

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

INARI AGRICULTURE, INC.,
Petitioner,

v.

CORTEVA AGRISCIENCE LLC,
Patent Owner.

Case No. PGR2023-00022
Patent No. 11,371,055

REPLY DECLARATION OF DR. ARON SILVERSTONE, Ph.D.

I, Aron Silverstone, Ph.D., hereby declare under penalty of perjury:

1. My name is Aron Silverstone, and I have been retained by counsel for Petitioner Inari Agriculture, Inc. (“Inari” or “Petitioner”) as an expert witness to provide assistance regarding U.S. Patent No. 11,371,055 (the “’055 Patent”). I previously submitted a declaration (Ex. 1003) in support of Inari’s Petition. I have personal knowledge of the facts and opinions set forth in this declaration and believe them to be true. If called upon to do so, I would testify competently thereto.

2. My opinions set forth in this declaration are based on my consideration of the following exhibits and papers:

Exhibit No.	Material Considered
Ex. 2011	Paragraphs 125-126 from the Declaration of Dr. Bollinger
Ex. 2085	Slide 2 from Protein presentation (CONFIDENTIAL – PROTECTIVE ORDER MATERIAL)
Ex. 2089	Protein sequences (CONFIDENTIAL – PROTECTIVE ORDER MATERIAL)
Ex. 2092	Protein presentation (CONFIDENTIAL – PROTECTIVE ORDER MATERIAL)
Ex. 2095	Protein sequences and analysis (CONFIDENTIAL – PROTECTIVE ORDER MATERIAL)
Ex. 1043	The portions of the transcript of the deposition of Dr. Bollinger (Feb. 29, 2024) cited in this declaration

3. Exhibits 2085, 2089, and 2095 describe [REDACTED]

[REDACTED]. [REDACTED]

[REDACTED], [REDACTED]

[REDACTED]

[REDACTED]. [REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]. '055 patent, 11:29.

4. [REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED].

[illegible]

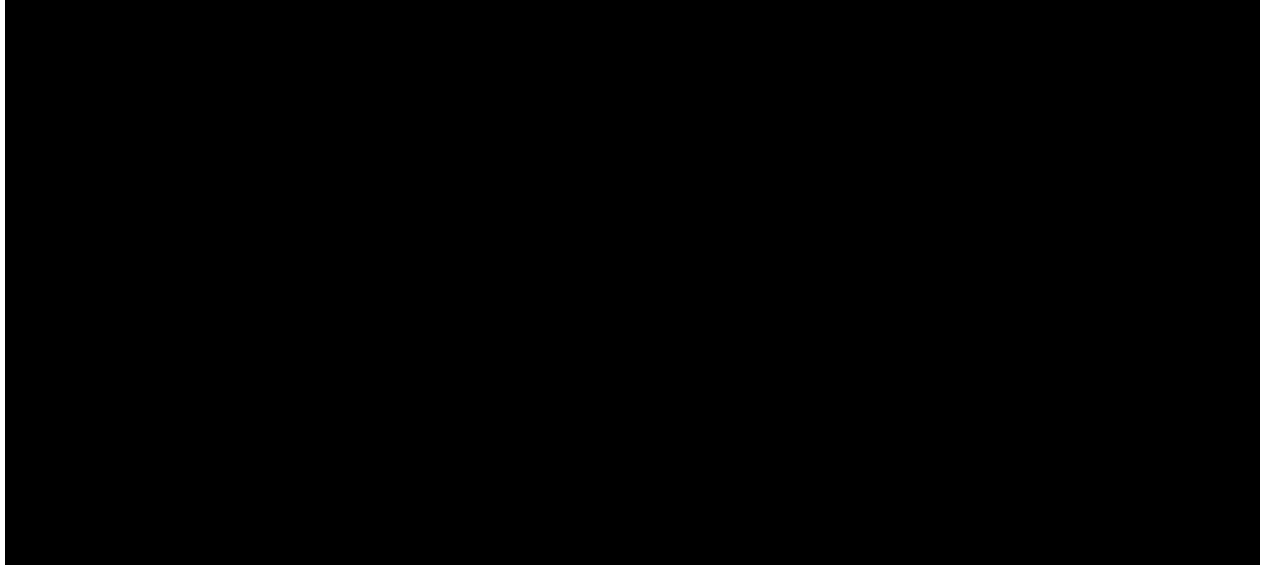
[REDACTED]. In Appendix A, I have [REDACTED]

[REDACTED]. Appendix A includes the positions of the alignment in Figure 2 of the '055 patent and the 292 positions of the amino acids in SEQ ID NO:2 (AAD-12). I have highlighted in green [REDACTED]

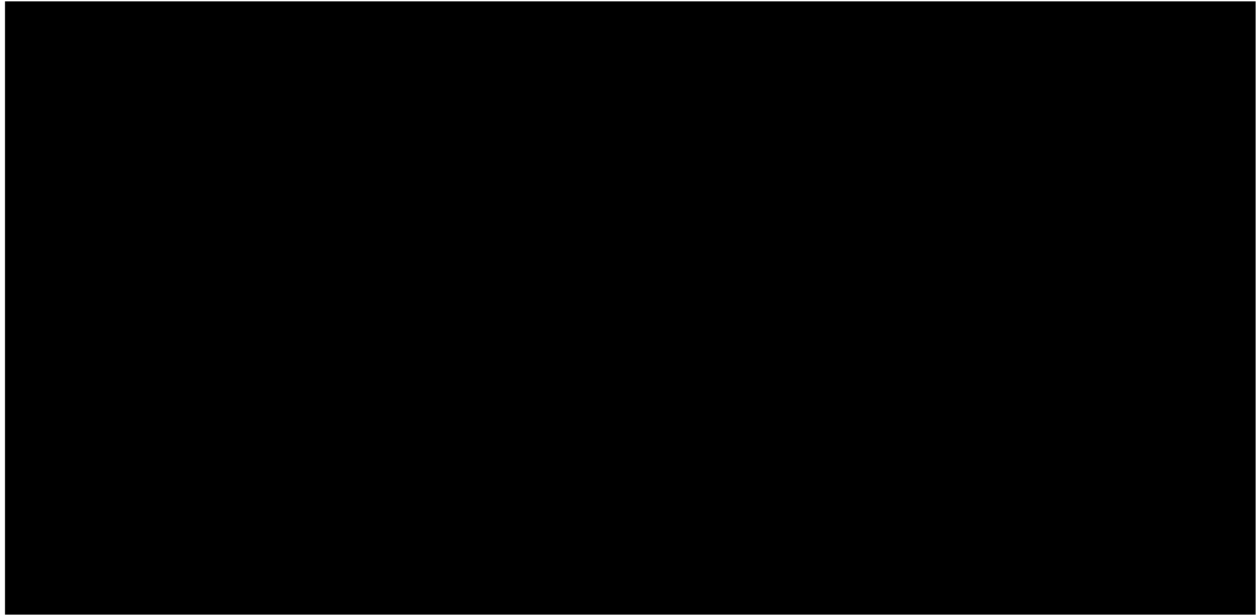
[REDACTED]

[REDACTED] ([REDACTED]). Using the positions of TauD, I have also identified the secondary structures (i.e., α -helixes and β -strands) identified in Elkins (Ex. 2022), Figure 5, which I have highlighted in yellow.

7. Exhibit 2092, [REDACTED]:



8. Exhibit 2092, [REDACTED] :



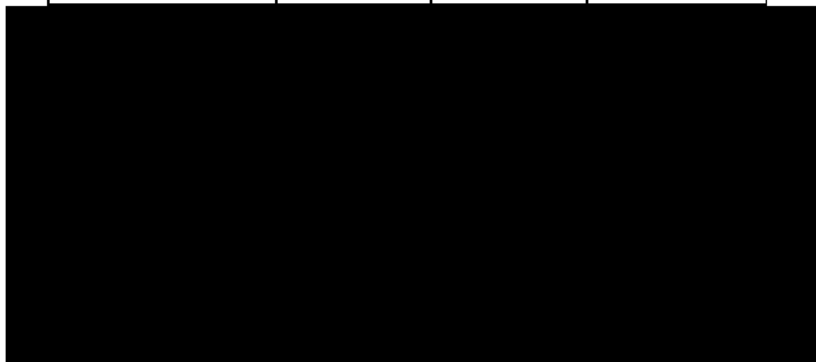
9. [REDACTED]

[REDACTED]. [REDACTED]

[REDACTED], are highlighted in

green:

Table A			
Variant No.	% Seq. Identity	% Activity	
		2,4-D	Triclopyr
AAD-12 wt	100.0%	100%	100%



[REDACTED]

10. As depicted in the table in Appendix A to this declaration, [REDACTED]

[REDACTED]

[REDACTED].

11. As depicted in Appendix A, [REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]. [REDACTED] Elkins identified as

having a secondary structure, which are highlighted in yellow.

12. [REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

13. As depicted in Appendix A, [REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]. [REDACTED]

[REDACTED] 57 positions that Dr. Bollinger identified as “strictly conserved” or
“somewhat conserved” in Figure 2 of the ’055 patent (Ex. 2011, ¶¶ 125-126),

which 57 positions are identified in red highlighting in the '055 patent Figure 2 position in Appendix A.

14. Dr. Bollinger identified 57 amino acids as “conserved” in Figure 2 of the '055 patent: he identified 28 as “strictly conserved” and he identified 29 as “somewhat conserved.” Ex. 2011, ¶¶ 125-126. This leaves 235 amino acids, i.e., $292 - 28 - 29 = 235$. Varying these 235 amino acids results in about 10^{78} possible AAD-12 variants. To get an estimate of a minimum number of variants a POSA would have had to choose from if they assume that both the “conserved” and “strictly conserved” are invariant from the AAD-12 (SEQ ID NO:2), they would have assumed that only 235 amino acids could change, and that up to 43 changes would be tolerated for an 85% homology. The equation I used to determine the number of different proteins is: $43^{19} * (235! / ((235-43)! * 43!))$. The solution for this is 2.69×10^{78} . Even if we were to assume that the 235 amino acids could only be substituted by one different amino acid (instead of 19), the total possible AAD-12 variants would still be on the order of 10^{50} . This is based on the following equation: $43^1 * (235! / ((235-43)! * 43!))$.

15. In his declaration, Dr. Bollinger stated: “Skilled artisans would readily identify in Figure 2 the residues that are identical across all five enzymes and generally avoid making substitutions to those strictly conserved residues.” Ex. 2011, ¶ 125. In his annotation of Figure 2, Dr. Bollinger identified position 71 as

one of the “strictly conserved” amino acids that a POSA would have generally avoided changing. Ex. 2011, ¶ 125. [REDACTED]

[REDACTED], as depicted in Appendix A.

16. I understand that Dr. Bollinger testified that, when using SIFT, “a POSA would have used the first four [of the sequences shown in Figure 2 of the ’055 patent], and I think it has been established since then that these alignments of functionally related but not strictly orthologous proteins helps in this, so inclusion of TauD is not a bad choice.” TauD is the fifth sequence shown in Figure 2 of the ’055 patent. Ex. 1043 (Bollinger Dep.), 159:22-160:7. I submitted to the SIFT website (<https://sift.bii.a-star.edu.sg/>) the five sequences in Figure 2 of the ’055 patent. SIFT generated the table attached as Appendix B to this declaration. For each of the 292 positions in AAD-12 (SEQ ID NO:2), SIFT predicted how many of the 20 natural amino acids would be tolerated if substituted. The table below summarizes SIFT’s results. SIFT predicts that over half of the amino acids would tolerate substitutions by 17 or more amino acids, as summarized in Table B below. Even assuming that 43 of the amino acids (i.e., 15% of 292) could tolerate substitutions by only four different amino acids (far fewer than the amount indicated by SIFT), the number of possible variants would be at least 10⁴⁵.

17. Using the output of the SIFT analysis in Table B below, the positions that can tolerate virtually any amino acid substitution (i.e., 17-19 amino acids) represents over half the amino acids in the protein sequence (153 amino acids). SIFT analysis indicated 37 amino acids are absolutely conserved and would not tolerate a substitution. If a POSA only examines the potential substitutions among the 153 positions that can tolerate the most changes, 17-19 amino acids, for 85% homology (that is up to 43 changes), there are still at least 1.23×10^{66} different proteins that fit these criteria. This is calculated by assuming the smallest number of amino acid substitutions (17) for a sequence that is 153 amino acids long that can tolerate up to 43 changes. The equation I used to determine the number of different proteins is: $43^{17} * (153! / ((153-43)! * 43!))$. The solution for this is 1.23×10^{66} . I streamlined this analysis by focusing on only the 153 amino acids that tolerate 17 or more substitutions, which simplifies the calculations. This approach does not take into account the other 102 amino acids (i.e., $292 - 153 - 37 = 102$) that can tolerate between 2 and 16 substitutions.

Table B			
# of Amino Acid Substitutions Tolerated	Positions	% of Total positions	Cumulative %
19	69	23.6%	23.6%
18	63	21.6%	45.2%
17	21	7.2%	52.4%
16	8	2.7%	55.1%
15	13	4.5%	59.6%
14	7	2.4%	62.0%
13	7	2.4%	64.4%
12	8	2.7%	67.1%
11	8	2.7%	69.9%
10	3	1.0%	70.9%
9	1	0.3%	71.2%
8	4	1.4%	72.6%
7	2	0.7%	73.3%
6	11	3.8%	77.1%
5	8	2.7%	79.8%
4	8	2.7%	82.5%
3	5	1.7%	84.2%
2	9	3.1%	87.3%
1	0	0.0%	87.3%
0	37	12.7%	100.0%
	292		

18. In signing this declaration, I recognize that the declaration will be filed as evidence in a contested case before the Patent Trial and Appeal Board of the United States Patent and Trademark Office. I also recognize that I may be subject to cross-examination in the case and that cross-examination will take place within the United States. If cross-examination is required of me, I will appear for cross-examination within the United States during the time allotted for cross-examination.

19. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code.

Date: April 28, 2024



Dr. Aron Silverstone
Durham, NC

APPENDIX A

'055 Pat. Fig. 2 position	16	17	18	19	20	21	22	23	24	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
TauD	M	S	E	R	L	S	I	T	P	L	G	P	Y	I	G	A	Q	I	S	G	A	D	L	T	R	P	L	S	D	N	Q	F	E	Q	L
Elkins sec. structures						β1	β1	β1	β1	β1					β2	β2	β2	β2	β2	β2									α1	α1	α1	α1	α1	α1	α1
AAD-12 position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		26	27	28	29	30	31	32	33	34
AAD-12 (SEQ ID NO:2)	M	Q	T	T	L	Q	I	T	P	T	G	A	T	L	G	A	T	V	T	G	V	H	L	A	T		L	D	D	A	G	F	A	A	L

'055 Pat. Fig. 2 position	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	81	82	83	84	85
TauD	Y	H	A	V	L	R	H	Q	V	V	F	L	R	D	Q	A	I	T	P	Q	Q	Q	R	A	L	A	Q	R	F	G					
Elkins sec. structures	α1	α1	α1	α1	α1	α1	α1		β3	β3	β3	β3	β3							α2	α2	α2	α2	α2	α2	α2	α2	α2	α2						
AAD-12 position	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					
AAD-12 (SEQ ID NO:2)	H	A	A	W	L	Q	H	A	L	L	I	F	P	G	Q	H	L	S	N	D	Q	Q	I	T	F	A	K	R	F	G					

'055 Pat. Fig. 2 position	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120			
TauD					E	L	H	I	H	P	V	Y	P	H	A	E	G	V	D	E	I	I	V	L	D	T	H	N	D	N	P	P						
Elkins sec. structures					β4	β4	β4													β5	β5	β5	β5	β5														
AAD-12 position					65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95			
AAD-12 (SEQ ID NO:2)					A	I	E	R	I	G	G	G	D	I	V	A	I	S	N	V	K	A	D	G	T	V	R	Q	H	S	P	A	E	W	D			

APPENDIX A

'055 Pat. Fig. 2 position	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155
TauD								D	N	D	N	W	H	T	D	V	T	F	I	E	T	P	P	A	G	A	I	L	A	A	K	E	L	P	S
Elkins sec. structures													β6	β6	β6									β7	β7	β7	β7	β7	β7	β7	β7				
AAD-12 position	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130
AAD-12 (SEQ ID NO:2)	D	M	M	K	V	I	V	G	N	M	A	W	H	A	D	S	T	Y	M	P	V	M	A	Q	G	A	V	F	S	A	E	V	V	P	A

'055 Pat. Fig. 2 position	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190
TauD	T	G	G	D	T	L	W	T	S	G	I	A	A	Y	E	A	L	S	V	P	F	R	Q	L	L	S	G	L	R	A	E	H	D	F	R
Elkins sec. structures				β8	β8	β8	β8	β8	β8			α3	α3	α3	α3	α3		α4	α4	α4	α4	α4	α4	α4	α4			β9	β9	β9	β9	β9	β9		
AAD-12 position	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
AAD-12 (SEQ ID NO:2)	V	G	G	R	T	C	F	A	D	M	R	A	A	Y	D	A	L	D	E	A	T	R	A	L	V	H	Q	R	S	A	R	H	S	L	V

'055 Pat. Fig. 2 position	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
TauD	K	S	F	P				E	Y	K	Y	R	K	T	E	E	E	H	Q	R	W	R	E	A	V	A	K	N	P	P	L	L	H	P	V
Elkins sec. structures																						α5	α5	α5	α5	α5	α5				β10	β10	β10		
AAD-12 position	166	167	168	169					170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196
AAD-12 (SEQ ID NO:2)	Y	S	Q	S					K	L	G	H	V	Q	Q	A	G	S	A	Y	I	G	Y	G	M	D	T	T	A	T	P	L	R	P	L

APPENDIX A

'055 Pat. Fig. 2 position	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260		
TauD	V	R	T	H	P	V	S	G	K	Q	A	L	F	V	N	E	G	F	T	T	R	I	V	D	V	S	E	K	E	S	E	A	L	L	S		
Elkins sec. structures	β11	β11	β11	β11					β12	β12	β12	β12	β12					β13	β13	β13	β13	β13	β13				α6	α6	α6	α6	α6	α6	α6	α6	α6		
AAD-12 position	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212		213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230		
AAD-12 (SEQ ID NO:2)	V	K	V	H	P	E	T	G	R	P	S	L	L	I	G	R		H	A	H	A	I	P	G	M	D	A	A	E	S	E	R	F	L	E		

'055 Pat. Fig. 2 position	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295		
TauD	F	L	F	A	H	I	T	K	P	E	F	Q	V	R	W	R	W	Q	P	N	D	I	A	I	W	D	N	R	V	T	Q	H	Y	A	N		
Elkins sec. structures	α6	α6	α6	α6	α6	α6					β14	β14	β14	β14	β14					β15	β15	β15	β15	β15	β15	β15	β15				β16	β16	β16	β16	β16		
AAD-12 position	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265		
AAD-12 (SEQ ID NO:2)	G	L	V	D	W	A	C	Q	A	P	R	V	H	A	H	Q	W	A	A	G	D	V	V	V	W	D	N	R	C	L	L	H	R	A	E		

'055 Pat. Fig. 2 position	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322
TauD	A	D	Y	L	P	Q	R	R	I	M	H	R	A	T	I	L	G	D	K	P	F	Y	R	A	G		
Elkins sec. structures								β17	β17	β17	β17	β17	β17	β17	β17	β17											
AAD-12 position	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292
AAD-12 (SEQ ID NO:2)	P	W	D	F	K	L	P	R	V	M	W	H	S	R	L	A	G	R	P	E	T	E	G	A	A	L	V

APPENDIX B

Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																					
																		1M	0.6	w	c	p	d	h	f	g	y	n	i	s	t	v	q	e	M	a	l	R	k		
																		2Q	0.6	w	c	m	p	i	g	h	d	n	Q	v	r	F	t	l	k	e	S	y	a		
																	w	3T	1	c	f	M	y	h	i	p	g	l	n	v	r	q	d	T	s	a	k	E			
																	w	4T	1	c	f	m	y	h	i	l	p	v	g	d	q	n	R	e	a	k	S	T			
							h	w	d	q	n	p	e	c	r	g	s	k	y	5L	1	t	a	f	m	V	L	l													
																		w	6Q	1	c	f	m	y	h	i	p	l	g	n	r	d	V	t	Q	k	e	S	A		
							w	h	g	d	n	r	q	y	e	k	c	s	p	f	7I	1	m	t	l	A	V	l													
																		w	8T	1	c	f	y	m	h	i	p	v	l	g	N	d	Q	R	a	T	s	e	k		
														w	c	m	f	y	i	h	9P	1	v	l	n	g	t	s	r	d	a	k	e	Q	P						
								w	h	c	d	g	n	y	p	q	e	r	10T	1	k	s	f	m	a	i	v	T	L												
																		11G	1	w	c	m	i	p	f	v	H	y	l	r	Q	n	d	G	T	a	s	e	k		
																		w	12A	1	f	m	y	h	c	i	l	v	r	n	q	d	k	e	P	T	G	s	A		
																		13T	1	c	w	p	d	m	e	q	k	n	g	r	i	T	s	V	a	H	L	f	Y		
								d	c	g	n	e	h	w	k	s	r	p	q	t	14L	1	y	a	m	v	F	l	L												
																		w	15G	1	h	m	f	y	i	c	n	q	r	d	l	k	e	t	p	V	s	G	A		
		w	h	y	f	m	i	q	r	c	l	n	d	k	e	v	t	p	16A	1	s	G	A																		
																		w	17T	1	c	f	y	m	h	i	p	v	l	G	n	r	T	Q	d	s	a	k	E		
		h	w	q	d	n	p	r	e	g	c	k	s	y	f	m	t	a	18V	1	l	l	V																		
														w	f	y	c	m	19T	1	h	i	l	p	v	g	r	q	n	d	k	a	E	S	T						
							w	m	i	f	c	v	l	y	r	h	p	q	20G	1	t	k	a	e	s	n	D	G													
							w	h	g	d	n	r	q	y	e	k	s	c	p	21V	1	f	m	t	A	L	l	V													
													w	m	c	i	f	v	l	22H	1	y	r	p	t	q	a	k	s	g	H	e	n	D							
y	w	v	t	s	r	q	p	n	m	k	i	h	g	f	e	d	c	a	23L	1	L																				
																		w	24A	1	c	f	m	y	h	i	p	l	v	g	n	d	q	e	s	T	A	R	k		
																		w	c	25T	1	f	y	m	h	i	p	v	l	g	n	d	q	s	T	a	R	E	K		
y	w	v	t	s	r	q	p	n	m	k	i	h	g	f	e	d	c	a	26L	1	L																				
																		w	27D	1	c	f	m	y	i	h	v	l	p	r	q	G	a	k	n	T	e	S	D		

APPENDIX B

Predict Not Tolerated																Position	Seq Rep	Predict Tolerated																						
															w	c	f	m	28D	1	y	i	h	l	v	r	q	t	g	P	k	a	n	e	S	D				
																		w	29A	1	c	f	y	m	h	i	p	v	l	G	r	q	N	d	T	k	A	S	e	
																	w	c	30G	1	y	f	m	h	i	v	p	l	G	n	r	T	Q	d	s	a	k	E		
																			31F	1	c	d	p	m	e	q	k	n	g	r	W	s	t	i	h	A	V	l	y	F
																	w		32A	1	c	f	y	m	h	i	p	v	l	g	t	N	q	d	R	s	A	k	E	
															w	c	f	y	m	33A	1	h	i	v	l	p	g	n	r	t	s	k	Q	d	A	E				
							h	w	d	q	n	p	e	c	r	g	s	k	y	34L	1	t	a	f	m	V	L	l												
																			35H	1	c	w	p	m	d	q	n	E	g	k	r	i	t	s	v	a	H	L	f	Y
																		w	36A	1	c	m	f	y	H	i	p	v	l	g	n	R	q	t	D	S	A	k	e	
																	w	h	37A	1	c	y	n	d	q	r	f	m	e	p	k	g	t	s	i	v	L	A		
																			38W	1	c	d	p	e	k	n	q	g	W	r	s	t	h	M	a	i	V	F	y	l
																			39L	1	w	c	m	p	i	H	r	v	g	q	f	t	n	k	D	s	L	a	y	e
																w	c	y	f	40Q	1	m	h	i	p	v	l	g	n	d	s	T	a	Q	R	E	K			
																			41H	1	c	w	m	p	d	e	g	i	n	q	t	s	v	a	r	l	f	K	H	Y
																	w		42A	1	c	f	y	m	h	i	l	v	p	n	r	g	d	t	k	Q	e	S	A	
		h	w	d	n	g	q	r	e	c	p	k	s	y	f	t	m	a	43L	1	i	L	V																	
					h	d	w	n	g	q	e	p	c	r	s	k	y	t	44L	1	a	f	m	V	l	L														
																			45I	1	c	p	d	w	e	q	n	k	g	r	m	s	t	h	a	F	Y	l	l	V
						d	n	c	g	e	h	k	r	p	q	s	t	w	a	46F	1	m	v	i	y	L	F													
																			47P	1	c	w	m	i	f	P	v	d	H	g	y	l	n	t	s	a	e	q	R	k
													w	m	i	f	c	v	l	48G	1	y	r	h	p	q	t	k	a	e	s	n	D	G						
y	w	v	t	s	r	p	n	m	l	k	i	h	g	f	e	d	c	a	49Q	1	Q																			
																			50H	1	w	c	m	f	i	H	y	P	v	l	g	r	t	q	n	s	D	A	k	e
				h	d	w	n	g	c	e	r	p	s	q	k	y	t	a	51L	1	f	m	v	L	l															
			w	f	y	h	m	c	i	l	r	q	e	g	k	v	d	p	52S	1	n	a	S	T																
																	w		53N	1	c	f	m	y	i	h	v	l	P	r	t	g	a	Q	s	k	D	e	N	
									c	w	f	y	m	i	h	v	l		54D	1	r	g	p	n	t	s	a	k	Q	D	E									

APPENDIX B

Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																					
y	w	v	t	s	r	p	n	m	l	k	i	h	g	f	e	d	c	a	55Q	1	Q																				
											w	c	m	i	f	v	p	y	56Q	1	l	g	t	s	a	n	d	e	r	k	H	Q									
																		w	57I	1	c	d	p	g	h	n	q	e	s	y	t	k	f	a	R	M	v	l	l		
								w	h	y	f	m	c	r	q	d	n	i	58T	1	l	k	e	p	g	v	s	T	A												
					d	n	c	g	e	h	k	r	p	q	s	t	w	a	59F	1	m	v	i	y	L	F															
			w	h	y	f	m	i	c	r	q	l	n	d	k	e	v	p	60A	1	t	g	S	A																	
																w	c	f	61K	1	m	y	i	h	v	p	g	d	n	t	s	L	a	e	Q	R	K				
															w	c	m	f	62R	1	i	y	v	p	h	l	t	a	g	s	d	e	q	k	N	R					
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	e	d	c	a	63F	1	F																				
y	w	v	t	s	r	q	p	n	m	l	k	i	h	f	e	d	c	a	64G	1	G																				
																w	c	f	y	65A	1	m	h	i	v	l	g	n	r	t	s	P	d	Q	k	A	E				
												w	d	c	h	p	n	g	66I	1	q	e	s	k	y	R	t	m	f	a	L	V	I								
										w	c	m	f	y	i	v	l		67E	1	r	p	t	g	s	n	a	q	k	H	D	E									
																	w		68R	1	c	f	m	y	h	l	P	v	l	G	n	R	t	q	D	s	a	k	e		
																			69I	1	w	c	m	p	d	n	G	l	q	r	e	k	t	H	V	s	f	A	l	y	
																			70G	1	w	c	m	P	i	d	n	q	G	h	v	t	R	e	F	s	l	k	a	y	
												w	c	p	d	q	h		71G	1	n	r	e	G	k	s	t	m	a	y	f	L	V	I							
																			72G	1	c	w	m	p	d	n	G	q	i	e	t	s	r	v	K	h	a	f	L	Y	
																	w		73D	1	c	y	f	m	h	i	P	V	l	g	n	r	q	T	D	s	a	K	e		
								w	d	p	c	q	e	n	k	r	g		74I	1	h	s	t	a	m	f	Y	L	V	I											
																	w		75V	1	c	f	y	m	h	i	P	V	l	g	N	r	q	t	D	s	A	k	e		
												w	c	f	y	m	i		76A	1	h	v	l	r	g	p	n	t	s	q	k	A	D	E							
		h	w	q	d	n	p	e	r	g	c	k	s	y	f	m	t	a	77I	1	l	V	l																		
																			78S	1	w	c	m	f	h	y	p	l	g	v	l	n	r	d	Q	a	k	e	t	S	
																			79N	1	w	c	p	h	M	g	d	q	N	r	f	y	e	k	s	t	a	i	l	V	
				h	w	d	q	n	p	e	r	g	c	s	k	y	t	a	80V	1	f	m	L	l	V																
																	w		81K	1	y	c	f	m	h	i	p	v	l	G	n	R	t	q	D	a	S	K	e		

APPENDIX B

Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																						
																		82A	0.6	w	c	m	f	y	h	p	i	g	n	v	L	d	q	t	r	s	A	e	K			
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	c	a	83D	0.6	D																					
y	w	v	t	s	r	q	p	n	m	l	k	i	h	f	e	d	c	a	84G	0.6	G																					
																w	c	f	85T	1	m	y	i	h	v	p	g	l	d	n	s	a	T	q	e	R	K					
																			86V	1	w	c	m	P	i	H	f	g	n	V	y	r	l	q	d	t	s	a	k	E		
																			87R	0.8	w	c	m	f	h	p	y	i	g	n	d	v	q	t	L	s	R	e	A	k		
																	w		88Q	0.6	c	m	f	y	h	i	p	l	v	n	g	r	t	d	s	k	Q	A	e			
																c	w		89H	0.6	m	f	i	y	v	p	d	g	l	n	H	t	s	a	e	q	R	K				
													w	c	m	f	y	i	90S	0.6	h	v	l	p	r	q	g	t	k	a	n	e	S	D								
															w	f	m	y	91P	0.6	h	c	i	l	v	r	n	q	d	k	e	t	g	P	S	A						
																	w		92A	0.6	c	m	f	y	h	i	p	v	l	n	d	g	t	q	s	e	A	R	k			
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	d	c	a	93E	0.2	E																					
y	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	a	94W	0.2	W																					
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	c	a	95D	0.2	D																					
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	c	a	96D	0.2	D																					
																	w		97M	0.8	c	f	M	y	h	i	p	v	l	g	N	r	q	d	T	s	a	k	E			
																			98M	1	w	c	M	p	i	H	g	f	V	N	d	r	q	l	t	y	s	k	a	E		
																	w		99K	1	c	f	y	m	h	i	p	V	L	g	n	r	t	q	D	S	a	K	e			
																			100V	1	w	c	m	p	d	q	N	G	r	e	k	i	t	h	s	V	a	F	l	y		
																			101I	1	w	c	m	f	h	l	y	P	v	g	l	N	d	q	t	R	s	a	e	k		
																			102V	1	w	d	c	n	g	e	q	k	P	r	s	h	m	t	a	y	F	i	V	L		
																	w		103G	1	c	m	f	h	y	l	p	v	l	r	n	G	q	t	D	s	k	A	e			
											w	m	i	f	c	v	l	y	104N	1	r	p	h	q	t	a	k	e	s	d	G	N										
																			105M	1	w	C	M	f	h	i	p	y	v	g	l	n	r	Q	D	t	s	a	k	e		
																	w		106A	1	c	m	f	y	h	i	p	v	L	g	r	N	q	t	D	s	A	k	e			
y	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	a	107W	1	W																					
y	w	v	t	s	r	q	p	n	m	l	k	i	g	f	e	d	c	a	108H	1	H																					

APPENDIX B

Predict Not Tolerated																			Position	Seq Rep	Predict Tolerated																				
												w	f	y	h	m	c	i	109A	1	l	r	q	p	v	d	g	e	k	n	A	S	T								
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	c	a	110D	1	D																				
																		w	111S	1	h	m	y	f	c	r	q	d	n	e	p	k	l	i	g	V	t	a	S		
			w	f	y	h	m	c	i	l	r	q	e	g	k	d	v	p	112T	1	n	a	S	T																	
		q	k	n	d	r	g	e	p	h	c	t	s	m	a	v	i	w	113Y	1	l	Y	F																		
																			114M	1	w	c	p	g	h	d	n	M	t	f	s	y	Q	e	v	R	k	a	l	L	
													w	c	f	y	m		115P	1	i	h	v	l	g	r	n	t	P	s	a	Q	k	D	E						
																	w		116V	1	h	g	y	f	c	d	n	m	r	q	P	k	s	e	l	T	I	A	V		
																	w		117M	1	h	c	y	f	n	d	q	r	M	i	k	e	t	l	g	P	v	s	A		
													w	h	y	f			118A	1	m	c	i	n	r	q	d	l	k	e	t	v	P	g	s	A					
																w	c		119Q	1	f	y	m	h	i	v	p	l	g	n	d	t	s	Q	A	R	e	K			
																			120G	1	c	w	p	d	m	e	q	k	n	r	G	i	t	s	v	h	A	I	F	Y	
												w	h	f	y	m	c		121A	1	r	n	q	d	i	l	p	k	e	g	t	V	S	A							
				h	w	d	n	q	e	p	g	c	r	s	k	y	t		122V	1	a	f	M	L	I	V															
			d	g	c	n	e	h	w	s	k	r	p	q	t	y	a		123F	1	v	i	M	F	L																
																	w		124S	1	c	f	m	y	h	i	l	v	p	n	q	d	g	t	e	k	R	A	S		
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	125A	1	A																				
																	w		126E	1	c	f	y	m	h	l	p	V	l	g	n	t	R	d	q	s	a	E	K		
																	w	c	127V	1	f	m	y	h	i	l	p	g	V	r	n	t	s	q	a	k	D	E			
		h	w	d	n	g	q	r	e	c	p	k	s	y	f	m	t	a	128V	1	i	L	V																		
													w	m	c	f	i		129P	1	y	l	v	h	q	r	k	t	e	a	g	s	d	N	P						
													w	y	c	f			130A	1	m	h	i	l	v	g	n	r	q	t	d	k	P	S	A	E					
																			131V	1	w	c	m	p	i	g	H	f	d	q	r	n	l	y	V	e	k	a	S	T	
y	w	v	t	s	r	q	p	n	m	l	k	i	h	f	e	d	c	a	132G	1	G																				
y	w	v	t	s	r	q	p	n	m	l	k	i	h	f	e	d	c	a	133G	1	G																				
														w	c	m	f		134R	1	i	y	v	l	h	p	q	t	a	R	g	k	s	e	N	D					
y	w	v	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	a	135T	1	T																				

APPENDIX B

Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																					
																		136C	1	w	C	m	i	p	h	f	v	y	G	n	L	r	q	d	t	s	k	E	a		
			q	n	k	d	r	g	h	e	p	c	t	s	m	a	v	i	137F	1	l	y	W	F																	
																		138A	1	w	m	h	C	d	n	p	r	f	g	q	y	k	e	s	i	L	T	A	v		
											w	m	f	c	i	y	l	v	139D	1	h	r	p	q	k	a	t	g	e	n	S	D									
																		140M	1	w	c	h	y	q	f	d	r	n	e	i	p	k	t	v	M	s	l	G	a		
																		141R	1	c	w	d	p	m	n	g	e	q	s	t	l	h	a	v	f	k	R	l	Y		
				w	h	y	f	m	c	r	q	d	n	i	k	l	e	p	142A	1	g	v	s	T	A																
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	143A	1	A																				
			d	q	n	k	p	r	c	e	g	h	m	t	s	a	i	v	144Y	1	l	f	W	Y																	
						c	w	f	m	y	i	l	v	h	r	t	g	p	145D	1	s	n	a	k	q	E	D														
				w	h	y	f	m	c	r	q	d	n	i	k	l	e	p	146A	1	g	v	s	T	A																
y	w	v	t	s	r	q	p	n	m	k	i	h	g	f	e	d	c	a	147L	1	L																				
																	w	148D	1	f	c	m	y	i	h	l	v	r	P	q	g	k	t	a	n	e	S	D			
																	w	149E	1	c	y	f	m	h	i	P	V	l	g	n	R	t	q	D	s	a	k	E			
																w	y	c	150A	1	f	m	h	i	v	P	l	g	n	r	T	q	D	s	A	k	E				
																		151T	1	c	w	d	p	g	n	e	k	q	r	s	h	T	a	M	y	F	v	i	L		
											c	w	f	m	y	i	d	v	152R	1	h	p	g	l	n	s	t	a	e	Q	K	R									
												w	f	c	y	m	h	153A	1	i	l	v	p	n	r	d	g	t	k	e	Q	S	A								
																	w	154L	1	c	m	f	h	y	p	i	g	n	r	v	L	q	d	T	s	a	k	E			
						h	w	d	q	n	p	e	r	c	g	s	k	y	155V	1	t	a	f	m	L	V	l														
																	w	c	156H	1	m	f	i	y	v	p	l	g	r	t	H	q	n	a	k	d	S	E			
																w	c	m	157Q	1	f	i	y	v	l	h	p	r	t	a	k	s	Q	n	e	D	G				
																	w	c	158R	1	d	p	h	g	n	y	s	e	t	q	f	m	a	v	i	k	R	L			
																	w	159S	1	c	m	f	y	h	i	p	V	l	g	N	q	d	R	t	a	S	e	k			
												w	h	d	y	n	160A	1	r	f	q	m	e	k	p	g	s	l	t	C	i	V	A								
																	w	161R	1	c	f	m	y	h	i	p	l	g	V	n	t	d	q	s	a	R	k	E			
y	w	v	t	s	r	q	p	n	m	l	k	i	g	f	e	d	c	a	162H	1	H																				

APPENDIX B

Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																					
																		163S	1	w	c	m	i	p	v	f	r	l	h	q	Y	k	a	e	t	g	D	S	n		
																		164L	1	c	d	w	p	n	e	g	k	q	r	h	s	t	m	y	A	v	F	i	L		
																		165V	1	w	c	p	M	g	h	d	n	q	f	R	s	y	e	k	T	i	a	L	V		
																		166Y	1	c	w	m	p	i	d	g	v	f	h	N	t	s	e	l	a	q	Y	R	K		
																	w	167S	1	h	m	y	f	c	r	q	d	n	e	p	k	l	i	g	V	t	a	S			
																		168Q	1	c	w	m	p	d	i	g	n	v	h	t	s	F	e	Q	a	l	y	R	k		
																		169S	1	w	c	m	i	h	P	q	r	d	F	v	n	k	l	e	t	y	G	S	a		
																	w	170K	1	c	f	y	m	h	i	p	v	L	g	n	r	t	q	d	S	a	K	E			
							d	c	p	n	e	g	q	k	r	h	s	t	w	171L	1	a	m	v	i	f	Y	L													
																		172G	1	w	c	m	p	i	v	f	h	t	q	l	e	d	s	a	r	n	Y	G	K		
																		173H	1	c	w	p	m	D	e	k	n	g	r	Q	i	t	s	v	a	H	I	F	Y		
																w	h	174V	0.8	y	f	c	g	m	d	r	n	q	p	k	e	s	l	i	A	T	V				
													w	c	f	y	m	i	175Q	0.8	h	v	l	g	p	r	n	t	s	a	k	D	Q	E							
																		176Q	0.8	w	c	m	p	i	Q	v	t	e	g	d	r	h	s	k	a	f	l	N	Y		
																w		177A	1	c	f	y	m	h	i	p	l	v	g	n	q	d	R	T	A	k	e	S			
																w	c	178G	0.6	f	m	y	i	h	v	p	l	G	d	n	t	s	a	q	e	R	K				
																		179S	0.6	w	c	m	i	p	f	v	l	H	y	q	r	g	e	k	a	d	t	n	S		
																	w	180A	0.6	c	m	f	h	y	p	g	n	i	r	d	l	Q	t	s	k	e	V	A			
																		181Y	0.6	c	w	m	d	p	i	g	f	v	n	h	s	t	l	a	Y	e	q	R	K		
																d	c	p	182I	0.6	q	n	e	g	r	k	h	s	W	m	t	a	y	f	l	V	I				
																	w	183G	1	c	f	y	M	h	i	p	v	l	G	n	R	t	q	D	s	a	k	E			
																	w	c	184Y	1	m	i	f	h	v	p	Y	l	g	r	n	t	s	q	k	A	D	E			
																		185G	1	c	f	y	m	h	i	p	V	l	G	n	r	t	Q	d	s	A	k	E			
																		186M	1	c	f	M	y	h	i	p	V	l	g	n	R	t	q	D	s	a	K	e			
																		187D	1	c	f	y	m	h	i	v	p	l	g	r	t	Q	N	A	s	D	k	e			
																		188T	1	c	f	y	M	h	i	p	v	l	G	n	r	q	d	T	s	A	K	e			
																		189T	1	w	c	M	p	i	g	h	D	N	v	q	r	F	l	T	k	s	e	y	a		

APPENDIX B

Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																							
																	w	c	190A	1	f	y	m	h	i	v	l	g	n	d	t	q	P	s	e	A	R	K					
																	w	c	191T	1	f	y	m	h	i	l	v	g	r	n	q	d	a	s	k	T	P	E					
																		w	192P	1	g	h	c	d	n	y	r	f	m	q	P	e	k	s	T	L	i	a	V				
																		w	193L	1	c	d	p	g	h	q	r	e	N	s	k	y	m	t	f	a	i	V	L				
																			194R	1	c	W	m	d	p	g	i	n	e	t	s	v	Q	a	f	H	l	y	R	k			
																w	c	m	f	195P	1	y	i	h	v	d	l	n	t	g	s	q	e	a	k	R	P						
					d	h	w	g	n	c	e	r	s	q	p	k	y	t	a	196L	1	f	m	i	V	L																	
y	w	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	a	197V	1	V																						
																	w	c	198K	1	f	m	y	i	d	h	p	g	l	n	V	s	t	a	e	q	R	K					
						w	h	y	g	f	d	r	c	q	m	n	e	p	k	199V	1	l	s	i	a	V	T																
y	w	v	t	s	r	q	p	n	m	l	k	i	g	f	e	d	c	a	200H	1	H																						
						w	h	y	f	m	c	i	n	r	q	l	d	k	e	201P	1	v	t	g	s	A	P																
																		w	202E	1	c	m	f	h	y	i	p	l	V	n	r	G	t	q	d	s	k	a	E				
																		w	203T	1	c	m	f	i	y	p	l	v	r	q	g	e	d	H	k	n	a	T	S				
																w	m	c	f	204G	1	i	y	h	v	l	p	t	q	e	d	n	s	a	k	R	G						
		c	w	f	m	d	i	y	v	g	p	h	s	l	n	t	a	e	205R	1	q	K	R																				
																	w	c	f	206P	1	m	y	i	h	v	l	g	n	d	t	P	s	a	Q	e	r	K					
																			207S	1	w	m	c	i	h	q	d	r	p	n	F	v	l	k	e	y	t	G	S	A			
y	w	v	t	s	r	q	p	n	m	k	i	h	g	f	e	d	c	a	208L	1	L																						
											d	c	p	k	q	n	e	g	r	209L	1	m	t	s	h	a	i	w	v	L	Y	F											
		h	w	q	d	p	n	e	r	c	g	s	k	y	t	a	f	m	210I	1	L	V	l																				
															w	m	i	f	c	211G	1	v	l	y	p	h	r	q	t	k	a	e	d	S	G	N							
																	w	y	212R	1	c	f	m	h	i	p	v	l	g	n	t	R	d	Q	S	A	k	E					
																			213H	1	c	w	p	d	m	e	q	k	n	g	r	t	i	s	v	a	l	F	Y	H			
																w	h	m	f	214A	1	y	r	d	q	n	e	k	p	l	i	g	C	s	v	T	A						
																			215H	1	w	c	m	f	H	i	y	p	v	l	G	r	n	Q	d	T	a	S	k	e			
																	w	c	216A	1	m	f	i	y	p	v	g	d	l	H	n	t	s	q	e	A	R	K					

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Predict Not Tolerated																	Position	Seq Rep	Predict Tolerated																					
		h	w	q	d	n	p	e	r	g	c	k	s	y	f	m	t	a	217I	1	l	V	l																	
																	w	218P	1	c	f	y	m	h	i	P	l	g	n	r	V	q	t	d	s	k	A	E		
											w	m	f	c	i	y	v	l	219G	1	h	p	r	q	t	k	e	a	n	S	D	G								
						d	h	g	w	n	c	e	r	s	k	p	q	y	220M	1	t	a	f	i	V	L	M													
																	w	221D	1	f	y	c	m	h	i	l	v	P	g	r	q	n	D	a	k	e	T	S		
																	w	222A	1	f	y	m	h	i	p	l	V	g	n	r	t	q	s	D	A	k	E			
																	w	223A	1	f	c	y	m	h	i	l	v	n	q	d	P	t	r	g	s	e	K	A		
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	d	c	a	224E	1	E																			
																	w	225S	1	m	f	i	y	h	c	l	r	q	v	e	k	p	t	d	n	G	a	S		
																w	c	f	226E	1	y	m	i	h	v	p	l	g	n	d	t	s	a	q	E	R	K			
																			227R	1	w	c	M	P	h	f	i	y	g	v	n	d	q	L	R	t	s	A	e	k
						d	g	c	n	h	e	k	r	s	p	q	w	t	a	228F	1	y	m	v	i	F	L													
y	w	v	t	s	r	q	p	n	m	k	i	h	g	f	e	d	c	a	229L	1	L																			
																	w	y	c	230E	1	f	m	h	i	p	v	l	g	n	t	R	d	Q	S	A	k	E		
																			231G	1	w	c	m	i	p	F	h	v	l	r	y	t	G	q	n	s	k	a	D	E
y	w	v	t	s	r	q	p	n	m	k	i	h	g	f	e	d	c	a	232L	1	L																			
																			233V	1	c	w	p	d	m	e	k	q	N	g	r	t	s	i	a	V	h	L	F	Y
											w	c	f	y	m	i	h	234D	1	v	l	r	g	p	n	t	s	q	k	A	D	E								
																			235W	1	c	m	p	W	d	q	e	i	g	t	n	s	v	r	k	a	f	l	y	H
																	w	h	236A	1	y	d	n	c	r	q	f	m	e	k	p	g	s	t	l	l	v	A		
													w	h	f	m	y	237C	1	r	q	e	d	k	p	g	l	n	i	C	v	a	s	T						
												c	w	f	m	y	i	238Q	1	v	d	h	p	g	l	n	s	t	a	e	R	K	Q							
																			239A	1	w	c	m	P	i	d	n	h	g	q	v	t	R	F	e	l	s	k	y	A
											w	c	f	m	y	i	h	240P	1	v	l	r	g	t	n	s	P	a	k	q	D	E								
																			241R	1	w	c	d	p	m	n	g	e	q	t	s	h	i	v	a	y	k	R	l	F
																	w	242V	1	c	h	f	y	m	g	p	n	d	r	e	k	Q	s	l	i	a	T	V		
																			243H	1	w	C	p	d	m	e	k	q	n	g	r	t	i	s	a	V	H	l	f	Y

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Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																					
																		244A	1	w	c	m	f	h	y	p	n	d	g	i	q	l	t	s	e	R	V	k	A		
																		245H	1	c	W	p	d	m	e	q	n	g	k	r	t	s	i	a	V	H	f	l	y		
										c	w	f	m	y	i	d	v	p	h	g	246Q	1	l	n	s	t	a	e	Q	K	R										
y	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	a	247W	1	W																				
																	w	c	248A	1	f	y	m	h	i	p	v	l	g	t	N	r	d	s	Q	A	e	K			
																			249A	1	w	c	m	f	h	y	P	i	g	n	L	r	d	q	V	t	s	K	A	e	
															w	m	i	c	250G	1	f	v	l	y	p	r	q	t	a	H	k	e	s	G	D	N					
									w	c	m	f	i	y	v	l	h	r	p	251D	1	t	g	s	a	k	n	e	Q	D											
				h	w	d	q	n	p	e	r	g	c	s	k	y	t	a	252V	1	f	m	L	l	V																
						w	h	d	g	n	y	r	q	c	e	k	p	s	253V	1	f	m	t	i	A	L	V														
						h	w	d	n	q	g	r	e	p	c	s	k	y	254V	1	f	t	a	l	M	l	V														
y	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	a	255W	1	W																				
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	c	a	256D	1	D																				
y	w	v	t	s	r	q	p	m	l	k	i	h	g	f	e	d	c	a	257N	1	N																				
																w	c	258R	1	d	y	f	m	p	h	g	n	s	t	i	v	e	a	q	L	k	R				
																		259C	1	w	d	m	h	n	p	g	r	f	e	k	y	Q	s	t	C	i	l	a	V		
																	w	260L	1	g	h	d	n	y	r	c	q	p	e	k	f	m	s	a	T	L	i	V			
										c	w	d	g	h	n	p	s	261L	1	e	y	r	t	k	a	Q	f	v	i	M	L										
y	w	v	t	s	r	q	p	n	m	l	k	i	g	f	e	d	c	a	262H	1	H																				
																c	w	263R	1	m	d	p	i	f	v	g	h	n	s	t	e	a	l	q	Y	k	R				
										w	h	m	f	y	i	c	n	264A	1	q	r	d	l	k	e	t	p	s	V	G	A										
																	w	265E	1	c	f	y	m	h	i	p	V	l	g	N	t	q	d	R	s	a	k	E			
																	w	266P	1	c	m	f	y	h	i	l	v	n	d	P	q	g	t	e	s	R	k	A			
																		267W	1	c	m	W	p	q	k	D	r	e	i	g	t	n	s	v	a	h	l	f	Y		
																		268D	1	w	m	c	i	v	p	r	l	h	f	q	t	k	a	Y	s	g	e	n	D		
																		269F	1	w	c	p	d	n	g	m	Q	e	k	r	s	t	h	A	l	v	F	y	L		
																	w	270K	1	c	f	y	m	h	i	v	l	P	r	G	n	q	t	d	S	a	K	e			

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Predict Not Tolerated																		Position	Seq Rep	Predict Tolerated																					
																	w	271L	1	c	f	m	y	h	i	p	v	L	g	n	t	d	Q	r	s	A	e	K			
																		272P	1	w	c	m	P	d	i	n	g	h	v	q	t	e	F	s	a	l	y	R	k		
y	w	v	t	s	q	p	n	m	l	k	i	h	g	f	e	d	c	a	273R	1	R																				
																		274V	1	w	c	m	p	D	g	n	q	r	l	k	t	h	E	s	V	f	a	l	Y		
				d	h	g	c	n	e	w	s	r	k	p	y	q	t	a	275M	1	f	v	i	M	L																
																		276W	1	c	W	m	p	d	g	n	i	e	q	s	T	v	H	a	f	R	l	k	y		
										c	w	m	f	i	d	v	p	y	277H	1	g	s	l	t	a	n	e	q	H	k	R										
											w	f	y	h	m	c	i	278S	1	l	r	q	p	d	v	n	e	k	g	T	S	A									
																	w	279R	1	c	f	m	y	h	i	p	g	d	l	v	n	q	e	a	s	R	k	T			
							w	h	d	g	n	q	r	e	p	c	y	k	s	280L	1	f	m	a	T	L	l	V													
																	w	281A	1	m	c	h	f	i	y	n	q	d	r	p	v	t	e	k	L	G	s	A			
							w	m	i	f	c	v	l	y	r	h	p	q	282G	1	t	k	a	e	s	n	D	G													
																	w	283R	1	c	f	m	y	h	i	p	V	l	g	n	R	q	D	T	s	a	k	e			
																	w	284P	1	y	c	f	m	h	i	v	l	P	g	n	t	q	d	R	s	A	K	E			
																	w	285E	1	c	m	f	y	h	i	g	n	l	r	q	t	s	P	d	V	k	a	E			
																		286T	1	w	c	d	m	p	g	n	q	r	h	e	k	s	F	y	i	T	l	A	V		
																		287E	0.8	w	c	m	p	d	g	i	n	q	t	h	V	R	s	E	f	k	a	l	Y		
																		288G	0.4	w	c	m	f	i	y	h	p	v	l	t	G	q	d	n	s	e	a	R	k		
y	w	v	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	289A	0.4	A																				
															w	m	h	f	290A	0.4	y	c	i	l	r	q	v	n	d	p	t	k	e	s	G	A					
y	w	v	t	s	r	q	p	n	m	k	i	h	g	f	e	d	c	a	291L	0.2	L																				
y	w	t	s	r	q	p	n	m	l	k	i	h	g	f	e	d	c	a	292V	0.2	V																				