Supporting Information Table 1. The predicted H-2k^{b}–restricted octameric epitopes and H-2D^{b}–restricted nonameric epitopes, derived from 81 MHV68 open reading frames, are highlighted in gray. The N-terminal residue of each individual epitope is highlighted in black to enable the discrimination of overlapping sequences. Epitopes identified to give an CD8^{+} T cells response in B6 mice are highlighted in red.

Locus Tag	Protein ID	Sequence and predicted epitopes
MuHV4gp01	**44841**	MQLATLCLLSCILGQSIAHWPSVVNIETYPFPEDDTKEDMRDYLFLVQNCLLQDNFNATYCSDSFEKLDKRSHFTL PDTCNVKTTFLVNYNRHKYGIFKFESRLPLPTMASATSGRVIKVLVLAEAGRPWKRHWANLAMVTYSNVVRLTDF NAKFRTRFSRIWSVTLDRHEVDLDLTFAGFLFAAPESVQLTLLMDYVPTFTWCGQISLNDPDLPVPSFQAIRTLPV MCFPMWRYLNGQDFHHQDGCHQESKWWNPTHIIPRLNPGTESHNITLNTCVCHVKYNDLQELDTAHRIKILTISN FFGFYKPLYVLVTYFGSSDVNVEGQAPPLQYCVVFIHRGNYGFFRTRQRGDPDCPCHFSLGRDEIVLVGHYVDVK RIVGITIFFDGQEHRISYLGKLSRAAVVGDDTTNKIIFPGQQS
MuHV4gp02	**44842**	MRFRFQVMAPTPPQGKIPNPWPGGCSQNPVLWGDGTDGNYRPSEPWILGQVPCDQRFPHPSGNKNSSSTSGG RPQRPPLPRTRFPKTIRRGFNKLRSTLKSPWKPRPSPVPSPEEVNPAGSPEENIYETANSEPVYIQPISTRSLMML DSGSTDSPENLGPPTRPLPKLPNQHPMNPEIRLPIIPPSKCHKGFVEWGEE
MuHV4gp03	**44843**	MAFLSTSVLIKCCILLLAGGLAESLTLGLAPALSTHSSGVSTQSVDLSQIKRGDEIQAHCLTPAETEVTECAGILKDV LSKNLHELQGLCNVKNKMGVPWVSVEELGQEIITGRLPFPSVGGTPVNDLVRVLVVAESNTPEETPEEEFYAYVE LQTELYTFGLSDDNVVFTSDYMTVWMIDIPKSYVDVGMLTRATFLEQWPGAKVTVMIPYSSTFTWCGELGAISEE SAPQPSLSARSPVCKNSARYSTSKFCEVDGCTAETGMEKMSLLTPFGGPPQQAKMNTCPCYYKYSVSPLPAMD HLILADLAGLDSLTSPVYVMAAYFDSTHENPVRPSSKLYHCALQMTSHDGVWTSTSSEQCPIRLVEGQSQNVLQV RVAPTSMPNLVGVSLMLEGQQYRLEYFGDH
MuHV4gp04	**44844**	MVGTQPRFLVKIHQKFYWAIRDDLIIHGGYKRSGLTSSFALVAMGPLGRPWAASFGFFFLAVVSLATPTPGEDDDI PVKIHRLTFVKGLVPDVTGGSSYYVCVYPSRKLFCTPTRWKDLSRFLNSETLNQVCSARTIYSVVPVEMLRIISLPL PPEIKSIVGGSIRSQYVSFPTFISLHPAKLPIWKSFANLKVSMKFRSSQWEVAFSVVSKTDYAITYWAEIPGFLIHES ATINLINQPLLALYADLHVDMVMRLTDKFIYCQTYTLQQKNLTDPRTGKRPTSSVLIPSPHVKNCQIRRRNETHFVD TCSSAWDNYTSEAHNISRNSSSRGSNATQLVNITANPCTLPTLWDNWPCYTNYRSSPVPEIVIHENILLEGRAIYIIY HQIGLFDQPRLCVATFWMSKEETLLMQLDYPCEVSVEKKGKKFFIKSVVSMYHAISMVTFIWEYGIEIYDFLE
MuHV4gp05	**44845**	MANFHFFCAVLVGIVGVNGDNMCHHLPQMPTLTSPKFTPPVKSGTTLQLRCRPGFTPGAGGRKTVTCLGDNMW TTVTPCNRKRCPHVTFPTNGGANYHFKDNDTSPSYGTEAVFYCDPGYNLLGESKLFCELQDNNKVGWSGESPIC DIKKCAPPEVKSPAYILRAKDVYNTREVTRFSCPINLKLYGPTHAVCEGPGWTPSTSPFCLEIPCGQPTIPHATIQS KPGAPPGSRELVVNCDPGYMPLDGTTLTCEGRGVWKLPLPECVASKPGNDGHSYVTPGISEAPEVPTSSDMSTT TWSTRKLTSNTPPDPEVQTLGSYEYEPDEPVYPTSPQTASTASPVTQTVPPPKKSSLMMVFKLLGLLLIPLLIVSV AVLGFLITRCCRL
MuHV4gp06	**44846**	METTNVCSQAPLGPAGYIYYQLVDDFPLEEASLLSTNFTSAKACLLPLVTGLTVEPGFNFNVKAPCQKIMFESLTV KPTKYFNHAIVFHNSNKIPPIFHGRGLEQLCEATRLMFGFSSFKPDASKGQWKSSTHLPQNPEKYIGWVVVAESFK ERLICGELAMLSAPMKTVTINNKLCFKVPLHDTRFLSSDQLLPFYDENVSRIMYESYYTNVAQAVRIRDVTGLIEAL QERAVTEQYKTAKLASLKTYPAENCGAGNLEYAVIDAAVSELAVSHGLAFLEAPQEESPIQNYVQWPMFSEDATP EGRIKALQEWNAKMAIHVHAQVLSANSVLYVTKVGQSAGKAVGGKQDDMFLGRYYMQHGLGHLNVQTRDENNT VVFPGVPDSCMNGSQYTVHHLAYAASMSPHILARLCYYLQMCQNQRLASTPQGTTVPAYVTTTANTSMCDLCGG DLPAVCLHTLFFRLRDRFPQVLATQKRDPYVVTGIAGPHNDMEILGNFGSFKEKDDDQENGQRYSYWQLNANLT ERLEEIGVTASTPACQLITDVDSFLTVFKKIDAIVDEETIRFNDGLVRNNINYKESVKSIAHVLQLQCNTNWLPPCPII HNLFTRSFFTILQDMSFPLCVTHHTENPLNYGTVSTWMSNHFQNLWSNFKSIWFDKGLLTCSDMRVVHTETSSD MENLAADLPKQRCAIRLSRAQIFAPKALKIKNRIIFSNSSSTESLSASFVKAGKAENPITAGPYMHFLTQLHKQLFPT TKTGAYYIWQTFMSSKKLPQAGSTNAKKLSEFISYLMTSSLAHDEVNVLDYVPTTLMAYAKQRLNNAILRLCGQTQ FYATTINFLQPTILSMPSLDYPHVAGPVPVQDLTTYMDMTRDQSATVIQSSCREDPAAVCKMRPIVTIPMMVNKYS GSNGNNSIFQSGNMGYFMGRGVDRKLLPDIPRMRKHVNTSMRRRYAFASPMTESLLTQPGKGTVRTYQLEKTR KIIHDIIASGNAEPENLVLELVKCLGHECATLTSDDVEFYLGEFSFMVNDVMEVLETLKASGCAFSEESVQALLPTS SPGTSESFVEVTDNIITSLPEISVTQFTAAPPKRRRIATFEDID
MuHV4gp07	**44847**	MSKEVAVLYAQIYGLCMDLSLVPYMDPSSLNLRSISNNYHKLCQIQKIIGGQLLENNTQTPCALTLELEHLLCNAVE LCKSVLSHENTYDHVLCSKQCVLDVSCLACFYGGDTVDIPLDTINKIDMLFKKLNVTFYCTSFHQTLPLLRNVFAQL GKFRGVSPIPSPGIYDICQPCIQCLQQVEYLPNQGLSKDTLLRKTICNHVFPMVPPEPIDFAQVEESPCAVSKPLEH DKAVLARPQAMVEYNVFSEPTSDVLQLSNLLYWTSCEQLTTSSNIHCSNLSNIYTRENKLLNASKQVGSLCHRSLR KYTPSPFELLFTGGLVTEHSKIVAALKDDCTSSFLKKTNYADSLKHKNEMFASLQSLLTGSQPSQKLTQENAPQQK NPEKGFAYDAHKRKEAYFKKLADEGLKRLTNSLDTNIGNLEKLLGIRIWGQSVYAELAKLLNHFLIRKFLVQNATST DWTVEEAREKSQFIKSILYGHSINREHIQSLGSVYYKLLNGPLIKERGLFKLPINILLAQSLDAAEVLPHQKIAMCFDV TNLKSPKDWIDVQFNQFYNFLPNTHLAGVQEQAWRYIRELVLSVTVYNVIWEKSLSICSPSDFQDIKDFEARSVDL DTVCLTFEASCPLILISKNQLRVFKDIYTMLNYHLYI
MuHV4gp08	**44848**	MYPTVKSMRVAHLTNLLTLLCLLCHTHLYVCQPTTLRQPSDMTPAQDAPTETPPPLSTNTNRGFEYFRVCGVAAT GETFRFDLDKTCPSTQDKKHVEGILLVYKINIVPYIFKIRRYRKIITQLTIWRGLTTSSVTGKFEMATQAHEWEVGDF DSIYQCYNSATMVVNNVRQVYVDRDGVNKTVNIRPVDGLTGNIQRYFSQPTLYSEPGWMPGFYRVRTTVNCEIV DMVARSMDPYNYIATALGDSLELSPFQTFDNTSQSTAPKRADMRVREVKNYKFVDYNNRGTAPAGQSRTFLETP SATYSWKTATRQTATCDLVHWKTFPRAIQTAHEHSYHFVANEVTATFNTPLTEVENFTSTYSCVSDQINKTISEYIQ KLNNSYVASGKTQYFKTDGNLYLIWQPLEHPEIEDIDEDSDPEPTPAPPKSTRRKREAADNGNSTSEVSKGSENP LITAQIQFAYDKLTTSVNNVLEELSRAWCREQVRDTLMWYELSKVNPTSVMSAIYGKPVAARYVGDAISVTDCIYV DQSSVNIHQSLRLQHDKTTCYSRPRVTFKFINSTDPLTGQLGPRKEIILSNTNIETCKDESEHYFIVGEYIYYY NLSSIATLDTFIALNISFIENIDFKTVELYSSTERKLASSVFDIESMFREYNYYTYSLAGIKKDLDNTIDYNRDRL VQDLSDMMADLGDIGRSVVNVVSSVVTFFSSIVTGFIKFFTNPLGGIFILLIIGGIIFLVVVLNRRNSQFHDAPIKMLYP SVENYAARQAPPPYSASPPAIDKEEIKRILLGMHQVHQEEKEAQKQLTNSGPTLWQKATGFLRNRRKGYSQLPLE DESTSL
MuHV4gp09	**44849**	MNFYNPYLRKGSKKKADQPCQERAGATENIQRLIPLCFQTPGTSGYKTFNSMLPPVTFLNDQQINLPLQPGQPPW TPPNNTASIKQKGGLVENLKFHVYDIISSCYSQDRCEDIPFRFQADIIPSGTVIHLLGKLENGQSVCVNVFGQKIYFY AKAPNSLVLSSAIQEVMSQFKGKRGPSFHITQEEKIPLVTYTEELTKVYKVTLSSSQLLYPICDKLKALGIELFETNV

		DACQRFMIDNNFSTFGWYTCDVADLRQSKKDSLCQLEIDCGLENICHHPELSSWPPYNILSFDIECLGECGFPCAL KEQDCIIQISCVTWNCATNSISKLLFSLGTCDPIEGTEVYECPSEYDLLMAFLIFMRDSGVEFISGYNIANFDLPYIIDR ATQIYNIDCTQFTKLVTMRTFEVRKPIDSGAGFMRAQTKIRISGVIPVDMYTVCKDKLSLSDYKLNTVAKHCLNMEK EDVSYKDIPILFKEGPTGRAKIGTYCVMDSQLVLDLLKYFMAHIEIAEIGKLAKIPVRRVLTDGQQIRVFSSLLDAARR ENYILPSNQAKCSNSGYQGATVIDPITGFYNTPVLVVDFASLYPSIIQAHNLCYSTIIPDNKLQMFPNLTPADYETFTL PSGTVHFVKKHKKCSLLSRLLTKWLAKRKEIRTQLAACEDPITKTILDKQQLAIKVTCNSVYGFTGVASGMLPCLQI AETITFQGRKMLEKSRAYIENMSSATLGALMHKTYNPDAYFRVIYGDTDSLFVETQGYTLEEVVEFGEMLADNTTK ALFVQPIKLEAEKTFKSLLMITKKRYVGTLSNNKLLLKGVDLVRKTACKFVQSATSNVVSLILNDNDVRAAAQTMSN WGKLDVYRRGLPSGFSKVIDALNHNHLQLITNSVDIDHLTFTTELSKPLTEYKTTNLPHLAVFKKLVSRQEELPQIH DRIPYVFIDGSEKGLKSDLAEHPAYVRQQNLRIAHKVYFDKLVHSVANIIQCLFDNDTDYTVKIIYNFLNIQPDNISEIA ELLNIQTGHGEVCPLDYS
MuHV4gp10	**44850**	MEKSAPSIILNHWCVTWQGHHFLCRNLSNIKILNRRNGYTTLDLPLTLGDLTQYRLAHGLSENLMALSPYSWTIPFL VSSSETPGIELLPKVINDFGTPLSLAIKTNLPSIPAHQLLFYIIFLRPSPLTSMSCYARPLSLASTPSTNGLCQSVSVLD NKPGLLITTPLHRDPASGKYTSNVQSPTTFNLFRVLYIKLSGEEGMVSQKVKHLTIDKDSLQEGFLQLCLNMCGVS YETLQCEILLELVQGPTNFIFPAAFPPPVSLPHRNCIELTCDTERCLKPGDVMKLKHRLLYELGQRGDTPQNAFLIV GAHSPETVWISPSLWLPGQPLYINIINLSHKPLLLSRHSILALAIPISYTRAPASAHEATDTTICYSGNSRVLTCGAAH VLEAHFKHPPITSRAITDGGESPMEWQTL
MuHV4gp11	**44851**	MAESHPWSGRPSSSPRRSSTFANYAWKHTIKPNRILIRNARPLVINFATDRLPIIKPVDQIILEDAGTVGSALNLPSE SICTRPGLLLFGHYNNDVPVTPLVDFKPDEPLQVVLTAHKTIVVPPGEFVMIIVCVNFEKIKSLDLIIHEMSTSNIPLPP TCGQTFKNFNTATPSLEIYGDVIECNDDQKTCVFTAVFPGLHRRCSLHGPLNFMGFVNSVNITGTILRVYYSGVSE AAPDSILVKFKTSSAVAFSKNPCQGHVPSHDDTLIPLVYTGPTLRLLPLETISIPFNTSFVAQNPDLKAIIYDNNLKDI RISATMWTGEQTPILAHNLTAAVKLIHSGTVFARAAFFSTKENKKACTLKLCPSTILLPGGELSLDTSTLPNCFK
MuHV4gp12	**44852**	MDSTGEFCWICHQPEGPLKRFCGCKGSCAVSHQDCLRGWLETSRRQTCALCGTPYSMKWKTKPLREWTWGEE EVLAAMEACLPLVLIPLAVLMIVMGTWLLVNHNGFLSPRMQVVLVVIVLLAMIVFSASASYVMVEGPGCLDTCTAK NSTVTVNSIDEAIATQQPTKTDLGLARETLSTRFRRGKCRSCCRLGCVRLCCV
MuHV4gp13	**44853**	MTAYSVGMGAEIQLCSHPIGLSKNQSRNPTKTLDSAKILACSLAQSKQPIRWEADPYNNIVYSIYYMELTLPTTPCR MLPQYQEKYGAVGRGTPYWIYYRKTLYLEIPLSERVGLKGGDTKMGIQDGTHQRDPPFYKPTPPPHIPPVLEKHT GWSYLCGYTWWTP
MuHV4gp14	**44854**	MAHTNGTLHSINPRPLHIFPLFWRSILVGPTCVAIPGGHLKVLLFDVFYSDIKAFTSLSGSFWFCSSTCADRFGFPS RAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSP TSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPE LGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRP PRPPPELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAGARIPDLPGPLPSW GPDPRPPRPPPELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAGARIPRPS RPPPELGPGSPRFPRPSRPPPELGPGSPDLPGPLPSWGPDPPTFPAPSRAGARIPPVPPTFPAPSRAGARIPRPP RPPPELGPGSPDLPGPLPSWGPVPPPSRPSPELGPVTKSSQKNRYTIVAPSTNILLTHATLLQ
MuHV4gp15	**44855**	MADAPIYVGGYVDIKKYPTLEKELVLDHDRLLQAVPSFKPVPINVEHLADAEVGWVQTIYPASHGLFCMGEVTNKQ FLHLVTQMAEESAASHITLTKQLPREPTLQMLHTWLPELSLSSISPHLMNSTPDTEIFHHVALCALGKRRGVVAVY GHSLDWVISKFESLKPGEISAIKECVESVSKRHGPNGQRPLNFSISMDSLLAKAIDASFIKNRLDLLKSDRQVAAVK QSAYLKASHVPQADPDPISQPTQSAIMTTVTAGMEENNLISVPKATLISLLTKAESSQRPQGGQASVPQILQPFQT PSSAITNHAAFSTPGAGLSYPHAGQWPIMPPWSPYCPPAYPLQASEGAPQSGPYWPPMYSYGHRDEARAGKRK RECEEEDQVSFPGETSKRGLYSELLSMAGSIASLKSELQSLKQSLPACAPPSTPASAYYPEAGSLLQYPGRHINP QQCYMSHPSPAPLPAASPAGAAAAPPPTVVESVPRPPETVPTVPVAQSVEREPDALVTTKKTVPAKRVDASKLA NHEKSKVQQLFCEELSK
MuHV4gp16	**44856**	MSTYPPTYIGASAMLGRYVIVGKPMSPGLQALLSKILFKDKLNTLSSTELRLLHAILCHLYNFTTNCYLFKYALYNTG TYDNGVLGRKVPIQFWTLLYEVCLESGLTTKDLTDETVAASLWYRLNTADDGTLCGFCEKIFKKLGLTHHVALDLV NLRDGNLLFNLGSTIPCRLLMCLLFCLKNWGAQGLEPWVRHYVGKFFLLYLILAGYLLPRKECVEFAATQSYAGLM ETICADILTFQGSQALSLPPDNYLQELDQLFTFNNSFISYTTATVTGSAPNTQK
MuHV4gp17	**44857**	MFVYLNPNPKNTLRIDAEALTETRRLAARAWDLKYQMTKQGMHQRMLRAELDNLEILERGHSAALTTNLSLLANV LLDQPAPPDPTQGEEKGLPPSSRVESRTEGVYTVTVYPGDPAFEIQDSLPQKIWPMLYLHQQRWLPSYGPWHIR FTSSAMQLRNFPRSLRGQANFQNSMSLKLITALTDVISRISLDFYSDLRHLSDTMSALCLIAAYYSEKNQTPLPTNL PELLGNITAKVTLLVRDLKRAAANKGFNFNRNSSSLLPAQGGLYSNDFFQEHALYSLFRTAGMLASSSSPEYPRA DSVLAITAAVFGDNIPPFAAYQWNLRSGLKALESLILLFLLLDVNVPATSNKRLHLEALLGESYSKGSRPPARRTGP LDAGGSVFSFLMENYLVPTLLHRPTTNMSALFPGLYLLQLEFSSGASTPHAIHLTDVKFRDIFNILVQSNVFQDSQE LIRAKQSLRVSCETGSGNLLESLSPGTTMRDIIRKEFMAQDVYDYVYFCVLGALPVTVAVV
MuHV4gp18	**44858**	MNELGAKQLLNKLPKRRARAGKLAHVRCYRAMQGASNILQLLESLKIAHQITHPVGSRLFFEVTLGRRVVDAIIVVF SESSPHIHCFLIELKTCKINFFNQHSTTREAQKVEGSNQLRDSAKALAVLAPVGTDPCRVTAHLIFKSQRGLNTLKS YTLNWMTHTVNTQKVALLNFLGLRADNELRACLTRGLPPANSPGSRRHHVCLPEPKPQKHLKNRRGGAHRNQK ARRQGVGPKVSNDKTRNAPTHAEGRAG
MuHV4gp19	**44859**	MASGGKNNPGFQPDSDSDEHVYAEPEEVYDNPFDAMRRQGVYSLLRPPYNRQEAVDSDDDATYATPSFDRIITR RPSTGEVERMPGTPSRRPPEQSDSESDYEDIGAYGQPARQSIYQTPRRSTIRCKVSSVGENYDIPRDTQANTVTV QTTHGGARPRSRAPRVLVRHPEAGGNKPDFLPVDKPLPSVPQHVPQGYEEMAGSPPPERDVRSPRPQRRPNP PVIIFSDSETESDAEAVGERQRGSKVDVPTSWKRLMMTKETGTKSKTAFDKLKGSFEKFMSGNTKNEGTEEHRS VVRRRGDGTGFRYSYMSKMSTDFPAGPTRCATVLYFDGGIAVGKTTALEAAAEFLHNILVISEPIPYWTSTFDKNV CQQIYDVVKTKEKGKKHSKKVLQCQMAFAQPFHATQHLLRRTCLGTKVSDGTCNNYVLIDRHMVSPTVIFPCLFF RLGVLRFCDLLSLLSVFSAQKFDNVVLFKLHPKVAATRVKERGRNPEGVINHTYLQLLNEVLDAIFCAWELLAIVPP EVIVDAMLSQTSVKTVFQKAGFVAPRARLMEQMFRDSIFNDLRENVRQLPLHGSSIPTLLHKFCYELSKPHMVKLD AGQFPNDVPGLWTHIYTQILTDPAIKTCDLKWNILEKGISGGDPQ
MuHV4gp20	**44860**	MVTCLKNLFLYCIFVSMMVWLVHGVGDRDSKGEGATIKVKRNDNGVISVYIDGKDYAYIFNVTKALQDLGRDPIRQI WRHSDVFKPLTRTLAERDSIFVTNDTIHIDSDSLFVCPVGRGYPTITSQVQWKDLPPGYLGKFGWQKNMALKEFN ENERFTMFSENEREKTLVVGKDKYVEYGSLTWMMPEWGGTYGVVTNSFAFVSVNITVESQVCSASIIFSHNKGG PSFKGSIVPEKILIGKTDLYSMYFIAFNTKPVCQTDIITGIELQNLFVQMVTELPENIMADIANDVAYFSAVNCHPLKIP VPRLIRTFTKLTISHFLTISGIVATKTDTVDVGCLIQQLADLRYLRESLSACSMAYSPHMFTSNFLKFLSGVQIERLPK ATQIPQADMSRAMAMLRFGITNYNVSAHAFTFMEEMFENIYREYSYVYSLTSETRKAMMGVSETLKHVAKLWKFT TKDLIKLFTIATSMCTNNEISTMVERHAPLWDIDAVETFSPCYLSLRFDFSANKINFEVEQTSQLTPKRTSGGVSGFL TDLHNHHLDLVATLPFVKCLSHVINNTDVILPLEKITYIISKEAVPGVTVYDVAETFLESKLVISVFTDECQPALQDTD

		VHRTVPVIYNISDSRCQFCGSIIMSYDESQGFLAAMYVSDKTIQTNLFLPESPFFDNHNTHVHYLWLMSNGSVVEL RGKYRRQIQSVFILFAVISLLCFLCFLVLQIIKYIFH
MuHV4gp21	**44861**	MLRILKKDCALTGGEVTLANQTKIFYVIKAPSLCSLVGSPSSDSVTSQELFKTFPCETPLSMPLVSTSNPLLSIVRLM VSPKPYDLTGVLCFGEDHETHYILRRVAKILTMTQEELDTICDIELHFSSNETLSSNRVPSRLTESIFPGLVPTVHFP QNMILSRGFFTGGNGPIIKHVAQTHHLTSDFVARVFYALKTPQAHAPGAAQLYRGLQIMNHAHNGLDFFPSDSDIN DMQQMFLKHVLLSRKGTDSCAQMFFQAYLPVAPEVLGPEVIERVELALAKIELFANNTVFCMSTISTIVRPRIQVTT SANIKYIRMANKYFTMFPPINKDTAVIFGAAVLDQICKETPIREIVLVLRKYAHVVRRPHTPTIKLYTVLTL
MuHV4gp22	**44862**	MTIFLPVFCDLPEVYQDCEYDENSQLSILFWISSNTYEVVENVQQFNILGKDLTFCLCRALRRLLLGIRLYPTCNTES NRYVVTGDRYVGNGLVVSPTGRHIQRIDTCTYVPVIYSFEQTDAHYDGMGPGKLRALYHEQLFFKGIDYSFVFSTL IRFLSMKQIDECYYSFIHTLEPWARSACKKNYLKLTECFKNVALTKLPVVDATFHLEYIKFNIKCFLDQWNDCPDLW VLRRTISANLSKKHLLATIGRLMSVCEIQLRNPLAYHDHLTMMKTFPQVTISAQKKPTTCLNQKLEIVMSGTESMWL VYTPASSMFRIMLCAAYISDIYYNNTVQQAIYDVTHDKPSNGEMLMNLYRRIDYLPKDSVETIARVCSTPWENPLIE RPPTMYHEYCPIKNLSINSFKVTIFNTNMVINTKISCKKITPRFRSFLDIPRLTNNFVVKKYSVKEPSFTISVFYSDDLC KSGAININISGTLIHFLFAMGCLKCFMPIKTINPVLISNWNSTFDLQGLENQEIVRTGRHDVFWTTNFPSAVSTKRGY NISWFKAATATVSKIHGGALLDQVRGEISQILLSSDAIINTNKNCIYTTLEKRNRFQIQTLHKRFLECLFESCVASKLN YHTVKRLCSTGIFDFSRHIISHSKNKHECALYGYRKCNLVPKILTGTKKTRLDELGRNSNYLSFNKSPLHHKKDASD FKKRLCLNRRRSNPCQPD
MuHV4gp23	**44863**	MDAPVENRAFAYVRTGANLTSQIKESAAEGLFKSFHLLVGKNVRENSVRFEALLGVYTNAIEFVKFLETSLAIACLN TEFKDLRRMVEGKIQFKVSVPTIAHGDGRRPSKQRQYLVMKSAHKHHISAEIELSTEDIELLFAEKETQLDVAEYVG AVKTITSALQFGIDALERGLINVVLTSKLRQAPPTFILQSINDPSAAQRGFGKAAKSDIVANFKKHLLEHTFFLDDGL RSQRGRDYVLAVLSDAVTAVNSESVFKGADFYTTEGGEPVSGVFETTDGTMQKLLNLVGQATSSIMAPAAYANY VIRGGNVVTAMSYGKVMKNFDSFLSRMIENGTNKSVTENDFYTENGDTDMDVSKTTIPAATIRIGEKVFAIESLQR MYRETQQAYPLIRTMQYAYYFPVGLYLPDPKYTTSGTLRGLEGGSPPLEAWVVNKNNLIQCFTFDNALKMLCHPR FHNPQLCIQNLPGEEFQHDHILGYGIQSRQIGHMNLYRMMYGYYDGKAVAHIPDVVAKSELSTSELLSPPMAHLLR LELHPLFDFYKIRGANGAIECRAVHRTHVGNIPEAFAPPKFQEGRGQQLESAAGLSHVIDQQTMELIQETAFDANY PPMCYVIEAMIHGQEDKFIMTSSIVALTITTYWNNTGHLAFVNSYFMIKYICKHFANGLIPREIYLIYKKIMAELITMEQ TLLKICGHEKVANVSVGQQYFNSIMDPALLPPFINDDILSKALKNKQRKVSFYIGDELYDNQERRDVYIKEIDTLENSY AAFDDIYTDMHDADHENRKVLLLGPEPAGDLILEKLFYYVFLPVCTNGHVCGMGVDYGHVIQTLGFNGPVCLPNV NGGDDLYQHLANGPLKDLLLASDLKPTVGMIRLLVACSLTTPAVTQIVRVEAERDSAQQLATHESGTKVRHSVLVN GIAAFVVADRNKHVIETMFYPVPFHKFYADPVVAATLHPLVNNYLNNIPSQRNGICFNVPSEFMAEYEEWHKSPML KYVRDCDVQPQALSTMLAMHMKLSPMGFIHMTKLKVHPGVALTVVRTDELLTENILYSNRASTSVFIGRPTVKRRE IRADAVGFDVSNEIASLDTAMGYSSTLIPARVAGITTDMGIHCQDLFKMYPTDNFKNRELTIFIKNKIGSERAPNANV VDPLAYMADPRHGSEMCGLAHGQLATCEVILTPVTSDLTYFQSPNSPRGRTGCVVSCDTYSPENAAKLLYDHGQ PDPAYEFRTTNNPWASQIGSLGDALYNNHNRQLVTPGLYSPCRQFFNKDMLLKNNKSLFTLIHEYITRLGGSPATS NTDVQYVVINGTDVFLEQPCMLLQEAYPTLSASHKGLLDEFMSNKKGHAPVHNMHYLVEEVAPLKRVLKIGNKT
MuHV4gp24	**44864**	MASNRNIVITLTSRLYADEISALQEMVGAVICLQHYHQVQDVTSIGLGHIIRPEGPVDWIAAFHYLRRCTFGILHEINP DSISIIRVDPGENYQIKNTSKPYVMWDEHDDLAIIPPIFGVQQCTIKLDSNDVNLVFPSVVPAGLAQMGIQKILMYNL YSNLLAAERNHDNVNALEHYTRNISYMGRTYNLDAMAQHQDGAMAVLDDVAMCTAVLAAIVPEVCNRVAMATIR EGQHPLVEVFADNVPMLQRGQELNVEQDIMLMGLFMAYTHKLGSIFNLSTRLCLGAYSHETKIGTCWL
MuHV4gp25	**44865**	MPEEIELRSLGRNSSGEVVLNGPYHCSENSRCPDCEKFSYLAYSFLIFLTVLLFSVYLLFVCPFEIKHLYGTWQSG DSILAGEVGPILNRTVTSKSCWRGPRCEMFIPNIPIILPNDTIYPNFTNYNGSYADYRTTLQEIIHTILYDQCNVTVLLH TSFGKTYGMDDVFFKTVMYKLITSFLMEGSTMCDLKTAARDVYVLHSLSHLHDVGKGCKLRLDNIYDESSGSHYS RECVKQFDCMLCIYPKSISVSFN
MuHV4gp26	**Seq 597855**	MWYVSENYTMTETTTISGQTSSGFSFHVPIMVIVLILLIIGLLLYGAYKCFFWVMYKRAQIMGLPAQALLSRVKV
MuHV4gp27	**44866**	MLQKDAKIFFISSVNSGEKTTSFLYNLKDANEKMVNVVSYVCSEHMEDFNKQSAITACPCYRLYVPEFITINDNIKC TTNLLLEGSFATELMGNMQSHTEVSGNSMIHESSLTRLDFYRCDTAGQGAPTTENTLFVYIDPAYGNNVHASGTG IVAMSHCKHTKKCIILGLEHFFLNNLTGTAAHNIASCATALLEGILFQHPWIQEIRCIIEGNSNQDSAVAIATFISHNIKL PTLFASYRDKTGMQWPIYMLSGDKTLAFQNFISSLNQGLLCASQTVVSNTVLLSSDPISYLIEQIKNTKCIYHKNKTI TFQSKTHTMSDDVLIACVMTCYVMTTNKISYISFSIK
MuHV4gp28	**44867**	MSAPGCSVNKSKNLVTDQDLLDVVNFFNRPLHALIAEVSKTTSDLELVRSTTQGIENICLLLDLVGTECIKDASAAK TSV
MuHV4gp29	**44868**	MYKRCKRGQDKCMMRPLSNPLTEAYNVQNLYQCLNCDDYHLCNGSLNCDPLVDREGIVCTVTGKYIQCNVRES PMCGAACLDVDIHPEDNTDCILRALFGDIVDIINKLDDIAEIKDKILAGDSLNEHIKKKIECTFPMCANIINCNSQGYSIL CSMFVHIIMSIYANKTIYGHMLFKCTRNKKYDTIAKKIREKWMYLE
MuHV4gp30	**44869**	MDVFRINKKSVPLQQDELLVDLFLPEHLLAIYGILPNRNFVYTSSVCDYQSGHVLPYRRVWGKFMKAGESGGPVG SQGLCVSIIVRVHQNLSCLDMALLKVSNWDEGFFRIIKFSLLNLLRMFYITSVPPVTRLKKTAFEELCNQVSSDKPP AHAAASFLLSLLPNTVCETTKTHCALENPGYIRGSNPPTCQTQPATETLPCKNRRTERQPRTEYSWKLLHHVENG APYYVEDTHNPIEAQHIHQKLLTVMTGDPPAKAPTDIFLMDTDFLHAVQNRFIDSIDLPGVKDGGLNIFQKFSIFITYD ETTKHLYEIFLDSLITLRSKSSKYPAWLMAYYHGPSFQGVWLDIVNATATGEVFKGDSIYLGKCHEGLSPTSIDKLL KGRGIFYNNLVLLLVHSDLTAWLLLPGGFVIKGTYILGIQEKAFVGRYYGNQRRYNSDISE
MuHV4gp31	**44870**	MATKEDIIQTFLNKECIWIVNKASCCRKKVFTCTTSISPSLKHHFGVPDDGAWCLNVTVLILKPKQSPFSVTVFINGK PILCSNSQLISIQKVSGREHMAVIYFGKFTGKSAIPVPMDPTILDPGSDSPHILCSDVMESSTLVDLPVVGSSKQVG YTAWLANNSIYEYMLSTEHQMMCPSLPVFPSLSKILNIMTSCTSPTCKKCAGYRRHCKVCSGYTDATGDGYSPSC PCTTSCALKPGDIIPITGHHTLLPLLFDPVNAHSVTRLRITPTSSPQPLDQIITGITESGESVPITLEAWKLVRLSDLYS HLYIISCKALKSHLHSC
MuHV4gp32	**44871**	MFIASKKSYFEAVYRSTVSSHSEEFWKSDDPVYFTQYKKQCNRLPNAYLGTLHSASKYSENFRHYVATFSNSPLD FPQSVFNERNPCEYSVPYLDSALQCSAKTLVGCSVSTTERNEYEVCKEATRCFKDAMSHKVLKVFLSNLSWFLK GHYKSKQAFLEPFQKQLILHSFMFVASIKCPETTTKLFDEFKFLLDMLYFDNTDLLTFLQKSPAFLIPRRHGKTWIVT AIISMLLTSVDDLHIGYVAHQKHVSLAVFLEISNILLAWFPRKNIDIKKENGVILYSHPGKKSSTLMCATCFNKNVSVI
MuHV4gp33	**44872**	MATLSDFFPEADPVLEKNYRRCVDLAINMSWSVPGQFKLVETPINSFLLVGDVLPNDMIESKPVNSTNLVNIPFPLS TLGVSTSKKSVEVTSYKSETEKFQEAASISEHSIRGSIVYEGLTWITAMGYNVTDFLVNMLEQMKCPENWSGLHPV DPLACVWLLYFGPKSRCSEIACVSELFIGKKGPILLPPHMYRGDTSVNSFAHHLCQYVKHLYADYEPEILSCPLDIT RVKGCLSDLRQVAESCVFLSQRCLLCHLYKQNAAVSKNILTASDCIILGGSGKSLLGTYMKSYKDPATHDSILLPTY NLEAIVNYILEHYGHETAGQEINWE
MuHV4gp34	**44873**	MDTKLLAKKLIGSSLRADIEKRAAVSLTDRFGKSHSLTQFQYTKAKRAERTASSAREHCHRIENMVSTKRELSDCV SELTHLKEICQNFSVEDAERLIEETTVLKEELEDTVNTVSAALQREESLSADSEQEESDITCWRLDGLPTVTARIG

MuHV4gp35	**44874**	MDYRQLPRVLGEDGEDTAASSWNTFLLMQSIEGALVIPYEKFPTMVSYMMYAANHVSTEDMDGKPSFIAPPIWER CFHTKFTPGDTLGEGGFGRVSTMASDDTLCIKYIPKLTALYKEAVLMDIIHLTSLFKPHGASNKVLQMMFACVECQ CIVLPKMRCSLDTYREWSPNSVADTLSGFRGLIDGLLYLNFTCGITHCDVSPSNILIGAGGLSDMVLSDLGIATII**C**A PGMPGEIPIFSKMLGRVTNLYSSSCPMFFAKRDYRPSTCLFLCYKAIKEQKAAESIPMYWRTPQEGLRLDLCCLYY SFQDCLLCM**A**GLQYRGLDFLKVSPPPPDRPGKYLAYMMQRTVVTQFICGVWGLSVETGLDIDGGSSNIHIPRTHR SYFKAVAEKALCLVRQQFTPEKRVTILSESVQA**F**VVPFLRLDSFNHCHGRVDYSGFF
MuHV4gp36	**44875**	MEGSIILDFFEKDDLLEVLGNMARE**N**QLESLATLNFSAFIRSPQVQELLATSKTSVRISDMRLTY**Y**YFLFLRLNEYIG NTAIMGVFKDMMHLTDNSEVSAVYAACRDVTPDIKYAVCQRIEALTRGQQDNELWDILRDGMISSSKFQWAVKQH SIN**K**KLFNPQPIKVNHYFAGPLAFGIRCEQTVKKILSELIHPNLPRFHDCGFLPSAIDGIFGVSLDTAFNVFTDSSGLV HFEPDSIVYEIKSRYKYQFSKSEFDGLAKKYLDLYKNPCEATFIKFINCISRPAVEYVPHGKLPSESDYLITHSMNWK TSNKRKRKITDSHICLKKCLLHNMYQQSTVYILSDPSETSGKITIKASFPIDVFVNPAHNYFYQVALQNMVVQDYIEF GQGVYKRLGHQKNFIASGFFRKRHFSDPAV**C**SIGNCGKLDTTDEIPVALIITPVRIPSTVLHEYLKKAIDFWNQ**C**AE ANFDHIPWGQLSDVARKPITP
MuHV4gp37	**44876**	MGAAFGCCKKTHNPLKDVRGQLIDLTKDFELISENTGLLVEDPSVGEGHLELKPKPYGSDTDSDTDIEYERGKHA
MuHV4gp38	**44877**	MPALKVPQLKKLEPSRSDSFLL**K**SWTNL**L**ALLTLLFVTSSTVPILASFRGVGFPCYFVNLVDYSTLNLTVRNSAKHL TPTLFLEGPEMFVYIVWSFLTEAINI**L**YFIFGAVTVYRLKKIFMPSL**N**AIQVWLTL**I**GGHSTLYLSIARLWTLQLFVHVL SFKQIFLAA**F**VYLFHFM**L**SYVHVHVFISRYVPQWQANDMEQKIPEGSSLEKLVLFYRPILANIQMSLLALEMLV**F**SLS VM**M**AVCNSFYILVSD**A**V**F**GAVNLFLI**I**SLVWHIGAEVFLAKYLRHHVGFYIGLFVAYVIMLLPVIRYD**A**IFVTSRLHKPI TINMTIIPIICLI**I**VVRIIRLRSQTSTKVTYKKLGISGAMEAQPFQSIPQPPRAKYTDLETESEDEL
MuHV4gp39	**44878**	MCRLQWHDVQVLNVSLYNISMPHKTGIWVITALKTATWDLCAFFRLEQLSETVPHIPGEMDPRPMSPFMHNENIC LFDLLMRYQSPLL**R**KLINLGRM**K**LGTSGKEILAVEEVETALTHQLTGGYLMCFGTTIRQEDDRGKLTSWKEHLLKD FNLCQPQVYLKTCRGVYVYDSRDIPAKKGRLDSLTIEDIFSPVDTILHVAGSPITVRTFETPFHILWIDKDSVWNGYL SEFFRALYVKLYGNFIGLKPILAYVFPAAVESPTFFNT**I**F**T**SFPFLCLRFGKPVKTSCVHLQKDCLKILAKLPNVIRSP LADKVLDIKAQKKPITSMWPLLTKELNGS**F**AEDNKVI**I**TKECNVVEIDFTKAFLISCNMP**Y**AVYWHEQMVEIVNVITD EMKDSLVSRYNEFLYAIISSGNKHNFTWVSISKCTVHMVGPDLVNDTQFLDEIFHRLSSVYNGHVGDITVSSQKLK VAMFTDILDEIKLIKPLCLEENRQPETFQSACEDILRYSLCLCKHSKEDILWKILLTMWQQRRNTSFWLKETMNIEHP TIRPKGLFFTIAPAFYLHTKHGMSFWMQDKPLPSCFDYTPYIMELCDILQLNDEERDMILSNYETLLNLS
MuHV4gp40	**44879**	MISSNIREARTVILPRLMLEITSNGTLTVASHTPIFQKLSLLDLPSLTAHLKTKLSGSMF**K**GFLFATL**C**ETEDHVTTLD MHPHVFEKRLVLYNPRNTCNKELCALISMVENLMDCDPKLPLSIYMRGKRLFQKNPGKD**S**CFLFKGL**S**TLISTHFA VYHPNFTVNDELLLPPLLAYKMHSTIEGIDEVSKGLLKAIYLDSYRMDNNIDDFQNPAGTFTLLCLPTIFTKHLTVPN VLILIKRAGLMYEAIDNIIL
MuHV4gp41	**44880**	MFMMNLSESAMLVHPTKN**S**MQLFESL**K**GK**Y**VYVNGQSVYTSLRSSGMFSKQLFLHLYRFALNSCTYETLFTSWA NFHNTMRKKWKKGTTSEDFLASSYASWVATLKLTLERLALPLINQLQYSRNLISYERYIDWVTTLGVVPVA**Q**VPEN KTTIQHLEDNLKVLVNTSGPGDKVITEMISSLIQEMKVILKTLSSLYIPDYSEVSIHKNLESGEWFGIYKSKRIPVEVM AAPVLCKEGYMFDSCVQRVFPTVMQCYRTQEHAKL**C**QLLNTIPV**K**TIVGNAQSPGYKDILEHLEKSNSKTDPKKEL LNLLINLAENKTVSGVTDVVEDFISDVSNNLIDRNKLFGNSNETTCAGLKKQVSNSVFKCLTKQINEQFDTIADLKKE RELYLARLQTVESHLLRIARNEKSIHDVD**V**NLLTADTMESLSEVRDLNLLSSTTEVPNGKSVLNSFFSQYVPPFREL GKDLANLWESELMSTFKLVPEVDPQGKMICVRYTPDTVSLLLGPFTYVITKLTSMDLIRDDMTSQSVHGLVD**I**VYK ESRLLVYITDIGSKLGTEVQLSTDGVEVLPP
MuHV4gp42	**44881**	MALSDRFIMNMTSDAKIRQIVTRIEDLSNTVTTNIPDMCWYDSQYDPLDEECMNLLPFTSFIITGTAGAGKSTSVSAI HQQLNCLITGATV**A**ASQNLSSM**L**KSYCPTIFQAFGFKSRHINMLCRQVPKTPITSIEQLQQYELAKYWSVVADIIQEI TQKKKMHQYQNMSEELYELMCLSCQPELWTTNIIIIDEAGTLPSYMLTTIVFFYWFYNSWLSTPLYRQGKVPCIVCV GSPTQTSAIQSIFNHSLQRNEIQKCDNVLSVLMENQVLRRYIDVDNNWALFINNKRCLDTEFSHMLKVMEYGLPVT DEVLQYIDR**F**VVPYAKI**C**DPLEYVGWTRLFVSHQEVKTFLSSLHLALTAKSHRLPNEVKLFTCPIVCEVYNQTFQKY KEKVNLTEITIMDWLKKNMFKASNYSQFVDQDMTIINTDITEDCTRITYQAKYVKNSFISLNGKTKRCICGYSGTYAS FKQVLDSDGFLESHTRDN**I**KYVYNFL**S**TLIFNSL**Y**QFYAYGIQTGDKKYLAS**I**QEQNIPSLLLSDDETVEGLTEDIFYL LATQPPLPSQSTITE**I**INWYSAIKQVYLDRLQVATDHFGEEFLLQPFSTYTTNIHIRDDVEFTSTETVITGLLDYASTV ESYQLKGYTFVSVSFGKQFSQRSDYMSKTMPMIIVQDSMGFISCLNTNFNKITEILEDGSSMVLGCTGDYGISSKL AMTIVKAQGMSLSKVAVAFGKYKTLQHSHAYVAISRATNPKYLVIDRNPMRSSELTMDTKSAGYIT**K**ALHNPKTLL VY
MuHV4gp43	**44882**	MDPFKKPVRMLPIKGAPISRPISVFTFDVFNPPDDSDGSSTPDSVFEAETSPARTPPTPALILPYDYVSSEDSDDEA QEHADNRDTNDQVSESSTSEDSDSESESSCDDTQQTFVDDESTSSSGEEDRDDPFESNDQGAQGGSTSESED DLPAILRAARETQSDSSSDSSGNSHKKRRVQEEESSRILKTPAPISGNGKYNWPWLD
MuHV4gp44	**44883**	MDTWLKTHVWSLNVMQRDSVMDFLPQSWIDYLQLSAFSSKKLEQIMAAVENRRKQNIVYPDSEDVMRWAFSCP PENVRVVILGQDPYHGGQANGLAFSVHENFPVPPSLHNIFQELKRSVPDFQIPPSGCLDKWAEQGVLLLNCILTVD KGRPGSHHKLGWGWFTDYVISTISEKNDKCVFMLWGNKAIEKEVLINGSKHLVLKAQHPSPLASLGGYSSKQAPF LGCNH**F**SIANTYLTQHNKPSISWNL
MuHV4gp45	**44884**	MMANVVLLCINADMFMYPGVLLERY**F**AVLTQHHL**F**IMFGSLLKTVL**L**TLAFVSLSTCDSKILPKHCCHISATPTEKKS WNFLSSITEIYLSSPSSCGNINVAQVKVKTKTGYHLECANGFGLMGFLEAVVSRFRDPTPDDVEFLKQLKLLHDQF DEVFSASTANSSSFKVAAW
MuHV4gp46	**44885**	MCSKMDLETREGGGCQQVSILMVTSDREKEQYEKFMNIL**K**NLSNCTDISQVVADAKKIYDSREFCYVPALLTLFKK LPSVHKWPENENCNEVLS**A**AFFVCQLLFFHNFPASPAFTVDEMFATVAARLKDLIEYSCDCENCELLAESL**T**NYKF SLVPIKIRPHTDTCVSLKTLQRLRT**A**MLGNPETLSIWTLDDLVEDPVVFKGYESAIRREFAEHVTCLNMCWVVKIILD C**M**SQPTALLRDCIQKGAKNNGLQLDTSSTWTWPAARIAEKEVIEHTMSVCVQDMTRSHDQEFYTEAFKEDLHIGL KRLVAMVLGQNHSWLDGFLTDTIVTGKA
MuHV4gp47	**44886**	MGDEFYYPSLESVVHTFCVIDTREHNRVSACLCKLQVLCKICQTLRHNLDTEPFLLPHLRELIIRHLTLLERLSTTSK FQ**R**ILDYMKLSLEANDSNLLQDLAIGTVNLLGCQSPEILSIPYDKDQPVHEWCACFLTSVDEEALRKISSMLDNKHF SYMYNFKTFLKYSLELETAADFDLSTGLNVLVYWVSVFKLFSVCVQSQFLLD**S**LVAFNAL**F**KNHVKELEAIVESDTN LLCYSTSVVWAKLSNLNHLLHRLQTSNNTLVFDEILICLRGLQIYIKCLPTLSAEGESESEAIAAEIPS
MuHV4gp48	**44887**	MFRNQKVRFNAKVHNRHPCGYISHHLIKYAIER**V**VYTTDRL**F**LTAPC**S**GVQLPQPLACSLFEILKDVRGKCTTAWR RLGAGRRHLMTFGRNVLDEFNSEKKSPGGISREVEAFIKICFPQMDLNKI**L**IPIYQHA**I**NIPPDCVPSCTIGDGNRKR APHGSLYSKDISSQKFCIPDPLFASPTEPGLGELHRGNMA**H**LLQNPEE**I**INLDPLHNTTEPCLYQMFSEAVTNPSKK RWLSS**F**NMVFSGLSPRARPETTYEPLGPFSPISPGPSSATEEFQFEFSPSPQTSPETSEQSYIPTPNSAMG**G**SFE YTGAVQPQLIPDNHTCSAKRLRESDEEVNYSSDGSPNKKPTARTSGHEQAYGFLAELLSSHRDTPVQHIVQSGST PAPPIVEPQGQDFVGKQDETCSNVFPEQITQEACPGSSEDAFIDDAIKEIFASL**D**SMANQDTADSDTCSILDPQSPT PPPSVPPITTLSLYDIYASILSPLDPNSLES

MuHV4gp49	**44888**	MCGVKSLAKCFLLFQIISFLGNHNLVWVPGAALGAAETVEGITSREMEINATKAPSSGATFSLLVTLSNNNPTTIMR PPVAQNGESVHKDARSASASDPTTSEPTSPGEEPTEADPKAAPSAGHVGETEPESPTPLPATPKPSSQEDNPTM TPPTAEPPTSNADVSTEHVDETEPESPTFLPPTPEPDTPTTPETTTPSQNQEDEPTLTTSSSDAPADTSDTSPPKQ EDDPVKPTESKPQAEPKDNSPSDVPETADSPTDPASPTVELTPPTEPPTPETVSPADSPVPQPTAPAEPSKPEPT PPVDPPATEPNTPADPSTPESTPPTDPPAPQPTPPAEPSNPEPTPPVDPPATPPNIPADPSTPESTPPADPPAPQ PTPPAEPSTPEPSTPAKAPAPEPTPPPSGPSMTPEATPPSTAGPGAETETPDGDTTTQPASPQTTAPMHPVPDIS TLLWIRPTIAILIFLLMTIFHIMYCVCLHE
MuHV4gp50	**44889**	MASKKPDKTYEEMVKEVERLKLENKTLKQKVKSSGAVSSDDSILTAAKRESIIVSSSRALGAVAMRKIEAKVRSRA AKAVTEQELTSLLQSLTLRVDVSMEETTVGASGGIGPSSQTETKKRRPRSKSRHRHDHE
MuHV4gp51	**44890**	MQVLVVVLFLMCAFVCGITQETTPTPKPDDSSDFYGHGCNADTYVPQWGSVSSVLAIINGSIVTVSSGVFLIYACF SKFLTTMTS
MuHV4gp52	**44891**	MKVEYSFVPKHFLECTHGWALTTQGTDLDPGTRLKFQNITPISVQPSEGTKVPLGLFIQKTSGFPLILNAICANSLVT GHTGLIDPGYRGEISVILATAAQSTVEIQPGQLTIYILPVSYTVPVITDDHLLKNPVYDEDAGFDFRASEDLCLLPKTR HTFQFDLTHLSGIAPEFTPVVLGRSGIACRGILVTPTGINMAEKFSLTLHNLTTEPIIIPQGIRIAQIVFISKSYSPSLLQ LLTSKECSMDIPGLAVVQFIRVPHEAADKSEIAEEKNRRYSKQRPGKPSREGRGFGSSGVN
MuHV4gp53	**44892**	MNCCGIWPFGKPGVPYKRLADVETDERMEMEIRLGMPPGVLAADLIRSTKDKQVLEQLYLLAVQANNLTEHIKRF TLGEIPEECKNVTRSQLEKLKSVQHIIWNTMISLAAGAISVDEATLPALLDKRAEETVALLEMEKIATAVKLDETAAW ATDIAGIVSSQPLATPPSESPDQIALKKATQLSNAVY
MuHV4gp54	**44893**	MARYHSNSCLVSPDTVRCIFSTDIDVIDAVVNLITHEGATEYKFTSLIHDCFSISGLKNISSISMCLPLNRPNKEKKYF ELFKVDISCDDAKQFLFNGRPLTSGQVASCLDYSHLKAQILPILKLIMSLDNRGEKEGTFLEMVRWYQSKLINFLRK LLKTTSSTQWFITTFGQDDLTFTLVIASYYFYKHACTVETLMHLARLFCGELGHSLIDVSSLQELGLFFSSSSILDSV PLFAEYVETKLNIDTLENEKIDQMINEIRGGLLLSNKDIVQFVYLAFYACFNKTAFLEFIGKTSPDNINTYSSEILHLKL CDEFLDKMSSYYNKEKYIHTHLLTKVVRVPGASLGSYGDTPGTLQAWFGQTSDLTALFDSINEDFPFYSSESSLKE LLKLASLSPQELDNPKDILFPEKPICPTYRSEFKNKTYFVMVATDSIEDYWKKHVIFPHSINLDELTDVRITELLTYCV NGCTSNTVEDNLMVSRHEYFNPHLPIYNVILDFDLPVEVPGYKIEDIYNLCLQIRQDIITVLSTILNLEMPPSHPVYFF KSECNSDIYMEPRPFCTCSKKIGLRIITPLPMRHAIVGATPLITLARVINRTIRLNKRVCELFPSISSTEFLFDTGIYSQ GRCIRLPHTYKFTSTGLPERLLKLFVCHPFPDKTSYVKNSFVLTNLLYHSTSEDLRSGDYNLILDIRDKDEDFLSCKT VASLPKNSLDIDKLEDILGCPVQSWIDTTLWPLFCEQLVKYLPQKNANELNNISFNVVSNNMLQLKPRRGPGFSCL THQHRTKSHNVRLFITLGKFSRDVITATLMSQCFANKCNNNKPVTHCTVHARV
MuHV4gp55	**44894**	MKKVSSQILHQLRSQRGQSGMWCTNLTHSSTTHHQHPRQTSSHLLQRLESAPCLLKLSTTLLCLEIQQSMSLHPK EAILTTPDAVHREKMLTRSRKGDQTHEDQTDGTRKARNNIGPPNLFWITAKFQEQSTKMPNCWCLQLVNCAQSSI LIGLWML
MuHV4gp56	**44895**	MLDEQLAWAYACLKHGRELPTDDILMSTSEKLSQQLVIKLIEVIKCIEKDGIFSRILKGVADAVCLKAQFLRGMITLKR TPCSLPMYTLFVYVLTIPTLRTRVIRDPLLTQCKDVVLKYQPGDCITLLKAALNCHQCNKDCDKCKYILDPLLGQTH RTKGVFFVCE
MuHV4gp57	**44896**	MKSHWSDVFLPLIVGGMSAVPFIWCLIFRTLYLPIECDWRCWIFVYGSMIWHITMFMSLLFKHKHGMIGWFKLCSA VAICLIIVLALLEQYCPYEMYIVPVIFIINIVLLSTWVPMALISTYMCNRIYARLLELGFLAAIIGYYVMLQIGAQESPAFW IPIPVLHIGGVYALLHFRTRPCFLHSVEKRHSIYYFGNNKYTVYPCETIVRMCSPEISLMIILIMMLAIGFPILAYYVKIV QGMQYFYMFLMLGPMVGGLIFDSKIVGTFFMMLALVTMIFAGIAPVWFPLMAERTFVISLILANFSAGCFLECMRVK LRRAINGVYFVYLVTVLYNLLVALIMIAVSM
MuHV4gp58	**44897**	MQTFQLDTERLCQAAKLYQHTKSDFGLNGMIQLSGSCNNMSLSVLGSIGGCAILRLELLEAARLHSSKDSSKSAIY SFRNASSLGREFTHGGELFGPKMESASLSFYGHHGVKYVEAQFVHDSSSKTVHTAAMQPITIPPSCAFDDREAN GIVTLSTKTAAALVKWLKQHTKTCQSPVKVSISEILGVMVLSVGDASMTVDVTPVNVSSGKKTRGGNKASDSGTIS ADATTVHVNGHCLIRSLIVCKVPGCTTPRVKFHACGILEVDGAPVKQGELTQVKLSVALLNVDSSTGRVLKEPVVTG ASKDRGASKSEDADGSPPVPDHPKESLTSDSDSSVPGPRSTDLSSLTHTPSDRFSSDLRSGCGGQQFLKRPPPK KDREPTTKRPKLHFNHFP
MuHV4gp59	**44898**	MDFVKEFLYVSDHAGFLELTTETWKNMWFPSQIPLSSDVAGIAQLNETDREFYKFLFVFLGLAERLVNFNIEDLVK EFNCHDATHYYAEQMAMENIHGKVYANILQLFFNGDMMKLKEYAVKVVADPTLKAKLDWLHTRVKNTKTRAEKVL IFLLIEGIFFISSFYSISLFRVRGMLNGICLANDYISKDELLHTRAAAVLYNSLIPAKERPDAAWIKRLFQEAVEVEYSFI AAKSKNVTLVVPGEIKKFLQATCDRILQSIGVEPIYGSHAPVTCPLSYNGCIKSVNFFEREGTDYSTKVTNDL
MuHV4gp60	**44899**	MATQTMDVEPVQTVNAIDAAIAELKLMAGHSHEANVLAGRLLHFKMREVCTQTVAQFLDAFSSVLDEGLCAFIGN YSQSLDEMVQRYVSGGFAAVKENGYLAAARFYDTYVLRNDVKYESVPHMFMRISAFCAYHCIQNECLFKTLKHM ELDRGNVVENAMDLITYFFEMIASQQVCCATPVMRSAGLRDANLSSCFIFAPALDSEEKTVDAVFSELTKLLACKS GVGMDLSTYSHGKNLHAVLKALDGQITYFNDHNIRPVSVAAYMEIWHTNIMDFLTAKLPENPERCGNLFQGVCIPE IFFRTYKNDPESNWYLFDPKKAEVLTNTYGYMFSIAYAGLVEQGAYEAVVPIKSVMFALVSCIIKTGGPYILNKKAIN RHDWHEWSTHQYRAINCANLCAEVIQYPGENVSTCNLANICLPKCLEDDKFVSGKSCLLTYEREFSIERLERATEA AVFIINACIHGGTLPTQRARRGQSDRSMGIGVQGLADTFAMMGLGYFDAGSEILDQKIAETLYFNALN G KGEPYANYEQSKHSIGVLHWHDWDMCSPMVYTRDEWEDLARSCEVHGVYNSQFVAYMPTAGTGQITGYSDSF YPFYSSMSSKVSNKEEILRPNMTLMSRMSDSEVQTLRECNWDIAKLPEPLLQKYRIFLSAFDYEPSLYVRRAMLRA PFIDQSQSMTLFLNEDYASSASNIKNLLMYGWECGLKTLMYYCRIRKTATSNEFECVRRNSQQKYVNCADGEGA GGEEPSENCIKAEGATCSLSVGASCLHCQ
MuHV4gp61	**44900**	MPFKLFKKLTISSVVTSATVNWATLASRTVFILPKRVLPYLRSVARLTRVVIAMDRYGGLLGGFLRAVPPVQKPLSL TDGNKFREGIMSEVGKYVSTLVDPRNMMLDSFHHLKHNKSLQGSFLVHAGTVSDQEVCGTPMFCYKDGLSNPEI DRLLTPISLTRLTVPNNENSDVFRIGNIIYSEDSGLFDIIPTLRTRLMERNLHEGLVFVGPLIKNINSSFVNKITTAIKGD TVLNESLSHGLVLKLPVEQFMDFETTNTFHYTGRLPMTHRSYIYYALGYVITADGTQSLLQKFFRTPIEGPEFTRLV RDYFAGEIRNFFLGDNDFGQGNFLMFGAVCRCGYFPEDSLLTRTRVSIKGGGLSLIEIPDFTVSRGPWQFI
MuHV4gp62	**44901**	MPSLNLFPSVSDSGFWTGGTALRNPPSRPPYLSIAMTTLVSLATDLKYGSTLLGRIKTVLDASVAQLTVADVTTEDI VNFLNSLNGIDHELFSFIRTYPVFFVLHLCTLDRTQTYTSGQVIKTIKHLITTFREVLCEDMGADNDSIISNSNILKDCS WYLTKLETEQMSTSIPHLPKSCITFPCMEQVHHLVHNATLATLPNSWTSPLPSLNSVYVQWFVLSYKHKVFPDEV PSSNIQDLADKMTNIYKHLFVPHTSQLTGASIILARSLDILSQFTPLEKIPSNSPAVAFGDDELSNIPSNCHLMFGHLI ESIYMGMTYACTLGAVEQFIREAFDVVLGVASEIKRTASLSDLPTVTKLVNIKRILIEHGLSETRCEEYAQALPKWQH REGIYPFEETLDHFHQKLSTLIKFCLEFYNTLMLVSPTSISHSYLKENNYLLQLDRKSAASQGQGPDDINLLEKVETF VYPQVPGQDLQRIHDAIDSDIMRTLFFSWVNRNWGIVLITQNPLMEPSCEHQVSEERVAAYCKRMPVGDLSYEPA MVSHKMFYKYFIRHIVGPTIQGIFSRKTSRNRALFQIRWLLSFAITDTPQLQEIRRPLGMFYFELLDIINGTNKPSAMK NLLDHALDLKKKINKINQTFSIPQDLILYLFVLDTGASYINSVDYITAIIPKVEHLLLRGRNILRLGSILCHTIKYNYHPLT HQFTILSSSGQILEVHLETLKSLISQVEKDHSQLLMEITDLEGELRGEYSTVLSLLQDLEAYKQHELGIEFDTEPWNQ

		LKQSFSGILSRISSGLSLLSKGCSSCLRKRFHDLFSQEIITPTILKAASAGNVEIIKNLKEIPVNLMAPPTDTSMTQAG GNPTDEDLTMLYSTYPQIFSQNAARGEKHPPQLKKYSSTYDRIPLDVNWQIFTQQTYTAEHAECPYTIVKIHDIIKLL S
MuHV4gp63	**44902**	MALPASLAGFRIEGTASTNQADCKFGENAGAQCLSNCIIYLMSSYFNNEAPITETHDLNKVLKFGAELDSNLRKLGL LSPGQYAQLDHVPCYVQTRKWSGFIYTSAEMFGLLGMPADISDSCITSLRDLLTANYSNTIQYILYICGQKSGAIIIQ GGRYTMFDPHCLKDIPESPAHVLSTSDPDALIKYVGGVSREYTACFLYFVPGHISPKNYIMSHYKVISFSDLHGSKII LEEYDLPTTNQSFCSSPQASSSPDPEVGSLLKYMSKAKRKRYPMSCGEEWTDANKKRKESGRTPPEKMTHPLP SPDIIDLTMDDDVIDLTGDDDMEDESEGDREAEPDRSGTSLPSVTLPNLAAVDQLLNSLTLPGHVPSFPALVDTDT GESYRLTRALHQLKNVLQQVLEIGVVSDSDYTPTEALNVLNYLMAWSKQLQIKNDDIKLLINSNLQIEKLFTLLKNNL ISDPNLADHVQAKVCACLPAMHANRATDLQKILLHCKNLTRALEISKSSLDIKDIITTFTESFPQDFFCVCSVEEANN LVSTVQDLKRVVSNNMALTSEQDARFKALMLSVLNNTDPPASLGPIYLETETRTPLLSSAIQEAVKAIEKDTVETLS ELISNIPSENAIETTFVPPVRTLLKNVTTLLTVINACVERAEIRTPEIDSSQQQLSYIGRELSKIIDETWPERAFREPVH VLDIFQKTSSHLNDLKKKMADSESLDKILSEINQTLKAIQDKAASPALINTLSDYIKNATVLAQASDPRLVEIQSQVTT LTTSTSYIESLLQKINIRTLPEVIPQLQAATKTEQGQLSLAAMNLSLIQITNSLINEALSSIHARSHNHLSNTFFNSLNS LMGLADIPGREDLIKTMESIMAVQEELVDCDDMECVEKGLTTFKYIKSSIRQYKFDKSFKTKIYLIITSEVRDLTKIKT DKQLEAWKQDVADFTPASIDDLNLFLDKAPTKTARSYATRQLKHFRDDLIKEQEMETETTPVPSTAEIERAIDLKIKA TWDKILTNLRDLTFHHIAPGDWQVLLTVFNDHKSALFTKMGGELLKALQGLTAYVDSILTPLLASQLPQGQRYVAP NSDWVETFDQNVKYYLRTFHLPRVSEQLDDLERKTLLLTKLVKFTDLSQSLIGTHLEKDWSIYQKLFNSLLTVYND HLIKTKTEVHAFLDKIASDPLLEPQAHPDLQKITQLFTEQEIIEINTLPDIFKESIKNNEKHYIASYQTEMKVFTSMVDA ALAKKTQSTTEYNTHLLKIVNNMLVQAPPYAASHPISSDAISYITSLVRDKHLLEKLSYAESLKNFNWLSRLITIILTNC HPSHKQHLQTLLDEILSREQTLTPLVALEDNANQSPTERTLQAALTTLNVERVLGRATTFQKWKSQLQELEEAVKT TTQVSLLIQTISSLHDKTVTEMDPTILSSHSQALADKLKELLALKPSLDETTMSLFHGMKAYAQFKHYFVQHYVITQP KIFDAYPLSHHGTVSSSGGHQATKFNPLMRLKAFSMVTDVKKMSVWREINTTVDPTGHTFIPAPPTPAMPPIHYNV LFSSFLQAEAINLALNSNQPPTKKFGLLPGLMDARVGVQGAMLLDNQWNDISTNSAKLLDHYVRSELTPNNSLTNS QFAAMTVFAHAMAMVTPHINSTRATIFPSKAIVLNQLQFLKLCLTMWPKFSGGLLRAPSFERVVQLARATLPTLLLS APRNTLNHFLANNYRPTDTLPNTEALLFYPNQHPLVNLEKLLLTSSPFHALSTSVLNTRISMLVWGILSLSEAVLQQ LWDSLYQESATFTTYIDLLRHLSAMNHKNSTLTTSTSLPQNNGPVVYSYGHTAGTTVATLEGSHPLDDGGQNIPM TLFEFVIFAIILKLKFHVFYTQEKALVNTQLGPLHLITHALDGTGDTEPFKTYISIPPQKYNGLGNLQQFCSQDEIQIFQ RQHEWLVGVTKQTSFSNEDLFIVLASADNKVLSVHTFNPPINSLESETPEIVAAPIQESWPKEITTVSFWDKPALEK SPQELITEVSLVAEIFSGSAIFNTFPPSYKMVSHTPSLHVETHQLENLSITEGTPPTSPPLPDSTTQDHMEEPDNKQ AKPPYQMTSPMKENTSTSGRPARSPSPSPPVLTPIKPIIPIPQATPTMPILSPFTPRLLPAAVKKHQNGAVWGHSG SLPPTHIQSSTPGPAQNTRDSGRRQIVSPVITILPGTKAGADSAGQNTSHKDISAYSPPPASKKTDRPSDTHVTAPL FSKSKLVTPRPAAKTDTGTFGPLLGHEKPPVTDLTAPVEPGHPSKVSPIIHLKPSNTGDRDPHPISDDEDSKQPPV PDTSRDKAQSRWKTPKQRPQNIFPPPKHEDDVPVTAPQPQGRKILVGGRQLPSLVYNPPTLRDIKTGMSDDKNP EPCVKENPPGVTHDPPLRIQHMEQTVNSSKYNVLLFIEKIIKSVHDHSSYMLSTLKRIKQLY
MuHV4gp64	**44903**	MNKDRVKAPAFHPELHNKLLERLKAAYGKDSIGKDPEEAPVPLLLHTCAVRFYEEYKELTRDNTLPTLVNKKGFPG DAKMMDPVLGIYHSGKKQGASSVPSSSGAFDGGSHGGPLPSVDLPQREGGLWYGLGPDKSGLGFVLPSDPGS MSDGNSFRMIPDPSSLTDKDDQNLGESTKTRSGNGKKK
MuHV4gp65	**44904**	MVMGALDYLRLMNISVDEFRSFCIYGHLSGQRGWGELLLSNLSFKRAVCHILKIQCETKKRWTNKVLVANSALSLL TLFRMVLHECVFSHKYFIPDRIEDMCFPLTKILTVPFLKALDLYLSQFSISCKFPIIKISTVNPTLLAFTKKKYLASVVS DQPIEVPAPSARPDPVRFTAAVPLASDEQSLVKALHSSTGTVQCGNPFYYMMTRLCLYGLMHGRGGIVPVSSSS KQSVYDVAIRFIGSRILSPIVRLPILSRALADLALTGHGHQITVCNECGHCLNLGRDKFLAVNFSPTSMFYCRDQKE KQFNICATTGRIYCSYCGATEFTVYDMVGRYATGEPFIRAVSSANSLSILDNSEQECDILIPCFGKSRSCSIKLRATF RELLYLTASVDNFICQKCSNKGDE
MuHV4gp66	**44905**	MANQKKLIDELCGIVTSFLCPQGIVPEIEKCSTKLPHFSKGGTKPVCTVRLQHGHTYHIEFVYKFWQHILGQLRLPL QPCFILTNNGLATTLKCFMSPPRDIDFQYGNRVNMACDVNLEKNSCVIIEDEDFLRFKSYHVFPKDVPIYNSMVVC RTYITDMRNAVQFFVVKPGNRRKIVHMLESIEEMPETPQQLYFCGGRGYKMIGAGLSLFFFAAIVALASKLVW
MuHV4gp67	**44906**	MTQEVFNTAILPLKYTGRHRVVKMYVPWSLETVTSHDSIMQMLLSKSYLPATPETGFHDPTLTHISSTLLPTSKCKI CNMLFEAVLEHNPPDSFFSEYATLCFYVLHAPVTWSATYITICDMLQIFSNAGLNHLITEKINSSKIMGIDFYLHFFAR QCFRHTTPDQVAQLENLHQVRLSLLSNTICNVQSAAHIQGIWSSSLETAHKKGAQSPDPPTGCPVKAVPHREFFS NTNRPSLLKIFSEAWKRSLLLDPDYSEPDTPVETVDTSQGPCLLSFPFSLKCRGNTSSVCVLCECLACHPEAARIL QEIKSTILTCLENNTSLLDRTAYTLMMYTTSKLIDDPDLAEIITSRGPNVLHKHLFCDPFCAINSLKTDPLVLFKYPSG PKFQIFTKALASGKYLAENALFDQPETELLVLALKACQLAQFPKKFEAEVLKGISRLGTTLTTVSPVHFFSVYT
MuHV4gp68	**44907**	MRSTGSAPSCSGESARAHRRRAGAMSIRSSRTKHSTAQKGAHRRRVSLAGFFNLIYKRQDLGLDFLREMSEPLC TSRPVLLPLNLKNIAPGRCISLTPFGHTDNLGFQCETCTDPNLNKSIPPKLEDPAFSKNELCSVTLTFYQQAEQVIQ HKQFYLSLLNLSMDAVRNSLTQPGLLYCYLVTKAFMLEGFPIFFEETNGMLGLYLVFRRDLLHLHESYLRLLIDNLG NYDISVDSVGRSYIIKLCPVGNVSRIPTIPADNVCLAVNNLDYGDDVKASWIECFNIVSRLSQQ
MuHV4gp69	**44908**	MLQHCISSFSAINFFLSNYLLIVFFLGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPER GSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAG CPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARP GVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCG SPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPA WGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEP VPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPP AGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDG GNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTG GTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRG PGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAKARSSTAEVRPVARRGAE
MuHV4gp70	**44909**	MGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGE PGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGD GAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPR SEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARE RAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLP GPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARG AGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVP RPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLG SRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGP

		PRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPKRGAA QQRSVQ
MuHV4gp71	**44910**	MGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGE PGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGD GAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPR SEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARE RAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLP GPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARG AGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLGSRSPPAGWGEPGGRGPGARERAARPGVRVP RPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGPPRRDGGNRGDGAPERGSGLPGPGCGSPGLG SRSPPAGWGEPGGRGPGARERAARPGVRVPRPGEPVPPGGMGGTGGTGPRSEGAGCPARGAGPPAWGAGP PRRDGGNRGDGAPERGSGLPGPGCGSPGLGSQSEEQHSRGPSSSEARRRMSPHRNQGLYITSVKKNTSKSVL LNYQQVIHKNRKRYQQVRRSGVDIP
MuHV4gp72	**44911**	MASQEFQGFLDSSLLNEEDCRQMIYRSEREHDARMVGVNVDQHFTSQYRKVLTTWMFCVCKDLRQDNNVFPLA VALLDELFLSTRIDRENYQSTAAVALHIAGKVRAYMPIKATQLAYLCGGATTADKLLTLEVKSLDTLSWVADRCLST DLICYILHIMHAPREDYLNIYNLCHPKIFCALCDGRSAMKRPVLITLACMHLTMNQKYDYYENRIDGVCKSLYITKEE LHQCCDLVDIAIVSFDENYFKINA
MuHV4gp73	**44912**	MSHKKSGTYWATLITAFLKTVSKVEELDCVDSAVLVDVSKIITLTQEFRRHYDSVYRADYGPALKNWKRDLSKLFT SLFVDVINSGRIVGFFDVGRYVCEEVLCPGSWTEDHELLNDCMTHFFIENNLMNHFPLEDIFLAQRKFQTTGFTFLL HALAKVLPRIYSGNVIYV
MuHV4gp74	**44913**	MPTSPPTTRNTTSGKTRSGCKRRCFNKPAAMPPKRRRAPKRPAPPPPPGCQGDEESSQGTQTPNPPSPPVPPS SPTLPSSPVPPSSPVHEPPSPSPPPAPPSPDVDVEGLDVGETDDPGPPPPKRYSRYQKPHNPSDPLPKKYQGM RRHLQVTAPRLFDPEGHPPTHFKSAVMFSSTHPYTLNKLHKCIQSKHVLSTPVSCLPLVPGTTQQCVTYYLLSFVE DKKQAKKLKRVVLAYCEKYHSSVEGTIVKAKPYFPLPEPPTEPPTDPEQPSTSTQASGTQHGPTASLDAGAEQGA TGSPGSSPGQQGQGSQT
MuHV4gp75	**44914**	MLVLRDLDLEDLQAFLENSSLSYDDYYDNATWIPDLASPCTVSLKYGVLFALALFMFVLSVLGNLTVVCVFCAYRA ACKGADVLMLVFCFVCMLASLAHVLEISHLLYTMPGSMLLCVLFTLYVSTLDFCIVFILMIISIHRCLLVMTPNRLFLN SKCFGACLAWFAVILAIGAAAVETVFVKPLDLSQIITHGAFICAMELGGTTRVSVRLAQQFLGIWIPVLIIVCFIMVVC RVRRMRMGKKYRIYVSFICTTILFLIFCVPGKIVALVDEVVRLGWVQETCEIRTVLATLGTASMILESLFCALVTLITSL FGSIFKKRMGESVRRAVCRLSS
MuHV4gp76	**44915**	MARHFAFIYFGDSQYNETEKELIEDTEAGRAPVDTSGHRFINIVCGSLIPSNPNNVNHEHVGIYKRIIQHAMSAESP RLPVTATPIDKSNSSRALALSYGPNTRWRPTTVSRELAAYLHDLIPEYSIRIESFRRVICTLENTPTNISNTRLLESAY GFLEDHFTANTVLSIMRPESAIENYETFTHSMLVSAPAPPPDPLTMKITYPNTTPLDSVLNHCSLGTYHRENLYPTM LHETLSTKFPMFLGQSADVQTAHWHTCSMFFNPGWVLENIYFASSWITGIDFQHSALGLYTLHPPEDQQPFHLVN KRSRAVLKKYSSLMRAMGLPICGGFSRPIRTTHALESGQDVLINASVTGTVPQNRLSTQDPRPGDLIVFLGDFVPT LHQETAPYLYTHSPLELNKILAVVKQLSDTTTQSCITKTIRPFGHPSMLEALTELIHPYGAYLDLNNLPQPIVSALNSS APAIHEEIVKHHFLSVHCPVYLLVISQDLGLEDAAERDATHNPLDMFLTFAENHKLPCGVIGTLVEDRGLHFCKELF DGGFPVKIEFTAQEATVPRGRLPRSRSFSRHKPMKFDQSFLWTTEHFNESVEAILKHPAVESKEYIVKHIDRLGQY TVGQQQGCGPLDLPVCDHSIMMCTALKTTPQPLDASGPRPTFTTLRVHSDSALDLINSPTCWLSNKEYSKPEVFP CVVTGVGEQYYKMQVDPVRGAVYGLVEAILNMLTSNCVHGWRKMAITGSISWSSDDPSYSLLYQTLMACKDFCY SLSIPITYTNATSGQTQDTGPRPGPTTNSIAFTAQCPGVMGTYRKTTPDFKSHGSYIIWLPMSQKLTLAGTIFQQIS KLKANKLHKLAPEYISNLAHALEMLTSRTAILSMHDVSDGGLIAAILEMAMAGNKGCNIEMPSYITRPFDMLISETPG MVIEVEKKSMEMVKAILKFKSLTYYKLGQVAKHGEEPVVEISHAGKQLFKAHLSTVMRWWRHTYSSHITQQCSNL SAKEKLYVLDYGNNKTDLGLMGPGMRSRHLRPVKCVDPDFGAYVCVACSPGQPPPHSLMSALSNSGFDPVPCN ILELAHTDLNEYSGIIFSGHSGAEKNVTAASILANSLVTNQDFTETLTRFYNKSHTFILGFGELGTQLLLALDIVNLDQ SNPQFISRTEERELFQHGALEPNASALLECLWLNFYVRQSRSVFLAPISGSVVPAWAVGTHLGINFNHDGAEQRL MTSGQISATFHGPEPGRNLEAAHYPRNPSGASNVAAFCSPDGRATAMLIDPSQSFFPWQWQYDAENLQCTPWQ ICFFRLLLWSLASRD
MuHV4gp77	**44916**	MDEDVWAIQVYARARTTLEEHVLNRLILSRTIHFPLRSTSICGVLTLTIRNSRTRNGRASSRRIRRWIQVAARLTCSD LTLDSTREPPDDGHGDAQRLDFIYGPFPGQRPLTWCNELTELLGYILPMGTTRMDYSRRICGIYTQPNAAILVMIEL LYWFIYGRERTQLEYDHLSTFEPSSRLTSPTVLSSEPDAVHANIMLAQGLGRTTYANSLSTFPEAVPTMIKLTGSE MATCHHTTITGPGNFLHANLSSISNMPGVIPVAINGGSYLICNQTVGDNPLAPCILTMLLKARSDHLRASGVPVTGG FIRPISSNQLTFPTEVNFVNFISKLSKDDYVSHNRPADPCNTFIVAVGSFCPLYRPDGPPYGYDSSPLTVRKLTRVL QEWTKDLSHACYIRSMMPQVRCSIQEILTELLSPMGALIDINDLPDPVCHGLRNRTQEELERGIRTKFLNVTTDQVF LLVQNETGTIQETQESVGTIEHLINLCAKYEVACSIVGKCCTEPNLHIISSTSNPVAVTYDTADIMLTIPLDYDHGQTG GLAASAPRPSREDGALNWASLNLRQVWSDIITHPAVESKEYILTHIRRVANGRVVQQPGCGPFDFPVADHSLVSL NSIHNTKSWTSDLTVVTSSEMVNRIMSDPDIWFCDPSTSDVPRLECVASAIGEQHYKVKEDPILGSTYGLVEALLN LNTCPGATLEKTIITCSVTCSQADVAHSELYDAIAECKNMCTMMGCTFMCDMAAKNPRNCDINSPLIVFSAKCIVDF PWRGRIGPNLKEHHNTLLWLPIHSQPTLAGSIFKTFNPHVPIHRLPQISVNALFKLLTNTQKLFEQDKIRSIHDVSDG GLLTCVAEMAMSGGKSVVMTLPDHIANPKAMLLSETPGYVIEVDNDSTDAILTFLQENSCVAMPIGRVVPLTESST FSVFHKSENLLSVPFFNVVGCWRRRHVDESTLLCTHLGPRRSIYAIEYGHNQFNFPGVSRYFLTSPVRSFRAPPH AQKRVCVIEFNGQTSLEGTLFMLQYAGFLPEIVHSSCLHDFETSLDRFCGIVFTGSMCTLHEHGGVLAAATRFTES HTVVSKLSAFCRRPDTFMLGFDQLGMQILLNLNILNITADKTMYDCKIDPLECMPLKKNASCTYESRWLNFYIPESN SLFFKPIQQNVFPSWIQGSNLGLPLDQHQESFWRNTRQICTYYQTEQPTPGIAAINYPRNPVAGSPVAGICSLDGR ITGCLIDPAESFFPWTWQFVPGNRALASTPWQLCFQQLLIWTLSTDGL
MuHV4gp78	**44917**	WTLRVFHPCSPSAEDLATQRGPPLAWGQNPGLECFLPTRVLECRAVLPSSEVDDRSRISMLFSRLAAAFTRDLSRR PRGFPRRPELLDFAYSHLQSLPPATALQELINSAVVGTHPLRANIRIDLTHHLLVTLLHEGSTLAEVTHRVLSYLHSWN RQLVTLPLGSDAETGLFPTSYRRPRPHPPDPVSSGIFLPRLGDRSSVCLGSTSPPLAYGTGYPLFLRGLTEVDHALD VRHTCLHLHARIQRPGHAVEPLLFLQAWLPGSRPVQSTLGLFILAPSQVTPLSSLQSTYAVQDQAGALYACGVGVP THENHELGFVVVHTSTTSSFDRNCHETWVNASHPAGGDIVLVGSLEDSPLADMPPHSNAQSPLIANGISQAIARLVG AIVKSIRPPYLSSLEELLLELLFPLSATIDLSYLSQDLLDELLASTDDNYEETCRQVFFNKVCCVIPLLVSNTPCIDHNTG DRLRQLCSSSGVTAVFLGRARPGAAGILVSDIRGAPPERRADFYLQDAYPRQPYYPLGPEPSNRGRTIPHHVRFPW SFMEFLLSHPDVESKEGIVRHLDRCGQGQVVQQQGCGPLDLPVSDYSTIYTGVYQSASKTIQVNTEIAQRLILDVDA VPTVLTNNHCICITTALGEQCRKVHLDPRRGVMYALLESLTNLFCSPHILVDDIHITAAVTCGPNLRHYELINYCLRCC EAGVCFSTTSASDSTPERSPSTPPLMTIVFTAQATGPLYLAPKPTPDFKSPGSHIIWVSLHPKFTLSASIAATILGLACT HRLVWKTLKTINHFLTRGAILSIHDISDGGLITCLLEMAMSGRRGAEIEIPAQVPCPYQFMLSETPGFICEVDPLRAQDI QGLCFAMIGFVSGNVPPATIRCMHNRNVIYQESLAHATMYWRSGFLREHMMKVGNLTPQEQQESLSLGYNRPYNL

		SKLCALSMAPGSSPPKVLLIVFPGQPTHHGTLTAFASMGFDIRPMDVTELYKTDPLTVSGCVIAGQRGTLLSETGGW LQNLQFLDWMNTFYQQKHTFILGFGEFATQVLLALNLTEWRCDRPFIATELEELINRPRLTANKVPLLQSLWLNVSLP FRPLHGSACPAWACGTHLGIDISSSSSGDTLSPGLIAARFATADGTAPATYYPRNPSGGTNVAALCSYDGRACTMV LYLHQWQHLDDQEAQESPWRQCLHHLLLWALAARET
MuHV4gp79	**44918**	MGENMRDTKPGPEECCDAETYLVGATHESGSGPEGRVEDAQTQSIRTDHWREDEAEPGDKTRETKIVRLALLSPL SPRLALSPPPPKKRGGGLISSLPARGPSPYPPPLGRQAPTAAQGSGVGGAGGWRGLEGGRPCQGVPVPPLPPP FPQSQSPGCPAVPRASRVALPPHSSDSGPLRPPRASSGPGALPAPTPPTPAPSAAPLPVLALSRVRVPVGGSRR GGGPGGGGV
MuHV4gp80	**44919**	MRQNLGTRRGRRKSFAWLSAPSPLAWLSAPHPPRRGGGGSSPASLPGGPAPTPHPWAGRHQQRPRAREWGV LGGGGGWRGEDPARESQCLPSPLPSPRARVQAAPQFPEPPGWRCRPTVQTLALSGLRGPAPAPAPSPPPLPRP QPPRRLPYLFWPSAGSGCLWAGPGGAGVRGAGVSSRGPPAGGRGTVSGDPRPPGAGPGLTFTLNFEGS
MuHV4gp81	**44920**	MAPQARPLPPGPEDGPRRAGAGGTGARRAPLPGAGPPPPGVGGRGRGPLPGRGTPPARPPSPGPGPPQASP ASPGPGSPGVGGGGARPPRGEEGLGPCSGMPSDRV

Supporting Information Table 2. The 192 highest scoring H-2K^b–restricted octameric epitopes from all 81 MHV68 open reading frames, as predicted by the consensus epitope prediction algorithm. The program, including documentation for its execution and sample data, is freely available at http://jura.wi.mit.edu/bioc/grotenbreg. Epitopes identified to give an CD8$^+$ T cells response in B6 mice are highlighted in red.

peptide	Orf	Position	arb-score	smm-score	uda-score	park-score	arb-rank	smm-rank	uda-rank	park-rank	median rank
ISMLFSRL	44917	64	-0.463	-2.478	-2.089	-4.796	1	1	1	180	**1**
RSYIYYAL	44900	272	-0.452	-2.424	-1.672	-7.003	3	2	18	2	**2.5**
AGYIYYQL	44846	15	-0.382	-2	-1.56	-7.367	20	12	27	1	**16**
WIFVYGSM	44896	42	-0.389	-1.868	-1.038	-6.174	16	20	171	26	**23**
FSPCYLSL	44860	499	-0.269	-1.808	-1.922	-6.398	193	26	5	20	**23**
KSLTYYKL	44915	940	-0.392	-1.904	-1.413	-5.663	14	18	44	55	**31**
YSFVFSTL	44862	147	-0.424	-2.009	-1.308	-5.394	6	11	69	112	**40**
AGLQYRGL	44874	315	-0.27	-1.785	-1.673	-5.576	189	30	17	58	**44**
LDFAYSHL	44917	98	-0.362	-1.635	-0.541	-6.182	32	64	729	25	**48**
VSLKYGVL	44914	42	-0.308	-2.031	-1.796	-5.481	99	10	12	87	**49.5**
IQFAYDKL	44848	459	-0.325	-1.807	-1.122	-6.269	74	27	135	21	**50.5**
ISNNYHKL	44847	35	-0.229	-1.662	-1.862	-5.576	386	55	6	59	**57**
SYLAYSFL	44865	39	-0.356	-1.827	-1.136	-5.489	38	24	124	79	**58.5**
FNMVFSGL	44887	237	-0.338	-1.773	-1.365	-4.883	60	34	57	171	**58.5**
FSIAYAGL	44899	334	-0.318	-2.138	-1.453	-5.394	87	5	37	111	**62**
TGFRYSYM	44859	304	-0.309	-1.802	-0.699	-6.451	98	29	481	15	**63.5**
FVVPFLRL	44874	414	-0.322	-1.69	-1.347	-4.606	76	47	63	272	**69.5**
ISLHPAKL	44844	176	-0.331	-1.686	-1.231	-2.675	65	50	84	1672	**74.5**
MYNLYSNL	44864	154	-0.278	-1.896	-1.22	-5.576	168	19	91	64	**77.5**
ATQSYAGL	44856	222	-0.321	-1.582	-1.225	-6.588	77	82	85	5	**79.5**
AIFVTSRL	44877	304	-0.46	-1.632	-1.195	-4.061	2	66	100	454	**83**
RGVMYALL	44917	700	-0.301	-1.806	-0.447	-5.671	112	28	878	54	**83**
SCLDYSHL	44893	108	-0.251	-1.5	-1.636	-5.671	278	119	20	53	**86**
IIYNFLNI	44849	993	-0.32	-2.099	-1.217	-5.47	81	8	92	94	**86.5**
YSLLYQTL	44915	750	-0.227	-1.723	-1.364	-5.299	403	41	59	117	**88**
FTFVYPQV	44901	465	-0.312	-1.559	-1.802	-3.871	92	86	10	524	**89**
AILKFKSL	44915	935	-0.292	-1.7	-1.41	-5.065	135	45	46	140	**90.5**
IIGYYVML	44896	140	-0.216	-1.513	-1.278	-5.576	456	110	75	72	**92.5**
TSFPFLCL	44878	270	-0.252	-1.608	-1.524	-5.299	268	73	31	116	**94.5**
SSFYSISL	44898	163	-0.394	-1.541	-1.211	-3.186	12	94	95	1037	**94.5**
VTVLYNLL	44896	330	-0.221	-1.613	-1.437	-5.299	436	70	42	120	**95**
INHTYLQL	44859	496	-0.165	-1.411	-2.005	-5.94	852	172	2	34	**103**
IKYVYNFL	44881	483	-0.175	-1.535	-1.154	-5.799	748	97	113	41	**105**
VSQKVKHL	44850	204	-0.343	-1.427	-1.443	-3.584	55	160	39	723	**107.5**
IIFLVVVL	44848	744	-0.296	-1.543	-1.457	-3.273	124	93	36	998	**108.5**
MSNHFQNL	44846	642	-0.327	-2.069	-1.096	-4.788	73	9	146	210	**109.5**
MQYFYMFL	44896	242	-0.255	-2.129	-0.973	-6.908	252	6	213	3	**109.5**
AAQLYRGL	44861	205	-0.267	-1.365	-1.618	-6.493	200	200	23	9	**111.5**
MTNIYKHL	44901	244	-0.159	-1.511	-1.396	-5.299	913	112	48	115	**113.5**
RILDYMKL	44886	81	-0.268	-1.998	-0.903	-5.94	196	13	273	33	**114.5**
SCFLFKGL	44879	139	-0.296	-1.502	-1.12	-5.394	121	116	137	96	**118.5**
SLPVFPSL	44870	180	-0.267	-1.355	-1.565	-5.8	199	208	25	40	**119.5**
IILIFLLM	44888	463	-0.3	-1.743	-1.131	-4.883	113	40	129	166	**121**
FLFVFLGL	44898	55	-0.366	-1.505	-0.936	-5.299	29	114	238	128	**121**
KGFLFATL	44879	61	-0.275	-1.748	-0.615	-5.576	177	39	595	68	**122.5**
SSYMLSTL	44902	2442	-0.294	-1.783	-1.144	-4.102	130	32	118	396	**124**
ASFGFFFL	44844	53	-0.284	-1.701	-0.846	-5.394	154	44	319	97	**125.5**
LSDLYSHL	44870	305	-0.357	-1.697	-0.98	-3.88	36	46	206	519	**126**
LSPFTPRL	44902	2142	-0.345	-1.404	-1.254	-4.19	51	176	78	349	**127**
YYFLFLRL	44875	66	-0.294	-1.582	-0.921	-5.299	132	81	250	124	**128**

LVVDFASL	44849	578	-0.274	-1.671	-1.172	-4.978	179	53	108	149	**128.5**
MSALFPGL	44857	406	-0.39	-2.31	-0.928	-4.606	15	3	244	259	**129.5**
STLIFNSL	44881	491	-0.247	-1.649	-1.56	-4.701	296	59	26	220	**139.5**
ISYITSLV	44902	1284	-0.278	-1.5	-1.39	-2.492	166	118	49	2297	**142**
IYFIFGAV	44877	104	-0.299	-1.688	-1.026	-3.091	114	49	180	1175	**147**
AAVLYNSL	44898	198	-0.18	-1.366	-1.497	-5.394	700	199	35	98	**148.5**
YSIYYMEL	44853	62	-0.044	-1.419	-1.143	-5.299	2759	166	120	131	**148.5**
MVFKLLGL	44845	357	-0.344	-1.638	-0.941	-3.178	54	63	235	1100	**149**
RSYATRQL	44902	968	-0.308	-1.484	-1.027	-4.882	101	128	179	176	**152**
SFPTFISL	44844	171	-0.261	-1.557	-0.869	-6.077	224	87	297	30	**155.5**
LILLFLLL	44857	336	-0.265	-1.521	-1.085	-4.883	208	106	150	165	**157.5**
KYVEYGSL	44860	175	-0.162	-1.412	-1.085	-5.481	884	171	148	82	**159.5**
MCFDVTNL	44847	535	-0.286	-1.528	-1.04	-3.455	149	103	170	808	**159.5**
RSPSTPPL	44917	772	-0.348	-1.413	-1.067	-4.19	45	169	157	354	**163**
FYPFYSSM	44899	604	-0.273	-1.455	-0.962	-6.493	181	146	222	12	**163.5**
MSCYARPL	44850	131	-0.296	-1.379	-1.113	-2.303	122	190	139	3457	**164.5**
IFTSFPFL	44878	268	-0.353	-1.531	-0.785	-4.701	40	101	390	231	**166**
RIIKFSLL	44869	110	-0.268	-1.646	-0.964	-5.16	198	61	218	138	**168**
ILFAVISL	44860	706	-0.346	-1.283	-1.445	-3.186	50	289	38	1051	**169.5**
SSPEYPRA	44857	294	0.207	-1.78	-1.687	-4.372	8354	33	16	307	**170**
IIPKVEHL	44901	670	-0.296	-1.343	-1.386	-3.956	123	218	50	497	**170.5**
VVYSYGHT	44902	1827	0.247	-1.704	-1.33	-4.605	8957	42	64	278	**171**
ILSQFTPL	44901	272	-0.279	-1.1	-1.285	-4.796	164	582	72	186	**175**
LTLAFVSL	44884	47	-0.241	-1.483	-1.184	-4.701	326	130	102	228	**179**
IWKSFANL	44844	185	-0.33	-1.457	-0.968	-3.369	69	144	216	913	**180**
IIYHQIGL	44844	384	-0.363	-2.262	-0.693	-4.284	30	4	494	336	**183**
VNFFNRPL	44867	24	-0.294	-1.325	-1.255	-3.178	127	243	77	1084	**185**
ANIKYIRM	44861	311	-0.119	-1.252	-1.851	-5.853	1415	332	7	39	**185.5**
SFCIYGHL	44904	21	-0.254	-1.334	-1.096	-5.394	255	234	145	103	**189.5**
LSKLFTSL	44912	71	-0.307	-1.404	-0.984	-3.187	102	177	204	1029	**190.5**
QIRVFSSL	44849	530	-0.293	-1.455	-0.936	-3.274	133	147	237	946	**192**
TKYNYHPL	44901	694	-0.089	-1.282	-1.214	-5.704	1896	291	93	50	**192**
MMYTTSKL	44906	333	-0.256	-1.703	-0.496	-5.064	244	43	805	142	**193**
IFLRPSPL	44850	121	-0.347	-1.346	-1.037	-2.675	49	213	173	1666	**193**
ASFLLSLL	44869	157	-0.318	-1.276	-1.222	-3.186	86	300	88	1046	**194**
LGSVYYKL	44847	491	-0.338	-1.246	-0.435	-5.758	58	336	915	42	**197**
IGGVYALL	44896	166	-0.253	-1.477	-0.881	-5.671	261	133	286	52	**197**
VITLTSRL	44864	8	-0.401	-1.518	-0.877	-3.273	9	107	290	994	**198.5**
IIVCFIMV	44914	226	-0.311	-1.848	-0.858	-2.675	94	21	306	1625	**200**
ITQQCSNL	44915	988	-0.393	-1.473	-0.91	-3.774	13	136	266	554	**201**
IAPEFTPV	44891	170	-0.242	-1.548	-1.382	-3.774	321	90	51	561	**205.5**
YSYVYSLT	44860	429	0.262	-1.465	-1.054	-4.7	9204	139	166	246	**206**
INFATDRL	44851	45	-0.332	-1.438	-0.915	-3.966	64	155	260	492	**207.5**
FTAVFPGL	44851	192	-0.287	-1.573	-0.644	-4.606	148	84	555	273	**210.5**
ILLPTYNL	44872	302	-0.44	-1.45	-0.899	-3.273	5	148	277	960	**212.5**
GSVYYKLL	44847	492	-0.201	-1.273	-1.202	-5.299	534	306	97	119	**212.5**
LSLAAMNL	44902	812	-0.33	-1.659	-0.815	-2.58	68	57	358	2011	**213**
YSTIYTGV	44917	634	-0.268	-1.334	-1.127	-3.091	194	235	133	1274	**214.5**
LSVPFFNV	44916	934	-0.262	-1.657	-0.963	-2.58	220	58	219	2090	**219.5**
SNTFFNSL	44902	845	-0.25	-1.28	-1.404	-4.883	284	295	47	170	**227**
VARVFYAL	44861	188	-0.38	-1.622	-0.79	-2.997	21	68	387	1302	**227.5**
HITMFMSL	44896	52	-0.276	-1.31	-0.428	-4.788	174	262	935	195	**228.5**
CHLMFGHL	44901	303	-0.269	-1.376	-0.515	-4.606	191	191	781	271	**231**
IVVRIIRL	44877	330	-0.356	-1.493	-0.823	-2.675	37	121	346	1676	**233.5**
MSQPTALL	44885	232	-0.341	-1.493	-0.631	-4.19	56	120	573	356	**238**
SYYFYKHA	44893	184	0.288	-1.554	-0.955	-4.7	9701	88	228	248	**238**
AVGSFCPL	44916	354	-0.318	-0.984	-0.917	-4.701	84	875	253	226	**239.5**
AMVTYSNV	44841	138	-0.245	-1.462	-1.036	-3.55	308	141	174	727	**241**

RGIFYNNL	44869	386	-0.182	-1.821	-0.727	-5.758	677	25	452	44	**248**
ATLCFYVL	44906	99	-0.302	-1.315	-0.694	-4.701	110	257	492	241	**249**
FVPHTSQL	44901	252	-0.294	-0.911	-1.007	-4.372	129	1116	192	310	**251**
FSFHVPIM	597855	24	-0.262	-1.287	-1.153	-2.996	217	286	115	1315	**251.5**
FNQFYNFL	44847	553	-0.257	-1.201	-0.913	-6.58	240	399	263	6	**251.5**
KLQMFPNL	44849	605	-0.298	-1.179	-0.794	-5.887	119	445	385	37	**252**
SVLNHCSL	44915	214	-0.285	-1.222	-1.553	-2.398	150	367	28	2762	**258.5**
AIYSFRNA	44897	74	0.206	-1.753	-0.992	-4.371	8326	37	201	320	**260.5**
AVVQFIRV	44891	253	-0.275	-1.233	-1.221	-2.493	176	352	90	2266	**264**
KIFDAYPL	44902	1478	-0.452	-1.492	-0.77	-3.36	4	122	406	936	**264**
VGTFFMML	44896	265	-0.241	-1.64	-0.418	-4.788	330	62	959	202	**266**
VNLVFPSV	44864	132	-0.222	-1.53	-1.769	-2.485	431	102	13	2417	**266.5**
FILGFGEL	44915	1125	-0.24	-1.753	-0.317	-4.788	336	38	1193	208	**272**
GALDYLRL	44904	4	-0.114	-1.168	-1.369	-5.481	1498	462	54	91	**276.5**
FVYLFHFM	44877	167	-0.163	-1.483	-0.751	-6.215	880	129	425	24	**277**
DIVQFVYL	44893	272	-0.239	-1.344	0.337	-4.788	342	215	4071	189	**278.5**
SVPPVTRL	44869	127	-0.257	-1.261	-1.948	-3.592	239	320	4	658	**279.5**
IAPVWFPL	44896	282	-0.249	-1.294	-1.314	-3.497	286	278	67	741	**282**
SVYGFTGV	44849	682	-0.237	-1.831	-0.959	-4.102	346	22	225	393	**285.5**
IPFPLSTL	44872	72	-0.26	-1.274	-0.906	-3.186	227	305	270	1061	**287.5**
LIPIYQHA	44887	127	0.245	-1.302	-0.99	-4.372	8927	268	202	308	**288**
VAVLYAQI	44847	5	-0.178	-1.302	-1.083	-4.372	723	269	151	313	**291**
LAWAYACL	44895	6	-0.179	-1.184	-1.082	-5.489	704	436	153	76	**294.5**
VIPDPSSL	44903	157	-0.252	-1.402	-0.845	-3.861	269	178	322	533	**295.5**
ISTVNPTL	44904	135	-0.298	-1.301	-0.837	-2.398	117	270	331	2800	**300.5**
GSIVYEGL	44872	113	-0.122	-1.158	-1.33	-5.394	1365	488	65	113	**300.5**
FRVLYIKL	44850	190	-0.249	-1.263	-1.009	-4.372	289	318	191	317	**303**
SGFIYTSA	44902	99	0.165	-1.783	-1.064	-4.061	7633	31	159	452	**305.5**
HVPSFPAL	44902	370	-0.202	-1.205	-0.955	-5.705	524	391	227	46	**309**
IYLIYKKI	44863	673	-0.135	-1.265	-1.279	-4.372	1191	316	73	305	**310.5**
MAPQARPL	44920	1	-0.232	-1.318	-1.441	-3.402	373	252	40	906	**312.5**
VVYTTDRL	44887	34	-0.147	-1.399	-0.759	-4.787	1054	180	414	214	**314**
STPHAIHL	44857	425	-0.271	-1.174	-1.133	-3.592	185	454	126	654	**319.5**
IVYSIYYM	44853	60	-0.32	-1.413	0.018	-4.007	79	170	2371	472	**321**
SGATFSLL	44888	57	-0.205	-1.504	-0.064	-5.16	510	115	2037	137	**323.5**
AAFFVCQL	44885	95	-0.341	-1.099	-1.348	-3.273	57	586	62	985	**324**
LIFRTLYL	44896	26	-0.328	-1.315	-0.691	-4.148	72	258	499	391	**324.5**
ALLNFLGL	44858	170	-0.245	-1.087	-0.826	-4.701	306	605	344	232	**325**
KIYFYAKA	44849	149	0.284	-1.567	-0.686	-5.064	9625	85	507	146	**326.5**
LHTLFFRL	44846	458	-0.256	-1.199	-0.712	-4.701	249	405	468	240	**327**
LSLDTSTL	44851	376	-0.266	-1.324	-0.77	-3.368	207	247	409	922	**328**
LVFCFVCM	44914	86	-0.166	-1.153	-1.059	-5.394	834	495	162	95	**328.5**
WIAAFHYL	44864	59	-0.223	-1.332	0.327	-4.788	423	238	4021	204	**330.5**
IVYKESRL	44880	533	-0.307	-1.511	-0.644	-1.981	104	113	553	3818	**333**
LSPLSPRL	44918	71	-0.278	-1.144	-1.205	-3.497	170	504	96	758	**337**
SQYTVHHL	44846	391	-0.097	-1.284	-1.314	-4.189	1778	288	68	386	**337**
FFLLYLIL	44856	200	-0.15	-1.238	-0.837	-5.299	1034	345	330	126	**337.5**
IVRVHQNL	44869	84	-0.231	-1.27	-1.641	-0.971	374	310	19	6564	**342**
AVFGAVNL	44877	251	-0.23	-1.271	-1.109	-3.273	384	309	141	979	**346.5**
SLVAFNAL	44886	208	-0.244	-1.216	-0.239	-4.701	313	380	1438	235	**346.5**
ISTNSAKL	44902	1604	-0.362	-1.255	-0.809	-2.675	31	328	368	1651	**348**
ISQAIARL	44917	405	-0.416	-1.66	-0.325	-3.592	7	56	1174	649	**352.5**
YNYYTYSL	44848	663	-0.26	-1.159	-0.624	-4.787	225	481	582	217	**353**
INLINQPL	44844	234	-0.227	-1.278	-1.17	-2.58	408	298	109	2143	**353**
SYLMTSSL	44846	790	-0.31	-1.261	-0.783	-3.186	96	319	392	1035	**355.5**
FYYVFLPV	44863	804	-0.205	-1.415	-0.976	-3.912	509	167	209	504	**356.5**
AIQVYARA	44916	7	0.159	-1.337	-0.751	-4.467	7504	226	423	291	**357**
SMQLFESL	44880	19	-0.254	-1.132	-0.721	-5.895	257	525	457	35	**357**

GSFEYTGA	44887	303	0.192	-1.429	-0.953	-3.966	8101	159	229	496	**362.5**
MDFLTAKL	44899	276	-0.271	-1.335	0.656	-3.966	184	231	6505	495	**363**
IAFNTKPV	44860	251	-0.284	-1.153	-0.947	-1.481	155	496	231	4497	**363.5**
VNALFKLL	44916	819	-0.108	-1.176	-0.895	-4.788	1609	451	279	206	**365**
RGPGFSCL	44893	775	-0.191	-1.485	0.053	-6.077	608	127	2528	29	**367.5**
IINWYSAI	44881	559	-0.237	-1.148	-0.781	-4.467	347	499	395	292	**371**
TNYKFSLV	44885	148	-0.133	-1.19	-1.278	-4.371	1221	422	74	323	**372.5**
LIRTFTKL	44860	310	-0.272	-1.588	-0.639	-3.733	183	78	562	571	**372.5**
FVVPYAKI	44881	319	-0.174	-1.175	-0.98	-4.372	760	453	207	297	**375**
SSHLLQRL	44894	41	-0.233	-1.212	-0.84	-2.398	366	386	327	2651	**376**
SILDSVPL	44893	229	-0.246	-1.219	-0.785	-2.762	300	371	389	1516	**380**
STFDLQGL	44862	507	-0.263	-1.475	-0.645	-3.273	213	135	549	959	**381**
WQLCFQQL	44916	1258	-0.234	-1.2	-0.568	-4.788	363	402	681	211	**382.5**
IVFFLGGM	44908	22	-0.35	-1.463	-0.595	-3.091	44	140	633	1191	**386.5**
CNRIYARL	44896	124	-0.129	-1.285	-1.798	-3.967	1260	287	11	487	**387**
VISKFESL	44855	159	-0.225	-1.229	-0.73	-5.065	417	358	447	141	**387.5**
ITYFFEMI	44899	164	-0.076	-1.214	-0.783	-5.201	2147	383	393	132	**388**
SGHRFINI	44915	36	-0.229	-1.288	-0.27	-4.138	389	285	1339	392	**390.5**
FYYMMTRL	44904	204	-0.242	-1.364	-0.218	-4.007	322	202	1495	475	**398.5**
KLFYYVFL	44863	802	-0.181	-1.039	-1.145	-5.992	689	725	117	31	**403**
MRFRFQVM	44842	1	-0.213	-1.24	-0.318	-4.277	467	343	1191	337	**405**
LSPPMAHL	44863	524	-0.24	-1.196	-0.779	-3.592	338	414	397	653	**405.5**
LAIGFPIL	44896	225	0.008	-1.164	-0.829	-4.701	4072	471	340	239	**405.5**
VLKKYSSL	44915	314	-0.241	-1.118	-1.251	-3.967	328	552	79	488	**408**
LIFLTVLL	44865	46	-0.282	-1.151	-0.831	-3.966	159	497	336	494	**415**
FSLTLHNL	44891	202	-0.219	-1.616	-0.784	-2.667	442	69	391	1700	**416.5**

Supporting Information Table 3. The 192 highest scoring H-2D^b–restricted nonameric epitopes from all 81 MHV68 open reading frames, as predicted by the consensus epitope prediction algorithm. The program, including documentation for its execution and sample data, is freely available at http://jura.wi.mit.edu/bioc/grotenbreg. Epitopes identified to give an CD8$^+$ T cells response in B6 mice are highlighted in red.

peptide	orf	Position	arb-score	smm-score	uda-score	park-score	Arb -rank	smm-rank	uda-rank	park-rank	mid-rank
AMLGNPETL	44885	178	-0.61	-1.599	-2.215	-3.933	7	23	5	12	**9.5**
FSLLNLLRM	44869	114	-0.566	-1.966	-1.76	-4.012	18	7	30	2	**12.5**
KALHNPKTL	44881	765	-0.654	-1.904	-1.85	-3.892	2	9	21	27	**15**
CALENPGYI	44869	176	-0.565	-1.468	-1.925	-3.971	19	37	16	7	**17.5**
MAVCNSFYI	44877	238	-0.51	-1.715	-1.884	-3.892	32	13	19	30	**24.5**
AHLTNLLTL	44848	11	-0.481	-0.9	-1.986	-3.898	51	170	13	24	**37.5**
ASPQTTAPM	44888	437	-0.541	-1.58	-1.607	-2.012	25	27	53	579	**40**
ALLQNLQFL	44917	1088	-0.435	-0.532	-2.025	-3.977	75	392	10	6	**42.5**
LAFVNSYFM	44863	648	-0.557	-1.67	-1.515	-3.494	21	16	77	109	**49**
CQLLNTIPV	44880	265	-0.495	-1.266	-2.391	-2.477	39	66	1	402	**52.5**
YQCYNSATM	44848	157	-0.631	-1.084	-2.034	-3.301	6	105	9	200	**57**
SATVNWATL	44900	17	-0.572	-0.799	-1.946	-3.535	13	212	14	101	**57.5**
DQLLNSLTL	44902	359	-0.495	-1.447	-1.491	-3.778	40	39	82	76	**58**
AQLENLHQV	44906	168	-0.481	-1.253	-1.812	-2.676	50	70	26	282	**60**
VALLNFLGL	44858	169	-0.37	-1.021	-2.132	-4.012	146	122	6	4	**64**
FSAVNCHPL	44860	295	-0.497	-0.991	-2.287	-3.535	37	133	3	100	**68.5**
FSLGTCDPI	44849	333	-0.467	-1.823	-1.417	-1.933	56	11	107	868	**81.5**
KSWTNLLAL	44877	23	-0.587	-1.02	-1.607	-3.494	11	123	52	112	**82**
AASQNLSSM	44881	92	-0.514	-1.053	-1.529	-3.614	30	112	70	98	**84**
YMFLMLGPM	44896	246	-0.412	-1.969	-1.432	-1.494	90	6	103	2497	**96.5**
FAVLTQHHL	44884	26	-0.482	-2.403	-1.233	-1.933	48	1	174	822	**111**
FQYGNRVNM	44905	104	-0.508	-1.549	-0.966	-3.342	33	28	364	195	**114**
CAEANFDHI	44875	463	-0.421	-1.108	-1.328	-2.795	81	101	129	253	**115**
FMMLALVTM	44896	269	-0.331	-1.584	-1.633	-1.535	206	26	45	2313	**125.5**
AMHMKLSPM	44863	1012	-0.336	-1.267	-1.501	-0.535	202	65	79	8101	**140.5**
FGAVNLFLI	44877	253	-0.353	0.105	-1.397	-3.614	173	1491	114	99	**143.5**
EQIKNTKCI	44866	296	-0.395	-0.807	0.243	-3.857	115	208	3771	35	**161.5**
YSPENAAKL	44863	1208	-0.292	-0.049	-1.85	-3.971	302	1113	22	8	**162**
HLLQNPEEI	44887	195	-0.304	-0.105	-1.517	-3.857	264	989	75	32	**169.5**
HVINNTDVI	44860	560	-0.34	-0.549	-1.291	-3.778	195	374	145	94	**170**
RVVSNNMAL	44902	548	-0.342	-0.511	-1.283	-3.778	191	407	150	72	**170.5**
FSNTNRPSL	44906	230	-0.317	-0.508	-1.988	-3.456	228	410	12	117	**172.5**
VNLLTADTM	44880	413	-0.393	-1.413	-1.163	-1.819	118	45	231	1501	**174.5**
KALAVLAPV	44858	122	-0.662	-1.185	-1.1	-0.67	1	85	271	6878	**178**
SMVVCRTYI	44905	149	-0.404	-0.885	-1.211	-2.012	102	175	190	601	**182.5**
QALSTMLAM	44863	1005	-0.479	-2.012	-1.033	-1.892	53	5	315	1096	**184**
RGMLNGICL	44898	174	-0.32	-0.012	-1.704	-3.415	226	1202	37	148	**187**
AALTTNLSL	44857	63	-0.55	-1.665	-0.962	-1.933	23	17	367	852	**195**
AAERNHDNV	44864	163	-0.315	-0.941	-1.251	-1.456	235	154	161	2702	**198**
HLLCNAVEL	44847	70	-0.284	0.03	-1.625	-3.778	324	1295	46	73	**198.5**
RVHQNLSCL	44869	86	-0.18	-0.673	-1.536	-3.459	741	291	68	113	**202**
SSQKNRYTI	44854	561	-0.314	-0.648	-1.239	-3.535	239	309	167	102	**203**
QAIRTLPVM	44841	220	-0.401	-1.948	-1.05	-1.971	111	8	305	746	**208**
LAAMNLSLI	44902	814	-0.309	-0.609	-1.233	-3.494	247	335	173	111	**210**
TVLTNNHCI	44917	673	-0.407	-0.622	-0.954	-3.819	97	327	380	53	**212**

RQFFNKDML	44863	1265	-0.23	-0.781	-1.236	-3.301	529	230	170	203	**216.5**
AAILVMIEL	44916	147	-0.408	-1.201	-0.988	-1.933	94	78	351	840	**222.5**
SGGTNVAAL	44917	1230	-0.284	0.418	-1.457	-3.456	323	2552	91	124	**223.5**
LALLTLLFV	44877	29	-0.395	-1.788	-1.01	-0.67	117	12	336	6863	**226.5**
KQLTNSGPT	44848	813	-0.289	-0.952	-1.309	-2.477	310	148	136	397	**229**
FMLQYAGFL	44916	1019	-0.642	-0.877	-1.074	-1.313	3	178	287	4461	**232.5**
LAIINGSIV	44890	55	-0.263	-0.956	-1.456	-2.591	401	144	93	328	**236**
SLVYNPPTL	44902	2373	-0.252	-0.241	-1.61	-3.819	442	763	51	50	**246.5**
VMTPNRLFL	44914	146	-0.235	-0.55	-1.585	-3.456	511	373	58	121	**247**
SAITNHAAF	44855	308	-0.279	-0.936	-2.13	-1.933	345	155	7	798	**250**
LSNNNPTTI	44888	67	-0.197	-0.557	-1.303	-3.415	669	365	138	150	**257.5**
VSLAVFLEI	44871	251	-0.318	-0.682	-1.159	-2.012	227	280	236	589	**258**
FAEDNKVII	44878	338	-0.088	-0.743	-1.141	-2.757	1456	249	250	268	**259**
FALALFMFV	44914	50	-0.632	-0.441	-1.661	-0.711	5	489	41	6683	**265**
KKLFNPQPI	44875	157	-0.262	-0.143	-1.325	-3.778	407	922	131	89	**269**
IQPDNISEI	44849	1000	-0.134	-0.433	-1.738	-3.819	1035	497	34	46	**271.5**
VTLPNLAAV	44902	350	-0.386	-0.183	-1.154	-2.597	125	846	240	322	**281**
LAVALLDEL	44911	72	-0.569	-0.706	-1.043	-1.971	15	264	306	754	**285**
KLLTNTQKL	44916	824	-0.32	0.039	-0.992	-3.778	225	1322	348	86	**286.5**
KQLILHSFM	44871	164	-0.504	-0.681	-1.066	-1.778	36	282	294	1795	**288**
APVHNMHYL	44863	1347	-0.26	-0.502	-1.243	-3.819	413	418	166	66	**289.5**
DHIANPKAM	44916	870	-0.351	-0.501	-0.158	-3.778	175	421	2072	69	**298**
FALVAMGPL	44844	39	-0.145	-1.652	-1.996	-2.012	961	18	11	585	**301.5**
YSEKNQTPL	44857	214	-0.166	-0.588	-2.231	-2.795	828	354	4	254	**304**
CAVSHQDCL	44852	28	-0.422	-0.77	-0.957	-1.892	80	238	374	1045	**306**
DATHNPLDM	44915	501	-0.28	-0.689	-0.354	-3.415	338	275	1428	144	**306.5**
SLPQNNGPV	44902	1819	-0.293	0.218	-1.665	-2.597	300	1799	40	313	**306.5**
KQRLNNAIL	44846	817	-0.568	-0.585	-0.394	-2.778	16	356	1332	262	**309**
SMLEALTEL	44915	431	-0.023	-1.006	-1.61	-2.091	2176	130	50	491	**310.5**
KALESLILL	44857	331	-0.406	-0.151	-1.557	-2.05	100	911	66	523	**311.5**
KALASGKYL	44906	394	-0.558	-0.459	-1.269	-1.892	20	472	155	1091	**313.5**
FAIESLQRM	44863	375	-0.589	-0.859	-0.88	-2.091	10	182	447	490	**314.5**
SMFFNPGWV	44915	261	-0.327	-0.498	-1.277	-2.155	218	428	153	451	**323**
NAIQVWLTL	44877	125	-0.457	-1.27	-0.679	-2.012	63	64	724	583	**323.5**
AGPHNDMEI	44846	487	-0.215	0.085	-1.558	-3.933	585	1434	65	13	**325**
AMTVFAHAM	44902	1632	-0.58	-0.569	-1.023	-1.535	12	362	325	2321	**343.5**
TLLKNVTTL	44902	637	-0.162	-0.335	-1.467	-3.898	855	615	86	22	**350.5**
SAIENYETF	44915	176	-0.109	-1.037	-1.623	-2.012	1240	118	47	598	**358**
KVYANILQL	44898	99	-0.288	-0.503	-0.655	-3.301	314	417	760	232	**365.5**
VSSANSLSI	44904	348	-0.21	0.055	-1.377	-3.456	607	1364	118	125	**366**
IQNYVQWPM	44846	289	-0.481	-1.049	-0.757	-1.342	52	115	618	3915	**366.5**
LMIVMGTWL	44852	92	-0.397	-2.109	-0.753	-1.971	113	2	623	732	**368**
QVPENKTTI	44880	146	-0.133	-0.314	-1.491	-3.857	1047	659	83	38	**371**
FLHANLSSI	44916	246	-0.208	-0.181	-1.728	-3.421	609	848	36	139	**374**
SAVVGTHPL	44917	120	-0.023	-0.923	-1.945	-2.012	2179	161	15	596	**378.5**
ASLAHVLEI	44914	95	-0.275	-0.509	-1.409	-1.933	355	409	110	819	**382**
ILIRNARPL	44851	35	-0.188	-0.255	-1.826	-3.819	705	747	24	59	**382**
SVLGNLTVV	44914	60	-0.224	-0.481	-1.583	-2.597	551	450	60	320	**385**
HMLESIEEM	44905	179	-0.516	-0.301	-1.45	-1.971	29	680	95	724	**387.5**
NQLESLATL	44875	26	-0.493	-0.048	-1.428	-1.977	43	1114	104	684	**394**
VQPQALSTM	44863	1002	-0.078	-1.289	-1.454	-1.977	1548	61	94	699	**396.5**
IAMTTLVSL	44901	34	-0.282	-0.848	-0.862	-1.535	329	186	470	2384	**399.5**

TVHVNGHCL	44897	230	-0.191	-0.378	-1.162	-3.421	698	567	234	142	**400.5**
LQIEKLFTL	44902	447	-0.372	-0.583	-0.879	-0.936	142	357	448	5647	**402.5**
FAHHLCQYV	44872	203	-0.456	-0.433	-1.037	-0.155	64	498	309	10236	**403.5**
NSLTNSQFA	44902	1623	0.043	-0.424	-1.574	-2.632	3061	510	61	302	**406**
ASKLNYHTV	44862	618	-0.298	-0.4	-1.199	-1.632	280	536	195	2233	**408**
VTLANQTKI	44861	16	-0.255	-0.366	-0.938	-3.819	425	582	393	58	**409**
SSISMCLPL	44893	61	-0.193	-1.586	-1.289	-1.933	688	25	146	872	**417**
TLPVMCFPM	44841	224	-0.247	-0.681	-0.955	-1.898	464	281	379	891	**421.5**
SSVVTSATV	44900	12	-0.482	-1.367	-0.633	-0.711	49	49	801	6693	**425**
ASVVSDQPI	44904	152	-0.315	-0.149	-1.11	-2.012	236	916	264	587	**425.5**
IVGVNGDNM	44845	14	-0.262	-0.414	-0.863	-3.421	402	523	468	128	**435**
RCMHNRNVI	44917	947	-0.2	0.125	-1.218	-3.301	652	1546	185	220	**436**
CSIGNCGKL	44875	419	-0.281	-0.395	-0.418	-3.892	334	545	1271	29	**439.5**
SVLLNYQQV	44910	700	-0.178	-0.43	-1.165	-2.518	751	501	229	378	**439.5**
VSVAVLGFL	44845	373	-0.299	-0.838	-0.37	-2.012	277	193	1390	609	**443**
FANNTVFCM	44861	286	-0.457	-1.47	-0.619	-1.456	62	36	830	2746	**446**
HGVYNSQFV	44899	578	-0.392	-0.243	-0.775	-2.591	119	760	579	324	**451.5**
KIIYNFLNI	44849	992	-0.3	-0.325	-0.281	-3.857	276	627	1673	41	**451.5**
DSVLNHCSL	44915	213	-0.034	-0.543	-0.809	-3.892	2030	380	529	28	**454.5**
FSIANTYLT	44883	230	-0.053	-0.369	-1.014	-2.632	1831	579	331	303	**455**
AGIVSSQPL	44892	158	-0.282	0.594	-1.586	-2.012	330	3409	57	581	**455.5**
TSLEGTLFM	44916	1012	-0.066	-0.754	-1.021	-2.012	1671	244	329	582	**455.5**
AAVKQSAYL	44855	226	-0.545	0.128	-1.032	-2.012	24	1557	316	595	**455.5**
FFLSNYLLI	44908	14	-0.142	-0.42	-0.93	-3.819	982	515	400	47	**457.5**
AAVCKMRPI	44846	889	-0.278	-1.098	-0.785	-0.933	348	103	567	5672	**457.5**
AMHANRATD	44902	480	-0.248	-0.992	1.199	-2.155	463	132	9677	460	**461.5**
LQKINIRTL	44902	786	-0.199	-0.166	-1.085	-2.778	653	886	280	266	**466.5**
WQLCFQQLL	44916	1258	-0.377	-0.245	-1.223	-1.778	135	757	182	1809	**469.5**
HAIVGATPL	44893	582	-0.106	-0.817	-1.519	-1.971	1268	202	72	744	**473**
PKLPNQHPM	44842	167	-0.258	-0.393	-0.808	-2.778	417	546	530	257	**473.5**
YSVGMGAEI	44853	4	-0.362	-1.291	-0.633	-1.892	157	60	798	1094	**477.5**
FMIDNNFST	44849	237	-0.147	-0.391	-0.919	-2.632	939	549	410	299	**479.5**
FSLSVMMAV	44877	232	-0.288	-0.524	-0.787	-0.632	313	396	564	7204	**480**
LSLFFFAAI	44905	209	-0.336	-0.059	-1.16	-1.971	203	1090	235	728	**481.5**
YAVYWHEQM	44878	369	-0.203	-0.962	-1.003	-1.193	637	143	344	5303	**490.5**
KAPAFHPEL	44903	7	-0.346	-0.213	-1.583	-1.892	184	798	59	1129	**491**
VAVGSFCPL	44916	353	-0.271	-0.163	-1.799	-2.012	370	891	29	612	**491**
MQLATLCLL	44841	1	-0.239	-1.053	-0.844	-1.857	494	113	493	1252	**493.5**
FATQVLLAL	44917	1116	-0.504	-0.923	-0.622	-1.614	35	162	826	2241	**494**
YVYVNGQSV	44880	30	-0.239	0.122	-1.004	-2.079	493	1535	343	503	**498**
LMLVSPTSI	44901	421	-0.309	-0.086	-1.463	-1.971	249	1034	89	747	**498**
HAVEPLLFL	44917	271	-0.14	-0.454	-0.855	-2.05	999	474	477	524	**500.5**
KGLTTFKYI	44902	892	-0.304	-0.862	-0.231	-1.971	267	181	1822	738	**502.5**
SAPMKTVTI	44846	164	-0.262	-0.347	-1.415	-0.933	406	601	108	5668	**503.5**
KAKRKRYPM	44902	269	-0.35	-0.637	-0.702	0.108	177	315	692	14404	**503.5**
GQLATCEVI	44863	1170	-0.28	-1.285	-0.715	-1.778	339	62	675	1928	**507**
TCLENNTSL	44906	316	-0.328	0.011	-0.628	-3.898	214	1252	808	16	**511**
FAYSHLQSL	44917	100	-0.253	-0.44	-0.799	-1.535	434	490	545	2379	**517.5**
SAVPFIWCL	44896	18	-0.277	-0.49	-0.763	-1.933	349	440	597	826	**518.5**
IAPVWFPLM	44896	282	-0.26	-0.325	-1.231	-1.392	412	625	176	3385	**518.5**
YVAPNSDWV	44902	1084	-0.307	0.087	-0.938	-2	251	1439	394	660	**527**
YMLSTEHQM	44870	168	-0.194	-1.625	-0.957	-1.892	682	21	376	1130	**529**

SVLVNGIAA	44863	914	-0.028	-0.257	-1.885	-2.597	2101	743	18	317	**530**
SSVTGKFEM	44848	133	-0.003	-0.882	-1.15	-1.933	2414	176	241	825	**533**
NNLMNHFPL	44912	126	-0.055	-0.092	-2.323	-3.819	1809	1018	2	49	**533.5**
HSLVSLNSI	44916	611	-0.225	0.631	-0.896	-2.05	550	3613	428	525	**537.5**
DSMANQDTA	44887	436	-0.184	-0.348	-1.225	-2.114	722	599	180	479	**539**
SGLTSSFAL	44844	33	-0.33	0.676	-1.61	-1.933	208	3849	49	873	**540.5**
LSPMGFIHM	44863	1017	0.214	-0.533	-1.106	-1.971	6474	391	268	705	**548**
SAPAIHEEI	44915	463	-0.3	0.768	-1.347	-1.933	275	4397	122	823	**549**
IQEQNIPSL	44881	517	-0.138	-0.206	-1.07	-2.722	1010	811	291	270	**551**
HSIMMCTAL	44915	634	-0.419	-1.698	-0.504	-1.892	85	14	1041	1032	**558.5**
WVNRNWGIV	44901	496	-0.235	0.204	-0.842	-2	506	1755	495	613	**559.5**
RKLINLGRM	44878	89	-0.225	-0.368	-0.484	-3.857	547	580	1092	44	**563.5**
ESLKNFNWL	44902	1304	-0.17	-0.615	-0.471	-4.05	802	330	1119	1	**566**
QGLENQEIV	44862	512	-0.162	0.069	-1.215	-2.67	852	1393	188	284	**568**
FTFDNALKM	44863	444	-0.24	-0.317	-0.223	-3.342	489	654	1853	185	**571.5**
SLPKNSLDI	44893	709	-0.125	0.455	-1.617	-3.898	1103	2728	48	21	**575.5**
KILTNLRDL	44902	1015	-0.283	-0.191	-0.324	-3.857	326	830	1536	40	**578**
NSLVLSSAI	44849	158	-0.277	0.235	-0.777	-2.012	350	1852	577	580	**578.5**
FSISCKFPI	44904	124	-0.188	-0.465	-1.462	-1.933	706	463	90	880	**584.5**
YSFRNASSL	44897	76	-0.137	-0.085	-2.113	-3.415	1021	1038	8	149	**585**
FQNITPISV	44891	36	-0.288	-0.695	-0.604	-0.041	312	269	861	12480	**586.5**
ANFQNSMSL	44857	168	-0.135	0.685	-1.414	-3.421	1033	3883	109	141	**587**
SGLKNISSI	44893	55	-0.078	-0.033	-1.757	-4.012	1550	1148	31	5	**589.5**
IAVGKTTAL	44859	335	-0.327	-0.655	-0.59	-0.933	219	300	883	5696	**591.5**
SAGCFLECM	44896	305	-0.303	-0.303	-0.825	-1.535	268	673	512	2350	**592.5**
AAVTCGPNL	44917	728	-0.358	-0.606	-0.395	-1.933	160	337	1329	850	**593.5**
VALTKLPVV	44862	196	-0.186	-0.452	-1.31	0.289	712	477	135	15939	**594.5**
SYVKNSFVL	44893	663	-0.173	-0.298	-0.825	-3.898	770	684	511	18	**597.5**
AAYCKRMPV	44901	526	-0.204	-0.38	-0.795	0.845	631	564	549	24722	**597.5**
FLPEHLLAI	44869	23	-0.237	0.53	-1.364	-1.977	499	3074	119	698	**598.5**
KNLSNCTDI	44885	40	-0.149	0.037	-1.096	-3.778	932	1319	276	93	**604**
SNLAHALEM	44915	858	-0.336	-0.097	-1.464	-1.819	204	1004	87	1767	**604**
KMVSHTPSL	44902	2044	-0.258	-0.293	-0.821	-1.892	415	690	519	1099	**604.5**
TMLAMHMKL	44863	1009	-0.267	-1.359	-0.466	-1.933	392	50	1136	820	**606**
SGVQLPQPL	44887	48	-0.21	0.531	-0.908	-2.012	604	3078	420	611	**607.5**
QNLQFLDWM	44917	1091	-0.279	-0.094	-0.891	-1.936	343	1012	432	787	**609.5**
FQHPWIQEI	44866	199	-0.242	-0.449	-0.67	-0.643	483	481	737	7100	**610**
MMLAIGFPI	44896	223	-0.472	0.38	-1.418	-1.892	54	2389	106	1124	**615**
CAPGMPGEI	44874	228	-0.342	-1.307	-0.418	-1.892	190	57	1272	1042	**616**
NVVENAMDL	44899	155	-0.168	-0.014	-0.906	-3.898	811	1198	421	15	**616**
LSLLTLFRM	44904	73	-0.244	-1.5	-0.178	-1.971	476	32	2023	756	**616**
AKLLNHFLI	44847	441	-0.118	0.212	-1.494	-3.819	1153	1780	81	56	**617**
AAMEACLPL	44852	76	-0.139	-0.751	-1.739	-1.535	1004	246	33	2344	**625**