	-1369	-50	-1616	-1384	303
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
298(D)	-1826	-3662	3559	1199	-3883	-1662	-1073	-3846	-1391	-3720	-3110	-272	-2222	-760	-2283	-1471	-1913	-3321	-3864	-2864	304
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
299(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	305
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
300(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	306
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
301(O)	-1048	-2608	205	2170	-2893	-1535	-505	-2680	-255	-2604	-1769	1814	-1849	2272	-789	-848	-1028	-2228	-2770	-2013	307
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
302(R)	1083	-1687	691	135	-2058	-1406	-178	-1755	214	-1793	-924	-145	-1553	247	1670	-383	1217	-1367	-2031	-1404	308
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
303(I)	-1915	-1536	-4077	-3667	2027	-3678	-2155	3137	-3381	144	94	-3225	-3506	-2848	-3202	-2914	-1871	345	-1522	-791	309
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
304(R)	-689	-2015	-494	24	-2395	-1582	-184	-2087	444	-2020	-1151	1161	-1687	1832	2131	626	-614	-1684	-2156	-1573	310
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
305(D)	387	-1967	1600	1359	-2275	-1391	1561	-2025	282	-1976	-1067	-25	-1525	342	1024	-369	-443	-1584	-2152	-1462	311
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
306(R)	-1460	-2315	-1793	-887	-2832	-2237	-431	-2288	2193	-2199	-1473	-946	-2245	-20	2708	-1394	-1275	591	-2248	-1861	312
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
307(V)	-941	-1027	-3099	-2832	-1692	-2234	-2324	470	-2665	-1003	-695	-2305	-2663	-2399	-2587	-1527	1858	2876	-2536	-2152	313
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
308(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4821	-3859	-4490	-4165	-3491	-4225	-3781	-3695	-3182	-3279	-4087	-3594	-4084	314
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
309(V)	-1090	-1215	-2097	-1824	-819	-2221	2699	-287	-1392	-1027	-591	-1674	-2482	-1446	-1482	-1482	-1143	2879	-1420	-707	315
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
310(L)	-2439	-1972	-4702	-4181	-588	-4401	-3258	1582	-3881	2757	587	-4061	-3862	-3093	-3590	-3689	-2344	-130	-2230	-2217	316
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
311(C)	2157	4166	-3012	-2973	-2780	1022	-2337	-2398	-2724	-2744	-1930	-1786	-1943	-2372	-2623	-540	-692	-1624	-3091	-2881	317
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
312(D)	-1732	-3453	3468	99	-3733	-1645	-1066	-3747	-1356	-3641	-3008	1690	-2201	-755	-2209	-1416	-1833	-3208	-3752	-2776	318
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
313(L)	-2477	-2023	-4713	-4122	1592	-4329	-2920	72	-3835	2593	2472	-3948	-3754	-2914	-3466	-3550	-2350	-634	-1927	-1830	319
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
314(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	320
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
315(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	321
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
316(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	322
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
317(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	323
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
318(K)	2	-2257	-1073	-374	-2740	-1908	-278	-2339	2328	-2192	-1373	-562	-1953	2273	1344	-952	-933	-1980	-2234	-1799	324
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
319(Y)	-3482	-2868	-3701	-3919	238	-3552	-1112	-3000	-3638	-2516	-2526	-3027	-3772	-3101	-3341	-3418	-3527	-3071	-441	4711	325
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
320(M)	-1559	-1267	-3829	-3380	-1103	-3357	-2655	805	-3067	-64	3046	-3065	-3326	-2779	-3011	-2591	-1556	2855	-2312	-1998	326
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												

Table 7

321(M)	1225	-489	-2256	-1879	1656	-1926	-870	90	-1398	-210	2763	-1424	-2028	-1129	-1411	-1008	712	154	-851	-586	327
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
322(N)	-738	-2094	-84	1704	-2416	-1495	-317	-2135	61	-2127	-1275	-163	-1704	1857	-405	-613	1930	-1734	-2331	-1668	328
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
323(O)	-1746	-3458	3540	90	-3744	-1650	-1081	-3767	-1381	-3662	-3036	1386	-2211	-772	-2239	-1429	-1850	-3226	-3765	-2769	329
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
324(P)	-2451	-1983	-4707	-4186	-582	-4409	-3259	1510	-3884	2776	592	-4069	-3865	-3091	-3590	-3698	-2355	-150	-2226	-2214	330
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
325(Q)	-2923	-2573	-2959	-2926	826	-3449	4553	-2508	-2463	-2054	-1948	-2278	-3499	-2191	-2397	-2761	-2855	-2540	123	2920	331
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
326(R)	373	-1957	-342	1025	-2297	-1472	-98	-2018	2111	-1954	-1056	906	-1570	352	685	-424	-473	-1592	-2105	-1469	332
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
327(S)	1739	-1008	-3509	-3043	-1376	-3028	-2406	1765	-2807	-615	-334	-2718	-3093	-2585	-2823	-2226	-1263	2376	-2322	-1931	333
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
328(T)	-2594	-2690	-3304	-3823	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	334
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
329(U)	-2594	-2690	-3304	-3823	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	335
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
330(V)	-1758	-1302	-4331	-3970	-1756	-4054	-3748	2976	-3840	-603	-533	-3731	-3877	-3693	-3914	-3372	-1750	2505	-3265	-2824	336
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
331(W)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4166	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	337
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
332(X)	1795	-1440	-730	-492	-2453	682	-812	-2151	-508	-2256	-1426	-624	-1796	2666	-901	-590	-889	-1636	-2510	-1971	338
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
333(Y)	-1771	-1603	-3750	-3689	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2828	-1917	3536	-3074	-2677	339
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
3334(M)	-2355	-1988	-4343	-3834	-504	-4051	-2868	105	-3385	1451	4460	-3680	-3671	-2806	-3171	-3327	-2274	-474	-2039	-1925	340
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3335(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-455	-2604	-2536	-3331	-3001	-2988	341
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3336(Y)	-1187	-974	-3186	-2638	-117	-2732	-1255	1905	-2270	73	1977	-2217	-2699	-1882	-2144	-1841	-1124	71	-907	3254	342
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3337(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3835	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	343
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3338(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3835	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	344
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3339(K)	-864	-1785	-860	-366	-2128	-1763	-407	-1612	2624	-1800	-1045	629	-1900	-28	62	-851	-805	1127	-2064	-1581	345
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
340(N)	602	-1686	-275	1008	-1926	-1415	1528	-1618	244	-1673	-815	1897	-1530	299	-244	-371	-391	322	-1934	-1306	346
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
341(G)	-1709	-2639	1362	-690	-3785	3257	-1671	-3805	-1946	-3792	-3137	-980	-2480	-1424	-2576	-1630	-1936	-3150	-3628	-3155	347
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
342(F)	-942	-799	-2828	-2226	1797	-2476	-1269	1109	581	1793	516	-1952	-2453	-1557	-1815	-1558	-875	52	-1138	-794	348
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
343(L)	-2451	-1993	-4707	-4186	-582	-4409	-3259	1510	-3884	2778	592	-4069	-3865	-3091	-3590	-3698	-2355	-150	-2226	-2214	349
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
344(H)	-3205	-3079	-2723	-2890	-2110	-3046	5295	-4135	-2617	-3813	-3561	-2886	-3482	-2833	-2620	-3291	-3356	-3895	-2397	-1681	350
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
345(G)	-2594	-2690	-3304	-3623	-4326	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	351
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

346(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	352
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
347(C)	774	4452	-2162	-1688	-1862	-1478	-1302	-1474	-844	-1796	-1088	-1351	-1979	-1147	1864	-732	-719	-1116	-2225	-1881	353
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
348(L)	-2387	-1922	-4674	-4155	-617	-4366	-3250	1869	-3865	2650	558	-4023	-3847	-3098	-3586	-3047	-2296	-38	-2247	-2224	354
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
349(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3266	-3156	355
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
350(C)	-1489	2972	-4007	-3563	-1524	-3541	-2939	2812	-3350	-617	-413	-3224	-3470	-3129	-3335	-2770	-1475	2269	-2657	-2248	356
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
351(T)	-364	-978	-2232	-2250	-2904	-1245	-2090	-2559	-2191	-2881	-2075	-1571	-1984	-1991	-2260	905	3428	-1762	-3159	-2858	357
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
352(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3778	-2839	-2981	-4004	-3688	-4222	358
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
353(K)	-1716	-2632	-2004	-1008	-3336	-2379	-444	-2764	2775	-2484	-1756	-1035	-2357	2151	1811	-1592	-1477	-2481	-2391	-2172	359
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
354(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3266	-3156	360
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
355(V)	-1771	-1339	-4275	-3816	-1235	-3919	-3194	2139	-3617	1520	-66	-3558	-3681	-3244	-3547	-3164	-1733	2390	-2634	-2369	361
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
356(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	362
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
357(E)	-2641	-3308	-866	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3385	363
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
358(N)	-823	-1917	-96	1188	-2187	-1547	-506	-1711	-265	-1955	-1191	2711	-1815	-144	-747	-757	-815	1140	-2287	-1666	364
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
3359(L)	-2153	-1779	-4360	-3884	-675	-3965	-3012	392	-3561	2726	467	-3673	-3662	-2955	-3355	-3239	-2102	1281	-2207	-2099	365
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3360(E)	1136	-2084	-175	2027	-2436	-1510	-274	-2147	1525	-2118	-1254	-175	-1692	152	-251	-593	-670	-1736	-2296	-1650	366
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3361(H)	893	-1761	1357	214	-2092	-1387	1862	-1810	229	-1825	-942	-83	-1527	293	-273	640	793	-1409	-2050	-1397	367
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3362(I)	608	-458	-2776	-2176	1666	-2202	-1113	1712	-1836	-222	338	-1782	-2245	-1512	-1731	-1292	867	1366	-1036	-694	368
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3363(P)	-922	-1912	1681	-141	-2123	-1604	-687	-1787	-550	187	-1245	-427	2677	-363	-1049	-882	-947	-1524	-2338	-1711	369
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3364(D)	-1692	-3605	3364	1256	-3770	-1599	-957	-3700	-1216	-3569	-2909	1025	-2138	-628	-2083	-1346	-1761	-3174	-3765	-2738	370
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3365(Q)	-877	-1646	-633	499	-1610	-1781	-505	-1210	-63	1648	-649	-558	-1931	2241	-360	-907	-814	-1097	-1882	-1395	371
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
3366(P)	-648	-2019	1139	203	-2354	-1436	-285	-2089	29	-2086	-1217	-114	1965	1445	-492	-529	1244	-1672	-2300	-1616	372
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-571	-7108	-1646	-894	-1115	-701	-1378*	*													
3367(R)	-422	-1009	-851	-304	1408	-1496	-193	-740	147	-894	-230	-440	775	21	2009	-539	-381	-568	-1136	-521	373
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-23	-6560	-7602	-894	-1115	-341	-2249*	*													
3368(D)	1472	-1688	1835	-70	-2356	-138															

Table 7

371(D)	-1275	-2955	2862	1330	-3205	-1556	-670	-3029	1508	-2936	-2141	-158	-1955	-280	-1213	-1025	-1281	-2554	-3111	-2272	377
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
372(V)	-1738	-1298	-4281	-3921	-1737	-3979	-3665	1917	-3774	-601	-528	-3671	-3634	-3628	-3843	-3293	-1735	3205	-3215	-2770	378
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
373(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3299	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	379
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
374(M)	-584	-1354	-847	-246	-1467	-1659	2505	-1087	212	-374	2571	-449	-1729	1171	1074	-634	-507	-876	-1617	-1128	380
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
375(P)	-910	-2031	-73	1195	-2792	-1488	-794	-2539	629	-2588	-1788	-401	3005	-439	-1131	612	-1014	-2050	-2815	-2151	381
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
376(W)	-1588	-1300	-3783	-3197	-329	-3245	-1926	2071	-2827	1801	558	-2822	-3072	-2297	-2616	-2381	-1508	-111	3483	-1042	382
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
377(E)	-1024	-2640	1844	2310	-2908	-1498	-505	-2711	-344	-2636	-1791	-107	-1824	1521	-957	207	-1011	-2243	-2817	-2021	383
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
378(N)	-826	-2349	1089	227	-2651	-1487	-341	-2416	1494	-2346	-1475	2601	-1724	1005	-522	-657	-787	-1868	-2511	-1791	384
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
379(P)	1932	-1116	-2232	-2301	-3058	-1358	-2206	-2706	-2336	-3009	-2238	-1674	3274	-2114	-2406	-739	-814	-1913	-3260	-3019	385
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
380(V)	-914	-773	-2713	-2129	-712	-2505	-1388	1452	1084	1324	204	-1926	-2507	-1580	-1808	-1591	-859	1713	-1424	-1081	386
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
381(Y)	-1484	-2331	-1762	-887	-2436	-2254	-420	-2325	2137	-2195	-1475	-949	-2258	-39	1983	-1411	-1295	-2075	-2087	2868	387
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
382(E)	1258	-1890	-206	1353	-2196	-1401	-89	-1930	812	-1898	-996	-45	547	1252	-162	-356	-414	-1507	-2083	-1416	388
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
383(Q)	-752	-2272	1566	1407	-2561	-1448	-308	-2329	-23	-2276	-1396	-71	-1677	1749	-577	-590	1569	-1881	-2459	-1727	389
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
384(G)	-2594	-2600	-3304	-3823	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	390
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
385(H)	-964	-2089	-200	-136	-2264	-1600	3833	-2320	-296	-2338	-1558	1362	1479	-276	-699	-881	-992	-1924	-2364	-1652	391
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
386(L)	-2451	-1983	-4707	-4186	-582	-4409	-3259	1510	-3884	2778	592	-4069	-3865	-3091	-3590	-3698	-2355	-150	-2226	-2214	392
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
387(Q)	1643	-1017	-1196	-721	-1189	-1714	-668	1336	-497	-907	-297	-823	-1893	2044	-794	-784	-569	-339	-1579	-1135	383
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
388(U)	-1760	-1308	-4323	-3961	-1730	-4039	-3721	3156	-3825	-575	-512	-3720	-3867	-3669	-3893	-3356	-1753	2241	-3236	-2802	384
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
389(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3935	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	395
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
390(K)	-1259	-2115	-1267	-676	-870	-2105	1794	-2040	2549	-1955	-1282	-808	-2165	-187	114	-1192	-1140	-1801	-1301	2517	396
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
391(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	397
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
392(N)	-2171	-2655	-1458	-1748	-3334	-2384	-2287	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	398
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
393(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3935	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	399
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
394(A)	3121	-934	-2489	-2561	-3081	-1203	-2295	-2766	-2533	-3080	-2234	-1669	-1953	-2234	-2533	936	-746	-1844	-3331	-3090	400
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
395(E)	-522	-1773	-240	1676	-2248	-1396	-289	-1968	50	-1989	-1115	-174	1198	131	-448	1226	677	-1538	-2214	-1565	401
	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

396(E)	-1481	-3230	1425	2936	-3481	751	-843	-3354	-954	-3256	-2520	-187	-2057	-492	-1711	-1193	-1527	-2852	-3445	-2523	402
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
397(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	403
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
398(A)	2847	-932	-2454	-2477	-3066	-1198	-2236	-2763	-2439	-3057	-2202	-1635	-1940	-2152	-2471	1777	-731	-1840	-3306	-3056	404
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
399(V)	-1771	-1603	-3750	-3669	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2628	-1917	3536	-3074	-2677	405
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
400(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	406
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
401(K)	-2620	-2981	-2481	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	407
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
402(I)	-1761	-1312	-4317	-3954	-1713	-4027	-3703	3225	-3814	-556	-498	-3712	-3859	-3653	-3877	-3344	-1754	2110	-3216	-2787	408
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
403(S)	-348	-981	-2200	-2194	-2989	-1227	-2073	-2666	-2157	-2970	-2136	-1541	-1946	-1946	-2253	3080	1398	-1824	-3217	-2916	409
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
404(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	410
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
405(V)	-917	-809	-2556	-1976	-827	-2491	-1367	1339	1455	721	94	-1841	-2501	-1487	-1710	-1570	-863	2038	-1514	-1151	411
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
406(K)	-1386	-2643	-447	1824	-3108	-1893	-570	-2762	2860	-2616	-1848	-552	-2117	-166	-3	-1217	-1300	-2388	-2847	-2154	412
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
407(N)	-537	-1563	-449	-36	-1889	1143	-307	-1529	932	-1655	-844	1794	-1658	73	-356	-518	-516	924	-1982	-1392	413
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
408(P)	-894	-2181	-369	1705	-2576	-1650	-357	-2268	243	-2210	-1375	-330	2093	63	1619	-774	-835	-1876	-2347	-1769	414
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*															
409(V)	-419	-634	-1376	-807	1053	-807	-1737	-499	-198	-623	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
410(I)	-1282	-1082	-3022	-2555	2426	-2683	1767	2555	-2191	-443	-88	-2038	-2692	-1794	-2075	-1793	-1220	-317	-361	552	416			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
411(T)	-499	-1595	-431	966	-1830	-1487	-185	-1448	1092	-1574	-754	-207	-1601	213	-206	-458	2067	159	-1877	-1296	417			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
412(G)	-2594	-2690	-3304	-3623	-4328	3747	-3482	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	418			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
413(P)	-632	-1230	-2074	-2144	-2996	-1453	-2116	-2631	-2128	-2928	-2213	-1658	3610	-2006	-2221	-852	1302	-1931	-3185	-2917	419			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
414(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	420			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
415(R)	-1454	-2316	-1780	-878	-2834	-2232	-428	-2292	2281	-2200	-1473	-940	-2240	-17	2627	-1386	-1270	588	-2249	-1960	421			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
416(V)	-1771	-1603	-3750	-3689	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2628	-1917	3536	-3074	-2677	422			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
417(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3845	-3490	-3420	-2566	-739	349	423			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
418(D)	-1572	-3426	2573	2447	-3613	-1583	-878	-3513	-1050	-3393	-2694	1292	-2085	-535	-1855	-1253	-1623	-3000	-3585	-2609	424			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
419(S)	-879	-1989	1498	-177	-3045	1600	-939	-2843	-904	-2867	-2046	-438	-1922	-591	-1483	2171	-1044	-2226	-3072	-2372	425			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																
420(E)	-2641	-3308	-866	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3365	426			
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	600	-1807	-475	475	313	-360	1389	-1016	1303	415		
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*																

Table 7

421(Q)	-705	-1925	-199	2112	917	-1534	-288	-1824	42	-1842	-1054	-210	-1709	2163	-420	-611	-656	-1502	-1997	-1291	427
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
422(H)	-569	-2048	1450	1526	-2349	-1405	1830	-2103	181	-2058	-1157	-37	-1569	272	-349	713	620	-1692	-2240	-1537	428
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
423(C)	1626	2878	-2671	-2107	1264	-1968	-1091	233	-1777	-334	250	-1672	-2128	-1459	-1691	-1096	-529	1209	-1066	-704	429
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
424(M)	-2042	-1634	-4379	-3826	-659	-3976	-2899	2765	-3546	1204	3085	-3605	-3604	-2896	-3318	-3183	-1961	195	-2135	-2058	430
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
425(E)	412	-2447	1356	2379	-2747	-1477	-445	-2527	-243	-2477	-1622	-107	855	-36	-831	-730	-894	-2073	-2668	-1906	431
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
426(A)	2822	-1031	-2418	-2539	-3226	1898	-2384	-2941	-2626	-3229	-2379	-1722	-2026	-2302	-2634	-654	-848	-1993	-3415	-3226	432
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
427(U)	-1772	-1325	-4307	-3877	-1405	-3993	-3393	2935	-3705	820	-217	-3632	-3761	-3400	-3682	-3260	-1742	2033	-2838	-2525	433
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
428(L)	-875	-1634	-575	959	-1581	-1769	-525	-1179	-135	1884	-625	-547	-1931	1405	-450	-909	-816	-1074	-1863	-1383	434
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
429(A)	1705	-1826	-180	949	-2318	-1410	-359	-2041	-53	-2067	-1204	1001	-1652	52	-561	1232	-595	-1609	-2298	-1843	435
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
430(D)	-1074	-2458	2381	60	-2921	1927	-658	-2710	-463	-2675	-1860	-271	-1918	-276	866	-915	-1100	-2245	-2845	-2124	436
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
431(K)	-688	-2117	785	888	-2469	-1529	-187	-2189	2380	-2108	-1221	-162	-1681	256	1134	-553	-819	-1760	-2240	-1607	437
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
432(I)	-2019	-1582	-4380	-3941	-1000	-4086	-3253	3295	-3671	1100	145	-3736	-3783	-3222	-3556	-3378	-1976	657	-2517	-2289	438
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
433(Q)	-490	-1797	-369	171	-2078	-1457	1762	-1779	1157	-1780	-905	1165	-1550	1798	-48	-396	-422	725	-1986	-1366	439
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 7

[illegible]

Table 7

4446(K)	-1060	-2058	-1088	-460	-2432	-1917	-357	-1970	2801	-1978	-1220	-632	-1990	1339	367	-998	-946	536	-2145	-1717	452
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4447(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	453
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4448(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	454
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4449(P)	-2931	-2878	-3420	-3706	-4181	-2825	-3468	-4821	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	455
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4450(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	456
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4451(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	457
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4452(P)	-1859	-2241	-2022	-1846	-3185	-2242	-1373	-3000	-450	-2936	-2274	-1824	3435	-1065	2095	-1730	-1750	-2593	-2816	-2613	458
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4453(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3385	459
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4454(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	460
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4455(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3935	-3797	-3288	-3484	-3713	-2869	-1136	-2394	-2220	461
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4456(K)	1368	-1491	-763	-332	-2319	-1417	-551	-1998	1786	-2068	-1221	-500	-1721	-160	-470	1631	-587	-1532	-2298	-1754	462
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4457(P)	-1500	-1738	-2514	-2380	-1555	-2358	-2022	-1126	-2063	1224	-841	-2189	3436	-2061	-2129	-1822	-1674	-1231	-2290	-1878	463
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	
4458(T)	-351	-974	-2208	-2185	-2894	-1237	-2041	-2561	-2125	-2863	-2046	-1539	-1948	-1923	-2218	1543	3230	-1758	-3139	-2834	464
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*	*	*	*	*	*	*	*	*	*	*	*	

Table 7

-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
459(S)	-897	-1482	-2333	-2543	-3185	-1640	-2474	-3294	-2886	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	485
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
460(M)	2706	-986	-2433	-2144	-1502	-1684	-1706	-700	-1858	-968	2744	-1705	-2188	-1713	-1932	-963	-862	-592	-2145	-1794	466
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
461(I)	-2103	-1659	-4461	-3992	-869	-4152	-3233	3082	-3723	1619	290	-3801	-3788	-3171	-3557	-3432	-2046	487	-2418	-2285	467
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
462(I)	-1761	-1312	-4317	-3954	-1713	-4027	-3703	3225	-3814	-556	-498	-3712	-3859	-3653	-3877	-3344	-1754	2110	-3216	-2787	468
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
463(G)	-2594	-2690	-3304	-3823	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	469
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
464(K)	1641	-2033	-323	914	-2415	-1565	-296	-2097	2052	-2080	-1233	-257	-1736	125	-133	-646	-702	-1707	-2258	-1657	470
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
465(G)	-2594	-2690	-3304	-3823	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	471
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
466(L)	-1699	-1807	-2268	-1925	-830	-2795	-1551	-455	-1225	2510	90	-1958	-2845	1927	-1308	-2067	-1651	-846	-1841	-1454	472
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
467(G)	-2594	-2690	-3304	-3823	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	473
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
468(D)	-863	-2415	2115	1717	-2702	-1488	-378	-2484	1085	-2417	-1546	-84	-1732	41	-699	696	-824	-2025	-2594	-1839	474
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
469(S)	-892	-1780	-931	-688	-2757	-1643	-830	-2472	1671	-2492	-1708	-799	-2018	-468	-365	2676	-1004	-1981	-2598	-2130	475
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
470(C)	-1135	3503	-3700	-3406	-1670	-2549	-2675	653	-3101	-916	-667	-2727	-2925	-2870	-3030	-1868	-1288	2927	-2619	-2222	476
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

471(A)	2590	-1035	-2404	-2530	-3236	2290	-2355	-2954	-2627	-3240	-2389	-1719	-2027	-2302	-2637	-656	-851	-1991	-3423	-3234	477
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
472(L)	-2632	-2152	-4630	-4185	1767	-4324	-2442	-61	-3679	2789	563	-3833	-3823	-2870	-3513	-3609	-2518	-738	-1527	-945	478
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
473(U)	-2073	-1632	-4434	-3975	-911	-4130	-3238	3164	-3706	1451	244	-3779	-3785	-3187	-3557	-3413	-2021	546	-2448	-2273	479
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
474(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	480
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
475(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	481
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
476(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3688	-4222	482
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
477(R)	-2957	-3022	-3318	-2735	-3796	-2998	-1968	-3912	-846	-3631	-3157	-2611	-3280	-1724	4056	-3026	-2913	-3650	-3086	-3185	483
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
478(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	484
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
479(S)	-897	-1462	-2333	-2543	-3185	-1840	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	485
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
480(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3688	-4222	486
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
481(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3688	-4222	487
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
482(T)	-359	-976	-2225	-2229	-2900	-1242	-2074	-2560	-2170	-2875	-2084	-1561	-1958	-1969	-2247	1110	3375	-1760	-3152	-2850	488
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
483(Y)	-3402	-2632	-3941	-4011	1064	-3924	3368	-2526	-3541	-1986	-1973	-2625	-3821	-2664	-3170	-3135	-3280	-2619	3420	3756	489
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
484(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-3953	-3748	-3779	-2839	-2981	-4004	-3668	-4222	490		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
485(M)	-2322	-1904	-4536	-3951	2387	-4112	-2676	67	-3649	2034	3156	-3710	-3633	-2803	-3311	-3309	-2204	-588	-1794	-1586	491
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
486(V)	-1771	-1603	-3750	-3689	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2628	-1917	3536	-3074	-2677	492
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
487(V)	-1771	-1603	-3750	-3689	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2628	-1917	3536	-3074	-2677	493
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
488(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-3953	-3748	-3779	-2839	-2981	-4004	-3668	-4222	494		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
489(H)	-3205	-3079	-2723	-2890	-2110	-3046	5295	-4135	-2617	-3813	-3561	-2886	-3482	-2833	-2620	-3291	-3356	-3895	-2397	-1681	495
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
490(V)	-1754	-1297	-4329	-3968	-1770	-4053	-3752	2604	-3840	-621	-545	-3728	-3878	-3699	-3917	-3370	-1746	2859	-3276	-2829	496
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
491(A)	2587	-828	-2477	-2155	-1837	-1468	-1728	-743	-1941	-1564	-954	-1607	-2033	-1725	-2034	-738	1178	1108	-2310	-1972	497
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
492(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3858	-4480	-4165	-3481	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	498
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
493(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2478	-2750	-3722	-3563	-3385	499
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
494(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	500
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
495(Y)	-866	-976	-1863	-1331	1353	-2145	1318	-556	-1116	-777	-173	-1242	-2197	1714	-1301	-1173	-802	888	-445	2749	501
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

496(D)	417	-1831	1647	1094	-2065	-1488	-353	-1618	-107	-1820	-1019	-189	-1698	30	-623	-603	-643	1629	-2154	-1520	502
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
497(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	503
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
498(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	504
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
499(T)	492	-1190	-706	-181	-1475	311	-333	-1099	-81	71	-509	570	1113	-8	-509	-450	1123	-835	-1880	-1161	505
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
500(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	506
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
501(A)	3103	-1036	-2445	-2572	-3222	1051	-2380	-2930	-2650	-3226	-2381	-1739	-2034	-2327	-2648	-664	-857	-1981	-3412	-3228	507
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
502(L)	-2239	-1892	-3711	-3400	301	-3520	-1210	-542	-2948	2564	-35	-2786	-3395	-2438	-2750	-2747	-2165	-945	-573	2562	508
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
503(V)	-1757	-1367	-4101	-3681	-1174	-3714	-3031	880	-3410	1254	-60	-3407	-3585	-3094	-3354	-2984	-1743	3014	-2536	-2219	509
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
504(Q)	-862	-2251	-866	971	-2711	-1822	-252	-2340	1444	-2194	-1356	-464	-1885	2646	1632	-858	-863	-1958	-2245	-1765	510
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
505(E)	-1162	-2771	2137	2238	-3046	-1528	-626	-2849	-546	-2792	-1983	-145	-1905	-242	-1192	-940	1396	-2385	-2990	-2169	511
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
506(G)	-1707	-2684	1591	-614	-3783	3190	-1613	-3795	-1887	-3775	-3119	-915	-2456	-1358	-2539	-1610	-1924	-3150	-3636	-3124	512
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
507(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	513
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*														
508(M)	-473	-522	-1819	-1236	-468	-1879	-687	1519	-996	566	1677	-1154	-1937	836	-1131	1078	-413	102	-957	-585	514
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
509(I)	-1761	-1312	-4317	-3954	-1713	-4027	-3703	3225	-3814	-556	-498	-3712	-3859	-3653	-3877	-3344	-1754	2110	-3216	-2787	515
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
510(T)	782	-1467	-550	1029	-2202	-1425	-709	-1791	-472	-1993	-1203	-528	-1787	-368	-902	-617	2685	-1400	-2333	-1783	516
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
511(U)	-1766	-1333	-4283	-3923	-1635	-3967	-3619	3388	-3759	-473	-437	-3672	-3822	-3576	-3804	-3285	-1764	1695	-3126	-2717	517
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
512(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	518
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
513(A)	2705	-1451	-1036	-913	-2506	-1504	-1143	-2174	-794	-2337	-1613	-946	-1993	2040	-1061	-809	-910	-1703	-2633	-2156	519
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
514(H)	-615	-1680	1444	66	-1883	168	2650	-1558	-86	-1691	-891	-223	-1680	31	-577	-571	-585	1267	-2007	-1397	520
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
515(K)	-654	-2006	-546	42	-2376	-1581	-133	-2066	1935	-1987	-1107	1132	-1658	1043	1058	-540	1180	-1660	-2113	-1532	521
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
516(N)	-933	-2085	-946	-284	-2472	-1822	-253	-2080	1711	76	-1204	1918	-1876	175	1799	-841	-817	-1755	-2132	-1663	522
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
517(E)	-416	-987	-843	1107	-1070	-1583	-338	-823	-183	879	-172	-489	-1679	-94	-565	544	813	265	-1379	-905	523
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
518(I)	-2258	-1804	-4588	-4084	-706	-4289	-3231	2527	-3807	2292	465	-3923	-3814	-3118	-3570	-3544	-2181	190	-2303	-2237	524
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
519(O)	-477	-1909	958	282	-2211	-1389	1484	-1953	285	-1921	-1018	-32	-1517	2318	-225	630	559	-1525	-2110	-1430	525
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
520(L)	-2127	-1743	-4402	-3796	1257	-3918	-2674	149	-3492	2527	2164	-3553	-3509	-2714	-3181	-3095	-2019	570	-1870	-1818	526
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

521(N)	-723	-2217	988	236	-2518	-1466	1611	-2279	1719	-2217	-1334	2285	-1666	166	-401	-570	-677	-1837	-2382	-1678	527
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
522(V)	-1754	-1287	-4330	-3968	-1770	-4053	-3752	2623	-3841	-620	-545	-3728	-3878	-3699	-3918	-3371	-1746	2846	-3277	-2830	528
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
523(S)	1545	-974	-2003	-1825	-2667	-1206	-1790	-2580	-1788	-2795	-1932	-1362	1626	-1586	-1999	2362	-672	-1755	-3057	-2721	529
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
524(D)	-1776	-3649	3326	1869	-3838	-1642	-1031	-3788	-1322	-3660	-3029	-245	-2192	-711	-2201	-1425	-1855	-3264	-3821	-2816	530
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
525(E)	423	-2950	1944	2696	-3223	-1545	-718	-3047	-715	-2979	-2196	-161	-1968	-347	-1403	-1043	-1314	-2569	-3177	-2316	531
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
526(E)	-2641	-3308	-866	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2580	-2478	-2750	-3722	-3583	-3385	532
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
527(L)	-2339	-1899	-4618	-4042	1570	-4204	-2849	1440	-3758	2558	676	-3825	-3700	-2902	-3418	-3418	-2226	-382	-1924	-1778	533
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
528(A)	2338	-1990	-241	938	-2395	-1557	-423	-2061	954	-2103	-1286	-301	-1791	-26	-375	-717	-784	-1691	-2330	-1728	534
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
529(R)	524	-2098	-789	-146	-2504	-1729	1632	-2153	1229	-2054	-1204	-378	-1789	1328	2313	-718	-724	-1774	-2150	-1637	535
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
530(R)	-2957	-3022	-3318	-2735	-3796	-2998	-1968	-3912	-846	-3631	-3157	-2611	-3280	-1724	4056	-3026	-2913	-3650	-3096	-3185	536
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
531(R)	-1895	-2713	-2327	-1192	-3484	-2502	-481	-2856	2144	-2544	-1842	-1181	-2458	1393	3023	-1770	-1619	-2599	-2421	-2259	537
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
532(A)	2935	-1714	-553	857	-2769	-1546	-1218	-2333	-1106	-2591	-1873	-809	-2065	-934	-1502	-954	-1103	-1872	-2898	-2374	538
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
533(A)	1291	-1874	-176	1227	-2177	-1392	-109	-1909	277	-1891	-995	1134	-1522	1248	-228	-361	562	-1492	-2090	-1419	539
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 7

-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
534(W)	-805	-687	-2581	-2028	138	-2236	-697	897	-1681	-421	141	-1645	-2282	-1369	-1627	-1315	636	-90	4479	1809	540
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
535(H)	-408	-1801	-274	1284	-2096	-1385	1500	-1822	1168	-1802	-899	-33	-1479	1381	-102	-303	595	221	-1996	-1339	541
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
536(Q)	-650	-1737	-627	-72	-1981	-1615	-209	-1625	1223	392	-866	-318	1222	2120	50	-598	-572	-1326	-1932	-1394	542
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
537(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	394	45	96	359	117	-369	-284	-249
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-324	-7108	-2368	-894	-1115	-701	-1378*	*												
538(A)	2195	-924	-968	-546	-1397	-1356	-583	-812	-365	-1167	-487	-618	-1660	1324	-684	-483	-404	462	-1703	-1242	544
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-18	-6804	-7846	-894	-1115	-428	-1961*	*												
539(P)	411	-1017	-1886	-1616	-1600	-1588	-1411	-962	-1408	495	-755	-1384	3156	-1323	-1577	-847	-785	-783	-2111	-1716	545
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
540(R)	-1612	-2397	-2037	-1033	-2897	-2352	-458	-2365	2184	665	-1520	-1051	-2334	-51	2602	-1545	-1395	-2143	-2262	-2014	546
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
541(Y)	712	-796	-2334	-1883	-370	-2028	-886	-143	-1607	-663	-131	-1587	-2243	-1383	-1656	-1178	-771	1114	-965	3479	547
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
542(T)	-527	-1669	1091	-27	-2315	-1379	-443	-2033	-151	-2081	-1218	-282	557	-41	-650	1128	2077	-1576	-2321	-1690	548
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
543(R)	-2957	-3022	-3318	-2735	-3786	-2998	-1968	-3912	-846	-3631	-3157	-2611	-3280	-1724	4056	-3026	-2913	-3650	-3096	-3185	549
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
544(G)	-2594	-2690	-3304	-3623	-4328	-3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	550
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												
545(V)	-1747	-1296	-4310	-3948	-1758	-4023	-3716	2215	-3813	-615	-540	-3705	-3860	-3670	-3887	-3339	-1741	3087	-3252	-2806	551
-	-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249
-	-	-16	-7108	-8150	-894	-1115	-701	-1378*	*												

Table 7

546(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3935	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	552
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
547(A)	2404	-890	-1926	-1629	-1803	1275	-1415	-1282	-1490	392	-963	-1316	-1930	-1328	-1674	-654	-644	-852	-2187	-1810	553
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
548(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	554
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
549(Y)	-3621	-2707	-4176	-4424	2950	-4049	-394	-2539	-4002	-1942	-1987	-2749	-3933	-2854	-3451	-3299	-3499	-2690	349	4094	555
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
550(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	556
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
551(H)	-1741	-2627	-2070	-1046	-3303	-2401	2713	-2751	2478	-2476	-1755	-1061	-2375	-27	2379	-1621	-1497	-2477	-2379	-2181	557
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
552(L)	-1014	-876	-2966	-2408	-582	-2550	-1528	1721	-2079	2042	345	-2114	-2581	-1775	-2028	454	-980	286	-1414	-1096	558
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
553(V)	933	-842	-2818	-2467	-1542	-1870	-1890	154	-2226	-1095	-617	-1932	-2326	-1995	-2259	-1126	1070	2769	-2180	-1826	559
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
554(S)	-787	-1522	-1486	-1172	-2714	-1599	-1112	-2500	-433	-2563	-1791	-1110	-2067	-796	1351	2916	-989	-1943	-2648	-2234	560
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
555(S)	-326	-1010	-1778	-1541	-2691	-1234	-1566	-2386	-1486	-2594	-1749	-1228	1196	-1330	-1747	2396	1967	-1662	-2876	-2496	561
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
556(A)	3121	-934	-2489	-2561	-3081	-1203	-2295	-2766	-2533	-3080	-2234	-1669	-1953	-2234	-2533	936	-748	-1844	-3331	-3090	562
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
557(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	563
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
558(R)	-588	-1873	-516	979	-2188	-1543	-123	-1869	1290	-353	-980	-202	-1622	314	1866	-491	782	-1495	-2024	-1439	564
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

Table 7

[illegible]

CLAIMS

What is claimed is:

1. A recombinant lactic acid bacterial cell comprising at least one
5 gene encoding a heterologous polypeptide having dihydroxy-acid
dehydratase activity wherein the bacterial cell is substantially free of
lactate dehydrogenase activity.
2. The recombinant lactic acid bacterial cell of Claim 1 wherein the
10 heterologous polypeptide having dihydroxy-acid dehydratase activity has a
specific activity of at least about $0.1 \mu\text{mol min}^{-1} \text{mg}^{-1}$ total soluble protein in
a crude cell extract.
3. The recombinant lactic acid bacterial cell of Claim 2 wherein the
15 heterologous polypeptide having dihydroxy-acid dehydratase activity has a
specific activity of at least about $0.6 \mu\text{mol min}^{-1} \text{mg}^{-1}$ total soluble protein in
a crude cell extract.
4. The lactic acid bacterial cell of Claim 1 wherein the dihydroxy-acid
20 dehydratase enzyme is expressed by a nucleic acid molecule that is
heterologous to the bacteria.
5. The lactic acid bacterial cell of claim 1 wherein the dihydroxy-acid
dehydratase is a [2Fe-2S] dihydroxy-acid dehydratase.
- 25 6. The lactic acid bacterial cell of Claim 5 wherein the dihydroxyacid
dehydratase polypeptide has an amino acid sequence that matches the
Profile HMM of table 7 with an E value of $< 10^{-5}$ wherein the polypeptide
additionally comprises all three conserved cysteines, corresponding to
30 positions 56, 129, and 201 in the amino acids sequences of the
Streptococcus mutans DHAD enzyme corresponding to SEQ ID NO:168.

7. The bacterial cell of Claim 1 comprising a disruption in at least one endogenous gene encoding a polypeptide having lactate dehydrogenase activity.
- 5 8. The lactic acid bacterial cell of claim 7 wherein the gene encoding lactate dehydrogenase is selected from the group consisting of IdhL, IdhD, IdhL1, and IdhL2.
9. The lactic acid bacterial cell of claim 1 wherein the lactic acid
10 bacteria is selected from the group consisting of *Lactococcus*,
Lactobacillus, *Leuconostoc*, *Oenococcus*, *Pediococcus*, and
Streptococcus.
10. The lactic acid bacterial cell of Claim 1 wherein the bacteria
15 produces isobutanol.
11. The lactic acid bacterial cell of Claim 10 wherein the bacteria comprises an isobutanol biosynthetic pathway.
- 20 12. The lactic acid bacterial cell of Claim 11 wherein the isobutanol biosynthetic pathway comprises genes encoding acetolactate synthase, acetohydroxy acid isomeroreductase, dihydroxy-acid dehydratase, branched-chain α -keto acid decarboxylase, and branched-chain alcohol dehydrogenase.
- 25 13. A method of making isobutanol comprising providing the lactic acid bacteria of claim 11 and growing the lactic acid bacteria under conditions wherein isobutanol is produced.

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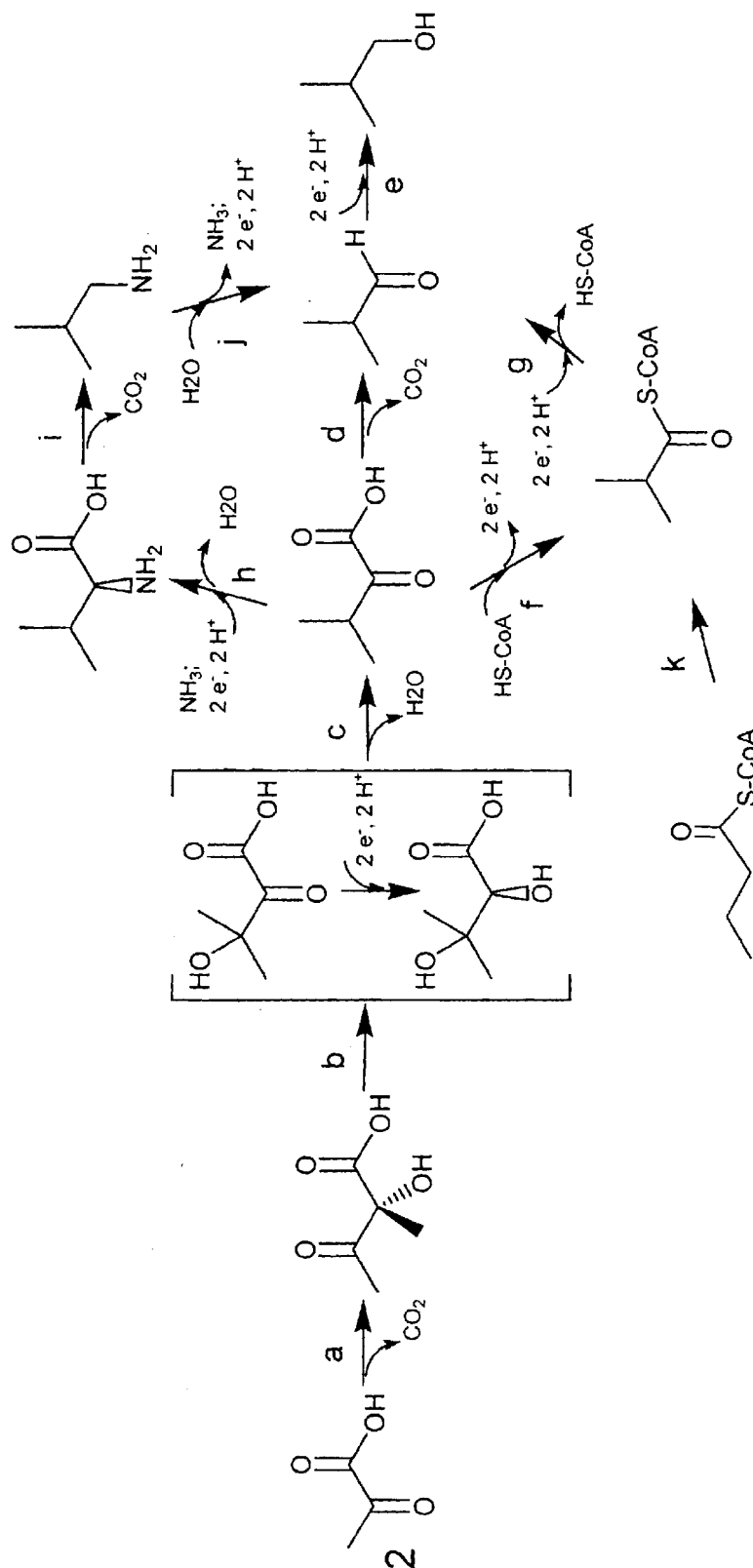


FIG. 1

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2009/058815

A. CLASSIFICATION OF SUBJECT MATTER

INV. C12N9/04 C12N9/88 C12P7/16 C12N15/74 C12R1/46
C12R1/225

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12N C12P C12R

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, COMPENDEX, BIOSIS, MEDLINE, EMBASE, FSTA

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2007/092957 A1 (DONALDSON GAIL K [US] ET AL) 26 April 2007 (2007-04-26) the whole document, in particular [0086], [0167] and Example 21	1-13
X	WO 2008/098227 A2 (UNIV CALIFORNIA [US]; LIAO JAMES C [US]; ATSUMI SHOTA [US]; SMITH KEVI) 14 August 2008 (2008-08-14) the whole document, in particular paragraph [00101], Table 1 and claims, mainly claims 1, 7, 24, 25, 28 -33, 45 ----- -/--	1-13

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

11 December 2009

Date of mailing of the international search report

13/01/2010

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Bassias, Ioannis

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2009/058815

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	KROGH A ET AL: "Hidden Markov Models in Computational Biology - Applications to Protein Modeling" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 235, no. 5, 3 February 1994 (1994-02-03), pages 1501-1531, XP024008598 ISSN: 0022-2836 [retrieved on 1994-02-03] -----	6

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2009/058815

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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WO 2008098227	A2	14-08-2008	AU 2008212799 A1 14-08-2008
		CA 2678261 A1 14-08-2008	
		EP 2118266 A2 18-11-2009	
		US 2009081746 A1 26-03-2009	