

## Sigma factor ECF subfamily (FeSreg)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	459	459	100%	2e-125	97%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	448	448	100%	4e-122	96%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	431	431	100%	4e-117	95%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	420	420	100%	9e-114	94%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	409	409	100%	2e-110	93%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	403	403	100%	9e-109	93%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	392	392	100%	2e-105	92%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	392	392	100%	2e-105	92%	<a href="#">CP011306.1</a>

### Stenotrophomonas maltophilia K279a complete genome, strain K279a

Sequence ID: [emb|AM743169.1](#) Length: 4851126 Number of Matches: 1

Range 1: 2742086 to 2742360 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
459 bits(248)	2e-125	266/275(97%)	0/275(0%)	Plus/Minus
Query 1	TTCATCGCGCGCTATCTCGACCCGGCCAGTACCGAGGACACCCTGCAGAACCTGTACCTG	60		
Sbjct 2742360	TTCATCGCGCGCTATCTCGACCCGGCCAGTACCGAGGACACCCTGCAGAACCTGTACCTG	2742301		
Query 61	AAGGCCAGCAGCGTGCCCGGCGATCCGCCATCCTCGAGCCGCGCGGCTATCTGTACCGG	120		
Sbjct 2742300	AAGGCCAGCAGCGTGCCCGGCGATCCGCCATCCTCGAGCCGCGCGGCTATCTGTACCGG	2742241		
Query 121	ATGGCCTACCACACGCGCTCAACCGCAGCCAGTCCGACGCCCGCGAGCGGCGTGCCATG	180		
Sbjct 2742240	ATGGCCTACCACACGCGCTCAACCGCAGCCAGTCCGACGCCCGCGAGCGGCGTGCCATG	2742181		
Query 181	GCCGAGTACGCCCTCGACATGGCCGAGGCCAGCCGCGATGGCGAGGCGCAGGCGCTGGAC	240		
Sbjct 2742180	GCCGAGTACGCCCTCGACATGGCCGAGGCCAGCCGCGATGGCGAGGCGCAGGCGCTGGAC	2742121		
Query 241	CAGGCGCAGCTGCGCGAGATCACCCGGACCATCCT	275		
Sbjct 2742120	CAGGCACAACGCGCGAGATCACCCGGACCATCCT	2742086		

### Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

FEATURES	Location/Qualifiers
source	1..275
	<a href="#">/organism="Stenotrophomonas maltophilia K279a"</a>
	<a href="#">/mol_type="genomic DNA"</a>
	<a href="#">/strain="K279a"</a>
	<a href="#">/db_xref="taxon:522373"</a>
	<a href="#">/country="United Kingdom"</a>
gene	complement(<1..>275)
	<a href="#">/locus_tag="Smlt2716"</a>
CDS	complement(<1..>275)
	<a href="#">/locus_tag="Smlt2716"</a>
	<a href="#">/note="similarity:fasta; BB4742; bbronchiseptica; ECF sigma factor; length 177 aa; id=39.8%; E()=1.7e-11; 133 aa overlap; query 6-136 aa; subject 30-162 aa"</a>
	<a href="#">/codon_start=1</a>
	<a href="#">/transl_table=11</a>
	<a href="#">/product="putative ECF sigma factor"</a>

## Iron siderophore receptor protein (FeSR)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	484	484	98%	3e-133	99%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia JV3 complete genome</a>	401	401	97%	3e-108	94%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2 complete genome</a>	396	396	97%	1e-106	94%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R complete genome</a>	396	396	97%	1e-106	94%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome strain K279a</a>	390	390	100%	7e-105	93%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	385	385	100%	3e-103	92%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3 complete genome</a>	385	385	98%	3e-103	93%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3 complete genome</a>	357	357	98%	7e-95	91%	<a href="#">CP011010.1</a>

### Stenotrophomonas maltophilia D457 complete genome

Sequence ID: [emb|HE798556.1](#) Length: 4769156 Number of Matches: 1

Range 1: 3908959 to 3909226 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
484 bits(262)	3e-133	266/268(99%)	0/268(0%)	Plus/Minus
Query 4	TCGCAGCGTACCTACCTCGACGCGGACCTGATCTCCAGCCTGACCATCACCAAGGGCCCCG	63		
Sbjct 3909226	TCGCAGCGCACCTACCTCGACCGGACCTGATCTCCAGCCTGACCATCACCAAGGGCCCCG	3909167		
Query 64	AGCCTGCAGGCCAACGCGTCCGGTGGCATCGGCGGCGTGGTCGAGATGGAGACGTTGAAG	123		
Sbjct 3909166	AGCCTGCAGGCCAACGCGTCCGGTGGCATCGGCGGCGTGGTCGAGATGGAGACGTTGAAG	3909107		
Query 124	ATCGGTGACGTGCTGCGCGAGGGCCGCGACGTGCGCGTGCCTGCGCGGCGGCGCTGGCC	183		
Sbjct 3909106	ATCGGTGACGTGCTGCGCGAGGGCCGCGACGTGCGCGTGCCTGCGCGGCGGCGCTGGCC	3909047		
Query 184	AATGGCAGTGCCAAACAGCCTGCCGTCTACAGTGCAGGACCGCGCACCGATCGCAGCGCC	243		
Sbjct 3909046	AATGGCAGTGCCAAACAGCCTGCCGTCTACAGTGCAGGACCGCGCACCGATCGCAGCGCC	3908987		
Query 244	ACCGGCAGCCAGTTCTTCAACGTGGCCG	271		
Sbjct 3908986	ACCGGCAGCCAGTTCTTCAACGTGGCCG	3908959		

## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

### FEATURES

source

Location/Qualifiers

1..268

/organism="Stenotrophomonas maltophilia D457"

/mol\_type="genomic DNA"

/strain="D457"

/db\_xref="taxon:1163399"

/country="Spain:Mostoles"

gene

complement(<1..>268)

/locus\_tag="SMD\_3500"

CDS

complement(<1..>268)

/locus\_tag="SMD\_3500"

/codon\_start=1

/transl\_table=11

/product="Iron siderophore receptor protein"



## Iron siderophore sensor protein (FeSS)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	427	427	100%	4e-116	99%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	411	411	100%	4e-111	98%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	311	311	100%	5e-81	90%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	311	311	100%	5e-81	90%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	285	285	99%	3e-73	89%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	272	272	100%	2e-69	87%	<a href="#">CP011010.1</a>

### Stenotrophomonas maltophilia K279a complete genome, strain K279a

Sequence ID: [emb|AM743169.1](#) Length: 4851126 Number of Matches: 1

Range 1: 3988174 to 3988410 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
427 bits(231)	4e-116	235/237(99%)	0/237(0%)	Plus/Minus
Query 1	ACGTCGTCGAGAACGTAACGCTGCCGATGGCAGCCGCGCAGTGTGGATGCGGACAGCG			60
Sbjct 3988410	ACGTCGTCGAGAACGTAACGCTGCCGATGGCAGCCGCGCAGTGTGGATGCGGACAGCG			3988351
Query 61	CGATCGCCGTGCGCTTCGATGCGCACGACGCGAGGTTGAGCTCTGCGCGGGCGCGTCT			120
Sbjct 3988350	CGATCGCCGTGCGCTTCGATGCGCACGACGCGAGGTCGAGCTGCTGCGCGGGCGCGTCT			3988291
Query 121	GGTTCGAGGTGAGCCGGATGCGCAGCGGCGTTTCAGCGTGCGTGCCGGCAATGGCGTGG			180
Sbjct 3988290	GGTTCGAGGTGAGCCGGATGCGCAGCGGCGTTTCAGCGTGCGTGCCGGCAATGGCGTGG			3988231
Query 181	TTGAGGACATCTCGACCGCGTTACCGTCGCGCGTGGCGATGACCTGGTGGAAACCC			237
Sbjct 3988230	TTGAGGACATCTCGACCGCGTTACCGTCGCGCGTGGCGATGACCTGGTGGAAACCC			3988174

## Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

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                        /strain="K279a"
                        /db_xref="taxon:522373"
                        /country="United Kingdom"
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     CDS               complement(<1..>237)
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                        /note="similarity:fasta; ECA1539; ecarotovora_atroseptica;
                        putative transmembrane sensor protein; length 322 aa;
                        id=31.5%; E()=3.9e-20; 317 aa overlap; query 25-318 aa;
                        subject 10-322 aa;
                        similarity:fasta; with=UniProt:Q1IGG4; Pseudomonas
                        entomophila (strain L48).; Putative FecR-like
                        transmembrane sensor.; length=325; id 33.974%; ungapped id
                        36.426%; E()=8.8e-21; 312 aa overlap; query 9-306; subject
                        7-311"
                        /codon_start=1
                        /transl_table=11
                        /product="putative transmembrane FecR sensor protein"

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## Heme oxygenase, associated with heme uptake (HemO/HO)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	520	520	100%	8e-144	100%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	514	514	100%	4e-142	99%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	436	436	100%	9e-119	95%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	431	431	100%	4e-117	94%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	431	431	100%	4e-117	94%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	364	364	100%	4e-97	90%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	364	364	100%	4e-97	90%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	353	353	100%	9e-94	89%	<a href="#">CP011010.1</a>

### Stenotrophomonas maltophilia strain 13637 genome

Sequence ID: [gb|CP008838.1](#) Length: 4989312 Number of Matches: 1

Range 1: 4804541 to 4804821 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
520 bits(281)	8e-144	281/281(100%)	0/281(0%)	Plus/Plus
Query 1	CAGCAATTTGCCCCGTTTCTGCGCGTGCAAGTATCGCTTCCACCGCAGCATCGATGCGCT	60		
Sbjct 4804541	CAGCAATTTGCCCCGTTTCTGCGCGTGCAAGTATCGCTTCCACCGCAGCATCGATGCGCT	4804600		
Query 61	GTATGCCAACCTGCGCTGGACGCACTGCTGCCGGACCTGGGCGAGCGCCGCCCTGAC	120		
Sbjct 4804601	GTATGCCAACCTGCGCTGGACGCACTGCTGCCGGACCTGGGCGAGCGCCGCCCTGAC	4804660		
Query 121	CCAGGTCGCGCGCGACCTGCAGGACCTGGAGCAGACCTGCCGGGGGCTGACATCGCGGC	180		
Sbjct 4804661	CCAGGTCGCGCGCGACCTGCAGGACCTGGAGCAGACCTGCCGGGGGCTGACATCGCGGC	4804720		
Query 181	GTTGCCGTCCGATCTGGAAGTGCCTGCCCGCGCTTGGGGTGGCTGTACGTGGCTGAAGGCTC	240		
Sbjct 4804721	GTTGCCGTCCGATCTGGAAGTGCCTGCCCGCGCTTGGGGTGGCTGTACGTGGCTGAAGGCTC	4804780		
Query 241	CAACCTGGGCGGCAACCTCTGTACAAGATGGCTGCCAAGC	281		
Sbjct 4804781	CAACCTGGGCGGCAACCTCTGTACAAGATGGCTGCCAAGC	4804821		

## Stenotrophomonas maltophilia strain 13637 genome

GenBank: CP008838.1

FEATURES	Location/Qualifiers
source	1..281
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	<a href="#">/mol_type="genomic DNA"</a>
	<a href="#">/strain="13637"</a>
	<a href="#">/db_xref="taxon:40324"</a>
gene	<1..>281
	<a href="#">/locus_tag="DP16_4486"</a>
CDS	<1..>281
	<a href="#">/locus_tag="DP16_4486"</a>
	<a href="#">/codon_start=1</a>
	<a href="#">/transl_table=11</a>
	<a href="#">/product="heme oxygenase family protein"</a>



## Heme ABC transporter, ATPase component (HmuV)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	483	483	100%	1e-132	99%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	477	477	100%	5e-131	98%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	383	383	98%	1e-102	92%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	364	364	97%	4e-97	91%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	364	364	97%	4e-97	91%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	339	339	98%	2e-89	89%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	327	327	98%	5e-86	89%	<a href="#">CP002986.1</a>

### Stenotrophomonas maltophilia K279a complete genome, strain K279a

Sequence ID: [embjAM743169.1](#) Length: 4851126 Number of Matches: 1

Range 1: 2400245 to 2400517 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
483 bits(261)	1e-132	269/273(99%)	0/273(0%)	Plus/Plus
Query 1	GAAGCTGCATGAGGTGGTGGTGCGCCGCCAGCAGCGCGAGATCCTGCATGGCATCTCGCT	60		
Sbjct 2400245	GAAGCTGCATGAGGTGGTGGTGCGCCGCCAGCAGCGCGAGATCCTGCATGGCATCTCGCT	2400304		
Query 61	CGCGTTTCGAGCCGGGTACCGTGATCGCGCTGGTTGGCCCGAACGGCGCAGGCAAGTCCAC	120		
Sbjct 2400305	CGCGTTTCGAGCCGGGTACCGTGACCGCGCTGGTTGGCCCGAACGGCGCAGGCAAGTCCAC	2400364		
Query 121	CTTGCTGGCGGTAGCGGCCGGCGACCTGCGCGCCGATGCGGGCGAGGTGAGCCTGTTGGG	180		
Sbjct 2400365	CTTGCTGGCGATAGCGGCCGGCGACCTGCGCGCCGATGCGGGCGAGGTGAGCCTGTTGGG	2400424		
Query 181	CAAGCCGCTGGCCAGCTACAAGGCCGGGCCGCTGGCGCGCGAGCGCGCGGTAATGCCGCA	240		
Sbjct 2400425	CAAACCGCTGGCCAGCTACAAGGCCGGGCCGCTGGCGCGCGAGCGCGCGGTAATGCCGCA	2400484		
Query 241	GGAGCACGGCGTTTCGTTTCGCCCTTCAGCGTAGA	273		
Sbjct 2400485	GGAGCACGGCGTTTCGTTTCGCCCTTCAGCGTAGA	2400517		

## Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

FEATURES	Location/Qualifiers
source	1..273 /organism="Stenotrophomonas maltophilia K279a" /mol_type="genomic DNA" /strain="K279a" /db_xref="taxon:522373" /country="United Kingdom"
gene	<1..>273 /locus_tag="Smlt2357"
CDS	<1..>273 /locus_tag="Smlt2357" /codon_start=1 /transl_table=11 /product="putative ABC transport protein, ATP-binding component."

## Hypothetical protein related to heme utilization (Hyp1)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	424	424	100%	6e-115	98%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	424	424	100%	6e-115	98%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	379	379	100%	1e-101	94%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	379	379	100%	1e-101	94%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	379	379	100%	1e-101	94%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	379	379	100%	1e-101	94%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	368	368	100%	3e-98	94%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	357	357	100%	6e-95	93%	<a href="#">CP011010.1</a>

### Stenotrophomonas maltophilia strain 13637 genome

Sequence ID: [gb|CP008838.1](#) Length: 4989312 Number of Matches: 1

Range 1: 4601859 to 4602105 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
424 bits(229)	6e-115	241/247(98%)	0/247(0%)	Plus/Plus
Query 1	GGCATCGTCGGCATCTTCGTGCCGGGCTGCCGACCACCGTATTCATCCTGATTTGGGCC	60		
Sbjct 4601859	GGCATCGTCGGCATCTTCGTACCGGGCTGCCGACCACCGTATTCATCCTGATTTGGGCC	4601918		
Query 61	TGGGCGCGCTCGCGTGGCTCCGAGCGCTGCACAACCTGGCTGCTGCAGCATCCACGCTTC	120		
Sbjct 4601919	TGGGCGCGCTCGCGTGGCTCCGAAACGCTGCACAACCTGGCTGCTGCAGCATCCACGCTTC	4601978		
Query 121	GGCCCGGCCATCGCCAACCTGGCAGGCACACGGGGCGGTACGCCGCTATGGCAAGTGGATG	180		
Sbjct 4601979	GGCCCGGCCATCGCCAACCTGGCAGGCACACGGGGCGGTACGCCGCTACGGCAAGTGGATG	4602038		
Query 181	GCCACGATCACCATGGCGGTATGCGCGGCCATCATGCTGTGGTGCCTACCGATTGCCTGG	240		
Sbjct 4602039	GCCACGATCACCATGGCGGTATGCGCGGCCATCATGCTGTGGTGCCTACCGATTGCCTGG	4602098		
Query 241	GTGAAGT	247		
Sbjct 4602099	GTGAAGT	4602105		

## Stenotrophomonas maltophilia strain 13637 genome

GenBank: CP008838.1

### FEATURES

source

Location/Qualifiers

1..247

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/strain="13637"

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CDS

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/product="hypothetical protein"



## Heme ABC transporter, permease protein (HmuU)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	420	420	100%	1e-113	92%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	403	403	100%	1e-108	91%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	398	398	100%	4e-107	91%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	398	398	100%	4e-107	91%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	381	381	100%	4e-102	90%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	375	375	100%	2e-100	89%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	375	375	100%	2e-100	89%	<a href="#">CP011306.1</a>

### Stenotrophomonas maltophilia K279a complete genome, strain K279a

Sequence ID: [emb|AM743169.1](#) Length: 4851126 Number of Matches: 1

Range 1: 2399866 to 2400164 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
420 bits(227)	1e-113	275/299(92%)	0/299(0%)	Plus/Plus
Query 1	ACGCCATTGGACATGCTGGCGCTGGGCGAGCGCCAGGCCAGCACCTGGGGCTGGATGTG	60		
Sbjct 2399866	ACGCCATTGGACATGCTGGCGCTGGGCGAACGCCAGGCGCAGCACCTCGGGCTGGACGTG	2399925		
Query 61	ACCCGCACGCGGGCTCGACTGGTGGCGTTACGCGCGCTGCTGGTGGGGGCGGCGGTGGCG	120		
Sbjct 2399926	ACCCGCACGCGGGCTCGCTGGTGGCGTTCAGTGCGCTGCTGGTGGGCGCGGCGGTGGCC	2399985		
Query 121	TTTGCGGGCTCGATCAGCTTCGTTGGCCTGGTGGTCCGCGACGTGGCGCGCTGCTGGTG	180		
Sbjct 2399986	TTTGCGGGTTCGATCAGTTTCGTTGGCCTGGTAGTGCCGCGACGTGGCGCGCTGCTGGTG	2400045		
Query 181	GGTCCCGGTATCGCTGGCTGCTGCCGTTGTCCGGCCTGCTGGGTGCACTGCTGATCGTG	240		
Sbjct 2400046	GGCCCCGGGATCGCTGGCTGCTGCCGTTGTCCGGCCTGCTGGGCGCGCTGCTGATCGTG	2400105		
Query 241	GTGGCGGATACGGCCGCGCGCACGCTGGATCCGCCCGCGGAGATTCCGCTGGGCTTGT	299		
Sbjct 2400106	GTGGCCGACACCGCGGCCCGCACGCTCGATCCGCCGCGGAGATTCCGCTGGGCTTGT	2400164		

## Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

### FEATURES

source

Location/Qualifiers

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/mol\_type="genomic DNA"

/strain="K279a"

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/country="United Kingdom"

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/locus\_tag="Smlt2356"

CDS

<1..>299

/locus\_tag="Smlt2356"

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/transl\_table=11

/product="putative FecCD-family transmembrane transport protein."

## Heme ABC transporter, cell surface heme and hemoprotein receptor (HmuT)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	499	499	100%	1e-137	97%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	455	455	100%	3e-124	94%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	455	455	100%	3e-124	94%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	444	444	100%	6e-121	93%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	444	444	100%	6e-121	93%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	444	444	100%	6e-121	93%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	427	427	100%	6e-116	92%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	399	399	100%	1e-107	91%	<a href="#">CP011010.1</a>

### Stenotrophomonas maltophilia D457 complete genome

Sequence ID: [emb|HE798556.1](#) Length: 4769156 Number of Matches: 1

Range 1: 2356617 to 2356916 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
499 bits(270)	1e-137	290/300(97%)	0/300(0%)	Plus/Plus
Query 1	CATGCGCCACGACTGATCCACGTCTCGGCAACCGGCGCTGGCGGCTCGCCCACTGTTGCC	60		
Sbjct 2356617	CATGCGCCACGACTGATCCACGTATCGGCCACCGGCGCTGGCGGCTCGCCCACTGTTGCC	2356676		
Query 61	GGTGCCGACAGCGCGTCCGCGCAGCTGATCGCCCTGGCCGGCGGCATCAACATCGGCACC	120		
Sbjct 2356677	GGTGCCGACAGCGCGTCCGCGCAGCTGATCGCGCTGGCCGGCGGCATCAACATCGGCACC	2356736		
Query 121	GAGGCCGGGGTGAAGAAGTACTCGCAGCTGAGCAACGAGGGCGTGGTGGCGGCGGCACCG	180		
Sbjct 2356737	GAGGCCGGGGTGAAGAAGTACTCGCAGCTGAGCAACGAGGGGGTGGTGGCGGCGGCACCG	2356796		
Query 181	GAAAGTGATCCTGGTGACCGAGCATGACCTGCAGCTGTTCCGGCGGTGCCGAAGGCCTGTGG	240		
Sbjct 2356797	GAAAGTGATCCTGGTGACCGAGCATGACCTGCAGCTGTTCCGGCGGTGCCGAAGGCCTGTGG	2356856		
Query 241	AAGGCGTACCCGACGCTGAAGCAGACCCCGGCCGGGCAGGCCAATCGGGTCTGGGTGATG	300		
Sbjct 2356857	AAGGCGTACCCGACGCTGAAGCAGACCCCGGCCGGGCAGGCCAATCGGGTCTGGGTGATG	2356916		

## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

### FEATURES

source

Location/Qualifiers

1..300

/organism="Stenotrophomonas maltophilia D457"

/mol\_type="genomic DNA"

/strain="D457"

/db\_xref="taxon:1163399"

/country="Spain:Mostoles"

gene

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/locus\_tag="SMD\_2121"

CDS

<1..>300

/locus\_tag="SMD\_2121"

/codon\_start=1

/transl\_table=11

/product="Heme ABC transporter, cell surface heme and hemoprotein receptor HmuT"



## Outer membrane receptor proteins, mostly Fe transport (Rp2)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	348	348	100%	3e-92	95%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia D457, complete genome</a>	342	342	100%	1e-90	95%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	327	327	99%	4e-86	94%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	327	327	99%	4e-86	94%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	327	327	99%	4e-86	94%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	315	315	100%	3e-82	92%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	315	315	100%	3e-82	92%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	278	278	99%	4e-71	89%	<a href="#">CP001111.1</a>

### Stenotrophomonas maltophilia D457 complete genome

Sequence ID: [emb|HE798556.1](#) Length: 4769156 Number of Matches: 1

Range 1: 3781688 to 3781908 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
342 bits(185)	1e-90	209/221(95%)	0/221(0%)	Plus/Minus
Query 1	AACGCATGCCCGACTACTGGGAGTTGTTCTCGCCCGACACGGCCCGGCGGTGA	60		
Sbjct 3781908	AACGCATGCCCGACTACTGGGAGCTGTTCTCGCCCGACACGGCCCGGCGGTGA	3781849		
Query 61	ACGCGTTTGCCGGCATCCAGCCCGAGCGCACCACCCAGCTCGACGTCGGCTGCAGTACA	120		
Sbjct 3781848	ACGCGTTTGCCGGCATCCAGCCCGAGCGCACCACCCAGCTCGACGTCGGCTGCAGTACA	3781789		
Query 121	AGGGACGACGCGTGCAGGCTGGGTCTCGGCCTACGCCGGGCAGATCCAGGACTACATCC	180		
Sbjct 3781788	AGGGACGCGCGTGCAGGCTGGGTCTCGGCCTACGCCGGGCAGATCCAGGACTACATCC	3781729		
Query 181	TGTTACCTACCACGGCAGCGGCATGATGGGCATGAGCCAG	221		
Sbjct 3781728	TGTTACCTACCACGGCAGCGGCATGATGGGCATGAGCCAG	3781688		

## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

### FEATURES

source

Location/Qualifiers

1..221

/organism="Stenotrophomonas maltophilia D457"

/mol\_type="genomic DNA"

/strain="D457"

/db\_xref="taxon:1163399"

/country="Spain:Mostoles"

gene

complement(<1..>221)

/locus\_tag="SMD\_3393"

CDS

complement(<1..>221)

/locus\_tag="SMD\_3393"

/codon\_start=1

/transl\_table=11

/product="Outer membrane receptor proteins, mostly Fe transport"

## Hemin uptake protein (Hup)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Brugia timori genome assembly B_timori_Indonesia_v1_0_4_scaffold BTMF_contig0011954</a>	370	370	100%	6e-99	100%	<a href="#">LK924066.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	370	370	100%	6e-99	100%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	364	364	100%	3e-97	99%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	359	359	100%	1e-95	99%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	359	359	100%	1e-95	99%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	359	359	100%	1e-95	99%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	353	353	100%	6e-94	99%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	353	353	100%	6e-94	99%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	353	353	100%	6e-94	99%	<a href="#">CP008838.1</a>

### Stenotrophomonas maltophilia D457 complete genome

Sequence ID: [emb|HE798556.1](#) Length: 4769156 Number of Matches: 1

Range 1: 784415 to 784614 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
370 bits(200)	6e-99	200/200(100%)	0/200(0%)	Plus/Plus
Query 1	ATGCTCATGAATGCTCAACCTGTACTGCTGCGCCCCGAAACGCTGACCTCCGCGATCGT	60		
Sbjct 784415	ATGCTCATGAATGCTCAACCTGTACTGCTGCGCCCCGAAACGCTGACCTCCGCGATCGT	784474		
Query 61	CCGGTCCGTGTCGTTCCGCCGGAAGAGGTCATCGACAGCGAAGCCCTGCTCAAGGGCCGT	120		
Sbjct 784475	CCGGTCCGTGTCGTTCCGCCGGAAGAGGTCATCGACAGCGAAGCCCTGCTCAAGGGCCGT	784534		
Query 121	CGTGAAATCCTGATCCAGCACGGCGACCGCTTCTATCGCCTGCGGCACACCAGCAACGAC	180		
Sbjct 784535	CGTGAAATCCTGATCCAGCACGGCGACCGCTTCTATCGCCTGCGGCACACCAGCAACGAC	784594		
Query 181	AAGCTGATCCTGACCAAGTA	200		
Sbjct 784595	AAGCTGATCCTGACCAAGTA	784614		

### Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

#### FEATURES

source

Location/Qualifiers

1..200

/organism="Stenotrophomonas maltophilia D457"

/mol\_type="genomic DNA"

/strain="D457"

/db\_xref="taxon:1163399"

/country="Spain:Mostoles"

gene

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/locus\_tag="SMD\_0678"

CDS

7..>200

/locus\_tag="SMD\_0678"

/codon\_start=1

/transl\_table=11

/product="Hemin uptake protein"



## Electron transfer flavoprotein, beta subunit (ETFb)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	398	398	100%	3e-107	100%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	392	392	100%	1e-105	99%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	381	381	100%	3e-102	99%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	381	381	100%	3e-102	99%	<a href="#">CP011306.1</a>
<a href="#">PREDICTED: Pantolops hodgsonii electron transfer flavoprotein subunit beta, mitochondria</a>	370	370	100%	7e-99	98%	<a href="#">XM_005963657.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	370	370	100%	7e-99	98%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	364	364	100%	3e-97	97%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	353	353	100%	7e-94	96%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	353	353	100%	7e-94	96%	<a href="#">CP008838.1</a>

### Stenotrophomonas maltophilia D457 complete genome

Sequence ID: [emb|HE798556.1|](#) Length: 4769156 Number of Matches: 1

Range 1: 621185 to 621399 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
398 bits(215)	3e-107	215/215(100%)	0/215(0%)	Plus/Minus
Query 1	CCTGGAACGCTGGAAGTCGATCTGCCGGCCGTGGTCACCAACGACCTGCGCCTGAACGA	60		
Sbjct 621399	CCTGGAACGCTGGAAGTCGATCTGCCGGCCGTGGTCACCAACGACCTGCGCCTGAACGA	621340		
Query 61	GCCGCGCTTCATCAAGCTGCCGGACATCATGAAGGCCAAGGCCAAGCCGCTGGAGACCCT	120		
Sbjct 621339	GCCGCGCTTCATCAAGCTGCCGGACATCATGAAGGCCAAGGCCAAGCCGCTGGAGACCCT	621280		
Query 121	GCAGCTGGCCGACCTCGGCGTTGAAGCCGCCGACACCTTCAAGACCACCCAGTACGCCGC	180		
Sbjct 621279	GCAGCTGGCCGACCTCGGCGTTGAAGCCGCCGACACCTTCAAGACCACCCAGTACGCCGC	621220		
Query 181	GCCGTCCAAGCGCAGCAAGGGTGTGATGGTCAAGG	215		
Sbjct 621219	GCCGTCCAAGCGCAGCAAGGGTGTGATGGTCAAGG	621185		

## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

### FEATURES

source

Location/Qualifiers

1..215

**/organism="Stenotrophomonas maltophilia D457"**

/mol\_type="genomic DNA"

/strain="D457"

/db\_xref="taxon:[1163399](#)"

/country="Spain:Mostoles"

gene

complement(<1..>215)

/gene="etfB"

/locus\_tag="SMD\_0543"

CDS

complement(<1..>215)

/gene="etfB"

/locus\_tag="SMD\_0543"

/codon\_start=1

/transl\_table=[11](#)

**/product="Electron transfer flavoprotein, beta subunit"**

## Ferric siderophore transport system, periplasmic binding protein (TonB)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	564	564	100%	4e-157	99%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	525	525	100%	2e-145	97%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	525	525	100%	2e-145	97%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	514	514	100%	4e-142	96%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	475	475	100%	2e-130	94%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	475	475	100%	2e-130	94%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	464	464	100%	5e-127	93%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	453	453	99%	1e-123	93%	<a href="#">CP001111.1</a>

### Stenotrophomonas maltophilia D457 complete genome

Sequence ID: [emb|HE798556.1](#) Length: 4769156 Number of Matches: 1

Range 1: 4553337 to 4553650 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
564 bits(305)	4e-157	311/314(99%)	0/314(0%)	Plus/Plus
Query 1	CGCGAGAACC	CGCATGTATGCGCCGGCCGGCGACAACGCCATCGAGTACTACCTCGCCCTG	60	
Sbjct 4553337	CGCGAGAACC	CGCATGTACGCGCCGGCCGGCGACAACGCCATCGAGTACTACCTCGCCCTG	4553396	
Query 61	CGCGACAAGACCCCGGACGACGCTCGGTGAAGAGCGCGCTGACCGACCTGCTGCCGTAC	120		
Sbjct 4553397	CGCGACAAGACCCCGGACGACGCTCGGTGAAGAGCGCGCTGACCGACCTGCTGCCGTAC	4553456		
Query 121	ACCCTGATCGCCGCCGAGCAGCACCTGGGGCGCGAGGACTACACCGAAGCGCAGCGACTG	180		
Sbjct 4553457	ACCCTGATCGCCGCCGAGCAGCACCTGGGGCGCGAGGACTACACCGAAGCGCAGCGGCTG	4553516		
Query 181	GTGGCACTGATCGAGAAGGTGGATGTCATCCGCGCCGGCCCTGCCGCGCCTGAAGGACGGC	240		
Sbjct 4553517	GTGGCGCTGATCGAGAAGGTGGATGTCATCCGCGCCGGCCCTGCCGCGCCTGAAGGACGGC	4553576		
Query 241	CTGGCCAAGGGCGTGCGAAGCGCGGCCAAGCGCACCGAGGCCGAAGCCGAGAAGGCCAAG	300		
Sbjct 4553577	CTGGCCAAGGGCGTGCGAAGCGCGGCCAAGCGCACCGAGGCCGAAGCCGAGAAGGCCAAG	4553636		
Query 301	AAGGACGCCGAGGA	314		
Sbjct 4553637	AAGGACGCCGAGGA	4553650		

## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

### FEATURES

source

### Location/Qualifiers

1..314

/organism="Stenotrophomonas maltophilia D457"

/mol\_type="genomic DNA"

/strain="D457"

/db\_xref="taxon:1163399"

/country="Spain:Mostoles"

gene

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CDS

<1..>314

/locus\_tag="SMD\_4053"

/codon\_start=1

/transl\_table=11

/product="Ferric siderophore transport system, periplasmic binding protein TonB"



## Ferric siderophore transport system, biopolymer transport protein (ExbB)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	459	459	100%	2e-125	99%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	453	453	100%	8e-124	99%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	420	420	100%	8e-114	97%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	420	420	100%	8e-114	97%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	375	375	100%	2e-100	94%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	370	370	100%	8e-99	93%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	364	364	100%	4e-97	93%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	353	353	100%	8e-94	92%	<a href="#">CP001111.1</a>

### Stenotrophomonas maltophilia K279a complete genome, strain K279a

Sequence ID: [emb|AM743169.1](#) Length: 4851126 Number of Matches: 1

Range 1: 1703311 to 1703561 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
459 bits(248)	2e-125	250/251(99%)	0/251(0%)	Plus/Plus
Query 1	GAGCGTTTCTGGTCCCTTCGGCGGACTGAAGTGCTGCCGCCCGGCCTCGGCCAGGAAGTG	60		
Sbjct 1703311	GAGCGTTTCTGGTCCCTTCGGCGGACTGAAGTGCTGCCGCCCGGCCTCGGCCAGGAAGTG	1703370		
Query 61	CGCAACTGGGCCGCCCGCGGCAAGCTCGACCCGGCCACCTGCAGACCTGCGGGCGAAC	120		
Sbjct 1703371	CGCAACTGGGCCGCCCGCGGCAAGCTCGACCCGGCCACCTGCAGACCTGCGGGCGAAC	1703430		
Query 121	TCGCCGCTGGGCGCGCTGCTGGCTGCCGCACTGGAAGCCCGCAACCGCCGCGACCAAG	180		
Sbjct 1703431	TCGCCGCTGGGCGCGCTGCTGGCTGCCGCACTGGAAGCCCGCAACCGCCGCGACCAAG	1703490		
Query 181	ATCCGCGAGCGCATCGAAGACACCGCCGCCACCTGGTGCACCGCATGGAGCGATTCTCTG	240		
Sbjct 1703491	ATCCGCGAGCGCATCGAAGACACCGCCGCCACCTGGTGCACCGCATGGAGCGATTCTCTG	1703550		
Query 241	AACGCACTGGG	251		
Sbjct 1703551	AACGCACTGGG	1703561		

### Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

#### FEATURES

source

#### Location/Qualifiers

1..251

[/organism="Stenotrophomonas maltophilia K279a"](#)

[/mol\\_type="genomic DNA"](#)

[/strain="K279a"](#)

[/db\\_xref="taxon:522373"](#)

[/country="United Kingdom"](#)

gene

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[/locus\\_tag="Smlt1638"](#)

CDS

<1..>251

[/locus\\_tag="Smlt1638"](#)

[/codon\\_start=1](#)

[/transl\\_table=11](#)

[/product="putative biopolymer transport protein"](#)

## Hemin transport protein (Htp)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	427	427	100%	4e-116	99%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	394	394	100%	4e-106	97%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	366	366	98%	9e-98	95%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	361	361	100%	4e-96	94%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	361	361	100%	4e-96	94%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	350	350	100%	1e-92	94%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	342	342	99%	2e-90	93%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	322	322	100%	2e-84	91%	<a href="#">CP002986.1</a>

### Stenotrophomonas maltophilia strain ISMMS2, complete genome

Sequence ID: [gb|CP011305.1](#) Length: 4509724 Number of Matches: 1

Range 1: 735723 to 735957 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
361 bits(195)	4e-96	222/235(94%)	1/235(0%)	Plus/Plus
Query 1	CACCGTGTGTGCTGTACACGCGGCAACGAGCTGGGCGGCTGGCGCCAGGCCGT	60		
Sbjct 735723	CACCGTGTGTGCTGTACACGCGGCAACGAGCTGGGTGGCTGGCGCCAGGCCGT	735782		
Query 61	ACGCGTACACGCTGCCAGGGCGTGGACAGCGAGGGCCTGCGCGAAAGCCTGTGCTTCCT	120		
Sbjct 735783	ACGCGTGCACGCTGCCAGGGCGTGGACAGTGAAGGCCTGCGCGAGAGCCTGTGTTTCCT	735842		
Query 121	TGATGGCCGCGGCGCGTGCCTGTGGCGCTGTACCTGCTGCCCGACAGCGATTTCTTGGC	180		
Sbjct 735843	CGATGGCCGCGGCGCGTGCCTGTGGCGTTTGTACCTGCTGCCCGACAGCGACTTCTTGGC	735902		
Query 181	CTGGGACCGCTCTGGTCGCGGCGCTGCCGCGGGACCGGAACACGATAGCGA-GGC	234		
Sbjct 735903	CTGGGACCGCCTGGTCGCGGCGCTGCCGCGGGACCGGAACACGACAGCGATGGC	735957		

### Stenotrophomonas maltophilia strain ISMMS2, complete genome

GenBank: CP011305.1

FEATURES	Location/Qualifiers
source	1..235 <div>/organism="Stenotrophomonas maltophilia"</div> <div>/mol_type="genomic DNA"</div> <div>/strain="ISMMS2"</div> <div>/isolation_source="blood"</div> <div>/host="Homo sapiens"</div> <div>/db_xref="taxon:40324"</div> <div>/country="USA: New York, NY"</div> <div>/lat_lon="40.7898553 N 73.9531696 W"</div> <div>/collection_date="2013"</div> <div>/collected_by="The Mount Sinai Hospital"</div>
gene	<1..>235 <div>/locus_tag="YH67_03255"</div>
CDS	<1..>235 <div>/locus_tag="YH67_03255"</div> <div>/inference="EXISTENCE: similar to AA</div> <div>sequence:RefSeq:WP_019661101.1"</div> <div>/note="Derived by automated computational analysis using</div> <div>gene prediction method: Protein Homology."</div> <div>/codon_start=1</div> <div><div>/transl_table=11</div></div> <div>/product="Hemin transport protein"</div>



## TonB-dependent hemin, ferrichrome receptor (FCR)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	691	691	100%	0.0	99%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	686	686	100%	0.0	99%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	647	647	100%	0.0	97%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	636	636	100%	1e-178	97%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	636	636	100%	1e-178	97%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	233	233	54%	2e-57	87%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	231	231	58%	6e-57	85%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	161	161	28%	8e-36	94%	<a href="#">CP011010.1</a>

### Stenotrophomonas maltophilia strain 13637 genome

Sequence ID: [gb|CP008838.1](#) Length: 4989312 Number of Matches: 1

Range 1: 746379 to 746758 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
686 bits(371)	0.0	377/380(99%)	0/380(0%)	Plus/Plus
Query 1	CGGAAATGAAGGCCGGTATCGAGTTTGGCGAACTCAGCCCGGCGCTGAAGGGCTGGGCGC	60		
Sbjct 746379	CGGAAATGAAGGCCGGCATCGAGTTCGGCGAACTCAGCCCGGCGCTGAAGGGCTGGGCGC	746438		
Query 61	TGCGCAGTGCGTTGGCATGGTCGCGTGGTGACAACCGGACCGATGACGAACCGCTGGCCT	120		
Sbjct 746439	TGCGCAGTGCGTTGGCATGGTCGCGTGGTGACAACCGGACCGATGACGAACCGCTGGCCT	746498		
Query 121	CGGTCGATCCGCTGCGTGCGCACGCTGGGCTGATGTACGACACCGATACCTGGGGCGTCG	180		
Sbjct 746499	CGGTCGATCCGCTGCGTGCGCACGCTGGGCTGATGTACGACACCGATACCTGGGGCGTCG	746558		
Query 181	AACTGGCCGGTACCTTCGTGCAGCGCAAGAAGCGCCTGCCGCCGCTGCGGCGCAGACCA	240		
Sbjct 746559	AACTGGCCGGTACCTTCGTGCAGCGCAAGAAGCGCCTGCCGCCGCTGCGGCGCAGACCA	746618		
Query 241	ATCCGAACGCACCGGCGCCGTTCTGTCTACCAAGCCGGCCGGCTACGGCGTGCTGGACCTGA	300		
Sbjct 746619	ATCCGAACGCACCGGCGCCGTTCTGTCTACCAAGCCGGCCGGCTACGGCGTGCTGGACCTGA	746678		
Query 301	TGGCGCACTGGAACCTTCGCGCCGGGTGCCACCTTCAATGTCGGCGTGTTCAACCTGGCCG	360		
Sbjct 746679	TGGCGCACTGGAACCTTCGCGCCGGGTGCCACCTTCAATGTCGGCGTGTTCAACCTGGCCG	746738		
Query 361	ACAAGCGCTACATCGAATGG	380		
Sbjct 746739	ACAAGCGTTACATCGAATGG	746758		

## Stenotrophomonas maltophilia strain 13637 genome

GenBank: CP008838.1

FEATURES	Location/Qualifiers
source	1..380 /organism="Stenotrophomonas maltophilia" /mol_type="genomic DNA" /strain="13637" /db_xref="taxon:40324"
gene	<1..>380 /locus_tag="DP16_685"
CDS	<1..>380 /locus_tag="DP16_685" /note="tonB-hemlactrns: TonB-dependent hemoglobin/transferrin/lactoferrin receptor family protein" /codon_start=1 /transl_table=11 /product="TonB-dependent hemoglobin/transferrin/lactoferrin receptor family protein"

### Predicted dye-decolorizing peroxidase, encapsulated subgroup (DyP)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	405	405	100%	2e-109	95%	<a href="#">HE798556.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	405	405	100%	2e-109	95%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	394	394	100%	5e-106	94%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	387	387	98%	8e-104	94%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	383	383	100%	1e-102	93%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	383	383	100%	1e-102	93%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	383	383	100%	1e-102	93%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	355	355	100%	2e-94	91%	<a href="#">CP011010.1</a>

Stenotrophomonas maltophilia K279a complete genome, strain K279a

Sequence ID: [emb|AM743169.1](#) Length: 485126 Number of Matches: 1

Range 1: 195850 to 196107 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
405 bits(219)	2e-109	245/258(95%)	0/258(0%)	Plus/Plus
Query 1		GTGCTGAAGGTGAAGGATGACGAGGCGTCGATCGCCAGGGCACGCGAGGTGCTGGCGAGC		60
Sbjct 195850		GTGCTGAAGGTGAAGGATGACGAGGCGTCGATCGCCAAGGCACGCGAGGTGCTGGCCAGC		195909
Query 61		ACCGATGACCTGATCAAGAACACCGCCATCCGCGAGATCGAGCGTACCTTCACCTGCAAC		120
Sbjct 195910		ACCGACGACCTGATCAAGAACACCGCCATCCGCGAGATCGAACGCACCTTCACCTGCAAC		195969
Query 121		GTGGCCATCGGCCACCGCGTGTGGCAGCCGCTGGTGGGCTCCACGCCGCCGCGCGAGCTG		180
Sbjct 195970		GTGGCCATCGGCCACCGCGTGTGGCAGCCGCTGGTGGGCACCACGCCGCCGCGCGAGTTG		196029
Query 181		AAGCCGTTCCGTGAGATCAAGGGCGCCACCCACACCGCCGTGTCCACGCCCGGTGACCTG		240
Sbjct 196030		CAGCCGTTCCGCGAGATCAAGGGCGCGACCCACACGCCGTGTCCACGCCGGGCGACCTG		196089
Query 241		CTGTACCACATCCGTGCA	258	
Sbjct 196090		CTGTACCACATCCGTGCA	196107	

**Stenotrophomonas maltophilia K279a complete genome, strain K279a**

GenBank: AM743169.1

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FEATURES
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            /mol_type="genomic DNA"
            /strain="K279a"
            /db_xref="taxon:522373"
            /country="United Kingdom"
    gene
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            /locus_tag="Smlt0187"
    CDS
        <1..>258
            /locus_tag="Smlt0187"
            /note="similarity:fasta; with=UniProt:Q2UBB0
            (EMBL:AP007162); Aspergillus oryzae.; Predicted
            iron-dependent peroxidase.; length=315; id 62.215%;
            ungapped id 62.215%; E()=1e-70; 307 aa overlap; query
            18-324; subject 8-314"
            /codon_start=1
            /transl_table=11
            /product="putative peroxidase"

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## Ferric uptake regulation protein FUR (Fur)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<a href="#">Stenotrophomonas maltophilia JV3, complete genome</a>	449	449	100%	1e-122	96%	<a href="#">CP002986.1</a>
<a href="#">Stenotrophomonas maltophilia K279a complete genome, strain K279a</a>	449	449	100%	1e-122	96%	<a href="#">AM743169.1</a>
<a href="#">Stenotrophomonas maltophilia strain 13637 genome</a>	438	438	100%	2e-119	95%	<a href="#">CP008838.1</a>
<a href="#">Stenotrophomonas maltophilia R551-3, complete genome</a>	427	427	100%	5e-116	94%	<a href="#">CP001111.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS3, complete genome</a>	416	416	100%	1e-112	94%	<a href="#">CP011010.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2, complete genome</a>	411	411	100%	5e-111	93%	<a href="#">CP011305.1</a>
<a href="#">Stenotrophomonas maltophilia strain ISMMS2R, complete genome</a>	411	411	100%	5e-111	93%	<a href="#">CP011306.1</a>
<a href="#">Stenotrophomonas rhizophila strain DSM14405 genome</a>	405	405	100%	2e-109	93%	<a href="#">CP007597.1</a>
<a href="#">Stenotrophomonas maltophilia D457 complete genome</a>	388	388	100%	2e-104	92%	<a href="#">HE798556.1</a>

### Stenotrophomonas maltophilia JV3, complete genome

Sequence ID: [gb|CP002986.1](#) Length: 4544477 Number of Matches: 1

Range 1: 1789191 to 1789469 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
449 bits(243)	1e-122	268/280(96%)	2/280(0%)	Plus/Plus
Query 1	TGACCGCCGAAGACATCTACCGCCAGCTGCTGGAGCACGGCGACGAGATCGGCCTGGCCA	60		
Sbjct 1789191	TGACCGCCGAAGACATCTACCGCCAGCTGCTGGAGCACGGCGACGAGATCGGCCTGGCCA	1789250		
Query 61	CGGTGTACCGGGTGTGACCCAGTTTCGAGGCCGCGGCCCTCGTGCTCAAGCACAATTTTCG	120		
Sbjct 1789251	CGGTGTACCGGGTGTGACCCAGTTTCGAGGCCGCGGCCCTCGTGCTCAAGCACAATTTTCG	1789310		
Query 121	AGGGCGGCCAGGCGGTCTACGAACTGGACCGTGGCGGCCACCACGACCACATGGTCGACG	180		
Sbjct 1789311	AAGGCGGCCAGGCGGTCTACGAGCTGGACCGTGGCGGCCACCACGACCACATGGTCGACG	1789370		
Query 181	TGGACAGTGGCAAGATCATCGAGTTTCGAAAGCCACGAGATCGAGGAGCTGCAGCGCA-GA	239		
Sbjct 1789371	TGGACAGCGGCAAGATCATCGAGTTTCGAAAGCCACGAGATCGAGGAGCTGCAGCGCAAGA	1789430		
Query 240	TTCCGCGCAGACCATGGCTACGAACTGGAAGAGCACTCGC	279		
Sbjct 1789431	-TCGCGGCCGACCACGGCTACGAGCTGGAAGAGCATTCGC	1789469		

## Stenotrophomonas maltophilia JV3, complete genome

GenBank: CP002986.1

FEATURES	Location/Qualifiers
source	1..279
	/organism="Stenotrophomonas maltophilia JV3"
	/mol_type="genomic DNA"
	/strain="JV3"
	/db_xref="taxon:868597"
	/country="Brazil"
	/note="isolated from plants"
gene	<1..>279
	/locus_tag="BurJV3_1637"
CDS	<1..>279
	/locus_tag="BurJV3_1637"
	/inference="protein motif:PFAM:PF01475"
	/note="PFAM: Ferric-uptake regulator;
	KEGG: smt:Smal_1594 Fur family ferric uptake regulator"
	/codon_start=1
	/transl_table=11
	/product="ferric uptake regulator, Fur family"

