

Supplementary Information for

Identification and comparative expression analysis of odorant binding protein genes in the tobacco cutworm *Spodoptera litura*

Shao-Hua Gu¹, Jing-Jiang Zhou², Shang Gao^{1,3}, Da-Hai Wang⁵, Xian-Chun Li^{1,4}, Yu-Yuan Guo¹, Yong-Jun Zhang^{1,*}

¹State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China.

²Department of Biological Chemistry and Crop Protection, Rothamsted Research, Harpenden, UK.

³Education Ministry Key Laboratory of Integrated Management of Crop Diseases and Pests, College of Plant Protection, Nanjing Agricultural University, Nanjing, China.

⁴Department of Entomology and BIO5 Institute, University of Arizona, Tucson, AZ 85721 USA

⁵Beijing Autolab Biotechnology Company, Beijing, China.

*Corresponding author

Yong-Jun Zhang, PhD. State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, 100193, China.

Email: yjzhang@ippcaas.cn; Tel.: +86 10 62815929; Fax: +86 10 62894786.

Supplementary Figures

Supplementary Figure 1. The full-length gels for each SlitOBPs presented in Figure 8.

Supplementary Tables

Supplementary Table 1.

A percent identity matrix of the 30 full-length SlitOBPs. The calculations are based on the alignment of amino acid sequence by Vector NTI 10.2. The percentage of identity of each pair is shown.

Supplementary Table 2.

A percent identity matrix of the 78 OBPs in *S. litura*, *S. littoralis* and *S. exigua*. The calculations are based on the alignment of amino acid sequence by Vector NTI 10.2. The percentage of identity of each pair is shown.

Supplementary Table 3.

Gene specific primers used for molecular cloning of *S. litura* OBP genes.

Supplementary Table 4.

The protein names and sequences of the 78 of OBPs from *S. litura*, *S. littoralis* and *S. exigua* used in Figure 5.

Supplementary Table 5.

The protein names and sequences of the 384 OBPs and 225 CSPs used in Figure 6.

Supplementary Table 6.

Primers used in RT-PCR for determination expression level of *S. litura* OBP genes.

Supplementary Table 7.

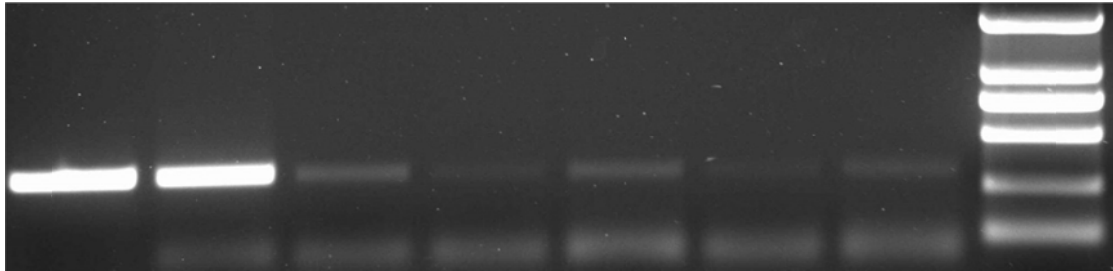
Primers used in real-time PCR for determination expression level of *S. litura* OBP genes.

Supplementary Table 8.

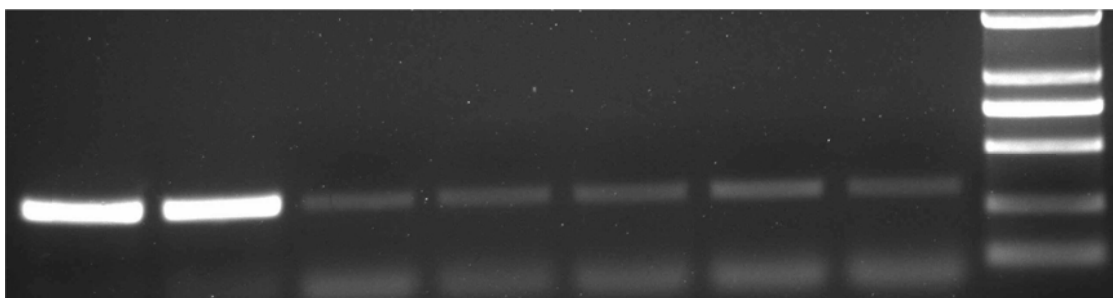
The protein names and sequences of the 193 Lepidoptera OBPs used in Figure 7.

Supplementary Figure 1.

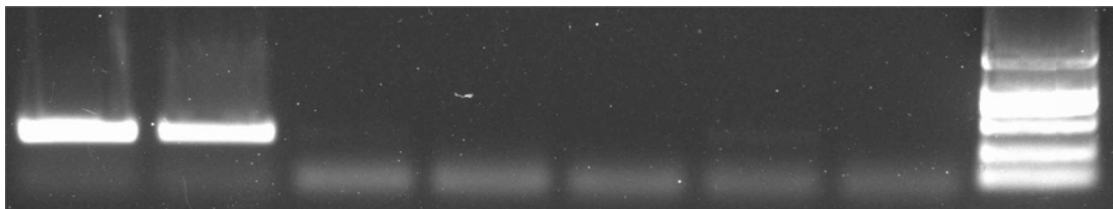
SlitPBP1



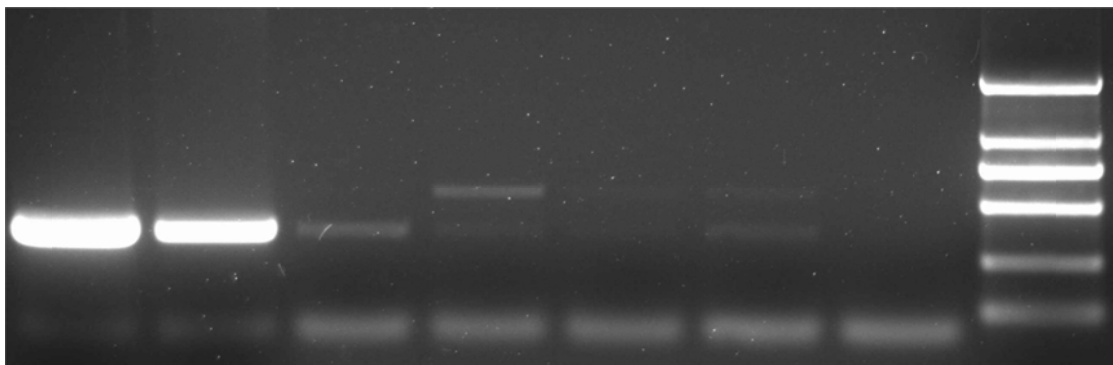
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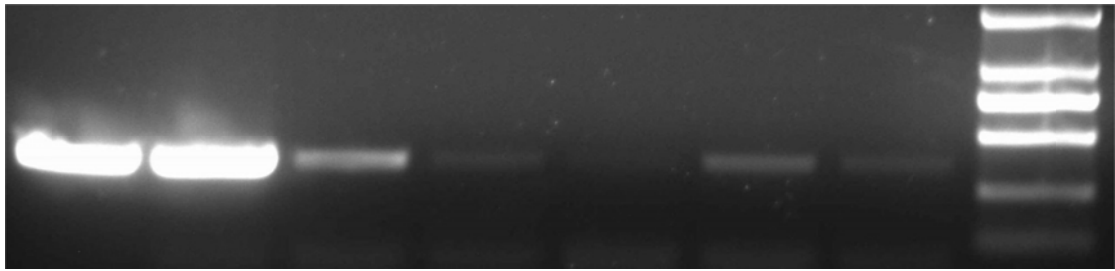
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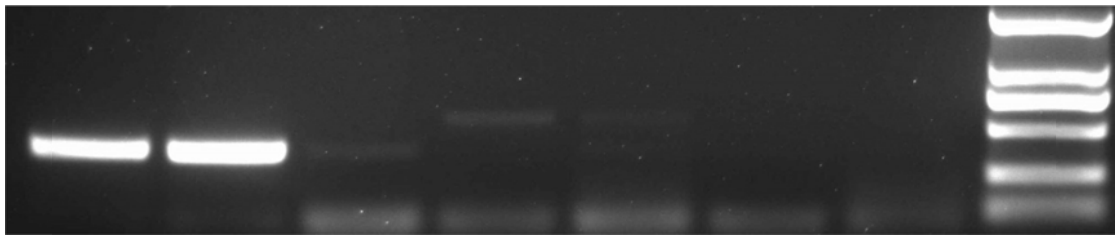
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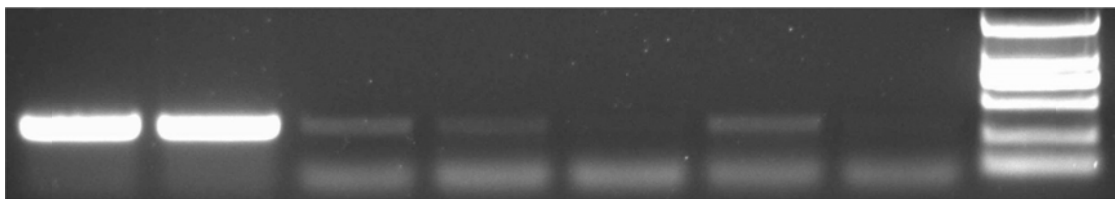
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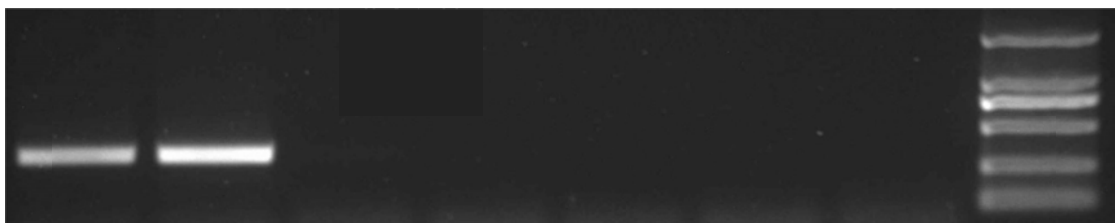
SlitOBP1



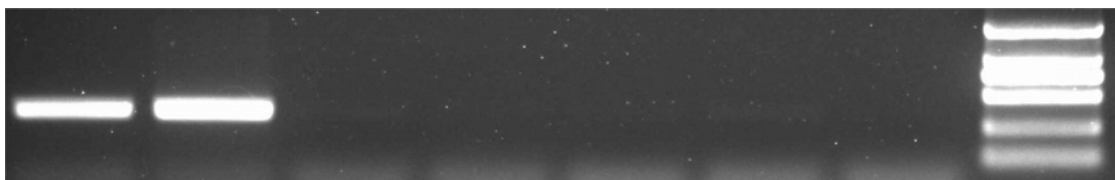
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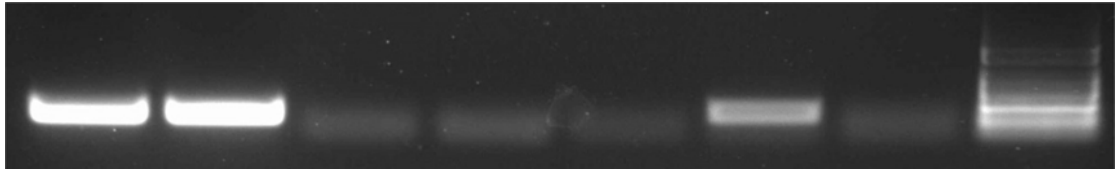
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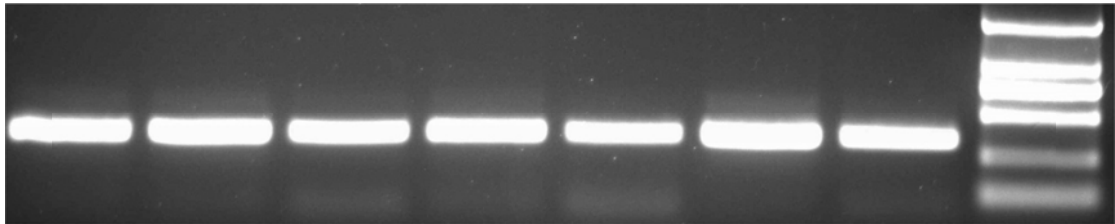
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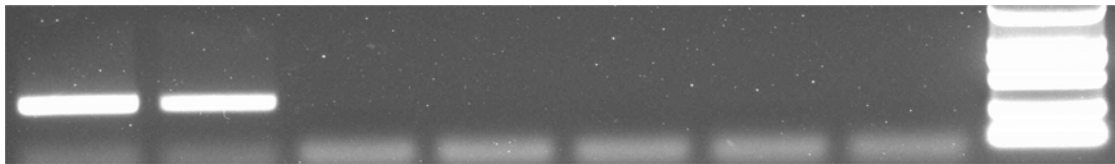
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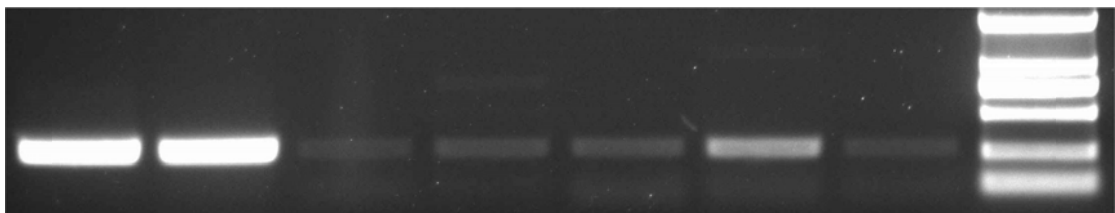
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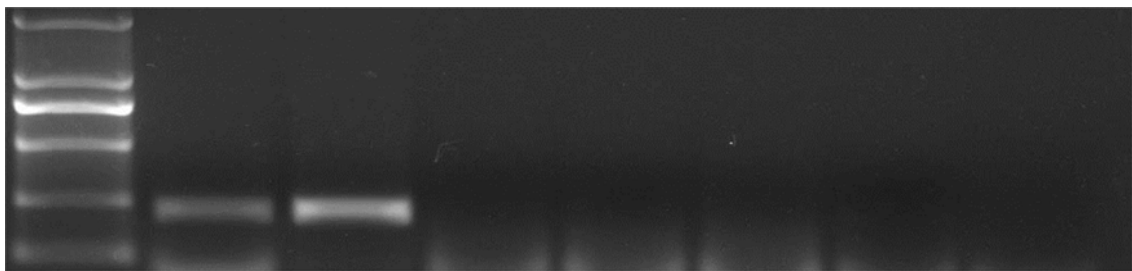
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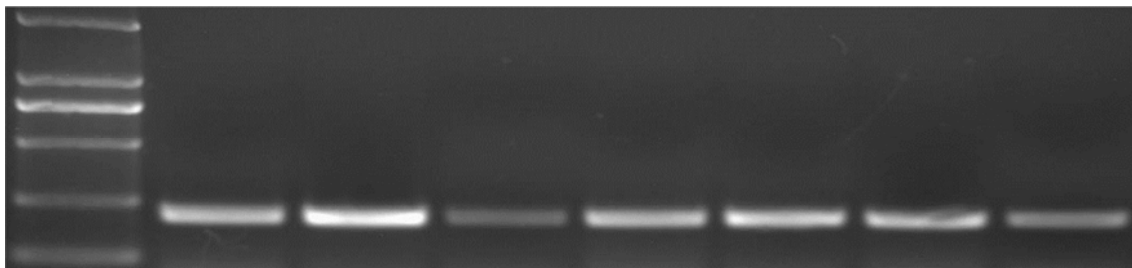
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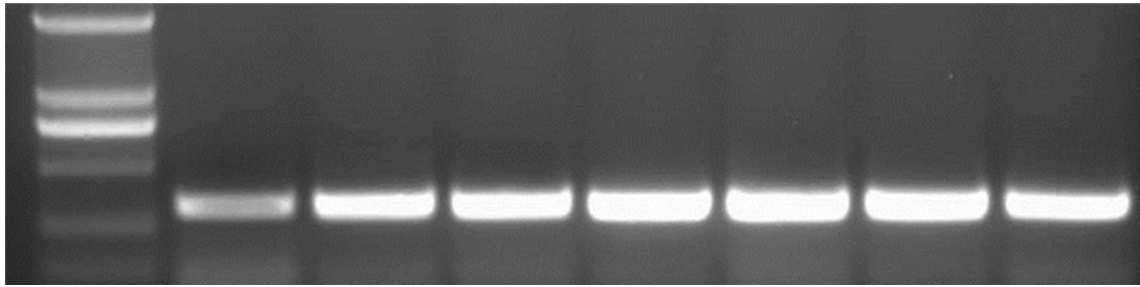
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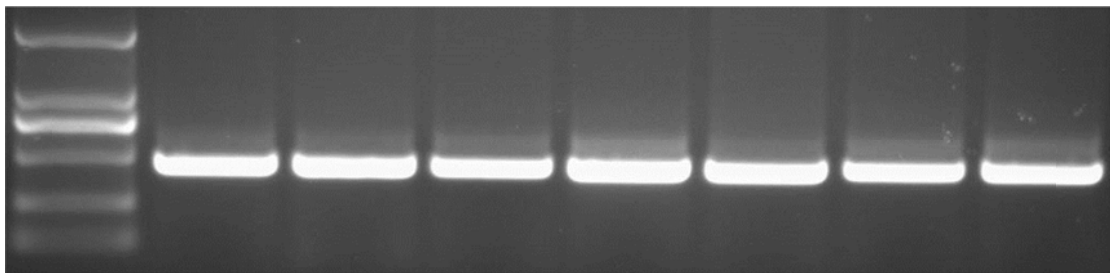
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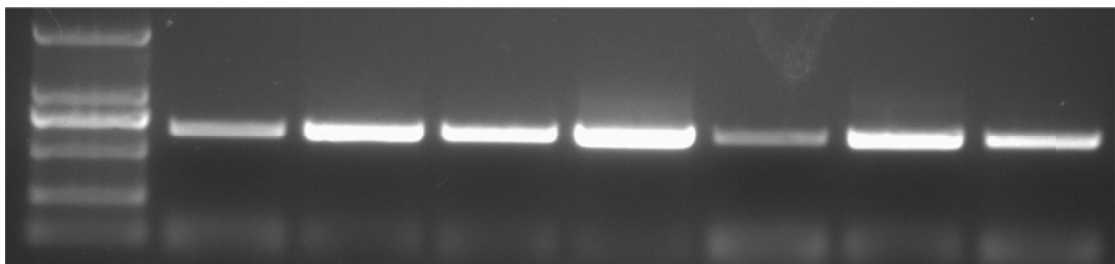
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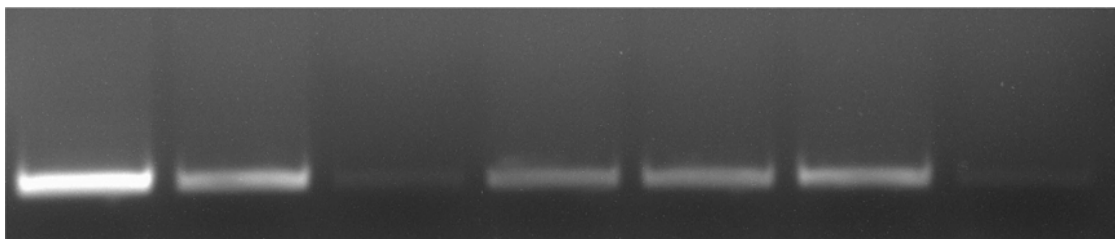
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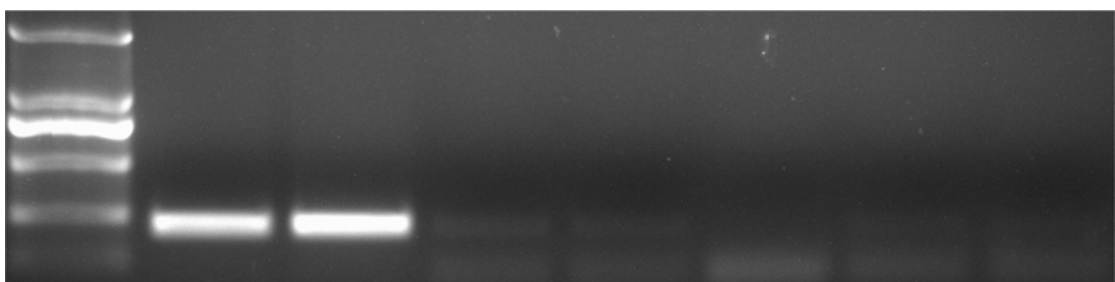
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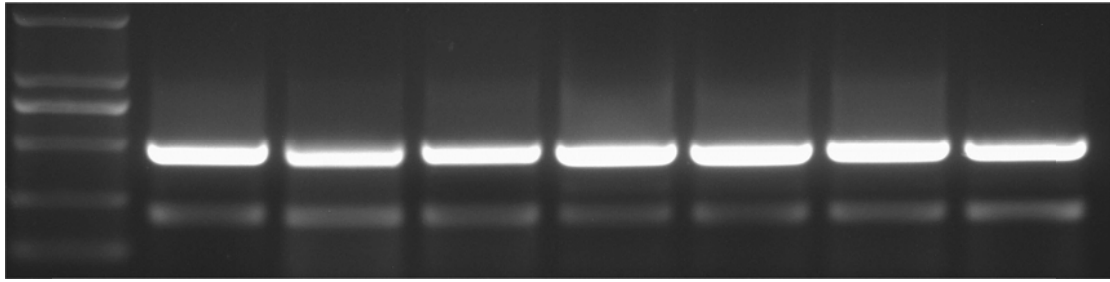
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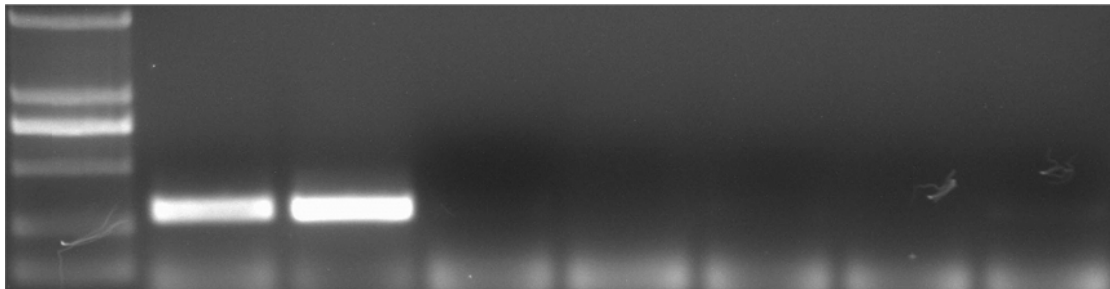
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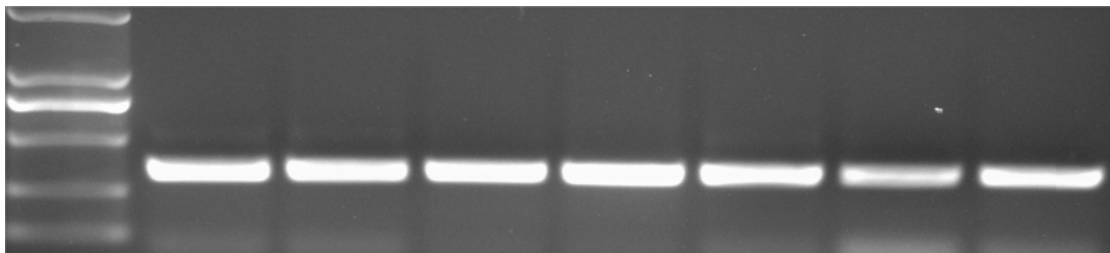
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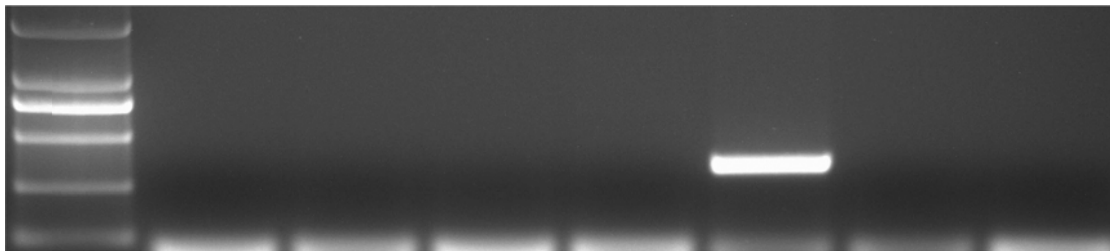
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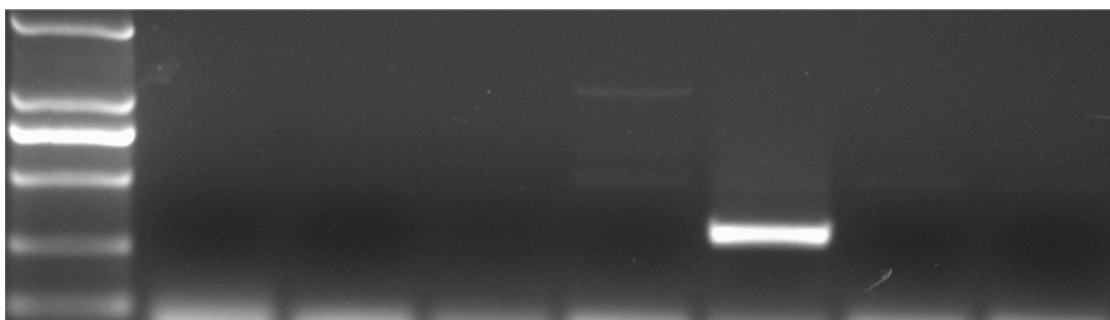
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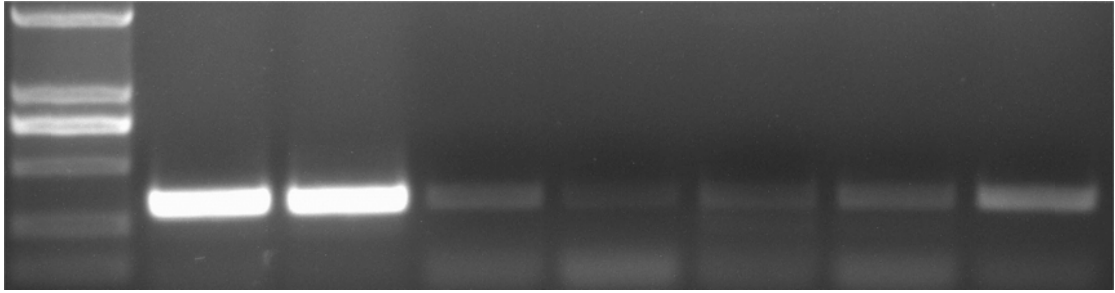
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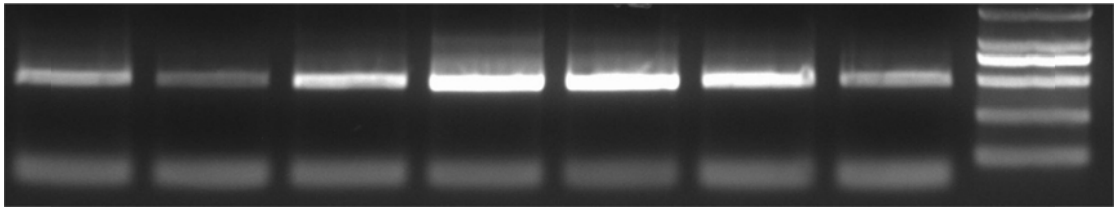
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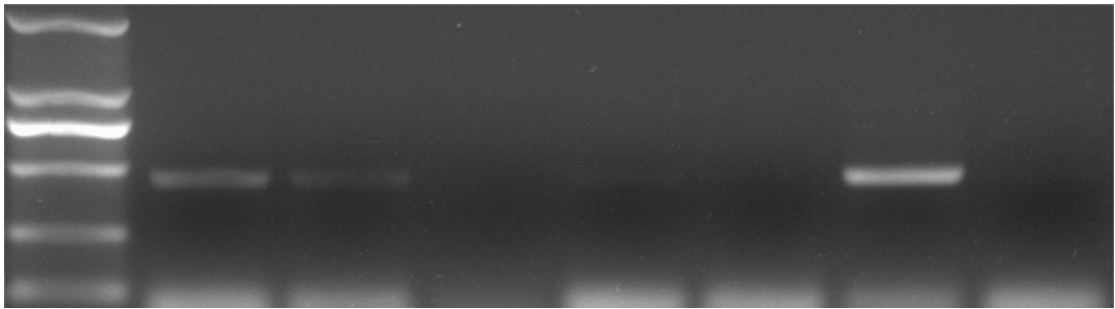
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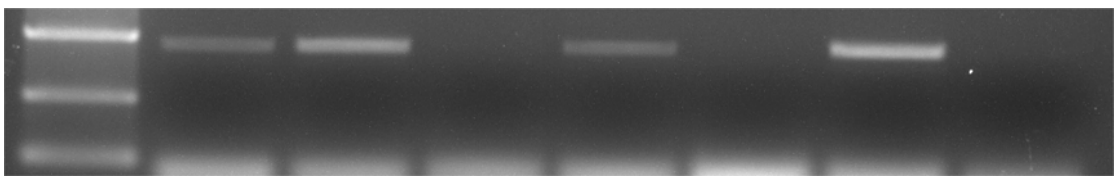
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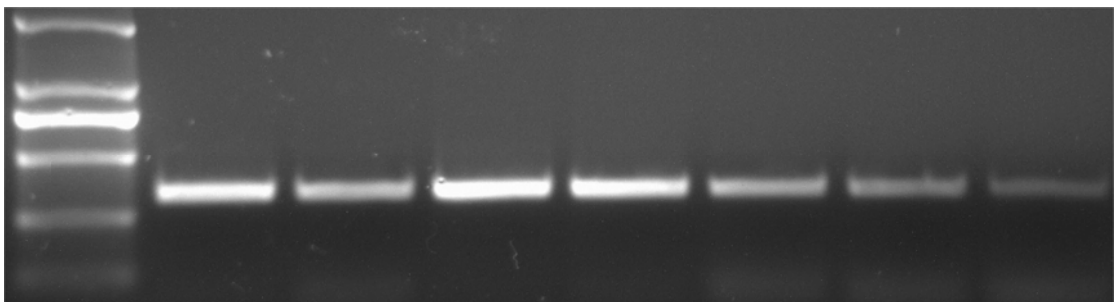
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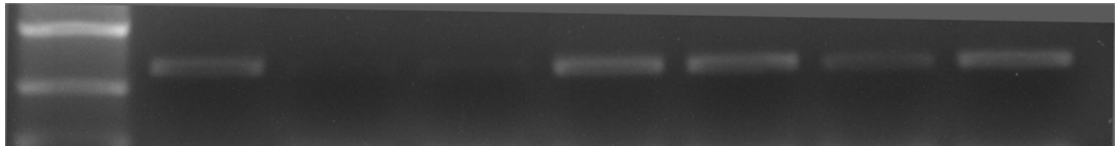
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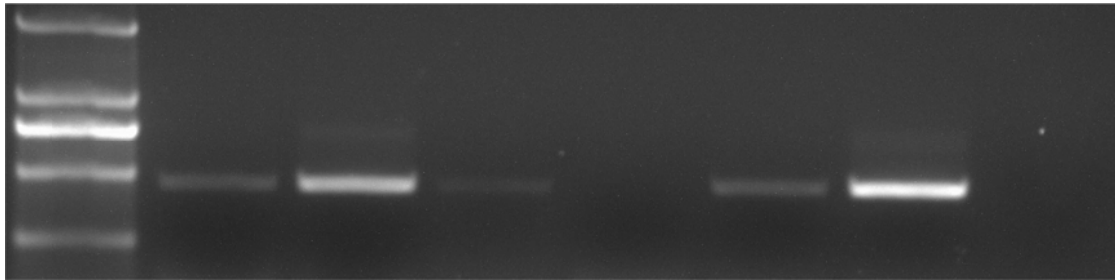
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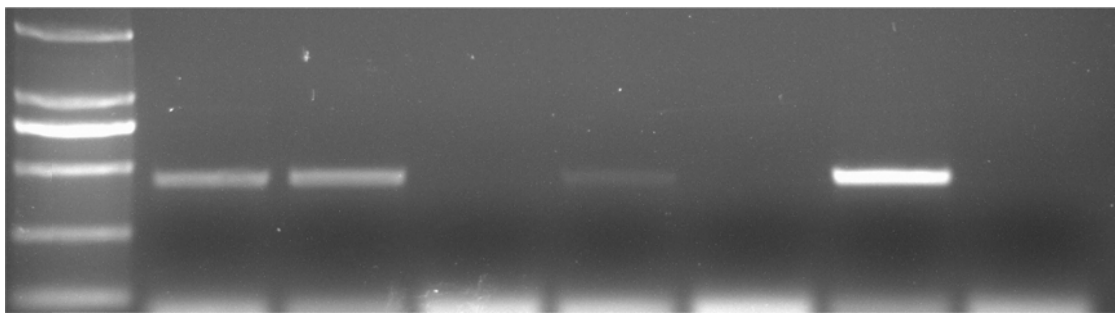
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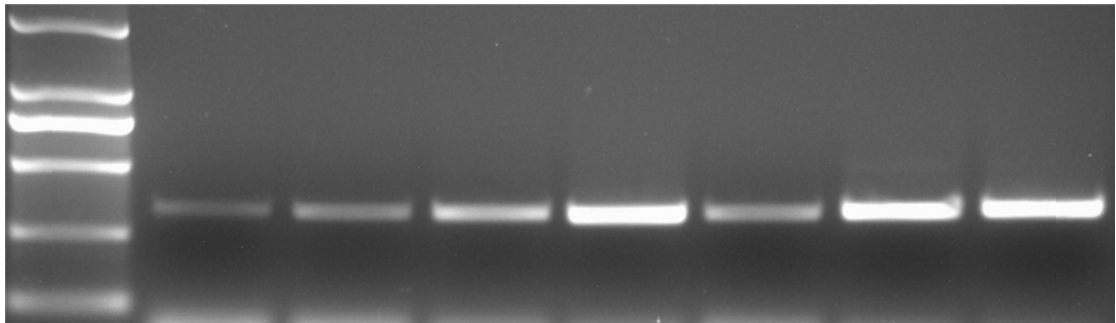
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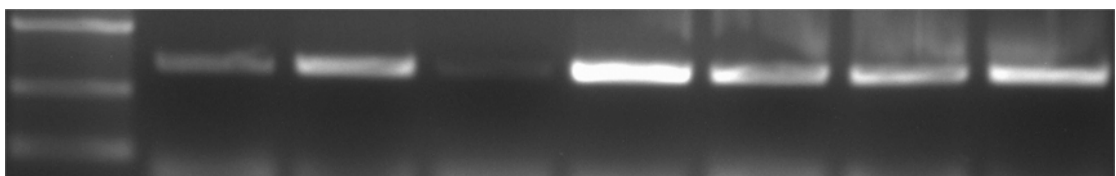
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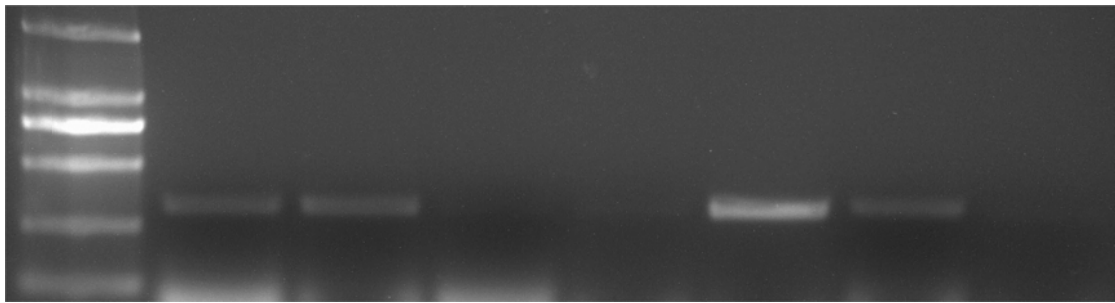
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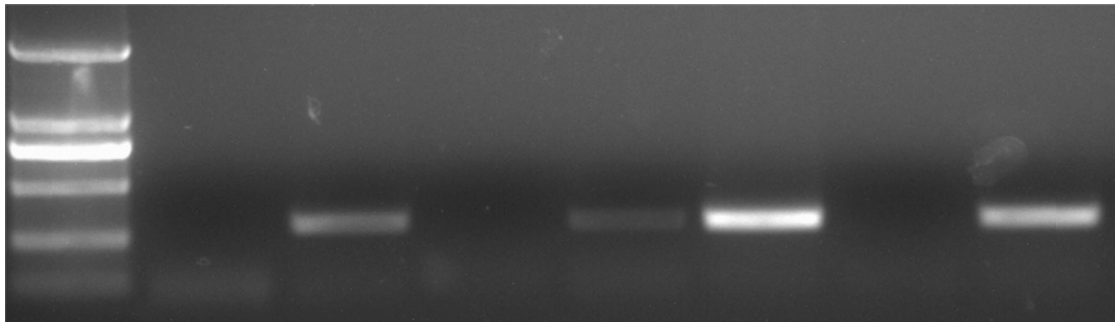
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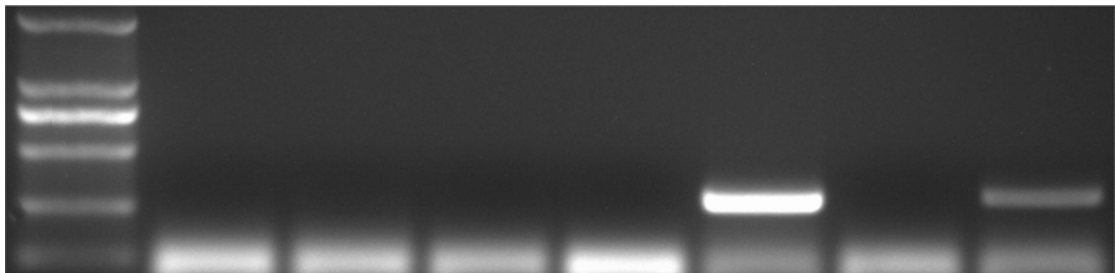
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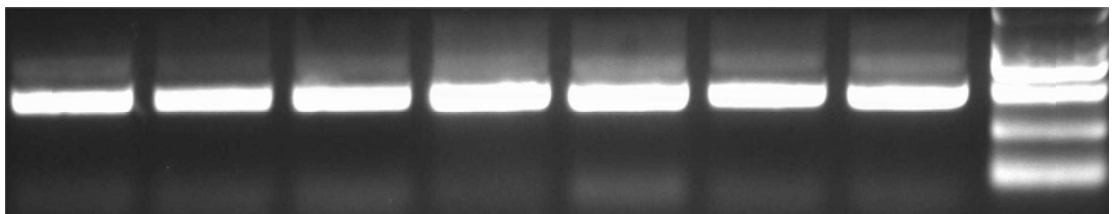
SlitOBP32



SlitOBP33



β -actin



Supplementary Table 3.

Gene	Forward primers (5'-3')	Reverse primers (5'-3')
<i>PBP1</i>	ATGGCGAACGCAAGATGG	TTACACGGCGGTCATGACCT
<i>PBP2</i>	ATGGCGTTCTGTCCATCGG	TTACACTTCAGCAAGCACCTCTC
<i>PBP3</i>	ATGGGATCGCGTAACGTCTTT	CTATATTTCCGTGAGGACCTCACTC
<i>GOBP1</i>	ATGTTGCTGTTGTTGCGCG	TCAGCGCGCCTCAGCCT
<i>GOBP2</i>	ATGACGTCTGAAGTGTGTTTGTCT	TCAGTACTTCTCCATAACAGCTTCAAT
<i>OBP1</i>	ATGAAAGAAGGGAACCGATACAG	CTATCCTGTCTGTTCCGTAGAAGATT
<i>OBP2</i>	ATGACTCGAGCACAAAGTTAAAAAGA	CTTTTCATACAAACATTTTCGATGC
<i>OBP3</i>	ATGTGGATGCAGGCGCTAGT	CTATATGAGGAAGTAGTCCGCCTTG
<i>OBP4</i>	ATGACTAAAGTACTGTTTGCCATCG	TTAAGATTTCTCATATCTTTCAATTTCC
<i>OBP5</i>	ATGTCCGTTGTGCGGTGTTT	TCACTCCATCTTCTTCTTAGTCTCAG
<i>OBP6</i>	ATGTCCAAGTTCACTTGTGTTGGTTT	TTAAGCGGAGATCTCGCTCTTGT
<i>OBP7</i>	ATGGATCAAAAAGAATATGTTTATTTG	TTATGCGAAAATAAAAATCTTCTGGC
<i>OBP8</i>	ATGCTTCTGACAAAAATTGTGAAGTT	TCAAGGAAAGTAAAATATAACCAGGATT
<i>OBP9</i>	ATGTGCCTCGTCAAGTACCATG	CTAGAACGTCAGGTCATCCTTCC
<i>OBP10</i>	ATGGTTCGTAATAATCAGTGGACTC	TTAGAGGCCGGAGGTTCCAC
<i>OBP11</i>	ATGAAATCGTTTGTGATTCTGTATC	TTACGAAGCGAACATAATGTGTGAT
<i>OBP12</i>	ATGAAGACTCTGTTTGTGTTTCGCT	TTACAAAAAATCGCATGCTTG
<i>OBP13</i>	ATGATAACATCATGTTTATTAGTACTAAGTGC	TTAACGAACTTCAAAATCTTTTATTGTT
<i>OBP14</i>	ATGGTTAAAGTTACTTACATAGCCTTGT	GGGGCAAGTAAACTCGCATC
<i>OBP15</i>	ATGTATTCCATTAAGTGTGTTTATTTTTC	GGGAACATGAAATTAGCTGGGT
<i>OBP16</i>	ATGTACCGCTTTGTGATCCTCA	TTATATGACTTTTCGCACATTTTCC
<i>OBP17</i>	ATGAAAACCTTTTCGACTACTCTGTTG	TCAAGGAAATACAAAATTTTTCG
<i>OBP18</i>	ATGTTTAAAGCTCTGTGTGTTCCCTTG	TTATACTGTACGTGGTTGTGTGTAGC
<i>OBP19</i>	ATGTTTCGCCGAACGCTG	TTAATAGTTAACCATTATTTTGTGTTTATTA
<i>OBP20</i>	ATGGAAAAATCCTAATTTTACTTTTATAA	TTACATTAGTAGAATTCTGTATAAATGTGTG
<i>OBP21</i>	ATGGCGCGGAGGCAGC	TCAGAATAAGAAGTATAAGTCTGGATCCT
<i>OBP22</i>	ATGTCTGAAGTTTACCTGCATTATCC	TTAGAACGGCATCTCAACTTTGTG
<i>OBP23</i>	ATGGCCAAGTTCTCTTGTCTTGTGTT	TTAGATGATGATACTAGTCTTATGCTCCAA
<i>OBP24</i>	TGTGTTTATAAAAAGACAGAATTTTGTG	TTTATGATCCAAAAGCATTGGGTT
<i>OBP25</i>	ATGGCTAAAGTTACGTGCATAGTCC	TTAATAATCAACACCAAACATATTTGG
<i>OBP26</i>	TGCTTCTTGGCCTGCATGAT	TTAGATGTCTGAACCCAAACTTAGAAG
<i>OBP27</i>	ATGTATAAATTTGTTATTTTGTGCTCTA	CTAGCACTTCCACGCTGTGTC
<i>OBP28</i>	ATGATCGTTTCGGTTTTTATTATGTTT	TTATGGTAATTTTATTCCCAGCTGAG
<i>OBP29</i>	ATGTGGAATTTATTGGTTGTGTTT	TTATAACTTGAATCCAAACTTGGGT
<i>OBP30</i>	GCTTTATCGATGGACGATCTAAAG	CCCTGGTCGTTTCATCATTCC
<i>OBP31</i>	CGAAACGAACACCGCGAG	AGCTCTATTAGCTTCTAATAAATGTTC
<i>OBP32</i>	CGAATTGATAGGAATGATATACCTTGTA	CTATTTCCATTCATCGGGATCTCT
<i>OBP33</i>	ATGACTTGCTCCAGGCGC	TTAGGAGTTGTTGTCTCAGTCTCGCT

Supplementary Table 4.

>SlitPBP1

MANARWRFVVFVYALYLSAVLGSQDLMVKMTKGFTRVDDCKTELNVGDHIMQDMYNYWREDYQLINRD
MGCMLLCMAKKLDLMDQTMHHGKTEDEFAKSHGADDDVAKKLVSVIHECEQQHAGIADDCMRVLEVAKCF
RTKIHCLKWAPSIEVIMEEVM TAV

>SlitPBP2

MAFCPSVTMSLRVALVVAASLLVVVQASQDVMKNLAVNFAKPLDDCKEMDLPDSVTTDFYNFWKEGYELTN
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>SlitPBP3

MGSRNVFVALVLTVMREIEPSKDPMKYIASGFVKVLEECKHELMNDHLIADLFHYWKLEYTLN RDTGCAI
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NWQPNVEVIVSEVLTEI

>SlitGOBP1

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>SlitGOBP2

MTSKCCLLLVMAAATSSVMGTAEVMSHVTAHFGKALEECREESGLSAEVLEEFQHFWRDFEVHRELGC A II
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AGIAPEVAMIEAVMEKY

>SlitOBP1

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>SlitOBP3

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TMETAGMMADGEVDIEAVLALLPPSLAEHNAPALRACGTQRGADHCDTAFRTQQCWQNANKADYFLI

>SlitOBP4

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KTPKCFIRCVFENVGIVSE DGKQFNPARAAVIFAGERNGKPMEDIADMTALCATDRQETCPCDRSYKFLRCLMS
MEIEREYKS

>SlitOBP5

MSVVRCSLLVAIFCFVSVNAISGDEEAGIKDALRPFVQECAD EFGITEEQFEEAKK KASAADIDPCFMSCFLKKA
EFFDSQGKFDVDSTMAFAKEH LTSEPAMKFVEAVGDECVKINDEDVSDGDKGCDRAKLLFECIAETKKKME

>SlitOBP6

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>SlitOBP7

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NVIKNNKLN YEASIKQIDLMYPPDVKESAKAAVECKDVQK KYKDICEASFYAAKCMYEFKPEDFIFA

>SlitOBP8

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GRVGSKENKNSRDDSRSKDKKGDGSMRDNRNDMMSSRRDDMMSRGDERNDNRKHRTDDRMGNDND
RSGNRGRGNKNNRNDMNGRDDRFRDDYFNGREDFPQSDYEGGDMGQYNNNYSTTQSSRRYKRERRP
SNSGQRSQYNPNNHKISGYEDNFRSDERNTTDDNNSKETDNKSCALHCFLENLEMTGEDGMPDRYLVTHAIT
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>SlitOBP11

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DVAIAKLPSGVDKAEAEKLLDSCSKTKGDAVETVYEIFKCYQHGTSHIMFAS

>SlitOBP12

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>SlitOBP13

MITSCLLVLSAVVQVLLAKQPVFESGPPEPWGPPERTSHPGQFQPRVPKRCWVPPQRINVYNCCPIPTLYPDED
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>SlitOBP15

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GQSVKGSTINHDMMLRQVDMMPNDMKAPVKSIAIEHCRPVAKNYKDLCEASYWTAKCIYDFDPANFMFP

>SlitOBP16

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KKGATDDGKLDIKKFEVITKEVGSDDKDLLEIKTNCINGDLNNGPPEFCDFMKIKHCVTLHMMNHCEWS
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>SlitOBP17

MKTFRLLCCILSIFLFFDQSYGMTRQQLKNSGKLMKKSCMPKNDVTEDEVGDIKGFIEIETRNVMCIACVYTM
SQVVKNNKLSYEAIVKQVDVMFPAEMRDAVKAATHCKETTKYKDLCESSYWTAKCMYDYDAQNFVFP

>SlitOBP18

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>SlitOBP19

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>SlitOBP20

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>SlitOBP21

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>SlitOBP23

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>SlitOBP25

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VDY
>SlitOBP27

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>SlitOBP28

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>SlitOBP29

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>SlitOBP33

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>SlittoPBP1

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>SlittoPBP2

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>SlittoPBP3

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>SlittoGOBP1

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>SlittoGOBP2

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>SlittoOBP1

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>SlittoOBP2

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>SlittoOBP3

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>SlittoOBP4

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>SlittoOBP5

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>SlittoOBP7

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>SlittoOBP8

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>SlittoOBP9

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>SlittoOBP10

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>SlittoOBP11

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>SlittoOBP12

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>SlittoOBP13

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>SlittoOBP14

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>SlittoOBP15

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>SlittoOBP16

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>SlittoOBP17

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>SlittoOBP18

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FP

>SlittoOBP19

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>SlittoOBP20

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>SlittoOBP26

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>SlittoOBP25

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>SlittoOBP24

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>SlittoOBP28

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>SlittoOBP23

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>SexiPBP1

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>SexiPBP2

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>SexiGOBP1

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>SexiGOBP2

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>SexiOBP1

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>SexiOBP2

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>SexiOBP4

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>SexiOBP5

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>SexiABP1

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>SexiOBP10

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>SexiOBP8

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>SexiOBP9

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>SexiOBP11

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Supplementary Table 5.

>BmorGOBP1

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>BmorGOBP2

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>BmorPBP1

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>BmorPBP2

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>BmorPBP3

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>BmorOBP5

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TF

>BmorOBP8

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>BmorOBP9

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FNI

>BmorOBP10

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>BmorOBP11

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>BmorOBP12

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>BmorOBP13

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>BmorOBP15

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>BmorOBP16

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>BmorOBP17

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>BmorOBP18

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>BmorOBP19

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>BmorOBP20

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>BmorOBP21

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>BmorOBP22

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>BmorOBP23

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>BmorOBP25

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>BmorOBP27

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>BmorOBP28

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>BmorOBP29

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>BmorOBP30

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>BmorOBP31

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>BmorOBP33

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>BmorOBP34

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>BmorOBP36

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>BmorOBP37

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>BmorOBP39

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>BmorOBP43

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>BmorOBP44

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>HarmPBP2

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>HarmPBP3

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>HarmGOBP2

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>HarmOBP17

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>AipsOBP18

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>SlitGOBP2

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>SlitOBP3

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>SlitOBP12

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>SlitOBP20

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>SlitOBP23

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>SlitOBP27

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>HmelGOBP2

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>HmelPBP_C

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>HmelPBP_D

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>HmelOBP3

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>HmeI OBP6

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CTQLY AISYRESDD

>HmeI OBP8

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>HmeI OBP12

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>HmeI OBP13

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>HmeI OBP14

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>HmeI-OBP16

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>HmeI-OBP17

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>HmeI-OBP18

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>HmeI-OBP19

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>HmeI-OBP21

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>HmeI OBP22

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>HmeI OBP23

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>HmeI-OBP2

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>HmeI OBP9

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>HmeI OBP10

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>HmeI-OBP11

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>HmeI-OBP24

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>HmeI OBP27

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>HmeI-OBP28

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>HmeI-OBP29

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>HmeI-OBP30

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>HmeI OBP31

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>HmeI OBP35

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>HmeI-OBP1

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>BmorCSP1

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>BmorCSP2

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>BmorCSP3

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>BmorCSP4

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>BmorCSP5

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>BmorCSP5a

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>BmorCSP6

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>BmorCSP7

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>BmorCSP8

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>BmorCSP9

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>BmorCSP10

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>BmorCSP14

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>BmorCSP14a

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>BmorCSP11

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>BmorCSP9a

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>BmorCSP13

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>BmorCSP12

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>BmorCSP15

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>BmorCSP16

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>PxutCSP1

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>PxutCSP5

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>PxutCSP7

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>PxutCSP13
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>PxutCSP11b
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>PxutCSP4a
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>HarmCSP18

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>HarmCSP9

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>HarmCSP12

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>HarmCSP24

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>HassCSP

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>AipsCSP1

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>AipsCSP2

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>AipsCSP3

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>AipsCSP5

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>AipsCSP7

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>AipsCSP10

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>AipsCSP11

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>SlitCSP1

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>SlitCSP4

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>MbraCSP2

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>HvirCSP4

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>HvirCSP11

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>HvirCSP13

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>HvirCSP14

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>SexiCSP3

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>SexiCSP2

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>CmedCSP12

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>CmedCSP15

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>CmedCSP22

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>CmedCSP13

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>CmedCSP17

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AGKDK

>CmedCSP10

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>CmedCSP4

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>CmedCSP14

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>CmedCSP19

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>CmedCSP8

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>CmedCSP2

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CTPKQRELIREVVSFGFQSKLPEVWAEVKKHDPEGAYKESFEAFLHAKN

>CmedCSP1

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>CmedCSP3

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>DhouCSP12

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>DhouCSP10

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>DhouCSP6

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>DhouCSP2

MRVLVVLAYLVAATYAAEKYNSKYDNFDVETLIQNERLLKAYINCFLDKGRCTAEGADFKKALPEAVETTCAKCTD
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>DhouCSP14

MNSIIILSCLLAVVACEQYTDKYDNTNLEEIMENDNLRQAYLKLLEEGPCTAEGKKLCELLTEALETECSKCTDKQ
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>DhouCSP7

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>DhouCSP11

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>DhouCSP3

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>DhouCSP9

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>DhouCSP5

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STDINTMPTRFTLGSSTELQPLSTAITFIDQIGYKIIRTELVTDILKNTVRAVVG

>DhouCSP4

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>DhouCSP1

MKLLLVTVISFCSFAINGEEKYDKKYDNINIDEILDNRLLVAYIKCILEKGKCTAEGYELKSHITDALQTGCKKCTK
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>DhouCSP16

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>DhouCSP13

MNFIITSFVIFQIFIINGEETSYTNEFDGLDLHEILTNNRLLTAYVNCLENGPCTPDGKELKKNLPDAIDNGCKKCT
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>DhouCSP17

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>DhouCSP8

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>DkikCSP7

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>DkikCSP12

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>DkikCSP1

MRVLVVLACLVAATFAAEKYNSKYDNFVETLIQNERLLKAYINCFLDKGRCTAEGADFKKALPEAVETTCAKCTD
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>DkikCSP11

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EEQPSTAEQDQAAEMPIVVPLSIPSKPISPNRFDNGELVLGSSSSASGSSRPATVKPATVNQVVPTRPTMWTNT
DINTMPTRFTLGSSTELQPLSTAITFIDQIGYKIIRTELVTDLKNTVRAVVG

>DkikCSP2

MKVFLITLCLAFAMAEDKYESVNDDFDINEVLKNDRLLSYIKCLLDKGPCTPEVKQVKDKLPEALATHCAKCT
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>DkikCSP17

MQRPIFLCLSAAILIALIPSLMGAPQMSDAQLEQALADSATMERHIKCALGEGPCDAVGRRLRTLAPLVLRGACP
QCTVQETRQIRRTLAFVQRNYPWEWAKIVRQYG

>DkikCSP9

MKTFCIIISIVSLVIADFYSRPRYDDFDIQPLENDRILLGYVKCFLDEGPCTPEAKDFKKVIPEALQTTGCKCTSKQK
ELIRTVIRAIQDHPESWEQLIDKFDKEKKYKDAFDKFLADKNE

>DkikCSP15

MQTSRIVFACVVLAVCAAQEQRPEVSDTALDDALSDKRFIQRQLKCALGEGPCDPIGKRLKTLAPLVLRGACPQ
CSPQETKQIQKTLVYVQRNYPQQWAKIVRQYAG

>DkikCSP16

MKFVVMVVIAMAAARPGNPNYEKFDNLDVDEVLGNSKLTSSLLKCMVDDGRCTPEGTDLKNLAPGAVQNKCA
DCTAEQKTKAAKFMRAAKKDYTELFNKLVIHDPNNEHTAELDEFQNTQ

>DkikCSP13

MNFIIITSFVIFQIFIINGEETPYTNEFDGLDLHEILTNDRLLTAYVNCLENGPCTPDGKELKKNLPDAIDNGCKKCT
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>DkikCSP6

MKGIIAVCVLSLAAVVLSDCPDGLYTDRTYDNTVDEIVSNDRLMTPYVSCLEKGNCTPEGKELKNHIAHALQTG
CECCTNQQKSKSRVIGHFINEKPDVWNELAAYDPKKVYTKKYEELRKLKS

>DkikCSP4

MKGIIFLGCLLAVVVSQKYTEKYDNVDYKEIMQNPCLFHPYFKCVLDQGSCTAEGKELKAHISEALENGCEQCTE
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>DkikCSP3

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KCTAKQKSSSDTVIRFLVKNRPDLWKELSHKYDPDNIYQERYKDKIDSVKGS

>DkikCSP10

MKILLCLLTVGYAHATETYTTENDDLIDRLVNNDDQFLSFIRCFDKQECNSVAADFCKDLPEAVQTACLKCTQ
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>DkikCSP5

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>DkikCSP8
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>PrapCSP
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AQEKGYTIIIEHLINKEKEIWEKLCAYDAEGKYRKKYEERAKSAGLAV
>PaegCSP
MQSIVILMTLLSMALAIQSQTYPDYDNFNAEDLVENVRLRSYGKCFLEKGPCTAEGSDIKKIPEALRTSCAKCT
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>SnonCSP1
MMKFVLLLCVMVAAMAEKYTDKYDNIDLDEILSNKRLLMAYVNCVLDKGCSPGKELKDHLSDAIETGCTK
CTDAQQKGYRVIIEHLIKNELDIWRELCAKYDPTGTWRKKYEDRAKANGIVIPE
>SnonCSP2
MKVVLLALCLALGVLAQDKYESANDDFNIKEVLENDRLLTAYSKCLLGTGPCTPEVKQVKDKLPEALETRCAKCT
DKQKEMGKTLAQEVKKNHPDIWKQLVAKYDPQGYQQAWKDFLQE
>SnonCSP3
MRVLIVLACLIVMAFAADKYNSKYDNFDVETLISNDRLLKAYINCFLDKGRCTPEGSDFKKTLPEAIETTCACKTEK
QKTNIRKVIKAIQQKHPKEWDDLKKNVPSGKNXANFDKFIQGSS
>SnonCSP4
MYSALATMLLIYLTIQSNATETSTYTTKYDGIDLDEILNERNLLNGYVNCMLDLGPCTADGKELKKNIPDAIENDC
KKCTDRQRDGS DRVMHYLIDHRPDDWVKLEKKYNSDGSYKLYLSSKTTEDNSVTNVSKSEEDTKNDSKE
>SnonCSP5
MNSFIILCLFGLVVAVARPDTTYTDKYDSVNLDEILGNRRLLTPYLKCMLDQGKCTPDGKELKSHIREALEEDCA
KCTKTQRDGRTRVLGHLINHEKDYWNQLKAKYDQSYXSSKXEEELRTLKQ
>SnonCSP6
MNFLVLSIVVTLAAFAATETYTDYDHINIDEIENRKL LVPYIKCTLEQGRCTPEGKELKAHIK DAMQTACSKCTEK
QKKGARKVVKHIKAKEQDYWKQIIAKYDPENQYSETYEAF LAEKE
>SnonCSP7
MQFKYAILCCVAVVSVAQTQRPAVSDTALEDALQDKRFIQRQLKCALGEAPCDPIGKRLKTLAPLVLRGACPQC
TPQETKQIQRTLSYVQRNFPQT VGGQNSPPIRGIIYKVKVSCIGNMIG
>SnonCSP8
MKSIVLVCVLSVAVMALARPEDAQYTDYDNVNLDEVLSNRLLVYPVKCVLDEGKCAPDAKELKEHIREALEN
KCAKCNEAQKGRTRRIGHLINHEADYWNQLTAKYDPERKFTAKYEKELKEITA
>SnonCSP9
MKAVICLCALVVAVARPEEQYTSKYDGTNIPEVLANERLLHSYIKGLDLGKCTTEGKELKSHLKEALETHCAKCT
DKQKEATRLVIKHLINNEADYWKQLSDKYDPEGKYAXKYEDELKTVS
>SnonCSP10
MPKYDQRYDYLDVDAIFTNKRLVRNYVDCLINSVRCTPEGKALKRILPEALRTKIRCTERQKRAAVKVIRRLKYE
YPDEWSKLASRWDPDTGDFTRYFEEFLAKEHFNTIPGSGSAIPTSAPLPPRNPTMPPTIASPAGPTVPTPPKPAI
NRFGDDGELMQGSSSVGMTPRPMTQATTRPTTMMKPANTKPIPRPTMTTWAGAASNTQPTRFPLRPSSD
LPPPYFHSNTH
>SnonCSP11
MKLLIVLALVAVASPDGDHYDSKYDSFNVDELIQSPRLLKSYAHCFIGDGKCTPEGKEFKGWIP EATTSSCGKC

TEKQKVLVAKFIKAIKEKFPEEY GALVKKSDPEGTHGGDLQKFIDKYGS

>SnonCSP12

MKFVCIVLLLAVIAVQAQYSTENDNLDIDALVANEESFKSYLGCFLDRVTCDAVPAEFK DIPDAVKTTCSKCTDA
QKQIFHKFLLGLKEKLPSDY EAFKNKYDPGNEYFTALEAAVANS

>SnonCSP13

MKADCVFLATLSVMVAADFYDSKYDSFDVQPLENDRILLGYSKCFLDQGPCTPDAKDFKKVIPEALETTGKCS
PKQKQLIKSVIKAVIDRHPDTWEQLSEKYDKDRKFESFDKFLAEED

>SnonCSP14

MKLIIAVALLCMVAMSWGQRTSTYTDKWDNINVDEILESERLMKAYVDCLDRGRCTPDGKALKETLPDALEN
ECSKCTAKQKTGSDKVIRHLVNRPELWRELSTKYDPDHIYQDKYKTQIESVKQ

>SnonCSP15

MINLNKCSFRGSLILTYLFLVTVLAQDKFYDRRYDYEIDTLIQNRLLRKYLECFLWKGPCPTIGRVFRQILPEAVS
TACKKCTXSQRRLARKAFNAFRKYFPEXYVELMKRLDPKNKYEAFEKAIXNA

>SnonCSP17

MKNWLLCLCVLTVVSCYSQGANRYENFNADAIQNDRILLAYKCVMDKGPCTRDGKNFKRVL PETLSTACGR
CNPTQKAIVRTLLLGIKSKSEPRFMELLDKYNPDRSNRDALYNFLVTGN

>SnonCSP18

MNALLIAVFALVAPSALAYDEIYDKIDVDKILGDDALFTTYINCMLDKGECTVEHSADFKLLPEVIATSCGKCSPI
QRQNVKRKTVKALSEKKPEEFTQFRAKYDPKGEHEKSFSFAFVMGTD

>SnonCSP19

MKTILALCLLVAVCAKPEATYDSRYDNFDVESLVGNTRLLKSYGHCFLGTGHCTAEGSAFKKQIPDALRTGCSKC
SPKQRHLIRVVVKGFTKTPDIWNQLVKKEDPTGEYKESFTKFLNSSD

>MsexCSP1

MKCICLLFLVVAVYAEKYTEENDDLDIEGVIKDADTMKAFTGCFMDTADCDHVSGDFKKDLPEAIQTACA KC
TDKQKHITKRYFEGLEEKYPELYQAFKNKYDPENKYFAALKAAIAKF

>MsexCSP4

MQVTYVLLVCVVVASCVAQQAQRQVTDTALEDALNDKRFIQRQLKCALGEAPCDPIGKRLKTLAPLVLRGACP
QCSPQETKQIQRTLSYVQRNYPQQWAKIVRQYAG

>MsexCSP13

MRTVIVLTFVAACFAAEKYNPKYDNFDVDTLISNERLLKAYINCFLDKGRCTPEGTDFFKKALPEAVETTC AKCTEK
QKVNIRKVIKAIQQKYPKQWEELVKKNDPSGKHRANFDKFIQGS

Supplementary Table 6.

Gene	Forward primers (5'-3')	Reverse primers (5'-3')
<i>PBP1</i>	AAACTGAGCTTAACGTGGGC	TCGTGGATCTTAGTGC GGAA
<i>PBP2</i>	GCGTTCTGTCCATCGGTTAC	TTCATGGCAAATTCCTGGGC
<i>PBP3</i>	CGCCTCAGGATTCGTGAAAG	TTAGCTCGTGGATACCGGTC
<i>GOBP1</i>	ACTGACGGAGGAGAAGATGG	AGCCTCCATGATGAACTCGG
<i>GOBP2</i>	GTGCAGAGAAGAGTCAGGGT	ATCATTGCGACTTCTGGTGC
<i>OBP1</i>	GCTTACATCAGTACCACGCC	ACGCAGCATCAAACATCGTT
<i>OBP2</i>	ACAGAAGAACAAGTTGGGAGAA	TCATACAAACATTTTCGATGCGT
<i>OBP3</i>	AGAGATGGACGAGGACATGG	TAGTCCGCCTTGTTAGCGTT
<i>OBP4</i>	CTGTTTGCCATCGTCCTCAC	TTTCCATTGCGTTCTCCAGC
<i>OBP5</i>	GTTCCCTCGTTATTGGTGGCG	AACTTCATAGCCGGCTCACT
<i>OBP6</i>	TGGTTTTGTGTGTTGTGGCT	TTTTCGTTGACTGAAGCGCA
<i>OBP7</i>	TCTGGAAGTGATGCCATGTCT	CTGGCTTAAACTCGTACATGCA
<i>OBP8</i>	AGTTGCAACGTGTGAAGCTA	ACATGAAATGACGCATCGCA
<i>OBP9</i>	ATGTGCCTCGTCAAGTACCATG	CGACCTCGGTCCCAGTCATT
<i>OBP10</i>	GATTCCGAGTCAAGATGCCG	GGTACACACACTGCAGCAA
<i>OBP11</i>	GTGTTCGTGGTTGGGGTTTG	TGTCTCCACGGCATCTTTTC
<i>OBP12</i>	ATGAAGACTCTGTTTGTTCGCT	TTACAAAAAATCGCATGCTTG
<i>OBP13</i>	GATAACATCATGTTTATTAGTACTAAGTG	TAACGAACTTCAAATCTTTTATTG
<i>OBP14</i>	GCCTTGTTTGTAGTAGCTGTGA	GGGGCAAGTAAACTCGCATC
<i>OBP15</i>	TGGGACAGAGCGTTAAAGGT	GGGAACATGAAATTAGCTGGGT
<i>OBP16</i>	ACCGCTTTGTGATCCTCAGT	TTCCGTCGTCCTCCATTCA
<i>OBP17</i>	CCTTTGACTACTCTGTTGCA	AGCATCCCTCATCTCAGCTG
<i>OBP18</i>	GTGGAGCAATAGACAAGGCG	GTAGCAGGCGTTACAAGAGC
<i>OBP19</i>	ATGACCGAGTGCTTGAAGGA	CATGAGGTCGTTCTGCAAT
<i>OBP20</i>	ATAACACTCTCCGGCTTCGCT	ATGTGTGCAGTCGTTGAAGACCT
<i>OBP21</i>	TGCTGTACTCATGGCGGTA	GGCATCGGTCTTATCTGGA
<i>OBP22</i>	ATGTGCAAGTTTACCTGCATTATCC	TTAGAACGGCATCTCAACTTTGTG
<i>OBP23</i>	ATGGCCAAGTTCTCTTGTCTTGT	TTAGATGATGATACTAGTCTTATGCTCCA
<i>OBP24</i>	TGTGTTTATAAAAAGACAGAATTTTG	CACCTCTCTCGCATCCAGCC
<i>OBP25</i>	TCAAGCAGATGATGGCAAGA	TTAATAATCAACACCAAACATATTTGG
<i>OBP26</i>	GGCCTGCATGATGAAGCAA	GCACCATCACTGACCGATT
<i>OBP27</i>	ATGTATAAATTTGTTATTTTGTGCTCTA	CTAGCACTTCCACGCTGTGTC
<i>OBP28</i>	ATGATCGTTTCGGTTTTTATTATGTTT	TTATGGTAATTTTATTCCCAGCTGAG
<i>OBP29</i>	GCTCAAGATGGAGTTCACAAAGTTA	GGGTGCATTTTCAACTGTGC
<i>OBP30</i>	TCTAAAGCAGAAGTATGTGGACA	CTGGTCGTTTCATCATTCCCG
<i>OBP31</i>	CGAACACCGCGAGAAAGAAA	AGCTCTATTAGCTTCTAATAAATGTT
<i>OBP32</i>	CGAATTGATAGGAATGATATACCTTGTA	CTATTTCCATTCATCGGGATCTCT
<i>OBP33</i>	CTGGGTAAGGAGGAGAAGGC	CGCCTTCTGTGATAGCCAC
<i>β-actin</i>	CGAGAAATCGTGCGTGACAT	ATCTGCTGGAAGGTGCGAGAG

Supplementary Table 7.

Gene	Forward primers (5'-3')	Reverse primers (5'-3')
<i>PBP1</i>	AAGATGACCAAGGGATTC	CGCCAGTAGTTATACATG
<i>PBP2</i>	CGAAACCTTTGGATGATT	TCCAGAAGTTGTAGAAAGT
<i>PBP3</i>	TACATCGCCTCAGGATTC	TGGAACAGGTCTGCTATG
<i>GOBP1</i>	GCCAGGAGAGTCAACTGA	CGGTGCTCGAACTTGAAG
<i>GOBP2</i>	ATGTCACCGCCATTTTCG	GGAACTCCTCTAACACCTCTG
<i>OBP1</i>	CAACTGATGACGACTATA	TGCTGGTATTATTCTTGT
<i>OBP2</i>	CTCAGTAACAGAAGAACAAGT	GCAAGCGACATAACACAT
<i>OBP3</i>	GCTCAAGTGCTACATCAAGT	TACAGCCTCGATGTCCAC
<i>OBP4</i>	AGTTCAATCCAGCGAGAG	ATGTCAGCGATGTCTTCC
<i>OBP5</i>	CGGTGTTCTCGTTATTG	ATACCTGCCTCTTCATCTC
<i>OBP6</i>	ATGGCATCAACTCCTGTT	TATCGGCGTCGTATTCTC
<i>OBP7</i>	CTATGAATTGACGAATGTGATAA	CGCAGATGTCCTTGTATT
<i>OBP8</i>	TTGCGGATGCCATAAAG	TACCAGGATTGTGATTGTAGATG
<i>OBP9</i>	CAATCCGAACAACCACAA	GTAACGCACACGACTTAT
<i>OBP10</i>	GATTACTCTGTGTCAGGATG	ATCGTGTGCTCTTCTTTG
<i>OBP11</i>	AATAGAGATGTAGCCATT	GTTGATAGCATTGAAGA
<i>OBP12</i>	CGCACTGAATGTCTAACT	GCCTCATTGTCCATCTTAT
<i>OBP13</i>	ATTCTTACACTGTATCCA	ATTACGCAATATCCTTCTT
<i>OBP14</i>	GAGCCTTAGTAGTGTTCA	AATTGTTCTTCAGAGATGTC
<i>OBP15</i>	GATATGAAGGCACCAGTTA	TCGCTGTCCAATAAGATG
<i>OBP16</i>	CTTAACAACACTACGGACCA	TCACTCCATTCAGAACAG
<i>OBP17</i>	AAGTGGTGAAGAATAACAA	ATCGTAGTCGTACATACA
<i>OBP18</i>	AATAGTAGTCTTGGAACC	GGCACCTGTATATGTTATC
<i>OBP19</i>	ACTGGTCCTATGCGAATT	GAACTTCCTTCAAGCACTC
<i>OBP20</i>	AATCCAGGAATCAGATGAAC	TCTAGTTGGTGAGCGATT
<i>OBP21</i>	GAGGAGGATATAACGAAT	AATCCACTGTATCATCAT
<i>OBP22</i>	AAACTGGACTTGGTAAACTAA	CGTCGCTTACAGATTTCAT
<i>OBP23</i>	AACTGGATTGAAGAACCT	ATCACTCACTGCCTTATC
<i>OBP24</i>	TAGCAATGATGATGATTAC	GTTAGTAGTACACCTCTC
<i>OBP25</i>	TGTAGTAGGTGTGAGTCT	AGTCGTCTATGATCTGATTC
<i>OBP26</i>	AATTGGTGTTATGGATGAC	GATTGCCCTCAGTTCTTC
<i>OBP27</i>	GACTGATTCCATTTACAAA	TTCTTCAACATAGCGATA
<i>OBP28</i>	ACTCAATAGCAATGACACAA	CTTCGTCGTTCACTTTCT
<i>OBP29</i>	TGTGTATGCTCGAAGAAG	ACCTCTCCATCCTTGTTA
<i>OBP30</i>	GTGGACAACATATTAGAATG	TATAAACACAGGCAAACA
<i>OBP31</i>	TTGTACTGTTCTCATTCG	GTTCTCTGTATCTTGTT
<i>OBP32</i>	CCTGTGCTCAGAACATTA	GTAGGACACTGCGTATAG
<i>OBP33</i>	CTGGGTAAGGAGGAGAAGGC	CGCCTTCTTGTATAGCCAC
<i>β-actin</i>	CATCCGTAAGGACTTGTA	TGATCTTGATCTTCATTGTG
<i>RL-31</i>	AAGTTGTAACCTCGTGAATAC	GTTCCCATTTGTTTCTCAG

Supplementary Table 8.

>BmorGOBP1

MWKLVVVLTVNLLQGALTDVYVMKDVTLGFGQALEQCREESQLTEEKMEEFFHFWNDDFKFEHRELGCAIQC
MSRHFNLLTDSSRMHHENTDKFIKSPNGEILSQKIDMIHTCEKKFDSEPDHCWRILRVAECFKDACNKSGLA
PSMELILAEFIMSEADK

>BmorGOBP2

MFSFLILVVASVADSVIGTAEVMSHVTAHFGKTLLEECREESGLSVDILDEFKHFWSDDFDVHRELGCAIICMS
NKFSLMDDDVRMHVNMDEYIKGFPNGQVLAEKMVKLIHNCEKQFDTETDDCTR/VKVAACFKKDSRKEGI
APEVAMIEAVIEKY

>BmorPBP1

MSIQGQIALALMVYMAVGSVDASQEVMMKNLSLNFQKALDECKKEMTLTDAINEDFYNFWKEGYEIKNRETGC
AIMCLSTKLNMLDPEGNLHHGNAMEFAKKHGADETM/AQQLIDIVHGCEKSTPANDDKCIWTLGVATCFKAEI
HKLNWAPSM/VAVGEILAEV

>BmorPBP2

MKLQVVVLTVEMVCGSRDVMNLSIQFAKPLEACKKEMGLTETVLKDFYNFWIEDYFTDRNTGCAILCMS
KKLELMDGDYNLHHGKAHEFARKHGADETM/AKQLVDLIHGCSQSVATMPDECERTLKVAKCFIAEIHKLKWAP
DVELLA/EVLNEVSWKS

>BmorPBP3

MARYNIVVAVLVGVVARGSSSEAMRHIATGFIRVLDECKQELGLTDHILDMYHFWKLDYSMMTRETGCAIIC
MSKKLDLIDGDGKLHHGNAQAYALKHGAATEVA/KLVEVIHGCEKLHESIDDQCSR/VLEVAKCFRTGVHELHW
APKLDVIVGEVMTEI

>BmorOBP5

MKQRLRVLLLRFILQTVLSESGVDVVKNLSL/SFARFFLECDEERHFQPEVRLKVMTFWYSESSTWDRDVGCAF
LCIFKKMEIDNPQDPSYRTHLELLSFANSE/DNKIANQMVEIFYACGENTETDPCLWALEQVKCYKNRINQLGLTP
TF

>BmorOBP7

AVTEELKIEFTKLVMKCTKDHPVDMSELMQLQQLIAPKKTESKLLACAYKLN/VMTSQQGLYNLEHAYKIAEM
SKNGDEKRLKNGK/VADICVKVNDVEVSDGEGK/CERAALIFKCTLENAPKVF/KFGSSEYN/CQ

>BmorOBP8

MLRVVVICVCF/LVIAPYGINASSLDD/LKMVYKNVIK/ECVGDYPITAADL/KLIKARQIPND/DIKCVFACAYKKTGM
MTEEGML/SVEGIK/DMSQKYLS/DNPEQLRKSKEFAEACSSVND/QQVSDGT/KGCERAALIFK/CKSTEKITNFGFEL

>BmorOBP9

MLRVVVICVCF/LVVAPYGINAVS/EQKIKIRDQLDRAGFECFKD/HKITEDDIK/NLRANKPATGEN/VPCFIACVMKK
TGVMNDQGVIRKGPVLELAKK/VLADDDK/DIKLQDYI/HSCSHVNS/ETVHDKGKGCEFAMQAYTCMSANASKFG
FNI

>BmorOBP10

MLRVVVICVCF/LVIAPYGINAVS/DEQKIKIREQIDKSGFECFKD/HKITEDDIK/NLRANKPATGEN/VPCFIACVMKKT
GVMNDQGV/IHTEPVLQ/LAKKVLTD/DKDIK/LQDYI/HSCSHVNS/KTVHDKGQ/GCEFAIQTYTCMSANASKFGFD
V

>BmorOBP11

MSANSFVV/LAFCALAVGVNALTEEQKAEITKSS/LPIAEC/SKEFSVN/QGDIDA/AAK/LGDP/SGLNSCFV/GCFMKKA
GIINASGLFDVAATIEKSKKYL/SEEDLKA/FEKLTET/CAPENDK/PVSDS/DKGCERAK/LLLD/CFVANKGSF/SFVSL

>BmorOBP12

MTSFMVFFVLSVLTLYSDALTDEQKNKIQSKFIEIGAECIVEHPISIDDINSFKNKKFSPSGVNAGCFVACIFNKIGL
FDDKGNLSHNSALEKAKGIFNADEEVKNLEEFNRCQAVNGEAVGDGVKGCERAKLAYNCLIENSLEFGFNIDF
>BmorOBP13

MLKIHVLLCFGMAILYFGSAKAVTPEESKAFAFAKPVIEQCQKDFGMDKESFAQKNLDEIDECLIACVVEKFGIT
NDEKIDGDALKALVTKFVGNNEERNKINKIVEECTEDANKSGDGT CNTSTILFLCLLNGKDLWGF

>BmorOBP14

MSRQQLKNSGKMLKKQCMGKNDVTEEEIGDIEKGFIEQKNVMCIACIYQMTQIIKNNKISYEASIKQIDLMI
PPELKESAKASAGRCKDVSCKYKDICEASYWTAKCMYEDNPKDFIFA

>BmorOBP15

MFLKNIFIECVLLYFVMLNTSFVNTMTKQKIKNSGKILKKACISKNDVTEQISDIDKGFIEDKNVMCIACVYS
MSQVVKNNKFVHDAMVKQVDMMFPTMRDAVKASIANCRGVAKNYKDICEASFWTAKCMYEFDPANFVFA

>BmorOBP16

MRIISFLISVITITFDSVFAMTRAQVKKMTIMKNQCMPKNGVTEQVQKIEEGIFLENHNVMCYIACVYKTI
QVVKNDRDKDLISKQIDVLPQEIRESTKKA VGDCINLQEKYDDWCEGIFRSTKCLYEKDPANFIFP

>BmorOBP17

MTRQQLKNSGKIMKKT CMPKNDVTEEEIGQIEQGFLEQRNVMCYIACIYTVTQVVKNNKLSYDAVIKQVDV
MFPAEMRPAVKA AENCKDISKTFKDICEASYWTAKCMYDFDPKNFVFP

>BmorOBP18

MILIVIAKFLILISLCETMTMKQIKNTGKMMRKSCQPKNNVDDEKINPINDGVFIEENEVKYIACIMKMANTM
KNGKLNFEAAMKQADLLLPDEMKEPTKEAIVACRQVADSYKDVCDASFHVTKCIYNHNPSVFFFP

>BmorOBP19

MTSAKTDVEIKAWFLGQAVECSKDHPVTTEELRMHKHELPSKNAKCLMKCVFRKCNWLD SKGMYDINAAY
ASSTKDFSDDKTKQENANKLFD TCKSVNEENVGDGEEGCDRSLLLAKCLTAA PQVSIYYS

>BmorOBP20

MAVHIFLILASYMALAAHGQLDDEIAELAAMVRENCADESSVDLNLVEKVNAGTDLATITDGKLCYIKCTMET
AGMMSDGVVDVEAVLSLLPDSLKTNEASLKKCDTQKGSDDCDTAYLTQICWQAANKADYFLI

>BmorOBP21

MITASLHVIFALLAFVYGGKDKPVLSEEIKEI IQTVHDECVGKTVSEEDITNCESGIFKEDVKLKYMFCLLEEAGL
VNDDGTVDYEMFTSLIPEEYFDRATKMIFSKELDTPDKDKCERAFEVHKCSYEKDPDFYFLF

>BmorOBP22

MLKV FVVVVCTLGASQLCAALYTQKVAVSFPKDKTTIVVEAMKSCIAKTGANPNVIEVISSGKVSSEDEKFEFFYC
ACNDIGVVNPDGHIVKECIELFPKETQPLVEPVIKNCDKEGVNKYDTLFKYLKCFQETSPVRVTLA

>BmorOBP23

MTSKVLLSCVVLAVLATTVLAEDSRKLVSAPEVAKLLKVLIQECLNENGLGEDAIEVIRAGEYREDEPFQNLVYCA
YKKFGALDENNRISQVAAASFPKDIDVVTVIESCGKEDGNTPVEQVFKYFKCFQKNSPVRMQLY

>BmorOBP25

MKSVVLI CLAFVFNCGADNVHLNEDEREKANWYTAECGVETGVSTEVINA AKIGKYSKDKAFK FVLCFFKKS
AILNSDGT LNMVVALAKLPSGVNKSEAQSVLEQCKNKTGQDAADKAFAILQCFHKGTKTHILF

>BmorOBP26

MKSVVLI CLAFVFNCGADNVHLAETQKEKAKQYTSECVRESGVSTEAINAAKIGKYSKDKAFKNFVLCFFNKSA
IFNSDGT LNMVVALAKLPPGVNKSEAQSVLQCKNKTGQGAADKAFEIFRCYKGT KTHILF

>BmorOBP27

MKSVVLI CLAFVFNCGADNVHLTETQKEKAKQYTSECVKESGVSTEVINA AKTGQYSEDKAFK FVLCFFNKSA

ILNSDGTLNMDVALAKLPPGVNKSEAQSVLEQCKDKTGQDAADKAFEIFQCYYKGTKTHILF

>BmorOBP28

MLKVFIVTFFAFQLSAIARLQANGCVAVPFPKDKTIIIVEAMKSCIAKTGANPNFIDVIRSGKVSSEDEKFKEFYYCT
CNDTGFVNPDPGHKVKECIELFPKETQPLVEPVIKNCDKEEGVNKYDTLFLKFLKCFQETSPVRVALA

>BmorOBP29

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HVYCVLLSCKMIGKDGKLLKAAILGKLAARPAGRDTVTKVLEACAEQPGASPEDVAWNIFRCGYNRKAVLFDYM
PAGGASSGNTENHP

>BmorOBP30

MRSFVILLNYGLCCGQFMAEDYDYDIVTRDPDDLREKENEVRALRAFQADCAEDVQVKPDLVNLKSGDW
QTEDVSLKKWALCVLMKLGMLTAQGVFKMNEAMSKIPDMNDKIIAEKLIDDCLSLQATTPHDAAWNLIKCHH
QKDPEGNFSSLNIF

>BmorOBP31

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DGKFKKDALAKVPNAEDKLVKVEKLIDACLANKGNSPHQTAWNVVKCYHEKDPKHALFL

>BmorOBP32

MYSHKYLNDFTNIPEIILLLSSVALMSYGYNTKLFHSLGSEPSLSILYARDKKSVDKVTNECLMEMYPKNLYKYPLR
IDRNDIPCIHCVLKKFGIISNDGFINIKNYRRVQAIHRYDPRILISDVGETCAQNINGMNLHDVCKKAKVFND
CTQLYAI SYREPEDW

>BmorOBP33

MYAHDKLSDMIADQCLNEMYPRSKRLEIEESDEPCIIFCVLKKFGIMSPTGVINLEAYRKRVLPEQLAQRNSIN
DFGSACLES AEATQHKQDVCKKAKVFNECTHLYKILLK

>BmorOBP34

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SGQCFATCMLEQSDIINHGVNRDLLVHLAGLVNGKNSRVVRKLNVSRLCLDSISGMTDRCQLASTYNDCLNE
NMIEFAFPLDIAEEAVRKMPFHLIQPK

>BmorOBP35

GMSTHVLDFKRNMT ECLKEVQNNDRPIKRLSPKQESPIHGELIACVLKKNQVIQNGKVNKDNLMALVSKFH
AKETKLMKKLEKNLDRGINISVKNHDECSLASQLNDCTNDIMASSKQKILFNY

>BmorOBP36

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GKCFVACILKRNLIKNKLSQENLLEVNRAVYGGDSEVMSRLKTAILECSKIVEDIFEICEYASVFND CMHMKM
EHILDKITMERRMEALGQMSSNPDEWSEEEDEMLKLVKDEL

>BmorOBP37

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>BmorOBP38

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DETDKTPKCYIRCVLEKTEILSENGVLNPATAALVFAGERNGKPMSDL EEMAVACADRHEKCKCEKAYNFVKCL
MYMEIDKYEKKN

>BmorOBP39

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NKREVPFTHDEKRIAGCLLQCVRKVKAVDGGFPTLEGLVGLYSDGVNERGYFMAVLEASRECLMKNHDKFS
RTTPMDNGRNCVDFIFECISDRIGEYCGTSGL

>BmorOBP40

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KGVVDVKSFIKLLDKFTNSYPVWNSAKARVITCLRKSLIAYDGGCELNNILACTFDVLSENCPLNGNNQTC

>BmorOBP41

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KKKVSDYFEQFAKDNPDWSAAVQNFKTTCLSDSLKPPQGVDTNCPAYDIIHCALISFIKFAFPSQWSTSEQCVYPR
QYAGACPVCPERCFAPSVPNGSCNACLALLRTP

>BmorOBP42

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CSKQNCLLKKYNLLKNDETPDIEAIKSLDKYIEKNPSFKSSVEKAKECLREDLPGPPQICLANRMTLCIGTVLLME
CPDEKWNTTDDCKAFKDHMTECQKYFPK

>BmorOBP43

MKVCVLF AIFTVAQA AKATLKPISACCNIPELGNPEPLAEC SNPKLPGPCKDIQCVFEKSGFLTENKTLIKEAYKTH
LRQWAKEHEGWSVAVEKAISDCVDKDLRQYLEFPCSAYDVFTCTGIAMLK KCPNEHWTC

>BmorOBP44

MSRLVFF TILVVLQEFIIINLYFN FITEIDSCCVKKYPKLF DSEFITECYNTQRKANDKCERDMCVARKL NLLTEEDSI
NKDALLRFVEEGFKTEIDL VNAIKKKCFEEDISNIGKPEMCEVAKYKICITSRMAEDCPKWDSKGICSSAQQKVEN
FMKMLS

>SlitPBP1

MANARWRFV FVVYALYLSAVLGSQDLMVKMTKG FTRVDDCKTELNVGDHIMQDMYNYWRE DYQLINRD
MGCMLLCMAK KLDLMD DQTMHHGKTEDFAKSHGADDVAKKLVSVIHECEQQHAGIADDCMRVLEVA KCF
RTKIH ELKWAPSIEVIMEEVM TAV

>SlitPBP2

MAFCPSVTMSLRVALVVAASLLVVVQASQDVMKNLAVNFAKPLDDCKKEMDLPDSVTTDFYNFWKEGYELTN
RQTGCAILCLSSKLEILDQELNLHHGRAQEFAMKHGADEAMAKQIVDMIHTCAQSTPDEAADPCM KALNVAK
CFKLVHELNWAPSVELIVGEV LAEV

>SlitPBP3

MGSRNVFVALVVLTVGMREIEPSKDPMKYIASGFVKVLEECKHELNMNDHLIADLFHYWKLEYTLN RDTGCAI
ICMGKKL DLDASGRMHGNAQEF AKKHGAGDEVASQIVQIIHDCEKKHERDDDECLRVLEVA KCFRTGIHEL
NWQPNVEVIVSEVLTEI

>SlitGOBP1

MLLLLRALPLLA AVLPLRADVNVMKDVT LGFGQALDKCRQESQLTEEKMEEFFHFWREDFKFEHRELGC AIQC
MSRHFNLLTDSRMH HENTEQFIQSFN GEVLARQMVELIHACEKQHDHEEDHCWRILHVAECFKQACVQR
GIAPSMEIMITEFIMEAEAR

>SlitGOBP2

MTSKCCLLLV LMAAATSSVMGTAEVMSHVTAHFGKALEECREESGLSAEVLEEFQHFWR EDFEVVHRELGC AI
CMSNKFSL LQDDSRMHVNMHDYVKSPNGHVLSEKLVGLIHNCEKQFDSMTDDCERVV KVAACFKVDAKA
AGIAPEVAMIEAVMEKY

>SlitOBP1

MKEGNRYSHERRITNDSGDQLMVINATDDDYSYGSGNMGEKLLTSVPRPATPSNNINKNNTSRTKRNEPLL N
RPDS DQCLSQC VFANLQVVDSRGIPREAE LWNKVQSSVTSQQSRSALHDQIQACFQELQSEAEDNGCSYSNKL
ERCLMLRFSDR KVDGKGN AKKSSTEQTG

>SlitOBP2

MTRAQVKKTMGIIKNQCMPKNSVTTEE QVGRIEQGVFIEDRNVMCYVACIYKSLQVVKN DKLDMALITKQIDILY

PPELKEPVKKSVAACFHSQDNYSDFCEGVFYASKCLYEK

>SlitOBP3

MWMQALVLTATLATAAAVEMDEDMAELARMVRDNCAGETGVDVALVEKVNAGAELMPDDKLCYIKC
TMETAGMMADGEVDIEAVLALLPPSLAEHNAPALRACGTQRGADHCDTAFRTQQCWQNANKADYFLI

>SlitOBP4

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KTPKCFIRCVFENVGIVSEDKQFNPARAAVIFAGERNGKPMEDIADMTALCATDRQETPCDRSYKFLRCLMS
MEIEREYKS

>SlitOBP5

MSVVRCSLLVAIFCFVSVNAISGDEEAGIKDALRPFVQECADEFGITEEQFEEAKKASAADIDPCFMSFCFLKKA
EFFDSQGKFDVDSTMAFAKEHLTSEPAMKFVEAVGDECVKINDEDVSDGDKGCDRAKLLFECIAETKKKME

>SlitOBP6

MSKFTCLVLCVAVSLSGVHATAEKAAFIEAVKPYVQECSEKHGVTPEDIKSAKAAGNADGINSFLSCVYKKA
EVITEKGEYDADKALEKLLKFFVSNEDDYAKFANIGKKCASVNEKSVSDGEAGCERAALLTSCFLEHKSEISA

>SlitOBP7

MDQKRICLFVIAMFLASGSDAMSRQQLKNSGKMLKKNMKNKIGVTEDQIGSIDKGGKFIEDRKVMCYIACIYELT
NVIKNNKLNYEASIKQIDLMYPPDVKESAKAAVEKCKDVQKYYKDICEASFYAAKCMYEFKPEDFIFA

>SlitOBP8

MLLTKIVKFFILVATCEAMTMKQIKNTGKMMRKTCPKNNAEDEKIDPISDGVFIDEKEVKCYMACIMKMANT
IKNGKLNDAAMKQADLLFPDDIKEPAKEAITACRKVADAHKDICDASFHVTKCIYNHNPGIFYFP

>SlittoPBP1

MANARWRFVVFVYALYLSAVLGSQDLMAKMTKGFTRVVDCKTELNVGDHIMQDMYNYWREDYQLINRD
MGCMLLCMAKLLDMDQTMHHGKTEDFAKSHGADDDVAKKLVSVIHECEQQHTGIADDCMRVLEVAKCF
RTKIHCLKWAPSMEVIMEEVMTAV

>SlittoPBP2

MSLRVALVVAASLLVVVQASQDVMKNLAINFAKPLDDCKKEMDLPDSVTTDFYNFWKEGYELTNRQTGCAILC
LSSKLEILDQELNLHHGRAQEFAMKHGADEAMAKQIVDMIHTCAQSTPDVAADPCMKTLNVAKCFKLVHEL
NWAPSVELIVGEVLAEV

>SlittoPBP3

MGRNVFVALVVLTVAMRETEPSKDPMKYIASGFVKVLEECKHELMNDHLIADLFHYWKLEYTLLNRDTGCA
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NWQPNVEVIVSEVLTEI

>SlittoGOBP1

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MSRHFNLLTSSRMHHENTEQFIQSFNGEVLARQMVELIHACEKQHDHEDDHCWRILHVAECFKQACVQR
GIAPSMEMMITEFIMEAEAR

>SlittoGOBP2

MATVTSSVMGTAEVMSHVTAHFGKALEECREESGLSAEVLEEFQHFWRDDFEVVHRELGCAIICMSNKFSLQ
DDSRMHVNMHDYVKSFPNGHVLSEKLVGLIHNCEKQFDSMTDDCERVVKVAACFKVDAKAAGIAPEVAMI
EAVMEKY

>SlittoOBP1

MFKLCVFLALGFVACHGASNSNPGTPNANPGTYCGVTPDNIRCLNNPRVVTPEVSTKCGSQFTECEKMTCIF
RELKWSKRGAIKAKVRAYFDQYETEHPWAQAVQHVKAFCLASELRAQGVFLNCPAYDIMQCVLASFIKHAS
PSVWSTATDCAYPKAYAADCPCVPCSDCYSPIPYGSCNACYTQPRTV*

>SlittoOBP2

MVRKISGLLCLCVFGISFSDSAISADSESRNPPPTAPQKIERVITLCQDEIKLSILREALDVIKEEHTMPAQRRRD
KREVPFTHDEKRIAGCLLQCVYRKVKAVDGYGFPTLEGLVGLYSYDGVNERGYFMAVLEASRECLMKNHDKFSRT
VPMDNDRNCDISDFIFECISDRIGEYCGTSGL

>SlittoOBP3

MKSFVVICIVFVVGVCATEKGNKIASECIKESGVKSDVLAEAKKGNLGGDDPAFKEFTYCFKVKVIVGEDGKLNDR
VAIAKLPSGVDKAEAEKLLDSCSKTGKDAVETVYEIFKCYQHGTKSHIMFAS

>SlittoOBP4

MKTLLVFAACILVAQALTDEQKEKLLKHRTECLTETKVDEQLVNKLGKGDYKMDNEALKKYALCMMMKSSELMT
KDGFKFDVALAKVNPADKPTVEKLIDACLANKGNTPHQTAWNYVKCYHEKDPKHAIFL*

>SlittoOBP5

MTKVLFAIVLTMVTFVAVLSASTKEAMTTTMSDQVNSIDVDVLAVMDMCNDSYRIDPTYLQALNESGSFIDET
DKTPKCFIRCVFENVGIVSEGDGKQFNPARAAVIFAGERNKPMEDIADMTALCATDRQETPCDRSYKFLRCLM
SMEIEREYS*

>SlittoOBP6

ESKFGIIVKRTVIATAHTCMDHVNATAKDLHLRDEPPYPETSACIVKCLLEKVKYMRKQTN

>SlittoOBP7

MFTEALPLFVILVAVTHGGKNKPVFSDEIKEIIQTVHDECVAKTGVAEEDITNCENGIFKEDAKLKYMFCLEEAS
LVDDDDTVDYDMLVSLIPDEYYERTTKMIFACKHLDTDPKDRQRAFEVHKCSYEKDPDLYFLF

>SlittoOBP8

MFGSKIVFSLMIVSVCYGAVDIKKYFKVCDRNAIDVNDMAEAVRQGIATMINGIDELGVPPIDPYLQKDFRLE
YKNNQLAAKLTLNKIYVEGLKEAIVHDARLRADDDKFHLEVDLSGPRVSVRSYYGEGQFNALKIVAYGQVNTT
MTDLVYTWKLAGVPEKNGTETYIRIKDFYMRPDVGSVLTFRNDNPESRELTDLGRFANENWRMLYKEFLPY
AQANWNRIGVRVANKLFLKVPYDQLFPTSS

>SlittoOBP9

MCLVKYHVLVLCVILVGSYALNCRSSGGPKAEELKNIYKCLKMQEGKNSSKGNASQDWKEPRVQIQSNDNDG
SGNRGRGNKNNRNDMNGRDRDFGRDDYFNGREDFPQSDYEGGDMGQYNNNYSTTQSSRRYKRERRPS
NSGQRSQYNPNNHKISGYEDNFRSDERNTTDNNSKETDNKSCALHCFLENLEMTGEDGMPDRYLVTHAITK
DVKNEDLRDFLQESIEECFQILDNENTEDKCEFSKLLIDLSVRE

>SlittoOBP10

MKEGNRYSHERRITNDSGDQLMVINATDDDYSGYSGNMGEKLLTSVPRPATPSNNINKNNINRTKRNEPLL
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ERCLMLRFSRDKVDGKGNNAKKSSTEQTG

>SlittoOBP11

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>SlittoOBP12

MSVVRCSFLVALFCFVSVNAMSGDEEAGIKEALRPVQECADFEFGITEEQFEEAKKASAADIDPCFMSFLK
AEFFDSQKFDVDSTMAFAKEHILTSEPAMKFVEAVGDECVKINDEDVSDGDKGCDRAKLLFECIAETKKKME

>SlittoOBP13

MITSSLLVLTAVVQVLFAQQPVFESGPPPEWGPQRPARRRQFLPRIPKRCWVPPQRINVYNCCPIPTLYPDED
MQSCGFECTSGNTDQPQKPVFRPEGTCKEYCVMGKFDLLFANNSVDFVKFREYLDNWAESYPEFANAIRIAK
QECAQDGGPEVPPICEPKLFLCLTSTIFWNCKLRDGDGCAALQEHMNECKQYYTRQMEPTMKDIEVR*

>SlittoOBP14

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TNVIKNNKLNYEASIKQIDLMYPPDVKESAKAAVEKCKDVQKYYKDICEASFYAAKCMYEYKPEDFIFA

>SlittoOBP15

MFNFCVYSMTREQIKNSGKLIKTCSTAKNDLDEVDKDVQKGFIEKDFMCIACVYKMGQTVKGSTINHD
MMLRQVDMFMFPNDMKAPVKAIEHCRPVAKNYKDLCEASYWTAKCIYDFDPANFMFP*

>SlittoOBP16

MLAEELKDCFDGSGPKDPMKCEIDLCAKKGKGFATDDGKLDIKKFEEVITKDVGSDDKLLDEIKTNCINGDLNNY
GPPEFCDFIKIKHCVTLHMMNHCSEWSDDGNCKVVKELVGKCAKVI*

>SlittoOBP17

MRTFRLLCCILSIFIFDQSYGMTRQQLKNSGKLMKSCMPKNDVTEDEVGDIEKGFIESTRNVMCIACVYTM
SQVVKNNKLSYEAVIKQVDVMFPAEMRDAVKAATHCKETTKYKDLCESSYWTAKCMYDYDAQNFVFP*

>SlittoOBP18

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MACIMKMANTIKNGKLNDAAMKQADLLFPDDIKEPAKEAITACRQVADAHKDICDASHVTKCIYNNHNSIFY
FP*

>SlittoOBP19

MYSKICILLFISYTCLVTADSVSFIKCKWDDGKCAKESGQNVQKFAAGISEYNVGVSDPLHIEYVDASSPNMKLI
VTDVVVTGLRNCEVKKIQRFEDESKLIVKLLCAAELNGKYDMKQQLFVPIEGNGGLYSKVPKIQINAEVDLNTKQ
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AVPIEDLSL

>SlittoOBP20

MWVQALVLTATLVTLVAAVEMDEDMAEARMVRDNCAGETGVDVALVEQVNAGAELMPDDKLCYIKCT
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>SlittoOBP21

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LDTDPDKDRCQRAFEVHKCSYEKDPDLYFLILRREQLASRDCCVAISGIN*

>SlittoOBP22

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>SlittoOBP26

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ASKFGFDI

>SlittoOBP31

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VSKRKNTPQCNSLFMEMVKATPADNQTVTKEKAXXNYEALPPRXVSDR

>SlittoOBP25

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>SlittoOBP24

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>SlittoOBP28

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P

>SlittoOBP29

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>SlittoOBP30

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QNRIMPDKPEIKLCLFACVYKLAGMMNDQGELSVGEVNAISRKYLAEDPEKLQKSEEFTEACRSVNDAPVSDGT
RGCDRAALIFKCTIEKSPEFNFV

>SlittoOBP27

QLFNSGVVFCIIVAVFLKNASAITDELKAHIEAKFLTVAECIKEHPLTIEDLSAFKNRVFPDGENAGCFSACIFNKL
GLFDDKGTLSHLTALENAKKVFEDQGELESIEKFLTTCAKVNDEEVSVDGEGKGERAKLAYNCFIPKTIEQLGFDL

>SlittoOBP23

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>HarmPBP1

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>HarmPBP2

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LGCMIMCMTAKLDLIGDDQKMHHGKAEFAKSHGADDALAKQLVGLIHGCETQHQAIEDHCSRALEIAKCFRT
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>HarmPBP3

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WQPKVEVIVSEVLTEI*

>HarmGOBP1

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IAPSMELMMTEFIMEAEAR*

>HarmGOBP2

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>HarmOBP1

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>HarmOBP2

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>HarmOBP3

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>HarmOBP4

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>HarmOBP5

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>HarmOBP6

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>HarmOBP7

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>HarmOBP7.2

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GFFDDAGKFDKAEKISFAKEHITSETAIKFLGAGGECVKINDEDVSDGDKGCDRAKLLFDCLDLKKKMS*

>HarmOBP8

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>HarmOBP9

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DMKEK*

>HarmOBP9.2

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DMKEN*

>HarmOBP13

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>HarmOBP18

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>HarmOBP15

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QHQVEVIVPDVLTEI*

>HarmOBP16

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NKERTAFLDNFVKQYPSWEVAIDVAKTSCLRSSGLKPGVFLDCPAYDIIQCVFANLVKNALPSQWSSMSQCN
HAREFAAACPICPDACFAPLPIGTCNACSAARRSS*

>HarmOBP17

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>HarmOBP18a

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MFPAEMRDAVKAATSKDITKSKDLCEAYWTAKCMYDYDAENFVFP*

>HarmOBP19

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>HarmOBP20

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YTWKLDGVPEKNGTETYIRIKEFYMRPDVGSIVTNFKNDNPESRELTDLGTRFANENWRTLYREFLPYAQANW
NKIGTKVANKLFLKVPYDQLFPTSS*

>HarmOBP21

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DALYPPELKEPVKKAVSLCIHSQDNYNDLCEKVFHASKCLYEKDPASFIFP*

>HarmOBP22

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>SexiPBP1

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KIHCLKWAPNMEVIMEEVMTAV*

>SexiPBP2

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NRQTGCAILCLSSKLEILDQELNLHHGRAQEFAMKHGADETMAKQIVDMIHTCAQSTPDVAADPCMKTNLVA
KCFKLIHELNWAPSMELIVGEVLAEV*

>SexiPBP3

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DWQPKVEVIVSEVLTEI*

>SexiGOBP1

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GIAPSMEMMMTEFIMEAEAR*

>SexiGOBP2

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>SexiOBP1

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>SexiOBP2

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>SexiOBP3

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DIINDKGLYDAEAGIAKIEKLLPNNEFLDKISGVLKSCESANEKSVGDGDAGCERAVLVATCYLEHKTAVIA*

>SexiOBP4

MWNFLVFLAICSCVYGLTEELKMEFTKLIMKCNKDGKVDMTLVQLQNYVVPTKQTTKCVLACAYKAAEVM
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L*

>SexiOBP5

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>SexiOBP6

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>SexiOBP7

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MSMEIEREYKS*

>SexiABP1

MSVVRYSSFVALFCLVSVNAMSGDEEAGVRDALRPYVQECADYEGITEEQFEEAKKKASADDIDPCFMSCFLK
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D*

>SexiOBP10

MDRKRICLFVIAMFLASGSDAMSRQQLKNSGKMLKKNCMNKIGVTEQVGSIDKGFIEDRKVMCIACIYEL
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>SexiOBP8

MARRQQGAMFTETLPLFVILVAVTHGGKDKPVFSDEIKEIQTVHDECVAKTGVAEEDITNCENGIFKEDAKLKC
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>SexiOBP9

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>SexiOBP11

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LERCLMLRFSDRKVDGKGNPKKSSTEQT*

>AipsPBP1

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IHDLKWAPSMDLIMGEVLAEV*

>AipsPBP2

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MHELKWAPSMEVAMEEIMTAV*

>AipsPBP3

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WQPKVEVIVSEVFTDM*

>AipsGOBP1

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>AipsGOBP2

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>AipsOBP1

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AYAAACPICPEDCFSAQVFPFGSCNACYLPPRTP*

>AipsOBP2

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>AipsOBP3

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>AipsOBP4

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SE*

>AipsOBP5

MKYFVLFVALVAGIHANVTLPPSEQSEKALKTASECIKETGVSKEVLAEAKKGHIADDEGLKKFTLCFFKAGIVDN
DGKLNLETALAKLPPGVDKAEAKKVLGECQAKSGKTPQDTAFIYKCYHAGAKTHIALAGI*

>AipsOBP6-PG

QRENKGASLPLSVCCDIPELGDPKHLAKCSNPKLPGPCNDVQCVFEESGFLTDKNTLNKEAYRNHLKQWEEN
NKGWTVAVDKAIKEVDNDPRQHLDIPCKAYDVFTCTGIAMLKCPDSAWKC*

>AipsOBP7

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>AipsOBP8

MYLRSTNGGVRSFPLGESAYTTKIVEICSKETGLKQVPPEEKEIKFSQRKGLREFNDCYLAKTGVTSDGKLNIDE
ALEKLPPGFAKPFVEHCQANIILGYIEENVNDFSTCFHQEVQNHLLSFYGFENYWVMLVLGTSFDKTRFTTLFFD
KHDFWLAERAGFVNL*

>AipsOBP9

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SVEGVNEMTRRYSDDPKIKKSEQFTEACKSVNDVPVSDGTRGCDRAALIFKCTVEKSPDFDL*

>AipsOBP10

CYRLKTQYSVFHFRKIKRYVLRFSNYVFFISDPFGFKCKSADEECVLENAKAGVVPFVNGIPEFGVNLDPDFL
R*

>AipsOBP11

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DIEVKGLKNCEAKKITRDLKAMKLSVKFLCAVDFKGVYDMKGQLFVLPFIEGNGDLTAHVPKIQLNAEVDMMVDTK
GKDGGKHWGVKSWRHSFELKEKSNVKFENLFPDNEFLRKTTEELIASNGNDVIVEVGPFIKAVTAKVIESIKLFL
DEVPVEELAIDE*

>AipsOBP12

MYSGTIFLFSFILLIVSNVTFVSSQMTREQVKNSGKLVKKTCSAKNDLTEDEVKDVDKGKFIEEKKFMCYVACVYK
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*

>AipsOBP13

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>AipsOBP14

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TMSDLVYTWKLDGVPEKNGSEYVRIKEFYMRPDLSSIVTSFRNENPETRETELGARFANENWRTLYKEFLPYA
QANWNRIGVRIANKLFLKVPYDQLFPSSS*

>AipsOBP15

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>AipsOBP16

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DCFLKKTGFVTS DGKLNIDKTLEKLPSPFVKPIVEHCQANIALNYTTESVENFSSCYHDGILNHIFAATEVGIFPIQ
TWKFFVPGTSFADTILILN*

>AipsOBP17

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>AipsOBP18

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>AipsOBP19

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ASLVDDDGTVDYDMLVSLIPDEYERTTKMIFACKHLDTDPDKCQRAFEVHRCSYEKDPDLYFLF*

>AipsOBP20

MLVINATDYDIEGYGTGNMGEKLLTSVPRPASSNNINNDTSRTRRSEPLLKPDLDQCLSQCVFANLQVDS
RGIPREAELWNKVQSSVTSQQRSALHDQIRACFQELQSEAEDNGCSYSNKLRLMLRFSRDRKVEGKASTPKP
ASTEQS*

>AipsOBP21

MLKFSVVCLYFVAAVNFVNVHCISEDEKKAFFIEAMKPMVEECGSDCGLTEEDYKHKHSGEDMDPCFKKMM
QKLGFLDEDGKYNRKQLHESISEYTGDKDEAKRVQEQLDSCFDANGDNDGDDEESQMKRVDVLFKCLKEIKE*

>AipsOBP22

MSMWFRAMVVVGALAAARCGVVMDEMAELARMVRESCVDETGADVKLVEAVNGGADLMEDDKLKYI
KCTMETAGMMSDGEVDIEAVMALLPPEMAEHNGPALKSCGTQRGADDCDTAWKTQVCWQNANKAEYFLI*

>AipsOBP23

MSKFTYLVLCFVAVSRVYANEDERAFAFHEAAKPILVECSKENGVSFDKLLAAKEAGSADGIDPCFFSVCVFKKTGVF

NSKGFDFLDNSLTKLKEFVSNDEYAKVAEVGKKCESVNEKDVSDGEAGCERASLLTACFLEHRAEIPV*

>AipsOBP24

MAKLLLAMILVTMFTALTMSATTKDAGTKEAIMTTTTVANQDSSIDSNDVDVLAVMNVNENEFRIEMSYIQALN
ESGSFVDETDKTPKCFIRCVFENVGIVSEDGRMFNPARAAVIFAGERNGKPMDDIADMTALCAADRKETPCD
RSYQFLRCLMSMEIEREYKS*

>AipsOBP25

SRKLREAMRPIIEQCSKEHGVTDADIQASKDSNNAASLPDCFNHCLFEKSGFIDKNGRYDRDSGLKNLSKYLKD
VNQYNKVVEVTKECASVEEKPATGCELGTRLTACLLDHQTSILI*

>AipsOBP26

MSKFTCIVLFFVAASLTKVTQAVSEEEKAVAREAMAPILAECSKAEGVSDIEDIEEAKKNPSVDAVNCSFIRCVMR
KTDALNEKGLFSDAALAKIRPFVKSDDEFKFEIGKACMSVNDKEVSDGEAGCDRAKLLACFLEHKAEMLY
*

>AipsOBP27

DSAISADAESRCRNPPPTAPQKIERVITLCQDEIKLSILREALDVIKEEHTMPAQRRRDKREVPFTHDEKRIAGCLLQ
CVYRKVKAVDGYGFPTLEGLVGLYSDGVNERGYFMAVLEASRECLMKNHDKFSRTMPMDNGRNCDSVDFIFE
CISDRIGEYCGTSGL*

>AipsOBP28

MTHIFSSFIPYMITVSMFSPVSVKIIISPTVPVTVVSSSVIITFMFDMYRLVLSIVAVTTVVADTDLQECRRLVHPH
SMRCKKSADAKEKMMKNDDLKECFDLPKDPVKEHELMAKKGITTSDDKLDKAKFEEVTKDIDDKDLVA
DIKANCINGDLTKYPPDFCFVVKMRHCMSMQILNHCTEWNDFGDCPQLKSIIGDCVKLVAA*

>SlitOBP9

MCLVKYHVLVLCVILVGSYALNCRSSGGPKEAELKNYKCKLKMQEGKNSSKGNSAQDWKEPRVQIQRNDWD
RGRVGSKENKNSRDDSRSKDKKGDGMRDNRNDMMSSRRDDMMSRGDERNDNRKHRTDDRMGNDN
DRSGNRGRGNKNNRNDMNGGRDDRFGRDDYFNGREDFPQSDYEGGDMGQYNNNNYSTTQSSRRYKRER
RPSNSGQRSQYNPNNHKISGYEDNFRSDERNTDNNSSKETDNKSCALHCFLENLEMTGEDGMPDRYLVTH
AITKDVKNEDLRDFLQESIEECFQILDNENTEDKCEFSKNLLICLSEKGRANCDDWKDDLTF*

>SlitOBP10

MVRKISGLLCCLVFGISFSDSAISADSESRCRNPPPTAPQKIERVITLCQDEIKLSILREALDVIKEEHTMPAQRRR
DKREVPFTHDEKRIAGCLLQCVYRKVKAVDGYGFPTLEGLVGLYSDGVNERGYFMAVLEASRECLMKNHDKFS
RTVPMMDNGRNCDSVDFIFECISDRIGEYCGTSGL*

>SlitOBP11

MKSFVVCIVFVVGVCATEKGNKIASCEKESGVKSDVLAEAKKGNLGDPAFKEFTYCFKVKVIGGEDGKLN
DVAIAKLPSGVDKAEAEKLLDSCSKTKGDAVETVYEIFKCYQHGTKSHIMFAS*

>SlitOBP12

MKTLFVFAACILLAQALTDEQKEKLRTECLTETKVDEELVNKLGKGDYKMDNEALKKYALCMMMSELM
TKDGKFKKDALAKVNPADKPTVEKLIDACLANKGNTPHQTAWNYVKCYHEKDPKHAIFL*

>SlitOBP13

MITSCLLVLSAVVQVLLAKQPVFESGPPEPWGPPERTSHPGQFQPRVPKRCWVPPQRINVYNCCPIPTLYPDE
DMQSCGFELSENKPKPVYRPEGTCKEGYCVMGKFDLLLANNVSDYVKFREYLDNWAESYPEFANAIIHIAKE
ECAQDGGPEVPPICEPDKLFLCLTSTIFWNCKLRDGECAALQEHMNECKQYYTRVMAPTIKDFEVR*

>SlitOBP14

MVKVTYIALFVVAVSLSSVQADDKNSKPEFNLDITTFQCAQKFDISEEQFSKAIMTFDASLLAPCFWS

>SlitOBP15

MYSINCFIVSILVIMFDNCFVYSMTREQIKNSGKLIKKTCSAKNDLTEDEVKDVDKGKFIKKDFMCIACVYK

MGQSVKGSTINHDMMLRQVDMMPNDMKAPVKS AIEHCRPVAKNYKDLCEASYWTAKCIYDFDPANFMF
P*

>SlitOBP16

MYRFVILSIVLVSALADDIDIRECGRIFHPPPHGCCKANNAVKNKDM LAEELKDCFDGSGPKDPMKCEIDL CIAK
KKG FATDDGKLDIKKFEEVITKEVGS DKDLLDEIKTNCINGDLNNYGPPEFCDFMKIKHCVTLHMMNHCSEWS
DDGNCKVVKELVGKCAKVI*

>SlitOBP17

MKTRFLLCCILSIFLFFDQSYGMTRQQLKNSGKLMKKSCMPKNDVTEDEVGDIEKGKFIETRNVMCYIACVYT
MSQVVKNNKLSYEAVIKQVDVMFPAEMRDAVKAATHCKETTKKYKDLCESSYWTAKCMYDYDAQNFVFP
*

>SlitOBP18

MFKLCVFLALGFVACHGAPNSSPGTPNANPGTYCGVTPDNIYRCLNNPRVVTPEVSTKCGSQFTECEKMT CIF
RELKWSKRG AIDKAKV RAYFDQYETEHP EWAQAVQHVKAFCLASELRAQGVFLNCPAYDIMQCVLASFIKHA
SPSVWSTATDCAYPKAYAADCPVCPSPDCYSPQIPFGSCNACYTQPRTV*

>SlitOBP19

MFRRLLLLFSIIYISACNGQTEAPEKNRMMGIDAVHDNNVKIDKDTIITRNLKLEKRSRGPKSVSNKNEDQIEPD
WSYANFPKEVSEHVEKFKNMTECLKEVQTS DKRPVKRLSPKMESPVHGECL IACVLKRNQVIINGKVNKDNL I
ALVSKFYKDRMLMKLEKNLDRCIEMSVRAQDDCALALVLNDCTNDLMASNKHKIMVNY*

>SlitOBP20

MEKILIFTITLSGFAHARISV MYAHDKLSDLVAQQCLSEMYPKNKRIEIQESDEPCIIFCVLKKFGIISASGVINLDI
YRKRQVIAHQLDQKTSIMDYGGSCMENA EATQHKQDVCKKAKVFNDCTHLYRILLM*

>SlitOBP21

MARRQRGAMFTEALPLFVILVAVTHGGKNKPVFSDEIKEIQTVHDECVAKTGVAEEDITNCENGIFKEDAKLK
CYMFCLLEEASLVDDDDTVDYDMLVSLIPDEYERTTKMIFACKHLDTDPDKDRCQRAFEVHKCSYEKDPDLYFL
F*

>SlitOBP22

MSKFTCIILCVVAASLTKVSHA AVTEEEKEAFREAMAPIIAECSEEHGVSEADIKAAKESASADNIKPCFLGCVMK
KIEVLDAKGLYDAETGLGKLRKFVKDDDEF AKFEDI AKKCLKVND ESVSDGEAGCDRAKLV LGCFIEHKVEMPF*

>SlitOBP23

MAKFSCLVLCVVAASLSI HVASGESLRESLRPVIVACSQEHGVTDAEIQA AKDAGSPASIKPCFIACVFKAGFI
NEQGQLDLETGLKNLRQFVKDDEYK KLEEVAKKCSQVKDKAVSDGAAGCERGVLLAGCFLEHKTSIII*

>SlitOBP24

CVYKTEFLNSKGEYDVDTALAKLKKYISNDDDYAKLSQVGKDCASVNSKPVGDGEAGCERGVLLTQCFLDHK

>SlitOBP25

MAKVTCIVL FVVGVSLSSIQADDGKNESEVEIDVNQIIDDCEIYHIPRRLFLAAAETGSTHALTPCFWSCCFKGV
GVLNSEGQYDIDATLDLSKKIFTDHEYEKVEIIVKKCESVNGAPVSNNGNIECEKSVLLADCLFDNAKHFPMFG
VDY*

>SlitOBP26

CFLACMMKQIGVMDDNGMVQKETALEMAKAVFDDPEELKAIEDYLHSCSHINTESVSDGAAGCERAMLAYK
CMTENASKFGFDI*

>SlitOBP27

MYKFVILCSIFVAASNADVAQTLTKRET KASLPLSVCCDIPELADEFQLAKCSPPPGPCEDVQCIFEVSGFLTD
RNTLNKAAYRSHLQKWEKNHPGWTD SIYKAITDCVDNDPRQHLEVPCKAYDVFTCTGIAM LKKCPDTAWKC
*

>SlitOBP28

MIVRFLLCLYIVEFYGAHARTDQEIKAWFFREGMDCNIEHPISPKEMLELKENKIPDTNNAKCFVACVFKKTGM
LDSKGMFDAENSIAMTQKDFANDPNRLESSKLLACKKVNDEAVSDGEGKGCERSVLLHKCFVETAPQLGIKLP
*

>SlitOBP29

MWNLLVVFLAICSCVYARRRSGAEINGLTEELKMEFTKLIMKCNKDGEVDMTELVQLQNYVVPTKQSTKCV
LACAYKAAEVMNAKGEYDIDHAYKVAEMMKNGDEKRLVNAKKMADLCVKVNELSVSDGEGKCDRAAMIFK
CTVENAPKFGFKL*

>SlitOBP30

ALSMDDLKQKYVDNILECSKQYPIDRADAEQLQNRIMPDKKEPIKCLFACVYKLAGMMNDQG

>SlitOBP31

RNEHREKEKMNKLTNIFASILFVLSFAFYLTISFTPLTKDEQMERYNKMTENVEPFRKNLTECARQVKASMAD
VENFMKRIPQASLQGKCFVACILKRNSIIKNNKISKEHLLEANRA

>SlitOBP32

RIDRNDIPCIHCVLKKFGIMTNDGYINIKNYRRVQAIHRYDPRILISDVGETCAQNINGMNLHDVCKKAKVF
NDCTQLYAVSYRDPDEWK*

>SlitOBP33

MTCSQALALLALVAISQQATTGCKNCIMLGKEEKAMFRAHSDACVAASRVEPRLVDAMLAGELLDEPALRKH
VYCVLLKCKLISKDGKQLQKAAVLGKMAARPDKNATKVLSCADQTGDTPEDLAWNLFRCGYDKKALLFDYM
PTNVASETDNNS*