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Supporting information for article:

The structure of *Synechococcus elongatus* enolase reveals key aspects of phosphoenolpyruvate binding

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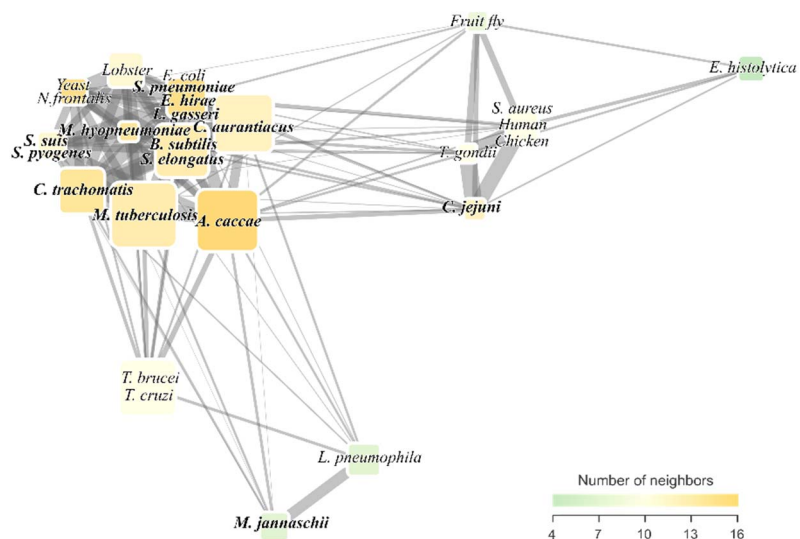


Figure S1 Sequence similarity subnetwork (18 rep nodes by 101 edges) comprising those rep nodes and edges in the family-wide SSN including at least one enolase sequence with known PDB structure. Colouring according to number of neighbours (also known as node degree) and edge thickness proportional to sequence similarity allow a better visualization of clusters in the network. Compare with the dendrogram in Figure 3.

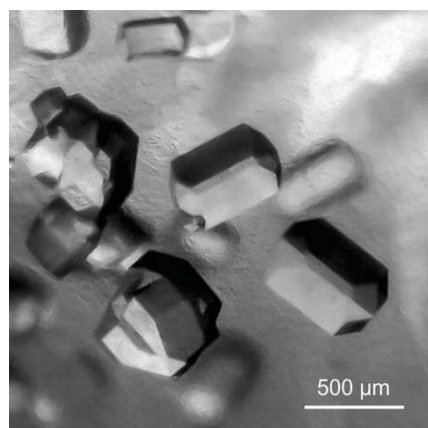


Figure S2 *SeEN* crystals.

Table S1 Buried area (in Å²) of selected enolase crystallographic structures for quaternary structure estimation, as calculated with the PISA server (Krissinel & Henrick, 2007).

Organism	UniProt	PDB	Dimer	Octamer
<i>Trypanosoma cruzi</i>	Q4DZ98	4G7F	0	0
<i>Coxiella burnetii</i>	Q83B44	3TQP	3,760	0
<i>Toxoplasma gondii</i>	B9PH47	3OTR	3,770	0
<i>Escherichia coli</i> (strain K12)	P0A6P9	1E9I	4,060	0
<i>Legionella pneumophila</i>	A0A2S6F4U1	6NBM	4,260	0
<i>Homarus gammarus</i> (European lobster)	P09104	1PDY	4,530	0
Human γ -enolase	Q97QS2	1TE6	4,820	0
<i>Saccharomyces cerevisiae</i> (Baker's yeast)	P00924	1EBG	4,920	0
Human α -enolase	Q38BV6	2PSN	4,960	0
<i>Trypanosoma brucei brucei</i>	Q9NDH8	2PTZ	5,670	0
<i>Trypanosoma brucei brucei</i>	P56252	2PU1	5,780	0
<i>Entamoeba histolytica</i>	P51555	3QTP	5,920	0
<i>Legionella pneumophila sub. pneumophila</i>	Q5ZTX1	6NB2	6,130	0
<i>Drosophila melanogaster</i> (Fruit fly)	P15007	5WRO	6,920	0
Human β -enolase	P13929	2XSX	8,670	0
<i>Streptococcus suis</i>	K7N5M7	4EWJ	3,350	22,870
<i>Lactobacillus gasseri</i>	Q042F4	4MKS	3,410	23,150
<i>Chloroflexus aurantiacus</i>	A9WCM4	4YWS	3,290	23,630
<i>Synechococcus elongatus</i>	Q5N3P4	4ROP	3,570	23,920
<i>Streptococcus pyogenes</i>	Q5XD01	3ZLH	3,650	24,770
<i>Streptococcus pneumoniae</i>	Q60173	1W6T	4,190	26,920
<i>Anaerostipes caccae</i>	B0MAG5	3UJ2	4,810	26,960
<i>Bacillus subtilis</i> (strain 168)	P37869	4A3R	3,480	27,120
<i>Campylobacter jejuni</i>	P42448	3QN3	4,750	29,170
<i>Staphylococcus aureus</i>	O69174	5BOE	5,270	31,760
<i>Enterococcus hirae</i>	Q8GR70	1IYX	4,780	32,180
<i>Mycobacterium tuberculosis</i>	P9WNL1	6L7D	5,380	32,670
<i>Mycoplasma hyopneumoniae</i>	A0A223MA21	6J36	5,840	33,530
<i>Methanocaldococcus jannaschii</i>	P06733	2PA6	4,310	34,170
<i>Chlamydia trachomatis</i>	B0BA40	6O4N	5,670	38,850

Table S2 PDB and associated UniProt entries present in the enolase SSN (Figure 3).

Organism	PDB	Entry
<i>Anaerostipes caccae</i>	3UJ2	B0MAG5
<i>Bacillus subtilis</i> (strain 168)	4A3R	P37869
<i>Campylobacter jejuni</i>	3QN3	P42448
<i>Chlamydia trachomatis</i>	6O4N	B0BA40
<i>Chloroflexus aurantiacus</i>	4YWS, 4Z17, 4Z1Y	A9WCM4
<i>Coxiella burnetii</i>	3TQP	Q83B44
<i>Drosophila melanogaster</i> (Fruit fly)	5WRO	P15007
<i>Entamoeba histolytica</i>	3QTP	P51555
<i>Enterococcus hirae</i>	1IYX	Q8GR70
<i>Escherichia coli</i> (strain K12)	1E9I, 2FYM, 3H8A, 5OHG, 6BFY, 6BFZ, 6D3Q, 6NPF	P0A6P9
<i>Gallus gallus</i> (Chicken)	2GUA	P51913
<i>Homarus gammarus</i> (European lobster)	1PDY, 1PDZ	P56252
Human α -enolase	2PSN, 3B97, 5JLZ, 5LAX, 5NI9, 5NIG, 5OCK	P06733
Human β -enolase	2XSX	P13929
Human γ -enolase	1TE6, 2AKM, 2AKZ, 3UCC, 3UCD, 3UJE, 3UJF, 3UJR, 3UJS, 4ZA0, 4ZCW, 5EU9, 5IDZ, 5TD9, 5TIJ	P09104
<i>Lactobacillus gasseri</i>	4MKS	Q042F4
<i>Legionella pneumophila</i>	6NBM	A0A2S6F4U1
<i>Legionella pneumophila sub. pneumophila</i>	6NB2	Q5ZTX1
<i>Methanocaldococcus jannaschii</i>	2PA6	Q60173
<i>Mycobacterium tuberculosis</i>	6L7D	P9WNL1
<i>Mycoplasma hyopneumoniae</i>	6J36	A0A223MA21
<i>Neocallimastix frontalis</i> (Rumen fungus)	2GE6	P42894
<i>Saccharomyces cerevisiae</i> (Baker's yeast)	1EBG, 1EBH, 1ELS, 1L8P, 1NEL, 1ONE, 1P43, 1P48, 2AL1, 2AL2, 2ONE, 2XGZ, 2XH0, 2XH2, 2XH4, 2XH7, 3ENL, 4ENL, 5ENL, 6ENL, 7ENL	P00924
<i>Staphylococcus aureus</i>	5BOE, 5BOF	O69174
<i>Streptococcus pneumoniae</i>	1W6T	Q97QS2
<i>Streptococcus pyogenes</i>	3ZLF, 3ZLG, 3ZLH	Q5XD01
<i>Streptococcus suis</i>	4EWJ	K7N5M7
<i>Synechococcus elongatus</i>	4ROP, 5J04	Q5N3P4
<i>Toxoplasma gondii</i>	3OTR	B9PH47
<i>Trypanosoma brucei brucei</i>	1OEP, 2PU1	Q9NDH8
<i>Trypanosoma brucei brucei</i>	2PTW, 2PTX, 2PTY, 2PTZ, 2PU0	Q38BV6
<i>Trypanosoma cruzi</i>	4G7F	Q4DZ98