

Table A – Matrix of CLUSTALW scores from pairwise sequence alignment.
Boxes where >30% sequence identity was detected by CLUSTALW alignment
are colored in orange.

	At1g30110	At3g10620	At5g06340	At1g12880	At1g14860	At1g73540	At1g18300	At2g01670	At3g12600	At3g26690	At1g28960	At2g33980	At5g45940
At1g30110	NA												
At3g10620	51	N/A											
At5g06340	48	51	N/A										
At1g12880	16	9	10	N/A									
At1g14860	17	13	12	47	N/A								
At1g73540	13	9	19	40	44	N/A							
At1g18300	14	7	8	38	47	73	N/A						
At2g01670	17	8	16	40	78	46	40	N/A					
At3g12600	7	5	15	44	42	38	36	45	N/A				
At3g26690	16	6	9	76	46	38	38	39	45	N/A			
At1g28960	17	8	6	10	15	10	12	5	8	6	N/A		
At2g33980	16	8	8	15	12	5	14	8	12	14	70	N/A	
At5g45940	11	6	14	11	10	18	11	10	10	7	50	48	N/A
At2g04430	13	6	4	7	10	13	9	7	9	10	5	10	7
At2g04450	15	13	10	15	17	22	15	7	10	11	8	12	8
At4g12720	13	10	7	9	15	12	12	7	12	8	4	4	4
At5g47240	14	16	9	8	7	16	10	10	11	9	8	13	8
At5g47650	15	12	13	7	11	6	10	8	11	4	4	6	12
At1g68760	18	12	14	9	17	12	10	17	17	10	12	21	14
At1g79690	16	7	8	11	15	6	9	9	8	4	7	10	15
At2g42070	12	10	9	7	16	9	11	9	12	5	5	11	6
At4g11980	12	13	12	6	10	5	6	9	18	10	10	9	8
At5g13570	16	13	7	16	10	15	16	7	11	12	8	12	10
At5g20070	18	8	9	10	12	16	17	8	9	8	5	4	11
At4g25440	9	16	5	7	12	7	1	10	6	8	3	5	6

	At2g04430	At2g04450	At4g12720	At5g47240	At5g47650	At1g68760	At1g79690	At2g42070	At4g11980	At5g13570	At5g20070	At4g25440
At1g30110												
At3g10620												
At5g06340												
At1g12880												
At1g14860												
At1g73540												
At1g18300												
At2g01670												
At3g12600												
At3g26690												
At1g28960												
At2g33980												
At5g45940												
At2g04430	N/A											
At2g04450	58	N/A										
At4g12720	54	61	N/A									
At5g47240	44	44	41	N/A								
At5g47650	44	47	48	48	N/A							
At1g68760	14	15	19	14	20	N/A						
At1g79690	15	14	8	8	13	15	N/A					
At2g42070	6	5	7	8	14	17	13	N/A				
At4g11980	10	9	9	11	13	13	6	3	N/A			
At5g13570	6	10	10	6	12	16	13	12	4	N/A		
At5g20070	7	13	7	11	10	18	8	18	5	9	N/A	
At4g25440	9	7	9	3	6	6	3	7	5	1	4	N/A

Figure A – Sequence alignment of Ap_nA hydrolases from plants

The protein products of the *Arabidopsis* genes At1g30110, At3g10620 and At5g06340 and their counterparts from *Lupinus angustifolius* (gi:1888557), *Oryza sativa* (gi:50929793) and *Hordeum vulgare* (gi:2564253) are aligned using the CLUSTAL W algorithm. Motif 4 present only in the At1g30110 gene product is underlined in red. The N-terminal extensions forming putative preprotein sequences in all proteins excluding the At1g30110 gene product are underlined in green.

Lupinus 1...MALCR·LVD·····SPTNHFRRKYP·SK·····FLKFSLSLAFR·Y·····CHSS 39
 At3g10620 1...MALYRPLLLHH·····PTSPSVTFFLRNYP·SK·····PIKFSLSLPLHPRGRKSRVSS·SS·····ARCOSS 65
 Hordeum 1...MTVAARCL·····ILTPTLSSSS·\$AAAA·····VLRIPRVAR·RPLS·CSASP·····LAVFAS 49
 Oryza 1...NWVSVARLPP·····ILVSPIRERT·TATR·····RLPSSALRLTEPLSSSCASP·····LAVVAS 54
 At5g06340 1QFNNDIADENSINEPPTETRAPHSPHATEHYDRLASEL·I·KEPTEINATGMHFATG·TKMAVVASGF·IGKSAISVHLDFSSSEPKVKSQKQF·SVSSGKQRLVLSVALSSPART 112
 At1g30110 ······

Lupinus 40 MDSPPEGYRRNVG·I·CLMN·NDKHI·FAASRLD·I·PDAWQPPDGG·I·DEGEDP·RNAAI·RELREETGY·TSAEVI·AEV·PYWL·TYDF·PPK·VRE·E·K·L·N·I·D·M·G·\$QNYGDAQDWFL·E·F·K·F·T·G 149
 At3g10620 58 MESPPEGYRRNVGVCLMN·SSKHI·FTASRLD·I·PSAWQPPDGG·I·DEGEDP·RVAVIRELKEETGY·HSAE·ILAE·APHWI·TYDF·PPD·VRE·E·K·L·K·V·R·M·G·\$QNYGDAQDWFL·L·K·F·T·G 185
 Hordeum 50 MDSPPEGYRRNVG·I·CLADP·SLTHI·FSASRLD·I·PTAWQPPDGG·I·DQGE·EP·RAAAI·RELREETGY·RSAE·I·VAE·AP·N·W·L·TYDF·PAD·V·K·D·L·N·R·M·G·\$QNYGDAQDWFL·F·R·L·T·G 180
 Oryza 55 METPPENYRTNVG·I·CLADP·SLTHI·FTASRL·DIANTWQPPDGG·I·DAGEDP·REAAI·RELREETGY·TSAEMVAE·V·P·V·W·L·TYDF·P·VD·V·K·E·L·N·R·M·G·\$QNYGDAQDWFL·F·R·F·T·G 188
 At5g06340 113 VESP·PV·G·Y·R·K·N·V·G·I·C·L·V·S·P·Q·R·K·I·F·T·A·S·K·I·H·I·P·D·I·W·Q·P·P·D·G·G·A·D·E·G·E·D·L·R·N·A·A·F·R·E·L·R·E·E·T·G·Y·T·S·A·E·F·I·A·E·I·P·N·W·L·T·Y·D·F·P·R·E·V·K·D·L·N·R·K·W·R·\$QNYGDAQDWFL·F·K·F·T·G 222
 At1g30110 1 MENTPPGYRPNVGVCLIN·\$DNLV·F·V·A·S·E·L·N·V·P·G·A·W·Q·P·P·D·G·G·I·E·D·G·E·D·P·K·S·A·M·R·E·L·D·E·E·T·G·Y·V·S·A·E·I·V·E·V·P·N·W·L·T·Y·D·F·P·P·A·V·H·A·V·V·R·L·M·G·\$ENHGDAQDWFL·V·R·L·R·N·D 110

Lupinus 150 DDE···I·NLLGDG·G·E·K·P·E·F·G·E·V·S·W·I·T·P·E·D·L·I·D·L·I·V·E·F·K·K·P·V·Y·K·E·V·S·I·V·F·A·P·H·L····· 189
 At3g10620 188 DEE···I·NLLGDG·G·E·K·P·E·F·G·E·V·S·W·I·T·P·D·Q·V·E·N·A·V·E·F·K·K·P·V·Y·K·E·V·S·A·F·A·S·H·L·D····· 218
 Hordeum 181 DDE···I·NLMGDG·G·E·K·P·E·F·S·E·W·A·M·I·T·P·K·I·D·V·I·E·K·A·V·D·F·K·K·P·V·Y·E·E·I·L·K·H·F·A·P·Y·L·Q·S·D·P·A·A·S·S····· 218
 Oryza 187 EDE···V·N·L·N·G·D·G·S·E·R·P·E·F·C·E·V·T·M·I·T·P·D·Q·V·I·E·K·A·V·E·F·K·K·P·V·Y·E·A·L·K·H·F·A·P·Y·L·Q·S·D·P·A·T·T·S·S····· 228
 At5g06340 223 EEE···I·NLLGDG·G·A·K·P·E·F·K·V·S·M·L·P·E·D·V·I·E·H·A·V·T·F·K·R·P·V·Y·E·H·V·I·N·Q·F·N·P·Y·F·V·D·E·E·K·D·S·I·M·N·S·S·K·D· 285
 At1g30110 111 EDEKEI·N·L·A·N·N·A·E·A·D·S·E·F·A·E·W·K·W·A·K·P·E·E·V·E·Q·A·V·D·Y·K·R·P·T·Y·E·E·V·I·K·T·F·G·S·F·L·N·D·T·G·R·A·K·K·S·A·K·W 175

