1
00:00:08,950 --> 00:00:06,389
[Music]

2
00:00:11,110 --> 00:00:08,960
welcome everyone we are in the edge

3
00:00:13,749 --> 00:00:11,120
science room tonight and we're going to

4
00:00:16,390 --> 00:00:13,759
hear alex alvarez discuss

5
00:00:18,150 --> 00:00:16,400
issues related to psy and looks like

6
00:00:20,470 --> 00:00:18,160
biochemistry to me some really

7
00:00:23,590 --> 00:00:20,480
interesting things coming out of an

8
00:00:26,710 --> 00:00:23,600
up-and-coming really booming

9
00:00:28,710 --> 00:00:26,720
uh laboratory in mexico that you're

10
00:00:30,870 --> 00:00:28,720
going to be seeing other presentations

11
00:00:33,110 --> 00:00:30,880
on over the next couple days

12
00:00:36,389 --> 00:00:33,120
uh we're really happy to have alex with

13
00:00:38,389 --> 00:00:36,399

us tonight and uh after this

14
00:00:40,549 --> 00:00:38,399
we're gonna have the standard q a that

15
00:00:43,270 --> 00:00:40,559
we'll have and then we're gonna have a

16
00:00:46,549 --> 00:00:43,280
final event that's going to be

17
00:00:48,869 --> 00:00:46,559
in the lounge at 8 00 p.m eastern time

18
00:00:50,150 --> 00:00:48,879
it's about an hour from now and that

19
00:00:52,389 --> 00:00:50,160
will be a

20
00:00:54,630 --> 00:00:52,399
performance art piece it should be

21
00:00:56,630 --> 00:00:54,640
really interesting gonna be different

22
00:00:58,869 --> 00:00:56,640
than what you've seen so far and it will

23
00:01:01,349 --> 00:00:58,879
definitely be informative and

24
00:01:03,430 --> 00:01:01,359
entertaining so i hope to see you over

25
00:01:05,509 --> 00:01:03,440
there for now i'm going to turn it over

26
00:01:06,630 --> 00:01:05,519
to lloyd thank you very much for being

27
00:01:07,990 --> 00:01:06,640
here lloyd

28
00:01:09,910 --> 00:01:08,000
thank you

29
00:01:11,830 --> 00:01:09,920
thanks john all right everybody so

30
00:01:14,070 --> 00:01:11,840
here's the deal um alex will get started

31
00:01:16,070 --> 00:01:14,080
here in a moment please put any of your

32
00:01:17,910 --> 00:01:16,080
questions in the chat um i will be kind

33
00:01:21,830 --> 00:01:17,920
of keeping an eye on the chat

34
00:01:24,230 --> 00:01:21,840
and at the end of alex's uh presentation

35
00:01:26,950 --> 00:01:24,240
i'll be asking questions on your behalf

36
00:01:29,590 --> 00:01:26,960
uh about 10 minutes or so to answer some

37
00:01:31,749 --> 00:01:29,600
questions at that point and then of

38
00:01:33,910 --> 00:01:31,759

course um i'll remind everybody about

39
00:01:35,030 --> 00:01:33,920
sally drucker's presentation

40
00:01:37,109 --> 00:01:35,040
at the end

41
00:01:39,510 --> 00:01:37,119
all right we are being recorded so alex

42
00:01:42,389 --> 00:01:39,520
alvarez please take it away thank you

43
00:01:45,270 --> 00:01:42,399
john for the introduction well i'm

44
00:01:49,190 --> 00:01:45,280
proceeding to share my screen

45
00:01:52,310 --> 00:01:49,200
i'm alex alvarez and i'm going to

46
00:01:55,590 --> 00:01:52,320
present the preliminary results of a

47
00:01:58,469 --> 00:01:55,600
series of bioinformatics analysis

48
00:01:59,990 --> 00:01:58,479
that a concern

49
00:02:02,389 --> 00:02:00,000
concerning

50
00:02:10,309 --> 00:02:02,399
protein that might be involved in the

51
00:02:13,589 --> 00:02:11,830
it is a

52
00:02:15,430 --> 00:02:13,599
a popular belief

53
00:02:18,470 --> 00:02:15,440
especially in

54
00:02:19,350 --> 00:02:18,480
some cultural and folkloric traditions

55
00:02:22,550 --> 00:02:19,360
that

56
00:02:23,830 --> 00:02:22,560
psychic abilities may run in families

57
00:02:26,070 --> 00:02:23,840
and

58
00:02:28,470 --> 00:02:26,080
fortunately we have

59
00:02:30,869 --> 00:02:28,480
evidence of different kinds

60
00:02:32,869 --> 00:02:30,879
that support this idea

61
00:02:36,869 --> 00:02:32,879
this comes from

62
00:02:38,390 --> 00:02:36,879
different esp studios

63
00:02:39,750 --> 00:02:38,400

from a

64
00:02:42,229 --> 00:02:39,760
service

65
00:02:44,630 --> 00:02:43,350
there is

66
00:02:47,030 --> 00:02:44,640
one

67
00:02:48,830 --> 00:02:47,040
pedigree analysis which is an analysis

68
00:02:51,270 --> 00:02:48,840
of the family history of different

69
00:02:55,030 --> 00:02:51,280
people this was

70
00:02:56,949 --> 00:02:55,040
done by sharokin in scotland

71
00:02:58,910 --> 00:02:56,959
and she

72
00:03:01,509 --> 00:02:58,920
interviewed around

73
00:03:04,550 --> 00:03:01,519
130 individuals

74
00:03:06,630 --> 00:03:04,560
that claimed to have an ability called

75
00:03:08,390 --> 00:03:06,640
second site this is a

76
00:03:11,670 --> 00:03:08,400
kind of

77
00:03:13,190 --> 00:03:11,680
it's like some sort of clairvoyance and

78
00:03:16,229 --> 00:03:13,200
mixed with

79
00:03:21,830 --> 00:03:18,630
and it's a typical ability

80
00:03:24,789 --> 00:03:21,840
in the scottish people

81
00:03:26,229 --> 00:03:24,799
mainly in the highlands of scotland

82
00:03:29,509 --> 00:03:26,239
so she

83
00:03:31,430 --> 00:03:29,519
found a consistent pattern across

84
00:03:32,470 --> 00:03:31,440
all of the individuals that she

85
00:03:33,270 --> 00:03:32,480
interviewed

86
00:03:34,789 --> 00:03:33,280
and

87
00:03:36,650 --> 00:03:34,799
proposed that

88
00:03:38,070 --> 00:03:36,660

this ability

89
00:03:39,750 --> 00:03:38,080
[Music]

90
00:03:41,670 --> 00:03:39,760
adjusted to an

91
00:03:45,190 --> 00:03:41,680
autosomal dominant

92
00:03:48,070 --> 00:03:45,200
model of inheritance this means that

93
00:03:49,430 --> 00:03:48,080
whatever is this trade it is not

94
00:03:51,910 --> 00:03:49,440
associated with

95
00:03:54,309 --> 00:03:51,920
sexual chromosomes

96
00:03:55,830 --> 00:03:54,319
and finally we have

97
00:03:58,550 --> 00:03:55,840
but i think it's the

98
00:04:03,429 --> 00:03:58,560
most striking evidence so far

99
00:04:09,350 --> 00:04:07,830
in which a team led by helani

100
00:04:10,470 --> 00:04:09,360
found a

101
00:04:18,390 --> 00:04:10,480
gene

102
00:04:22,069 --> 00:04:20,870
that uh well dejean has

103
00:04:23,749 --> 00:04:22,079
their

104
00:04:25,830 --> 00:04:23,759
specific variant in

105
00:04:30,390 --> 00:04:25,840
non-psychic people and

106
00:04:32,629 --> 00:04:30,400
another variant in psychic people

107
00:04:34,710 --> 00:04:32,639
so

108
00:04:36,710 --> 00:04:34,720
well before we

109
00:04:37,990 --> 00:04:36,720
proceed there's

110
00:04:42,230 --> 00:04:38,000
a couple of

111
00:04:45,350 --> 00:04:44,150
to show you

112
00:04:47,670 --> 00:04:45,360
in order to

113
00:04:50,070 --> 00:04:47,680

understand what's coming next the first

114
00:04:52,150 --> 00:04:50,080
one is the single nucleotide

115
00:04:56,469 --> 00:04:52,160
polymorphism

116
00:04:59,270 --> 00:04:56,479
or snip as it is abbreviated

117
00:05:01,350 --> 00:04:59,280
refers to a variation in a unique

118
00:05:02,790 --> 00:05:01,360
position of a

119
00:05:04,710 --> 00:05:02,800
nucleotide of

120
00:05:06,070 --> 00:05:04,720
any human gene

121
00:05:09,270 --> 00:05:06,080
and

122
00:05:11,350 --> 00:05:09,280
well in order to be considered a sleep

123
00:05:14,310 --> 00:05:11,360
it has to be present in at least one

124
00:05:15,670 --> 00:05:14,320
percent of a given population

125
00:05:16,870 --> 00:05:15,680
if

126
00:05:17,990 --> 00:05:16,880
because

127
00:05:19,430 --> 00:05:18,000
many times

128
00:05:21,350 --> 00:05:19,440
we can have

129
00:05:25,510 --> 00:05:21,360
specific variations both that are only

130
00:05:26,870 --> 00:05:25,520
present in a very few people

131
00:05:28,710 --> 00:05:26,880
so

132
00:05:31,110 --> 00:05:28,720
the snips are present in at least one

133
00:05:32,310 --> 00:05:31,120
percent of a population

134
00:05:34,230 --> 00:05:32,320
the other

135
00:05:36,710 --> 00:05:34,240
concept is the

136
00:05:39,990 --> 00:05:36,720
protein isoforms

137
00:05:42,710 --> 00:05:40,000
a protein isoform is a variation of a

138
00:05:47,909 --> 00:05:46,310

that is encoded by the same

139
00:05:48,950 --> 00:05:47,919
gene

140
00:05:50,070 --> 00:05:48,960
in this case

141
00:05:53,430 --> 00:05:50,080
we have the

142
00:05:56,070 --> 00:05:53,440
gene the dna which is first

143
00:05:57,670 --> 00:05:56,080
partly transcribed into three messenger

144
00:05:59,670 --> 00:05:57,680
rna

145
00:06:02,870 --> 00:05:59,680
and we have two types of gradients the

146
00:06:05,590 --> 00:06:02,880
coding regions which are the

147
00:06:07,909 --> 00:06:05,600
boxes and the non-coding ones which are

148
00:06:11,430 --> 00:06:07,919
the black lines so

149
00:06:15,189 --> 00:06:11,440
through alternative splicing which is

150
00:06:16,950 --> 00:06:15,199
a way of processing this

151
00:06:18,710 --> 00:06:16,960
piece of

152
00:06:22,070 --> 00:06:18,720
rna

153
00:06:23,270 --> 00:06:22,080
we can have different uh

154
00:06:26,070 --> 00:06:23,280
pro

155
00:06:27,029 --> 00:06:26,080
splice and rnas

156
00:06:29,510 --> 00:06:27,039
and

157
00:06:31,990 --> 00:06:29,520
this will be translated into

158
00:06:34,550 --> 00:06:32,000
slightly different proteins which is

159
00:06:35,990 --> 00:06:34,560
what we call protein ice forms

160
00:06:38,790 --> 00:06:36,000
as you can see

161
00:06:42,230 --> 00:06:38,800
protein ice forms share some

162
00:06:43,749 --> 00:06:42,240
parts of the gene both differ norms

163
00:06:45,189 --> 00:06:43,759

and

164
00:06:49,350 --> 00:06:45,199
finally

165
00:06:52,870 --> 00:06:49,360
the concept of homologous characters

166
00:06:55,990 --> 00:06:52,880
at structural and molecular level

167
00:06:58,150 --> 00:06:56,000
when we look at a phylogenetic tree

168
00:06:59,749 --> 00:06:58,160
we have a series of

169
00:07:00,830 --> 00:06:59,759
characters

170
00:07:06,870 --> 00:07:00,840
and

171
00:07:11,830 --> 00:07:09,990
these characters need to be uh

172
00:07:14,309 --> 00:07:11,840
evolutionarily related in order to be

173
00:07:16,710 --> 00:07:14,319
placed in a phylogenetic tree but many

174
00:07:18,870 --> 00:07:16,720
times the these

175
00:07:19,990 --> 00:07:18,880
evolutionary relationships are not so

176
00:07:21,270 --> 00:07:20,000
obvious

177
00:07:24,150 --> 00:07:21,280
for example

178
00:07:27,270 --> 00:07:24,160
we take the fin of a whale the arm of a

179
00:07:28,830 --> 00:07:27,280
human being the leg of a lizard and the

180
00:07:31,749 --> 00:07:28,840
wing of a

181
00:07:33,909 --> 00:07:31,759
bird at first we may think that

182
00:07:36,469 --> 00:07:33,919
there is no relationship between them

183
00:07:38,950 --> 00:07:36,479
but when we look at the bones

184
00:07:41,350 --> 00:07:38,960
each of these structures we are going to

185
00:07:43,830 --> 00:07:41,360
see that they are exactly the same bones

186
00:07:45,830 --> 00:07:43,840
but they have suffered different

187
00:07:47,189 --> 00:07:45,840
modifications

188
00:07:49,110 --> 00:07:47,199

so

189
00:07:51,510 --> 00:07:49,120
these all of these

190
00:07:53,350 --> 00:07:51,520
characters are said to be homologous

191
00:07:56,710 --> 00:07:53,360
because

192
00:07:58,950 --> 00:07:56,720
they come from a single common ancestor

193
00:08:00,629 --> 00:07:58,960
and this also happens at the molecular

194
00:08:03,909 --> 00:08:00,639
level

195
00:08:09,029 --> 00:08:06,390
we have two kinds of

196
00:08:11,909 --> 00:08:09,039
homologous genes

197
00:08:15,029 --> 00:08:11,919
the first one is ortollo blue genes this

198
00:08:17,270 --> 00:08:15,039
is the same protein in

199
00:08:18,790 --> 00:08:17,280
in different organisms you take for

200
00:08:21,350 --> 00:08:18,800
example the

201
00:08:23,270 --> 00:08:21,360
the monologuing gene from the frog the

202
00:08:25,830 --> 00:08:23,280
human and the mouse

203
00:08:26,950 --> 00:08:25,840
it is the same gene but is present in

204
00:08:29,589 --> 00:08:26,960
different

205
00:08:31,510 --> 00:08:29,599
organs so this is what we call

206
00:08:32,870 --> 00:08:31,520
orthologues or

207
00:08:34,070 --> 00:08:32,880
ortolos

208
00:08:36,550 --> 00:08:34,080
and

209
00:08:38,310 --> 00:08:36,560
we also can have within the same

210
00:08:41,029 --> 00:08:38,320
organism

211
00:08:43,750 --> 00:08:41,039
different genes that are evolutionarily

212
00:08:47,190 --> 00:08:43,760
related like the

213
00:08:49,910 --> 00:08:47,200

alpha chain of the hemoglobin from mouse

214
00:08:53,590 --> 00:08:49,920
and also the beta chain and

215
00:08:54,389 --> 00:08:53,600
another protein called myoglobu

216
00:08:57,110 --> 00:08:54,399
so

217
00:08:59,350 --> 00:08:57,120
these are present in the same organism

218
00:09:03,509 --> 00:08:59,360
and are evolutionarily related this is

219
00:09:03,519 --> 00:09:06,630
well

220
00:09:11,030 --> 00:09:09,910
so what's what about the tnrc

221
00:09:13,670 --> 00:09:11,040
engine

222
00:09:15,750 --> 00:09:13,680
as we said this is the gene that

223
00:09:17,300 --> 00:09:15,760
uh what they tell proposed in their

224
00:09:18,389 --> 00:09:17,310
studio to be

225
00:09:20,790 --> 00:09:18,399
[Music]

226
00:09:22,550 --> 00:09:20,800
that it could be involved in

227
00:09:24,550 --> 00:09:22,560
psychic function

228
00:09:26,389 --> 00:09:24,560
this gene encodes a massive protein

229
00:09:28,470 --> 00:09:26,399
which is 10 times

230
00:09:31,509 --> 00:09:28,480
the size of the average protein

231
00:09:35,269 --> 00:09:31,519
the average protein is around 300 amino

232
00:09:37,590 --> 00:09:35,279
acids this protein is around 3 000 amino

233
00:09:40,550 --> 00:09:37,600
acids its function and structure have

234
00:09:42,070 --> 00:09:40,560
not been properly elucidated yet

235
00:09:44,230 --> 00:09:42,080
and

236
00:09:45,269 --> 00:09:44,240
but it's known that it expresses in many

237
00:09:47,190 --> 00:09:45,279
organs

238
00:09:48,550 --> 00:09:47,200

throughout the body and in different

239
00:09:52,310 --> 00:09:48,560
brain regions

240
00:09:53,590 --> 00:09:52,320
and this gene has nine isoforms which is

241
00:09:56,870 --> 00:09:53,600
also

242
00:09:57,910 --> 00:09:56,880
far above the avarage of

243
00:10:00,070 --> 00:09:57,920
most of

244
00:10:07,430 --> 00:10:00,080
human proteins which have

245
00:10:10,310 --> 00:10:09,030
well

246
00:10:12,150 --> 00:10:10,320
as i said

247
00:10:15,110 --> 00:10:12,160
this gene expresses

248
00:10:18,150 --> 00:10:15,120
different brain structures specifically

249
00:10:21,509 --> 00:10:18,160
in the cerebral cortex the hypocampus

250
00:10:22,389 --> 00:10:21,519
the caudate nucleus and the cerebellum

251
00:10:24,710 --> 00:10:22,399
and

252
00:10:26,870 --> 00:10:24,720
it has different levels of expressions

253
00:10:29,430 --> 00:10:26,880
depending on the

254
00:10:33,750 --> 00:10:29,440
the cell type of each of these

255
00:10:36,630 --> 00:10:35,350
and

256
00:10:37,750 --> 00:10:36,640
what i

257
00:10:42,470 --> 00:10:37,760
did here

258
00:10:46,150 --> 00:10:42,480
was a series of bioinformatics analysis

259
00:10:49,350 --> 00:10:46,160
i initially took the sequence of the dnr

260
00:10:50,310 --> 00:10:49,360
c18 gene from human

261
00:10:51,670 --> 00:10:50,320
and

262
00:10:53,030 --> 00:10:51,680
launch it

263
00:10:55,190 --> 00:10:53,040

to a

264
00:10:57,670 --> 00:10:55,200
specific database of completely

265
00:10:59,590 --> 00:10:57,680
sequenced genomes

266
00:11:02,710 --> 00:10:59,600
in order to look for

267
00:11:05,110 --> 00:11:02,720
homologous or evolutionarily related

268
00:11:11,030 --> 00:11:07,990
then i perform a series of structural

269
00:11:15,509 --> 00:11:13,350
specifically the prediction of the

270
00:11:16,630 --> 00:11:15,519
secondary structure of a protein which

271
00:11:19,030 --> 00:11:16,640
is the

272
00:11:21,110 --> 00:11:19,040
specific conformations that

273
00:11:22,550 --> 00:11:21,120
some parts of the proteins

274
00:11:24,790 --> 00:11:22,560
adopt

275
00:11:27,269 --> 00:11:24,800
i also

276
00:11:30,150 --> 00:11:27,279
did an empirical modeling of possible

277
00:11:31,509 --> 00:11:30,160
protein domains a protein domain

278
00:11:33,269 --> 00:11:31,519
is a

279
00:11:34,389 --> 00:11:33,279
protein region that

280
00:11:35,430 --> 00:11:34,399
has a

281
00:11:37,829 --> 00:11:35,440
specific

282
00:11:41,110 --> 00:11:37,839
structure and function

283
00:11:43,190 --> 00:11:41,120
this function can be catalytic but also

284
00:11:44,550 --> 00:11:43,200
regulatory

285
00:11:46,310 --> 00:11:44,560
or strong

286
00:11:48,389 --> 00:11:46,320
and

287
00:11:50,629 --> 00:11:48,399
well i also predicted

288
00:11:52,790 --> 00:11:50,639

the composition in terms of disordered

289
00:11:57,030 --> 00:11:52,800
radiance this in contrast with the

290
00:11:59,750 --> 00:11:57,040
protein domains are radians that as its

291
00:12:02,470 --> 00:11:59,760
name says is our disorder they do not

292
00:12:04,790 --> 00:12:02,480
adopt a specific structure

293
00:12:07,590 --> 00:12:04,800
and finally i perform a series of

294
00:12:08,470 --> 00:12:07,600
sequence alignments

295
00:12:11,990 --> 00:12:08,480
with

296
00:12:15,190 --> 00:12:12,000
some of the domains that i identified

297
00:12:17,030 --> 00:12:15,200
in order to see if they were present in

298
00:12:19,750 --> 00:12:17,040
this program

299
00:12:21,590 --> 00:12:19,760
in the tnr c18

300
00:12:24,870 --> 00:12:21,600
well

301
00:12:27,509 --> 00:12:24,880
the first part of the results concerning

302
00:12:31,750 --> 00:12:27,519
the distribution of the

303
00:12:33,350 --> 00:12:31,760
sequences found in this database

304
00:12:35,350 --> 00:12:33,360
these are the

305
00:12:38,389 --> 00:12:35,360
this is the distribution of the

306
00:12:39,190 --> 00:12:38,399
dnrc8 potential homologs and

307
00:12:48,870 --> 00:12:39,200
i

308
00:12:53,670 --> 00:12:48,880
mostly an exploratory search

309
00:12:56,629 --> 00:12:53,680
so far it is not possible to discern if

310
00:12:59,030 --> 00:12:56,639
all of the sequence that i found are

311
00:13:00,069 --> 00:12:59,040
really evolutionarily related

312
00:13:03,509 --> 00:13:00,079
or

313
00:13:05,750 --> 00:13:03,519

they are similar to the tnr18 protein

314
00:13:09,110 --> 00:13:05,760
because of chance this is

315
00:13:11,509 --> 00:13:09,120
something that happens a lot in

316
00:13:13,190 --> 00:13:11,519
when someone

317
00:13:15,590 --> 00:13:13,200
searches a

318
00:13:17,509 --> 00:13:15,600
specific gene sequence against a very

319
00:13:18,310 --> 00:13:17,519
large database

320
00:13:20,470 --> 00:13:18,320
so

321
00:13:22,710 --> 00:13:20,480
in this case

322
00:13:27,990 --> 00:13:25,190
proteins that are similar and

323
00:13:30,069 --> 00:13:28,000
are mainly found in animals

324
00:13:31,670 --> 00:13:30,079
which is the

325
00:13:34,389 --> 00:13:31,680
thing is like

326
00:13:38,230 --> 00:13:34,399
some kind of orange color here

327
00:13:41,110 --> 00:13:38,240
and also in plants which is

328
00:13:42,069 --> 00:13:41,120
this great slice

329
00:13:45,829 --> 00:13:42,079
and

330
00:13:50,470 --> 00:13:45,839
i found a very few heats in

331
00:13:54,790 --> 00:13:50,480
fungi in protists and in prokaryotes

332
00:13:59,509 --> 00:13:58,710
so within animals i found that most of

333
00:14:03,030 --> 00:13:59,519
the

334
00:14:05,189 --> 00:14:03,040
chordates

335
00:14:06,470 --> 00:14:05,199
which is the group to which

336
00:14:08,550 --> 00:14:06,480
we belong as

337
00:14:09,509 --> 00:14:08,560
human beings

338
00:14:12,150 --> 00:14:09,519

and

339
00:14:14,310 --> 00:14:12,160
also a vast number of new

340
00:14:15,509 --> 00:14:14,320
arthropods and to a lesser degree in

341
00:14:16,710 --> 00:14:15,519
moles

342
00:14:18,870 --> 00:14:16,720
worms

343
00:14:21,030 --> 00:14:18,880
sea urchins and

344
00:14:23,030 --> 00:14:21,040
jellyfish

345
00:14:24,629 --> 00:14:23,040
and this is the

346
00:14:27,030 --> 00:14:24,639
interesting part

347
00:14:33,750 --> 00:14:30,710
these are not potential homologs but

348
00:14:35,590 --> 00:14:33,760
the dnrc18 gene

349
00:14:39,430 --> 00:14:35,600
but

350
00:14:41,509 --> 00:14:39,440
found in many other organisms other than

351
00:14:43,269 --> 00:14:41,519
humans

352
00:14:46,310 --> 00:14:43,279
as you can see

353
00:14:49,829 --> 00:14:46,320
it is mainly found in mammals

354
00:14:52,710 --> 00:14:49,839
but also in almost all main vertebrae

355
00:14:55,430 --> 00:14:52,720
groups like fish

356
00:14:56,829 --> 00:14:55,440
reptiles which are divided into

357
00:15:01,750 --> 00:14:56,839
crocodiles and

358
00:15:06,629 --> 00:15:04,550
and we also found it in

359
00:15:10,710 --> 00:15:06,639
some art roblox

360
00:15:13,509 --> 00:15:10,720
and in one flat one the only

361
00:15:16,710 --> 00:15:13,519
vertebrate rooting which i did not found

362
00:15:18,710 --> 00:15:16,720
any kids for this protein

363
00:15:19,590 --> 00:15:18,720

was the amphibians

364
00:15:22,069 --> 00:15:19,600
but

365
00:15:24,949 --> 00:15:22,079
this not necessarily means that

366
00:15:26,949 --> 00:15:24,959
it is not present in amphibians it could

367
00:15:27,670 --> 00:15:26,959
also mean that

368
00:15:31,749 --> 00:15:27,680
the

369
00:15:34,870 --> 00:15:31,759
sequence of this gene has diverged

370
00:15:36,629 --> 00:15:34,880
at a very fast rate and

371
00:15:39,110 --> 00:15:36,639
it is no longer

372
00:15:42,550 --> 00:15:39,120
identified through simple searches like

373
00:15:45,910 --> 00:15:42,560
this we will need to perform uh most

374
00:15:47,030 --> 00:15:45,920
robust searches and analysis if we want

375
00:15:49,990 --> 00:15:47,040
to

376
00:15:55,590 --> 00:15:50,000
identify if this gene is really absent

377
00:15:58,389 --> 00:15:56,629
so

378
00:16:00,710 --> 00:15:58,399
what about the functions

379
00:16:03,590 --> 00:16:00,720
associated with all of the sequences

380
00:16:07,350 --> 00:16:06,470
here is the number of hits that

381
00:16:10,870 --> 00:16:07,360
are

382
00:16:14,310 --> 00:16:10,880
annotated with a specific function

383
00:16:18,470 --> 00:16:17,350
the most common function is this the bah

384
00:16:19,560 --> 00:16:18,480
which

385
00:16:21,509 --> 00:16:19,570
stands for the

386
00:16:23,350 --> 00:16:21,519
[Music]

387
00:16:25,430 --> 00:16:23,360
this is the name of the a specific

388
00:16:28,550 --> 00:16:25,440

domain

389
00:16:30,310 --> 00:16:28,560
and it is found mainly in plants

390
00:16:34,470 --> 00:16:30,320
uh but also

391
00:16:39,590 --> 00:16:37,189
this

392
00:16:43,350 --> 00:16:39,600
protein domain is involved in the

393
00:16:48,470 --> 00:16:45,829
we also found the

394
00:16:51,269 --> 00:16:48,480
the specific tnrc18

395
00:16:52,870 --> 00:16:51,279
function which corresponds to the

396
00:16:55,110 --> 00:16:52,880
previous slide

397
00:16:56,790 --> 00:16:55,120
to this run

398
00:16:58,069 --> 00:16:56,800
all of these

399
00:16:59,509 --> 00:16:58,079
hits are

400
00:17:01,189 --> 00:16:59,519
grouped into

401
00:17:02,069 --> 00:17:01,199
this function

402
00:17:05,429 --> 00:17:02,079
and

403
00:17:07,750 --> 00:17:05,439
we find also

404
00:17:10,949 --> 00:17:07,760
some proteins that are

405
00:17:14,390 --> 00:17:10,959
involved in chromatin remodeling

406
00:17:15,990 --> 00:17:14,400
and others like the winged dye

407
00:17:20,789 --> 00:17:16,000
it's a

408
00:17:22,230 --> 00:17:20,799
protein typical of arthropods and if

409
00:17:25,270 --> 00:17:22,240
the term

410
00:17:27,270 --> 00:17:25,280
times the

411
00:17:29,990 --> 00:17:27,280
the specific position of

412
00:17:33,669 --> 00:17:30,000
several parts of the body and

413
00:17:35,270 --> 00:17:33,679

finally to a much lesser degree the phd

414
00:17:40,470 --> 00:17:35,280
function

415
00:17:45,750 --> 00:17:43,909
so regarding the structural analysis of

416
00:17:47,830 --> 00:17:45,760
this zoom

417
00:17:50,630 --> 00:17:47,840
is the

418
00:17:53,750 --> 00:17:50,640
distribution of disordered radiance this

419
00:17:59,510 --> 00:17:55,430
these are

420
00:18:02,870 --> 00:17:59,520
defined everything that is above this

421
00:18:04,630 --> 00:18:02,880
line is considered to be a disordered

422
00:18:06,470 --> 00:18:04,640
region

423
00:18:08,390 --> 00:18:06,480
but this below is

424
00:18:11,909 --> 00:18:08,400
likely to be uh

425
00:18:14,789 --> 00:18:11,919
a protein domain so

426
00:18:17,830 --> 00:18:14,799
what is reported in the many databases

427
00:18:19,270 --> 00:18:17,840
is this domain the bih which as you can

428
00:18:21,430 --> 00:18:19,280
see

429
00:18:24,310 --> 00:18:21,440
corresponds to only a small portion of

430
00:18:27,270 --> 00:18:24,320
the protons about a tenth of the protein

431
00:18:29,350 --> 00:18:27,280
and the the hypothetical function of

432
00:18:33,029 --> 00:18:29,360
this protein is

433
00:18:35,590 --> 00:18:33,039
predicted based on this specific

434
00:18:40,070 --> 00:18:35,600
but i

435
00:18:48,390 --> 00:18:43,590
the genes that

436
00:18:52,390 --> 00:18:49,750
responding to the functions that i

437
00:18:54,310 --> 00:18:52,400
showed you in the previous slide and

438
00:18:57,029 --> 00:18:54,320

i found that

439
00:18:58,549 --> 00:18:57,039
another domain called the tutor domain

440
00:19:01,270 --> 00:18:58,559
is also

441
00:19:03,430 --> 00:19:01,280
it aligns

442
00:19:07,270 --> 00:19:03,440
very well with this

443
00:19:08,630 --> 00:19:07,280
other region of the tnrc18 protein

444
00:19:10,470 --> 00:19:08,640
and

445
00:19:13,350 --> 00:19:10,480
this this is

446
00:19:14,630 --> 00:19:13,360
has been reported in the territory but

447
00:19:17,350 --> 00:19:14,640
only in

448
00:19:19,750 --> 00:19:17,360
two or three cases but

449
00:19:22,310 --> 00:19:19,760
the novelty here is this other domain

450
00:19:24,950 --> 00:19:22,320
the hoax 9 domain

451
00:19:27,590 --> 00:19:24,960
this has not been previously reported to

452
00:19:31,029 --> 00:19:27,600
be part of this protein but

453
00:19:33,430 --> 00:19:31,039
when i aligned the sequence of

454
00:19:36,710 --> 00:19:33,440
protein with half this domain

455
00:19:39,350 --> 00:19:36,720
with the dnrc8 protein

456
00:19:42,310 --> 00:19:39,360
there is a high similarity

457
00:19:43,990 --> 00:19:42,320
between both of them and it

458
00:19:45,350 --> 00:19:44,000
aligns exactly

459
00:19:46,630 --> 00:19:45,360
this region

460
00:19:49,029 --> 00:19:46,640
which

461
00:19:51,590 --> 00:19:49,039
the algorithm predicts to be and

462
00:19:52,470 --> 00:19:51,600
non-disordered version

463
00:19:53,830 --> 00:19:52,480

so

464
00:19:56,150 --> 00:19:53,840
at least

465
00:20:00,549 --> 00:19:56,160
we have three different protein domains

466
00:20:07,190 --> 00:20:03,110
all of these domains the va

467
00:20:12,149 --> 00:20:07,200
h the two layer holds b9 are somehow

468
00:20:14,630 --> 00:20:13,590
so

469
00:20:18,470 --> 00:20:14,640
this

470
00:20:20,630 --> 00:20:18,480
suggests us that the tnr18 protein

471
00:20:22,310 --> 00:20:20,640
could be part of a transcriptional

472
00:20:23,830 --> 00:20:22,320
regulation network

473
00:20:26,310 --> 00:20:23,840
and those

474
00:20:33,270 --> 00:20:26,320
might not be the only one responsible

475
00:20:37,590 --> 00:20:36,710
there is evidence uh

476
00:20:39,270 --> 00:20:37,600
other

477
00:20:41,530 --> 00:20:39,280
brain aspects

478
00:20:42,870 --> 00:20:41,540
that are dependent on

479
00:20:45,190 --> 00:20:42,880
[Music]

480
00:20:47,909 --> 00:20:45,200
this kind of

481
00:20:51,110 --> 00:20:47,919
networks for example some aspects of

482
00:20:54,630 --> 00:20:53,990
some brain disorders

483
00:20:55,990 --> 00:20:54,640
in which

484
00:20:57,430 --> 00:20:56,000
[Music]

485
00:21:00,470 --> 00:20:57,440
a brain a

486
00:21:04,470 --> 00:21:00,480
transcriptional regulation network is

487
00:21:08,870 --> 00:21:06,950
so you may wonder if

488
00:21:10,390 --> 00:21:08,880

how could a

489
00:21:15,029 --> 00:21:10,400
single

490
00:21:16,630 --> 00:21:15,039
sleep could make all the difference in

491
00:21:19,909 --> 00:21:16,640
this case well

492
00:21:23,190 --> 00:21:19,919
so far we do not know

493
00:21:25,430 --> 00:21:23,200
the results that reported

494
00:21:25,440 --> 00:21:30,230
very preliminary

495
00:21:36,070 --> 00:21:34,230
they report a aberration in a single

496
00:21:38,950 --> 00:21:36,080
position of

497
00:21:40,870 --> 00:21:38,960
a non-coding region of this gene

498
00:21:43,029 --> 00:21:40,880
but

499
00:21:46,470 --> 00:21:43,039
in the literature it has been reported

500
00:21:49,270 --> 00:21:46,480
that in other genes

501
00:21:51,350 --> 00:21:49,280
when we have a variation in

502
00:21:53,350 --> 00:21:51,360
unique slip we think

503
00:21:55,590 --> 00:21:53,360
also the infrared gradients or the

504
00:21:58,149 --> 00:21:55,600
non-coding gradients of the gene

505
00:22:00,870 --> 00:21:58,159
well this can result in the expression

506
00:22:03,909 --> 00:22:00,880
of different protein ice forms

507
00:22:05,270 --> 00:22:03,919
so a possibility is that

508
00:22:07,990 --> 00:22:05,280
people that

509
00:22:09,430 --> 00:22:08,000
have the let's call it the psychic

510
00:22:10,549 --> 00:22:09,440
variant

511
00:22:12,630 --> 00:22:10,559
express

512
00:22:13,789 --> 00:22:12,640
some protein isoform

513
00:22:17,510 --> 00:22:13,799

and a

514
00:22:20,549 --> 00:22:17,520
non-sticky people express

515
00:22:22,470 --> 00:22:20,559
another isotope of the same

516
00:22:25,350 --> 00:22:22,480
protein

517
00:22:27,669 --> 00:22:25,360
and just to show you the importance of a

518
00:22:28,549 --> 00:22:27,679
single nucleotide change in a gene

519
00:22:30,149 --> 00:22:28,559
and

520
00:22:37,830 --> 00:22:30,159
i

521
00:22:41,350 --> 00:22:37,840
normal red blood cells and

522
00:22:45,510 --> 00:22:41,360
secant cell anemia

523
00:22:53,830 --> 00:22:47,110
as

524
00:22:55,270 --> 00:22:53,840
that affects

525
00:22:59,669 --> 00:22:55,280
large part of

526
00:23:03,029 --> 00:22:59,679
the population specifically in africa

527
00:23:07,590 --> 00:23:05,830
the only difference between

528
00:23:10,470 --> 00:23:07,600
this kind of cells and

529
00:23:17,350 --> 00:23:12,230
other

530
00:23:20,310 --> 00:23:17,360
is a mutation in a single nucleotide

531
00:23:21,669 --> 00:23:20,320
not within the known sequence but in the

532
00:23:25,350 --> 00:23:21,679
coding sequence

533
00:23:26,870 --> 00:23:25,360
so this results in a change of a single

534
00:23:29,270 --> 00:23:26,880
amino acid

535
00:23:31,270 --> 00:23:29,280
in this case volume instead of glutamic

536
00:23:31,990 --> 00:23:31,280
acid and

537
00:23:34,070 --> 00:23:32,000
the

538
00:23:36,710 --> 00:23:34,080

molecule in chains are

539
00:23:39,750 --> 00:23:36,720
have an altered confirmation

540
00:23:42,149 --> 00:23:39,760
and ultimately this results in

541
00:23:43,750 --> 00:23:42,159
the production of abnormal

542
00:23:44,710 --> 00:23:43,760
red blood cells

543
00:23:47,510 --> 00:23:44,720
so

544
00:23:51,190 --> 00:23:49,669
yeah a single

545
00:23:53,110 --> 00:23:51,200
change in

546
00:23:55,430 --> 00:23:53,120
a single neuropathy

547
00:23:59,269 --> 00:23:55,440
can have very dramatic

548
00:23:59,279 --> 00:24:03,269
so what can be completed here

549
00:24:07,350 --> 00:24:05,269
the first thing is that the molecular

550
00:24:10,630 --> 00:24:07,360
basis for psychic abilities are more

551
00:24:13,350 --> 00:24:10,640
likely to rely on a protein network than

552
00:24:17,430 --> 00:24:13,360
on a single gene or a single

553
00:24:24,149 --> 00:24:21,590
perhaps even the functions identified

554
00:24:27,430 --> 00:24:24,159
for three of the domains that are likely

555
00:24:29,510 --> 00:24:27,440
to be present in the dnrc8 protein

556
00:24:32,149 --> 00:24:29,520
this network is a transcriptional

557
00:24:36,950 --> 00:24:32,159
regulation one

558
00:24:39,430 --> 00:24:36,960
and if the human pnrc18 gene is

559
00:24:41,110 --> 00:24:39,440
somehow associated with

560
00:24:41,990 --> 00:24:41,120
side

561
00:24:44,230 --> 00:24:42,000
it is

562
00:24:46,549 --> 00:24:44,240
likely that this is also the case in

563
00:24:51,430 --> 00:24:46,559

different organisms in which

564
00:24:58,830 --> 00:24:54,789
as you can remember the tnrc 18 gene is

565
00:25:01,269 --> 00:24:58,840
found in all main vertebrates all about

566
00:25:01,800 --> 00:25:01,279
confidence and

567
00:25:04,230 --> 00:25:01,810
we can

568
00:25:06,070 --> 00:25:04,240
[Music]

569
00:25:08,310 --> 00:25:06,080
if we

570
00:25:09,190 --> 00:25:08,320
turn to the evidence

571
00:25:12,789 --> 00:25:09,200
from

572
00:25:18,230 --> 00:25:15,029
we find that

573
00:25:21,909 --> 00:25:19,669
animals

574
00:25:24,710 --> 00:25:21,919
in which

575
00:25:26,390 --> 00:25:24,720
you suggested that they have some level

576
00:25:29,029 --> 00:25:26,400
of side

577
00:25:30,789 --> 00:25:29,039
yeah

578
00:25:33,750 --> 00:25:30,799
and uh

579
00:25:38,310 --> 00:25:36,390
just to elaborate a little bit more into

580
00:25:43,029 --> 00:25:38,320
this

581
00:25:46,070 --> 00:25:43,039
tree

582
00:25:49,510 --> 00:25:46,080
relax the amphibians because

583
00:25:54,390 --> 00:25:49,520
we did not find the tnrc 18g

584
00:26:01,029 --> 00:25:57,590
what we do have is this

585
00:26:04,230 --> 00:26:01,039
the presence of the tnrc18 protein in

586
00:26:06,870 --> 00:26:04,240
fish birds non-human mammals and

587
00:26:11,909 --> 00:26:08,950
according to the principles of

588
00:26:16,950 --> 00:26:11,919

evolutionary biology

589
00:26:21,269 --> 00:26:19,430
we can use the principle of maximum

590
00:26:22,390 --> 00:26:21,279
parsimony

591
00:26:23,590 --> 00:26:22,400
and

592
00:26:24,470 --> 00:26:23,600
say well

593
00:26:26,549 --> 00:26:24,480
these

594
00:26:27,590 --> 00:26:26,559
three seems

595
00:26:29,669 --> 00:26:27,600
to be

596
00:26:32,470 --> 00:26:29,679
complicated because

597
00:26:34,789 --> 00:26:32,480
it would mean that this gene appeared

598
00:26:37,350 --> 00:26:34,799
independently

599
00:26:41,590 --> 00:26:37,360
within each of these

600
00:26:44,310 --> 00:26:43,190
each of them

601
00:26:45,990 --> 00:26:44,320
each of these

602
00:26:47,750 --> 00:26:46,000
characters is

603
00:26:49,350 --> 00:26:47,760
considered

604
00:26:50,870 --> 00:26:49,360
is called a step

605
00:26:53,510 --> 00:26:50,880
and

606
00:26:55,750 --> 00:26:53,520
this means that this specific phylogeny

607
00:26:59,430 --> 00:26:55,760
isotopical phylogenetic three has four

608
00:27:01,990 --> 00:26:59,440
steps but there is a most parsimonious

609
00:27:03,990 --> 00:27:02,000
explanation

610
00:27:06,710 --> 00:27:04,000
which is this

611
00:27:07,990 --> 00:27:06,720
this means that tnrc18

612
00:27:09,590 --> 00:27:08,000
gene

613
00:27:10,710 --> 00:27:09,600

originated

614
00:27:12,870 --> 00:27:10,720
at a time

615
00:27:14,390 --> 00:27:12,880
before the divergence of

616
00:27:15,430 --> 00:27:14,400
all of these groups

617
00:27:18,549 --> 00:27:15,440
and

618
00:27:20,630 --> 00:27:18,559
well when they diverge they already have

619
00:27:22,389 --> 00:27:20,640
this specific gene

620
00:27:24,870 --> 00:27:22,399
this tree is

621
00:27:26,549 --> 00:27:24,880
less complicated it involves only one

622
00:27:28,310 --> 00:27:26,559
step

623
00:27:30,710 --> 00:27:28,320
and

624
00:27:33,510 --> 00:27:30,720
it has been shown in

625
00:27:36,470 --> 00:27:33,520
many cases that

626
00:27:37,590 --> 00:27:36,480
we have two hypotheses the left one and

627
00:27:39,110 --> 00:27:37,600
the right one

628
00:27:40,549 --> 00:27:39,120
there

629
00:27:43,750 --> 00:27:40,559
most likely

630
00:27:45,510 --> 00:27:43,760
is this one

631
00:27:48,950 --> 00:27:45,520
the one with the

632
00:27:52,950 --> 00:27:48,960
less number of steps and

633
00:27:54,470 --> 00:27:52,960
these perhaps could also apply to the

634
00:27:56,549 --> 00:27:54,480
site

635
00:27:58,630 --> 00:27:56,559
if we review the

636
00:28:00,230 --> 00:27:58,640
all of the experiments

637
00:28:03,669 --> 00:28:00,240
done in the field of

638
00:28:10,470 --> 00:28:08,630

it has been suggested in fish birds in

639
00:28:13,430 --> 00:28:10,480
non-human mammals and

640
00:28:14,830 --> 00:28:13,440
obviously in humans

641
00:28:17,029 --> 00:28:14,840
so it is a

642
00:28:18,549 --> 00:28:17,039
pattern pretty much like

643
00:28:23,029 --> 00:28:18,559
the one of the

644
00:28:25,669 --> 00:28:23,039
distribution of the tnrc8 engine and

645
00:28:27,110 --> 00:28:25,679
perhaps a simpler hypothesis would be

646
00:28:28,470 --> 00:28:27,120
this that

647
00:28:31,190 --> 00:28:28,480
psy did not

648
00:28:33,669 --> 00:28:31,200
originated independently in

649
00:28:37,110 --> 00:28:33,679
each of these groups but

650
00:28:40,870 --> 00:28:37,120
originated at least before the

651
00:28:43,830 --> 00:28:40,880
divergence of vertebrates

652
00:28:46,470 --> 00:28:43,840
it could also be have

653
00:28:47,669 --> 00:28:46,480
could also have originated even before

654
00:28:49,990 --> 00:28:47,679
but uh

655
00:28:52,389 --> 00:28:50,000
with the evidence so far this is the

656
00:28:54,310 --> 00:28:52,399
farthest we can go

657
00:28:56,630 --> 00:28:54,320
and finally the

658
00:28:58,870 --> 00:28:56,640
which are the perspectives

659
00:29:00,389 --> 00:28:58,880
for the well

660
00:29:02,789 --> 00:29:00,399
obviously further

661
00:29:04,710 --> 00:29:02,799
phylogenetic analysis with distantly

662
00:29:05,510 --> 00:29:04,720
related molecules

663
00:29:07,510 --> 00:29:05,520

which

664
00:29:11,510 --> 00:29:07,520
could help us to elucidate the

665
00:29:12,549 --> 00:29:11,520
evolutionary history of the dnrc8 engine

666
00:29:14,950 --> 00:29:12,559
and

667
00:29:17,190 --> 00:29:14,960
if we combine these with more robust

668
00:29:20,630 --> 00:29:17,200
genetic studies that follow the line of

669
00:29:26,310 --> 00:29:23,190
this could give us a wider picture of a

670
00:29:27,190 --> 00:29:26,320
molecular basis of sight in functioning

671
00:29:29,830 --> 00:29:27,200
and

672
00:29:31,830 --> 00:29:29,840
we could make use of for example the

673
00:29:35,669 --> 00:29:31,840
microarray technologies

674
00:29:36,630 --> 00:29:35,679
transcriptomics and proteomics and also

675
00:29:40,460 --> 00:29:36,640
a

676
00:29:42,310 --> 00:29:40,470
in order to

677
00:29:44,230 --> 00:29:42,320
[Music]

678
00:29:45,669 --> 00:29:44,240
try to detect if

679
00:29:50,389 --> 00:29:45,679
psychic

680
00:29:54,389 --> 00:29:51,590
have

681
00:29:57,269 --> 00:29:54,399
a specific anomaly of in a particular

682
00:29:59,110 --> 00:29:57,279
brain structure that is lacking in

683
00:29:59,909 --> 00:29:59,120
people that are

684
00:30:02,149 --> 00:29:59,919
have

685
00:30:03,029 --> 00:30:02,159
a non-sized bearing

686
00:30:05,269 --> 00:30:03,039
and

687
00:30:06,950 --> 00:30:05,279
well that's pretty much it thank you

688
00:30:08,630 --> 00:30:06,960

very much

689
00:30:11,669 --> 00:30:08,640
thank you alex

690
00:30:13,350 --> 00:30:11,679
we do have one question

691
00:30:15,750 --> 00:30:13,360
first i see actually two questions now

692
00:30:17,430 --> 00:30:15,760
so one question is does this imply

693
00:30:19,269 --> 00:30:17,440
that psi potential may have been

694
00:30:22,789 --> 00:30:19,279
developed before fish in the

695
00:30:25,110 --> 00:30:22,799
evolutionary time frame

696
00:30:27,430 --> 00:30:25,120
yeah yeah it is

697
00:30:30,230 --> 00:30:27,440
a hypothesis uh

698
00:30:31,990 --> 00:30:30,240
as i showed you in the

699
00:30:34,830 --> 00:30:32,000
this hypothetical

700
00:30:36,630 --> 00:30:34,840
phylogenetic tree

701
00:30:39,510 --> 00:30:36,640
fish

702
00:30:41,110 --> 00:30:39,520
there have been several studies with

703
00:30:42,470 --> 00:30:41,120
fish which

704
00:30:44,389 --> 00:30:42,480
suggested that

705
00:30:47,190 --> 00:30:44,399
they do have

706
00:30:48,470 --> 00:30:47,200
some levels of site

707
00:30:50,149 --> 00:30:48,480
so

708
00:30:52,070 --> 00:30:50,159
if we uh

709
00:30:53,520 --> 00:30:52,080
but well not only fish

710
00:30:54,870 --> 00:30:53,530
also reptiles and

711
00:30:56,470 --> 00:30:54,880
[Music]

712
00:31:04,470 --> 00:30:56,480
i

713
00:31:06,310 --> 00:31:04,480

so

714
00:31:10,549 --> 00:31:06,320
this

715
00:31:14,789 --> 00:31:13,269
organisms belong to the same clad the

716
00:31:17,029 --> 00:31:14,799
vertebrates

717
00:31:23,990 --> 00:31:21,190
if fish have some level of sight

718
00:31:26,950 --> 00:31:24,000
the most likely explanation is that this

719
00:31:28,149 --> 00:31:26,960
trait appeared before the divergence of

720
00:31:31,029 --> 00:31:28,159
fish

721
00:31:33,110 --> 00:31:31,039
which would mean that

722
00:31:37,029 --> 00:31:33,120
even before the divergence of

723
00:31:39,029 --> 00:31:37,909
okay

724
00:31:41,110 --> 00:31:39,039
thank you

725
00:31:42,549 --> 00:31:41,120
another question are there other snps

726
00:31:44,149 --> 00:31:42,559
that were found that are found across

727
00:31:45,509 --> 00:31:44,159
the phylum genetic

728
00:31:47,269 --> 00:31:45,519
trees

729
00:31:48,070 --> 00:31:47,279
could you repeat the question please

730
00:31:50,789 --> 00:31:48,080
sure

731
00:31:54,070 --> 00:31:50,799
are there other snps that are found

732
00:31:55,269 --> 00:31:54,080
across the phylogenetic tree if so why

733
00:31:56,950 --> 00:31:55,279
would this be

734
00:32:00,310 --> 00:31:56,960
why would this one be involved in psy

735
00:32:03,830 --> 00:32:00,320
versus others

736
00:32:07,350 --> 00:32:06,070
i'm sorry i think i

737
00:32:08,630 --> 00:32:07,360
it's not

738
00:32:09,590 --> 00:32:08,640

[Music]

739
00:32:11,350 --> 00:32:09,600
other

740
00:32:13,430 --> 00:32:11,360
snips

741
00:32:15,830 --> 00:32:13,440
i assume it's i assume the question is

742
00:32:16,630 --> 00:32:15,840
related to snips

743
00:32:19,350 --> 00:32:16,640
well

744
00:32:21,350 --> 00:32:19,360
so far the only one that has been

745
00:32:24,230 --> 00:32:21,360
identified is

746
00:32:26,710 --> 00:32:24,240
this one the from the snip from this

747
00:32:28,350 --> 00:32:26,720
gene the dnrc 18

748
00:32:30,870 --> 00:32:28,360
gene

749
00:32:33,669 --> 00:32:30,880
[Music]

750
00:32:36,389 --> 00:32:35,430
something that can be done is

751
00:32:39,269 --> 00:32:36,399
take the

752
00:32:40,070 --> 00:32:39,279
the intronic sequence of which this snip

753
00:32:41,029 --> 00:32:40,080
is

754
00:32:44,470 --> 00:32:41,039
and

755
00:32:47,269 --> 00:32:44,480
compare it with the sequences of

756
00:32:49,669 --> 00:32:47,279
fish genes or reptile genes

757
00:32:55,590 --> 00:32:51,990
perform an alignment of all of these

758
00:32:57,909 --> 00:32:55,600
sequences and here you can find if

759
00:32:59,029 --> 00:32:57,919
this particular sniff is consistent

760
00:33:02,310 --> 00:32:59,039
across

761
00:33:05,190 --> 00:33:02,320
the vertebrates or on is only present in

762
00:33:06,470 --> 00:33:05,200
humans or in humans and some other group

763
00:33:08,389 --> 00:33:06,480

and

764
00:33:11,269 --> 00:33:08,399
you

765
00:33:13,269 --> 00:33:11,279
could also detect other

766
00:33:15,830 --> 00:33:13,279
particular snips

767
00:33:20,470 --> 00:33:18,470
i think it

768
00:33:23,029 --> 00:33:20,480
you could not say these

769
00:33:27,190 --> 00:33:23,039
snips are somehow

770
00:33:29,570 --> 00:33:28,630
you are not

771
00:33:31,029 --> 00:33:29,580
evaluating

772
00:33:32,710 --> 00:33:31,039
[Music]

773
00:33:43,110 --> 00:33:32,720
the presence of sight in this other

774
00:33:49,909 --> 00:33:46,870
other animals they have

775
00:33:53,190 --> 00:33:49,919
some level of psy and also

776
00:33:55,029 --> 00:33:53,200
their ancestors also had it and

777
00:33:59,509 --> 00:33:55,039
something quite similar to

778
00:34:04,230 --> 00:34:01,430
but at least for this specific variant

779
00:34:10,950 --> 00:34:07,350
you can find out it is present in

780
00:34:14,149 --> 00:34:11,990
okay

781
00:34:16,629 --> 00:34:14,159
so and i just want to thank ramses and

782
00:34:20,149 --> 00:34:16,639
analysis for posting a couple of links

783
00:34:23,510 --> 00:34:20,159
both to your abstract and also to uh the

784
00:34:25,510 --> 00:34:23,520
wabib article um

785
00:34:27,190 --> 00:34:25,520
we do have another question

786
00:34:30,069 --> 00:34:27,200
how were your participants or samples

787
00:34:35,669 --> 00:34:32,389
could you repeat it please how were your

788
00:34:36,710 --> 00:34:35,679

participants or samples selected

789
00:34:38,869 --> 00:34:36,720
oh yeah

790
00:34:41,909 --> 00:34:38,879
uh

791
00:34:45,430 --> 00:34:44,149
the my sample consisted of

792
00:34:48,790 --> 00:34:45,440
[Music]

793
00:34:49,990 --> 00:34:48,800
the genes that were

794
00:34:51,430 --> 00:34:50,000
reported in

795
00:34:54,069 --> 00:34:51,440
this database

796
00:34:59,510 --> 00:34:56,629
it contains a genome completely

797
00:35:00,390 --> 00:34:59,520
sequenced genomes from

798
00:35:02,870 --> 00:35:00,400
many

799
00:35:10,870 --> 00:35:02,880
organisms not not only

800
00:35:18,790 --> 00:35:14,829
organisms from or all kingdoms right

801
00:35:20,790 --> 00:35:18,800
and this is what i took to be my

802
00:35:24,230 --> 00:35:20,800
sample

803
00:35:25,829 --> 00:35:24,240
given the sequence of the human

804
00:35:27,910 --> 00:35:25,839
protein

805
00:35:32,069 --> 00:35:27,920
this is search against all of these

806
00:35:37,910 --> 00:35:35,030
in order to detect if it is present in

807
00:35:38,630 --> 00:35:37,920
these organs

808
00:35:43,109 --> 00:35:38,640
i

809
00:35:45,670 --> 00:35:43,119
the sample of people that

810
00:35:48,630 --> 00:35:45,680
was used to detect this specifically

811
00:35:53,910 --> 00:35:50,710
was selected by helen

812
00:36:04,870 --> 00:35:54,710
i

813
00:36:07,990 --> 00:36:06,150

so

814
00:36:09,270 --> 00:36:08,000
well i only

815
00:36:11,109 --> 00:36:09,280
consider

816
00:36:12,790 --> 00:36:11,119
genomes

817
00:36:14,230 --> 00:36:12,800
gene sequences

818
00:36:15,030 --> 00:36:14,240
okay

819
00:36:16,390 --> 00:36:15,040
all right well here here's an

820
00:36:17,829 --> 00:36:16,400
interesting actually two related

821
00:36:19,910 --> 00:36:17,839
questions um

822
00:36:22,710 --> 00:36:19,920
how did you learn about hawaiian wabe's

823
00:36:24,069 --> 00:36:22,720
article and what inspired you

824
00:36:26,390 --> 00:36:24,079
oh

825
00:36:28,310 --> 00:36:26,400
yeah well

826
00:36:30,230 --> 00:36:28,320
uh i do not want

827
00:36:32,069 --> 00:36:30,240
to spoil you guys because this is

828
00:36:34,470 --> 00:36:32,079
something that i will mention

829
00:36:37,589 --> 00:36:34,480
my talk of tomorrow about uh

830
00:36:41,109 --> 00:36:37,599
did i learn about this

831
00:36:44,550 --> 00:36:41,119
i was interested in this because

832
00:36:47,190 --> 00:36:44,560
as an evolutionary biologist i

833
00:36:49,990 --> 00:36:47,200
this is something that i do i

834
00:36:52,150 --> 00:36:50,000
i'm not an experimental biologist not

835
00:36:55,430 --> 00:36:52,160
also a field biologist but i'm

836
00:36:56,870 --> 00:36:55,440
a informed information

837
00:36:58,870 --> 00:36:56,880
so it's

838
00:37:01,430 --> 00:36:58,880

in my master

839
00:37:02,630 --> 00:37:01,440
and my phd is

840
00:37:04,069 --> 00:37:02,640
what i'm used to

841
00:37:07,030 --> 00:37:04,079
so

842
00:37:10,390 --> 00:37:08,870
i uh

843
00:37:11,589 --> 00:37:10,400
around

844
00:37:14,630 --> 00:37:11,599
a year ago

845
00:37:17,510 --> 00:37:14,640
i think perhaps a year and a half in the

846
00:37:20,470 --> 00:37:17,520
website of the institute of sciences i

847
00:37:21,589 --> 00:37:20,480
found a pro this project the genetics of

848
00:37:22,950 --> 00:37:21,599
psychic

849
00:37:24,150 --> 00:37:22,960
abilities

850
00:37:27,510 --> 00:37:24,160
and

851
00:37:29,620 --> 00:37:27,520
i also found that a

852
00:37:31,030 --> 00:37:29,630
consultant on this project was a

853
00:37:32,390 --> 00:37:31,040
[Music]

854
00:37:35,589 --> 00:37:32,400
very famous

855
00:37:36,870 --> 00:37:35,599
geneticist dr gary nolan from stanford

856
00:37:39,910 --> 00:37:36,880
university

857
00:37:43,670 --> 00:37:39,920
and so i began to follow this

858
00:37:43,680 --> 00:37:45,990
well

859
00:37:51,589 --> 00:37:47,589
i think in

860
00:37:54,790 --> 00:37:51,599
the 2019 meeting within writing shows

861
00:37:58,310 --> 00:37:54,800
some preliminary results of this project

862
00:38:00,710 --> 00:37:59,349
when i

863
00:38:02,630 --> 00:38:00,720

read a

864
00:38:03,670 --> 00:38:02,640
paper

865
00:38:05,109 --> 00:38:03,680
what

866
00:38:08,950 --> 00:38:05,119
came to my mind

867
00:38:12,550 --> 00:38:10,870
but we have finally a

868
00:38:13,510 --> 00:38:12,560
gene which

869
00:38:15,829 --> 00:38:13,520
has

870
00:38:17,829 --> 00:38:15,839
with reported sequences a reported

871
00:38:20,150 --> 00:38:17,839
sequence

872
00:38:23,510 --> 00:38:20,160
can be analyzed through this kind of

873
00:38:23,520 --> 00:38:27,990
i decided to

874
00:38:30,710 --> 00:38:29,349
it would be a

875
00:38:32,790 --> 00:38:30,720
some

876
00:38:33,990 --> 00:38:32,800
kind of easy task

877
00:38:35,910 --> 00:38:34,000
so i

878
00:38:38,230 --> 00:38:35,920
took the this sequence from the

879
00:38:40,150 --> 00:38:38,240
[Music]

880
00:38:43,030 --> 00:38:40,160
that they reported and i began to

881
00:38:44,069 --> 00:38:43,040
perform different uh analysis

882
00:38:46,870 --> 00:38:44,079
and

883
00:38:49,109 --> 00:38:46,880
i finally came to what i will show you

884
00:38:50,470 --> 00:38:49,119
here

885
00:38:51,670 --> 00:38:50,480
okay

886
00:38:54,390 --> 00:38:51,680
so uh do you have any plans for

887
00:38:54,400 --> 00:38:57,750
yeah they are definitely

888
00:39:07,589 --> 00:38:59,030

i

889
00:39:10,150 --> 00:39:07,599
reconstruct the phylogeny or the

890
00:39:11,750 --> 00:39:10,160
evolutionary history of

891
00:39:14,150 --> 00:39:11,760
this gene

892
00:39:16,310 --> 00:39:14,160
but it's

893
00:39:24,230 --> 00:39:16,320
i

894
00:39:25,910 --> 00:39:24,240
but

895
00:39:27,109 --> 00:39:25,920
i need

896
00:39:30,390 --> 00:39:27,119
perhaps

897
00:39:32,310 --> 00:39:30,400
hundreds or thousands of sequences

898
00:39:35,109 --> 00:39:32,320
uh

899
00:39:40,230 --> 00:39:38,230
want to have a more robust analysis and

900
00:39:43,430 --> 00:39:40,240
uh

901
00:39:46,390 --> 00:39:43,440
i have looked in the literature and

902
00:39:48,470 --> 00:39:46,400
specifically for this gender as

903
00:39:51,160 --> 00:39:48,480
i have not found any

904
00:39:52,470 --> 00:39:51,170
revolutionary analysis

905
00:39:54,550 --> 00:39:52,480
[Music]

906
00:39:57,510 --> 00:39:54,560
let alone

907
00:39:58,870 --> 00:39:57,520
the phylogeny of this specific gene so i

908
00:40:01,270 --> 00:39:58,880
think

909
00:40:01,280 --> 00:40:05,349
i can publish if i

910
00:40:11,030 --> 00:40:08,069
reconstruct this phylogeny i think it

911
00:40:12,309 --> 00:40:11,040
can be published okay

912
00:40:14,470 --> 00:40:12,319
all right do we have any other questions

913
00:40:18,309 --> 00:40:14,480

anyone else

914
00:40:23,030 --> 00:40:19,829
what are the next steps for this line of

915
00:40:27,829 --> 00:40:24,870
what's your next step

916
00:40:29,430 --> 00:40:27,839
my my next step for using search

917
00:40:31,990 --> 00:40:29,440
for the line for this particular line of

918
00:40:36,309 --> 00:40:32,000
research for the results

919
00:40:41,750 --> 00:40:38,390
this was a very

920
00:40:46,790 --> 00:40:43,349
what i

921
00:40:50,309 --> 00:40:46,800
would need to do is to

922
00:40:54,230 --> 00:40:51,829
my sample

923
00:40:57,510 --> 00:40:56,150
because in this specific database there

924
00:40:59,829 --> 00:40:57,520
are

925
00:41:01,910 --> 00:40:59,839
i think around a thousand

926
00:41:04,230 --> 00:41:01,920
genomes

927
00:41:08,470 --> 00:41:04,240
i will need to

928
00:41:10,870 --> 00:41:08,480
if we look at the for example the

929
00:41:13,990 --> 00:41:10,880
ncbi database

930
00:41:16,390 --> 00:41:14,000
to which the pubmed resource belongs we

931
00:41:21,349 --> 00:41:18,150
tens of thousands of

932
00:41:23,829 --> 00:41:21,359
genomes so

933
00:41:25,829 --> 00:41:23,839
that would be a first step

934
00:41:28,230 --> 00:41:25,839
look in the

935
00:41:32,069 --> 00:41:28,240
tiger quantity of genomes that are

936
00:41:33,270 --> 00:41:32,079
available publicly publicly available

937
00:41:36,550 --> 00:41:33,280
and

938
00:41:41,589 --> 00:41:38,470

i think different

939
00:41:43,030 --> 00:41:41,599
structural analysis

940
00:41:46,470 --> 00:41:43,040
with

941
00:41:50,309 --> 00:41:46,480
more robust algorithms

942
00:41:52,790 --> 00:41:50,319
that uh can

943
00:41:55,750 --> 00:41:52,800
tell us more about the specific

944
00:42:01,430 --> 00:41:57,910
structure of this protein

945
00:42:01,440 --> 00:42:04,950
i i don't know

946
00:42:04,960 --> 00:42:09,030
i look but i

947
00:42:14,710 --> 00:42:11,270
what i have in mind is the

948
00:42:16,630 --> 00:42:14,720
evolutionary history of these genetics

949
00:42:18,069 --> 00:42:16,640
i think it's the that would be the next

950
00:42:21,829 --> 00:42:18,079
step

951
00:42:23,510 --> 00:42:21,839
and it will take a little while

952
00:42:24,470 --> 00:42:23,520
okay we only have a minute or two here

953
00:42:26,470 --> 00:42:24,480
um

954
00:42:28,150 --> 00:42:26,480
so a couple of quick questions first uh

955
00:42:31,750 --> 00:42:28,160
do you know if a gene for creativity has

956
00:42:34,150 --> 00:42:33,190
did you know

957
00:42:35,030 --> 00:42:34,160
that

958
00:42:39,109 --> 00:42:35,040
yeah

959
00:42:41,990 --> 00:42:40,470
is that a question

960
00:42:43,510 --> 00:42:42,000
that's a question yeah the question is

961
00:42:46,630 --> 00:42:43,520
whether you know whether or not a gene

962
00:42:47,750 --> 00:42:46,640
for creativity oh okay okay okay yeah

963
00:42:50,390 --> 00:42:47,760

uh

964
00:42:53,349 --> 00:42:52,069
i think there are

965
00:42:56,069 --> 00:42:53,359
there are

966
00:42:59,030 --> 00:42:56,079
some studies that

967
00:43:00,630 --> 00:42:59,040
for example are

968
00:43:03,589 --> 00:43:00,640
i remember one that

969
00:43:05,670 --> 00:43:03,599
has to do with a musical ability with

970
00:43:06,170 --> 00:43:05,680
relative musical ability

971
00:43:08,309 --> 00:43:06,180
and

972
00:43:09,750 --> 00:43:08,319
[Music]

973
00:43:10,790 --> 00:43:09,760
they found a

974
00:43:13,109 --> 00:43:10,800
uh

975
00:43:15,270 --> 00:43:13,119
i don't remember if it was a single gene

976
00:43:16,880 --> 00:43:15,280
or a

977
00:43:18,710 --> 00:43:16,890
couple of jeans there

978
00:43:19,990 --> 00:43:18,720
[Music]

979
00:43:23,349 --> 00:43:20,000
but

980
00:43:27,670 --> 00:43:25,829
talk about a more wider picture

981
00:43:29,829 --> 00:43:27,680
involving

982
00:43:32,950 --> 00:43:29,839
for example genius or

983
00:43:39,349 --> 00:43:36,870
i i do not know if there is some gene

984
00:43:41,829 --> 00:43:39,359
related to that there is

985
00:43:43,670 --> 00:43:41,839
for example this gene that

986
00:43:45,270 --> 00:43:43,680
has to do with

987
00:43:47,349 --> 00:43:45,280
religious

988
00:43:49,829 --> 00:43:47,359

experiences that

989
00:43:58,870 --> 00:43:49,839
i i don't know i don't remember the name

990
00:44:03,510 --> 00:44:00,230
all right if you can answer this uh

991
00:44:05,829 --> 00:44:03,520
relatively quickly uh if psy comes in on

992
00:44:08,710 --> 00:44:05,839
different perceptual channels you know

993
00:44:15,910 --> 00:44:08,720
visual auditory so on wouldn't there

994
00:44:21,109 --> 00:44:18,630
this is a complicated one because

995
00:44:24,550 --> 00:44:21,119
it's part of the

996
00:44:27,990 --> 00:44:25,910
tomorrow but

997
00:44:29,910 --> 00:44:28,000
uh

998
00:44:31,430 --> 00:44:29,920
so then we have people tune in tomorrow

999
00:44:33,349 --> 00:44:31,440
they can they can watch your session

1000
00:44:35,589 --> 00:44:33,359
tomorrow and and uh for the answer to

1001
00:44:41,030 --> 00:44:35,599
that

1002
00:44:44,470 --> 00:44:42,069
well

1003
00:44:45,829 --> 00:44:44,480
we so far we do not know

1004
00:44:48,470 --> 00:44:45,839
where does this

1005
00:44:51,030 --> 00:44:48,480
gene express well we know

1006
00:44:52,790 --> 00:44:51,040
it expressing some

1007
00:44:55,589 --> 00:44:52,800
specific brain gradients

1008
00:44:58,950 --> 00:44:56,710
we don't know

1009
00:45:00,550 --> 00:44:58,960
what uh

1010
00:45:04,950 --> 00:45:00,560
this

1011
00:45:05,990 --> 00:45:04,960
what the protein is doing perhaps it is

1012
00:45:07,430 --> 00:45:06,000
involving

1013
00:45:10,550 --> 00:45:07,440

making more

1014
00:45:11,510 --> 00:45:10,560
neuronal connections or

1015
00:45:12,710 --> 00:45:11,520
new

1016
00:45:20,950 --> 00:45:12,720
specific

1017
00:45:20,960 --> 00:45:31,030
[Music]

1018
00:45:37,750 --> 00:45:33,030
resulting phenotype

1019
00:45:41,109 --> 00:45:38,870
all right well thank you for your time

1020
00:45:43,190 --> 00:45:41,119
thank you for your presentation alex

1021
00:45:44,710 --> 00:45:43,200
um i just wanted to

1022
00:45:46,950 --> 00:45:44,720
yeah i just want to let first of all i

1023
00:45:49,270 --> 00:45:46,960
gotta say i got to ask you um

1024
00:45:51,910 --> 00:45:49,280
your funko pop figures in the back you

1025
00:45:53,349 --> 00:45:51,920
collect particular characters

1026
00:45:57,109 --> 00:45:53,359
yeah

1027
00:46:01,750 --> 00:45:58,829
the ones in

1028
00:46:05,829 --> 00:46:01,760
this this part are from

1029
00:46:10,790 --> 00:46:09,430
and the ones that are above me are from

1030
00:46:16,150 --> 00:46:10,800
the boys

1031
00:46:18,630 --> 00:46:16,160
all right just had to ask i've got my