Electronic Supplementary Material (ESI) for Food & Function.

SUPPORTING INFORMATION

Ixocarpalactone A from dietary tomatillo inhibits pancreatic cancer growth by targeting PHGDH

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Table S1. ^{1}H and ^{13}C NMR Spectroscopic Data for IoxA (in $CDCl_3$; ^{1}H NMR, 600 MHz; ^{13}C NMR, 150 MHz).

No.	δ_C	δ_H (J in Hz)
1	202.2	
2	132.5	6.19 d (9.9)
3	142.0	6.92 dd (9.9,5.8)
4	70.1	3.75 d (5.8)
5	64.1	
6	62.6	3.22 br s
7	31.2	2.06-2.13 m 1.31
8	29.0	
9	44.2	
10	47.8	
11	21.9	1.81-1.84 m
12	40.1	2.06-2.13 m
13	43.3	
14	54.5	
15	37.3	2.24-2.29 m
16	73.7	4.52 m
17	58.2	1.38 d (7.2)
18	15.0	1.12 s
19	17.6	1.40 s
20	79.3	
21	23.2	1.36 s
22	74.0	4.46 s
23	78.6	3.93 br s
24	41.8	2.24-2.29 m
25	40.2	2.64-2.70 m
26	180.3	
27	14.3	1.16 d (7.1)
28	13.2	1.22 d (6.9)

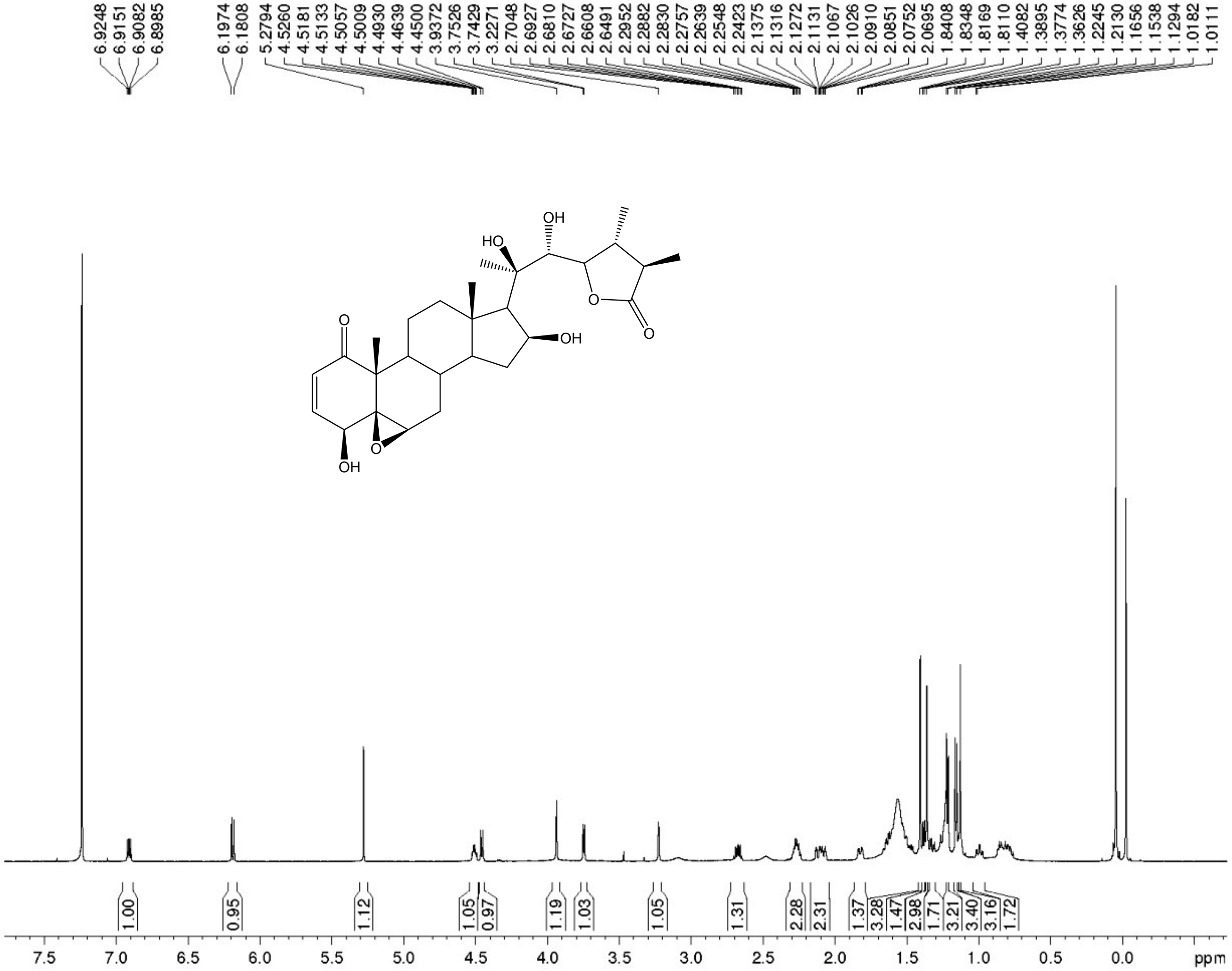


Figure S1. ^{1}H-NMR spectrum of **IoxA** (600 MHz, $CDCl_3$)

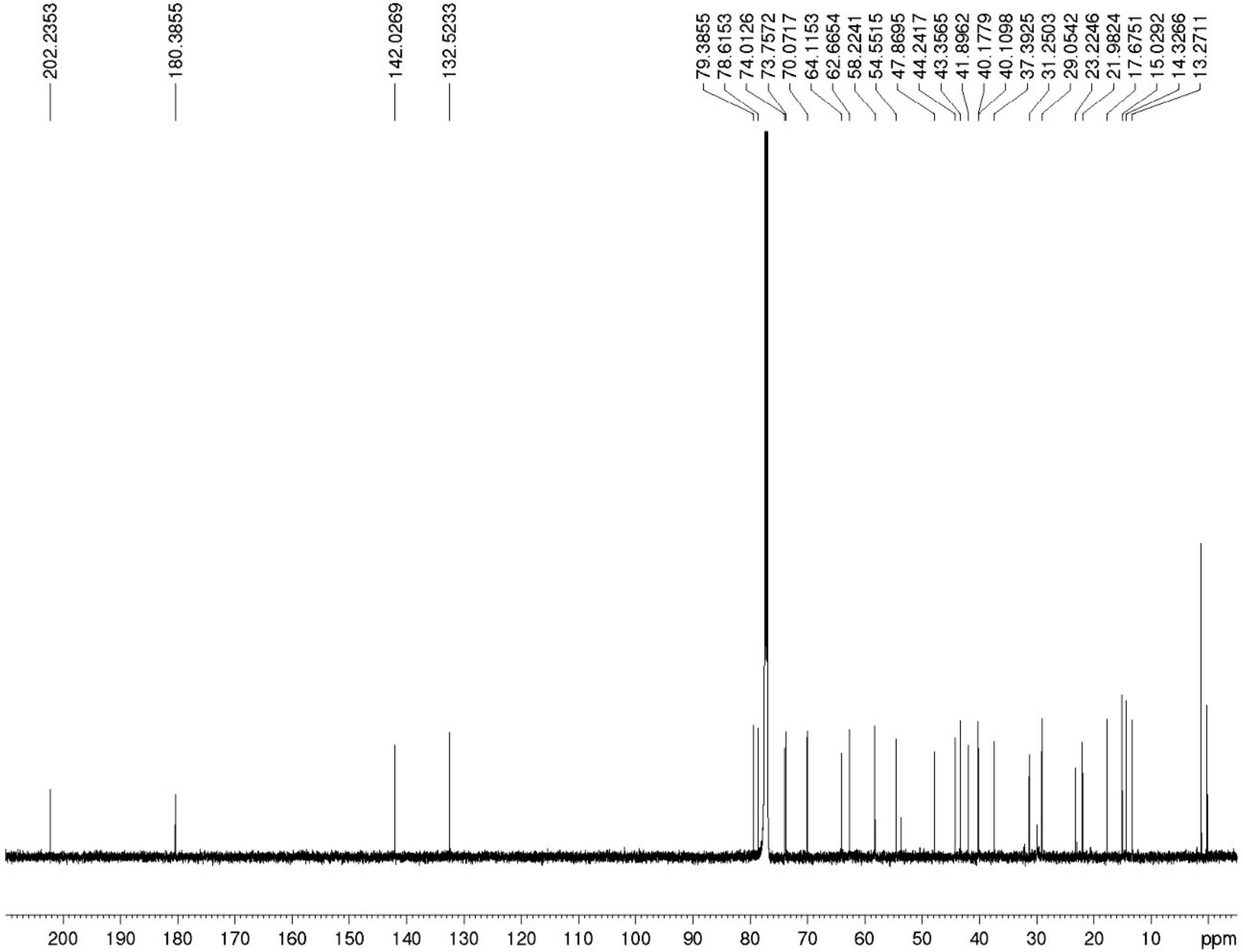


Figure S2. ^{13}C-NMR spectrum of **IoxA** (150 MHz, $CDCl_3$)

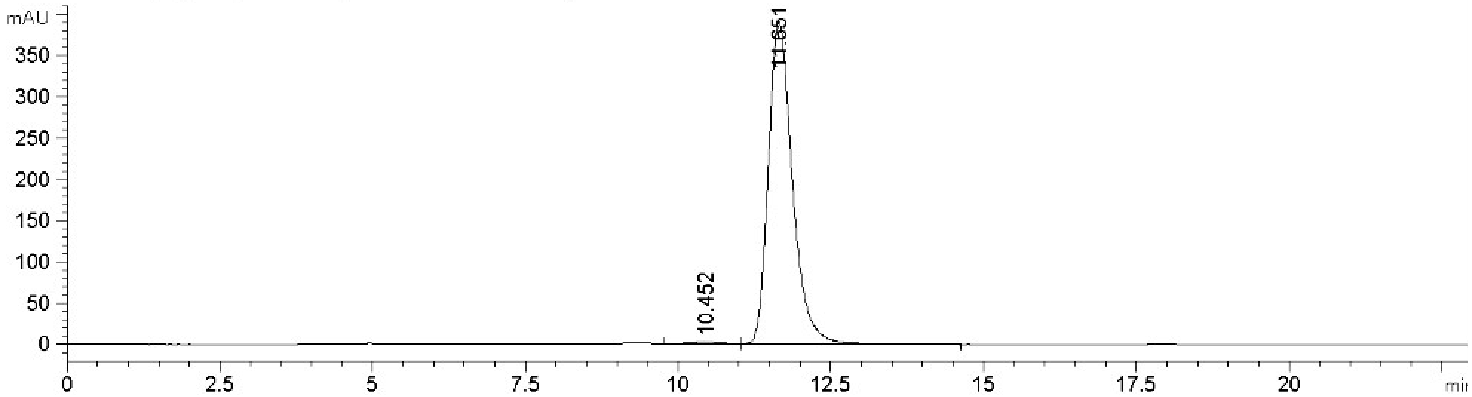
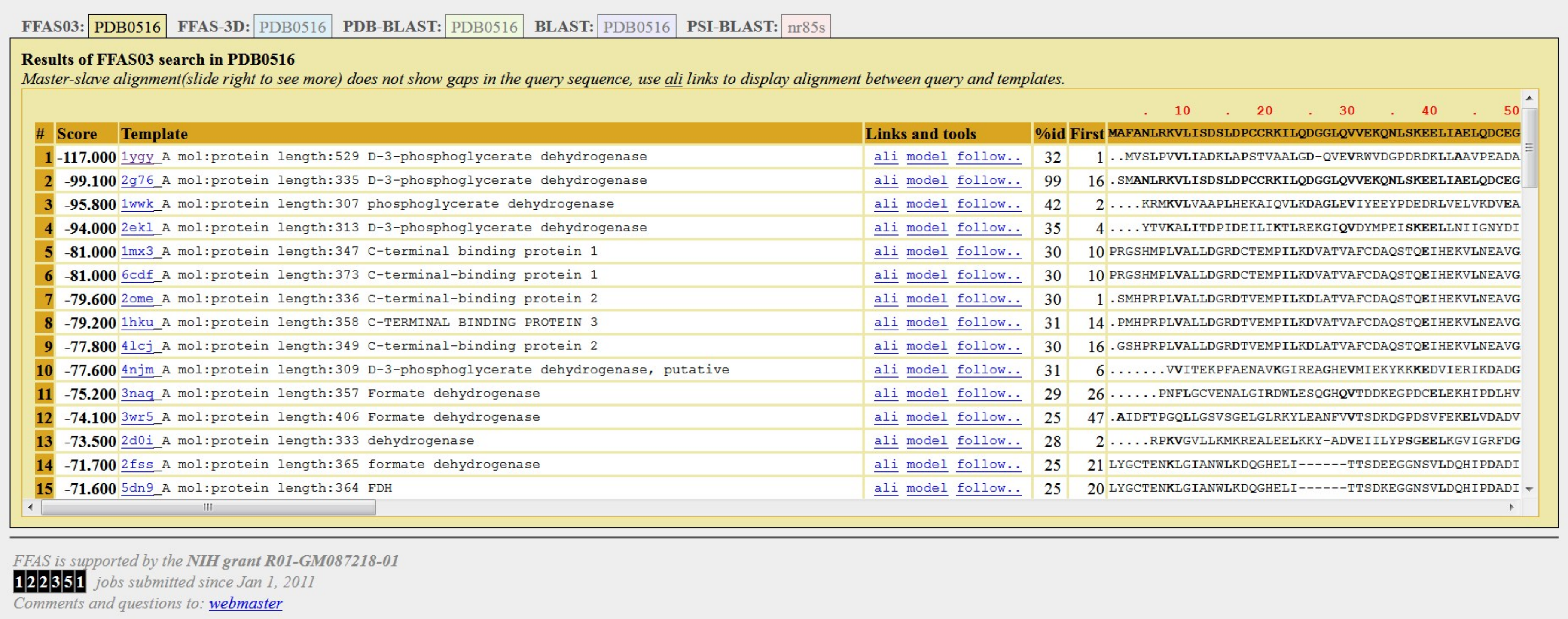


Figure S3. HPLC analysis of **IoxA** (230 nm, MeOH:H_2O=60:40)



Results of FFAS03 search in PDB0516

Master-slave alignment(slide right to see more) does not show gaps in the query sequence, use ali links to display alignment between query and templates.

. 10 . 20 . 30 . 40 . 50

#	Score	Template	Links and tools	%id	First	MAFANLRKVLISDSLDPCCRKILQDGGLQVVEKQNLSKEELIAELQDCEG
1	-117.000	1ygy_A mol:protein length:529 D-3-phosphoglycerate dehydrogenase	ali model follow..	32	1	..MVSLPVVLIADKLAPSTVAALGD-QVEVRWVDGPDRDKLLAAVPEADA
2	-99.100	2g76_A mol:protein length:335 D-3-phosphoglycerate dehydrogenase	ali model follow..	99	16	.SMANLRKVLISDSLDPCCRKILQDGGLQVVEKQNLSKEELIAELQDCEG
3	-95.800	1wwk_A mol:protein length:307 phosphoglycerate dehydrogenase	ali model follow..	42	2	....KRMKVLVAAPLHEKAIQVLKDAGLEVIYEEYPDEDRLVELVKDVEA
4	-94.000	2ekl_A mol:protein length:313 D-3-phosphoglycerate dehydrogenase	ali model follow..	35	4	....YTVKALITDPIDEILIKTLREKGIQVDYMPEISKEELLNIIGNYDI
5	-81.000	1mx3_A mol:protein length:347 C-terminal binding protein 1	ali model follow..	30	10	PRGSHMPLVALLDGRDCTEMPILKDVATVAFCDAQSTQEIHEKVLNEAVG
6	-81.000	6cdf_A mol:protein length:373 C-terminal-binding protein 1	ali model follow..	30	10	PRGSHMPLVALLDGRDCTEMPILKDVATVAFCDAQSTQEIHEKVLNEAVG
7	-79.600	2ome_A mol:protein length:336 C-terminal-binding protein 2	ali model follow..	30	1	.SMHPRPLVALLDGRDTVEMPILKDLATVAFCDAQSTQEIHEKVLNEAVG
8	-79.200	1hku_A mol:protein length:358 C-TERMINAL BINDING PROTEIN 3	ali model follow..	31	14	.PMHPRPLVALLDGRDTVEMPILKDVATVAFCDAQSTQEIHEKVLNEAVG
9	-77.800	4lcj_A mol:protein length:349 C-terminal-binding protein 2	ali model follow..	30	16	.GSHPRPLVALLDGRDTVEMPILKDLATVAFCDAQSTQEIHEKVLNEAVG
10	-77.600	4njm_A mol:protein length:309 D-3-phosphoglycerate dehydrogenase, putative	ali model follow..	31	6	.......VVITEKPFAENAVKGIREAGHEVMIEKYKKKEDVIERIKDADG
11	-75.200	3naq_A mol:protein length:357 Formate dehydrogenase	ali model follow..	29	26	......PNFLGCVENALGIRDWLESQGHQVTDDKEGPDCELEKHIPDLHV
12	-74.100	3wr5_A mol:protein length:406 Formate dehydrogenase	ali model follow..	25	47	.AIDFTPGQLLGSVSGELGLRKYLEANFVVTSDKDGPDSVFEKELVDADV
13	-73.500	2d0i_A mol:protein length:333 dehydrogenase	ali model follow..	28	2	.....RPKVGVLLKMKREALEELKKY-ADVEIILYPSGEELKGVIGRFDG
14	-71.700	2fss_A mol:protein length:365 formate dehydrogenase	ali model follow..	25	21	LYGCTENKLGIANWLKDQGHELI------TTSDEEGGNSVLDQHIPDADI
15	-71.600	5dn9_A mol:protein length:364 FDH	ali model follow..	25	20	LYGCTENKLGIANWLKDQGHELI------TTSDKEGGNSVLDQHIPDADI

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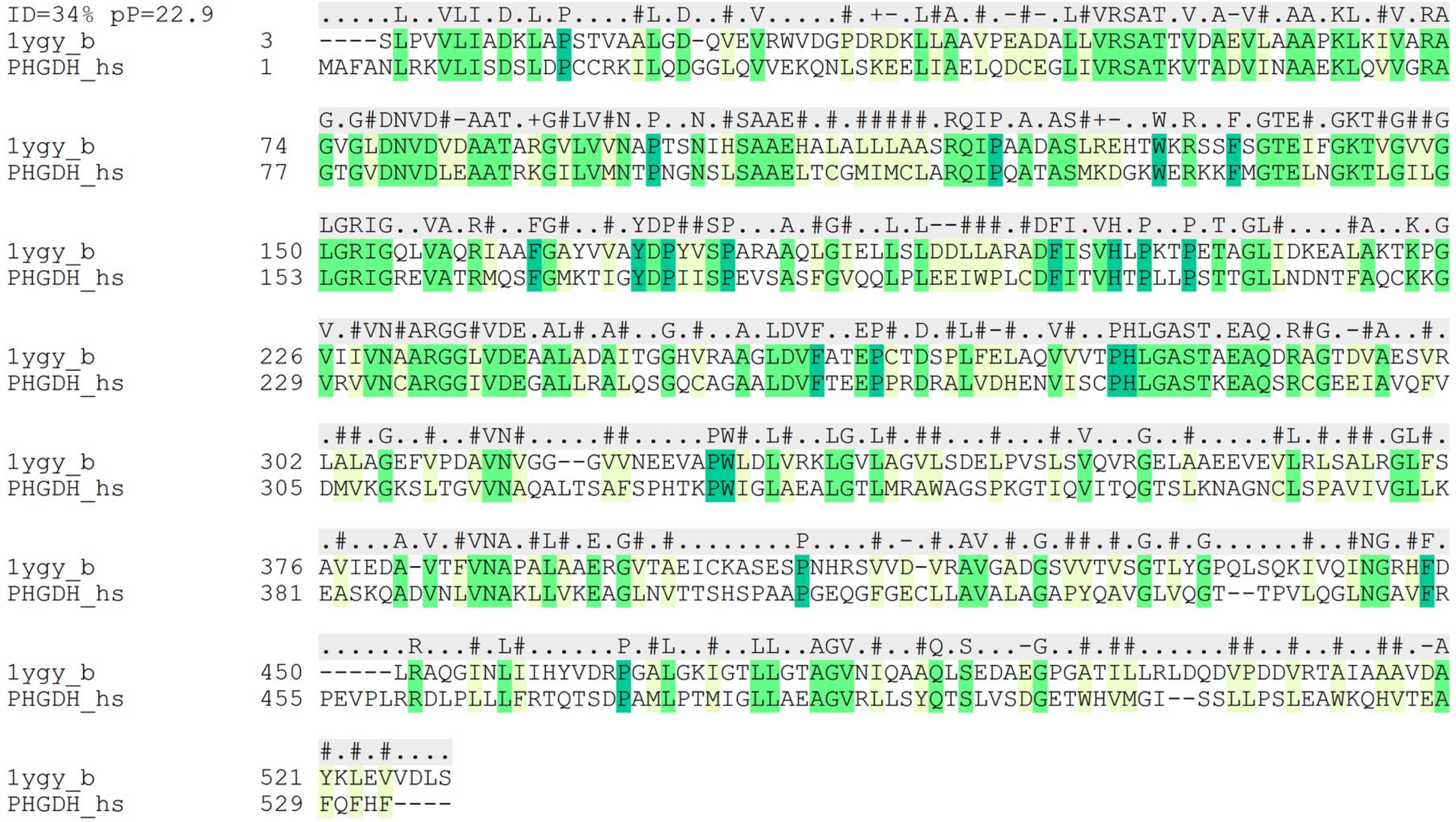
122351 *jobs submitted since Jan 1, 2011*

Comments and questions to: webmaster

Figure S4. Human PHGDH sequence searched in the FFAS server, finding the most resembling structure.



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ID=34% pP=22.9         .....L..VLI.D.L.P....#L.D..#.V.....#.+-.L#A.#.-#-.L#VRSAT.V.A-V#.AA.KL.#V.RA
1ygy_b            3    ----SLPVVLIADKLAPSTVAALGD-QVEVRWVDGPDRDKLLAAVPEADALLVRSATTVDAEVLAAAPKLKIVARA
PHGDH_hs          1    MAFANLRKVLISDSLDPCCRKILQDGGLQVVEKQNLSKEELIAELQDCEGLIVRSATKVTADVINAAEKLQVVGRA

                       G.G#DNVD#-AAT.+G#LV#N.P..N.#SAAE#.#.#####.RQIP.A.AS#+-..W.R..F.GTE#.GKT#G##G
1ygy_b            74   GVGLDNVDVDAATARGVLVVNAPTSNIHSAAEHALALLLAASRQIPAADASLREHTWKRSSFSGTEIFGKTVGVVG
PHGDH_hs          77   GTGVDNVDLEAATRKGILVMNTPNGNSLSAAELTCGMIMCLARQIPQATASMKDGKWERKKFMGTELNGKTLGILG

                       LGRIG..VA.R#..FG#..#.YDP##SP...A.#G#..L.L--###.#DFI.VH.P..P.T.GL#....#A..K.G
1ygy_b            150  LGRIGQLVAQRIAAFGAYVVAYDPYVSPARAAQLGIELLSLDDLLARADFISVHLPKTPETAGLIDKEALAKTKPG
PHGDH_hs          153  LGRIGREVATRMQSFGMKTIGYDPIISPEVSASFGVQQLPLEEIWPLCDFITVHTPLLPSTTGLLNDNTFAQCKKG

                       V.#VN#ARGG#VDE.AL#.A#..G.#..A.LDVF..EP#.D.#L#-#..V#..PHLGAST.EAQ.R#G.-#A..#.
1ygy_b            226  VIIVNAARGGLVDEAALADAITGGHVRAAGLDVFATEPCTDSPLFELAQVVVTPHLGASTAEAQDRAGTDVAESVR
PHGDH_hs          229  VRVVNCARGGIVDEGALLRALQSGQCAGAALDVFTEEPPRDRALVDHENVISCPHLGASTKEAQSRCGEEIAVQFV

                       .##.G..#..#VN#.....##.....PW#.L#..LG.L#.##...#...#.V...G..#.....#L.#.##.GL#.
1ygy_b            302  LALAGEFVPDAVNVGG--GVVNEEVAPWLDLVRKLGVLAGVLSDELPVSLSVQVRGELAAEEVEVLRLSALRGLFS
PHGDH_hs          305  DMVKGKSLTGVVNAQALTSAFSPHTKPWIGLAEALGTLMRAWAGSPKGTIQVITQGTSLKNAGNCLSPAVIVGLLK

                       .#...A.V.#VNA.#L#.E.G#.#........P....#.-.#.AV.#.G.##.#.G.#.G......#..#NG.#F.
1ygy_b            376  AVIEDA-VTFVNAPALAAERGVTAEICKASESPNHRSVVD-VRAVGADGSVVTVSGTLYGPQLSQKIVQINGRHFD
PHGDH_hs          381  EASKQADVNLVNAKLLVKEAGLNVTTSHSPAAPGEQGFGECLLAVALAGAPYQAVGLVQGT--TPVLQGLNGAVFR

                       ......R...#.L#......P.#L..#..LL..AGV.#..#Q.S...-G..#.##......##..#..#..##.-A
1ygy_b            450  -----LRAQGINLIIHYVDRPGALGKIGTLLGTAGVNIQAAQLSEDAEGPGATILLRLDQDVPDDVRTAIAAAVDA
PHGDH_hs          455  PEVPLRRDLPLLLFRTQTSDPAMLPTMIGLLAEAGVRLLSYQTSLVSDGETWHVMGI--SSLLPSLEAWKQHVTEA

                       #.#.#....
1ygy_b            521  YKLEVVDLS
PHGDH_hs          529  FQFHF----
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Figure S5. Structure based sequence alignment of human PHGDH with *M. tuberculosis* PHGDH.

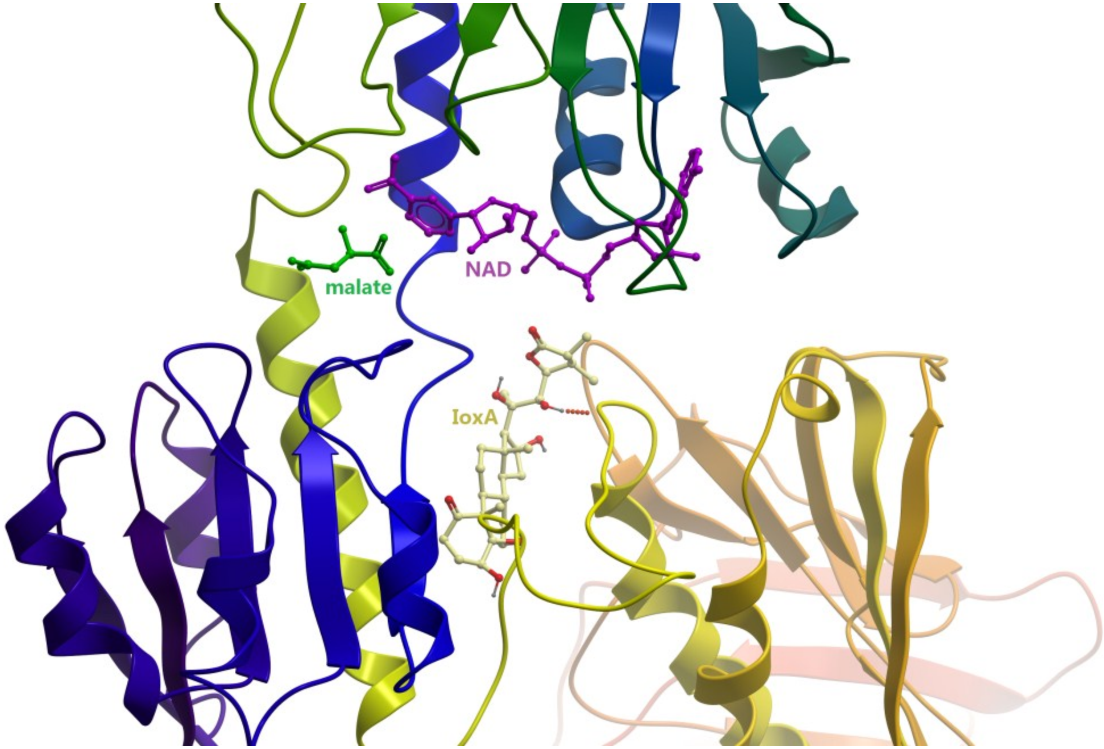

Figure S6. Binding mode of IoxA with human PHGDH. IoxA (yellow) was well fitted an allosteric site of the enzyme, where it was in the back side of the active site, where NAD (purple) and malate (green) were bound.