
AB
GRAD
CON23

1
00:00:14,089 --> 00:00:10,870
[Music]

2
00:00:15,530 --> 00:00:14,099
I'm gonna call back a little bit to a

3
00:00:18,230 --> 00:00:15,540
couple of the sites that Emily mentioned

4
00:00:19,609 --> 00:00:18,240
before and uh what's exciting for me is

5
00:00:21,590 --> 00:00:19,619
that I'm in San Diego for the first time

6
00:00:23,150 --> 00:00:21,600
so I finally might be able to go see one

7
00:00:24,650 --> 00:00:23,160
of the field sites I'm about to talk

8
00:00:27,349 --> 00:00:24,660
about and I had no idea that there were

9
00:00:29,630 --> 00:00:27,359
actually palm trees down here around my

10
00:00:33,049 --> 00:00:29,640
supposedly extreme field site so that'll

11
00:00:34,250 --> 00:00:33,059
be a a funny dichotomy there but um so

12
00:00:36,650 --> 00:00:34,260
yeah we're gonna be following the salt

13
00:00:39,530 --> 00:00:36,660

uh uh and it's going to be a lot of salt

14
00:00:41,690 --> 00:00:39,540
so uh uh hang tight there

15
00:00:44,150 --> 00:00:41,700
so the first field site South Bay

16
00:00:47,750 --> 00:00:44,160
saltworks which is down the road

17
00:00:50,569 --> 00:00:47,760
um is a salt Farm which as water is

18
00:00:51,770 --> 00:00:50,579
taken from the bay it is uh brought in

19
00:00:53,750 --> 00:00:51,780
and

20
00:00:56,510 --> 00:00:53,760
um the the people there are are

21
00:00:58,610 --> 00:00:56,520
basically taking the the hay light out

22
00:01:00,350 --> 00:00:58,620
and using that to I believe soften the

23
00:01:02,630 --> 00:01:00,360
water here and then the magnesium

24
00:01:04,910 --> 00:01:02,640
chloride also gets concentrated and and

25
00:01:07,370 --> 00:01:04,920
separated and so you get these

26
00:01:09,890 --> 00:01:07,380
um these really sodium chloride

27
00:01:11,390 --> 00:01:09,900
concentrated uh regions and magnesium

28
00:01:13,429 --> 00:01:11,400
concentrated magnesium chloride

29
00:01:15,950 --> 00:01:13,439
concentrated regions and then you also

30
00:01:18,289 --> 00:01:15,960
have uh regions which are a lot more

31
00:01:19,910 --> 00:01:18,299
like seawater and so

32
00:01:21,350 --> 00:01:19,920
um that's South Bay salt works that's

33
00:01:23,390 --> 00:01:21,360
one of the sites I'll be talking about a

34
00:01:24,289 --> 00:01:23,400
lot today and what we're investigating

35
00:01:26,570 --> 00:01:24,299
there

36
00:01:28,850 --> 00:01:26,580
um with oceans across space and time uh

37
00:01:31,370 --> 00:01:28,860
is can bioseignature molecules be

38
00:01:34,249 --> 00:01:31,380

detected in these sites um with these

39
00:01:36,230 --> 00:01:34,259
super high salinities and uh then how

40
00:01:38,630 --> 00:01:36,240
does that input impact our search for

41
00:01:41,690 --> 00:01:38,640
life elsewhere and

42
00:01:43,010 --> 00:01:41,700
um then how do these vary with things

43
00:01:44,390 --> 00:01:43,020
like water activity and ion

44
00:01:46,550 --> 00:01:44,400
concentration

45
00:01:48,109 --> 00:01:46,560
and then here's another analog site in

46
00:01:49,550 --> 00:01:48,119
Western Australia this is Lake Campion

47
00:01:50,749 --> 00:01:49,560
which is a very interesting site that we

48
00:01:52,910 --> 00:01:50,759
looked at

49
00:01:56,330 --> 00:01:52,920
um and uh so these are transient lakes

50
00:01:58,249 --> 00:01:56,340
and so uh they um they evaporate during

51
00:02:00,230 --> 00:01:58,259
the drier warmer months and then they

52
00:02:02,030 --> 00:02:00,240
fill up during the winter months and so

53
00:02:04,969 --> 00:02:02,040
you get these salt crusts which build up

54
00:02:07,010 --> 00:02:04,979
on the bottom of them and so uh these

55
00:02:08,870 --> 00:02:07,020
are really interesting because uh the

56
00:02:10,309 --> 00:02:08,880
the evaporation process is happening

57
00:02:11,270 --> 00:02:10,319
very actively so we can get a modern

58
00:02:13,550 --> 00:02:11,280
look

59
00:02:14,990 --> 00:02:13,560
um at what's happening there and so in

60
00:02:16,910 --> 00:02:15,000
general analog sites can give us

61
00:02:19,070 --> 00:02:16,920
training grounds for robotic exploration

62
00:02:21,650 --> 00:02:19,080
on other planets they can help us test

63
00:02:25,369 --> 00:02:21,660

our instruments and uh particularly we

64
00:02:29,270 --> 00:02:25,379
want to know how salt and acid acidic uh

65
00:02:31,490 --> 00:02:29,280
um low PH environments affect our uh our

66
00:02:33,530 --> 00:02:31,500
instruments and then it can give us

67
00:02:35,690 --> 00:02:33,540
insight into the environmental processes

68
00:02:39,290 --> 00:02:35,700
and the biology happening there

69
00:02:41,509 --> 00:02:39,300
and so uh now I'm gonna uh shout out uh

70
00:02:42,949 --> 00:02:41,519
Luke Fisher's review paper in

71
00:02:44,449 --> 00:02:42,959
environmental microbiology where he

72
00:02:46,790 --> 00:02:44,459
talks all about the bioseignature

73
00:02:48,830 --> 00:02:46,800
preservation uh in Brian's particularly

74
00:02:51,050 --> 00:02:48,840
in deep hyper saline anoxic basins which

75
00:02:52,790 --> 00:02:51,060
I won't be talking about today but when

76
00:02:55,190 --> 00:02:52,800
it comes to brines themselves as opposed

77
00:02:57,890 --> 00:02:55,200
to evaporates or salt crystals

78
00:03:00,530 --> 00:02:57,900
um we know that DNA and RNA are well

79
00:03:03,470 --> 00:03:00,540
preserved while mRNA is not as well

80
00:03:05,869 --> 00:03:03,480
preserved and that ATP preservation has

81
00:03:10,009 --> 00:03:05,879
been observed by uh to ovala at all in

82
00:03:12,770 --> 00:03:10,019
1987 but not much has been done about

83
00:03:15,170 --> 00:03:12,780
that since then and lipid preservation

84
00:03:17,149 --> 00:03:15,180
is being studied more and more recently

85
00:03:19,130 --> 00:03:17,159
and so that's good but but these aren't

86
00:03:19,729 --> 00:03:19,140
nearly as well explored

87
00:03:23,570 --> 00:03:19,739
um

88
00:03:24,890 --> 00:03:23,580

as genetic uh compounds and so uh one

89
00:03:26,809 --> 00:03:24,900
compound that we're looking at ATP

90
00:03:29,210 --> 00:03:26,819
adenosine triphosphate it's a

91
00:03:32,270 --> 00:03:29,220
short-lived molecule and it's used

92
00:03:34,490 --> 00:03:32,280
um in astrobiology and in ecology as a

93
00:03:36,410 --> 00:03:34,500
marker of microbial activity and so if

94
00:03:37,790 --> 00:03:36,420
you have a lot of ATP means that a lot

95
00:03:39,830 --> 00:03:37,800
of microbial activity is happening if

96
00:03:41,210 --> 00:03:39,840
you don't have any microbial activity

97
00:03:44,330 --> 00:03:41,220
then you're probably not going to have

98
00:03:47,330 --> 00:03:44,340
much ATP but it's very highly evolved so

99
00:03:49,369 --> 00:03:47,340
as a biosignature it might be less

100
00:03:51,530 --> 00:03:49,379
agnostic than for example amino acids

101
00:03:54,050 --> 00:03:51,540
and so we could look at polypeptides or

102
00:03:56,930 --> 00:03:54,060
we could look at individual amino acids

103
00:03:59,270 --> 00:03:56,940
and we target biological amino acids in

104
00:04:02,030 --> 00:03:59,280
this study as well as osmolite amino

105
00:04:03,890 --> 00:04:02,040
acids which are solute compounds that

106
00:04:09,110 --> 00:04:03,900
are accumulated by microbes when they're

107
00:04:10,970 --> 00:04:09,120
under high stress in hyper saline sites

108
00:04:13,550 --> 00:04:10,980
so and that's well understood in the

109
00:04:15,649 --> 00:04:13,560
literature that these osmolites exist

110
00:04:17,810 --> 00:04:15,659
and so first I'll talk about the methods

111
00:04:19,849 --> 00:04:17,820
that we used in in the field

112
00:04:22,850 --> 00:04:19,859
um or near the field in the motel room

113
00:04:24,590 --> 00:04:22,860

we looked for ATP using a luciferase

114
00:04:25,629 --> 00:04:24,600
assay and so say you have a beautiful

115
00:04:28,490 --> 00:04:25,639
Crystal

116
00:04:30,290 --> 00:04:28,500
from the crust of a lake like this from

117
00:04:32,510 --> 00:04:30,300
Western Australia then you take it to

118
00:04:35,450 --> 00:04:32,520
your Western Australia motel room and

119
00:04:38,030 --> 00:04:35,460
you do a uh you set out your samples we

120
00:04:41,510 --> 00:04:38,040
weigh them out we extract them in hot

121
00:04:43,670 --> 00:04:41,520
water and then we add our luciferase and

122
00:04:46,790 --> 00:04:43,680
luciferin and we have a field portable

123
00:04:50,510 --> 00:04:46,800
luminometer in order to do our analyzes

124
00:04:52,730 --> 00:04:50,520
and so that's how we uh quantify ATP

125
00:04:55,189 --> 00:04:52,740
and moving on to what we do at Georgia

126
00:04:57,590 --> 00:04:55,199
Tech when we bring the samples home so

127
00:04:59,270 --> 00:04:57,600
uh I was so glad to hear that uh another

128
00:05:00,710 --> 00:04:59,280
uh person here was using capillary

129
00:05:03,110 --> 00:05:00,720
electrophoresis so I don't need to

130
00:05:05,090 --> 00:05:03,120
explain it in its entirety again but um

131
00:05:06,409 --> 00:05:05,100
it's a separation method that uh in our

132
00:05:08,390 --> 00:05:06,419
lab we pair with laser-induced

133
00:05:10,010 --> 00:05:08,400
fluorescence and so laser-induced

134
00:05:12,350 --> 00:05:10,020
fluorescence mean means that we're

135
00:05:15,110 --> 00:05:12,360
tagging our amino acids our compounds of

136
00:05:17,570 --> 00:05:15,120
Interest with a fluorescent dye so we're

137
00:05:19,730 --> 00:05:17,580
targeting specific compounds

138
00:05:21,230 --> 00:05:19,740

um and so this is a targeted technique

139
00:05:24,529 --> 00:05:21,240
which has very low limits of detection

140
00:05:27,770 --> 00:05:24,539
and very high sensitivity and so

141
00:05:29,150 --> 00:05:27,780
um we did this at South Bay saltworks on

142
00:05:31,969 --> 00:05:29,160
one of the samples that has a water

143
00:05:34,070 --> 00:05:31,979
activity of below 0.4 and magnesium

144
00:05:36,469 --> 00:05:34,080
concentration of more than four molar

145
00:05:39,170 --> 00:05:36,479
and uh this is only a one to ten

146
00:05:42,590 --> 00:05:39,180
dilution so using a method that

147
00:05:45,890 --> 00:05:42,600
um Marshall Seton and I developed uh we

148
00:05:48,529 --> 00:05:45,900
got the concentration of amino acids in

149
00:05:50,510 --> 00:05:48,539
this sample down to tens of nanomolar

150
00:05:52,430 --> 00:05:50,520
the limits of detection for this method

151
00:05:54,409 --> 00:05:52,440
General are in the tense of picomolar

152
00:05:55,670 --> 00:05:54,419
and we did this using a commercial

153
00:05:56,270 --> 00:05:55,680
instrument

154
00:05:57,950 --> 00:05:56,280
um

155
00:06:00,650 --> 00:05:57,960
and again it was only a one to ten

156
00:06:02,629 --> 00:06:00,660
dilution for this uh hyper saline uh

157
00:06:04,730 --> 00:06:02,639
sample so we were delighted that uh the

158
00:06:07,430 --> 00:06:04,740
results came out like this and then for

159
00:06:09,710 --> 00:06:07,440
an untargeted analysis we can use uh

160
00:06:11,629 --> 00:06:09,720
microchip capillary electrophoresis

161
00:06:14,629 --> 00:06:11,639
paired with uh high resolution Mass

162
00:06:16,249 --> 00:06:14,639
spectrometry so if we take the same

163
00:06:18,350 --> 00:06:16,259

sample and we look at it using an

164
00:06:21,409 --> 00:06:18,360
untargeted method where we can get the

165
00:06:23,809 --> 00:06:21,419
master charge ratio of the compounds

166
00:06:25,550 --> 00:06:23,819
that we're interested in then uh

167
00:06:29,270 --> 00:06:25,560
combining the zip chip commercial setup

168
00:06:30,650 --> 00:06:29,280
with a thermocute exactive orbitrap we

169
00:06:34,550 --> 00:06:30,660
this is what the chip looks like it's

170
00:06:36,950 --> 00:06:34,560
very cute uh we get a very interesting

171
00:06:40,129 --> 00:06:36,960
set of compounds which we didn't

172
00:06:43,129 --> 00:06:40,139
necessarily Target and so

173
00:06:45,830 --> 00:06:43,139
uh moving back to the LIF analyzes for

174
00:06:47,510 --> 00:06:45,840
the results what we first observed was

175
00:06:49,550 --> 00:06:47,520
that as we increase in magnesium

176
00:06:51,770 --> 00:06:49,560
concentration and decrease in water

177
00:06:54,950 --> 00:06:51,780
activity and increase in chaotropicity

178
00:06:57,469 --> 00:06:54,960
we get a significant increase in the

179
00:06:59,749 --> 00:06:57,479
dissolved free primary amines that we

180
00:07:01,249 --> 00:06:59,759
were targeting and so that would be our

181
00:07:04,129 --> 00:07:01,259
biological amino acids which you've

182
00:07:05,990 --> 00:07:04,139
identified here and as you go up you

183
00:07:08,330 --> 00:07:06,000
have higher magnesium sites and we have

184
00:07:10,129 --> 00:07:08,340
a lot higher Peaks and we also have a

185
00:07:13,550 --> 00:07:10,139
lot higher values for Quantified amino

186
00:07:16,249 --> 00:07:13,560
acids and so we attribute this to evapo

187
00:07:17,510 --> 00:07:16,259
concentration as the sites which have a

188
00:07:19,070 --> 00:07:17,520

lot of water and a lot of salt and then

189
00:07:20,870 --> 00:07:19,080
evaporate and leave the salts and the

190
00:07:23,089 --> 00:07:20,880
Organics behind the concentration is

191
00:07:25,490 --> 00:07:23,099
higher so that's pretty straightforward

192
00:07:27,650 --> 00:07:25,500
and simple but it is very useful in the

193
00:07:30,170 --> 00:07:27,660
case where we're looking at very low

194
00:07:32,809 --> 00:07:30,180
biomass regions so

195
00:07:35,210 --> 00:07:32,819
uh next we then put it in micro uh micro

196
00:07:37,430 --> 00:07:35,220
microchip cems and we looked for these

197
00:07:39,529 --> 00:07:37,440
same compounds and we found a lot of

198
00:07:42,170 --> 00:07:39,539
them there and so you can see uh

199
00:07:45,350 --> 00:07:42,180
histidine Glycine alanine isoleucine and

200
00:07:47,990 --> 00:07:45,360
leucine are resolved there serine Etc et

201
00:07:49,850 --> 00:07:48,000
cetera glutamic and aspartic acid

202
00:07:51,710 --> 00:07:49,860
um and this was only a one to four

203
00:07:52,969 --> 00:07:51,720
dilution of that same sample so we were

204
00:07:55,909 --> 00:07:52,979
really delighted by these results as

205
00:07:58,010 --> 00:07:55,919
well and in the same separation just um

206
00:08:01,129 --> 00:07:58,020
looking at different traces different M

207
00:08:04,249 --> 00:08:01,139
over Z's we see a couple polypeptides

208
00:08:07,010 --> 00:08:04,259
and we see some adenine and guanidine in

209
00:08:08,809 --> 00:08:07,020
there as well and so these are things

210
00:08:10,850 --> 00:08:08,819
that we didn't necessarily look for in

211
00:08:12,890 --> 00:08:10,860
the celif but now that we're combining

212
00:08:14,089 --> 00:08:12,900
it with an untargeted method we can we

213
00:08:16,129 --> 00:08:14,099

can get a look at some more compounds

214
00:08:18,170 --> 00:08:16,139
that we didn't necessarily expect

215
00:08:20,089 --> 00:08:18,180
and then also osmolites which we did

216
00:08:21,950 --> 00:08:20,099
expect and did want to look for we found

217
00:08:25,189 --> 00:08:21,960
those like ornithine sarcosine and

218
00:08:26,749 --> 00:08:25,199
betaine in our samples with very high

219
00:08:29,089 --> 00:08:26,759
salt stress being applied to any of the

220
00:08:31,369 --> 00:08:29,099
microbes that were alive there

221
00:08:33,230 --> 00:08:31,379
um and and so these are are there in

222
00:08:35,990 --> 00:08:33,240
significant quantity

223
00:08:37,250 --> 00:08:36,000
and in Western Australia uh briefly I'll

224
00:08:39,529 --> 00:08:37,260
just show you some preliminary results

225
00:08:41,510 --> 00:08:39,539
this is Lake Brown which has a sodium

226
00:08:44,810 --> 00:08:41,520
concentration of near five molar and a

227
00:08:46,610 --> 00:08:44,820
water activity of 0.89 so not nearly

228
00:08:48,769 --> 00:08:46,620
um as low water activity as the South

229
00:08:50,090 --> 00:08:48,779
Bay saltwork sample I just showed you

230
00:08:52,250 --> 00:08:50,100
um but it has high relative

231
00:08:53,810 --> 00:08:52,260
concentrations of a lot of these uh

232
00:08:57,410 --> 00:08:53,820
compounds including the osmolite

233
00:08:58,970 --> 00:08:57,420
compound baiting and uh some lower

234
00:09:01,070 --> 00:08:58,980
concentrations of other compounds

235
00:09:03,889 --> 00:09:01,080
including a polypeptide

236
00:09:06,530 --> 00:09:03,899
and then conversely at Lake Gunter which

237
00:09:09,350 --> 00:09:06,540
has a higher water activity and a lower

238
00:09:11,389 --> 00:09:09,360

sodium concentration we see that there

239
00:09:13,430 --> 00:09:11,399
really isn't any easy way to detect

240
00:09:14,630 --> 00:09:13,440
those organic compounds with the method

241
00:09:17,030 --> 00:09:14,640
that we're using right now so just

242
00:09:19,250 --> 00:09:17,040
diluting these samples so perhaps this

243
00:09:20,389 --> 00:09:19,260
indicates that the uh and of course

244
00:09:22,430 --> 00:09:20,399
there's only two data points with

245
00:09:24,350 --> 00:09:22,440
Western Australia but you know looking

246
00:09:26,210 --> 00:09:24,360
at what we found at South Bay salt Works

247
00:09:28,370 --> 00:09:26,220
perhaps these saltier sites are actually

248
00:09:30,230 --> 00:09:28,380
places where it might be easier to

249
00:09:31,370 --> 00:09:30,240
detect biomolecules because of evapot

250
00:09:34,329 --> 00:09:31,380
concentration

251
00:09:36,590 --> 00:09:34,339
and we also want to look at the

252
00:09:38,990 --> 00:09:36,600
normalized abundance of certain amino

253
00:09:41,329 --> 00:09:39,000
acids just to see what sort of patterns

254
00:09:43,490 --> 00:09:41,339
we could find and if we have water

255
00:09:44,509 --> 00:09:43,500
activity increasing from left to right

256
00:09:48,050 --> 00:09:44,519
here

257
00:09:51,050 --> 00:09:48,060
that certain amino acids are upright

258
00:09:53,810 --> 00:09:51,060
regulated in this magnesium heavy site

259
00:09:56,509 --> 00:09:53,820
and others are down regulated

260
00:09:59,449 --> 00:09:56,519
and with that information we decided

261
00:10:02,090 --> 00:09:59,459
maybe we could classify our sites based

262
00:10:04,130 --> 00:10:02,100
on the amino acid distribution so if you

263
00:10:06,050 --> 00:10:04,140

take the distribution in you put in a

264
00:10:08,449 --> 00:10:06,060
classifier either logistic regression or

265
00:10:10,250 --> 00:10:08,459
random Forest you could get out one of

266
00:10:12,110 --> 00:10:10,260
these three different site types and

267
00:10:13,790 --> 00:10:12,120
this is a small data set and more of a

268
00:10:15,470 --> 00:10:13,800
proof of concept than anything but it's

269
00:10:17,750 --> 00:10:15,480
interesting to see that we have a very

270
00:10:20,990 --> 00:10:17,760
good area under the curve of you know 1

271
00:10:22,910 --> 00:10:21,000
or 0.83 which uh and and we also can see

272
00:10:25,550 --> 00:10:22,920
which compounds are driving that the

273
00:10:27,889 --> 00:10:25,560
most and so that's an interesting thing

274
00:10:29,690 --> 00:10:27,899
to take note of that might be used in

275
00:10:30,889 --> 00:10:29,700
the future if we have much larger data

276
00:10:32,630 --> 00:10:30,899
sets

277
00:10:36,590 --> 00:10:32,640
and so the last thing I wanted to talk

278
00:10:38,449 --> 00:10:36,600
about ATP if you remember so uh on the

279
00:10:40,490 --> 00:10:38,459
x-axis here's magnesium concentration

280
00:10:42,170 --> 00:10:40,500
and then we have three y axes because

281
00:10:44,210 --> 00:10:42,180
why not and

282
00:10:46,490 --> 00:10:44,220
um uh first of all I want to mention the

283
00:10:49,310 --> 00:10:46,500
cell counts by microscopy which is uh

284
00:10:51,710 --> 00:10:49,320
from Ben klempe uh showed that the

285
00:10:53,269 --> 00:10:51,720
number of active cells in these sites go

286
00:10:55,430 --> 00:10:53,279
down as you get to the super high

287
00:10:56,329 --> 00:10:55,440
magnesium concentration regions which is

288
00:10:58,550 --> 00:10:56,339

also

289
00:11:02,090 --> 00:10:58,560
um what Emily showed in her talk and so

290
00:11:04,550 --> 00:11:02,100
uh what we then can look at is the ATP

291
00:11:08,210 --> 00:11:04,560
concentration which strangely goes up

292
00:11:10,250 --> 00:11:08,220
even as the concentration of active

293
00:11:12,110 --> 00:11:10,260
cells goes down and the expected

294
00:11:15,050 --> 00:11:12,120
activity goes down and so we wondered

295
00:11:17,449 --> 00:11:15,060
why is that happening because

296
00:11:18,889 --> 00:11:17,459
um as we know the amino acids are

297
00:11:20,509 --> 00:11:18,899
concentrating but amino acids don't

298
00:11:22,790 --> 00:11:20,519
Decay on really short time scales

299
00:11:26,329 --> 00:11:22,800
they're not broken up by hydrolysis or

300
00:11:28,670 --> 00:11:26,339
by atpase enzymes but

301
00:11:30,470 --> 00:11:28,680
we think is that something must be

302
00:11:34,970 --> 00:11:30,480
driving this and if it's not evapo

303
00:11:36,949 --> 00:11:34,980
concentration uh well uh we're wondering

304
00:11:41,030 --> 00:11:36,959
you know since the ATP hydrolysis rate

305
00:11:43,790 --> 00:11:41,040
is uh much quicker than the evapo

306
00:11:45,350 --> 00:11:43,800
concentration rate uh why would the ATP

307
00:11:47,210 --> 00:11:45,360
accumulate doesn't really make much

308
00:11:49,850 --> 00:11:47,220
sense but perhaps

309
00:11:51,829 --> 00:11:49,860
it's being preserved so this to ovala at

310
00:11:54,769 --> 00:11:51,839
all paper from 1987 that I mentioned way

311
00:11:57,949 --> 00:11:54,779
earlier uh they found that ATP was

312
00:12:00,350 --> 00:11:57,959
preserved in low water activity sites

313
00:12:02,930 --> 00:12:00,360

and so that could be preventing the

314
00:12:05,630 --> 00:12:02,940
enzymatic uh and natural hydrolysis of

315
00:12:08,930 --> 00:12:05,640
ATP leaving it to uh persist in the

316
00:12:10,730 --> 00:12:08,940
solution and additionally it could also

317
00:12:12,889 --> 00:12:10,740
be used as an osmolite compound as well

318
00:12:15,290 --> 00:12:12,899
and be accumulated by those

319
00:12:18,170 --> 00:12:15,300
microorganisms before they end up in a

320
00:12:19,910 --> 00:12:18,180
super high magnesium site and not very

321
00:12:22,850 --> 00:12:19,920
active themselves

322
00:12:25,850 --> 00:12:22,860
so in conclusion we can detect

323
00:12:28,130 --> 00:12:25,860
biosignatures at micromolar

324
00:12:31,730 --> 00:12:28,140
concentrations in near saturation brines

325
00:12:34,190 --> 00:12:31,740
using celaf and microce Ms

326
00:12:35,930 --> 00:12:34,200
and amino acid distribution ratios can

327
00:12:37,069 --> 00:12:35,940
be well classified based on their brine

328
00:12:39,590 --> 00:12:37,079
type

329
00:12:41,389 --> 00:12:39,600
and osmolites are present and detectable

330
00:12:43,730 --> 00:12:41,399
in some but not all of the South Bay

331
00:12:45,889 --> 00:12:43,740
saltworks in Western Australia Brines

332
00:12:48,550 --> 00:12:45,899
and we found preservation of ATP at

333
00:12:51,290 --> 00:12:48,560
Southbay SolidWorks and so

334
00:12:53,090 --> 00:12:51,300
basically my argument is then why don't

335
00:12:54,829 --> 00:12:53,100
we follow the salt and see if we can

336
00:12:59,990 --> 00:12:54,839
find biosignatures there on other worlds

337
00:13:00,000 --> 00:13:03,670
foreign

338
00:13:03,680 --> 00:13:16,870

we have time for two questions

339
00:13:21,769 --> 00:13:19,430
Chad thank you for the talk um that was

340
00:13:23,569 --> 00:13:21,779
a beautiful separation that you showed

341
00:13:26,449 --> 00:13:23,579
uh showed earlier

342
00:13:30,170 --> 00:13:26,459
um so I'm I'm curious uh you did a

343
00:13:33,050 --> 00:13:30,180
connotation of amino acids using celf

344
00:13:38,110 --> 00:13:33,060
method and it looks like you've done

345
00:13:42,530 --> 00:13:38,120
some work using cems have you tried uh

346
00:13:45,769 --> 00:13:42,540
quantifying the amino acid content in

347
00:13:47,629 --> 00:13:45,779
the same sites using microchip cems and

348
00:13:49,550 --> 00:13:47,639
seeing what those look like to try and

349
00:13:50,930 --> 00:13:49,560
like cross validate both methods and the

350
00:13:53,030 --> 00:13:50,940
using the same sample yet or have you

351
00:13:55,730 --> 00:13:53,040
not got to that yet nope so we just

352
00:13:58,310 --> 00:13:55,740
started doing the micro CMS work over

353
00:14:00,410 --> 00:13:58,320
the past month and so we're really happy

354
00:14:02,509 --> 00:14:00,420
how it's been doing with qualitative

355
00:14:04,430 --> 00:14:02,519
untargeted work but we haven't gone into

356
00:14:05,470 --> 00:14:04,440
quantitative because the ion suppression

357
00:14:08,210 --> 00:14:05,480
effects

358
00:14:09,710 --> 00:14:08,220
might be a bit of a challenge to

359
00:14:11,329 --> 00:14:09,720
overcome so that'll probably be a little

360
00:14:12,949 --> 00:14:11,339
bit of a longer project what we have

361
00:14:16,069 --> 00:14:12,959
done to try to corroborate the amino

362
00:14:18,410 --> 00:14:16,079
acid concentrations is look at the

363
00:14:20,629 --> 00:14:18,420

expression of um or not the expression

364
00:14:21,730 --> 00:14:20,639
rather but the presence of certain

365
00:14:25,910 --> 00:14:21,740
proteins

366
00:14:28,190 --> 00:14:25,920
in the genetic code of the microbes that

367
00:14:32,150 --> 00:14:28,200
are were found to be present here by

368
00:14:32,750 --> 00:14:32,160
other uh host collaborators and

369
00:14:35,090 --> 00:14:32,760
um

370
00:14:36,769 --> 00:14:35,100
we find a moderate correlation between

371
00:14:39,290 --> 00:14:36,779
the amino acids we see and the amino

372
00:14:40,730 --> 00:14:39,300
acids that they see but since we don't

373
00:14:42,170 --> 00:14:40,740
have transcriptomes from all of these

374
00:14:44,210 --> 00:14:42,180
sites we don't know exactly what

375
00:14:46,550 --> 00:14:44,220
proteins are being made and so I think

376
00:14:48,650 --> 00:14:46,560
that's the next step is is to connect

377
00:14:50,509 --> 00:14:48,660
those from metabolomics to

378
00:14:53,750 --> 00:14:50,519
transcriptomics to genomics just as the

379
00:14:59,269 --> 00:14:53,760
talk last night uh was uh was discussing

380
00:14:59,279 --> 00:15:10,250
any last question for Chad

381
00:15:14,150 --> 00:15:12,050
um I have a two question actually oh

382
00:15:17,269 --> 00:15:14,160
maybe I didn't really catch you what's a

383
00:15:19,129 --> 00:15:17,279
pH of the site that you show the

384
00:15:21,230 --> 00:15:19,139
Magnesium concentration is more than

385
00:15:22,550 --> 00:15:21,240
four molar that's a great question I

386
00:15:23,810 --> 00:15:22,560
don't know off the top of my head but I

387
00:15:25,189 --> 00:15:23,820
can get back to you in a moment yeah

388
00:15:27,710 --> 00:15:25,199

okay

389
00:15:29,470 --> 00:15:27,720
um and also how would you determine your

390
00:15:32,150 --> 00:15:29,480
atp's

391
00:15:34,730 --> 00:15:32,160
accumulated or protected under high

392
00:15:37,670 --> 00:15:34,740
selling water or like a low water

393
00:15:40,610 --> 00:15:37,680
activity how did I sorry say again how

394
00:15:44,210 --> 00:15:40,620
did I how do you know that your ATP is

395
00:15:47,210 --> 00:15:44,220
not hydrolysis so yeah I don't know that

396
00:15:49,550 --> 00:15:47,220
it's not hydrolyzed necessarily but I am

397
00:15:50,870 --> 00:15:49,560
predicting that so the the typical

398
00:15:53,329 --> 00:15:50,880
destruction

399
00:15:54,590 --> 00:15:53,339
um method of ATP uh either in the cell

400
00:15:57,290 --> 00:15:54,600
or in the environment is through

401
00:15:59,230 --> 00:15:57,300
hydrolysis either performed by proteins

402
00:16:01,850 --> 00:15:59,240
or just

403
00:16:04,430 --> 00:16:01,860
happening naturally in the environment

404
00:16:07,550 --> 00:16:04,440
with water and so those are the those

405
00:16:10,129 --> 00:16:07,560
are the things that must uh from what

406
00:16:13,490 --> 00:16:10,139
I'm observing have been stopped

407
00:16:16,009 --> 00:16:13,500
if the ATP is going to persist so long

408
00:16:17,389 --> 00:16:16,019
for it to be evapo concentrated to those

409
00:16:19,790 --> 00:16:17,399
high of levels

410
00:16:22,069 --> 00:16:19,800
um the huge Spike there likely wouldn't

411
00:16:25,129 --> 00:16:22,079
have been possible if uh of Apple

412
00:16:28,250 --> 00:16:25,139
concentration weren't a component and so

413
00:16:31,250 --> 00:16:28,260

um you know unless uh the uh the

414
00:16:33,410 --> 00:16:31,260
osmolite effect is is uh so much more

415
00:16:35,210 --> 00:16:33,420
significant than I had thought

416
00:16:37,970 --> 00:16:35,220
um that could be another reason but I

417
00:16:41,269 --> 00:16:37,980
still think that uh the the preservation

418
00:16:44,629 --> 00:16:41,279
of ATP is yeah is linked to the the lack

419
00:16:47,749 --> 00:16:44,639
of a um a rapid breakdown mechanism uh

420
00:16:48,670 --> 00:16:47,759
have you ever considered that ATP with

421
00:16:51,530 --> 00:16:48,680
um

422
00:16:53,629 --> 00:16:51,540
form some nanostructures to make the

423
00:16:56,030 --> 00:16:53,639
things happen yeah so whether it

424
00:16:59,150 --> 00:16:56,040
stabilizes it in some way the yeah so

425
00:17:00,710 --> 00:16:59,160
I've I don't honestly know much about

426
00:17:02,389 --> 00:17:00,720
how it would investigate that I've

427
00:17:04,549 --> 00:17:02,399
spoken to someone recently about um

428
00:17:08,329 --> 00:17:04,559
potentially modeling it uh using

429
00:17:10,669 --> 00:17:08,339
molecular Dynamics but uh I haven't you

430
00:17:12,350 --> 00:17:10,679
know waded into the um you know the

431
00:17:14,569 --> 00:17:12,360
actual uh

432
00:17:15,770 --> 00:17:14,579
the structural chemistry of whether of

433
00:17:17,809 --> 00:17:15,780
whether that would happen but if you

434
00:17:20,210 --> 00:17:17,819
have any ideas I'd love to hear so