



**Figure S1. Multiple sequence alignment and classification of ASADHs.** ASADH sequences were extracted from the clustering analysis dataset. The sequence from the  $\alpha 6$  –  $\alpha 6$  -  $\alpha 7$  loop region shows a major discrepancy, providing a basis to classify ASADHs into three types.

**Table S1. Aspartate semialdehyde dehydrogenases used for clustering analysis.**

	Uniprot code	Organisms
Type I	Q8FCR6.2	[ <i>Escherichia coli</i> CFT073]
	P0A9Q9.1	[ <i>Escherichia coli</i> K-12]
	P0A1F8.1	[ <i>Salmonella enterica</i> subsp. enterica serovar Typhimurium str. LT2]
	P44801.1	[ <i>Haemophilus influenzae</i> Rd KW20]
	Q9KQG2.1	[ <i>Vibrio cholerae</i> O1 biovar El Tor str. N16961]
	Q51344.2	[ <i>Pseudomonas aeruginosa</i> PAO1]
	Q44151.1	[ <i>Actinobacillus pleuropneumoniae</i> ]
	P30903.2	[ <i>Neisseria meningitidis</i> MC58]
	P57008.1	[ <i>Neisseria meningitidis</i> Z2491]
	Q89AB8.1	[ <i>Buchnera aphidicola</i> str. Bp (Baizongia pistaciae)]
	P57523.1	[ <i>Buchnera aphidicola</i> str. APS (Acyrtosiphon pisum)]
	P41399.1	[ <i>Bordetella pertussis</i> Tohama I]
	Q8K9B5.1	[ <i>Buchnera aphidicola</i> str. Sg (Schizaphis graminum)]
	P96198.1	[ <i>Azotobacter vinelandii</i> ]
Type II	PgASADH	[ <i>Porphyromonas gingivalis</i> ]
	O67716.1	[ <i>Aquifex aeolicus</i> VF5]
	Q55512.2	[ <i>Synechocystis</i> sp. PCC 6803 substr. Kazusa]
	Q59291.2	[ <i>Campylobacter jejuni</i> subsp. jejuni NCTC 11168 = ATCC 700819]
	Q04797.1	[ <i>Bacillus subtilis</i> subsp. subtilis str. 168]
	O31219.1	[ <i>Legionella pneumophila</i> ]
	P49420.2	[ <i>Prochlorococcus marinus</i> subsp. marinus str. CCMP1375]
	Q56732.1	[ <i>Shewanella</i> sp. DB6705]
	Q56734.2	[ <i>Shewanella violacea</i> DSS12]
	P23247.2	[ <i>Vibrio cholerae</i> O1 biovar El Tor str. N16961]
	P10539.2	[ <i>Streptococcus mutans</i> UA159]
	O25801.1	[ <i>Helicobacter pylori</i> 26695]
	Q9ZK28.1	[ <i>Helicobacter pylori</i> J99]
	Q60080.1	[ <i>Vibrio mimicus</i> ]
	Q1RIB3.1	[ <i>Rickettsia bellii</i> RML369-C]
	Q53612.1	[ <i>Streptomyces akiyoshiensis</i> ]
	Q4UM57.1	[ <i>Rickettsia felis</i> URRWXC12]

	Q68X56.1	[ <i>Rickettsia typhi</i> str. Wilmington]
	P0A543.1	[ <i>Mycobacterium tuberculosis</i> variant bovis AF2122/97]
	Q92IJ0.1	[ <i>Rickettsia conorii</i> str. Malish 7]
	P41400.1	[ <i>Corynebacterium flavescens</i> ]
	Q9ZDL2.1	[ <i>Rickettsia prowazekii</i> str. Madrid E]
	P0C1D9.1	[ <i>Corynebacterium melassecola</i> ]
	P0C1D8.1	[ <i>Corynebacterium glutamicum</i> ATCC 13032]
	P41404.1	[ <i>Mycolicibacterium smegmatis</i> ]
Type III	O28766.1	[ <i>Archaeoglobus fulgidus</i> DSM 4304]
	Q57658.1	[ <i>Methanocaldococcus jannaschii</i> DSM 2661]
	O26890.1	[ <i>Methanothermobacter thermautotrophicus</i> str. Delta H]
	P41394.2	[ <i>Leptospira interrogans</i> serovar Lai str. 56601]
	Q75FC8.1	[ <i>Leptospira interrogans</i> serovar Copenhageni str. Fiocruz L1-130]
	P13663.1	[ <i>Saccharomyces cerevisiae</i> S288C]
	P78780.2	[ <i>Schizosaccharomyces pombe</i> 972h-]