

Table S2. Evidence of similarities to S15 catalytic domains found in metatranscriptomes from the deep subsurface. Shown are the hits to the Pfam of bathyaminopeptidase in Peru Margin Ocean Drilling Program Leg 201 marine sediment metatranscriptomes.

MG-RAST ID	Depth (mbsf)	S15 Hits (PF02129) (e-value $\geq 1e-5$)	Total Gbp	S15/total genes	S15/Gbp
4510337.3	5	1	18.9	6.82E-05	5.29E-02
4510335.3	30	14	11.4	1.21E-04	1.23E-00
4510336.3	50	8	23.2	3.46E-04	3.45E-01
4515477.3	70	1	16.5	3.69E-05	6.06E-02
4515478.3	91	3	34.7	1.16E-04	8.64E-02
4515476.3	159	3	25.8	9.77E-05	1.16E-01

Table S3: Inhibition constants for various compounds, against L-Phe-AMC.

Inhibitor	K_i , μM
D-Leu-NH ₂	1450
D-Leu-OMe	890
D-Phe-NH ₂	4500
D-Phe-OMe	845
D-Phg-NH ₂	2100
D-Phg-OMe	1950
L-Leu-NH ₂	2290
L-Leu-OMe	107
L-Phe-NH ₂	242
L-Phe-OMe	56
L-Phg-NH ₂	1910
L-Phg-OMe	1770

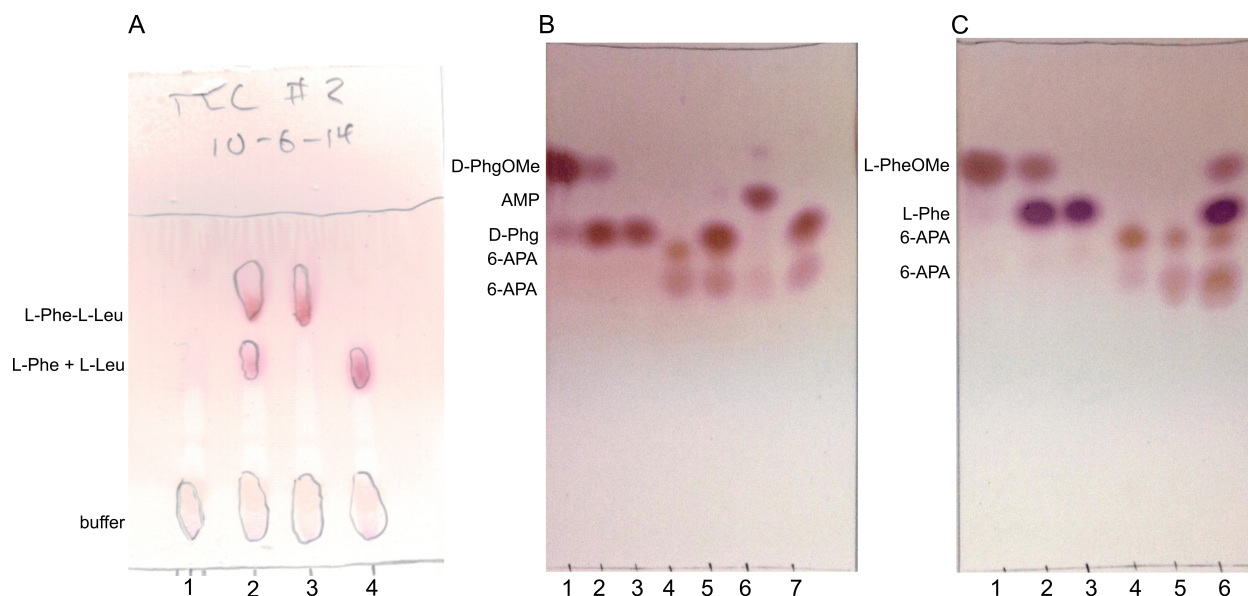


Fig. S1. TLC-based assay for BAP activity. A) Lanes: 1 – BAP alone, 2 – L-Phe-L-Leu + enzyme, 3 – L-Phe-L-Leu + enzyme + L-Leu + L-Phe, 4 – L-Leu + L-Phe. B) Lanes: 1 – D-Phg-OMe, 2 – D-Phg-OMe with BAP, 3 – D-Phg, 4 – 6-APA with BAP, 5 – D-Phg-OMe with 6-APA and BAP, 6 – ampicillin (AMP), 7 – ampicillin with BAP. C) Lanes: 1 – L-Phe-OMe, 2 – L-Phe-OMe with BAP, 3 – L-Phe, 4 – 6-APA, 5 – 6-APA with BAP, 6 – L-Phe-OMe with 6-APA and BAP. Note, that 6-APA migrates as two species, which is most likely attributed to two protonation states.