

Supplementary information for “Degradation of CP4-EPSPS with a psychrophilic bacterium *Stenotrophomonas maltophilia* 780”

Figure S1. The sequence of CP4-EPSPS

5'TTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGT
TAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTGTAAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGG
AACTGCATCCAAAAGTGGCAAGCTAGAGTATGGTAGAGGGTGGTGAATTCCTGTGTAGCGGTGAAATGCGTAGA
TATAGGAAGGAACACCAAGTGGCGAAGGCGACCACTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGC
AAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGG
CGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATTGACGGGGGCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCCAATGAACCT
TCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGCTGAGATGT
TGGGTAAAGTCCCGTAACGAGCGCAACCCCTTGCCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGC
CGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC
AATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCATAAAACCGATCGTAGTCCGGATCGCAGT
CTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTC-3'

Table S1. Strains obtained from CCTCC

Serial number	Molecular Taxonomy	Identity (%)	Geographical sources
CCTCC S2016780	<i>Mucilaginibacter gotjawali</i>	97.38	South Pole, Astronomical observatory
CCTCC S2016784	<i>Pseudomonas mandelii</i>	99.64	South Pole, Astronomical observatory
CCTCC S2016802	<i>Massilia eurypsychrophila</i>	99.36	South Pole, Astronomical observatory
CCTCC S2016808	<i>Arthrobacter oryzae</i>	99.49	South Pole, Astronomical observatory
CCTCC S2016809	<i>Pseudomonas chlororaphis</i>	98.39	South Pole, Astronomical observatory
CCTCC S2016709	<i>Massilia eurypsychrophila</i>	98.10	South Pole, the Larsemann Hills
CCTCC S2016713	<i>Arthrobacter oxydans</i>	98.45	South Pole, Inexpressible Island
CCTCC S2016714	<i>Arthrobacter globiformis</i>	98.15	South Pole, Inexpressible Island
CCTCC S2016723	<i>Arthrobacter oxydans</i>	98.73	South Pole, Inexpressible Island
CCTCC S2016730	<i>Arthrobacter oxydans</i>	98.66	South Pole, Inexpressible Island
CCTCC S2016741	<i>Pseudomonas marginalis</i>	99.7	South Pole, Larsemann Hills
CCTCC S2016742	<i>Pseudomonas marginalis</i>	99.7	South Pole, Larsemann Hills
CCTCC S2016746	<i>Sphingomonas oligophenolica</i>	98.6	South Pole, Larsemann Hills
CCTCC S2016754	<i>Brevundimonas intermedia</i>	99.69	South Pole, Larsemann Hills
CCTCC S2016766	<i>Sphingomonas asaccharolytica</i>	98.4	South Pole, Inexpressible Island
CCTCC S2016769	<i>Arthrobacter scleromae</i>	98.51	South Pole, Inexpressible Island
CCTCC S2016770	<i>Arthrobacter oxydans</i>	98.51	South Pole, Inexpressible Island
CCTCC S2016771	<i>Arthrobacter scleromae</i>	99.07	South Pole, Inexpressible Island
CCTCC S2016773	<i>Arthrobacter globiformis</i>	97.95	South Pole, Inexpressible Island
CCTCC S2016774	<i>Arthrobacter scleromae</i>	98.85	South Pole, Inexpressible Island
CCTCC S2016776	<i>Arthrobacter oxydans</i>	98.37	South Pole, Inexpressible Island

Figure S2. The 16S rDNA alignment of *Pseudomonas* sp. 780

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

Description	Max score	Total score	Query cover	E value	Perc. ident	Accession
<input type="checkbox"/> Stenotrophomonas sp. strain DT 16S ribosomal RNA gene, partial sequence	2603	2603	100%	0.0	99.93%	MH814356.1
<input type="checkbox"/> Stenotrophomonas sp. LY-2 gene for 16S ribosomal RNA, partial sequence	2603	2603	100%	0.0	99.93%	LC136883.1
<input type="checkbox"/> Stenotrophomonas maltophilia strain 7K14 16S ribosomal RNA gene, partial sequence	2603	2603	100%	0.0	99.93%	KT825837.1
<input type="checkbox"/> Stenotrophomonas maltophilia R551-3, complete genome	2603	10395	100%	0.0	99.93%	CP001111.1
<input type="checkbox"/> Uncultured bacterium clone KRA30-21 16S ribosomal RNA gene, partial sequence	2603	2603	100%	0.0	99.93%	AY081992.1
<input type="checkbox"/> Stenotrophomonas sp. 16S rRNA gene, isolate S3	2603	2603	100%	0.0	99.93%	AJ002814.1
<input type="checkbox"/> Stenotrophomonas maltophilia strain JZFX-2 16S ribosomal RNA gene, partial sequence	2599	2599	99%	0.0	99.93%	MF170829.1
<input type="checkbox"/> Bacterium strain YCR3A-3 16S ribosomal RNA gene, partial sequence	2599	2599	99%	0.0	99.93%	MF143454.1
<input type="checkbox"/> Stenotrophomonas maltophilia strain SBR01 16S ribosomal RNA gene, partial sequence	2597	2597	100%	0.0	99.86%	KX018309.2
<input type="checkbox"/> Stenotrophomonas maltophilia strain IARI-ABL-34 16S ribosomal RNA gene, partial sequence	2597	2597	100%	0.0	99.86%	KC581677.1
<input type="checkbox"/> Stenotrophomonas sp. Bg1a partial 16S rRNA gene, isolate Bg1a	2597	2597	100%	0.0	99.86%	HF48402.1
<input type="checkbox"/> Stenotrophomonas maltophilia strain KNUC2106 16S ribosomal RNA gene, partial sequence	2597	2597	100%	0.0	99.86%	JN084034.1
<input type="checkbox"/> Uncultured bacterium clone 16slp101-2c06 p1k 16S ribosomal RNA gene, partial sequence	2597	2597	100%	0.0	99.86%	GQ157164.1
<input type="checkbox"/> Uncultured bacterium clone 16slp101-3h04 p1k 16S ribosomal RNA gene, partial sequence	2597	2597	100%	0.0	99.86%	GQ157162.1
<input type="checkbox"/> Uncultured bacterium clone 10A-13 16S ribosomal RNA gene, partial sequence	2597	2597	100%	0.0	99.86%	DQ006850.1

Tax BLAST report [Taxonomy report description](#)

RID [9HZZH7AE015](#) (Expires on 03-26 17:31 pm)

Query ID [Id|Query_97843](#)

Description None

Molecule type nucleic acid

Query Length 1412

Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.9.0+ [Citation](#)

Lineage Report [Organism Report](#) [Taxonomy Report](#)

Organism	Blast Name	Score	Number of Hits	Description
Bacteria	bacteria		104	
• Stenotrophomonas	g-roteobacteria		88	
• • Stenotrophomonas sp.	g-roteobacteria	2603	2	Stenotrophomonas sp. hits
• • Stenotrophomonas sp. LY-2	g-roteobacteria	2603	1	Stenotrophomonas sp. LY-2 hits
• • Stenotrophomonas maltophilia	g-roteobacteria	2603	28	Stenotrophomonas maltophilia hits
• • Stenotrophomonas maltophilia R551-3	g-roteobacteria	2603	1	Stenotrophomonas maltophilia R551-3 hits
• • Stenotrophomonas sp. IARI-HHS2-27	g-roteobacteria	2603	1	Stenotrophomonas sp. IARI-HHS2-27 hits
• Stenotrophomonas sp. KSR5	g-roteobacteria	2603	1	Stenotrophomonas sp. KSR5 hits

Figure S3.The 16S rDNA alignment of *S.maltophilia* 780

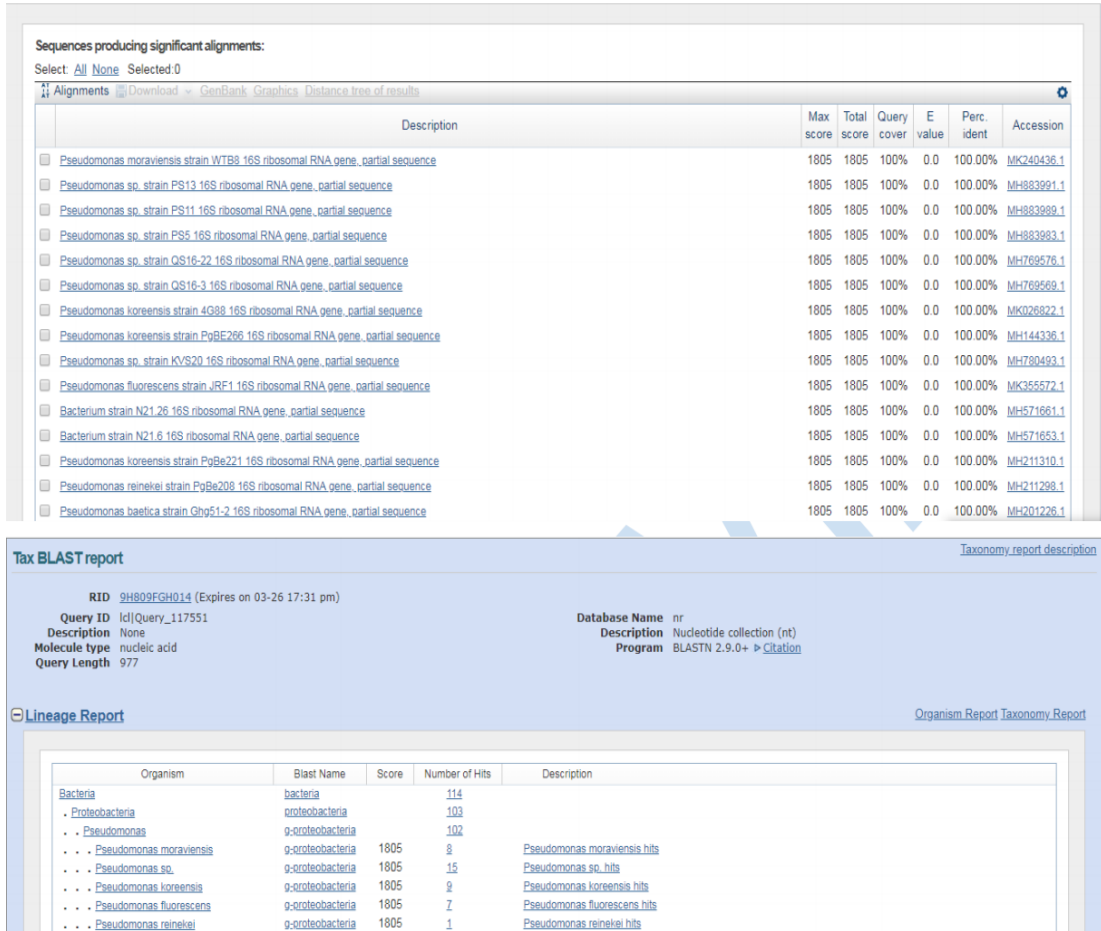
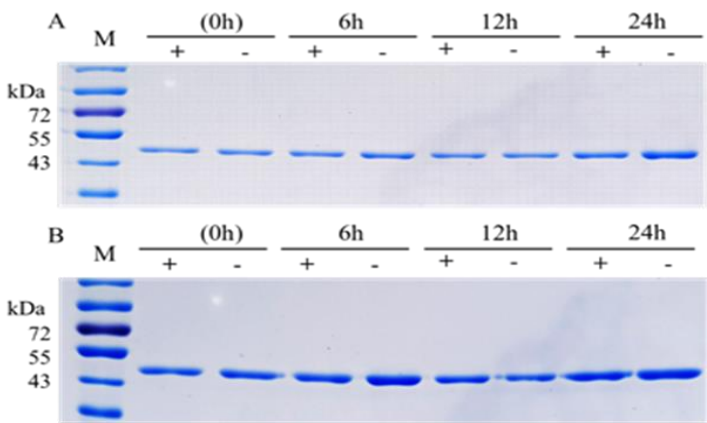


Figure. S4 The time course of the degradation of the recombinant CP4-EPSPS with extracellular proteases of *Pseudomonas* sp. 780



A. The degradation of 6×HIS-CP4-EPSPS; B. The degradation of CP4-EPSPS-6×HIS. (-): the negative control (degradation with supernatant of cell culture heated at 100°C for 30 min); (+) the extracellular proteases of *P.sp.* 780. M: protein molecular weight marker (the size of each band was indicated on the left).

Table S2. The putative ORFs coding proteases and peptidases in *S.maltophilia* 780

ID	E-value	Description
gi 692316381 ref WP_032127221.1	1.30E-124	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 501502945 ref WP_012511135.1	9.10E-301	peptidase S15 [<i>Stenotrophomonas maltophilia</i> R551-3]
gi 916992288 ref WP_051599000.1	0.00E+00	peptidase C39 [<i>Stenotrophomonas rhizophila</i>]
gi 504459148 ref WP_014646250.1	4.00E-290	peptidase M20 [<i>Stenotrophomonas maltophilia</i>]
gi 896534951 ref WP_049437628.1	9.70E-178	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 501501736 ref WP_012509956.1	0.00E+00	peptidase M14 carboxypeptidase A [<i>Stenotrophomonas maltophilia</i> R551-3]
gi 515925935 ref WP_017356518.1	0.00E+00	peptidase M13 [<i>Stenotrophomonas maltophilia</i>]
gi 501501696 ref WP_012509917.1	0.00E+00	peptidase M28 [<i>Stenotrophomonas maltophilia</i> R551-3]
gi 754363485 ref WP_041864589.1	1.10E-160	peptidase S41 [<i>Stenotrophomonas maltophilia</i>]
gi 896596053 ref WP_049480189.1	1.40E-232	Xaa-Pro aminopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 760006256 ref WP_043689563.1	8.10E-145	D-alanyl-D-alanine endopeptidase [<i>Luteimonas huabeiensis</i>]
gi 489189576 ref WP_003098955.1	1.30E-91	Lipoprotein signal peptidase [<i>Pseudomonas aeruginosa</i>]
gi 758873846 ref WP_043034335.1	4.50E-281	carboxypeptidase C (Cathepsin A) [<i>Stenotrophomonas maltophilia</i> WJ66]
gi 896525868 ref WP_049429646.1	0.00E+00	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 896504914 ref WP_049412562.1	0.00E+00	peptidase M20 [<i>Stenotrophomonas maltophilia</i>]
gi 491557240 ref WP_005414827.1	0.00E+00	Dipeptidyl peptidase IV [<i>Stenotrophomonas maltophilia</i> EPM1]
gi 896551079 ref WP_049451894.1	1.20E-233	metalloendopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 896545089 ref WP_049446379.1	3.40E-142	Methionine aminopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 896525822 ref WP_049429600.1	0.00E+00	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 475058159 emb CCP15559.1	7.90E-308	Plasma glutamate carboxypeptidase Flags: Precursor [<i>Stenotrophomonas maltophilia</i> RA8]
gi 493427208 ref WP_006382890.1	8.80E-151	Signal peptidase I [<i>Stenotrophomonas maltophilia</i> RA8]
gi 896551216 ref WP_049451966.1	1.60E-248	peptidase PmbA [<i>Stenotrophomonas maltophilia</i>]
gi 757859886 gb KIS38398.1	6.10E-102	endopeptidase YdhO [<i>Stenotrophomonas maltophilia</i> WJ66]
gi 922916199 gb KOO79758.1	0.00E+00	peptidase M13 [<i>Stenotrophomonas maltophilia</i>]

gi 612088648 gb EZIP47245.1	0.00E+00	putative endopeptidase [<i>Stenotrophomonas sp. RIT309</i>]
gi 612085737 gb EZIP44404.1	0.00E+00	Dipeptidyl-peptidase [<i>Stenotrophomonas sp. RIT309</i>]
gi 501503487 ref WP_012511663.1	1.40E-168	peptidase M48 Ste24p [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 696407508 ref WP_032978712.1	2.80E-147	Peptidase [<i>Stenotrophomonas sp. RIT309</i>]
gi 815697551 ref WP_046431082.1	2.10E-172	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 501503155 ref WP_012511339.1	1.30E-92	peptidase A24A prepilin type IV [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 498166821 ref WP_010480977.1	0.00E+00	peptidase S41 [<i>Stenotrophomonas maltophilia</i>]
gi 922919146 gb KOO82692.1	4.80E-181	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 759684756 ref WP_043401703.1	1.20E-98	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 501501432 ref WP_012509656.1	0.00E+00	peptidase M56 BlaR1 [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 504458374 ref WP_014645476.1	1.10E-251	peptidase C69 [<i>Stenotrophomonas maltophilia</i>]
gi 740905942 ref WP_038691190.1	0.00E+00	dipeptidyl carboxypeptidase II [<i>Stenotrophomonas rhizophila</i>]
gi 896565148 ref WP_049461671.1	9.80E-113	signal peptidase I [<i>Stenotrophomonas maltophilia</i>]
gi 501503709 ref WP_012511878.1	1.90E-120	peptidase M22 glycoprotease [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 501503686 ref WP_012511856.1	8.90E-160	Peptidase M23 [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 194350216 gb ACF53339.1	6.30E-133	Serine-type D-Ala-D-Ala carboxypeptidase [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 501501639 ref WP_012509860.1	3.60E-106	peptidase M15D vanX D-ala-D-ala dipeptidase [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 490240882 ref WP_004139140.1	7.60E-270	Endopeptidase ykfC [<i>Stenotrophomonas maltophilia RA8</i>]
gi 896553556 ref WP_049453837.1	0.00E+00	peptidase S8 [<i>Stenotrophomonas maltophilia</i>]
gi 896549217 ref WP_049450159.1	6.10E-189	peptidase M23 [<i>Stenotrophomonas maltophilia</i>]
gi 922921281 gb KOO84819.1	2.10E-183	proline iminopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 501504211 ref WP_012512377.1	0.00E+00	peptidase M3A and M3B thimet/oligopeptidase F [<i>Stenotrophomonas maltophilia R551-3</i>]
gi 756166387 ref WP_042614603.1	8.90E-255	aminopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 647597629 ref WP_025874228.1	0.00E+00	peptidase [<i>Stenotrophomonas maltophilia</i>]

gi 692317689 ref WP_032128510.1	2.10E-147	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 692317678 ref WP_032128499.1	2.10E-231	peptidase M19 [<i>Stenotrophomonas maltophilia</i>]
gi 501501962 ref WP_012510180.1	6.90E-235	peptidyl-Asp metalloendopeptidase [<i>Stenotrophomonas maltophilia</i> <i>R551-3</i>]
gi 692318258 ref WP_032129064.1	0.00E+00	dipeptidyl-peptidase 7 [<i>Stenotrophomonas maltophilia</i>]
gi 815699437 ref WP_046432751.1	0.00E+00	endopeptidase IV [<i>Stenotrophomonas maltophilia</i>]
gi 896549036 ref WP_049450010.1	2.10E-270	cytosol aminopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 896524539 ref WP_049428541.1	0.00E+00	peptidase M61 [<i>Stenotrophomonas maltophilia</i>]
gi 896531560 ref WP_049434638.1	7.40E-98	peptidase A8 [<i>Stenotrophomonas maltophilia</i>]
gi 647600489 ref WP_025877046.1	6.60E-120	endopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 756165275 ref WP_042613527.1	0.00E+00	peptidase M20 [<i>Stenotrophomonas maltophilia</i>]
gi 475058091 emb CCP15635.1	1.30E-106	methionine aminopeptidase [<i>Stenotrophomonas maltophilia</i> RA8]
gi 493434413 ref WP_006389956.1	4.80E-106	LON peptidase N-terminal domain and RING finger protein 2 [<i>Stenotrophomonas maltophilia</i> RA8]
gi 896545772 ref WP_049447062.1	2.50E-145	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 896565889 ref WP_049462250.1	0.00E+00	peptidase S46 [<i>Stenotrophomonas maltophilia</i>]
gi 896509486 ref WP_049416816.1	4.70E-258	proline dipeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 503804357 ref WP_014038351.1	1.30E-252	peptidase M24B X-Pro dipeptidase/aminopeptidase domain protein [<i>Stenotrophomonas maltophilia</i> JV3]
gi 653607042 ref WP_027618358.1	4.80E-127	peptidase S24 [<i>Pseudomonas</i> sp. <i>URHB0015</i>]
gi 491553502 ref WP_005411093.1	9.50E-96	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 756166096 ref WP_042614321.1	0.00E+00	peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 922683161 gb ALA83957.1	0.00E+00	prolyl oligopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 515923736 ref WP_017354319.1	9.50E-213	D-alanyl-D-alanine carboxypeptidase [<i>Stenotrophomonas</i> <i>maltophilia</i>]
gi 756166822 ref WP_042615018.1	0.00E+00	aminopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 922682389 gb ALA83185.1	0.00E+00	dipeptidyl carboxypeptidase II [<i>Stenotrophomonas maltophilia</i>]
gi 692318908 ref WP_032129696.1	0.00E+00	aminoacyl peptidase [<i>Stenotrophomonas maltophilia</i>]
gi 501504117 ref WP_012512283.1	2.70E-281	peptidase M56 BlaR1 [<i>Stenotrophomonas maltophilia</i> <i>R551-3</i>]

gi 896542396 ref WP_049443938.1	0.00E+00	oligopeptidase A [<i>Stenotrophomonas maltophilia</i>]
gi 896493993 ref WP_049402634.1	6.10E-262	peptidase S41 [<i>Stenotrophomonas maltophilia</i>]
gi 503801718 ref WP_014035712.1	0.00E+00	peptidase M28 [<i>Stenotrophomonas maltophilia</i> JV3]
gi 501501832 ref WP_012510051.1	5.90E-178	Peptidase M23 [<i>Stenotrophomonas maltophilia</i> R551-3]
gi 917542362 ref WP_052148779.1	1.50E-181	proline iminopeptidase [<i>Stenotrophomonas maltophilia</i>]
gi 566142589 ref WP_024011406.1	1.60E-10	peptidase [<i>Pseudomonas moraviensis</i> R28-S]
gi 917755073 ref WP_052269126.1	1.70E-200	peptidase M42 [<i>Pseudomonas fluorescens</i>]
gi 493413088 ref WP_006369023.1	9.60E-215	Uncharacterized metalloprotease [<i>Stenotrophomonas maltophilia</i> RA8]
gi 493412491 ref WP_006368434.1	0.00E+00	protease domain-containing protein [<i>Stenotrophomonas maltophilia</i> RA8]
gi 746376602 ref WP_039420382.1	1.00E-169	serine protease [<i>Xanthomonas vesicatoria</i>]
gi 922918882 gb KOO82428.1	0.00E+00	Clp protease ClpC [<i>Stenotrophomonas maltophilia</i>]
gi 896276656 ref WP_049263841.1	1.10E-179	Clp protease ClpC, partial [<i>Pseudomonas aeruginosa</i>]
gi 758873988 ref WP_043034476.1	1.30E-275	cysteine protease [<i>Stenotrophomonas maltophilia</i>]
gi 896505601 ref WP_049413215.1	1.70E-200	stomatin/prohibitin-family membrane protease subunit [<i>Stenotrophomonas maltophilia</i>]
gi 922682618 gb ALA83414.1	1.20E-267	protease TldD [<i>Stenotrophomonas maltophilia</i>]
gi 872686407 emb CRQ79460.1	5.20E-307	protease TldD [<i>Pseudomonas aeruginosa</i>]
gi 696406882 ref WP_032978097.1	0.00E+00	Zinc protease [<i>Stenotrophomonas</i> sp. RIT309]
gi 493410619 ref WP_006366596.1	8.80E-57	ATP-dependent Clp protease adapter protein clpS [<i>Stenotrophomonas maltophilia</i> RA8]
gi 740903143 ref WP_038688391.1	1.30E-147	Clp protease ClpX [<i>Stenotrophomonas rhizophila</i>]
gi 501503709 ref WP_012511878.1	1.90E-120	peptidase M22 glycoprotease [<i>Stenotrophomonas maltophilia</i> R551-3]
gi 515926406 ref WP_017356989.1	2.50E-41	ATP-dependent Clp protease proteolytic subunit [<i>Stenotrophomonas maltophilia</i>]
gi 495543884 ref WP_008268463.1	6.20E-300	protease [<i>Stenotrophomonas</i> sp. SKA14]
gi 922686726 gb ALA91477.1	6.40E-155	membrane protease HflC [<i>Stenotrophomonas maltophilia</i>]

gi 504459393 ref WP_014646495.1	6.80E-252	zinc metalloprotease [<i>Stenotrophomonas maltophilia</i>]
gi 872681110 emb CRR57107.1	1.90E-111	Protease synthase and sporulation protein PAI 2 [<i>Pseudomonas aeruginosa</i>]
gi 872680093 emb CRR70935.1	1.80E-117	Protease production enhancer protein [<i>Pseudomonas aeruginosa</i>]
gi 740576582 ref WP_038362377.1	3.10E-205	Clp protease ClpP [<i>Pseudomonas chlororaphis</i>]
gi 493437803 ref WP_006393294.1	1.10E-216	ATP-dependent protease ATP-binding subunit HslU [<i>Stenotrophomonas maltophilia</i> RA8]
gi 518167463 ref WP_019337671.1	9.70E-16	ATP-dependent protease [<i>Stenotrophomonas maltophilia</i>]
gi 501503639 ref WP_012511810.1	4.10E-290	protease Do [<i>Stenotrophomonas maltophilia</i> R551-3]
gi 490254907 ref WP_004152871.1	7.00E-134	cell division protease FtsH [<i>Stenotrophomonas maltophilia</i> RA8]
gi 748748842 ref WP_040006958.1	0.00E+00	serine protease [<i>Stenotrophomonas</i> sp. <i>SKA14</i>]
gi 219719191 gb EED37716.1	4.80E-106	ATP-dependent zinc-metallo protease [<i>Stenotrophomonas</i> sp. <i>SKA14</i>]
gi 647601653 ref WP_025878144.1	3.00E-121	Lon protease [<i>Stenotrophomonas</i> sp. <i>RIT309</i>]
gi 490248191 ref WP_004146319.1	1.00E-100	ATP-dependent protease ATP-binding subunit ClpX [<i>Stenotrophomonas maltophilia</i> RA8]
gi 748192953 ref WP_039764045.1	8.60E-20	Clp protease [<i>Pseudomonas fluorescens</i>]
gi 734951378 ref WP_034151555.1	3.50E-48	serine protease [<i>Pseudomonas fluorescens</i>]