

## 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	TTCATCGCGCGTATCTCGACCCGGCCAGTACCGAGGACACCCTGCAGAACCTGTACCTG			60
Sbjct 2742360	TTCATCGCGCGTATCTCGACCCGGCCAGTACCGAGGACACCCTGCAGAACCTGTACCTG			2742301
Query 61	AAGGCCAGCAGCGTGCCCGGCGATCCGCCATCCTCGAGCCGCGGGCTATCTGTACCGG			120
Sbjct 2742300	AAGGCCAGCAGCGTGCCCGGCGATCCGCCATCCTCGAGCCGCGGGCTATCTGTACCGG			2742241
Query 121	ATGGCCTACCACACGCGCTCAACCGCAGCCAGTCCGACGCCCGCGAGCGGGCTGCCATG			180
Sbjct 2742240	ATGGCCTACCACACGCGCTCAACCGCAGCCAGTCCGACGCCCGCGAGCGGGCTGCCATG			2742181
Query 181	GCCGAGTACGCCCTCGACATGGCCGAGGCCAGCCGCGATGGCGAGGCGCAGGCGCTGGAC			240
Sbjct 2742180	GCCGAGTACGCCCTCGACATGGCCGAGGCCAGCCGCGATGGCGAGGCGCAGGCGCTGGAC			2742121
Query 241	CAGGCCAGCTGCGCGAGATCACCCGGACCATCCT		275	
Sbjct 2742120	CAGGCCAACAAGTGCAGGATCACCCGGACCATCCT		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

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Query 4      TCGCAGCGTACCTACCTCGACGCGGACCTGATCTCCAGCCTGACCATCACCAAGGGCCCG 63
Sbjct 3909226 TCGCAGCGCACCTACCTCGACCGGACCTGATCTCCAGCCTGACCATCACCAAGGGCCCG 3909167
Query 64      AGCCTGCAGGCCAACGCGTCCGGTGGCATCGGCGGCGTGGTCGAGATGGAGACGTTGAAG 123
Sbjct 3909166 AGCCTGCAGGCCAACGCGTCCGGTGGCATCGGCGGCGTGGTCGAGATGGAGACGTTGAAG 3909107
Query 124     ATCGGTGACGTGCTGCGCGAGGGCCGCGACGTCGGCGTGCGCGTGCAGCGGCGGCGCTGGCC 183
Sbjct 3909106 ATCGGTGACGTGCTGCGCGAGGGCCGCGACGTCGGCGTGCGCGTGCAGCGGCGGCGCTGGCC 3909047
Query 184     AATGGCAGTGCCAACAGCCTGCCGTCTACAGTGCGGCACCGCGCACCGATCGCAGCGCC 243
Sbjct 3909046 AATGGCAGTGCCAACAGCCTGCCGTCTACAGTGCGGCACCGCGCACCGATCGCAGCGCC 3908987
Query 244     ACCGGCAGCCAGTTCTTCAACGTGGCCG 271
Sbjct 3908986 ACCGGCAGCCAGTTCTTCAACGTGGCCG 3908959
  
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## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

FEATURES	Location/Qualifiers
source	1..268 <div style="border: 1px solid red; padding: 2px;">/organism="Stenotrophomonas maltophilia D457"</div> /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 <div style="border: 1px solid red; padding: 2px;">/product="Iron siderophore receptor protein"</div>

## 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	ACGTCGTGCAGAACGTAACGCTGCCCGATGGCAGCCGCGCAGTGTGGATGCGGACAGCG			60
Sbjct 3988410	ACGTCGTGCAGAACGTAACGCTGCCCGATGGCAGCCGCGCAGTGTGGATGCGGACAGCG			3988351
Query 61	CGATCGCCGTGCGCTTCGATGCGCACGCACGCGAGGTTGAGCTCTGCGCGGGCGCGTCT			120
Sbjct 3988350	CGATCGCCGTGCGCTTCGATGCGCACGCACGCGAGGTCGAGCTGCTGCGCGGGCGCGTCT			3988291
Query 121	GGTTCGAGGTGAGCCGGATGCGCAGCGGCGTTTCAGCGTGCCTGCCGGCAATGGCGTGG			180
Sbjct 3988290	GGTTCGAGGTGAGCCGGATGCGCAGCGGCGTTTCAGCGTGCCTGCCGGCAATGGCGTGG			3988231
Query 181	TTGAGGACATCTCGACCGCGTTCACCGTGCAGCGTGGCGATGACCTGGTGGAAACCC			237
Sbjct 3988230	TTGAGGACATCTCGACCGCGTTCACCGTGCAGCGTGGCGATGACCTGGTGGAAACCC			3988174

## Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

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FEATURES             Location/Qualifiers
     source            1..237
                        /organism="Stenotrophomonas maltophilia K279a"
                        /mol_type="genomic DNA"
                        /strain="K279a"
                        /db_xref="taxon:522373"
                        /country="United Kingdom"
     gene              complement(<1..>237)
                        /locus_tag="Smlt3899"
     CDS                complement(<1..>237)
                        /locus_tag="Smlt3899"
                        /note="similarity:fasta; ECA1539; ecaratovora_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     GTATGCCAACCCCTGCGCTGGACGCACTGCTGCCGGACCTGGGCGAGCGCCGCCCTGAC 120
Sbjct 4804601  GTATGCCAACCCCTGCGCTGGACGCACTGCTGCCGGACCTGGGCGAGCGCCGCCCTGAC 4804660
Query 121    CCAGGTCGCGCGCGACCTGCAGGACCTGGAGCAGACCCGCGGGGGCTGACATCGCGGC 180
Sbjct 4804661    CCAGGTCGCGCGCGACCTGCAGGACCTGGAGCAGACCCGCGGGGGCTGACATCGCGGC 4804720
Query 181    GTTGCCGTCCGATCTGGAAGTCCCGCGCGTTGGGGTGGCTGTACGTGGCTGAAGGCTC 240
Sbjct 4804721    GTTGCCGTCCGATCTGGAAGTCCCGCGCGTTGGGGTGGCTGTACGTGGCTGAAGGCTC 4804780
Query 241    CAACCTGGGCGGCACCACTTCTGTACAAGATGGCTGCCAAGC 281
Sbjct 4804781    CAACCTGGGCGGCACCACTTCTGTACAAGATGGCTGCCAAGC 4804821
  
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## Stenotrophomonas maltophilia strain 13637 genome

GenBank: CP008838.1

FEATURES	Location/Qualifiers
source	1..281
	<a href="#">/organism="Stenotrophomonas maltophilia"</a>
	<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		GAAGCTGCATGAGGTGGTGGTGCGCCGCCAGCAGCGAGATCCTGCATGGCATCTCGCT		60
Sbjct 2400245		GAAGCTGCATGAGGTGGTGGTGCGCCGCCAGCAGCGAGATCCTGCATGGCATCTCGCT		2400304
Query 61		CGCGTTTCGAGCCGGGTACCGTGATCGCGCTGGTTGGCCCGAACGGCGCAGGCAAGTCCAC		120
Sbjct 2400305		CGCGTTTCGAGCCGGGTACCGTGACCGCGCTGGTTGGCCCGAACGGCGCAGGCAAGTCCAC		2400364
Query 121		CTTGCTGGCGGTAGCGGCCGGCGACCTGC CGCGCCGATGCGGGCGAGGTGAGCCTGTTGGG		180
Sbjct 2400365		CTTGCTGGCGATAGCGGCCGGCGACCTGC CGCGCCGATGCGGGCGAGGTGAGCCTGTTGGG		2400424
Query 181		CAAGCCGCTGGCCAGCTACAAGGCCGGGCCGCTGGCGCGCAGCGCGCGGTAATGCCGCA		240
Sbjct 2400425		CAAACCGCTGGCCAGCTACAAGGCCGGGCCGCTGGCGCGCAGCGCGCGGTAATGCCGCA		2400484
Query 241		GGAGCACGGCGTTTCGTTTCGCC TTCAGCGTAGA 273		
Sbjct 2400485		GGAGCACGGCGTTTCGTTTCGCC TTCAGCGTAGA 2400517		

## Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

FEATURES	Location/Qualifiers
source	1..273 <div style="border: 1px solid red; padding: 2px;">/organism="Stenotrophomonas maltophilia K279a"</div> /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 <div style="border: 1px solid red; padding: 2px;">/product="putative ABC transport protein, ATP-binding component."</div>

## 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

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Query 1      GGCATCGTCGGCATCTTCGTGCGGGCCTGCCGACCACCGTATTCATCCTGATTTCCGGCC 60
Sbjct 4601859 GGCATCGTCGGCATCTTCGTACCGGGCCTGCCGACCACCGTATTCATCCTGATTTCCGGCC 4601918

Query 61     TGGGCCGCGCTCGCGTGGCTCCGAGCGCCTGCACAACCTGGCTGCTGCAGCATCCACGCTTC 120
Sbjct 4601919 TGGGCCGCGCTCGCGTGGCTCCGAAACGCTGCACAACCTGGCTGCTGCAGCATCCACGCTTC 4601978

Query 121    GGCCCGGCCATCGCCAACCTGGCAGGCACACGGGGCGGTGAGCCGCTATGGCAAGTGGATG 180
Sbjct 4601979 GGCCCGGCCATCGCCAACCTGGCAGGCACACGGGGCGGTGAGCCGCTACGGCAAGTGGATG 4602038

Query 181    GCCACGATCACCATGGCGGTATGCGCCGCCATCATGCTGTGGTGCCTACCGATTGCCTGG 240
Sbjct 4602039 GCCACGATCACCATGGCGGTATGCGCCGCCATCATGCTGTGGTGCCTACCGATTGCCTGG 4602098

Query 241    GTGAAGT 247
Sbjct 4602099 GTGAAGT 4602105
  
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## Stenotrophomonas maltophilia strain 13637 genome

GenBank: CP008838.1

FEATURES	Location/Qualifiers
source	1..247 <div style="border: 1px solid red; padding: 2px; display: inline-block;">/organism="Stenotrophomonas maltophilia"</div> /mol_type="genomic DNA" /strain="13637" /db_xref="taxon:40324"
gene	<1..>247 /locus_tag="DP16_4312"
CDS	<1..>247 /locus_tag="DP16_4312" /note="conserved hypothetical protein" /codon_start=1 /transl_table=11 <div style="border: 1px solid red; padding: 2px; display: inline-block;">/product="hypothetical protein"</div>

## 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	ACCCGACGCGGGCTCGACTGGTGGCGTTTCAGCGCGCTGCTGGTGGGGCGGGCGGTGGCG			120
Sbjct 2399926	ACCCGACGCGGGCTCGCCTGGTGGCGTTTCAGTGCCTGCTGGTGGGCGGGCGGTGGCC			2399985
Query 121	TTTGCGGGCTCGATCAGCTTCGTTGGCCTGGTGGTGC CGCACGTGGCGCGCCTGCTGGTG			180
Sbjct 2399986	TTTGCCGGTTCGATCAGTTTCGTTGGCCTGGTAGTGC CGCACGTGGCGCGCCTGCTGGTG			2400045
Query 181	GGTCCCGGTATCGCTGGCTGCTGCCGTTGTCCGGCCTGCTGGGTGCACTGCTGATCGTG			240
Sbjct 2400046	GGCCCCGGGCATCGCTGGCTGCTGCCGTTGTCCGGCCTGCTGGGCGCGCTGCTGATCGTG			2400105
Query 241	GTGGCGGATACGGCCGCGCGCACGCTGGATCCGCCCGGGAGATTCCGCTGGGCTTGT			299
Sbjct 2400106	GTGGCCGACACCGCGGCCCGCACGCTCGATCCGCCGGAGATTCCGCTGGGCTTGT			2400164

## Stenotrophomonas maltophilia K279a complete genome, strain K279a

GenBank: AM743169.1

FEATURES	Location/Qualifiers
source	1..299 <div style="border: 1px solid red; padding: 2px;">/organism="Stenotrophomonas maltophilia K279a"</div> /mol_type="genomic DNA" /strain="K279a" /db_xref="taxon:522373" /country="United Kingdom"
gene	<1..>299 /locus_tag="Smlt2356"
CDS	<1..>299 /locus_tag="Smlt2356" /codon_start=1 /transl_table=11 <div style="border: 1px solid red; padding: 2px;">/product="putative FecCD-family transmembrane transport protein."</div>

## 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	GGTGCCGACAGCGCGTCCGGCAGCTGATCGCCCTGGCCGGCGGCATCAACATCGGCACC	120		
Sbjct 2356677	GGTGCCGACAGCGCGTCCGGCAGCTGATCGCGCTGGCCGGCGGCATCAACATCGGCACC	2356736		
Query 121	GAGGCCGGGGTGAAGAAGCTACTCGCAGCTGAGCAACGAGGGCGTGGTCGCGGGCGGCCG	180		
Sbjct 2356737	GAGGCCGGGGTGAAGAAGCTACTCGCAGCTGAGCAACGAGGGGGTGGTCGCGGGCGGCCG	2356796		
Query 181	GAAGTGATCCTGGTGACCGAGCATGACCTGCAGCTGTTCCGGCGGTGCCGAAGGCCTGTGG	240		
Sbjct 2356797	GAGGTGATCCTGGTGACCGAGCATGACCTGCAGCTGTTCCGGCGGTGCCGAAGGCCTGTGG	2356856		
Query 241	AAGGCGTACCCGACGCTGAAGCAGACCCGGCCGGGCAGGCCAATCGGGTCTGGGTGATG	300		
Sbjct 2356857	AAGGCGTACCCGACGCTGAAGCAGACCCGGCCGGGCAGGCCAATCGGGTCTGGGTGATG	2356916		

## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

FEATURES	Location/Qualifiers
source	1..300 <div style="border: 1px solid red; padding: 2px;">/organism="Stenotrophomonas maltophilia D457"</div> /mol_type="genomic DNA" /strain="D457" /db_xref="taxon:1163399" /country="Spain:Mostoles"
gene	<1..>300 /locus_tag="SMD_2121"
CDS	<1..>300 /locus_tag="SMD_2121" /codon_start=1 /transl_table=11 <div style="border: 1px solid red; padding: 2px;">/product="Heme ABC transporter, cell surface heme and hemoprotein receptor HmuT"</div>

## 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	AACGCATGCCCGACTACTGGGAGTTGTTCTCGCCCGACCACGGCCCGGCGGTGA	60		
Sbjct 3781908	AACGCATGCCCGACTACTGGGAGCTGTTCTCGCCCGACCACGGCCCGGCGGTGA	3781849		
Query 61	ACGCGTTTGCCGGCATCCAGCCCGAGCGCACCCAGCTCGACGTCGGCTGCAGTACA	120		
Sbjct 3781848	ACGCGTTTGCCGGCATCCAGCCCGAGCGCACCCAGCTCGACGTCGGCTGCAGTACA	3781789		
Query 121	AGGGACGACGCGTGCAGGCCCTGGGTCTCGGCCTACGCCGGGCAGATCCAGGACTACATCC	180		
Sbjct 3781788	AGGGACCGCGCGTGCAGGCCCTGGGTCTCGGCCTACGCCGGGCAGATCCAGGACTACATCC	3781729		
Query 181	TGTTACCTACCACGGCAGCGGCATGATGGGCATGAGCCAG	221		
Sbjct 3781728	TGTTACCTACCACCGCAGCGGCATGATGGGCATGAGCCAG	3781688		

## Stenotrophomonas maltophilia D457 complete genome

GenBank: HE798556.1

### FEATURES

FEATURES	Location/Qualifiers
source	1..221 <a href="#">/organism="Stenotrophomonas maltophilia D457"</a> /mol_type="genomic DNA" /strain="D457" /db_xref="taxon: <a href="#">1163399</a> " /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 <a href="#">/product="Outer membrane receptor proteins, mostly Fe transport"</a>

## 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

Location/Qualifiers
source
1..200
<a href="#">/organism="Stenotrophomonas maltophilia D457"</a>
<a href="#">/mol_type="genomic DNA"</a>
<a href="#">/strain="D457"</a>
<a href="#">/db_xref="taxon:1163399"</a>
<a href="#">/country="Spain:Mostoles"</a>
gene
7..>200
<a href="#">/locus_tag="SMD_0678"</a>
CDS
7..>200
<a href="#">/locus_tag="SMD_0678"</a>
<a href="#">/codon_start=1</a>
<a href="#">/transl_table=11</a>
<a href="#">/product="Hemin uptake protein"</a>

## 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: Pantholops 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	CCTGGAAACGCTGGAAGTCGATCTGCCGGCCGTGGTCACCACCGACCTGCGCCTGAACGA	60		
Sbjct 621399	CCTGGAAACGCTGGAAGTCGATCTGCCGGCCGTGGTCACCACCGACCTGCGCCTGAACGA	621340		
Query 61	GCCGCGCTTCATCAAGCTGCCGGACATCATGAAGGCCAAGGCCAAGCCGCTGGAGACCCT	120		
Sbjct 621339	GCCGCGCTTCATCAAGCTGCCGGACATCATGAAGGCCAAGGCCAAGCCGCTGGAGACCCT	621280		
Query 121	GCAGCTGGCCGACCTCGGCGTTGAAGCCGCCGACACCTTCAAGACCACCCAGTACGCCGC	180		
Sbjct 621279	GCAGCTGGCCGACCTCGGCGTTGAAGCCGCCGACACCTTCAAGACCACCCAGTACGCCGC	621220		
Query 181	GCCGTCGAAGCGCAGCAAGGGTGTGATGGTCAAGG	215		
Sbjct 621219	GCCGTCGAAGCGCAGCAAGGGTGTGATGGTCAAGG	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	CGCATGTATG	CGCCGGCCGG	CGACAACGCC	ATCGAGTACT	ACCTCGCCCTG	60
Sbjct 4553337	CGCGAGAACC	CGCATGTACG	CGCCGGCCGG	CGACAACGCC	ATCGAGTACT	ACCTCGCCCTG	4553396
Query 61	CGCGACAAG	ACCCCGGAC	GACGACCTCG	GGTGAAGAG	CGCGCTGACC	GACCTGCTG	120
Sbjct 4553397	CGCGACAAG	ACCCCGGAC	GACGACCTCG	GGTGAAGAG	CGCGCTGACC	GACCTGCTG	4553456
Query 121	ACCCTGATC	CGCCCGGAG	CAGCACCTGG	GGCGCGAGG	ACTACACCGA	AAGCGCAGC	180
Sbjct 4553457	ACCCTGATC	CGCCCGGAG	CAGCACCTGG	GGCGCGAGG	ACTACACCGA	AAGCGCAGC	4553516
Query 181	GTGGCACTG	ATCGAGAAG	GTGGATGCAT	CCGCGCCGG	CCCTGCCGCG	CCTGAAGGAC	240
Sbjct 4553517	GTGGCGCTG	ATCGAGAAG	GTGGATGCAT	CCGCGCCGG	CCCTGCCGCG	CCTGAAGGAC	4553576
Query 241	CTGGCCAAG	GGCGTGCAGA	AACGCGGCCA	AAGCGCACCG	AGGCCGGAAG	CCGAGAAGGC	300
Sbjct 4553577	CTGGCCAAG	GGCGTGCAGA	AACGCGGCCA	AAGCGCACCG	AGGCCGGAAG	CCGAGAAGGC	4553636
Query 301	AAGGACGCC	GAGGA	314				
Sbjct 4553637	AAGGACGCC	GAGGA	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

<1..>314

/locus\_tag="SMD\_4053"

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	GAGCGTTTCTGGTCCCTTCGGCGGACTGAAGTGCTGCCGCCCGGCCTCGGCCAGGAAAGTG	60		
Sbjct 1703311	GAGCGTTTCTGGTCCCTTCGGCGGACTGAAGTGCTGCCGCCCGGCCTCGGCCAGGAAAGTG	1703370		
Query 61	CGCAACTGGGCCGCGCCGCGGCAAGCTCGACCCGGCCACCTGCAGACCTGCGGGCGAAC	120		
Sbjct 1703371	CGCAACTGGGCCGCGCTCGCGGCAAGCTCGACCCGGCCACCTGCAGACCTGCGGGCGAAC	1703430		
Query 121	TCGCCGCTGGGCGCGCTGCTGGCTGCCGCACTGGAAGCCCGCAACCGCCGCGGACCAAG	180		
Sbjct 1703431	TCGCCGCTGGGCGCGCTGCTGGCTGCCGCACTGGAAGCCCGCAACCGCCGCGGACCAAG	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	Location/Qualifiers
source	1..251 <a href="#">/organism="Stenotrophomonas maltophilia K279a"</a> /molecule_type="genomic DNA" /strain="K279a" /db_xref="taxon:522373" /country="United Kingdom"
gene	<1..>251 /locus_tag="Smlt1638"
CDS	<1..>251 /locus_tag="Smlt1638" /codon_start=1 <a href="#">/translation_table=11</a> <a href="#">/product="putative biopolymer transport protein"</a>



## 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	CGGAAATGAAGGCCGGTATCGAGTTTGGCGAACTCAGCCGGCGCTGAAGGGCTGGGCGC			60
Sbjct 746379	CGGAAATGAAGGCCGGCATCGAGTTCGGCGAACTCAGCCGGCGCTGAAGGGCTGGGCGC			746438
Query 61	TGCGCAGTGCCTGGCATGGTCGCGTGGTGACAACCGGACCGATGACGAACCGCTGGCCT			120
Sbjct 746439	TGCGCAGTGCCTGGCATGGTCGCGTGGTGACAACCGGACCGATGACGAACCGCTGGCCT			746498
Query 121	CGGTCGATCCGCTGCGTGGCAGCTGGGCCGTGATGTACGACACCGATACCTGGGGCGTCG			180
Sbjct 746499	CGGTCGATCCGCTGCGTGGCAGCTGGGCCGTGATGTACGACACCGATACCTGGGGCGTCG			746558
Query 181	AACTGGCCGGTACCTTCGTGCAGCGCAAGAAGCGCCTGCCGCCGCTGCGGGCGCAGACCA			240
Sbjct 746559	AACTGGCCGGTACCTTCGTGCAGCGCAAGAAGCGCCTGCCGCCGCTGCGGGCGCAGACCA			746618
Query 241	ATCCGAACGCACCGGCGCCGTTCTGCTACCAAGCCGGCCGGCTACGGCGTGTGGACCTGA			300
Sbjct 746619	ATCCGAACGCACCGGCGCCGTTCTGCTACCAAGCCGGCCGGCTACGGCGTGTGGACCTGA			746678
Query 301	TGGCGCACTGGAACCTTCGCGCCGGGTGCCACCTTCAATGTCGGCGTGTTCACACTGGCCG			360
Sbjct 746679	TGGCGCACTGGAACCTTCGCGCCGGGTGCCACCTTCAATGTCGGCGTGTTCACACTGGCCG			746738
Query 361	ACAAGCGCTACATCGAATGG	380		
Sbjct 746739	ACAAGCGTTACATCGAATGG	746758		

## Stenotrophomonas maltophilia strain 13637 genome

GenBank: CP008838.1

```

FEATURES             Location/Qualifiers
     source            1..380
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                        /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"

```



## 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
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Sbjct 1789191	TGACCGCCGAAGACATCTACCGCCAGCTGCTGGAGCACGGCGACGAGATCGGCCTGGCCA			1789250
Query 61	CGGTGTACCGGGTGTGACCCAGTTTCGAGGCCGCGGCCCTCGTGCTCAAGCACAAATTCG			120
Sbjct 1789251	CGGTGTACCGGGTGTGACCCAGTTTCGAGGCCGCGGCCCTCGTGCTCAAGCACAAATTCG			1789310
Query 121	AGGGCGGCCAGGCGGTCTACGAACTGGACCGTGGCGGCCACCACGACCACATGGTCGACG			180
Sbjct 1789311	AAGGCGGCCAGGCGGTCTACGAGCTGGACCGTGGCGGCCACCACGACCACATGGTCGACG			1789370
Query 181	TGGACAGTGGCAAGATCATCGAGTTTCGAAAGCCACGAGATCGAGGAGCTGCAGCGCA-GA			239
Sbjct 1789371	TGGACAGCGGCAAGATCATCGAGTTTCGAAAGCCACGAGATCGAGGAGCTGCAGCGCAAGA			1789430
Query 240	TTCCGCCGACACCATGGCTACGAACTGGAAGAGCACTCGC		279	
Sbjct 1789431	-TCGCGGCCGACACCGGCTACGAGCTGGAAGAGCATTTCG		1789469	

## Stenotrophomonas maltophilia JV3, complete genome

GenBank: CP002986.1

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