

SUPPORTING INFORMATION

Human 2-Oxoglutarate Dehydrogenase Complex E1 Component Forms a Thiamin-derived Radical by Aerobic Oxidation of the Enamine Intermediate.

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SI Table S1. Peptic peptides originated from E1o-h ^a

No.	Position	Peptides Sequence	Monoisotopic Mass [M+H] ⁺ (Da)		Error (ppm)
			Experimental	Theoretical	
1	2-8	SAPVAAE	644.3248	644.3250	-0.2
2	9-17	PFLSGTSSN	909.4309	909.4312	-0.3
3	18-22	YVEEM	670.2756	670.2753	0.5
4	22-32	MYCAWLENPKS	1341.5956	1341.5966	-0.8
5	34-47	HKSWDIFFRNTNAG	1692.8260	1692.8241	1.1
6	41-65	FRNTNAGAPPGTAYQSPLPLSRGSL	2572.3259	2572.3267	-0.3
7	66-74	AAVAHAQSL	867.4678	867.4683	-0.5
8	75-84	VEAQPNVDKL	1112.5938	1112.5946	-0.7
9	85-89	VEDHL	612.2986	612.2988	-0.2
10	90-94	AVQSL	517.2980	517.2980	0.0
11	95-114	IRAYQIRGHHVAQLDPLGIL	2270.2893	2270.2880	0.6
12	115-135	DADLDSSVPADIISSTDKLGF	2166.0460	2166.0448	0.5
13	136-143	YGLDESDL	911.3996	911.3993	0.3
14	144-151	DKVFHLPT	956.5211	956.5200	1.1
15	153-161	TFIGGQESA	909.4305	909.4312	-0.8
16	163-187	PLREIIRLEMAYCQHIGVEFMFIN	3078.5865	3078.5838	0.9
17	186-207	INDLEQCQWIRQKFETPGIMQF	2724.3279	2724.3273	0.2
18	207-216	FTNEEKRTLL	1250.6742	1250.6739	0.2
19	220-228	VRSTRFEEF	1170.5917	1170.5902	1.3
20	229-245	LQRKWSSEKRFLEGCE	2053.0306	2053.0284	1.1
21	246-264	VLIPALKTIIDKSENGVD	2012.1267	2012.1274	-0.3
22	265-291	YVIMGMPHRGRLNVLANVIRKELEQIF	3196.7582	3196.7598	-0.5
23	292-326	CQFDSKLEAADEGSGDVKYHLGMYHRRINRVTDNRN	4080.9581	4080.9515	1.6
24	327-331	ITLSL	546.3501	546.3497	0.7
25	332-338	VANPSHL	737.3941	737.3941	0.0
26	339-354	EAADPVVMGKTKAEQF	1720.8570	1720.8574	-0.3
27	355-375	YCGDTEGKKVMSILLHGDAAF	2255.0829	2255.0835	-0.3
28	376-385	AGQGIVYETF	1084.5312	1084.5310	0.3
29	386-406	HLSDLPSYTTHTGTVHVVVNNQ	2318.1550	2318.1524	1.1
30	407-434	IGFTTDPMARSSPYPTDVARVVNAPIF	3078.5865	3078.5830	1.2
31	435-445	HVNSDDPEAVM	1213.5153	1213.5154	-0.1
32	446-453	YVCKVAAE	882.4385	882.4390	-0.5
33	454-466	WRSTFHKDVVVDL	1601.8450	1601.8435	1.0
34	467-481	VCYRRNGHNEMDEPM	1850.7719	1850.7731	-0.7
35	482-487	FTQPLM	736.3700	736.3698	0.2

36	488-504	YKQIRKQKPVLLQKYAEL	2133.2548	2133.2543	0.2
37	505-528	LVSQGVVNQPEYEEEISKYDKICE	2799.3407	2799.3393	0.5
38	529-565	EAFARSKDEKILHIKHWLDSPWPGFFTLDGQPRMSC	4330.1352	4330.1325	0.6
39	566-573	PSTGLTED	819.3732	819.3731	0.2
40	574-589	ILTHIGNVASSVPVEN	1649.8873	1649.8857	1.0
41	590-596	FTIHGGL	744.4050	744.4039	1.4
42	597-616	SRILKTRGEMVKNRTVDWAL	2373.3207	2373.3183	1.0
43	620-625	MAFGSL	625.3010	625.3014	-0.7
44	626-638	LKEGIHIRLSGQD	1465.8143	1465.8122	1.5
45	639-678	VERGTFSHRHHVLHDQNVDKRTCIPMNLWPNQAPYTVCN	4750.2876	4750.2837	0.8
46	682-687	SEYGVV	667.3298	667.3297	0.1
47	688-693	GFELGF	669.3250	669.3243	1.1
48	694-701	AMASPNAL	774.3812	774.3815	-0.3
49	702-708	VLWEAQF	892.4561	892.4563	-0.3
50	715-734	AQCIIQFICPGQAKWVRQN	2318.1550	2318.1533	0.8
51	736-759	IVLLLPHGMEGMGPEHSSARPERF	2660.3449	2660.3436	0.5
52	760-770	LQMCNDDPDVL	1262.5412	1262.5392	1.6
53	771-778	PDLKEANF	933.4684	933.4676	0.8
54	779-783	DINQL	602.3142	602.3144	-0.3
55	784-788	YDCNW	700.2408	700.2395	1.8
56	789-833	VVNCSTPGNFFHVLRRQILLPFRKPLIIFTPKSLLRHPEARSSF	5230.9478	5230.9455	0.4
57	834-842	DEMLPGTHF	1046.4593	1046.4612	-1.7
58	843-864	QRVIPEDGPAQNPENVKRLLF	2491.3439	2491.3416	0.9
59	865-887	CTGKVYYDLTRERKARDMVGQVA	2659.3447	2659.3443	0.1
60	888-902	ITRIQLSPFPDLL	1788.9894	1788.9894	0.0
61	903-914	LKEVQKYPNAEL	1431.7835	1431.7842	-0.5
62	915-928	AWCQEEHKNQGYD	1770.7188	1770.7177	0.7
63	929-945	YVKPRLRTTISRAKPVW	2071.2293	2071.2287	0.3
64	946-967	YAGRDPAAPATGNKKTHLTEL	2282.1902	2282.1888	0.6
65	968-975	QRLDPTAF	963.5263	963.5258	0.6
66	976-992	DLDFKFNFSLEHHHHHH	2149.0136	2149.0111	1.2

Table S2. Peptic peptides derived from E2o-h.

Position	Sequence	Monoisotopic Mass [M+H] ⁺ (Da)		Error (ppm)
		Experimental	Theoretical	
6-33	VKTPAFAESVTEGDVVRWEKAVGDTVAE	2891.4419	2891.4	-0.1
21-48	RWEKAVGDTVAEDEVVCEIETDKTSVQV	3135.5089	3135.5	-2.0
51-59	PANGVIEAL	883.4881	883.5	-0.3
59-75	LLVPDGGKVEGGTPLFT	1699.9258	1699.9	-0.4
76-94	LRKTGAAPAKAKPAEAPAA	1819.0558	1819.1	0.5
95-105	AAPKAEPTAAA	997.5299	997.5	-1.4
106-134	VPPPAAPIPTQMPPVSPSQPPSGKPVSA	2828.5017	2828.5	0.1
135-180	VKPTVAPPLAEAGAGKGLRSEHREKMNRMRQRIARLKEAQNTCAM	5128.7045	5128.7	-0.9
181-186	LTTFNE	724.3506	724.4	-0.8
187-216	IDMSNIQEMRARHKEAFLKKNLKLGFMSA	3543.8502	3543.8	0.1
217-223	FVKASAF	769.4239	769.4	-0.5
224-233	ALQEQPVVNA	1068.5677	1068.6	-0.6
234-246	VIDDTTKEVVYRD	1552.7853	1552.8	0.0
247-252	YIDISV	709.3771	709.4	0.6
253-272	AVATPRGLVVPVIRNVEAMN	2106.1837	2106.2	-0.7
273-292	FADIERTITELGEKARKNEL	2333.2448	2333.2	-0.5
293-301	AIEDMDGGT	908.3661	908.4	-0.6
302-313	FTISNGGVFGSL	1198.6095	1198.6	-0.7
314-350	FGTPIINPPQSAILGMHGIFDRPVAIGGKVEVRPMMY	4009.0976	4009.1	-0.9
350-364	YVALTYDHRLIDGRE	1820.9286	1820.9	-0.2
365-368	AVTF	437.2396	437.2	0.3
369-383	LRKIKAAVEDPRVLL	1721.0796	1721.1	0.0

^a For peptic digestion, samples of E1o-h (25 μ L) and E2o-h (25 μ L) were prepared in 20 mM NH₄NCO₃ (pH 7.0). Peptic digestion was as reported by us recently (SI ref S1 and ref S2)

SI References

- S1. Chandrasekhar, K., Wang, J., Arjunan, p., Sax, M., Park, Y. H., Nemeria, N. S., Kumaran, S., Song, J., Jordan, F., and Furey, W. (2013) Insight to the interaction of the dihydrolipoamide acetyltransferase (E2) core with the peripheral components in the *Escherichia coli* pyruvate dehydrogenase complex via multifaceted approaches. *J. Biol. Chem.* **288**, 15402-15417
- S2. Wang, J., Nemeria, N. S., Chandrasekhar, K., Kumaran, S., Arjunan, P., Reynolds, SD., Calero, G., Brukh, R., Kakalis, L., Furey, W., and Jordan, F. (2014) Structure and function of the catalytic domain of the dihydrolipoyl acetyltransferase component in *Escherichia coli* pyruvate dehydrogenase complex. *J. Biol. Chem.* **289**, 15215-15230