



# Detailed Protein Report

## Project Info

**Name:** David Leitsch\_Tricho **Date:** November 28, 2011

## Sample Info & Protocols

**Name:** Trichos\_metronidazole suseptible **Date:** November 28, 2011

## Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
HCT_NCBI_Eucaryota_PE_2011-11-28 08:27:32	/David Leitsch_Tricho/Trichos_metronidazole suseptible/DK_David_T39_BB5_01_3747.d	Mascot, 2.3.02	NCBIInr, NCBIInr_20110828.fasta	47/499

**Protein 1:** alcohol dehydrogenase 1 [Trichomonas vaginalis G3]  
**Accession:** gi|154415151 **Score:** 1794.06  
**Database:** NCBIInr **MW [kDa]:** 39.10  
**Seq. Coverage [%]:** 57.30 % **pI:** 6.15  
**No. of Peptides:** 38

**Modification(s):** Carbamidomethyl, Oxidation, Deamidated

10	20	30	40	50	60	70	80	90	100	110	120
MTFELPKTMK	AFAMRKIGEY	GWIEKPVPEC	GPNDICRPL	ALAPCTSDIH	TVWAGAIGER	HDMILGHEAV	GQVVKIGSEV	KNLKVGDKVL	VPAVTPDWGS	EAAQEGFPAH	SGGMLGGWKF
130	140	150	160	170	180	190	200	210	220	230	240
SNFKDGVFAE	YFHVNEADAN	LAKLPEGLTP	RDVIMCSDDM	TTGFHGAELA	EVLGDIVVV	IGIGPVGLMS	VRGAALMGAS	RIFAVGSRPH	CCDTAVQYGA	TDIINYKNGD	IVEQILKATG
250	260	270	280	290	300	310	320	330	340	350	360
GKGVDRVILIA	GGDVHTFAQA	IKMIRAGGVI	GNVNYLGEGE	MIDVPRVEWG	VGMGHKFIHG	GLTPGGALRM	EKMANLIKYY	KVDPTKLITH	EFKGLEKVED	ALMLMKDKPV	DLIKPVLIE
370											
YNDKL											



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Cmpd.	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
121	2	545.0000	81.24	3	40.8	107.4	0	61-75	R.HDMILGHEAVGQVVK.I	
309	3	1051.5000	-9.24	3	63.0	30.4	0	89-119	K.VLVPVTPDWGSEAAQEGFPAHS GGMLGGWK.F	Deamidated: 16
305	4	1051.6000	397.92	3	62.7	44.0	0	89-119	K.VLVPVTPDWGSEAAQEGFPAHS GGMLGGWK.F	
280	3	793.1000	273.89	4	59.2	57.4	0	89-119	K.VLVPVTPDWGSEAAQEGFPAHS GGMLGGWK.F	Oxidation: 26; Deamidated: 16
248	2	1055.9000	-84.71	2	55.3	54.6	0	125-143	K.DGVFAEYFHVNEADANLAK.L	Deamidated: 11
256	6	704.4000	101.19	3	56.5	59.6	0	125-143	K.DGVFAEYFHVNEADANLAK.L	Deamidated: 16
249	4	704.3000	425.11	3	55.7	99.9	0	125-143	K.DGVFAEYFHVNEADANLAK.L	
87	3	441.8000	100.03	2	36.2	64.2	0	144-151	K.LPEGLTPR.D	
187	2	825.8000	531.01	3	48.6	39.9	0	152-173	R.DVIMCSDMMTTGFHGAELAEVK. L	Carbamidomethyl: 5; Oxidation: 8, 9
149	2	831.0000	369.13	3	44.5	46.0	0	152-173	R.DVIMCSDMMTTGFHGAELAEVK. L	Carbamidomethyl: 5; Oxidation: 4, 8, 9
177	4	825.6000	288.69	3	47.9	53.6	0	152-173	R.DVIMCSDMMTTGFHGAELAEVK. L	Carbamidomethyl: 5; Oxidation: 4, 9
187	4	825.8000	531.01	3	48.6	58.9	0	152-173	R.DVIMCSDMMTTGFHGAELAEVK. L	Carbamidomethyl: 5; Oxidation: 4, 8
38	2	417.2000	-44.43	2	25.7	46.8	0	193-201	R.GAALMGASR.I	
17	7	425.2000	-37.62	2	17.4	55.2	0	193-201	R.GAALMGASR.I	Oxidation: 5
211	1	565.2000	-192.11	2	51.3	36.6	0	228-237	K.NGDIVEQILK.A	Deamidated: 7
215	5	565.3000	855.86	2	51.6	54.3	0	228-237	K.NGDIVEQILK.A	
244	4	565.9000	1046.15	2	54.8	57.5	0	228-237	K.NGDIVEQILK.A	Deamidated: 1
210	1	547.6000	-70.11	3	51.0	46.4	0	247-262	R.VIIAGGDVHTFAQAIK.M	Deamidated: 13
189	6	547.4000	163.73	3	49.0	130.7	0	247-262	R.VIIAGGDVHTFAQAIK.M	
255	2	1080.9000	-123.34	2	56.3	68.8	0	266-286	R.AGGVIGNVNYLGE GEMIDVPR.V	Deamidated: 9
255	2	1080.9000	-123.34	2	56.3	77.8	0	266-286	R.AGGVIGNVNYLGE GEMIDVPR.V	Deamidated: 7
228	2	1088.5000	-35.63	2	53.2	83.0	0	266-286	R.AGGVIGNVNYLGE GEMIDVPR.V	Oxidation: 16
255	2	1080.9000	331.94	2	56.3	99.7	0	266-286	R.AGGVIGNVNYLGE GEMIDVPR.V	
238	2	726.6000	-116.00	3	54.2	20.4	0	266-286	R.AGGVIGNVNYLGE GEMIDVPR.V	Oxidation: 16; Deamidated: 7, 9
238	4	726.6000	335.53	3	54.2	35.0	0	266-286	R.AGGVIGNVNYLGE GEMIDVPR.V	Oxidation: 16; Deamidated: 7
238	4	726.6000	335.53	3	54.2	39.5	0	266-286	R.AGGVIGNVNYLGE GEMIDVPR.V	Oxidation: 16; Deamidated: 9



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Cmpd.	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
59	1	558.2000	-123.16	2	30.3	31.2	0	287-296	R.VEWGVGMGHK.F	Oxidation: 7
88	1	550.6000	597.34	2	36.4	43.9	0	287-296	R.VEWGVGMGHK.F	
119	3	432.7000	280.15	3	40.4	74.3	0	297-309	K.FIHGGLTPGGALR.M	
54	4	444.2000	-119.08	2	29.2	37.8	0	327-333	K.LITHEFK.G	
150	3	533.8000	994.66	2	44.4	47.2	0	338-346	K.VEDALMLMK.D	Oxidation: 6
109	3	533.3000	57.05	2	39.2	50.0	0	338-346	K.VEDALMLMK.D	Oxidation: 8
176	1	525.3000	53.08	2	47.6	54.7	0	338-346	K.VEDALMLMK.D	
84	3	541.6000	615.16	2	36.0	59.1	0	338-346	K.VEDALMLMK.D	Oxidation: 6, 8
261	2	700.5000	621.85	3	56.9	58.8	0	347-364	K.DKPVDLIKPVVLLIEYNDK.L	
263	1	525.6000	102.14	4	57.1	35.2	0	347-364	K.DKPVDLIKPVVLLIEYNDK.L	Deamidated: 16
301	4	738.1000	17.13	3	61.6	48.9	1	347-365	K.DKPVDLIKPVVLLIEYNDK.L-	Deamidated: 16
301	4	738.1000	461.74	3	61.6	88.3	1	347-365	K.DKPVDLIKPVVLLIEYNDK.L-	

**Protein 2:** keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens]

**Accession:** gi|119581148

**Score:** 330.87

**Database:** NCBIInr

**MW [kDa]:** 57.50

**Seq. Coverage [%]:** 19.50 %

**pl:** 7.61

**No. of Peptides:** 16

**Modification(s):** Deamidated



# Detailed Protein Report

10	20	30	40	50	60	70	80	90	100	110	120	
MSCRQFSSSY	LSRSGGGGGG	GLGSGGSIRS	SYSRFSSSGG	GGGGRFSSS	SGYGGSSRV	CGRGGGSFG	YSYGGSGGG	FSASSLGGGF	GGGSRFGGA	SGGGYSSSGG	FGGGFGGGSG	
130	140	150	160	170	180	190	200	210	220	230	240	
GGFGGGYGSG	FGGFGGFGG	AGGGDGGILT	ANEKSTMQEL	NSRLASYLDK	VQALEEANN	LENKIQDWYD	KKGPAAIQKN	YSPYYNTIDD	LKDQIVDLTV	GNNRLLDID	NTRMTLDDFR	
250	260	270	280	290	300	310	320	330	340	350	360	
IKFEMEQLNR	QGVADINGL	RQVLDNLIME	KSDLEMQYET	LQEELMALKK	NHKEEMSQLT	GQNSGDVNV	INVAPGKDLT	KTLNDRQY	EQLIAKNRKD	IENQYETQIT	QIEHEVSSSG	
370	380	390	400	410	420	430	440	450	460	470	480	
QEVQSSAK	EV	TQLRHGVQEL	EIELQSQLSK	KAALKSLED	TKNRYCGQLQ	MIQEISNLE	AQITDVRQEI	ECQNQEYSL	LSIKMRLEKE	IETYHNLE	GQEDFESSGA	GKIGLGRRG
490	500	510	520	530								
SGGSYGRGIQ	GRKWRQLWWR	RKWRWLWWRK	WVQGRKWRQL	RWRKFWRR								

Cmpd.	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
40	2	616.7000	-166.24	2	25.9	72.6	0	14-29	R.SGGGGGGGLGSGGSIR.S	
26	2	618.3000	51.76	2	21.4	61.0	0	47-59	R.FSSSSGYGGGSSR.V	
39	2	533.2000	-99.96	2	25.9	50.5	0	155-163	K.STMQELNSR.L	
336	1	968.5000	31.29	3	68.3	39.2	1	200-224	K.NYSPYYNTIDDLKDQIVDLTVGN NK.T	Deamidated: 24
336	1	968.5000	31.29	3	68.3	39.2	1	200-224	K.NYSPYYNTIDDLKDQIVDLTVGN NK.T	Deamidated: 23
336	1	968.5000	31.29	3	68.3	42.8	1	200-224	K.NYSPYYNTIDDLKDQIVDLTVGN NK.T	Deamidated: 7
336	1	968.5000	31.29	3	68.3	48.3	1	200-224	K.NYSPYYNTIDDLKDQIVDLTVGN NK.T	Deamidated: 1
336	1	968.5000	370.10	3	68.3	48.5	1	200-224	K.NYSPYYNTIDDLKDQIVDLTVGN NK.T	
336	1	968.5000	31.29	3	68.3	51.5	1	200-224	K.NYSPYYNTIDDLKDQIVDLTVGN NK.T	Deamidated: 15
97	1	579.3000	1.55	2	37.8	33.7	0	251-261	R.QGVADINGLR.Q	
277	1	1089.3000	118.61	3	58.7	38.8	0	340-368	K.DIENQYETQITQIEHEVSSSGQE VQSSAK.E	Deamidated: 22



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Cmpd.	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
277	1	1089.3000	419.89	3	58.7	45.7	0	340-368	K.DIENQYETQITQIEHEVSSSGQE VQSSAK.E	
277	1	1089.3000	118.61	3	58.7	49.6	0	340-368	K.DIENQYETQITQIEHEVSSSGQE VQSSAK.E	Deamidated: 4
277	1	1089.3000	118.61	3	58.7	51.7	0	340-368	K.DIENQYETQITQIEHEVSSSGQE VQSSAK.E	Deamidated: 5
277	1	1089.3000	118.61	3	58.7	52.6	0	340-368	K.DIENQYETQITQIEHEVSSSGQE VQSSAK.E	Deamidated: 12
277	1	1089.3000	118.61	3	58.7	61.5	0	340-368	K.DIENQYETQITQIEHEVSSSGQE VQSSAK.E	Deamidated: 9

**Protein 3:** Chain E, Leech-Derived Trypsin InhibitorTRYPSIN COMPLEX

**Accession:** gi|3318722

**Score:** 107.15

**Database:** NCBIInr

**MW [kDa]:** 23.50

**Seq. Coverage [%]:** 4.50 %

**pl:** 9.53

**No. of Peptides:** 3

**Modification(s):** Deamidated

10	20	30	40	50	60	70	80	90	100	110	120
IVGGYTCAAN	SIPYQVSLNS	GSHFCGGSLI	NSQWVSAAH	CYKSRIQVRL	GEHNIDVLEG	NEQFINAAKI	ITHPNFNGNT	LDNDIMLIK	LSSPATLNSRV	ATVSLPRSCA	AAGTECLISG
130	140	150	160	170	180	190	200	210	220	230	
WGNTKSSGSS	YPSLLQCLKA	PVLSOSSCKS	SYPGQITGNM	ICVGFLEGGK	DSCQGDSSGP	VVCNGQLQGI	VSWGYGCAQK	NKPGVYTKVC	NYVNWIQQTI	AAN	

Cmpd.	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
64	1	523.6000	-338.83	2	31.2	32.2	0	90-99	K.LSSPATLNSR.V	Deamidated: 8
61	1	523.3000	944.84	2	30.8	44.0	0	90-99	K.LSSPATLISR.V	
64	4	523.6000	601.08	2	31.2	63.1	0	90-99	K.LSSPATLNSR.V	



# Detailed Protein Report

**Protein 4:** malic enzyme [Trichomonas vaginalis G3]  
**Accession:** gi|123402375 **Score:** 63.07  
**Database:** NCBIInr **MW [kDa]:** 16.80  
**Seq. Coverage [%]:** 6.90 % **pl:** 5.42  
**No. of Peptides:** 1

10	20	30	40	50	60	70	80	90	100	110	120
MAEITNSDLK	KGTLAEVIK	ADVFIGVSAP	KTLTQEMVKS	MAEKPIVFPM	ANPIPEIMPD	EAKAAGAAVV	GTGRSDFPNQ	INNVLAFFAL	FRGALDVRAS	RITNEMNIAA	ARAIASLVSD
130	140	150	160								
EELSADYILP	NPFDKRIKET	VSKAVAEAAI	KSGVARINQ								

Cmpd.	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
27	2	465.3000	82.12	2	22.4	63.1	0	64-74	K.AAGAAVVGTR.S	