والالمطاركة والكرفية

	*:***:::* .	:* * * .*	:*.* * .*	* *:.:.:.**	**:*:::*	*:.*			
AlgE1 A1	EVLLQSYDDTAGV	SGNFYVTTGT	LEGNVISC	SANSTYGIQER	ADGTDYSSLY	NSIDGVQTGA	VRLYGANSTVS	SQSGSGQQAT	395
ALGE1 A2	EVILOAFDDSO-V	IGE LYETINT	RIEGNLIDAS	DNAN YAVRER	DDGSDYTTLVI	ND I S <mark>GGOV</mark> AS	VOLSGAHSSLS	GGTV	321
ALGE2 A	E ILLOSYDDTAGY:	SGN FYTTTGT	NIEGNTIVG:	SANSTYGIOER	DDGTDYSSLY	NSVSNVONGS	VRLYGANSVVS	DLPGTGOOAT	385
ALGES AL	EVILOSYDDTAGV:	S <mark>GN FYVTTG</mark> TI	ALEGNVIS GS	ANST FGI OER	ADG TDYSSLY	NTIDGVONGT	VRLYGANSTVS	EQPSSGOOAT	385
ALGES A2	EVILOSENDVG-V	SGN FYATTGT	NI EGNVI S GS	ANSTYGIEER	NDG TDYSSLYA	NTIDGVOTGA	VRLNGAHSIVS	DOPGTGOOAT	327
AlgB4 A	EVILOSEDDTAGA	SGT YYTTLNTI	RIEGNTIS GS	SANSTYGIOER	NDGTDYSSLIL	ND IAGVOOPI		~	364
ALGES A	E ILLOSYDDTAGY:	SGN FYTTTGT	XIEGNTIVGS	ANSTYGIOER	ADG TDYSSLY	ANSVSNVOSGS	VRLYGTNSVVS	DLPGTGOOAT	385
AlgE6 A	EVILOSYDDTLGV								382
ALGEMI	EVILOSYDDTAGV								364
AlgEM2	EILLOSYDDTAGY							DL	377
ALGEMS	EVILOSEDDTAGA								364
ALGEM4	EVILOSEDDTAGA								364
ALGEMS	EVILOSEDDTAGA								364
AlgEM6	EVLLOSEDDTAGA								363
RIGERO	210	220	2 20	240	250	260	270	200	303

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			للأليسي				
AlgE1 A1							**:**::.**:*.* ****:: VRVYGAQDVQILDNQIHDNSQNGAYA 300
AlgE1 A2							VRLYGTEDVOILDNOIHDNSONGTYP 243
AlgE2 A							VRVYGAEDVQILDNYIHDNSQNGSYA 300
AlgE3 A1	FDPHEQT INLT IRDSVAHDNGLDC	FVAD YQV GGVFENNVS YNN	ORH GFN IVTSTND FVL SNNVAY	GNGGAGLVVQRGSYDLPH	YD ILIDGGAYYDNALEGV <u>Q</u> LF	MTHDVTLQNAE I YGNGLYG'	VRVYGAQDVQLLDNQIHDNSQNGAYA 300
AlgE3_A2							VRLYGTEDVQILNNQIHDNAQNVAYA 243
AlgB4 A AlgB5 A	FDPHEQT INLT IRD SVAHDNGLDC	FVADYLVDSVFENNVAYAN	ORH GFNVVT STHD FVMTNNVAY	GNGSSGLVVQRGLEDLAL	SNILIDGGAYYDNARE GVLLP	MTSDITLQNADIHGNGSSG	VRVYGAQDVQILDNQIHDNAQAAAVP 300
AlgE5 A							VRVYGAEDVQILDNYIHDNSQS <mark>G</mark> SYA 300 VRVYGAQGVQILGNQIHDNA <mark>K</mark> TAVAP 300
AlgE6 A AlgEMI							VRVIGAOGVOILGNOIHDNAATAVAP 300 VRVIGAODVOILDNOIHDNSONGAYA 300
AlgEM2							VRVYGAEDVQILDNYIHDNSQSGSYA 300
ALGEMS							VRVYGAODVOILDNOIHDNAQAAAVP 300
AlgEM4	FDPHEQT INLT IRD SVAHDNGLDO	FVAD FQI GGVFENNVS YNN	ORH GFNVVTSTND FVLSNNVAY	GNGGAGLVVQRGLEDLAL	SNILID <mark>GG</mark> AYYDNAR <mark>EGVLL</mark> F	MTSDITLQNTDIHGNGSSG	VRVYGAQDVQILDNQIHDNAQAAAVP 300
AlgEM5							V <mark>RVYG</mark> AQDVQILDNQIHDNAQAAAV <mark>P 300</mark>
AlgEM6							VRVYGAQDVQILDNQIHDNAQAAAVP 299
	160 170			220			

Figure S		
31-01 31	:::.* *:*:****: ** ****************	150
Alge1_A1 Alge1_A2	THE RECEIPTION OF THE ACTION O	93
AlgE2 A	MDYNVKD FGALGDGVS DDTAAIQAAIDAAYAAGGGTVYLPAGE YRVSGGEEPSDGCLTIKSNVHIVGAGMGETVIKLVDGWDQDVTGIVRSAYGEETSNFGMSDLTLDGNRDNTSGKVDGWFNGYIPGEDGADRDVTLERVEIREMSGYG	150
AlgB3 Al	MDFNVKDFGALGDGASDDTAAIQAAIDAAHAAGGGUVYLPAGEYRVSGCEEPSDGALTIKSNVYIVGAGMGETVIKMVDGWTQNVTGAVRSAYCEETSNFGMSDLTLDGNRDNLSAKVDGWFNGYIPGQDGADRDVTLERVEIREMSGYG	150 93
Alge2 A Alge3 A1 Alge3 A2 Alge4 A	MD YNVKD FGALGDGVSDDRASI GAA IDAAYA AGGGTVYLPAGEYRV SAAGEPGDGCULKDGVVLAGAGHGETVIKLIDGSDGKI UGWPSAYGETSNFGKDLIDGNDDNISGXVDGWPGYLPGGCGADRDVILERVEWENSGYG	150
AlgE5 A AlgE6 A	MDYNVKD FGALGDGVS DDTAAI QAAIDAAYAAGGGTVYLPAGEYRV SGGEEPSDGCLTIKSNVYIVGAGMGETVIKLVDGWDQDVTGIVRSAYGEETSNFGMSDLTLDGNRDNTSGKVDGWFNGYIPGEDGADRDVTLERVEIREMSGYG	150
alge6 a Algemí	MD YNVKD FGALGDGVS DDRVAI QAAIDAAHAAGGGTVYLP PGE YRV SAAGE PSDGCLTLRD NVYLAGAGMGQTVI KLVDG SAQKI TGIVRSPFGE ETSNFGMRDLTLDGNRANTVDKVDGWFMGYAPGQPGADRNVTI ERVE VREMSGYG MD YNVKD FGALGDGVS DDTAAI OAAIDAAYAAGGGTVYL PAGE YRV SGGEE PSDGCLTIKSNVHIVGAGMGETVI KMVDGWTONVTGMVRSAYGE ETSNFGMSDLTLDGNRDNLSAKVDGWFMGYI PGODGADRD VTLERVE I REMSGYG	150 150
AlgEM1 AlgEM2	MD YW KD FGALGOG VS DDTAAL GALDAAVA AGGGTV LIP AGE WY SGGBEP BUGCLTIK IN VY IV GACHGETV I KMYDGWTON VTGWYR SA YGE FSNFGMSDL ILDGWRDH DALAAVD GWR NG Y IP GOCGADDATLER VE IREMSGYG	150
AlgEM2 AlgEM3	MDFNVKD FGALGDGAS DDTAAI QAAIDAAHAAGGGTVYLPAGEYRV SGGEEPSDGALTIKSNAHIVGAGMGETVIKLVDGWDQDVTGIVRSAYGEETSNFGMSDLTLDGNRDNTSGKVYGWFMGYIPGEDGADRDVTLERVE IREMSGYG	150
AlgEM4 AlgEM5	MDFNVKD FGALGDGAS VDTAAIQAAIDAAHAAGGGTVYLPAGEYRV SGGEEPSDGALTIKSNVYIVGAGMGETVIKMVDGWTQNVTGMVRSAYGEETSNFGMSDLTLDGNRDNLSAKVDGWFNGYIPGQDGADRDVTLERVEIREMSGYG MDYKVKD FGALGDGVSDDTAAIQAAIDAAHASGGGTVYLPAGEYRV SGGEEPSAGCITTKSNVHIVGAGMGETVIKMVDGWTQNVRSAYGEETSNFGMSDLTLDGNRDNLSAKVDGWFNGYIPGGDGADRDVTERVEVREMSGYG	150 150
ALGEMS	MD YNYKD FGALGOGVSDDTAAI OAAIDAAYA AGGGYVLLPAGEYKY SGGEEPSDGCLTIKSNYTIYGACHGETYIKLDGWDDDVTGTYRSAYGETSNFGHRDLIDGWDDNTSGKYDGWPNGYTDGGYGADRDVTIERVEYREMSGYG	150
	$1 \dots \dots 10 \dots \dots 20 \dots \dots 30 \dots \dots 40 \dots \dots 50 \dots \dots 60 \dots \dots 70 \dots \dots 80 \dots \dots 90 \dots \dots 100 \dots \dots 110 \dots \dots 120 \dots \dots 130 \dots \dots 140 \dots \dots 150$	

Fi Q1 A

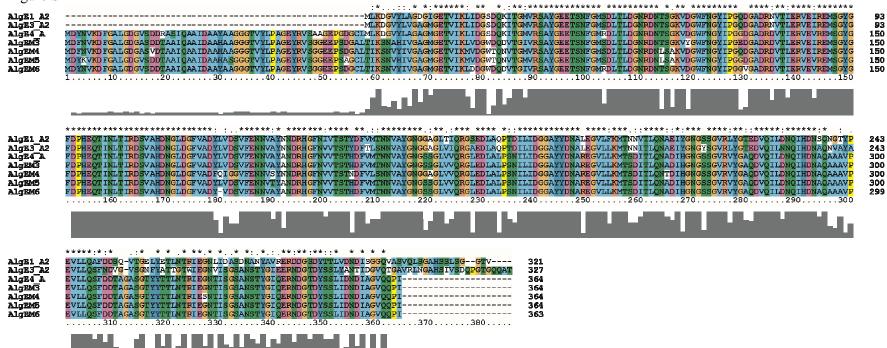


Figure S1 B

Figure S		
Alge1 A1 Alge2 A Alge3 A1 Alge5 A Alge6 A AlgeM1 AlgeM2	MD YNVKD FGALGDGVS DDTAAL GAAIDAAHA AGGGTVYLPAGEYRVSGGEEP SDGCLTIKSNVHIVGAGMGETVIKWDGWTONVTGMVRSAYGEETSNFGMSDLTLDGRRDNLSAKVDGWFNGYIPGCDGADRDVTLERVEIREMS GYG MD YNVKD FGALGDGVSDDTAAL GAAIDAAYAAGGGTVYLPAGEYRVSGGEEP SDGCLTIKSNVHIVGAGMGETVIKLVDGWDOVTGMVRSAYGEETSNFGMSDLTLDGRRDNLSAKVDGWFNGYIPGCDGADRDVTLERVEIREMS GYG MD YNVKD FGALGDGVSDDTAAL GAAIDAAHAAGGGTVYLPAGEYRVSGGEEP SDGCLTIKSNVHIVGAGMGETVIKLVDGYTGMVRSAYGEETSNFGMSDLTLDGRRDNLSAKVDGWFNGYIPGCDGADRDVTLERVEIREMS GYG MD YNVKD FGALGDGVSDDTAAL GAAIDAAHAAGGGTVYLPAGEYRVSGGEEP SDGCLTIKSNVHIVGAGMGGTVIKLVDGYTGMVRSAYGEETSNFGMSDLTLDGRRDNLSAKVDGWFNGYIPGCDGADRDVTLERVEIREMS GYG MD YNVKD FGALGDGVSDDTAAL GAAIDAAHAAGGTVYLPAGEYRVSGGEEP SDGCLTIKSNVHIVGAGMGGTVIKLVDGYTGMVRSAYGEETSNFGMSDLTLDGRRDNLSAKVDGWFNGYIPGCDGADRDVTLERVEIREMS GYG MD YNVKD FGALGDGVSDDTAAL GAAIDAAHAAGGTVYLPAGEYRVSGGEEP SDGCLTIKSNVHIVGAGMGGTVIKLVDGYTGMVRSAYGEETSNFGMSDLTLDGRRDNLSAKVDGWFNGYIPGCDGADRDVTLERVEIREMS GYG MD YNVKD FGALGDGVSDDTAAL GAAIDAAHAAGGTVVLPAGEYRVSGGEEP SDGCLTIKSNVHIVGAGMGETVIKWDGWTGNVTGMVRSAYGEETSNFGMSDLTLDGRRDNLSAKVDGWFNGYIPGCDGADRDVTLERVEIREMS GYG 11020304050	150 150 150 150 150 150
Alge1 A1 Alge2 A Alge5 A1 Alge5 A Alge6 A Algem1 Algem2	FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGAGLVVQRGSYDLPHPYDILLDGGAYUDNALGGVGLKAHHDVTLQNAEIYGNGUAGVGLUDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGAGLVVQRGSDVAHPYDILLDGGAYUDNALGGVGLKMHHDVTLQNAEIYGNGUAGVGLUDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGAGLVVQRGSDVAHPYDILLDGGAYUDNALGGVGLKMHHDVTLQNAEIYGNGUAGVGUADVGLUDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGAGLVVQRGSDVAHPYDILLDGGAYUDNALGGVGLKMHHDVTLQNAEIYGNGUAVGUADVGLUDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGAGLVVQRGSDVQHDFQSYDNGLGGVGLKMHHDVTLQNAEIYGNGUAVGAVGAVGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGAGLVVQRGSDLAHPENILLDGGAYUDNGLGGVGLKMHHDVTLQNAEIYGNGUAVGAVGAVGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGAGLVVQRGSENLAHPENILLDGGSYNDNGLGGVLKMSNVTVQNADIHGNGSSGVRVYGAQGVQLLDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGNGLVVQRGSENLAHPENILLDGGSYNDNGLGGVLKMSNNVTVQNADIHGNGSSGVRVYGAQGVQLLDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNGLDGFVAD FQLGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNGGNGLVVQRGSENLAHPENILLDGGSYNDNGLGGVLKMSNNVTVQNADIHGNGSSGVRVYGAQGVQILDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNSLDGFVAD FQLGGVFENNVSYNDRHGFNIVTSTNDFVLSNNVAYGNGGNGLVVQRGSYDLHPATILDGGAYNDNARGGVLKMSNNVTVQNADIHGNGSSGVRVYGAQGVQILDNQIHDNSQNGAYA FDPHEQTINLTIRDSVAHDNSLDGFVAD FQLGGVFENNVSYNDRHGFNIVTSTNDFVLSNNVAYGNGGNGLVVQRGSYDLHPATILDGGAYNDNARGVLKMSNNVTVQNADIHGNGSSGVRVYGAQDVQILDNQIHDNSQNGAYA FDFHEQTINLTIRDSVAHDNSLOGFVAD FQLGGVFENNVSYNDRHGFNVTSTNDFVLSNNVAYGNGGNGLVVQRGSVDLHPYDSILLDGGAYDNARGVLKMSNNTVQNADISLGGVZCDVGLQGVGLNGUNGSSGVRVYGAQDVQILDNQIHDNSQNGAYA FDFHEQTINLTIRDSVAHDNSLGFVAD FQLGSVSQNCQQUQULDNQIHDNSSNDFNGNZ FDFHEQTINLTIRDSVAHDSSDGFVAD FQLGFVAD FQLGGVGSSGVRVGGVQLGGVQUGGSSGVRVGGNQUGGNGLVQQGSGVQQQQUQULDNQIHDNSQNGAYA FDFHEQTINLTIRDSVAHDNSLGFVAD FQLGFVAVGSNDRHGFNVVTSTNDFVLSNNVAYGNGGSZVZQQQQUQULDNQIHDNSQNGAYA FDFHEQTINLTIRDSVAHDNSSNDFNGTVQ	300 300 300 300 300 300 300
Algel Al Algez A Alges Al Alges A Alges A Algem Algem2	************************************	

Figure S1: Multiple sequence alignment of epimerase A-module from *Azotobacter vinelandii* and the mutant A-modules for AlgEM1-6. Standard colour code for the amino acid types in ClustalX2 software is used. *indicates residues identity, : means conserved amino acids, · shows semi-conserved amino and the height of the bar indicate the degree of conservation (ClustalX2 definitions). (A) Multiple sequence alignment of epimerase from AlgE1-AlgE6 from *A. vinelandii* and the mutant A-modules for AlgEM1-6. (B) Multiple sequence alignment of MG –block forming epimerase from AlgE1,AlgE3 and AlgE4 from *A. vinelandii* and the mutant A-modules for AlgEM3-6. (C) Multiple sequence alignment of GG –block forming epimerase from AlgE1-AlgE3 and AlgE5-AlgE6 from *A. vinelandii* and the mutant A-modules for AlgEM3-6. (C) Multiple sequence alignment of GG –block forming epimerase from AlgE1-AlgE3 and AlgE5-AlgE6 from *A. vinelandii* and the mutant A-modules for AlgEM3-6. (C) Multiple sequence alignment of GG –block forming epimerase from AlgE1-AlgE3 and AlgE5-AlgE6 from *A. vinelandii* and the mutant A-modules for AlgEM3-6. (C) Multiple sequence alignment of GG –block forming epimerase from AlgE1-AlgE3 and AlgE5-AlgE6 from *A. vinelandii* and the mutant A-modules for AlgEM1-2.

Plasmid	Description	Reference or source
pLITMUS28	Cloning vector, Ap ^r	New England BioLabs
pUC128	Cloning vector, Ap ^r	1
pTrc99A	Expression vector, Ap ^r	2
pBL5	pTrc99A encoding AlgE4	3
pBL6	pTrc99A encoding AlgE2	3
pBG29	pTrc99A encoding AlgE6	4
pHE37		5
pHE133		
pHH5	pTrc99A encoding AlgE5	6
pHE88	Expression plasmid encoding the A2-module of AlgE3	7
pHE58	Expression plasmid encoding the A2-module of AlgE1	5
pBS5	pLITMUS28 in which a 0.3 kb EcoRI-EcoRV fragment from pBG29 was inserted	This study
pBS7	pLITMUS28 in which a 1.6 kb NcoI-KpnI fragment from pHE133 was inserted.	This study
pBS8	pTrc99A encoding the A- module of AlgE5. <i>algE5A</i> was PCR-amplified as a 1.13 kb NcoI-XmaI fragment using pHH5 as template and M13/pUC rev and EU5-E5 as primers and inserted into the same sites of pTrc99A.	This study
pBS9	pTrc99Å encoding the A1-module of AlgE1. algE1A1 was PCR-amplified as a 1.085 kb NcoI- XmaI fragment using pHE37 as template and M13/pUC rev and EU12-E1.1 as primers and inserted into the same sites in pTrc99A.	This study
pBS10	pTrc99A encoding the A-module of AlgE4. A 1.13 kb NcoI-KpnI fragment from pBL5 containing <i>algE4A</i> was inserted into the same sites in pTrc99A.	This study
pBS11	pTrc99A encoding the A-module of AlgE2. A 1.13 kb NcoI-KpnI fragment from pBL6 containing <i>algE2A</i> was inserted into the same sites in pTrc99A.	This study
pBS12	pTrc99A encoding the A1-module of AlgE3. algE3A1 was PCR-amplified as a 1.085 kb NcoI- XmaI fragment using pBS7 as template and M13/pUC rev and EU6-E3.1 as primers and inserted into the same sites in pTrc99A.	This study
pBS13	A 1.127 kb PCR-amplified NcoI-XmaI fragment containing <i>algE3A2</i> was cut with NcoI and EcoRV and the resulting 0.704 kb fragment was inserted into the same sites of pLITMUS28. pHE88 was used as template and EU10-E3.5 and EU11-E3.6 as primers.	This study
pBS14	A 1.127 kb PCR-amplified NcoI-XmaI fragment	This study

Table S1. Plasmids used in this study

	containing AlgE3A2 was cut with EcoRV-XmaI and	
	the resulting 0.437 kb fragment was inserted into the	
	same sites of pUC128. pHE88 was used as template	
	and EU10-E3.5 and EU11-E3.6 as primers.	
pBS15	Derivative of pBS5 where an internal XmaI site was	This study
	removed by site-directed mutagenesis. Primers used	
	were EU2-E6.1 and EU3-E6.2.	
pBS17	Derivative of pBS13where an internal XmaI site was	This study
-	removed by site-directed mutagenesis. Primers used	-
	were EU8-E3.3 and EU9-E3.4.	
pBS18	Derivative of pBS29 in which a 0.218 kb PshAI-	This study
Î	EcoRI fragment from pBS15 was inserted.	-
pBS20	Derivative of pBS17 in which a 0.473 kb EcoRV-	This study
1	EcoRI fragment from pBS14 was inserted.	
pBS21	pTrc99A in which a 1.120 kb PCR-amplified NcoI-	This study
I	Xmal fragment containing <i>algE6A</i> was inserted.	5
	pBS18 was used as template and M13/pUC rev and	
	EU4-E6.3 as primers.	
pBS22	pTrc99A encoding the A2-module of AlgE3. A 1.127	This study
r - ~	kb NcoI-XmaI fragment from pBS20 was inserted	
	into the same sites of pTrc99A.	
pBS23	pTrc99A in which a 1.084 kb PCR-amplified NcoI-	This study
r - ~	Xmal fragment containing <i>algE1A2</i> was inserted.	
	pHE58 was used as template and EU14 and EU13 as	
	primers.	
pBS29	pTrc99A encoding the A2-module of AlgE1. A	This study
r - ~ - >	nucleotide was inserted into pBS23 by site-directed	
	mutagenesis. Primers used were EU23 and EU24.	
pBS30	pTrc99A encoding the A-module from AlgE6. A	This study
r = ~ ~ ~ ~	nucleotide was inserted into pBS21 by site-directed	
	mutagenesis. Primers used were EU25 and EU26.	
pAT111	pTrc99A encoding AlgE4 with D119Y substitution.	This study
P	A synthetic ^{1} algE4 A-module with mutations leading	
	to D119Y was inserted into pBL5 as a NcoI-SexAI	
	fragment.	
pTB68	pTrc99A encoding AlgE4 with D119F substitution	This study
pTB77	pTrc99A encoding AlgE4 with D119A substitution	This study
pAT112	pTrc99A encoding AlgEM3 with Y119D	This study
F	substitution. A synthetic ¹ <i>algEM3</i> A-module with	
	mutations leading to D119Y was inserted into pBL5	
	as a NcoI-SexAI fragment.	
pAT113	pTrc99A encoding AlgEM3 with Y119R	This study
r	substitution. A synthetic ¹ gene fragment encoding the	
	<i>algEM3</i> A-module with mutations leading to Y119R	
	was inserted into pBL5 as a NcoI-SexAI fragment.	
pAT114	pTrc99A encoding the A-module of AlgEM1	This study
P	combined with the R-modules of AlgE6. A synthetic ¹	
	gene fragment encoding the R-modules of AlgE6 was	
	inserted as a XmaI-EcoRI fragment into the vector	
	encoding AlgEM1 isolated from the mutant library	
	encouning righting isolated from the induite florary	

pAT115	pTrc99A encoding the A-module of AlgEM2	This study
	combined with the R-modules of AlgE6. A synthetic ¹	
	gene fragment encoding the R-modules of AlgE6 was	
	inserted as a BglII-EcoRI fragment into the vector	
	encoding AlgEM2 isolated from the mutant library	

1. Synthetic gene fragments were obtained from Genescript.

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- 2. Amann, E., Ochs, B., and Abel, K. J. (1988) *Gene* **69**, 301-315
- 3. Bjerkan, T. M., Lillehov, B. E., Strand, W. I., Skjåk-Bræk, G., Valla, S., and Ertesvåg, H. (2004) *Biochem J* **381**, 813-821
- 4. Svanem, B. I. G., Skjåk-Bræk, G., Ertesvåg, H., and Valla, S. (1999) *J. Bacteriol.* 181, 68-77
- 5. Ertesvåg, H., and Valla, S. (1999) J. Bacteriol. 181, 3033-3038
- 6. Ramstad, M. V., Ellingsen, T. E., Josefsen, K. D., Høidal, H. K., Valla, S., Skjåk-Bræk, G., and Levine, D. W. (1999) *Enzyme Microb. Technol.* **24**, 636-646
- 7. Ertesvåg, H., Høidal, H. K., Schjerven, H., Svanem, B. I., and Valla, S. (1999) *Metab* Eng 1, 262-269

Primer name	Restriction site in primer sequence	Sequence (5'-3') ^{a, b}
M13/pUC rev		AGCGGATAACAATTTCACACAGGA
EU12-E1.1	XmaI	CGC <u>CCCGGG</u> CTGCACACC
EU14-E1.3	NcoI	CGCAAGA <u>CCATGG</u> TCAATGCC
EU13-E1.2	XmaI	AGCTGC <u>CCCGGG</u> GCGACC
EU23		CCAGGTCGGCCCCGGGGATCC
EU24		GGATCCCCGGGGCCGACCTGG
EU6-E3.1	XmaI	GTACCGT <u>CCCGGG</u> CTGCAC
EU10-E3.5	NcoI	CAGA <u>CCATGG</u> TCAATGCCAAGG
EU11-E3.6	XmaI	CTGGCCGGT <u>CCCGGG</u> CTG
EU8-E3.3		CACCGGGGATCCTGGCGACGGCT
EU9-E3.4		AGCCGTCGCCAGGATCCCCGGTG
EU5-E5	XmaI	TGGCCGGT <u>CCCGGG</u> CAGGTC
EU2-E6.1		CTGAACACGGGTCGAGGGCAAC
EU3-E6.2		GTTGCCCTCGACCCGTGTGTTCAG
EU4-E6.3	XmaI	ACAGTG <u>CCCGGG</u> ACCGTCG
EU25		CGAATTCGACGGTACCCGGGGATC
EU26		GATCCCCGGGTACCGTCGAATTCG
EU20		GAGCTGGTCGTCCGTGTCGC
Britt 35		AGCTTATCATCGACTGCACGGTG
Britt 28		CACACTACCATCGGCGCTACG

Table S2. Primers used for the staggered extension process, error prone PCR and for construction of StEP templates

^a Restriction sites are underlined ^b Nucleotides shown in bold are not part of *A. vinelandii* wild type sequence

Table S3. NMR analysis of polyM epimerised with AlgE6 and mutant epimerases AlgEM1-6. Epimerisation was performed with polyM (10 mg) and enzyme (0.2 mg) in MOPS, pH 6.9 with 100 mM NaCl and 1.5 mM CaCl₂

Enzyme	F _G	F _M	F _{GG}	F _{MG} /F _{GM}	F _{MM}	F _{MGM}
AlgE6	0.77	0.23	0.69	0.074	0.16	0.048
AlgEM1	0.85	0.15	0.78	0.061	0.094	0.030
AlgEM2	0.83	0.17	0.74	0.088	0.085	0.027
AlgEM3	0.54	0.46	0.22	0.33	0.13	0.25
AlgEM4	0.67	0.33	0.44	0.23	0.10	0.15
AlgEM5	0.59	0.41	0.31	0.28	0.13	0.21
AlgEM6	0.40	0.60	0.039	0.36	0.23	0.33

14010 51.		<u>• p: sper</u> 0	New amino acid						
							·		residues introduced by
Enzyme	E1A1	E1A2	E2	E3A1	E3A2	E4	E5	E6	mutagenesis ²⁾
AlgEM1	93	74	87	92	80	84	86	76	D/A/G354Y
AlgEM2	89	73	92	88	78	76	93	77	D/S61I, V136A,
-									G/A332S
AlgEM3	81	75	81	82	78	92	80	77	V63A, D119Y
AlgEM4	85	74	82	86	78	88	82	77	D17V, A265T, G327S
AlgEM5	83	74	79	82	76	92	79	77	N4K, A32S, D54A,
									S/A190T
AlgEM6	81	76	81	80	78	95	81	79	V/I78D, P/D130V

Table S4. Sequence properties of the A-modules from epimerase mutants AlgEM1-6

1) Given as % amino acid identity over 376 N-terminal residues constituting the A-module.

2) Residues before the position number indicates amino acids present in the wild type A-modules.

Table S5. NMR analysis of polyM epimerised with AlgE4 and AlgEM3 and derivatives of these enzymes with substitutions in residue 119. Epimerisation was performed with polyM (10 mg) and enzyme (0.2 mg) in MOPS, pH 6.9 with 100 mM NaCl and 1.5 mM CaCl₂.

Epimerase	F_{G}^{*}	F _{GG} *	F _{MGM} *
AlgE4 (D119)	0.47	0	0.47
AlgE4 D119Y	0.50/0.50	0.083/0.085	0.41/0.40
AlgE4 D119F	0.50	0.089	0.41
AlgE4 D119A	0.48	0.044	0.44
AlgEM3 (Y119)	0.64/0.64	0.39/0.38	0.17/0.18
AlgEM3 Y119D	0.57/0.58	0.27/0.27	0.23/0.23
AlgEM3 Y119R	0.36/0.37	0.024/0.032	0.35/0.33

*Were two values are shown, the results are obtained from two independent epimerization experiments.