

# Supporting Information

## The identification and use of robust transaminases from a domestic drain metagenome

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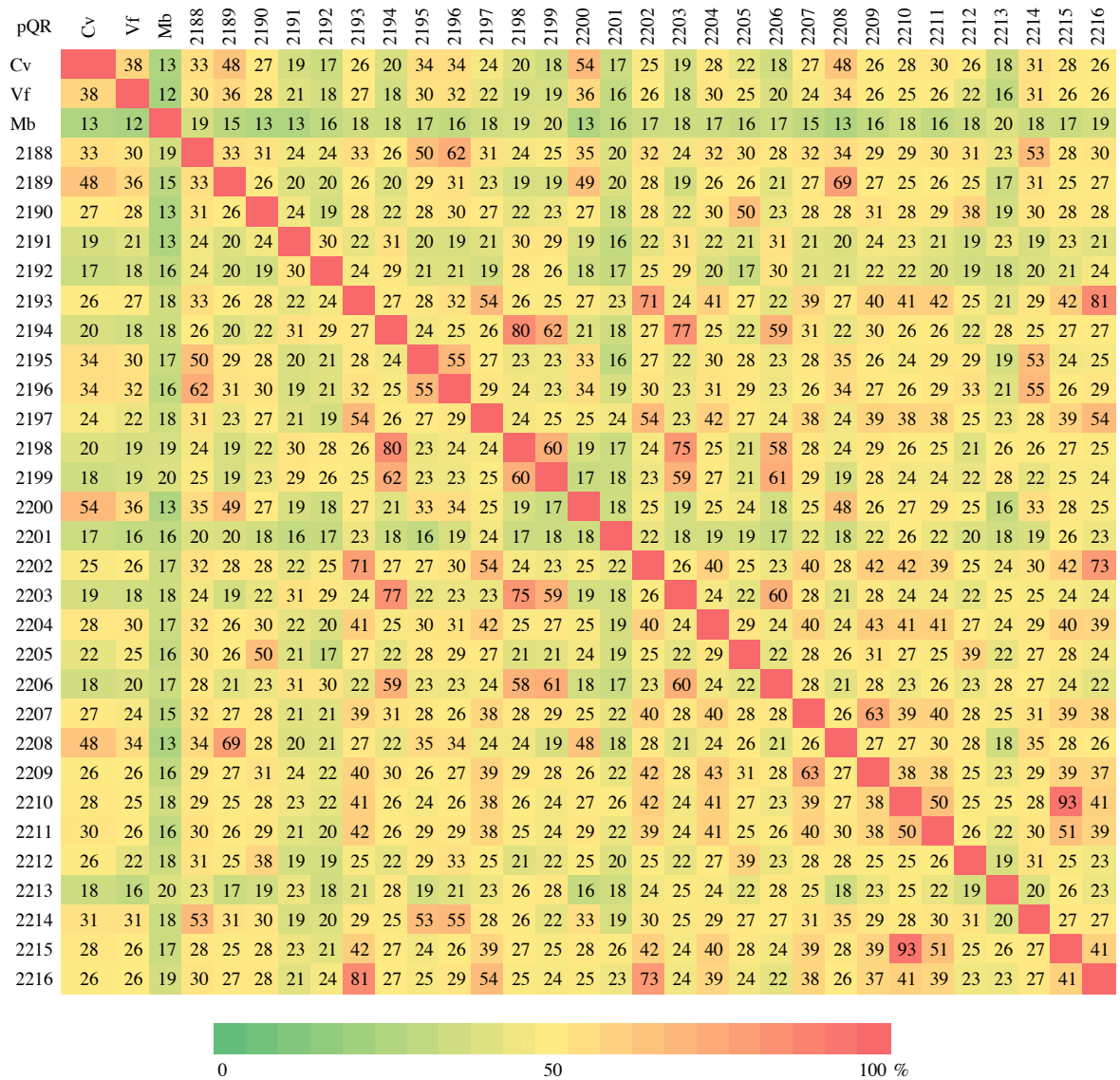
## 1. Taxonomic assignment of drain Class III TAmS

**Table S1.** Protein length, predicted molecular weight (MW) (calculated using ExPASy ProtParam), protein annotation and organism and percentage identity to closest homologue in NCBI database. Data have been deposited in GenBank and the accession number of each enzyme coding sequence is listed below beside the pQR number.

pQR	Accession number	Length (aa)	Predicted MW (kDa)	Function	Taxonomic Assignment	% Ident. to NCBI
2188	MK121624	483	52.3	Aspartate aminotransferase family protein	<i>Pseudoxanthomonas sp.</i>	97
2189	MK121625	484	52.3	Aminotransferase	<i>Sphingopyxis sp.</i>	96
2190	MK121626	490	54.6	Adenosylmethionine-8-amino-7-oxononanoate transaminase	<i>Perlucidibaca sp.</i>	71
2191	MK121627	450	49.2	Glutamate-1-semialdehyde 2,1-aminomutase	<i>Novosphingobium aromaticivorans</i>	63
2192	MK121628	701	77.8	Glutamate-1-semialdehyde aminotransferase	<i>Herbaspirillum lusitanum</i>	77
2193	MK121629	417	44.4	Acetylmethionine aminotransferase	<i>Azonexus hydrophilus</i>	85
2194	MK121630	456	48.1	Glutamate-1-semialdehyde aminotransferase	<i>Candidatus Propionivibrio aalborgensis</i>	83
2195	MK121631	478	51.5	Omega amino acid-pyruvate aminotransferase	<i>Acidovorax sp.</i>	99
2196	MK121632	469	51.1	Aspartate aminotransferase family protein	<i>Mesorhizobium</i>	90
2197	MK121633	414	44.5	Acetylmethionine aminotransferase	<i>Alkanindiges illinoisensis</i>	78
2198	MK121634	454	47.7	Aspartate aminotransferase family protein	<i>Azospira oryzae</i>	99
2199	MK121635	468	49.8	Aspartate aminotransferase family protein	<i>Alkanindiges illinoisensis</i>	76
2200	MK121636	460	50.9	Aminotransferase	<i>Pseudoxanthomonas mexicana</i>	97
2201	MK121637	1494, 504	54.5	Lysine 6-aminotransferase	<i>Pseudoxanthomonas mexicana</i>	97
2202	MK121638	394	42.4	Acetylmethionine aminotransferase	<i>Candidatus Accumulibacter phosphatis</i>	83
2203	MK121639	433	45.7	Aspartate aminotransferase family protein	<i>Azonexus hydrophilus</i>	96

2204	MK121640	401	42.8	Acetylnithine transaminase	<i>Sphingopyxis sp.</i>	98
2205	MK121641	447	48.4	Adenosylmethionine-8-amino-7-oxonanoate transaminase	<i>Roseateles depolymerans</i>	76
2206	MK121642	436	45.9	Glutamate-1-semialdehyde aminotransferase	<i>Pseudoxanthomonas sp.</i>	98
2207	MK121643	402	42.9	Acetylnithine transaminase	<i>Azospira oryzae</i>	98
2208	MK121644	1380, 466	50.1	Aspartate aminotransferase family protein	<i>Sphingomonas sp.</i>	83
2209	MK121645	404	42.4	Acetylnithine aminotransferase	<i>Curvibacter delicatus</i>	69
2210	MK121646	416	44.3	Acetylnithine aminotransferase	<i>Pseudoxanthomonas sp.</i>	94
2211	MK121647	412	44.2	Acetylnithine aminotransferase	<i>Pseudomonas lavalieres</i>	100
2212	MK121648	423	46.2	Denosylmethionine-8-amino-7-oxonanoate transaminase	<i>Sphingopyxis</i>	94
2213	MK121649	453	47.9	Aminotransferase	<i>Sphingopyxis</i>	87
2214	MK121650	459	49.5	Omega amino acid-pyruvate aminotransferase	<i>Aquabacterium parvum</i>	70
2215	MK121651	414	44.1	Acetylnithine aminotransferase	<i>Pseudoxanthomonas sp</i>	96
2216	MK121652	396	42.0	Acetylnithine aminotransferase	<i>Dechloromonas aromatica</i>	87

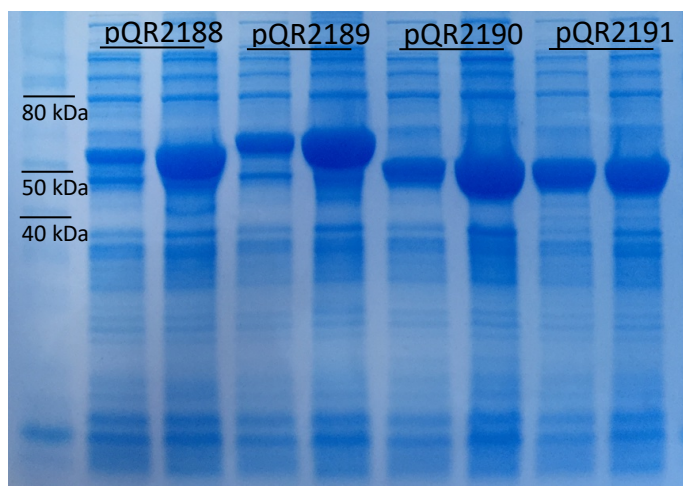
## 2. Percentage Identity Matrix



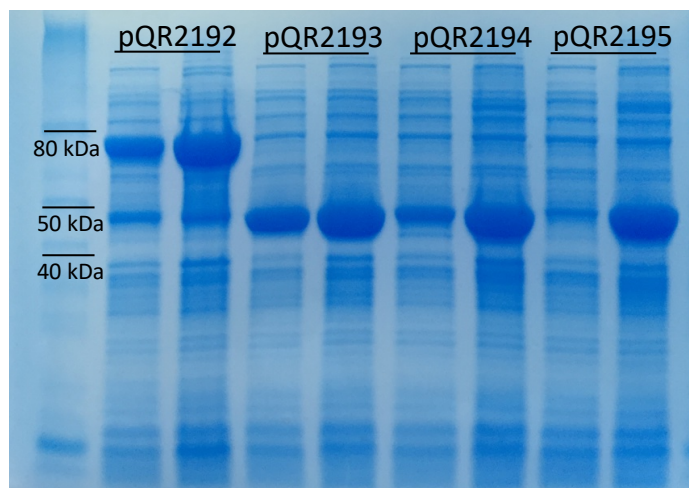
**Figure S1.** Heat map of the percentage identity of 29 cloned drain TAmS. Percentage identity matrix generated using Clustal Omega Multiple Sequence Alignment tool and visualised using Excel. Cv: *Chromobacterium violaceum* CV2025 accession number WP\_011135573.1, Vf: *Vibrio fluvialis* JS17 accession number AEA39183.1, Mb: *Mycobacterium vanbaalenii* ABM15291.1.

### 3. Expression of 29 TAMs

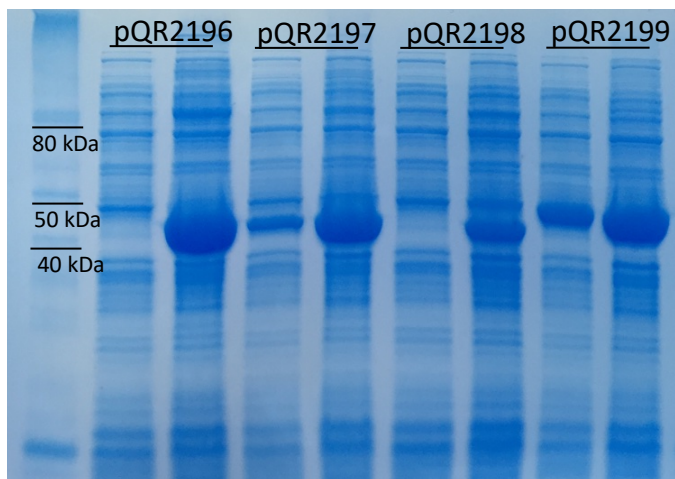
In the following SDS-Page gels, lane 1 is always ladder - NEB Broad Range protein ladder (10-250 kDa) (Figure S2-S4) or NEB color protein standard (Figure S5-S9), each protein is in two wells – the first is the cell free extract (CFE) and the second is the total protein (TP) fraction.



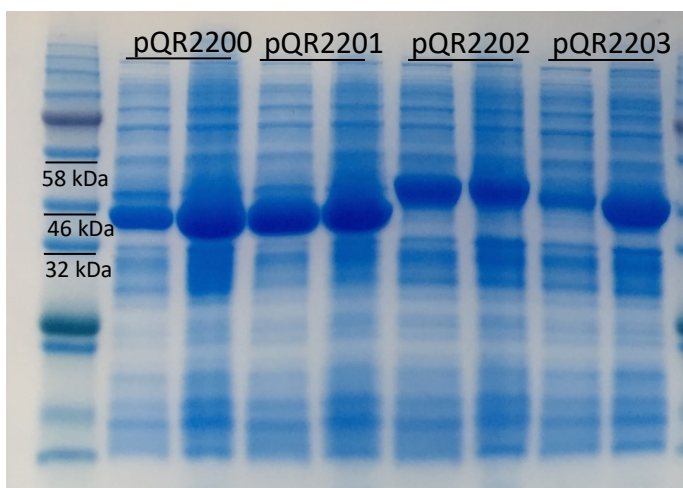
**Figure S2.** SDS-Page gel of pQR2188-2191.



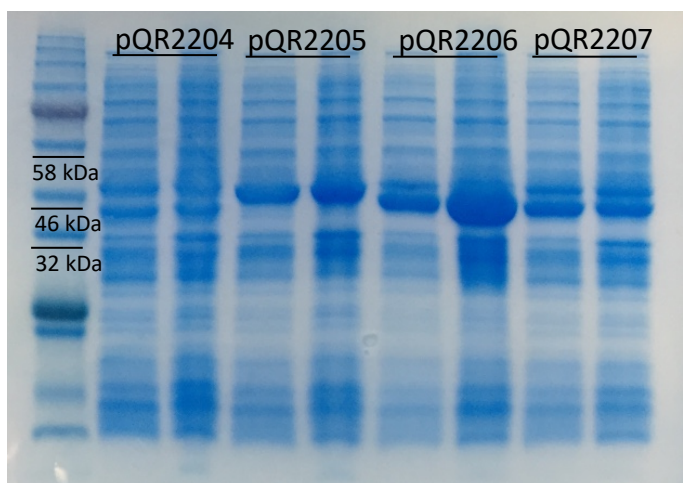
**Figure S3.** SDS-Page gel of pQR2192-2195.



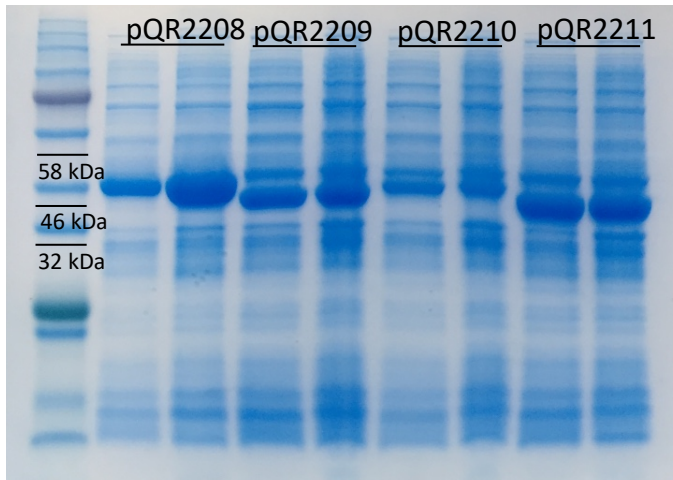
**Figure S4.** SDS-Page gel of pQR2196-2199.



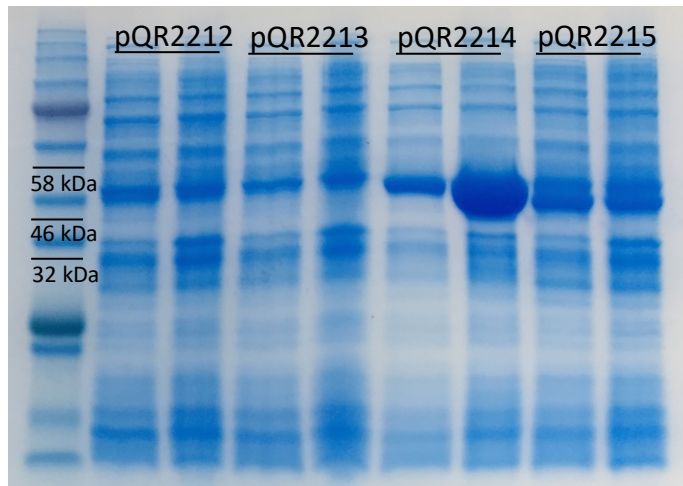
**Figure S5.** SDS-Page gel of pQR2200-2203.



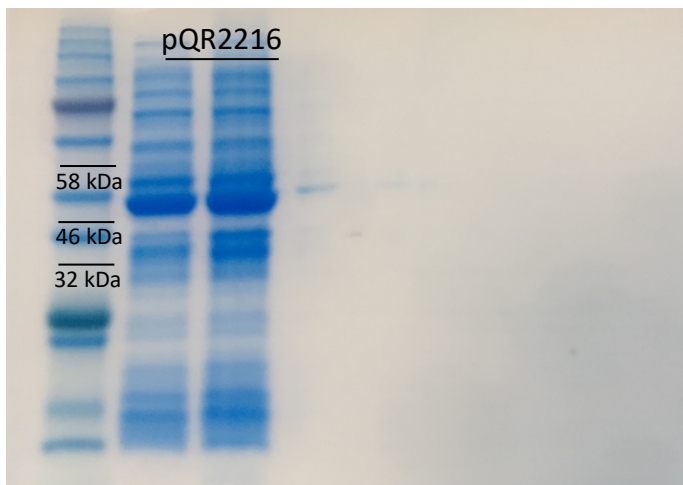
**Figure S6.** SDS-Page gel of pQR2204-2207.



**Figure S7.** SDS-Page gel of pQR2208-2211.



**Figure S8.** SDS-Page gel of pQR2212-2215.



**Figure S9.** SDS-Page gel of pQR2216.



#### 4. DNA Sequences

##### >pQR2188

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##### > pQR2189

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**> pQR2195**

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**> pQR2196**

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**> pQR2197**

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**> pQR2198**

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**> pQR2199**

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**>pQR2200**

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**> pQR2201**

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**> pQR2202**

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**> pQR2203**

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**> pQR2204**

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**> pQR2205**

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**> pQR2206**

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**> pQR2207**

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GCTGGCGCGCAAGTGGGGGCAGAAGCACAAAGGGCGCGCCACGAGATCATCACCT  
CGCCGGCGGCTTCCACGGCCGCACCCTGGCCACCATGTCGGCCTCCGGCAAGCCGG  
GCTGGGACACCCTGTTCCGCCCCAGGTGCCGGGCTTCCCAAGGCCAGCTGAACG  
ACCTGGATTCGGTGGCGGCCCTCATCAACGAGCGCACCGTGGCCATCATGCTGGAGC  
CGATCCAGGGCGAAGGCGGGGTGGTGCCGGCCAGTGTGGAATTCCTGCAACTGTTGC  
GGCAGATCTGCGACGACCGGGGCTGCTGCTGATCGTGGACGAGGTGCAGACCGGC  
ATGGGCCGCACCGGCAAGCTCTTCGCCACCAGCACGCCGGCATCGAGCCGGACATC  
ATGACCCTGGGCAAGGGCATCGGCGGGCGGCGTGCCCTCTCGGCCCTGCTGGCCAA  
GGAATCGGTCTGCTGCTTCGAGGCCGGCGACCAGGGTGGCACCTACAACGGCAATCC  
GCTGATGACCGCCGTCCGGCGTCCCGTGTGGAAGTGTGACGGCCCCCGGCTTCT  
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CCGACGAGCGGGGCCCGCCATCGTCGAGGCGGCCCGGGAGCGGGGCCCGAGGG  
TCTGCTGCTAACCGCGCCGCCGCCACCTGCTGCGCTTCATGCCGTCCCTGACGGT  
GAGCCGGGAGGAGATCGACCAGATGCTGGCCTGGCTGGAGGAACTGCTGGGGGCCT  
GA

**> pQR2208**

ATGACCCTGCGTAATTACGACATGGCCGAGCTCAAGCGGCTCGACCTCGCCCATCATC  
TGCCCGCGCAGGCAAGCTACGGCCTGATCCGCGACCTGGGCGGCAGCCGGATCATCA  
CCCGCGCCGAAGGATCGACGATCTGGGATGCGGAGGGCAATGCGATCCTCGACGGGA  
TGCGGGGCTGTGGTGCCTCGACGTCGGCTATGGCCGCGCCGAGCTGGCCGAGGTC  
GCACGCGAGCAGATGCTCGAGCTTCCCTATTACAACACCTTCTTCCGCACCGCGACGC  
CGCCACCGGTGAAGCTTGCCGCGAAGATCGCCGGACTGCTCGGCGGATCGCTCCAGC  
ATATCTTCTTCAACTCGTCGGGCTCCGAATCGAACGATACGGTGTTCGGCCTCGTGCG  
CACCTATTGGGCGCTGAAGGGACAGCCCGAACGCACGATCTTCATCTCGCGCCGCAA  
CGCCTATCATGGCTCGACCGTCCCGGCGTCAAGCCTGGGCGGCATGGCGGCGATGCA  
TGCGCAGGGCGGGCTCCCGATCGCCGGCATCGAGCATGTGATGCAGCCTTATGCGTT  
CGGCGAAGGCTTCGGCGAGGATCCCGAGGCGTTCGCCGCGCGCGCCGCTCAGGAGA  
TCGAGGATCGTATATTGGCTGTCGGGCTGAAAAGGTCGCTGCCTTCATCGGCGAGCC  
GGTGCAGGGCGCCGGCGGCGTCAATCCCGCCCCCGGATACTGGCCGCGGGTGC  
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CGGGCGGCTGGGCGAATGGTTCGGCTTCCAGAAATATGGCTATACGCCCGATATCGTT  
TCGATGGCGAAGGGGCTGTGCTCGGGCTATCTGCCGATCTCGGCCACGGGCGTGAGC  
AGCGAGATTGTCGAGACGCTGCGCGCGTCCGGGCGACGATTCGTCCACGGCTATACC  
TATTCGGGGCATCCGGTGGCCGCGGCCGTGGCGCTGCGCAATCTGGAGATTATCAAG  
CGCGAAGGGCTGGTCGATCGCGTGCAGCGACGATCTGGCACCCCTATTCGCGAAGGCG  
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CGGCGCGGTGGAGATCGTTTCCGAGAAGGGCACCAACCACCGCTTCGGCGGCAAGGA  
AGGCACCGCCGGGCCGGTTCGTGCGCGATCACTGCATCGCGGGCGGGGCTGATGGTGC  
GCGCGATCCGTGACTCGATCGTCAATGTGCCCGCCCTATGTTATCACGCATGACGAGAT  
CGACCGGATGGTTGCCATCATCCGCTCGGCGCTCGACAAGGCTGCGGTGATCTGGG  
TGGAGGCGCCTGA

**> pQR2209**

ATGAACCATCCATCCGCCCTTCCCTCCGCCGCCAGCCTGATGCCGATCGCCACCCGCC  
CGGACGTCCTCTTCGTCCGCCGCCAAGGCGCCTGGCTGTTTCGATGCCGCAGGCCGCC  
GCTACCTCGACTGGATGCAGGGCTGGGCGGTCAATTGCCTGGGCCATTCCGCCGAGG  
TGATCGTCGATGCCGTCCGCAACAGGCGGCGACGCTGCTCAACCCCGGCCCGCCT  
TCCACAACCTGCCGGCGATGCGCCTGGCCGAGAACTCACCGCGCACAGCGGCTTCG  
ACCACGTCTTCTTCGCCAGTTCCGGGGCCGAAGCCAACGAAGGCGCGATCAAGCTGG  
CGCGCAAATGGGGGCAGTTGCACAAGGGCGGCGCGCACGAGATCGTCACCTTCGTCCG  
ACGGCTTCCACGGGCGCACGCTGGCGACCATGTCCGGCCAGCGGCAAGCCC GGCTGG  
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GCCACGGTCCGACCGGCTGATCGGACCAAAAACCGTCGCCGTCATGCTCGAACC GATC  
CAGGGCGAAGCCGGCGTCATCCC GGCCAGCGGCGACTTCTGCGCCAGTTGCGGCA  
ACTGTGCGACGAACGCCAACTGCTGCTCATCGTCGACGAAGTGCAGACCGGCGTCCG  
CCGCACCGGCCACCTCTTCGCCCATAGCGCGCACGGCATCCAGCCGGACATCATGAC  
GCTCGGCAAGGGCCTCGGGCGGCGGCTGCCGATCTCGGCCCTGCTCGCCACCCGCG  
CCGCTTCTGCTTCGCCCCCGGCGACCAAGGGCGGCACCTACTGCGGCAACCCGCTGG  
TCTGTGCCGCCGGGCTGGCCGTGCTCGACACCCTGCTCGCCGACGGCTTCTCGCCG  
CCAGCCGGCAGCGCGGGCGAGCAGCTCGCCGACGCACTGCGCACGCTGTCCGCCGAA  
CTCGGCCTCGGCGCAGTGC GCGGCGAAGGTTTCTGCTCGCGCTCGAACTCGGCGCC  
GACCTCGGCCCGGCCATCGCCACCCGCGCCCGCGACCTCGGCCTGCTGGTCAACGC  
GCCGCGCGCGCACTGCCTGCGCCTGATGCCGGCGCTGAACACCAGCGCCGCCGAAA  
TCGCCGAAGGCATCGCCCTGCTCCGCCGCGCCATTGCCGACGTGCAAGAGGCACAAG  
CATGA

**> pQR2210**

ATGAGCGTCTCCACCACCGCCGACCTGCTGGCCCACGGCCAGCGCTATTACCTGCCG  
GTGTACCGCCCGCGCGAGGTGATCCTGGAGCGCGGCGAGGGCGCACGCGTGTGGGA  
CAGCGAGGGCCGCGAATACCTGGACCTGTCCGCGGGCATCGCCGTATGCGGGCTGG  
GCCACAACGATCCGGATCTGGTGGCTGCACTACCGAGCAGGCCGGCAAGCTCTGGC  
ATACCAGCAACGTGTTCTACAGCGAACC GCCGCTGCGATTGGCCGAGGAACTGGTCAC  
TGCTTCGCGCTTCGCCGAACGCGTCTTCTGTGCAACTCCGGCGCCGAGGCCAACGA  
GGCCGCGATCAAGCTGGTGC GCAAATGGGCGGCATCGCAGGGCCCGCGCGCCGGACC  
AGCGCGTCATCGTGACCTTCCGCGGCAGCTTCCACGGCCGCACGCTGGCCGCGGTCA  
CCGCCACCGCGCAACCCAAGTACCAGGAAGGCTACGAGCCCTTGCCCGGCGGCTTCC  
GCTACGTTCGATTTCAACGATGTGACCCAGCTCGAGATCGCCATGTCTGCGGCGACGT  
GGCCGCGGTGATGCTGGAGCCGGTGCAGGGCGAGGGCGGGGTGATGCCGGCCGCG  
TCCGGCTTCTGCGCGCGGTGCGCGAGCTGTGCGACCACCACGGCGCATTGCTGGTG  
CTGGACGAGATCCAGGCCGGCATGGGCCGCACCGGCACGCTGTTCCGCGCACTGGCA  
GGATGGCGTGGTGC CCGACATCGTGACGCTGGCCAAGGCCCTGGGCGGCGGGTTCC  
CGATCGGTGCGATGCTGGCCGGCCCCAAGGTGGCGCAGGCGATGCAGTTCGGCGCG  
CATGGCACCACTTCGGCGGCAACCCGCTGGCCGCCGCGGTGGCGCGCGTGGCGCT  
GCGCAAGCTGGCCTCGCCGCGAGATCGCCAACAACGTGGCGCGTCAGTCGGTCGCGCT  
GCGCAAGGGGCTGGATGCGATGAACGCCGAACTCGGCCTGTTCTCGCAGGTGCGTGG  
TCGCGGCCTGATGCTGGGCGCCGTGCTCGACGCGAAGTACGCCGGCCGTGCGGGCG  
AGGTA CTGGACCTGGCCGCCGCGAAGGGCCTGCTGATGCTGCAGGCGGGCCCCGAC  
GTGCTCCGCTTTCGTGCCGTGCTGAACATCACCGATGAGGAAGTCGGCGAGGGCCTC  
AGTCGCCTGCACGCAGCGCTGAGGGCGTTCCGCAAGCCGGGCTGA

**> pQR2211**

ATGTCCGTTTCAGCACGATCCGGTGCAACGCGCCGATTTTCGATCAGTATCTGGTCCCCA  
ACTATGCCCTGCGCCTTTGTTCCGGTGC GTGGCCTGGGTTCCGCGAGTCTGGGATCA  
GAGCGGTCCGCGAGCTGATCGATTTCCGCCGGCGGTATCGCCGTCAACGCCCTCGGTCA  
CTGCCATCCGGCACTGGTCAAGGCGCTGACCGAGCAGGCCAACACCCTGTGGCACAT  
CTCCAACGTGTTACCAACGAGCCGACCCTGCGCCTGGCCACAAGCTGGTTCGATGC  
AACCTTCGCCGAGCGCGTGTCTTCTGCAACTCCGGCGCCGAGGCCAACGAAGCCGC

CTTCAAGCTGGCCCGTCGCGTCGCCCATGACCGTTTCGGCCCGGAGAAGTACGAGAT  
CATCGCCGCGCTCAACAGCTTCCACGGTCGTACCCTGTTACCGTCAGCGTTGGTGGC  
CAGCCCAAGTACTCCGATGGTTTCGGGCCGAAGATCGAGGGCATCACCCATGTCCCGT  
ACAACGACCTGGACGCGCTGAAGGCGGCCATTTCCGACAAGACCTGCGCCGTGGTCC  
TGGAGCCGATCCAGGGCGAGGGCGGTGTGCTGCCGGCCGACAAGGCCTACCTGGAA  
GGCGCCCGTGGCCTGTGCGACCAGCACAAACGCGCTGCTGGTGTTCGACGAGGTGCAG  
AGCGGCATGGGCCGACGCGCCGAGCTGTTACCTATATGCACTACGGCGTCACCCCG  
GACATCCTCTCCAGCGCCAAGAGCCTGGGCGGCGGTTTCCCCATCGGGCCCATGCTG  
ACCACCACCGAGCTGGCCAAGCACCTGGCCGTGGGCACCCACGGCACCCACCTACGGC  
GGCAACCCGCTGGCCTGCGCGGTGGCCGAAGCGGTACTGGACATCGTCAACACCCCA  
GAAGTGCTGCAGGGCGTGAAGGCCAAGAGCGAGCAGTTCAAGCAGCGCCTGCTGGCC  
ATCGGCGAGCGTTATGGCATGTTCCGCCGAAGTACGTGGCCTGGGCCTGCTGCTCGGC  
TGCGTGCTCAACGATGCCTGGAAGGGCAAGGCCAAGGCCGTGCTGGATGCCGCTGCC  
GCCGAGGGCGTGCTGGTGTGCTGCAGGCCAGCCCGGACGTGGTGCCTTTCGCGCCAG  
CCTGGTGGTAGAAGAGGCCGATATCGTCGACGGTCTGGACCGTTTGAACGCGCCGT  
CGCCAAGCTCGCGCAGGGCTGA

**> pQR2212**

ATGGCCGATACCTCCCCGTCTGGCACCCCTTACCCAGCACGGCCTCGGGACCCC  
ATTCCGCTGATAAGCCACGCTAAAGACGCCAAGCTCTACGCCGCCGACGGGCAAAGCT  
GGATCGACGCCATCTCCAGCTGGTGGGTACCACCCACGGCCACGCCACCCCGCGCA  
TCATGGCCGCGATCCGCGCCAGACCGAAAAGCTCGACCAGCTCATCTTTGCCGGCT  
GGACGCACGAGCCCGCCGAAAGCCTCGCCGCCGAGCTGATCCGGATCACCCCGCC  
CCGCTACCCGCGTCTTCTTCTCGGACTCGGGCTCGACCAGCGTCGAGGTCGCGCTC  
AAGATGGCGCTCGGCTATTGGTATAACATCGGCCGAGCCGCGCAGCCGCATCCTCGTC  
CTCGAACATAGCTATCATGGCGACACGATCGGCACGATGTGCGTCCGGCAGCGCGGC  
GTCTACAATCGCGCCTGGCAGCCTTTGCTGTTTCGACGTAGACACCATCCCCTTTTCTTA  
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CGCCGCCTTCATCGTCGAACCCTTGATCCTCGGCGCCGGCGGCATGCTCATCTACCCC  
GCGTGGGTGCTCGCCGAGATGCGCGCGATCTGCGCGCGCCACGGCGTCTCTTCATC  
GCCGACGAGGTAATGACCGGCTGGGGCCGCACCGGCACGCGCTTCGCCTGTGATTCT  
GCGGGCGTCATCCCGGACATCGTCTGCCTGTGCAAAGGCCTCACCGGCGGAGCGCTC  
CCGCTCGCGGTACGCTCTGCATCGAACCGATCTTCGAAGCCCATTTCTCGACCGACC  
GCAGCAAGACCTTCTATCATTGAGCAGCTACACCGCGAACCCGATCGCCTGCGCCCG  
CGCAAACGCCAATCTCGAAATCTGGCGCGAAGAGCCCGTCCAGCAGCGTATCGACGC  
GCTCGCCGAAGCGCAGGCCGCACACCTCTCGCTGCTCAGCCACGATCCGCGCGTCCA  
AAATCCCCGCGTCTCGGCACAATCGCCGCGCTCGACATCGTTCGTCGCGGACTCAGG  
CTATCTCTCGAACCTCGCCCCGCGCCTGATCGCCTTCTATCGCGACCATGGCGTCTTG  
CTCCGCCCCGCTCGGCAACACGCTCTACGTATGCCGCCCTATTGCATTACGCCTGACG  
AGCTCGCGCAGGTGTGGAGCGCGATAACGGCCTCGCTCGACGCCGTATGA

**> pQR2213**

ATGATCTCGCCCGCCGCCATCGCGCGCGTTGCCGAGCGCGAGGCCGACCGCTTTCGC  
GCCGCTAATACGCGCGCGTTCGCGCATCATGCGGCGGCGACGGGTTGGTTCCAGTCG  
GTGCCCTTCCACTGGATGAAGGACTGGCCAGCCCGGTGCCAATCGTCGCAGCGTCG  
GCAAAAGATGCGGCGCTGACTAGCATCGACGGTCAAACCTACGATGACTTCTGCCTTG  
GCGACACCGCAAGCCTGTTCCGCCACTCACCGCCCGCACTCGCCGCCGCGCTAGCGA  
GGCAGGCAGGCGAAGGCTTGAGCTATATGCTCCCGACCGGACGCGGTGCCGCGCTGT  
CGGAGCGACTCGCGGTGATGTTCCGCGCTGCCGCAATGGCAGGTCACGACGACCGCCA  
GCGAGGCCAATCGAGCGGTGATCCGCTGGTGCCGCGGGATCAGCGGGCGACCCAAG  
ATCCTGACCTTCAACGGAGCCTATCATGGCGCGGTGACGACGCATTTCGTCGACCTGA  
AGGCTGGCGCTCCCACGATGCGAGCCAGCCTGATCGGTCAGGCTCACGATTTGTGCA  
CGACCACCGCGGTGATCGAGTTCAACGACGAAGACGCGCTTGCAAACGCCCTGCGTG  
GCGGCGACGTGCGCTGTGTGCTCGCCGAGCCGGTATGACCAATGTTGGTATGGTGC  
GCGACGCGCCGGGCTTTCTTGCAACCCTCCGCAGGCTTTGCGATGAAACGGGCACGTT

GCTGGTCTTCGACGAAACCCACACCATCTCCTCGGGCTACGGCGGCCATAGCGTTACG  
CACGGCCCCGCCCCGGACCTGATAGTCATCGGCAAGTCGATCGGCGGGCGGCGTGCC  
CTGTGCGATCTATGGATTTTCGGCTGTGGTGGCGGAACGGATGGCGGGCGCTCAACCAA  
TCACGCCCTCCAGGACATAGCGGCATCGGCACCACGCTTTCGGCCAACGCCCTAGCC  
ATCACTGCGATGGATGCGATGCTGGGCGAGGTCATCACGTCGGCTGCCTATGACCATA  
TGCTGCGCGGGCGCCGCGCGGCTCGTCGCCGGGCTCGAACAGGAAATAGCGCACGTC  
GGTCTCGACTGGCACGTCACCCAGGTCGGCGCCCCGCGTCGAATTCCTGACCTGCCCC  
ACCCCGCCCCGCAACGGTAGCGAGGCAAAGGCGGCGATGCATCTCGAACTCGAAGCG  
GCGATGCACCTTTTCCTTGCCAATCGCGGGATTTTGCTGGCGCCGTTTCACAATATGAT  
GTTGGTGAGCCCGTTACCACGGACGATCAGATCGACCGGCTGGTCGGCGCATTTCG  
CGACAGCGTGCAGGCATTGAAGGAGTGA

**> pQR2214**

ATGAACTATCCGGAATCAATCGCTGCACAGGTCGGTACGCCGCAGGGGCTGGACAACT  
ACTGGCTGCCGTTTACGCCCAATCGCTATTTCCGCGAGCATCCGAAGCTGATCGCCGG  
GGCCGAGGGCGCTTACTTCAATTCTTTCGGACGGCCGCAAGCTGTTTCGATGCCCTGTCC  
GGGCTGTGGTGTGTCCGCTCGGCCACGGCAACCCGAAGATCGTTGAGGCGCTGGCG  
AAGCAGGCGAAGGCGCTCGATTACGCGACGGCCTTCCAGTTCGCCAATCCGGTGACG  
CTCTCGCTCGCCGAACGCATCGCGACGATGGCGCCGGAAGGGCTGACGCGCGTGTTTC  
TTCGCCAACTCGGGTTCGAGTCGGTCGATACGGCGTTGAAGGTGGCCTACGGCTACC  
AGCGGCTGCGCGGGCGAGGGCGGGCGCACCCGCTTCATCGGGCGCGAGAAGGGCTAT  
CACGGCGTCCGTTTTCGGCGGCATGTCCGTCGGCGGCATGGTCGCCAACCGCAAGATG  
TTCGGACCGATCATGGTGCCCGGCGTCGATCACCTGCCGCACACCTACAACCTCTCGC  
AGATGGCCTTCTCCAAGGGCATGCCGACCTGGGGCGCGCATCTGGCCGAGGAACTGG  
AACGGATCGTCGCGCTGCATGACGCCTAACGATCGCCGCCGTCATCGTCGAACCGAT  
GCAGGGTTCGGTCGGCGTCATCGCGCCCGCGGTCGGCTACCTGCAGAAGCTGCGCGA  
CATCTGCACCAAGCACGGCATCCTGCTCATCTTCGACGAAGTGATCACCGGCTTCGGG  
CGCATGGGTACCAACTTCGGCTCCGATTTCTTTGGCGTCACGCCCCGACATCATCTGCTT  
CGCCAAGGGCGTCACCAACGGCACCGTGCCGATGGGCGGCATCATCGTGCGCGAGG  
AAATCTACCAGGCGTTCATGGGCGTCAACGCGCCGGAGTACGCCGTCGAGTTGATGCA  
CGGCTACACGTATTCGGGTTCATCCGCTGGCGGGCCCGGTCGGTCACGTCGCGCTCGA  
TGCGCTGGTGAACGACGGCCTGATCCAGCGTGCGGGCGGAACTCGCGCCGGTGCTCGA  
AGACGTGATCCACGGACTCAAGGGTGAGCCCGGCGTCATCGACATCCGCAACGTCCG  
CCTGGCGGGCGGGCGGTTCGATCTCGAAGGCATTCCGGGCAAGGTCGGGCTGCGCGCGC  
TGCGTACCTTCGAAGCGGGCATCGAGGAAGGGCTGATGCTGCGCTTCACCGCCGACA  
CGATCGCCATGGGGCCGCCCTTCATCTCTACGCGCGACGAGATCGAGGCGCTCGGCG  
AGAAGCTGCGCCGGGCGATCCGCAAGGCGTTCTCGCAAACCTGA

**> pQR2215**

ATGAGCGCCACGACCCCGACCTGCTGTGCAACGGACAGCGCTATTACCTGCCGGTC  
TACCGTCCGCGCGAGGTGATCCTGGAGCGCGGCCAGGGCGCGCGCGTCTGGGACAG  
CGAGGGCCGCGAGTACCTGGACCTGTCCGGCCGGCATCGCCGTGTGCGGTCTGGGCC  
ACAACGATCCGGACCTGGTCGCCGCGCTCACCGAGCAGGCGGGCAAGCTGTGGCACA  
CCAGCAACGTGTTCTACAGCGAGCCCGCTGAGGCTGGCCGAGGAACTGGTGAGCG  
CCTCGCGTTTTCGCCGAGCGCGTGTTCTGTGCAACTCCGGTGCGGAGGCCAACGAAG  
CGGCGATCAAGCTGGTGCGCAAGTGGGCGACCTCGCAGGGCCGTCGCGCCGGACCAG  
CGCGTCATCGTGACCTTCCGCGGCAGCTTCCACGGCCGCACGCTGGCGGGCGGTACCC  
GCGACCGCGCAGCCCAAGTACCAGGAAGGCTACGAGCCGCTGCCGGCCGGCTTCCG  
CTATGTGACTTCAACGACCTGACCCAGCTGGAGATCGCCATGTGTCGCGGCGACGTC  
GCCGCGGTGATGCTCGAGCCGGTGCAGGGCGAGGGCGGCGTGATGCCGGCCGCCCC  
CGGCTTCTGAGCGCCGTCCGTGCGCTGTGCGACCACCATGGCGCGCTGCTGGTGCT  
GGACGAGATCCAGGCCGGCATGGGCCGCACCGGCACGCTGTTCCGCGCACTGGCAGG  
ACGGCGTGGTGCCGGACATCGTGACGCTGGCGAAGGCGCTGGGCGGGCGGCTTCCCG  
ATCGGCGCGATGCTGGCCGGACCGAAGGTGGCCGAGGTGATGCAGTTCGGCGCGCA  
CGGCACCACCTTCGGCGGGCAATCCGCTGGCCGCCCGGTCGCACGCGTGCGGCTGC

GCAAGCTGGCGTCGCCGCAGATCGCCAACAACGTGGCGCGCCAGTCGGCCGCCCTG  
CGCAAGGGACTGGATGCAATCAACGCCGAGCTCGGCCTGTTCTCGCAGGTGCGCGGT  
CGCGGCCTGATGCTGGGCGCGGTGCTCAACGCGAAGTACGCCGGCCGCGCCGGCGA  
GGTGCTGGATCTCGCCGCGGCACAGGGCCTGCTGATGCTGCAGGCCGGCCCCGATGT  
GCTGCGCTTCGTGCCGTCGCTCAACATCACCGACGCGGAAGTGGCCGAAGGGCTGAA  
GCGCCTGCATACCGCGCTGAAGGCGTTCGCTGCGCGCTGA

**> pQR2216**

ATGTCGCATGTGATGAATACCTATGCCCGCCTGCCGGTAACCTTCAGTCACGGTTGCG  
GGTCCCGCCTGTTTCGATGTGCGAGGGCAAGGAGTATCTCGACGCCTTGTCCGGCATTGC  
CGTTTCGACCTTGGGCCACGCCCATCCGAAACTGGTTGCCGCGCTTGCCGCTCAGGCT  
GGCCGCATGCTGCATGTCTCCAACCTGTACCGGATCGCCGAGCAGGAACAACCTGGCC  
GACAAGCTGTGTTTCGCTGTCCGGGATGCAGGAAGTCTTTTTTCGGCAATTCAGGCGCCG  
AAGCCAACGAGGCGGCAATCAAGCTGGCACGTTTTCTACGGCCACAAGAAGGGCGTTG  
AACTCCCGACGGTGATCGTCATGGAGAAAGCCTTTCACGGTCGCACTATGGCGACCTT  
GTCCGGGACCGCCAACCGCAAGGCGCAGGCCGGTTTTCGAGCCGCTGGTCAGCGGTTT  
CGTCCGGGTTCCCTACGGCGATCTCGACGCCATCAAGGCGGTGGCCGAGCACAACAA  
GAACATCGTCGCGGTGATGTTTTGAAATCATCCAGGGCGAAGGCGGCATCCATCTCGTC  
GATCCGGCTTTCTATCGCGGCGTGCGCGAGCTTTGCGACCGGAACGAATGGCTGATGA  
TGTGCGACGAAGTCCAGTGCGGCATGGGACGAACCGGCAAATGGTTCCGCTTCCAGA  
CCGCCGGCGTCCAGCCGGATGTCGCGACCCTGGCCAAGGGCCTGGGTTCCGGGGTG  
CCGATCGGCGCCTGCCTGGCCGGTGGCAAGGCCGCCGGCCTGTTCCGGGCCGGGCAA  
CCACGGTTCGACCTTCGGCGGCAATCCGCTGGTGGCGACCGCGGCCCTGACCACCAT  
CGCGGTGATCGAGGAAGAGGGTTTTGCTCGACAATGCCGCCAAGATCGGCGTGTTGAT  
CCGCCAGGGCTTTGCCGAGGCACTGGCCGGGGTCAAGGGCGTGGTTCGAGATTCGTG  
GCCACGGACTIONGATGATCGGCATCGAACTCGAGCGTCCGTGCGGCGAACTGGTTGGCC  
AGGCGCTGGCCGCCGGCCTGCTGATCAACGTCACGGCCGATACGGTGGTACGCTTCC  
TGCCGCCGCTGAACTTCACCGAAAACGATGCCCGTGAGCTGGTTCGACCGTGTGCGAC  
CGCTGATCAAGGCATTCTCGCAGGGTGA

## 5. Amino acid sequence

Protein sequences correspond to cloned genes; amino acids in **bold** correspond to the vector sequence.

### > pQR2188

**MGSSHHHHHHSSGLVPRGSHMS**ADDTPSALAEHYARQNLDAPGSLDHFWMPTANKQF  
KAKPRLLASASGMYYKDVDGNEVLDATEAGLWCCNAGHARPRIVEAVRQQIGTLDFAPNFS  
MSSPLPFKLAERLAALAPGDLNRVFFSNSGSEAVDSALKIALAYHRVRGEGQRTRFIGREK  
GYHGVGFGGMSVGGPLPNNRWFGPGLPAVSHIRHTLDVARNAFSKGLPPHGIELAEDLER  
QIALYDASTIAAVIVEPVSGSAGVVIPPEGYLQRLREICDKHGILLIFDEVITGFGRVGHAFGA  
QRFVTPDMITAAKGITNGCVPMGATFVSERLFD AFMNGPDNAIDMFHGYTYSGHPLACA  
AALATLDTYEEEHLFDKALSLGDYWQEALHSLKGLPNIIDIRNIGLVGAIELAPRAGAPGTRA  
YDVFARAFHEGHLLTRVTGDVIALSPPLIVEKDHIDRIVNVLADTIRATA**EHHHHHH**

### > pQR2189

**MGSSHHHHHHSSGLVPRGSHM**PRNHDAELRRLDVAHHLPAQADWAEIEKLGGSRIITHAE  
GCYIHDGDGHRILDGMAGLWCVNVGYGREELVEAAAQMRLELPFYNTFFKTATPPTVTLA  
AKIASLTGNRLPHIFFNASGSEANDTVFRMVRHYWKLKGEKRTVFISRWNAYHGSTVAGV  
SLGGMKAMHAQGDLPPIGIEHVRQPYSFGEGQGMTEEEFCDACVHAIEDKILEVGPENCAA  
FIGEPVQGAGGVVIPPVKGYWPKVEAVARKYGLLVVSDEVICGFGRTGKMWGHETMGFTPD  
LMSMAKGLSSGYLPISATAVATHVVDVLKTGGDFVHGFTYSGHPVAAAVALKNIEIIEREGLV  
ERTGSVTGPHLAKALATLNDHPLVGETRSIGLLGAVEIVGEKVTRARFGGAEGTAGPMARD  
ACIANGLMVRGIRDSLVMCPPLIISTEQIDEMVAIIRKSLDEVMPKLRAL**EHHHHHH**

### > pQR2190

**MGSSHHHHHHSSGLVPRGSHM**NKNERLAQRDLRHVWHPCTQMQDHEQLPIVPIQRGQG  
VWLEDFEGRRYLDAVSSWVNLFGHANPRINNAVKEQLDTLEHVILAGFTHEPIVELSERL  
VQLAPKGLTRCFYADNGSAATEIALKMSLHFWRNVGKAEKTRFICLENGYHGETLGSLSVT  
DIPLFSATYAPLLKDHLRAPSPDCSRRDEGESWESFSRRQFAAMEALLEKHHAEVSAVILEP  
LVQGAAGMKMYHPVYLTLLREACDRYGVHLLADEIAVGFGRGTGLFACEQAGITPDFLCLSK  
GLTAGYLPMSVMTTDTVYNFYDSYESLKGFLHSHSYTGNALAARAALASLDIFASDNVLE  
KNKLLAATMTDALRGLGDHGHVLEVRQTGMIAAVELVQDRRTRQPFDRERRGLQIFQHA  
LDKGVLLRPIGSVVYFIPPYVITPEEIRLMVDVAAAIDVATAGTASRPGPGNIAL**EHHHHHH**

### > pQR2191

**MGSSHHHHHHSSGLVPRGSHM**SGQRDQELRARAAKVMPSSAFGHVGTALLPANYPQFF  
ERAEGAYVWDADGNRYLDYMCAGFPNLLGYRDRVESAASAQAARGDVMTPGPSPLAVEL  
AEKFVEIVSHADWAFFCKNGTDATTIARTIARAQTGRRKILIAEGSYHGAAPWCNPFPAQTV  
PEDRAHMLTFTFNDIASLEAAVAEAGDDLAGIATPFKHEAFANQEFPTQDYARRCREICDA  
SGAVLVVDDVRAGFRLAVDCSWATVGVKPDLSWGWKCFANGYSISAVMGSNRVKQGADS  
IFATGSFWQSAISMAAALATLDIIRDGKVIKTVRLGQRLRDGLDEVSRRHGFTLNQTPVQ  
MPQILFEGDPDFRVGFVWTSAMIDRGFYLHPWHNMFLCDAMTEEDIDQTIEAADSFAFATVR  
AALPTLQPHERVLALFSARA**EHHHHHH**

### > pQR2192

**MGSSHHHHHHSSGLVPRGSHM**TRIVAVQARMGSTRLPNKVMRPIAGIPMIEVLLKRLAQS  
QRIDQICLATADDVRNQPLVAHVQQLYAVYQGSEHDVLDRFYHAAEQMQADVIRITGDC  
PLIDAALVDLVIDRFLQGDVDYVSNVPPYTPDGLDTEVFSMAALRQAWQQATSTFDHEHV  
TPYLRDSGKFR LAVVSGEHDYSGERWTVDEPADFDVITQIFAHFAPRLDFSWTEVLALCHT  
QPQLFAANQHLIRNEGAMGTGQKLWKRANKVIAGGNMLLSKRPEMFLPEQWPAYFSRA  
QGCTVWDLDNQAYTDMIMIGTNTLGYGHPEVDDAVRRTIDAGNMSTFNCPEEVYLAEKLI  
ELHPWADMVRFARSGGEANAIAIRVARAATGKSKVAICGYHGWHDWYLAANLGDDKNLAG

HLLPGLEPNGVPESLRGTIYPFNYNFAELEALVNSQDIGVIKMEVSRNHGPEDEGFLHKVRE  
LATARGIVLIFDECTSGFRQTFGGLHKLYGVEPDMAMFGKALGNGYAITATIGRREVMEAAQ  
TTFISSTFWTERIGPTAALKTLEVMERERSWDITQTGLAITERWKTLAARHGLSINTNGLPA  
LTGFANSPNALAYKTLITQEMLGKGYLAGTSVYVCTAHTPEIVDGYFAALDPIFGVIRECED  
GRDVMSLLKGPICHAGFKRLEHHHHHH

> pQR2193

**MGSSHHHHHSSGLVPRGSHMSHVMNTYARLPVAFSHGKGSRVTDTEGREYLDALSGIA**  
VNTLGHHAHPRLVAAIAEQAGRLIHTSNLYGAVGQERLADRLCALSGMQEVFFGNSGAEANE  
AAIKLARFYGHKKGIELPTVIVMEKSFHGRMTATLSATGNYKVQVGFEPVAGFVRVPYGD  
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> pQR2194

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LKTMRALCTQHGAFLIFDEVMTGFRVGPQCAQGFYGITPDLTTLGKVIGGGMPVGAFFGK  
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> pQR2195

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DILNFAKQVTNGAQLGGVIASKEIYDTFMAAGGPEYMLEFPHGYTSAHPVACAAGIAALD  
ILQKEDMIGRVKALAPYFENAVHSLKGAKHVADIRNFGLAAGFTIAAVPGEPAKRPYEIAMKC  
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> pQR2196

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> pQR2197

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> pQR2198

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> pQR2199

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>pQR2200

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NDTILRMVRHFVAVQDQPQKNIFGRHDGYHGTTMAGASLGGMKGMHKQGGLPIPIHHI  
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RICRQHDVLLVADEVICGFGRTGEWFGSQYFGFQPDIMPIAKGITSGYIPLGAAMFNDRVAK  
VLKEQGGELAHGATYSGHPVCAVALENIRILQDEKIVETAKNDIAPYLAQRWAEELGEHRLV  
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AQVDELFDKTWRALNDTATDLGMHHHHHH

> pQR2201

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VLEAMARPQVMANIMTPSLSQLRFDRALRNEIGHTRGGCPFAKFLCLNSGSESVGLAARIA  
DINSKLMTPDGRHAGRTIKRIVVKGSFHGRTERPALYSDSSRKSQQHLASYRGEDSVIAI  
PPYDVALKQAFADAEAKGWFVEAVFLEPVMGEGDPGRSVPPAFYAAARELTRSHGSLFL  
VDSIQAGLRAHGVLSIIDYPGFEGLDAPDMETYSKALNAAQYPLSVLAVNERAAGLYRKGVY  
GNTMTTNPRALDVACATLAQLTPQVRENIRKRGVEAVQKLQQLQGELGGLITNVQGTGLLF  
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> pQR2202

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QEGGINIADLDYQRALRQLCDENGWLLICDEVQCGMGRTGTWFGFQHAGIRPDIVTLAK  
GLGGGVPIGACLTAGKAAFLKPGNHGSTFGGNQLATTAALTTIDVVERDRLIANAESVDEL  
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> pQR2203

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YNDPQGLAEAFKTHGDKIAAVIVEPVVGNMNLIAPTPEFLKAMRDLTAQYGAVLIFDEVMTG

FRVGLKSAQGLFGITPDLSTFGKVVGGGMPMGAFGGRRIMEKIAPLGPVYQAGTLSGNPI  
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GSYDEVLCADKEAFNRFFHAMIEAGHYFAPS SAFEAGFVSAAHSDAEIAATVAAADAWFATQ  
RHHHHHH

**> pQR2204**

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GEGGIRPASQPFLQALRDICDKRDLMLIFDEVQCGVARTGHLYAYEHFGVTPDIMASAKGIG  
GGFPMGACLATEKAARGM VIGTHGSTYGGNPLACAAGQAVLDVVLEEGFLASVRTTGERL  
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**> pQR2205**

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RAHTVESPDERRGNEAAALAAMRALLAERA EHIAAVIVEPLVQGAAGMVMHGPYLRGLR  
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AVYRAFWS EDVGRGFLHSHSYTGNALACAAANAVLDRFDAGQAERVRVQAACLATHCAP  
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**> pQR2206**

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SYNDFEGATALFEQYGSEIACLIIEPVVGNANCLPPREGYLQHLRALCTQH GALLIFDEVMT  
GFRVALGGAQAHYGITPDLTTFGKIIGGGMPVGAYGGRRALMQQIAPAGPIYQAGT LSGNP  
VAMAAGLAMLELIQARGFHDGLAAATAALCEGMEAAARDAGVPLTTTRVGAMFGLFFTDQ  
QVDTYAQAVACDTAAFNRFFHAMLERG VYLAPS SAFEAGFMSSAHTPDVIDATISAARDAFK  
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**> pQR2207**

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RTVAIMLEPIQEGGGVVPASVEFLQLLRQICDDRGLLLIVDEVQTGMGRTGKLF AHQHAGIE  
PDIMTLGKGIGGGVPLSALLAKESVCCFEAGDQGGTYNGNPLMTAVGVAVLEVL TAPGFLD  
EVAAKGEYLGAGLQRLSDRLGLRGERGELL RALLLADERGPAIVEAARERGPEGLLLNAP  
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**> pQR2208**

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VDAICRKYGILLVSDEVICGFGRGGEWFGFQKYGYTPDIVSMAKGLSSGYLPISATGVSSEIV  
ETLRASGDDFVHGTYTSGHPVAAAVALRNLEI IKREGLVDRVRDDLAPYFAKALATLDDHPL  
VGEARSVGLLGAVEIVSEKGTNHRFGGKEGTAGPVVRDHCIAGGLMVRAIRDSIVMCP PYY  
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> pQR2209

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KTVAVMLEPIQGEAGVIPASGDFLRQLRQLCDERQLLLIVDEVQGTGVGRTGHLFAHSAHGIQ  
PDIMTLGKGLGGGLPISALLATRAASCFAFGDQGGTYCGNPLVCAAGLAVLDTLLADGFLA  
ASRQRGEQLADALRTLSEELGLGAVRGEFLLALELGADLGPATRRARDLGLLVNAPRAH  
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> pQR2210

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IAMSCGDVAAMLEPVQGEAGVMPAASGFLRAVRELCDHHGALLVLDEIQAGMGRTGTLF  
AHWQDGVVPDIVTLAKALGGGFPIGAMLAGPKVAQAMQFGAHGTTFGGNPLAAAVARVAL  
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> pQR2211

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VAHDRFGPEKYEIIAALNSFHGRTLFTVSVGGQPKYSDGFGPKIEGITHVPYNDLDALKAAIS  
DKTCAVVLEPIQGEAGVLPADKAYLEGARALCDQHNALLVFDEVQSGMGRSGELFTYMHY  
GVTPDILSSAKSLGGGFPIGAMLTTELAKHLAVGTHGTTYGGNPLACAVAEAVLDIVNTPE  
VLQGVKAKSEQFKRLLAIGERYGMFAEVRGLGLLLGCVLNDAWKGKAKAVLDAAAAGV  
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> pQR2212

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SAGVIPDIVCLSKGLTGGALPLAVTLCEPIFEAHFSTDRSKTFYHSSSYTANPIACAAANANL  
EIWREEPVQQRIDALAEQAHLSSLSHDPRVQNPRLGTIAALDIVVADSGYLSNLAPRLIA  
FYRDHGVLLRPLGNTLYVMPYPYCITPDELAQVWSAITASLDAVHHHHHH

> pQR2213

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SRPPGHSGIGTTLSANALAITAMDAMLGEVITSAAYDHMLRGAARLVAGLEQEIAHVGLDW  
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DDQIDRLVGAFADSVQALKEHHHHHH

> pQR2214

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HLPHTYNLSQMAFSKGMPTWGAHLAEELERIVALHDASTIAAVIVEPMQGSVGIAPPVGYL  
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YQAFMGVNAPEYAVELMHGYTYSGHPLAAAVGHVALDALVNDGLIQRAAELAPVLEDVIHG  
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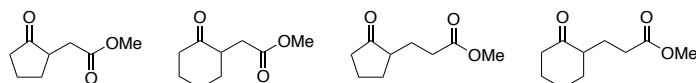
> pQR2215

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> pQR2216

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KGLGSGVPIGACLAGGKAAGLFGPGNHGSTFGGNPLVATAALTTIAVIEEEGLLDNAAKIGV  
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FTENDARELVDRVAPLIKAFLAGHHHHHH

## 6. Other Substrates



**Figure S10.** Substrates that showed no activity with any of the enzymes.

## 7. Analytical Methods

### 7.1 Achiral methods

Quantitative analysis of enzymatic reactions was analytical reverse phase HPLC analysis with respect of chemical standards using an Agilent 1260 Infinity or Dionex Ultimate 3000 with an Ace 5 C18 column 150 × 4.6 mm. Elution was carried out at 1 mL/min with a linear gradient of acetonitrile/0.1% TFA in water, injection volume 10 μL and column temperature 30 °C. Chromatograms showing retention times included below.

#### *Method A:*

Products were detected at 250 nm using a linear gradient 15 - 72% acetonitrile over 15 min. This method was used to detect acetophenone.

#### *Method B:*

Products were detected at 204 nm using a linear gradient 5 - 72% acetonitrile over 15 min. This method was used to detect all amine products **18b-25b**.

### 7.2 Chiral methods

Enantiomeric excess of **18b** and **20b** was determined by GC analysis using an Agilent 7820A GC System with a Supelco Beta Dex 225 capillary GC column 30 m × 250 μm × 0.25 μm with flame ionization detector at 300 °C, a temperature gradient and 1 μL injection volume. Chromatograms showing retention times included below.

#### *Method A:*

Initial temperature 140 °C, 1 min hold, ramp 5 °C/min to 210 °C, 2 min hold. This method was used to detect **18b**.

#### *Method B:*

Initial temperature 150 °C, 1 min hold, ramp 10 °C/min to 210 °C, 3 min hold. This method was used to detect **TFA-20b**

## 8. HPLC and GC Traces

### 8.1. HPLC traces

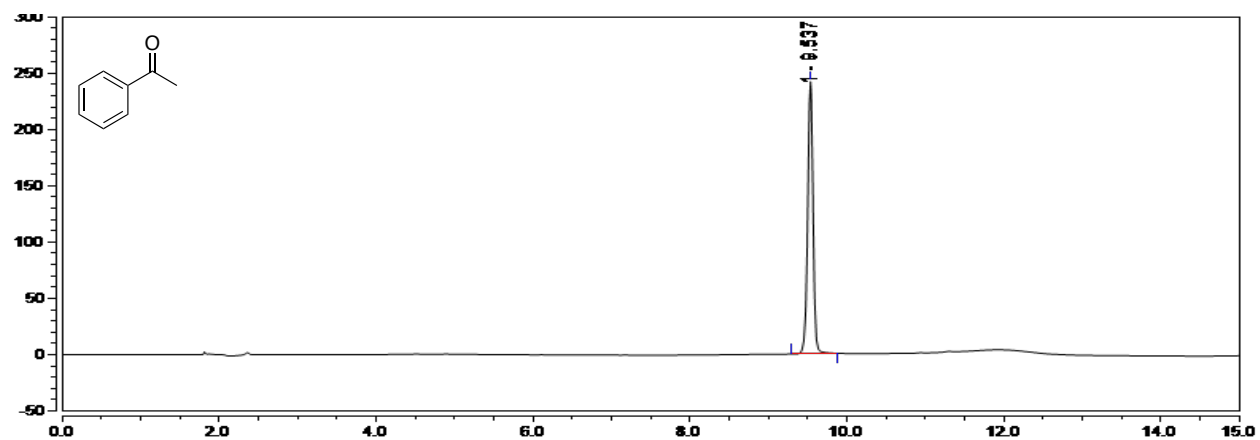


Figure S11. Chromatogram of acetophenone using HPLC method A. Retention time 9.5 min

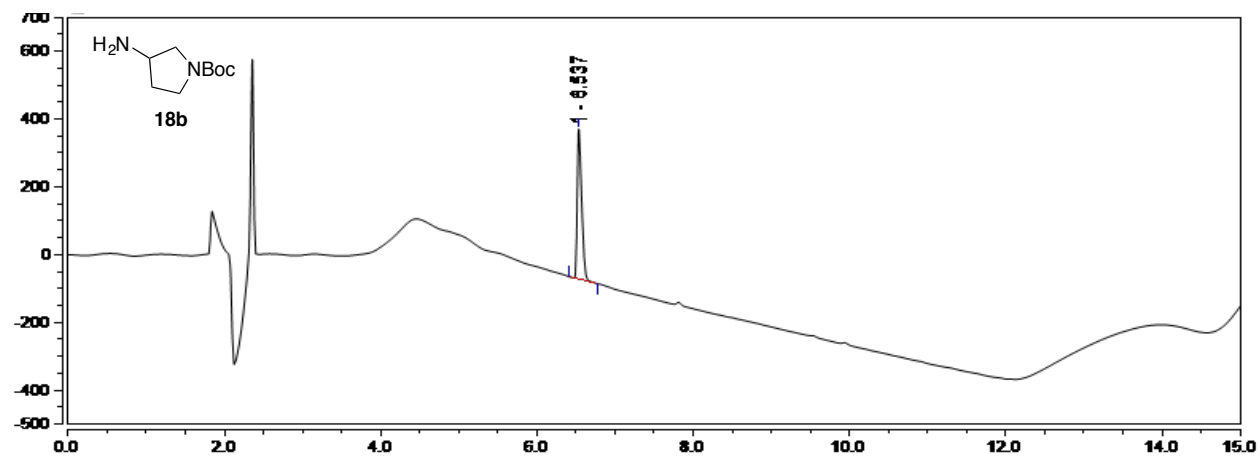


Figure S12. Chromatogram of amine **18b** using HPLC method B. Retention time 6.5 min.

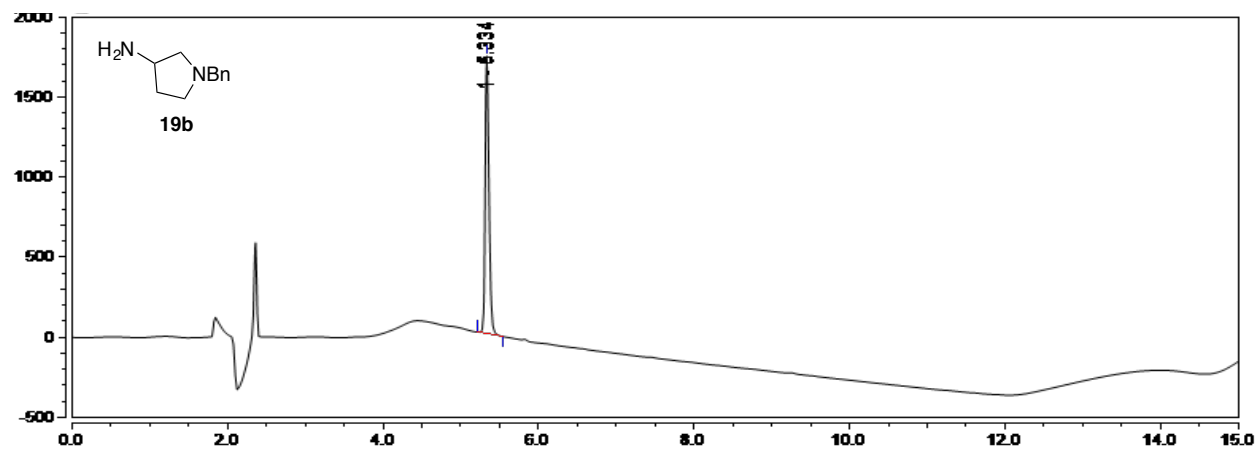


Figure S13. Chromatogram of amine **19b** using HPLC method B. Retention time 5.3 min.

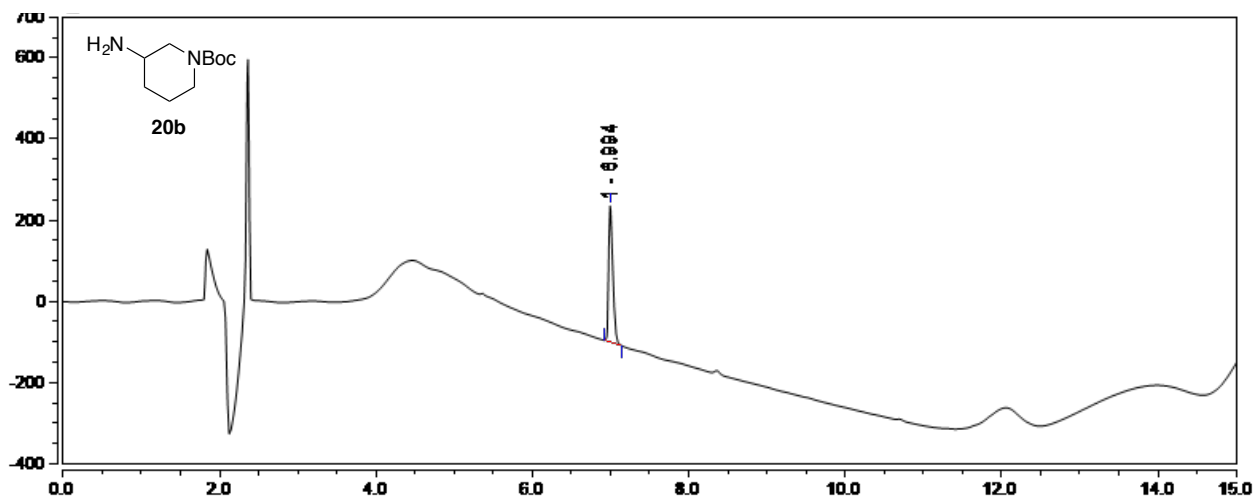


Figure S14. Chromatogram of amine **20b** using HPLC method B. Retention time 7.0 min.

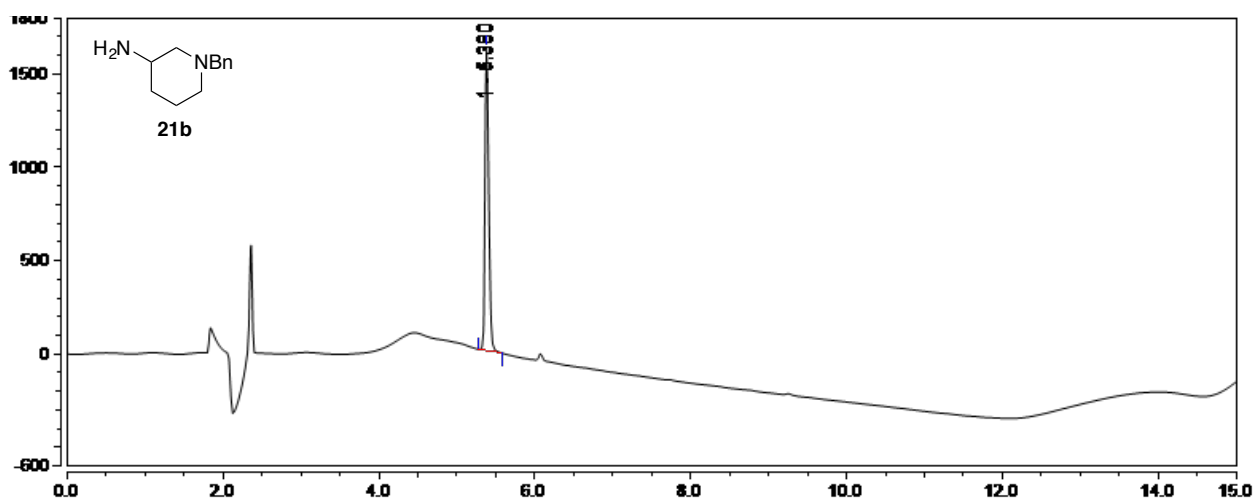


Figure S15. Chromatogram of amine **21b** using HPLC method B. Retention time 5.4 min.

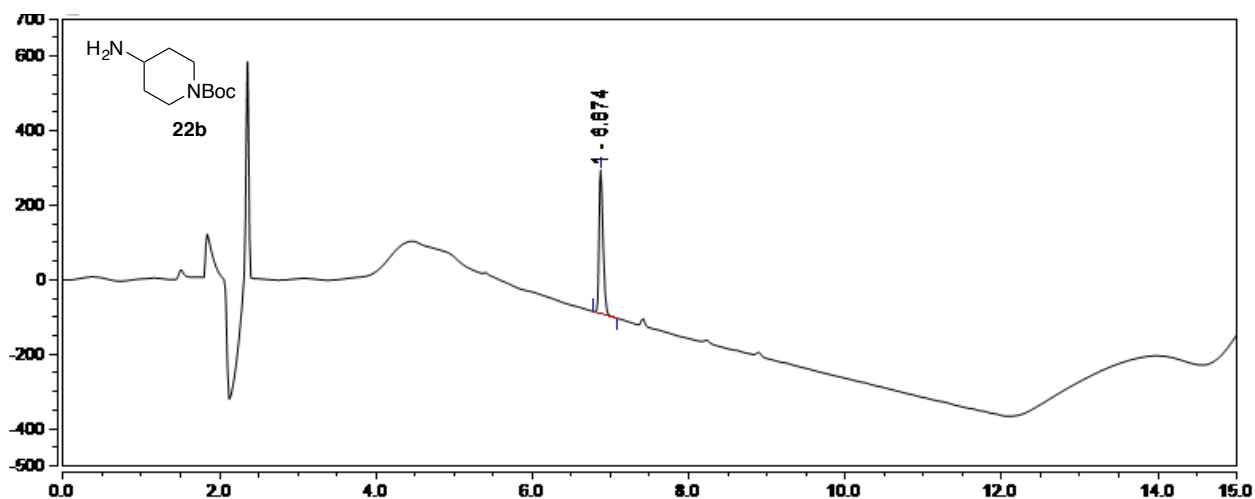


Figure S16. Chromatogram of amine **22b** using HPLC method B. Retention time 6.7 min.

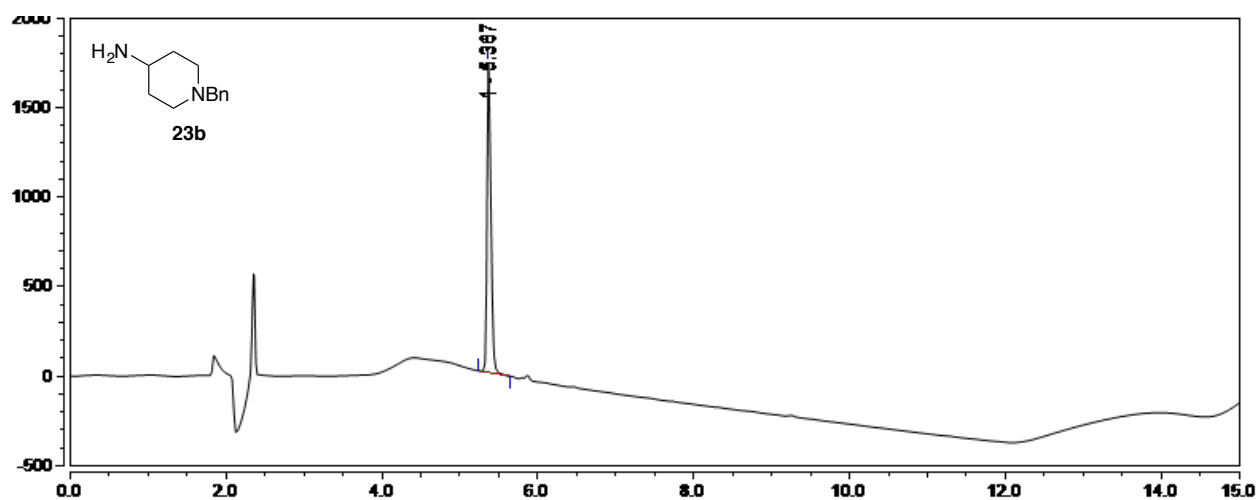


Figure S17. Chromatogram of amine **23b** using HPLC method B. Retention time 5.4 min.

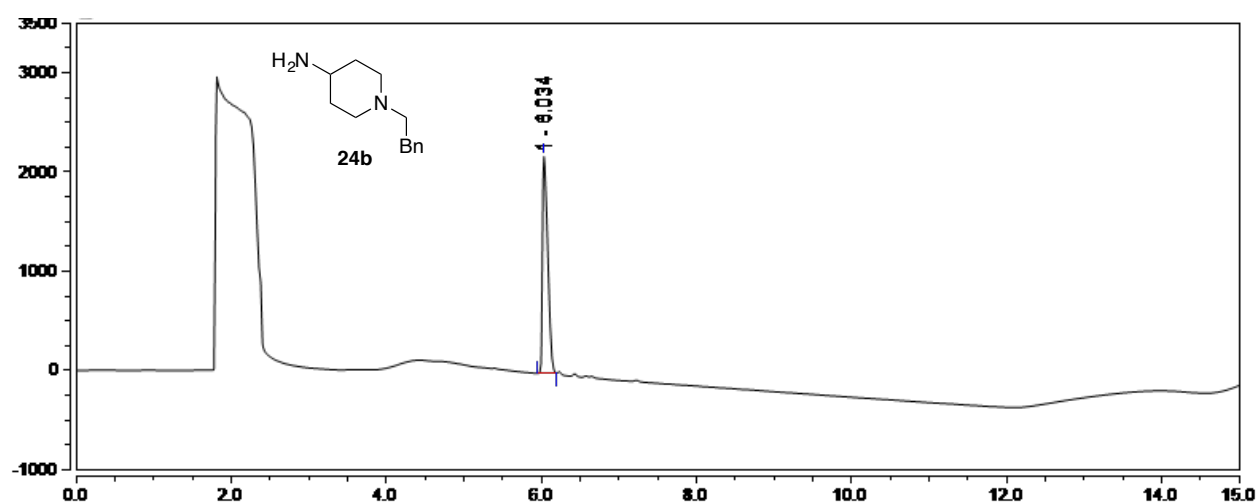


Figure S18. Chromatogram of amine **24b** using HPLC method B. Retention time 6.0 min.

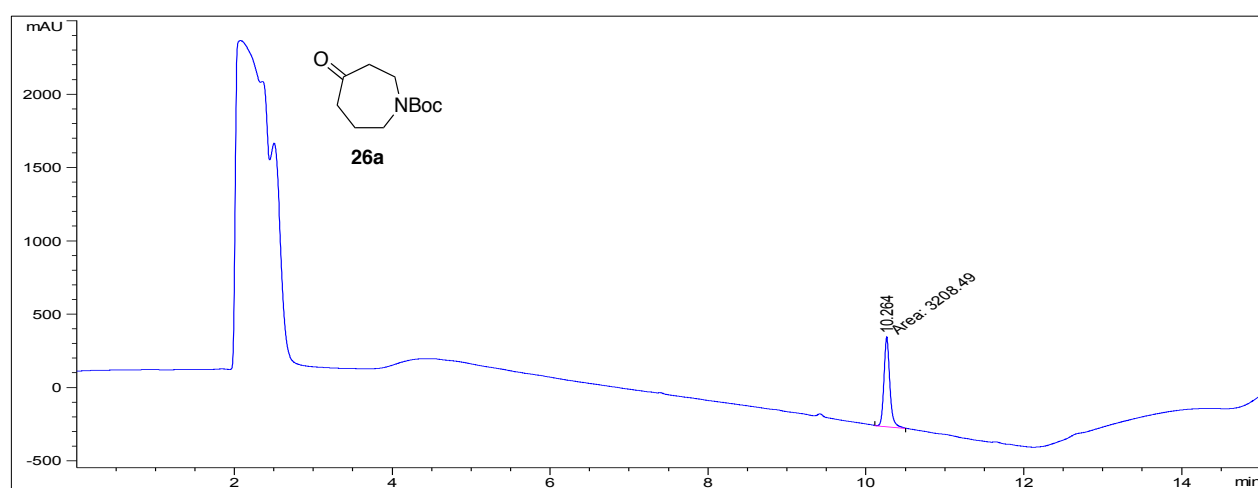
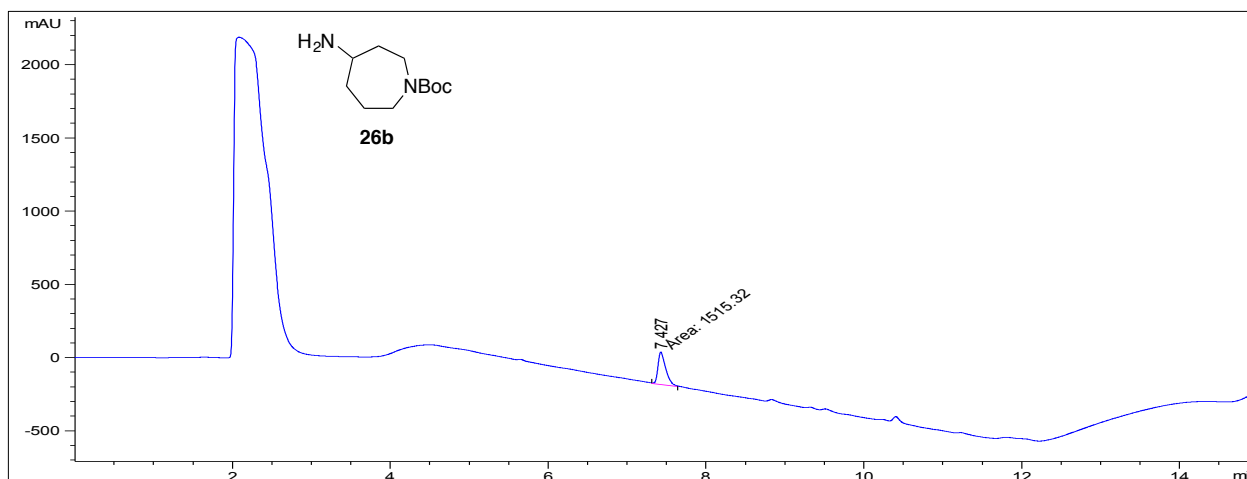


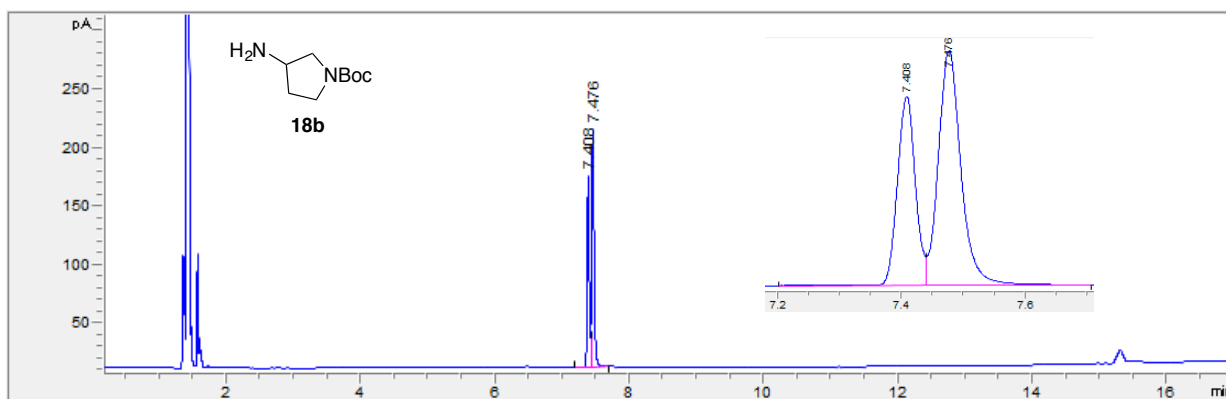
Figure S19. Chromatogram of ketone **26a** using HPLC method B. Retention time 10.3 min.



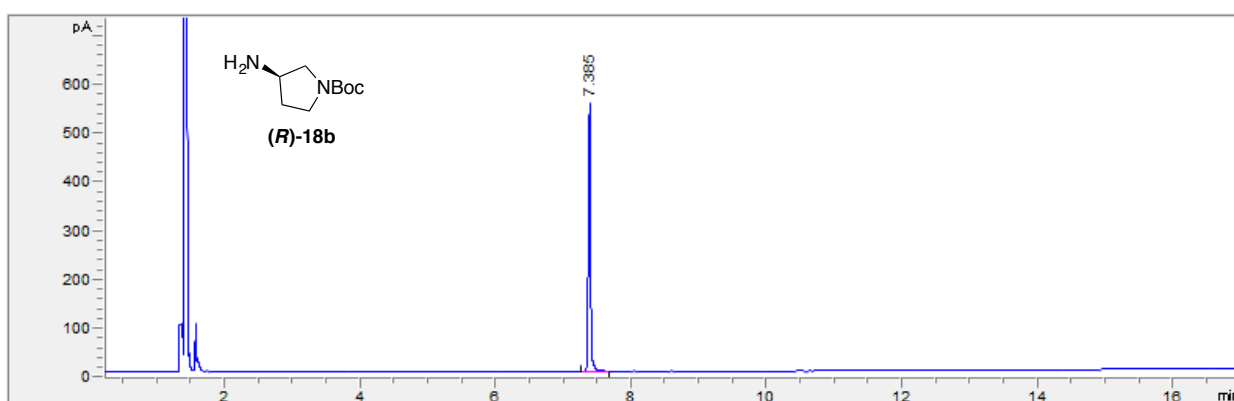


**Figure 20.** Chromatogram of amine **26b** using HPLC method B. Retention time 7.4 min.

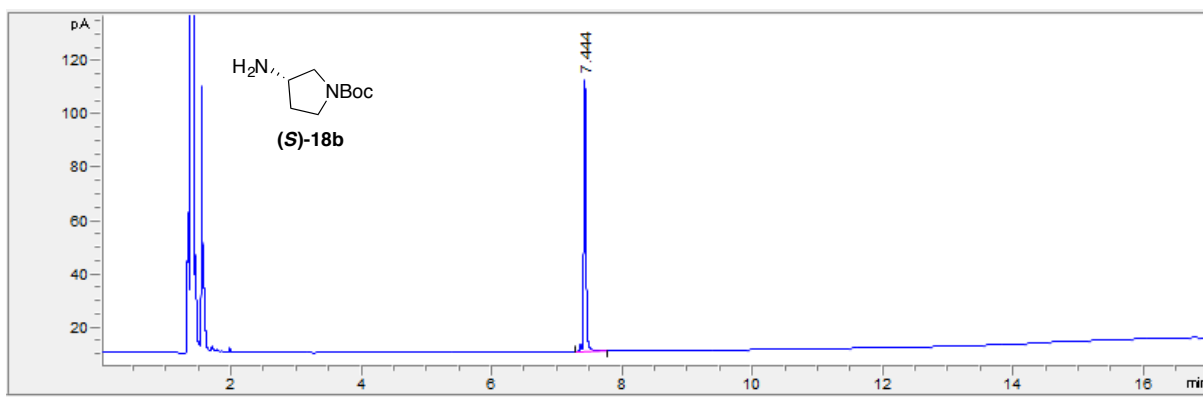
## 8.2. GC Traces



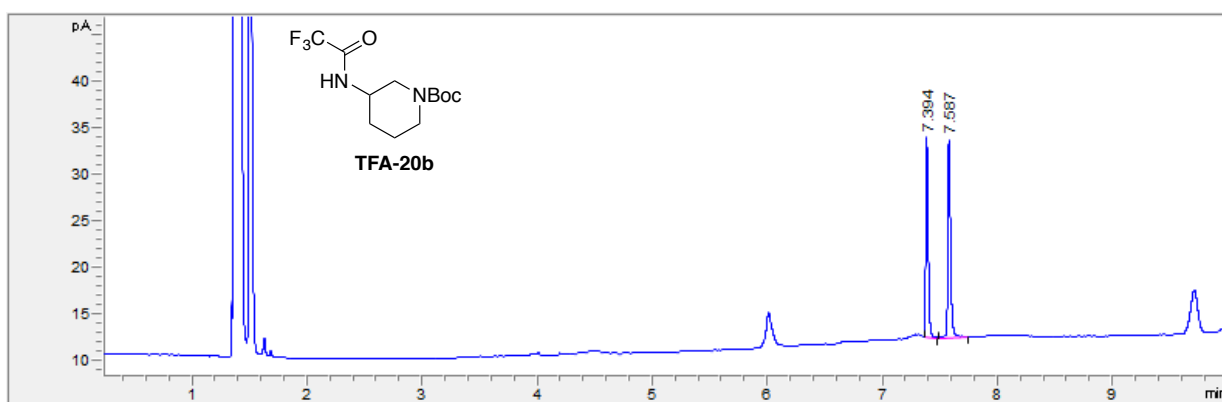
**Figure S21.** Chromatogram of racemic **18b** using GC method A. Retention times 7.4 & 7.5 min.



**Figure S22.** Chromatogram of (*R*)-**18b** using GC method A. Retention times 7.3 min.



**Figure S23.** Chromatogram of (S)-18b using GC method A. Retention times 7.4 min.



**Figure S24.** Chromatogram of racemic TFA-20b using GC method A. Retention times 7.4 and 7.6 min. Enantioselectivity inferred from 18b.

## 9. Calibration Curves

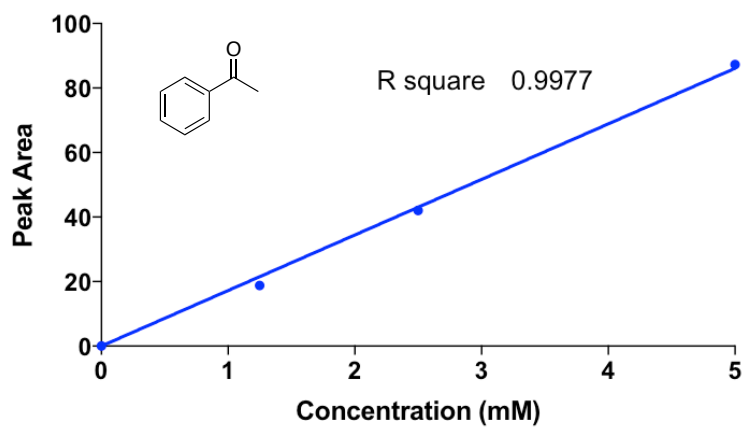


Figure S25. Calibration curve for acetophenone using HPLC method A.

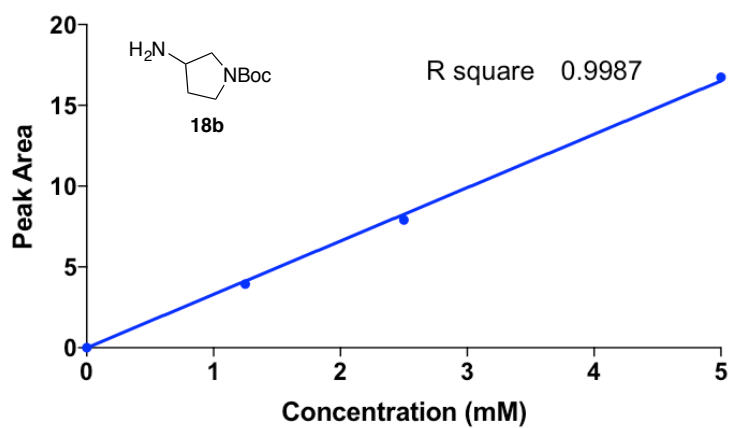


Figure S26. Calibration curve for amine **18b** using HPLC method B.

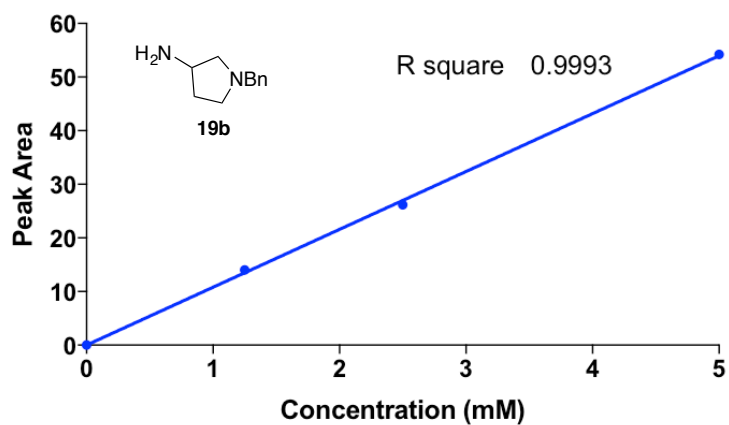


Figure S27. Calibration curve for amine **19b** using HPLC method B.

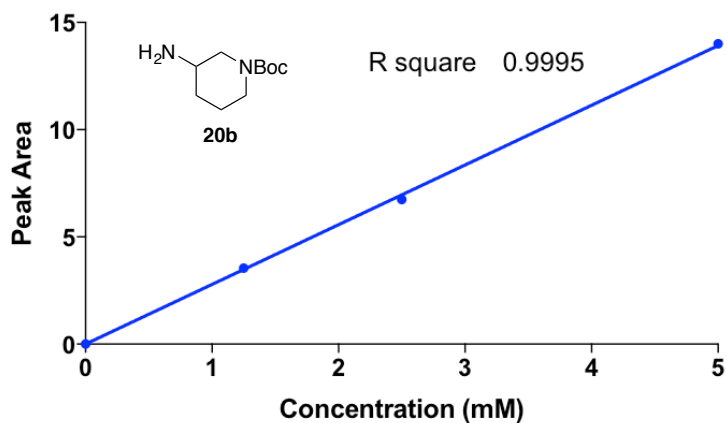


Figure S28. Calibration curve for amine **20b** using HPLC method B.

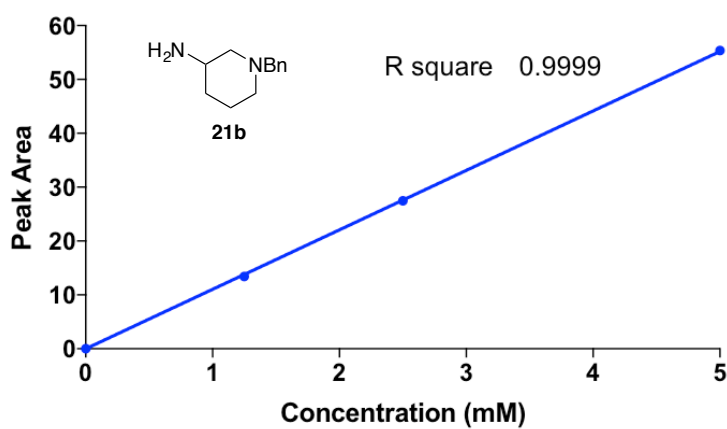


Figure S29. Calibration curve for amine **21b** using HPLC method B.

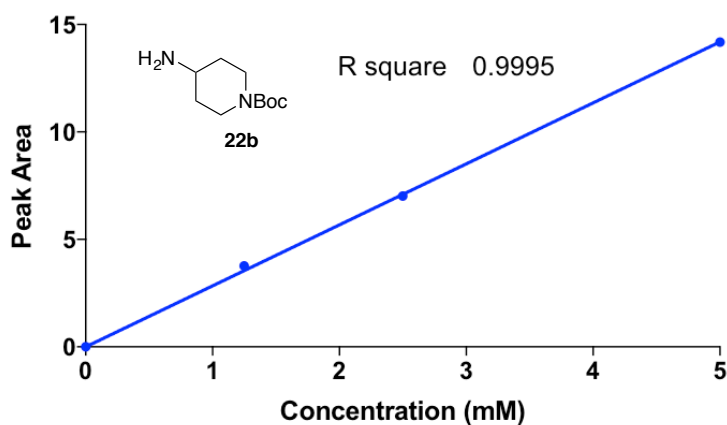


Figure S30. Calibration curve for amine **22b** using HPLC method B.

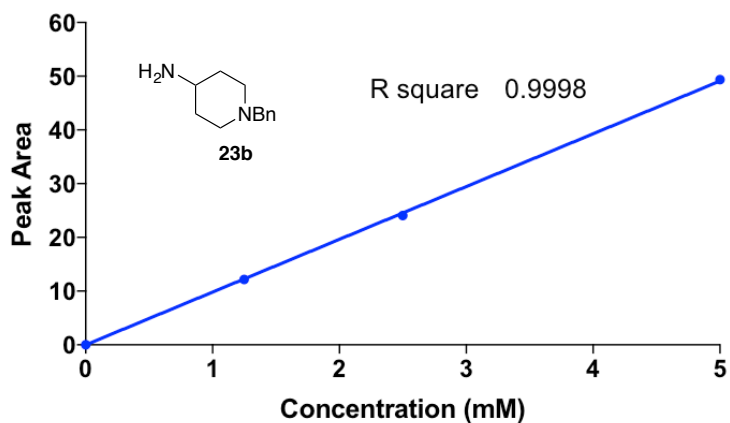


Figure S31. Calibration curve for amine **23b** using HPLC method B.

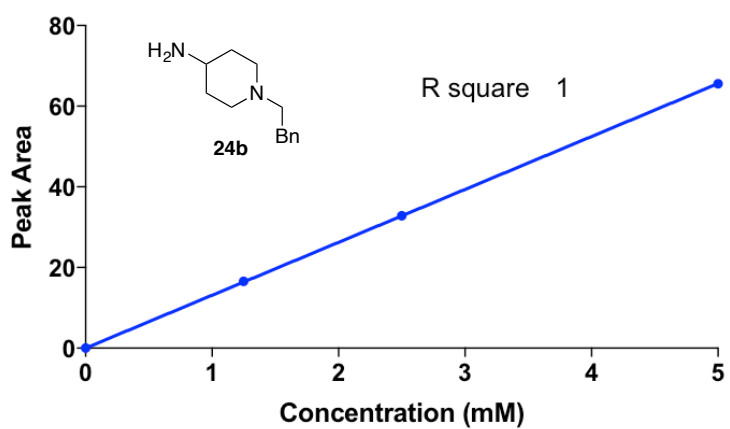


Figure S32. Calibration curve for amine **24b** using HPLC method B.

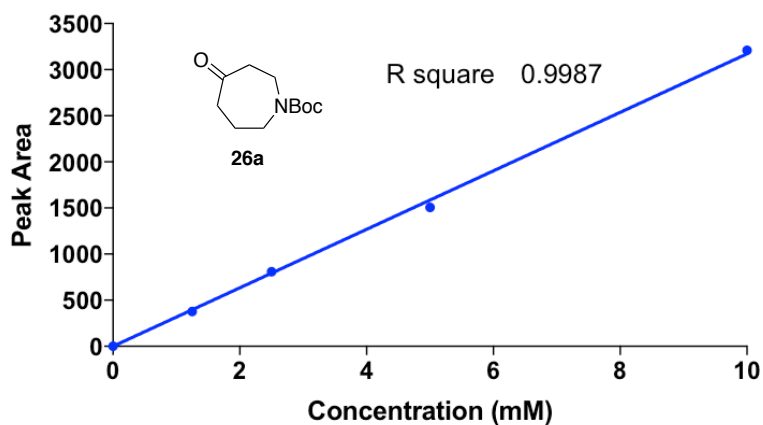
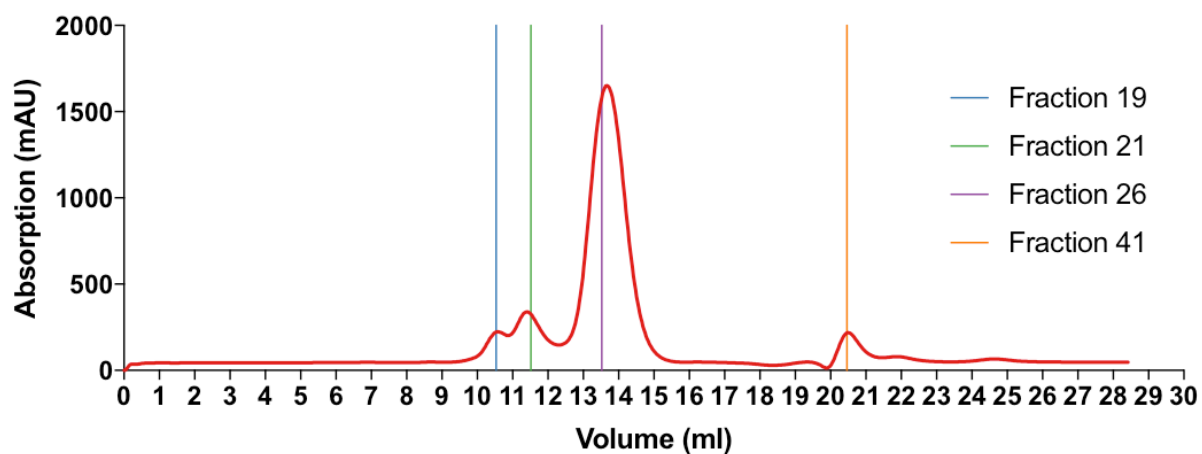
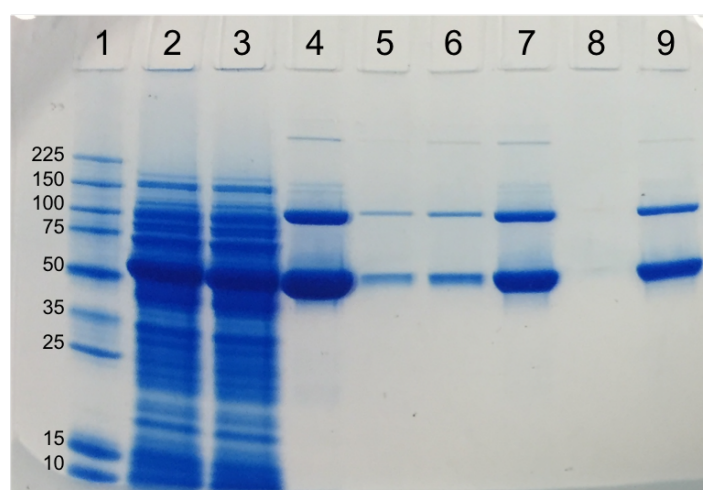


Figure S33. Calibration curve for ketone **26a** using HPLC method B.

## 10. Purification of pQR2189



**Figure S34.** Trace of gel filtration of pQR2189 and His-tag purification. Vertical lines show the fractions that were run on a gel shown in Figure S35.



**Figure S35.** SDS-Page gel of pQR2189 purification. **Lane 1:** Promega broad range protein molecular marker. **Lane 2:** TP fraction. **Lane 3:** CFE fraction. **Lane 4:** pQR2189 after His-tag purification. **Lane 5:** Gel filtration fraction 19. **Lane 6:** Gel filtration fraction 21. **Lane 7:** Gel filtration fraction 26. **Lane 8:** Gel filtration fraction 41. **Lane 9:** Pure protein fractions used in kinetics studies.

## 11. Kinetics Graphs

### 11.1. Pyruvate and (S)-MBA

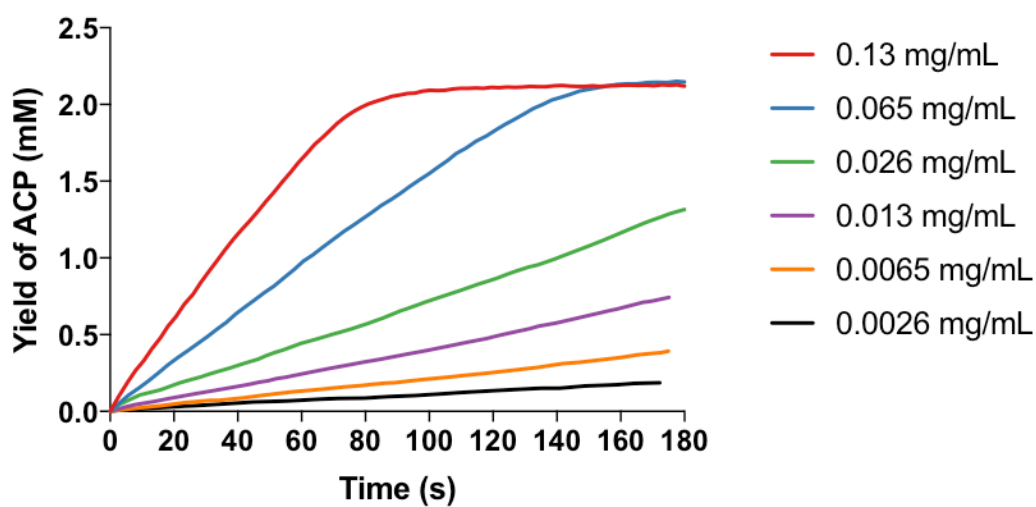


Figure S36. Effect of enzyme concentration on acetophenone formation.<sup>1,2</sup>

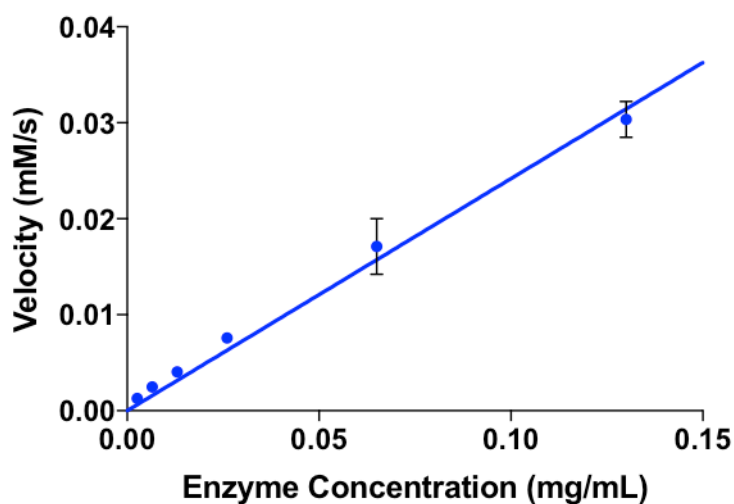


Figure S37. Enzyme concentration vs. velocity.

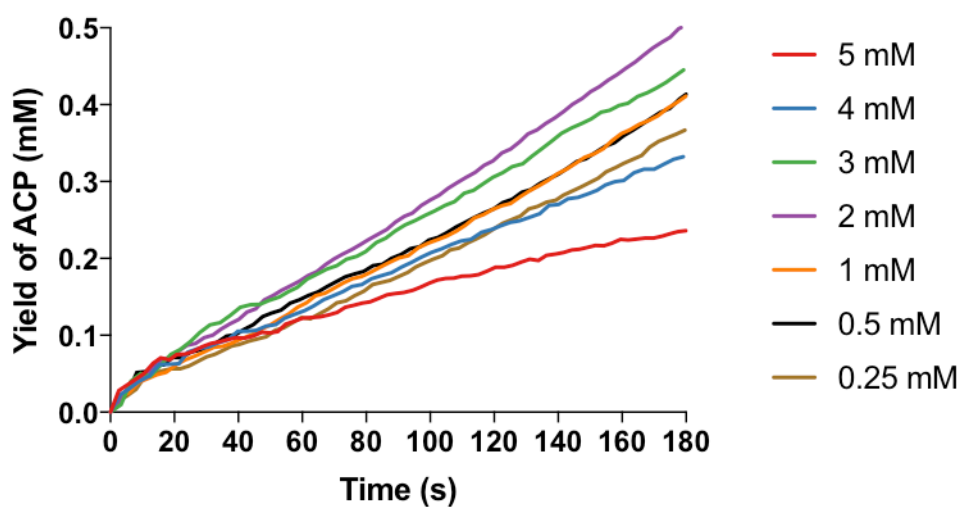


Figure S38. Effect of varying pyruvate concentration on acetophenone formation.<sup>1,2</sup>

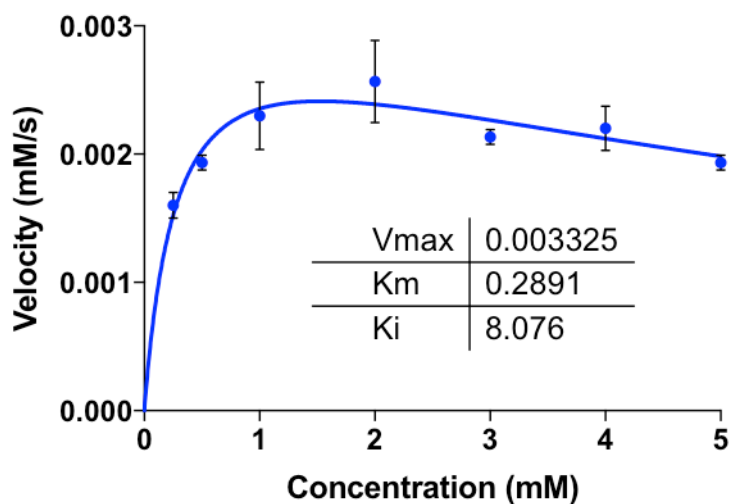


Figure S39. Michaelis-Menten plot of pyruvate concentration,  $K_m = 0.29$  mM.



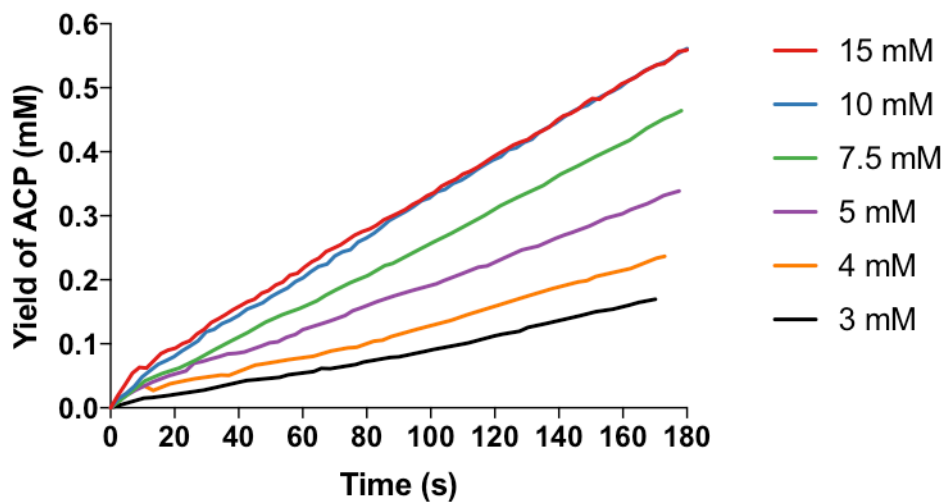


Figure S40. Effect of varying (S)-MBA (S)-7 concentration on acetophenone formation.<sup>1,2</sup>

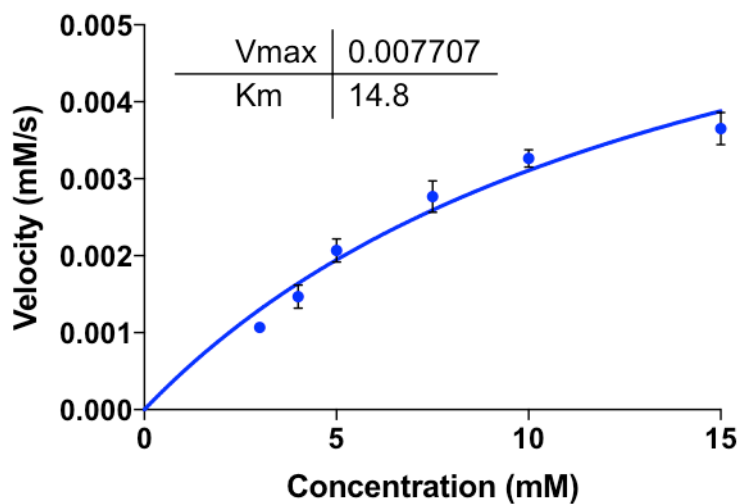


Figure S41. Michaelis-Menten plot of (S)-MBA concentration,  $K_m = 14.8$  mM.

## 11.2. 1-Boc-3-pyrrolidinone and IPA

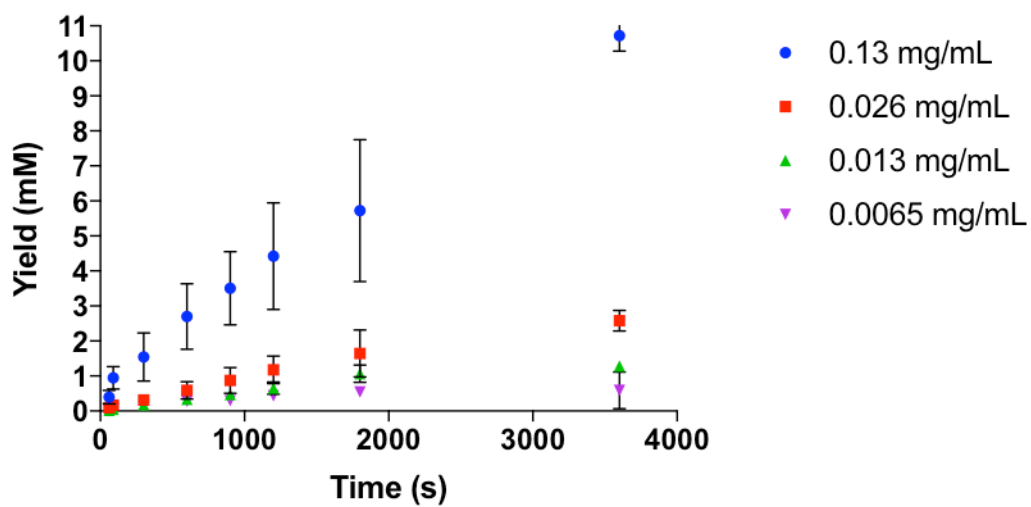


Figure S42. Effect of enzyme concentration on formation of **18b**.<sup>2</sup>

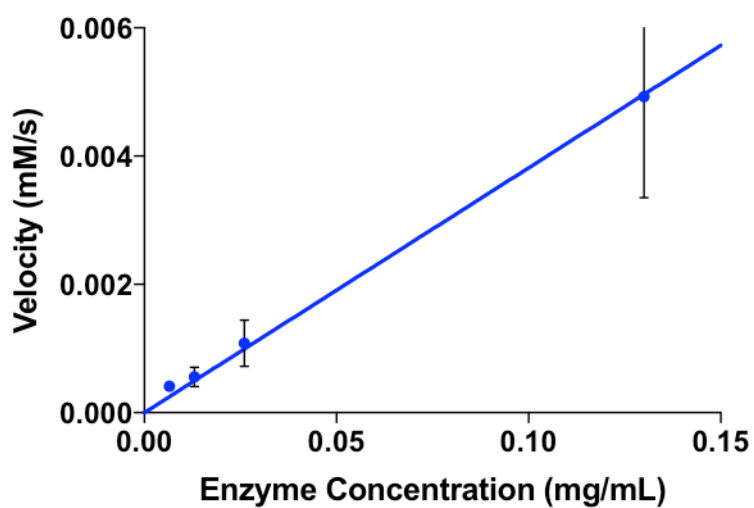


Figure S43. Enzyme concentration vs. velocity.

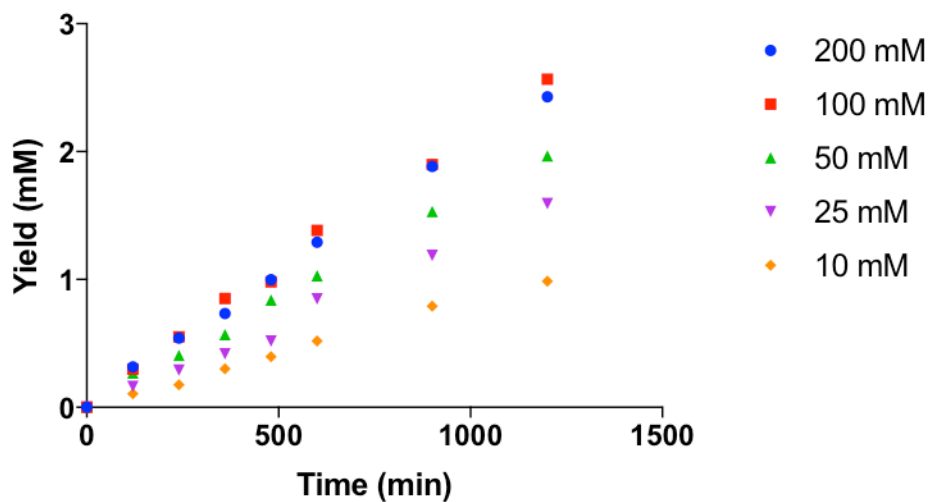


Figure S44. Effect of varying ketone **18a** concentration on formation of **18b**.<sup>2</sup>

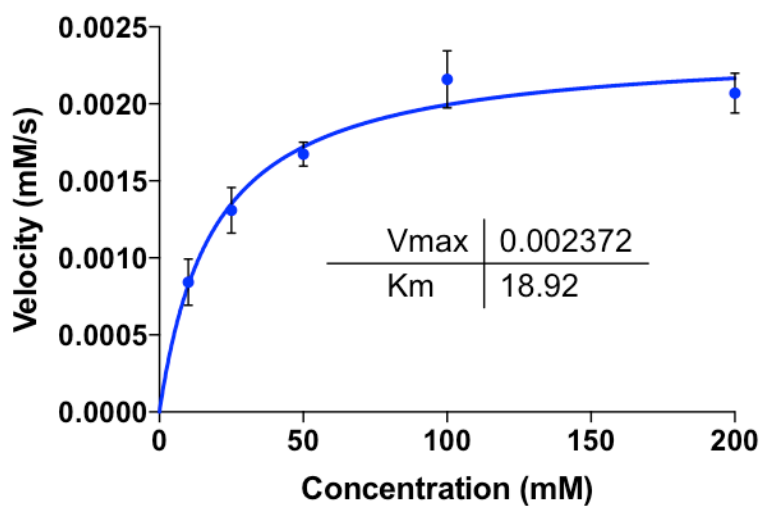


Figure S45. Michaelis-Menten plot of 1-boc-3-pyrrolidinone **18a**,  $K_m = 18.9$  mM.

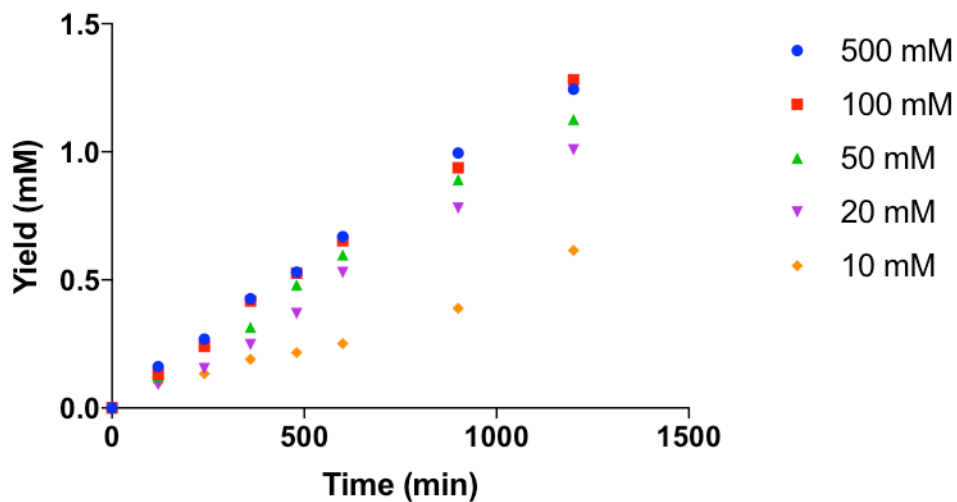


Figure S46. Effect of varying IPA 27 concentration on formation of 18b.<sup>2</sup>

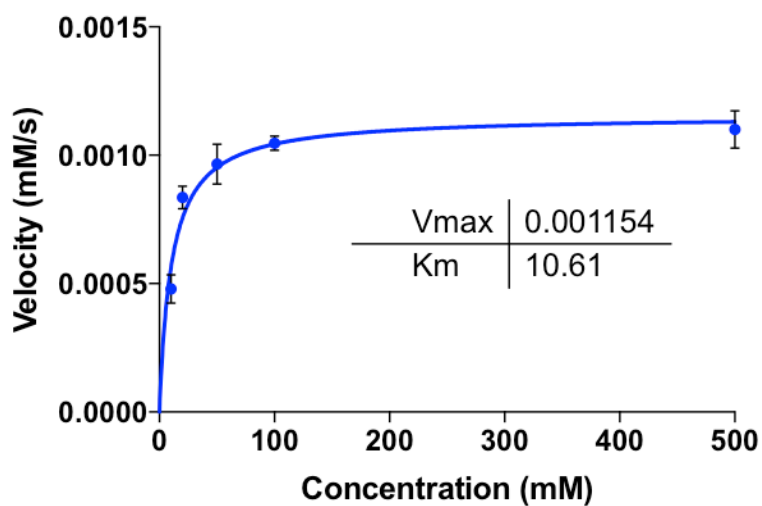
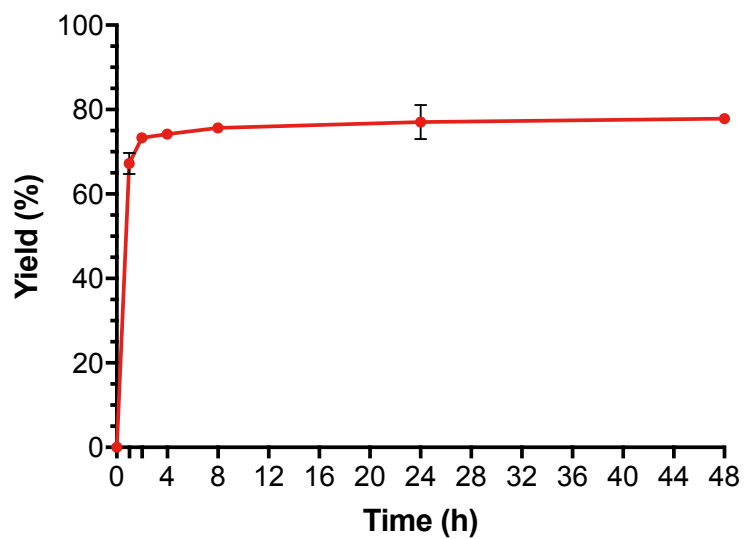
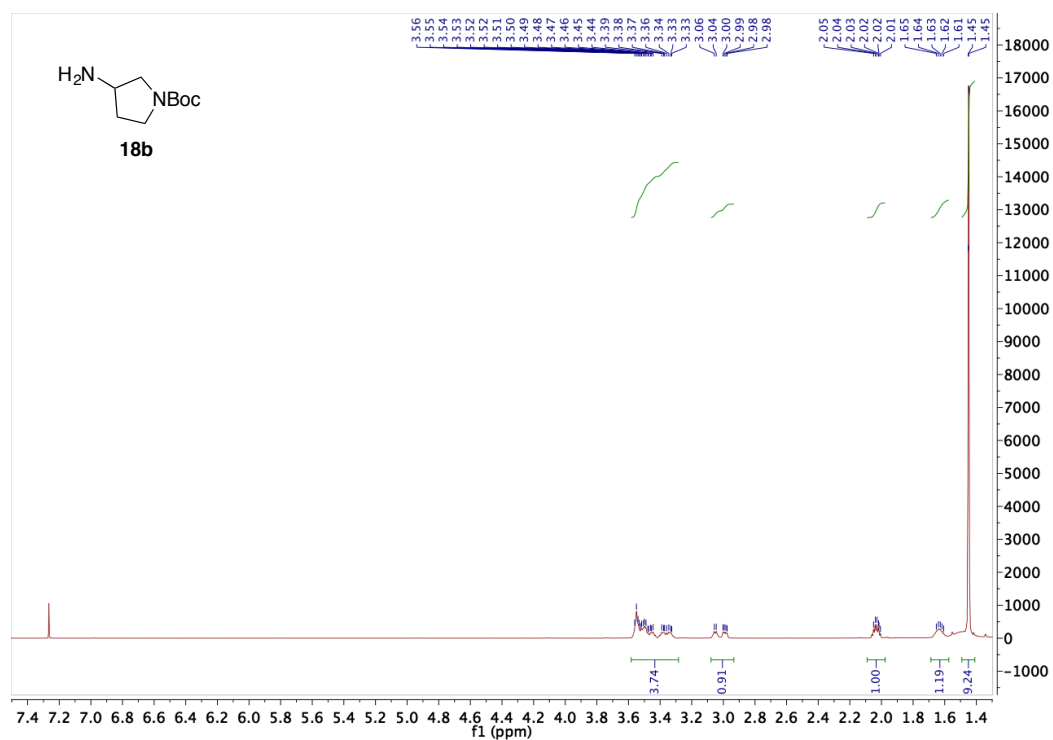


Figure S47. Michaelis-Menten plot of IPA 27,  $K_m = 10.6$  mM

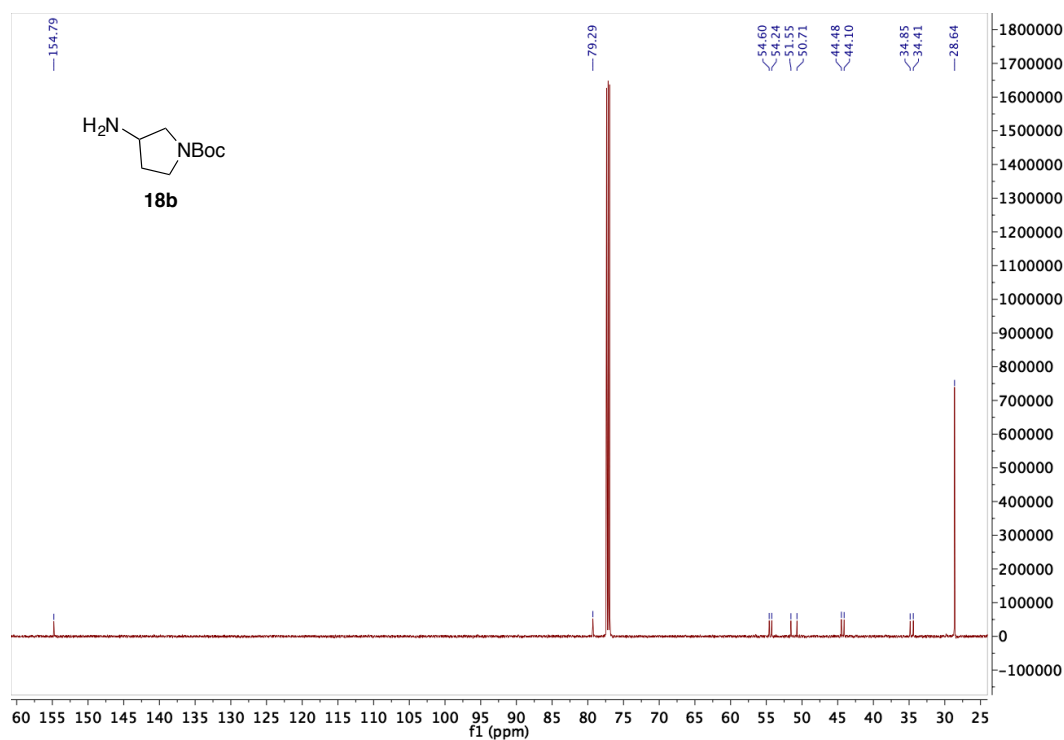


**Figure S48.** Percentage yield of **18b** using IPA **27** as an amine donor over time for pQR2189 using crude cell lysate.

## 12. NMR Spectra



**Figure S49.**  $^1\text{H}$  NMR spectrum of amine **18b** in  $\text{CDCl}_3$ .



**Figure S50.**  $^{13}\text{C}$  NMR spectrum of amine **18b** in  $\text{CDCl}_3$ .

### 13. References

- 1 S. Schätzle, M. Höhne, E. Redestad, K. Robins and U. T. Bornscheuer, *Anal. Chem.*, 2009, **81**, 8244–8248.
- 2 N. Al-Haque, P. A. Santacoloma, W. Neto, P. Tufvesson, R. Gani and J. M. Woodley, *Biotechnol. Prog.*, 2012, **28**, 1186–1196.