

## Supplementary Information

**Table S1.** Structures for the members of the transcarbamylase family deposited in PDB.

Protein	Source	Note	Ligands	PDB ID	Resolution (Å)	Reference
ATCase	<i>E. coli</i>	R54A mutant	Zn(II), PALA	1ACM	2.8	[89]
		R-state	Zn(II), PAM, Malonate	1AT1	2.8	[90]
		R-state	PALA	1D09	2.01	[91]
		Catalytic trimer	PALA	1EKX	1.95	[41]
		P268A mutant T-state	Zn(II)	1EZZ	2.70	[92]
		P268A mutant R-state	PALA, Zn(II)	1F1B	2.30	[92]
		R105A mutant Catalytic trimer		1GQ3	2.01	
		R105A mutant	PALA, Zn(II)	1I5O	2.80	[93]
		T82A mutant	Malic acid, Zn(II)	1NBE	2.60	[94]
		R-state	PALA, Zn(II)	1Q95	2.46	[95]
		R-state	Citrate, Zn(II), Phosphate	1R0B	2.90	[95]
		T-state	Zn(II), Phosphate, NCD	1R0C	2.37	[96]
		T-state	CTP	1RAA, 1RAB, 1RAC, 1RAD, 1RAE, 1RAF, 1RAG, 1RAH, 1RAI	2.50	[97]
		K244N mutant	Malonate, Zn(II)	1SKU	2.60	[98]
		E50A mutant	PALA, Zn(II)	1TTH	2.80	[99]
		E50A mutant	PAM, Zn(II)	1TU0	2.55	[99]
		E50A mutant	PAM, Malonate, CTP, Zn(II)	1TUG	2.10	[99]

Table S1. *Cont.*

Protein	Source	Note	Ligands	PDB ID	Resolution (Å)	Reference
		Q137A mutant	PALA, Zn(II)	1XJW	2.71	[100]
			CTP, Zn(II)	1ZA1	2.20	[71]
			CTP, CP, Zn(II)	1ZA2	2.50	[71]
		D236A mutant	PAM, Zn(II)	2A0F	2.90	[101]
			PAM, Malonate, Zn(II)	1AT1	2.80	[90]
			Zn(II)	2ATC	3.00	[102]
			PAM, Zn(II)	3AT1	2.80	[90]
		Catalytic trimer		3CSU	1.88	[40]
			ATP, Zn(II)	4AT1	2.60	[103]
			CTP, Zn(II)	5AT1	2.60	[103]
			Zn(II)	6AT1	2.60	[103]
			PAM, Malonate, ATP, Zn(II)	7AT1	2.80	[103]
			PAM, Malonate, CTP, Zn(II)	8AT1	2.80	[103]
			PALA, Zn(II)	8ATC	2.50	[104]
			Zn(II)	9ATC	2.40	[105]
			CP, Alanosine	2AIR	2.00	[106]
		T-state	CTP, EOA	2FZC	2.46	[107]
		T-state	CTP, EOB	2FZG	2.25	[107]
			CTP, EOZ	2FZK	2.50	[107]
		R-state	PALI	2IPO	2.60	[108]
		R-state	PALI	2H3E	2.30	[109]
		R-sate D236A	PAM, aspartate	2HSE	2.60	Unpublished

Table S1. Cont.

Protein	Source	Note	Ligands	PDB ID	Resolution (Å)	Reference
		rH20A		2QGF	2.20	[110]
		rD19A		2PG9	2.70	[110]
		pH = 8.5		3D7S	2.80	[111]
		R-state	ATP	4KGV	2.10	[112]
		R-state	CTP	4KGX	2.20	[112]
		R-state	ATP, Mg <sup>2+</sup>	4KH0	2.25	[112]
			dCTP	4FYV	2.10	[113]
			CTP	4FYX	2.10	[113]
			dCTP, CTP, Mg <sup>2+</sup>	4FYW	2.10	[113]
		R-state	UTP	4F04	2.30	[114]
		K164E/E239K		4E2F	2.80	[115]
		C47A/A241C		3NPM	2.10	[116]
		Natural source		4WTO	2.30	Unpublished
		C47A/A241C		3MPU	2.86	[116]
<i>M. jannaschii</i>		Regulatory dimer	ATP	2YWW	2.00	Unpublished
		Catalytic trimer		2RGW		[46]
		Catalytic trimer		3E2P	3.0	[45]
				4EKN	2.50	[47]
<i>M. profunda</i>		V2A T-state		2BE7	2.85	[48]
<i>P. abyssi</i>		Catalytic trimer	PALA	1ML4	1.80	[42]
<i>S. acidocaldarius</i>		T-state	Zn(II)	1PG5	2.60	[43]
		T-state	CTP	2BE9	2.60	[44]
<i>A. aeolicus</i>		Complexed with DHO		3D6N	2.3	[50]
		Complexed with DHO	PALA	4BJH	2.2	[51]
<i>B. subtilis</i>		Catalytic trimer		2AT2	3.0	[7]
				3R7D	2.2	[49]
			CP	3R7F	2.10	[49]
			PALA	3R7L	2.59	[49]
<i>T. cruzi</i>		Catalytic trimer		4IV5	2.10	Unpublished
<i>Y. pestis</i>		Catalytic trimer		3LXM	2.0	Unpublished
aOTCase	<i>E. coli</i>	Trimer		1AKM	2.8	[54]
			Psorn	1DUV	1.7	[53]
			PALO	2OTC	2.80	[52]
	Human	Trimer	CP, Norvaline	1C9Y	1.90	[117]
			CP	1EP9	2.40	[60]

Table S1. Cont.

Protein	Source	Note	Ligands	PDB ID	Resolution (Å)	Reference
			CP	1FVO	2.60	[60]
			PALO	1OTH	1.85	[58]
	Ovine	Trimer		1FB5	3.50	[61]
	<i>B. anthracis</i>	Trimer	CP, norvaline	4NF2	1.74	Unpublished
				4EP1	3.25	Unpublished
	<i>V. vulnificus</i>	Trimer		4KWT	1.86	Unpublished
		Trimer	Pi, Citrulline	4JQO	2.08	Unpublished
			CP, arginine	4JHX	1.85	Unpublished
			CP	4JFR	2.17	Unpublished
			CP, norvaline	4H31	1.70	Unpublished
				3UPD	2.90	Unpublished
	<i>T. thailandensis</i>		Pi	4F2G	2.10	[118]
	<i>Py. furiosus</i>	Dodecamer	Phosphate	1A1S	2.70	[57]
				1PVV	1.87	[77]
	<i>T. maritima</i>	Dodecamer	Phosphate	1VLV	2.25	Unpublished
	<i>T. thermophilus</i>	Trimer		2EF0	2.0	Unpublished
	<i>M. tuberculosis</i>	Trimer	CP Norvaline	2I6U	2.2	[119]
		Trimer		2P2G	2.7	[119]
	<i>G. lamblia</i>	Trimer	PALO	3GRF	2.0	[120]
	<i>C. jejuni</i>	Trimer		3TPF	2.70	[121]
	<i>C. immitis</i>			3SDS	2.80	[122]
	<i>B. melitensis</i>	Trimer		4OH7	1.50	Unpublished
	<i>G. violaceus</i>	hexamer		3GD5	2.10	Unpublished
cOTCase	<i>Ps. aeruginosa</i>	Dodecamer	Phosphate	1DXH	2.50	Unpublished
				1ORT	3.0	[55]
	<i>M. penetrans</i>	Dodecamer		4AMU	2.5	[19]
				4ANF	2.6	[19]
	<i>L. hilgardii</i>	Hexamer		2W37	2.1	[20]
AOTCase	<i>X. campestris</i>	Trimer	Sulfate	3KZC	2.20	[21]
			ACT, Sulfate	3KZK	1.90	[21]
			CP	3KZM		[62]
			AORN	3KZN		[62]
			CP, ANOR	3KZO		[62]
		E92A	CP, SNOR	3L02	2.30	[25]
		E92P	CP, SNOR	3L04	2.50	[25]
		E92S	CP, SNOR	3L05	2.80	[25]

Table S1. *Cont.*

Protein	Source	Note	Ligands	PDB ID	Resolution (Å)	Reference
		E92V	CP, SNOR	3L06	2.81	[25]
			PALAO	3M4J	2.2	[123]
		K302A	PALAO	3M4N	1.9	[123]
		K302E	PALAO	3M5C	1.85	
SOTCase	<i>B. fragilis</i>	Trimer	Phosphate	1JS1	2.0	[23]
			Sulfate, SNOR	2FG6	2.80	[24]
			CP, SNOR	2FG7	2.90	[24]
		P90E	CP, ANOR	2G7M	2.90	[25]
PTCase	<i>E. faecalis</i>	R54G	Guanidinine	4AM8	1.99	Unpublished
		Trimer	PALP	4A8H	2.50	[29]
			PALO	4A8P	2.00	[29]
		Hexamer	PALO	4A8T	1.59	[29]
		Trimer		3TXX	3.20	[30]
YTCase	<i>E. coli</i>	Trimer		3Q98	2.0	[32]
	<i>E. faecalis</i>	Trimer		2YFK	2.55	Unpublished
			CP	2YFF		Withdrawn
			CP + Taurine	2YFM		Withdrawn