

Supplement Fig. S1: Alignments of chlorviral, *Arabidopsis thaliana* (At), and *Pseudomonas aeruginosa* (Pa) AIH and CPA sequences. (A) AIH. (B) CPA.

**A**

AtAIH	.MEESRESEAEHGYYMPAEWDSHAQTWIGWPERQDNWRHNALPAQRVAFADVAKAISKKEFVTVCASPAQWENARKQLP.FDIRVVEMSMNDSWFRDSCPTFTIVRKRFPVKLSSLNRNTAGI	118
PaAIH	.MSNPTSIPRADGRMPAEWEPHEQTMVWVPEREDNWRNGGKPAQAAFAAVAKAIAARFEPVTVCASAGQYENARARLDGNIIRVVEISDDAVWRDTGPTFVHDDK.....GDVRGV	111
PBCV-1 AIH	.....MTPKQTFGYMPGFEFQHKRTWMIFPERNDNWRQEAVPAQKTITNLARKISEFEVIMIVSRDHLNKAMDLLHDSGVKMTADSDDCWARDTCATFITNGK.....NVKAI	105
NY-2A AIH	.....MTPKQTFGYMPGFEFQHKRTWMIFPERNDNWRQEAVPAQKTITNLARKISEFEVIMIVSRDHLNKAMELLHDSGVKMTADSDDCWARDTCATFITNGK.....NVKAI	105
AR158 AIH	.....MTPKQTFGYMPGFEFQHKRTWMIFPERNDNWRQEAVPAQKTITNLARKISEFEVIMIVSRDHLNKAMELLHDSGVKMTADSDDCWARDTCATFITNGK.....NVKAI	105
MT325 AIH	MFCICIMFPESEDGRMPGFEFQKHSQTWMIFPERNDNWRDFAAQEQLCALANLVGKYEKVIMLVPRRYVRRALGLVS.TDVSIIIVKLTDDAWWRDTGATFVFNNGK.....EVRGV	110
Consensus	p g mp e h tw p r dnwr aq a e v a d w rd g f	

AtAIH	DWNFNWGGANDGQYNDWSEDLIVSRKILALERTIPRFQHS.MILEGGSIHVDGEGTQLVTEECLLNKNRNPMSKEQTEEBLKKYLGVQSFITWLPRLGLYCDDETNGHIDNMCCFARPGVV	237
PaAIH	DWGFNAWGGFEGGLYFPWQRDDQVARKILLETERRARYRTLDFVLEGGSIHVDGEGTLITTEECLLNHNRNPHLSQAEIERILRDYLAVESIILWLPNGLYND.ETDGHVDNFCYARPGEV	230
PBCV-1 AIH	SWDFNSWGGNFDGLYTTWKNDQKIAEYMARISNPIIKTPGFVLEGGSIHVDGEGTLITTTKECLLSIICRNPTMSQODIEYYLKEYLNVEKIIWLEYGVADD.ETNGHVDNMACFSRPGEV	224
NY-2A AIH	SWDFNSWGGNFDGLYTTWKNDQKIAEYMARISNPIIKTPGFVLEGGSIHVDGEGTLITTTKECLLSACRNPTMSQODIEYYLKEYLNVEKIIWLEYGVADD.ETNGHVDNMACFSRPGEV	224
AR158 AIH	SWDFNSWGGNFDGLYTTWKNDQKIAEYMARISNPIIKTPGFVLEGGSIHVDGEGTLITTTKECLLSACRNPTMSQODIEYYLKEYLNVEKIIWLEYGVADD.ETNGHVDNMACFSRPGEV	224
MT325 AIH	SDFNAWGGDIDGLYQSWDIDAQVGRVYMKARGFKMYTTPGFVLEGGSIHVDGEGTLITTEECLLSACRNPHITRDEIETNLKMYLGVKIVWLEYGTVDD.ETNGHVDNMACFARPGEV	229
Consensus	fn wgg g y w d leggs hvdgegt t e cll rnp i e l y l v w l g d t g h d n c r p g v	

AtAIH	ILSWTDDETDPCYERSVEALSIVLSNSIDARGRKIQVIRKLYIPEPLYMTEEBSSGITQDGEAIPRLAGTRIAASYVNFYIANGGIIAPQFGDPIRDKEAIRVLSDFPHHSVVGIIENAREI	357
PaAIH	LLAWTDDQDDPNYLRCQAALRVLEESRDAKGRKLVVHKMIPGELYATQEECDGVDIVEGSCPRDPSIIRLACSYNFLTIVNCGIIPAFSDDPK.DAEARAILQRVFFHEHVMVP.GREI	348
PBCV-1 AIH	ILAWTDDPKHPCYERSKSNAYKLLTKERDAKGRKLIHKIHIPSDMFITEEBAIGVVNSGLAVPRRAGDRIAASYVNFVMPNCAIIFPTFGDEKYDALAHKKFEEIFPEREIVGFY.SREI	343
NY-2A AIH	ILAWTDDPKHPCYERSKSNAYKLLTKERDAKGRKLIHKIHIPSDMFITEEBAAGVNTGLAVPRRAGDRFAASYVNFIMPNGAIIFFPTFGDEKYDALAHKKFEEIFPEREIVGFY.SREI	343
AR158 AIH	ILAWTDDPKHPCYERSKSNAYKLLTKERDAKGRKLIHKIHIPSDMFITEEBAAGVNTGLAVPRRAGDRFAASYVNFIMPNGAIIFFPTFGDEKYDALAHKKFEEIFPEREIVGFY.SREI	343
MT325 AIH	MLAWTDDKPKHPCYERSKSNAYEVLKTTLDKAKGRKRVVHKIHIPKDMYITHTIANGVVGQ..HTIPRIVGDRFAASYVNFIMPNGAIIFFPTFGDDEYDSLAKKKFEEIFPEREIVGFY.SREI	346
Consensus	l w t d d p y r a l d a r k k i p t e g p r r a s y n f n g i i p f d d a f p r e	

AtAIH	VLGGNTHCITQQQPAEPTSVAENGH	383
PaAIH	LLGGNTHCITQQQPAPRKA.....	368
PBCV-1 AIH	LLGGNTHCITQQQPV.....	359
NY-2A AIH	LLGGNTHCITQQQPV.....	359
AR158 AIH	LLGGNTHCITQQQPV.....	359
MT325 AIH	LLGGNTHCITQQQPSV.....	363
Consensus	l ggn hc tqqp	

**B**

AtCPA	METEGRREVVVSSLOFACSDDISINVAEAERLVREAFAKGANITLQELFEGYYFCQAREDFFKRAKFKYKNHPTIARMQKLAKELGVVIVPSFFFEANTAHYNSIATIDADGTDLCIY	120
PaCPA	.....MTRNVTVAAITQMACSWDRPANLARAERLVRQAARGAQITLQELFETPYFCQKPNPDYLCIATITVEENAAIAHFQALARELQVVLPTISFFFERAQRARFNSIAVIDADGGNLCVY	115
PBCV-1 CPA	.....MSRKVTIATITQFACTHDIFGNTERAEMLVRNAAANGAQVIVLQELFATKYFCQTCSPQYFKFADFPADDSVIVVEIFSKLAKELGVVIVPIEPPFEKDGNNYNSVAVADADGSIVGVY	115
NY-2A CPA	.....MTRKVTIATITQFACTHDIFGNTERAEMLVRNAAANGAQVIVLQELFATKYFCQTCSPQYFKLADFPADDSVIVVEIFSKLAKELGVVIVPIEPPFEKDGNNYNSVAVADADGSIVGVY	115
AR158 CPA	.....MTRKVTIATITQFECTIKDVMGNLERAERMIRNAAANGAQVIVLQELFEMMYICQICQYPKFKKHAEPVKNKSGTVHMFNLAKELCVVIVPIEPPFEKDGNNYNSVAVADADGSIVGVY	115
MT325 CPA	.....MKITITAAALQFSVSKNAEDNLRTAERMVRNAAANGANVIVLPELFCARYFCQEQKQKWFALAEITVEESHVVRSHAKLAGELGVVIVPIEPPFERDRNNYNSVAVADADGSIIIGTY	113
FR483 CPA	.....MKITITAAALQFSVSKNAEDNLRTAERMVRNAAANGANVIVLPELFCARYFCQEQKQKWFALAEITVEESHVVRSHAKLAGELGVVIVPIEPPFERDRNNYNSVAVADADGSIIIGTY	113
Consensus	q n ae r a a g a i e l f y c q a l a e l v v p f f e n s a d a d g g y	

AtCPA	RKSHIPDGPYQEKFYFNPGLDIGFKVFOTKFAKIGVAICWDQWFEEAARAVLQGAELLFYPTAIGSEPEQDQGLDSRDHWRRVMQGHAGANVPLVASNRIGKEIIETEHGPSQITIFVGT	240
PaCPA	RKSHIPDGPYHEKYYFNPGLDIGFKVQTRYARIGVGCWDQWFEEASARSMALLGAELLFYPTAIGSEPHDASISSRDHWQRVQGHAGANLPLVASNRIGRE...EQDGYDITIFVGS	231
PBCV-1 CPA	RKTHIPQSKCYEEKFYFTPSNPNYEVFETKFGKMGVLCWDQWFSEAAKCLALEGADFIVYPTAIGSEPEFPNGESYLHWARTITIGHAAATGVPVIVANRIGRE...RFGTKIDFFCG	231
NY-2A CPA	RKTHIPQSKCYEEKFYFTPSNPNYEVFETKYGKLGVLICWDQWFSEAAKCLALEGADFIVYPTAIGSEPEFPNGESYLHWARTITIGHAAATGVPVIVANRIGRE...RFGTKIDFFCG	231
AR158 CPA	RKTHIPQSECYEEKFYFTPSNPNYRVFETKFGKMGVLCWDQWFSEAAKCLALEGADFIVYPTAIGTEPEFPDGETYLHWARTITIGHAAATGVPVIVANRIGHE...ELGSEIDFYCG	231
MT325 CPA	RKTHIPQGDICYNEKYFTPGNNGYGVFNTKFGVMGVLICWDQWNEEAARCLALDGAADFIVYPTAIGSEPAFPDGESEYMHWARTIQGSAASGIPVIVANRIGRE...RFGTKIDFYCG	229
FR483 CPA	RKTHIPQGDICYNEKYFTPGNNGYGVFNTKFGVMGVLICWDQWNEEAARCLALDGAADFIVYPTAIGSEPAFPDGESEYMHWARTIQGSAASGIPVIVANRIGRE...RFGTKIDFYCG	229
Consensus	rk hip y ek yf p v t gv icwdqw e a l ga yptaig ep hw r g a p nr ge i f g	

AtCPA	SFIADGTCGAVVITQVGGVPEKNGGVDPEPVDLKGYTKYTFDLDALLENHRAFVWGLYRDRRPELYSRLV.....AVLVAQFDLDMIKSKRQSWCVFRDRRPDLVKVLTMDGNL..	299
PaCPA	SFIADPFCGKVEELNRTEF.....GILVHTFDLDALETRSAWCVFRDRRPDLVGLKTLTDGSLES	292
PBCV-1 CPA	SFIADGTCGAVVITQVGGVPEKNGGVDPEPVDLKGYTKYTFDLDALLENHRAFVWGLYRDRRPELYSRLV.....	298
NY-2A CPA	SFIADGTCGAVVITQVGGVPEKNGGVDPEPVDLKGYTKYTFDLDALLENHRAFVWGLYRDRRPELYSRLV.....	298
AR158 CPA	SFIADGTCGAVVITQVGGVPEKNGGVDPEPVDLKGYTKYTFDLDALLENHRAFVWGLYRDRRPELYSRLV.....	299
MT325 CPA	SFIATNNKCEVVAQVGGEPQKNGGVDPEPVMKSHIKITITDTEENDMFRAWGLYRDRRPELYNRLVI.....	296
FR483 CPA	SFIATNNKCEVVAQVGGEPQKNGGVDPEPVMKSHIKITITDTEENDMFRAWGLYRDRRPELYNRLVI.....	296
Consensus	sf g v d r wg rdr rp ly l	