

TPRpred analysis results for ALoR receptors

Supplementary data 1

Peptide-based quorum sensing systems in *Paenibacillus polymyxa*

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> PPTDRAFT_00471_AloR1

MKHTPTIRAELDRYLQQEGMSLTQFGHVAGMNRGIVSAIVTGNKSMQSVNQLDLITEAMGLPEGHFYDLFIENYIIDHPPNMRRIEPLLFRC
AELDKLEAIRRVVGAIMDNLLYSPKLFIEAEELLSQERHAAAALLLYEGVAEAEKYQHSERLAVCQYRIFTIQVGDDQSRNHKAAILFEPYVERL
DDLEQLDALKDLANVYRSLRKWDKVDIARVMRAKAEIQYNWKHQKQNKERNEAAKLSRPMFVYITYADLLCASVCDARGDYQQALQ
YTYAYADLDWVRETDDDTLYWVEMYQDWARCNIIYVNKLLSGDVSLSDYVEYIAETADTMEGEKLSKLLNVMIAANQYNLDVDDVLSRF
KKDIDAFTQLPTSTDMYSQQVVPDYIAWFGYELAYYYLNRERYSDGFKQLLFAMVKSHIINNETYFINCIGLFMRQVYATPEIKTEFSNLIEK
VWVGNVEKNRTVNCCE

The sequence name: **PPTDRAFT_00471_AloR1**

Per-protein P-value for being TPR: **4.6E-03**

Probability for being TPR: **0.02%**

Per-protein P-value for being SEL1: **5.6E-02**

Probability for being SEL1: **0.00%**

Repeat	Begin	Alignment	End	P-value
TPR	114	--SPKLFETAEELLSQERHAAAALLLYEGVAEAEKYQ--	147	2.7e-03
TPR	191	--LDALKDLANVYRSLRKWDKVDIARVMRAKAEIQ--	224	1.2e-03

>PPTDRAFT_00474_AloR2

RAAAVFEAFVERLDEIDQLDALKDLANVYRSLRKWDKVDMAKKMRAKAEIQYTLKHQQNSREHTEFTDKLSRPLFVYISYADLLCASVCEA
QDDYQQALDYTYTYANLDWVMETDEDTRHWISLFSKSWAEGNTYVYKLLSGDINVLHDYVEYIVATSATNENEKISKLLNVIIAANQYSIDV
DDILKRFESEINSFSEHPLSDDMYTQQVIPDYIAWFGYELAYYYLHRGSYNDGFKHLMYSMVSYHILNNETYFINCMGLFSHFREYASHETKA
SFLNLIKVVMTNVEKNGTADHCG

The sequence name: **PPTDRAFT_00474_AloR2**

Per-protein P-value for being TPR: **7.0E-03**

Probability for being TPR: **0.01%**

Repeat	Begin	Alignment	End	P-value
TPR	19	--LDALKDLANVYRSLRKWDKVDMAKKMRAKAEIQ--	52	7.0e-03

>PPTDRAFT_01046_AloR3

MEITPTIQAEVQTYLKRKSLTMEFGHTIDLNVGTVSGIVTGNRSMSVHQLDSITAGMNLPPDYFYERYIEECIEECPNLWKKISPFLYRCIEL
GRLDCLQRVVILLDNPNYLPSLFEVAENVYQDGYNEAAAYLYKVAESEKQQHSERLAICQYRLFQIKVGGQDRAVNLQAAIEFAPFVDRDL
EIEQLDALKDLANVYRSLSMWDKVEFAHQMGQLGQLQYHLVHNSKRKGTEPRKLSRPLFVYIVYAEELLCANACDAKGNHDDQALEHIRG
YADLNWVKEQSDSTLYWKRKYQQWAKINTYVNRMLMSGDISVLPDYVEHIAAEEKILAELLNVLEVANRYNVDVDHILRRFESQIAAYQESP
SSDMYTQQVLTTEEYVRFWYKIAKYSLNKGRYTYGFKLLIAFEKAVTINHVLIIANCFGLFLHFKTNAAPKTQAQFHSIYEEVWEKNDQKDG
FLLGGN

The sequence name: PPTDRAFT_01046_AloR3

Per-protein P-value for being TPR: 2.9E-05

Probability for being TPR: 1.19%

Repeat	Begin	Alignment	End	P-value
TPR	114	--LPSLF ₁₁₄ EVAEN ₁₁₅ VYQ ₁₁₆ DGYNEAAAYLY ₁₁₇ KKVAE ₁₁₈ SEK ₁₁₉ Q ₁₂₀ --	147	6.2e-03
TPR	149	--SERLA ₁₄₉ ICQ ₁₅₀ YRLF ₁₅₁ QIK ₁₅₂ VGQ ₁₅₃ DRAV ₁₅₄ NLQAAIE ₁₅₅ FAP ₁₅₆ FFV--	182	1.5e-01
TPR	191	--LDAL ₁₉₁ KDLAN ₁₉₂ VYRSL ₁₉₃ SMWD ₁₉₄ KVYEF ₁₉₅ AHQMG ₁₉₆ QLG ₁₉₇ LQ ₁₉₈ LQ--	224	4.0e-04
TPR	340	--EVAN ₃₄₀ RYNV ₃₄₁ DVDH ₃₄₂ ILRR ₃₄₃ FESQ ₃₄₄ IAAY ₃₄₅ QES ₃₄₆ PSS ₃₄₇ DMYT--	373	4.4e-02
TPR	382	--VRF ₃₈₂ WYK ₃₈₃ IAK ₃₈₄ YSL ₃₈₅ NKGR ₃₈₆ YTYG ₃₈₇ FKCL ₃₈₈ LIA ₃₈₉ FEK ₃₉₀ AVTI--	415	3.8e-04

>PPTDRAFT_01711_AloR4

LYNTTTTILTEIAKHMRDHD₁₁₄LILSD₁₁₅LARAAEM₁₁₆NPGT₁₁₇MSSII₁₁₈NGN₁₁₉RTL₁₂₀SVD₁₂₁QLDR₁₂₂ITQAM₁₂₃GYPV₁₂₄GY₁₂₅YERY₁₂₆VSEY₁₂₇LAEAN₁₂₈PNW₁₂₉RRM₁₃₀SPFI₁₃₁HN
CARLNK₁₃₂LDCI₁₃₃HVVN₁₃₄LLMD₁₃₅KLGYS₁₃₆ESL₁₃₇FELAE₁₃₈EEL₁₃₉FHEK₁₄₀MYQA₁₄₁ATILY₁₄₂ENVAI₁₄₃SEK₁₄₄KQY₁₄₅SERL₁₄₆AMC₁₄₇QYR₁₄₈LFH₁₄₉TRQ₁₅₀GD₁₅₁NQEK₁₅₂NYEAA₁₅₃VQF₁₅₄EIY₁₅₅V
DRLDEI₁₅₆EQLD₁₅₇ALKDL₁₅₈ANTY₁₅₉RS₁₆₀LRK₁₆₁W₁₆₂DKV₁₆₃ELFA₁₆₄KALG₁₆₅DKAKI₁₆₆QYK₁₆₇LEQ₁₆₈ERH₁₆₉PSK₁₇₀KEN₁₇₁AKK₁₇₂PS₁₇₃PLF₁₇₄AYW₁₇₅AFS₁₇₆HLL₁₇₇RAE₁₇₈VCEA₁₇₉HKDY₁₈₀EKAL₁₈₁QHT
YKYGD₁₈₂LSW₁₈₃VKET₁₈₄DDTT₁₈₅LK₁₈₆WR₁₈₇QYEE₁₈₈WAV₁₈₉GNTY₁₉₀LNK₁₉₁ILAGE₁₉₂ICV₁₉₃LS₁₉₄VDY₁₉₅LVY₁₉₆ISS₁₉₇RKDE₁₉₈ILP₁₉₉ALDI₂₀₀IVD₂₀₁SAN₂₀₂RYH₂₀₃FD₂₀₄VD₂₀₅VIL₂₀₆KQF₂₀₇EGE₂₀₈ISS₂₀₉LLE₂₁₀Q₂₁₁
KIESF₂₁₂YTKR₂₁₃FITER₂₁₄FMH₂₁₅FSK₂₁₆ELSI₂₁₇YLT₂₁₈KKR₂₁₉YSD₂₂₀GFK₂₂₁LISC₂₂₂LEK₂₂₃STL₂₂₄INN₂₂₅KSYI₂₂₆IKC₂₂₇MK₂₂₈LYE₂₂₉SYRE₂₃₀YAS₂₃₁FD₂₃₂VKT₂₃₃AYR₂₃₄KLINE₂₃₅VD₂₃₆QDEA

The sequence name: PPTDRAFT_01711_AloR4

Per-protein P-value for being TPR: 7.9E-06

Probability for being TPR: 3.04%

Per-protein P-value for being SEL1: 8.1E-02

Probability for being SEL1: 0.00%

Repeat	Begin	Alignment	End	P-value
TPR	3	--NTTTT ₃ ILTEI ₄ AKHMRD ₅ HD ₆ LILSD ₇ LARAAEM ₈ NPGT--	36	9.7e-03
TPR	115	--SESL ₁₁₅ FELAE ₁₁₆ EEL ₁₁₇ FHEK ₁₁₈ MYQA ₁₁₉ ATILY ₁₂₀ ENVAI ₁₂₁ SEK ₁₂₂ KQ--	148	1.7e-04
SEL1	154	--AMC ₁₅₄ QYR ₁₅₅ LFH ₁₅₆ TRQ ₁₅₇ GD ₁₅₈ NQEK ₁₅₉ NYEAA ₁₆₀ VQF ₁₆₁ EIY ₁₆₂ VD ₁₆₃ R ₁₆₄ LDEI--	189	3.9e-03
TPR	192	--LDAL ₁₉₂ KDLAN ₁₉₃ TYR ₁₉₄ SLR ₁₉₅ KKW ₁₉₆ DKV ₁₉₇ ELFA ₁₉₈ KALG ₁₉₉ DKAKI ₂₀₀ Q--	225	4.1e-03

>PPTDRAFT_01713_AloR5

MEIIPTIRAEVQTYLIRKSL₁₁₄TMTE₁₁₅FGHI₁₁₆IDL₁₁₇NVGT₁₁₈VS₁₁₉GIVT₁₂₀GNR₁₂₁PIS₁₂₂VH₁₂₃QLDR₁₂₄ITM₁₂₅GMN₁₂₆LPP₁₂₇DYF₁₂₈ERY₁₂₉IDEC₁₃₀IEE₁₃₁PLN₁₃₂WRR₁₃₃ISP₁₃₄FLY₁₃₅RC₁₃₆VV₁₃₇LG
RLDCL₁₃₈RRV₁₃₉VGM₁₄₀LLDN₁₄₁PVY₁₄₂LPSL₁₄₃FVAE₁₄₄DSF₁₄₅KKGN₁₄₆TEAA₁₄₇FLY₁₄₈ENV₁₄₉SEGE₁₅₀KYQ₁₅₁SERL₁₅₂AVC₁₅₃QYR₁₅₄LFT₁₅₅IRIG₁₅₆DD₁₅₇QEK₁₅₈NYDAA₁₅₉IQF₁₆₀EPY₁₆₁VD₁₆₂R₁₆₃LDEI
DQLEA₁₆₄LKDL₁₆₅ANTY₁₆₆RS₁₆₇LRK₁₆₈W₁₆₉DKV₁₇₀ELFA₁₇₁KAMG₁₇₂DKAKI₁₇₃QYK₁₇₄LQ₁₇₅QR₁₇₆HH₁₇₇VHK₁₇₈DNS₁₇₉KK₁₈₀PN₁₈₁FL₁₈₂FAY₁₈₃WAF₁₈₄S₁₈₅HLL₁₈₆RSQ₁₈₇AC₁₈₈GER₁₈₉KDY₁₉₀EKGL₁₉₁QH₁₉₂HI₁₉₃KY
ADLSW₁₉₄VTDT₁₉₅DEE₁₉₆ALK₁₉₇WR₁₉₈KKY₁₉₉EDW₂₀₀AVV₂₀₁NTY₂₀₂VN₂₀₃KL₂₀₄SG₂₀₅DES₂₀₆VLS₂₀₇DY₂₀₈VAY₂₀₉ISAR₂₁₀KDEI₂₁₁LPAL₂₁₂DIM₂₁₃IEA₂₁₄AN₂₁₅RYH₂₁₆FD₂₁₇VD₂₁₈NIL₂₁₉KQF₂₂₀EEI₂₂₁S₂₂₂FLE₂₂₃Q₂₂₄KKV
EGLY₂₂₅TQR₂₂₆FTT₂₂₇ERY₂₂₈TH₂₂₉FARE₂₃₀LAI₂₃₁YLL₂₃₂RK₂₃₃GK₂₃₄FS₂₃₅DG₂₃₆FT₂₃₇FL₂₃₈SC₂₃₉LEK₂₄₀SAE₂₄₁ANN₂₄₂R₂₄₃IQAI₂₄₄RC₂₄₅MRL₂₄₆F₂₄₇TH₂₄₈FKE₂₄₉HAS₂₅₀AH₂₅₁TRAV₂₅₂YG₂₅₃KL₂₅₄IKAV₂₅₅NE₂₅₆DEE

The sequence name: PPTDRAFT_01713_AloR5

Per-protein P-value for being TPR: 5.4E-05

Probability for being TPR: 0.74%

Per-protein P-value for being SEL1: 3.9E-02

Probability for being SEL1: 0.00%

Repeat	Begin	Alignment	End	P-value
TPR	114	--LPSL ₁₁₄ FVAE ₁₁₅ DSF ₁₁₆ KKGN ₁₁₇ TEAA ₁₁₈ FLY ₁₁₉ ENV ₁₂₀ SEGE ₁₂₁ KYQ--	147	1.8e-03
TPR	191	--LEA ₁₉₁ LKDL ₁₉₂ ANTY ₁₉₃ RS ₁₉₄ LRK ₁₉₅ W ₁₉₆ DKV ₁₉₇ ELFA ₁₉₈ KAMG ₁₉₉ DKAKI ₂₀₀ Q--	224	3.6e-03
TPR	251	--AFS ₂₅₁ HLL ₂₅₂ RSQ ₂₅₃ AC ₂₅₄ GER ₂₅₅ KDY ₂₅₆ EKGL ₂₅₇ QH ₂₅₈ IK ₂₅₉ KYAD ₂₆₀ LSW ₂₆₁ VT--	284	8.6e-03

>PPTDRAFT_01722_AloR6

MKITPTIRAELEQYLKQEGLTLSQFGQITGMNIRGISSIVTGNKSMSINQLDRITEAMGLPEGHFYDLFIENYIIDHPPNMRRIEPFLYRCAELE
KLDAIRRVVGAIMDNLLYSPKLFIEAEGLLAQGRLEAALILYEGVAEAEKYQHSERLAICQYRLFQIKIGNDQEKNFQSALQFEPFVKRLDAID
QLDALIDLANVYRSLRKWERVKEIAKDLRTLAKAQYSLEYSQKRGECKPQRPLFFYIAFSKSLIGGVYEEQKYELALQIAYESCDLDWVKETD
EEALRWKSLFQEWGEANICLTKLMAGDTEVLPYIDLSTNREELLPLWNIMIVANRYKLNVDLSILSQFEWEISNIHDQEGRQTNDKQININ
DQLVGFSEADYYLTNGQYKKGISYLLDCMRISTIINNERSILRCVRFERCRQFVTDEAKVEYRNLVEMG

The sequence name: **PPTDRAFT_01722_AloR6**

Per-protein P-value for being TPR: **2.8E-11**

Probability for being TPR: **99.48%**

Per-protein P-value for being SEL1: **1.1E-02**

Probability for being SEL1: **0.01%**

Repeat	Begin	Alignment	End	P-value
TPR	114	--SPKLFIEAEGLLAQGRLEAALILYEGVAEAEKYQ--	147	2.6e-04
TPR	191	--LDALIDLANVYRSLRKWERVKEIAKDLRTLAKAQ--	224	1.4e-04
SEL1	222	-KAQYSLEYSQKRGECKPQRPLFFYIAFSKSLIGGVY-	257	8.5e-03
TPR	247	--AFSKSLIGGVYEEQKYELALQIAYESCDLDWVK--	280	1.1e-03
SEL1	264	-ELALQIAYESCDLDWVKETDEEALRWKSLFQEWGEA-	299	9.7e-04
TPR	379	--VGFLSELADYYLTNGQYKKGISYLLDCMRISTII--	412	1.0e-03

>PPTDRAFT_02243_AloR7

VDDLHSDITDLDTLVNMIKLSFSFMDGTHMIALCDQLYYHVNQKYQEWQLYKAFKKPIQPIHTKRPLVYYYGYSHLMKGMMAFQKQGKYE
AARDICIEKYAELGWFNGLDPYGEAEVDYRHAARANLYALDILSGRSEMQLQEYVQFLRDNPEELLPGLLSIVEGATRHDYPLERVLESFAEQI
EDFKYFEFPVNVSYFRFCYQLALYYIKLRQFRVALGYILQSLKLSDTLGMEHEHEFRKCTAIFEIFRSQATATQQDQYITILKGVKDEKIDFTP
VVAQSV

The sequence name: **PPTDRAFT_02243_AloR7**

Per-protein P-value for being TPR: **1.8E-10**

Probability for being TPR: **98.46%**

Repeat	Begin	Alignment	End	P-value
TPR	73	--GYSHLMKGMMAFQKQGKYEAAARDICIEKYAELGWFN--	106	1.7e-06
TPR	199	--FRFCYQLALYYIKLRQFRVALGYILQSLKLSDTL--	232	1.2e-04

>PPTDRAFT_02798_AloR8

MKHTPTIRAEADRYLKQEGLNLTQFGHIAGINRGIVSGIVTGNSSMSVNIQDRITEAMGLPEGYFYDLYVENYIIDIPPNMRRIEPFLYRCAEL
DKLDAIRRVVGAIMDNLLYSPKLFDAIEELLAQERHDAALLLYESVAEVEKYQHSERLAICQYRIFTIQIDDDQSRNLRAAILFEPYVERLDEIEQ
LDALEDLANVYRSLRKWDKVDEIARKMRAKAEIQYTLKHQQSSRERTESTKKLTRPMPFVYITYADLLCASVCEARGDYQQALQYTYAYTDLD
WVKETDEDQYWISLQHWAEAGNAYVNLMSGNTSVLLDFVEYIGTTANESEKLSKLLNIIIVANRYNLDIDGVLTKFKIDIDASTQLPTSTD
MYTQQVVPDYIALFCYEMAYYNLNRKKYSDGFKQLLSAMVKAHILNNETYFINCTGLFAHFQAYASPETREEYFKLLEKVWLDNVEKNGTV
NRCE

The sequence name: PPTDRAFT_02798_AloR8

Per-protein P-value for being TPR: 1.5E-04

Probability for being TPR: 0.34%

Per-protein P-value for being SEL1: 3.8E-02

Probability for being SEL1: 0.00%

Repeat	Begin	Alignment	End	P-value
TPR	114	--SPKLF ^D IAE ^E LLAQ ^R HDAA ^L LLY ^E SVAE ^V EKYQ--	147	3.0e-04
TPR	191	--LDA ^L EDLAN ^V YRSL ^R KK ^W DK ^V DEI ^A ARK ^M RAKAEIQ--	224	3.2e-04

>PPTDRAFT_02818_AloR9

MKHTPTIRAELDRYLQQEGLSMTEFGHIAGMNRGAVSAIVSGNKSMSVNQLDLITEAMGLPEGHFYDLFIENYIIDHPPNMRRIEPFLFRC
AELDKLDAIRRVVGAIMDNLLYSPKLF^EIAE^ELLVQGR^HKAALL^LYEG^VAE^AERYQH^SERLAV^CQYRIFTIQIGDDQSQNV^RVAAVFEAF^VER
LDEIEQLDALKDLAN^VYRSL^RKK^WDK^VDEMAR^QMRAKAVIQ^SVFHNE^QHKDGTLEK^KTRG^PLF^GYIAYADLLCAS^VCEARGDYQQALQ^YT
YAYADLDWVKEDDEDTKHWMN^LFSQWAEGNTY^VYKLLSGDIN^VLHDYVEYIVATSETNENEKIS^KLLNVIIAANQ^SIDVDDILKRFETLIG^T
FSQQLSSDDMYTRQVIPDYIAWFGYELGFYFLHRGKYIDGFKYLMNAMVKSHIINNETYFINCMGLFVRFQAHAVPETKA^EYFN^LIERV^WE
NNVQKSGTSNHCG

The sequence name: PPTDRAFT_02818_AloR9

Per-protein P-value for being TPR: 4.7E-04

Probability for being TPR: 0.13%

Per-protein P-value for being SEL1: 5.1E-02

Probability for being SEL1: 0.00%

Repeat	Begin	Alignment	End	P-value
TPR	114	--SPKLF ^E IAE ^E LLVQGR ^H KAALL ^L YEG ^V AE ^A ERYQ--	147	7.3e-04
TPR	191	--LDAL ^K DLAN ^V YRSL ^R KK ^W DK ^V DEMAR ^Q MRAKAVIQ--	224	4.1e-04

>PPTDRAFT_03195_AloR10

MKITPTIRAELEHFLQQENL^TLSQFGQITGMN^RGIISSIVTGN^KSMSINQLDRITEAMGLPEGHFYDLFIENYIIDTPPNMRRIEPFLFRC^AE^LD
KLD^AIRRVVGAIMDNLLYSPKLF^EIAE^ELLSQGR^HEAA^LLILYEG^VAE^AERYQH^SERLAV^CQYRIFTIQVGGDDQSRNIRAAAVFEAF^VERLDEID
QLDALKDLAN^VYRSL^RKK^WDK^VDEI^AARK^MKQKAKTQYLLKHQ^HKNRECDEYK^KLSR^LPFVYISYADLLCAGVYEAQGDY^NOALQYTYAYAD^L
DWVKETDEDTKHWISL^FQHW^AQANVIVN^KLLSGDMK^VLN^DYVEYIAASSD^TTDQDRVTQLLNIMMTANRYQIDVNDILQRFETDVNS^LL
QLPQFNDVY^TQHV^IPEQFARLGYELAYYYLHQGT^YDDGFKYLMYSLVSYHRLNNETYFIKCLVLFERYRVYAVSETKAAYLEFIERV^WIA^DV^K
KNGAIDRRN

The sequence name: PPTDRAFT_03195_AloR10

Per-protein P-value for being TPR: 5.8E-08

Probability for being TPR: 51.55%

Per-protein P-value for being SEL1: 1.0E-02

Probability for being SEL1: 0.01%

Repeat	Begin	Alignment	End	P-value
TPR	114	--SPKLF ^E IAE ^E LLSQGR ^H EAA ^L LILYEG ^V AE ^A ERYQ--	147	9.7e-05
TPR	191	--LDAL ^K DLAN ^V YRSL ^R KK ^W DK ^V DEI ^A ARK ^M KQKAKTQ--	224	2.4e-05
TPR	388	--ARL ^G YELAYYYLHQGT ^Y DDGFKYLMYSLVSYHRL--	421	1.5e-03

>PPTDRAFT_04223_AloR11

LSFIKFAHSKFVLKGFIMENTPTIRAEIVKYLKQKDLTMTTEFGHIIDLNVGTISGIVTGNRSISVHQLDSTMGMNLPDPYFYERFIEECIEDFS
LNWRKISPFLYRCVELNRLDCVQRVVSMLLDNPAYPPLLFEAENSFQKGYKDTAAYLYEKIAESEKHQHSELAICQYRLFTIGIGEDQIQNL
QIAARFEPFIDRLDEVDQLDALKDLANLYRALGQWDKVVYFAQMMRERAKLRYGMKQESHKRPSRPPFVYIAYGDLLCAYACDARGNYE
QGLKHLKAHTDLSWVKEKDSQHWLGLFQGWAKINTYVNRMLMSGDVSVLPDYVEYISGEKEIFAELNNVVEAANRYNLDIDHILDRFESHI
AAYREPKATDIYTQQVLSDEYARFWYKLAKYKLFGRGEYPYGFKCLMDAFEKSVKINNVLLISNCSGLFERFRVHADPETLAQYQSMFLEVWE
RNEKKDGLFSS

The sequence name: **PPTDRAFT_04223_AloR11**

Per-protein P-value for being TPR: **2.1E-07**

Probability for being TPR: **29.80%**

Repeat	Begin	Alignment	End	P-value
TPR	132	--PPLLFELAE ^{NS} FQKGYK ^{DTAAYLYEKIAESEKHQ} --	165	1.6e-04
TPR	167	--S ^{ER} L ^{AICQYRLFTIGIGEDQIQNLQIAARFEPFI} --	200	1.0e-01
TPR	209	--L ^{DALKDLANLYRALGQWDKVVYFAQMMRERAKLR} --	242	9.3e-05
TPR	393	--A ^{RFWYKLAKYKLFGRGEYPYGFKCLMDAFEKSVKI} --	426	3.3e-04
TPR	435	--C ^{SGLFERFRVHADPETLAQYQSMFLEVWERNEK} --	468	4.5e-02

>PPTDRAFT_04756_AloR12

LEKNTTIRAEIEKYIQSEGISMQCFADASKVNPGLTSGILNRNPPRPISVNQLDLITEAMGLEEGSLFEMYVDECFIHSPLPHWRRLRPFLRCSE
LNKLDICIRSVLGYLMDLNSVPAIFETA^{AMFEDGRHEASMLLYDCVIESEKYT}HSERLAISYFRIFQIQIKDNQRNLKAAVQFHLYRSRLPEIY
ALEGLHMLSQVFALKMQWSEMEMYADELRELAQALYRNRNRFGEHLELIKPLVYYAQAQHLLKASCYEFQGRYEESKQWIEGYADLSW
FEGLDDEGWKVVNLHRVYAQGNRLCIEIKMGNTSAIYEYITYLREHPDETLEGLNLTLESANRFGYFVDAEELFNQQLKRIWELAPEQWDT
HYRKHFNAFRFASFKVYAEYYFRKGDYPKGLGQTLHCLQLSVDNSYTEHIIGCMALFEQHRNFATPEQQQLYQSLCLGVRANEKNHAYD
HSAGGYL

The sequence name: **PPTDRAFT_04756_AloR12**

Per-protein P-value for being TPR: **8.0E-10**

Probability for being TPR: **95.64%**

Per-protein P-value for being SEL1: **4.5E-02**

Probability for being SEL1: **0.00%**

Repeat	Begin	Alignment	End	P-value
TPR	116	--V ^{PAIFETA} E ^{AMFEDGRHEASMLLYDCVIESEKYT} --	149	1.0e-04
TPR	192	--L ^{EGLHMLSQVFALKMQWSEMEMYADELRELAQAL} --	225	4.1e-03
TPR	248	--A ^{QHLLKASCYEFQGRYEESKQWIEGYADLSWFE} --	281	1.8e-03
TPR	383	--A ^{SFCKVYAEYYFRKGDYPKGLGQTLHCLQLSVDN} --	416	1.3e-03
SEL1	384	- ^{SFCKVYAEYYFRKGDYPKGLGQTLHCLQLSVDNSYT} -	419	1.1e-03

>PPTDRAFT_04976_AloR13

LENATTIRSEIEKELKGGYTFNSFGQATGLNRGIFSAMLNGNPPKISVRQMDLITKALNYPEDWLYDLYVDECFYDGRPHWKRVPFLIRC
VEVGNLQCVEKVL^{SRLMEDLNHIPTIFALAEELYDGGK}LQEAIPFYECVIENEKYQHSELAISHYKLFRAKIGENTEINLKA^{AIQFEPFR}LPE
CHQLDGLLH^{LNTNIYSSLHKWQETITHSDELWEQSKIYEEENKRRARKNRSYVPKTERHLVVY}YGQGLLMKAYALQKIGDYEKAKKIVA^{EYA}

DLSWFEGLDTVGKREVEKFKVWSMGNSYTLDLLLGDTSVLPQYVNLLENNDLILPGLVNILESANRNFFSVDSILDQFIKIDTFKTTQDVIF
MDDYYNFNFLAIYYRRNKRHKDAINAILQCIQTSFFLKNVESFAQSMVFFENLRALCDEVQIEIYKSIKGVCKDEEGFSFTLAFSNESSQ

The sequence name: **PPTDRAFT_04976_AloR13**

Per-protein P-value for being TPR: **4.0E-12**

Probability for being TPR: **99.80%**

Repeat	Begin	Alignment	End	P-value
TPR	79	--GRPHWKRVPFLIRCVGVNLCQVEKVLRLMED--	112	9.9e-02
TPR	116	--IPTIFALAEELYDGGKLEAIPFYECVINEKYQ--	149	3.0e-06
TPR	151	--SERLAISHYKLFRAKIGENTEINLKAAIQFEPFR--	184	1.4e-01
TPR	193	--LDGLLHLTNIYSSLHKWQETITHSDELWEQSKII--	226	1.5e-04
TPR	255	--GQGLLMKAYALQKIGDYEKAKKIVA EYADLSWFE--	288	8.3e-03
TPR	345	--ESANRNFFSVDSILDQFIKIDTFKTTQDVIFMD--	378	7.8e-02
TPR	381	--YNFNFQLAIYYRRNKRHKDAINAILQCIQTSFFL--	414	5.9e-05

>PPTDRAFT_04977_AloR14

MEHTPTIRSTIETELKQRGYTFSSFSKISGINRGTFSTMLNSNPPKPISVRQMDLITKALGYPDGWLYELYIDECFHEGKGHWKRIKPFLLRCV
DLGRKDCIQKVLRLTEDWSYVSTVFEFAEELHKVGGKNEAVPFYECVENERYYHSERLAICQYRLFCYLSNLDLNNRQAAIRFAPFPKNL
PENYQLDALLKLTNTNFQFYDYDMAIHYAKELEVLVTGIFWDQAQARAKNREVRTLNTERHLIVVYGOAYLMQGNLSLEKQGLYEAMKFI
PYYENLRIEGLDEVGMIEAEKFEIWGKANRLNLQILMGDKDSLPAVELIRDNPQEILLGLLTIIESANNYSYSVDDTLVLFADINKFRELRT
NISYYHTNNSLLTYSRFFLELSRYFFSKGSYTEAINNMLISLEASSQLNDKTYIYKISITLLFEKYKDHSTEEQRTEYEKAIKAVEYNTRQMTS

The sequence name: **PPTDRAFT_04977_AloR14**

Per-protein P-value for being TPR: **3.2E-08**

Probability for being TPR: **61.74%**

Repeat	Begin	Alignment	End	P-value
TPR	116	--VSTVFEFAEELHKVGGKNEAVPFYECVENERYY--	149	1.5e-05
TPR	157	--CQYRLFCYLSNSDLNDRQAAIRFAPFPKNLPEN--	190	2.7e-01
TPR	193	--LDALLKLTNTNFQFYDYDMAIHYAKELEVLVTGI--	226	1.8e-03
TPR	387	--SRFFLELSRYFFSKGSYTEAINNMLISLEASSQL--	420	2.8e-05
TPR	426	--YIKSITLLFEKYKDHSTEEQRTEYEKAIKAVEYN--	459	6.2e-02

>PPTDRAFT_05290_AloR15

VEEVLNQRGAIYLLSDSHALDKACELFRISYTHNDWDEANKVADYLHSLAESLYHTQLRNAADGKYETLDTKHPLVFFYAYSYLAKSIYYQNI
GQYEEARDYIMKYSEMGMGLDQSGHEEVERFRFLAKANLYMIDLLSGKALLPEYVQFLHSNDEELLPGLVSITEAANLNNWDIDELLN
EFADDIEIFEGYEDRANRVYLLKLVNQLAIYYLKKKQYIFALNYILVSLQFSIGVEADADFRTLVALFETYRDLATPSQQEQYQTILLRGLHNEKG
IKLDNYGLSVS

The sequence name: **PPTDRAFT_05290_AloR15**

Per-protein P-value for being TPR: **5.3E-07**

Probability for being TPR: **18.02%**

Repeat	Begin	Alignment	End	P-value
TPR	2	--EEVLNQRGAIYLLSDSHALDKACELFRISYTHND--	35	2.6e-02
TPR	43	--ADYLHSLAESLYHTQLRNAADGKYETLDTKHPLV--	76	5.1e-03

Repeat	Begin	Alignment	End	P-value
TPR	80	--AYSYLAKSIYYQNIHQYEEARDYIMKYSEMGMWF--	113	5.2e-05
TPR	123	--VERFRFLAKANLYMIDLLSGKKALLPEYVQFLHS--	156	5.9e-01
TPR	163	--PGLVSITEAANLNNWDIDELLNEFADDIEIFEGY--	196	9.5e-02
TPR	206	--LKLNVQLAIYYLKKKQYIFALNYILVSLQFSIGV--	239	1.6e-03

>PPTDRAFT_05358_AloR16

LKETTITIRAELEQYIRREGITISKFGENTGINAGTISAIINGNRPIAMLLLDRIAAGMGLEEGSLYELYIDEFIRNTAPNWRRVRPFLHRCAELNK
LDCIKQVVEFIMDYLIYAPALFETAEEFSEGRLEAAAIYKNVAESEKYQHSERLALCQYRLFTITVGDDQDENLWAATHFESFVERLGEADQ
LDALRDLANTYASLRRWDKVEWFAEKMAQKAKLQYEQKYGNTRKSERGKEPKGPLFMYIVYSYVLRAGVWDERGDYQKALEYVSLYSDL
SWVQEDTEEARHLKALCSNWAEANRYLYQLMSGSLDVIPQYVNYLEKNEGEILVGLHKIMVAANRYDFNVDHVLQHFQKQIEAFADQHA
KVGTYTEQMSADLYARFLAEMACYDLNKHRYSKGMKFLLESLSYSVVLNGNPVTIKCVGLFEKYRHTATSEDKKEYKNLLGEVEYIYDKKDRF
FSARI

The sequence name: **PPTDRAFT_05358_AloR16**

Per-protein P-value for being TPR: **6.2E-08**

Probability for being TPR: **50.32%**

Per-protein P-value for being SEL1: **2.4E-02**

Probability for being SEL1: **0.00%**

Repeat	Begin	Alignment	End	P-value
TPR	114	--APALFETAEEFSEGRLEAAAIYKNVAESEKYQ--	147	1.1e-04
TPR	191	--LDALRDLANTYASLRRWDKVEWFAEKMAQKAKLQ--	224	2.4e-04
TPR	250	--VYSYVLRAGVWDERGDYQKALEYVSLYSDLSWVQ--	283	8.1e-05