>SEQUENCE\_01|HIGH

MKKTAIAIAVALAGFATVAQAMQTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG

>SEQUENCE\_02|LOW

MKQSTIALALLPLLFTPVTKAMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRALRQMHHHHHH

>SEQUENCE\_03|MEDIUM

MKYLLPTAAAGLLLLAAQPAMALPSGSDPAFSQPKSVLDAGLTCQGASPSSVSKPILLVPGTGTTGPQSFDSNWIPLSTQLGYTPCWISPPPFMLNDTQVNTEYMVNAITALYAGSGNNKLPVLTWSQGGLVAQWGLTFFPSIRSKVDRLMAFAPDYKGTVLAGPLDALAVSAPSVWQQTTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVSNSPLDSSYLFNGKNVQAQAVCGPLFVIDHAGSLTSQFSYVVGRSALRSTTGQARSADYGITDCNPLPANDLTPEQKVAAAALLAPAAAAIVAGPKQNCEPDLMPYARPFAVGKRTCSGIVTP

>SEQUENCE\_04|MEDIUM

MKKIWLALAGLVLAFSASALPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHTSSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIEEQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSHKIDNYLKLLKCRIIHNNNC

>SEQUENCE\_05|LOW

MKRNILAVIVPALLVAGTANAFPQMLRDLRDAFSRVKTFFQTKDEVDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPEAKDHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQIKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTIKAR

>SEQUENCE\_06|MEDIUM

MKRNILAVIVPALLVAGTANASEEAKPATTTTIKNTKPQCRPEDYATRLQDLRVTFHRVKPTLQREDDYSVWLDGTVVKGCWGCSVMDWLLRRYLEIVFPAGDHVYPGLKTELHSMRSTLESIYKDMRQCPLLGCGDKSVISRLSQEAERKSDNGTRKGLSELDTLFSRLEEYLHSRK

>SEQUENCE\_07|MEDIUM

MKKKNIYSIRKLGVGIASVTLGTLLISGGVTPAANAAQHDEAVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDAQAPKVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDAQAPKVDANSYNLICYFTNWAQYRPGLGSFKPDDINPCLCTHLIYAFAGMQNNEITTIEWNDVTLYKAFNDLKNRNSKLKTLLAIGGWNFGTAPFTTMVSTSQNRQTFITSVIKFLRQYGFDGLDLDWEYPGSRGSPPQDKHLFTVLVKEMREAFEQEAIESNRPRLMVTAAVAGGISNIQAGYEIPELSKYLDFIHVMTYDLHGSWEGYTGENSPLYKYPTETGSNAYLNVDYVMNYWKNNGAPAEKLIVGFPEYGHTFILRNPSDNGIGAPTSGDGPAGPYTRQAGFWAYYEICTFLRSGATEVWDASQEVPYAYKANEWLGYDNIKSFSVKAQWLKQNNFGGAMIWAIDLDDFTGSFCDQGKFPLTSTLNKALGISTEGCTAPDVPSEPVTTPPGSGSGGGSSGGSSGGSGFCADKADGLYPVADDRNAFWQCINGITYQQHCQAGLVFDTSCNCCNWPARGHPFEGKPIPNPLLGLDSTRTGHHHHHH

>SEQUENCE\_08|LOW

MRRTTGRAIAMAMLLALGQHAWAAACPGWAEGTAYKVGDVVSYNNANYTALVAHTAYVGANWNPAASPTLWTPGGSCAGGDPTPPTPPNPPTPPSPPPGNTVPFAKHALVGYWHNFANPSGSAFPLSQVSADWDVIVVAFADDAGNGNVSFTLDPAAGSAAQFIQDIRAQQAKGKKVVLSLGGQNGSVTLNNATQVQNFVNSLYGILTQYGFDGIDLDLESGSGIVVGAPVVSNLVSAVKQLKAKIGPNFYLSMAPEHPYVQGGFVAYGGNWGAYLPIIDGLRDDLSVIHVQYYNNGGLYTPYSTGVLAEGSADMLVGGSKMLIEGFPIANGASGSFKGLRPDQVAFGVPSGRSSANSGFVTADTVAKALTCLTTLQGCGSVKPAQAYPAFRGVMTWSINWDRRDGYTFSRPVAASLRQQPVAAQAGKKKAARATRTAWHHHHHH

>SEQUENCE\_09|MEDIUM

MMRGSHHHHHHGMARGYGRKKRRPASPGASMMHHHHHHMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEA

>SEQUENCE\_10|MEDIUM

ADAQQNKFNKDQQSAFYEILNMPNLNEEQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPKMSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK

>SEQUENCE\_11|MEDIUM

ADAQQNKFNKDQQSAFYEILNMPNLNEEQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPKMATKAVCVLKGDGPVQGIINFEQKESNGPVKVWGSIKGLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGRTLVVHEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQL

>SEQUENCE\_12|MEDIUM

MKVKNTIAATSFAAAGLAALAVAVSPPAAAGDLVGPTSSNKSTTGSGETTTAAGTTASPGAASGPKVVIDGKDQNVTGSVVCTTAAGNVNIAIGGAATGIAAVLTDGNPPEVKSVGLGNVNGVTLGYTSGTGQGNASATKDGSHYKITGTATGVDMANPMSPVNKSFEIEVTCS

>SEQUENCE\_13|LOW

MTMITPNSSSVPGDPLESTCRHASLLAVVLQRRDWENPGVGDLVGPTSSNKSTTGSGETTTAAGTTASPGAASGPKVVIDGKDQNVTGSVVCTTAAGNVNIAIGGAATGIAAVLTDGNPPEVKSVGLGNVNGVTLGYTSGTGQGNASATKDGSHYKITGTATGVDMANPMSPVNKSFEIEVTCS

>SEQUENCE\_14|HIGH

MKKTAIAIAVALAGFATVAQAMANPYERGPNPTDALLEASSGPFSVSEENVSRLSASGFGGGTIYYPRENNTYGAVAISPGYTGTEASIAWLGERIASHGFVVITIDTITTLDQPDSRAEQLNAALNHMINRASSTVRSRIDSSRLAVMGHSMGGGGTLRKASQRPDLKAAIPLTPWHLNKNWSSVTVPTLIIGADLDTIAPVATHAKPFYNSLPSSISKAYLELDGATHFAPNIPNKIIGKYSVAWLKRFVDNDTRYTQFLCPGPRDGLFGEVEEYRSTCPF

>SEQUENCE\_15|MEDIUM

MKIKTGARILALSALTTMMFSASALAKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITK

>SEQUENCE\_16|MEDIUM

MNNNDLFQASTTTFLAQLGGLTVAGMLGPSLLTPRRATAKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITKRKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFGYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK

>SEQUENCE\_17|LOW

MNNNDLFQASTTTFLAQLGGLTVAGMLGPSLLTPRRATAMAEVQLVESGGSLVKPGGSLRLSCAASGFTFSNYSMNWVRQAPGKGLEWISSISGSSRYIYYADFVKGRFTISRDNATNSLYLQMNSLRAEDTAVYYCVRSSITIFGGGMDVWGRGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPASVSGSPGQSITISCAGTSSDVGGYNYVSWYQQHPGKAPKLMIYEDSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLAVLGAAAEQKLISEEDLNGAAHHHHHH

>SEQUENCE\_18|MEDIUM

MKIKTGARILALSALTTMMFSASALAKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITKMAEVQLVESGGSLVKPGGSLRLSCAASGFTFSNYSMNWVRQAPGKGLEWISSISGSSRYIYYADFVKGRFTISRDNATNSLYLQMNSLRAEDTAVYYCVRSSITIFGGGMDVWGRGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPASVSGSPGQSITISCAGTSSDVGGYNYVSWYQQHPGKAPKLMIYEDSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLAVLGAAAEQKLISEEDLNGAAHHHHHH

>SEQUENCE\_19|MEDIUM

MKTILPAVLFAAFATTSAWAHHHHHHDDDDKGVAPLHLGKCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISD

>SEQUENCE\_20|MEDIUM

MKIKTGARILALSALTTMMFSASALAHHHHHHKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITKEKLYFQGAGTACSCGNSKGIYWFYRPSCPTDRGYTGSCRYFLGTCCTPAD

>SEQUENCE\_21|HIGH

MKKTAIAIAVALAGFATVAQADIQMTQSPSSLSASVGDRVTITCRASQDISNYLSWYQQKPGKAPKLLIYYTSKLHSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGKMLPWTFGQGTKVEIKRTVAAPSVF

>SEQUENCE\_22|MEDIUM

MKYLLPTAEAGLLLLLAAPQIASDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

>SEQUENCE\_23|LOW

MKIKTGARILALSELTTMMFSASALASDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

>SEQUENCE\_24|MEDIUM

MKKTAIAIAVALAGFATVAQASEANGAALSNPNANQTTKNVYSWLANLPNKSNKRVVSGHFGGYSDSTLAWIKQCARELTGKMPGILSCDYKNWQTRLYVADQISYGCNQELINFWNQGGLVTISVHMPNPGFHSGENYKTILPTSQFQNLTNHRTTEGRRWKDMLDKMADGLDELQNNGVTVLFRPLHEMNGEWFWWGAEGYNQFDQTRANAYISAWRDMYQYFTHERKLNNLIWVYSPDVYRDHVTSYYPGANYVDIVALDSYHPDPHSLTDQYNRMIALDKPFAFAEIGPPESMAGSFDYSNYIQAIKQKYPRTVYFLAWNDKWSPHNNRGAWDLFNDSWVVNRGEIDYGQSNPATVLYDFENNTLSWSGCEFTDGGPWTSNEWSANGTQSLKADVVLGNNSYHLQKTVNRNLSSFKNLEIKVSHSSWGNVGSGMTARVFVKTGSAWRWNAGEFCQFAGKRTTALSIDLTKVSNLHDVREIGVEYKAPANSNGKTAIYLDHVTVRHHHHHH

>SEQUENCE\_25|LOW

MGSSHHHHHHSSGLVPRGSHMASMTGGQQMGRGSEFCNHLRHQDANFSWKSLQLLQNTAPPPPQPCPQQDVTFPFPETLLKSKDKKQAAITTLRILQHLFNMLSSPHTPKHWIDRTRHSLLNQIQHYIHHLEQCFVNQGTRSQRRGPRNAHLSINKYFRSIHNFLQHNNYSACTWDHVRLQARDCFRHVDTLIQWMKSRAPLTASSKRLNTQHHHHHH

>SEQUENCE\_26|MEDIUM

MKKTAIAIAVALAGFATVAQAMNEVLEERYDARFWQSRLEDLVEHYRPFSSSGRNAEYIPALGKIDSNQLGICVIGSDQTMIKAGNSDVSFTLQSISKVISFIAACLTKGISYVLDRVDVEPTGDAFNSIIRLEMHKPGKPFNPMINAGALTVSSILPGESALGKIESLHDVIEKMIGKRLEINEEVFRSEWQTAHRNRALAHYLKETGFLEADVEETLEVYLKQCSMEGSTEDIALIGMILANDGYHPFRREHVIPKDVARLTKALMLTCGMYNASGKFAAFVGIPAKSGVSGGIMCAVPASVKREQPFQHGCGIGIYGPAIDDYGNSMTGGMLLKHIAREWDLSIFHHHHHHHHHHLDYKDDDDK

>SEQUENCE\_27|LOW

MGSHHHHHHKELNRFADLTYHEFKNKYLSLRSSKPLKNSKYLLDQMNYEEVIKKYRGEENFDHAAYDWRLHSGVTPVKDQKNCGSCWAFSSIGSVESQYAIRKNKLITLSEQELVDCSFKNYGCNGGLINNAFEDMIELGGICPDGDYPYVSDAPNLCNIDRCTEKYGIKNYLSVPDNKLKEALRFLGPISISVAVSDDFAFYKEGIFDGECGDQLNHAVMLVGFGMKEIVNPLTKKGEKHYYYIIKNSWGQQWGERGFINIETDESGLMRKCGLGTDAFIPLIE

>SEQUENCE\_28|LOW

MGSSHHHHHHSSGLVPRGSHMAPLCLSQQLRMKGDYVLGGLFPLGEAEEAGLRSRTRPSSPVCTRFSSNGLLWALAMKMAVEEINNKSDLLPGLRLGYDLFDTCSEPVVAMKPSLMFLAKAGSRDIAAYCNYTQYQPRVLAVIGPHSSELAMVTGKFFSFFLMPQVSYGASMELLSARETFPSFFRTVPSDRVQLTAAAELLQEFGWNWVAALGSDDEYGRQGLSIFSALAAARGICIAHEGLVPLPRADDSRLGKVQDVLHQVNQSSVQVVLLFASVHAAHALFNYSISSRLSPKVWVASEAWLTSDLVMGLPGMAQMGTVLGFLQRGAQLHEFPQYVKTHLALATDPAFCSALGEREQGLEEDVVGQRCPQCDCITLQNVSAGLNHHQTFSVYAAVYSVAQALHNTLQCNASGCPAQDPVKPWQLLENMYNLTFHVGGLPLRFDSSGNVDMEYDLKLWVWQGSVPRLHDVGRFNGSLRTERLKIRWHTSDNQKPVSSAWSHPQFEK

>SEQUENCE\_29|LOW

MATPVVRKGRCSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLKNGVQTCLNPDSADVKELIKKWEKQVSQKKKQKNGKKHQKKKVLKVRKSQRSRQKKTT

>SEQUENCE\_30|LOW

MKYLLPTAAAGLLLLAAQPAMAAPADKPQVLASFTQTSASSQNAWLAANRNQSAWAAYEFDWSTDLCTQAPDNPFGFPFNTACARHDFGYRNYKAAGSFDANKSRIDSAFYEDMKRVCTGYTGEKNTACNSTAWTYYQAVKIFG

>SEQUENCE\_31|MEDIUM

MVKQSTIALALLPLLFTPVTKAAVGTNHLLSGEILDTNGHLRNGDFDLVMQEDCNAVLYNGNWQSNTANKGRDCKLTLTNRGELIIKNGDGSIVFRSGSQSERGDYALVVHPEGKLVIYGPSVFEINPWVPGLEHHHHHH

>SEQUENCE\_32|LOW

MKKLLFAIPLVVPFYSHSTMELEMVHNISLSSRKALHNVHLPYMVQLPKPTGYNVALKNAAEGYDKARRMVAWLYDIADYESSIPQTFTLQQKTDKYTWELSDNFPPHLAVVPPDQSVSAPSIFSPVRLAQTLLIMSSLWYDDHTDLAPGPEQNTMQKLTQWNQERHKDQGWLIKDMFNAPNIGLRNDWYTDEVFAQQFFTGPNSTTITLASDVWLTAFTSEAKAQGKDKVIALFESAPPNSFYVQDFSDFRRRMGAKPDEELFNDSDGAMRYGCAAVALFYLTAMGKLHPLAIIPDYKGSMAASVTIFNKRTNPLDISVNQANDWPWRYAKTCVLSSDWALHEMIIHLNNTHLVEEAVIVAAQRKLSPSHIVFRLLEPHWVVTLSLNALARSVLIPEVIVPIAGFSAPHIFQFIRESFTNFDWKSLYVPADLESRGFPVDQLNSPKFHNYAYARDINDMWTTLKKFVSSVLQDAQYYPDDASVAGDTQIQAWCDEMRSGMGAGMTNFPESITTVDDLVNMVTMCIHIAAPQHTAVNYLQQYYQTFVPNKPSALFSPLPTSIAQLQKYTESDLMAALPLNAKRQWLLMAQIPYLLSMQVQEDENIVTYAANASTDKDPIIASAGRQLAADLKKLAAVFLVNSAQLDDQNTPYDVLAPEQLANAIVIHHHHHH

>SEQUENCE\_33|MEDIUM

MKYLLPTAAAGLLLLAAQPAMAMAEVQLVQSGAEVAKPGASVKVSCKASGYSFSTYNIHWVRQAPGQGLEWIGTIYPGIGDTSYNQKFKGKATLTADKSTSTAYLELSSLRSEDTAVYYCARSDIYYGNYNALDYWGQGTLVTVSSSGGGSGGGGTGGGGSIVMTQSPLSLPVTPGEPASISCRASQSIVHSYGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQRSYVPWTFGQGTKVEIKRAAALEHHHHHH

>SEQUENCE\_34|MEDIUM

MSANKNIWIIRLGVAFVCVAIGAAQANEKDGSAVTSGNWSLLGGGNEQHYFSALKDVNKSNVKNLGLSWFTDMEAGDGLVGNPLVADGVIYQGGPPGKIYANDLKTGKNLWTYTPEVQYDKDTSWTGFWFTHVNRGLAVDDDNVYIGSYCKLLAVSRTTHKLTWSSQSCDPKKMQAITGAPRVGGGKVFIGNASGDFGGDRGHLDAFDAKTGKHLWRFYTMPGDPSKPFENDLLAKASKTWGTDYWKYTKGGVSPWDAITYDEASDTLYFGTDGPSPWSPAQRAPDAGDELFSHSIIAVDASTGAYKWHFQTVQNDGSNMSATMHIMLADLPVEGVSKRVVMTAPKNGYFYVLDASTGKFISADHYVPVNWTKGLDPKTGRPIPSNEANYWERPGEMTIPLPGDVGGHNWEAMAYNPELRTVYIPSTLVPVTVVASKDTGELDLDYYYGMRPDATIKTQGDLVAWDPLLQKEKWRAKRSLPVNGGVLATAGGLVFQGTGDGHFEAFDANTGEKLWSFHVGGSILAAPTTVEVDGDQYLIVASGNGGASGMRGIPRLMNNLQSQGPARLLAFRLGGKTELPITSTPDFPKPQYPKPTSAMAESGRHIFNANACGACHGFNAEGSTPGLPDLRRSDKLDLAVMKSIVIDGAFKPLGMPGHPHISDADLQALQAFILQKAWTAYDTQQTLKTSDTGAQ

>SEQUENCE\_35|MEDIUM

MKCILFKWVLCLLLGFSSVSYSREFTIDFSTQQSYVSSLNSIRTEISTPLEHISQGTTSVSVINHTPPGSYFAVDIRGLDVYQARFDHLRLIIEQNNLYVAGFVNTATNTFYRFSDFTHISVPGVTTVSMTTDSSYTTLQRVAALERSGMQISRHSLVSSYLALMEFSGNTMTRDASRAVLRFVTVTAEALRFRQIQREFRQALSETAPVYTMTPGDVDLTLNWGRISNVLPEYRGEDGVRVGRISFNNISAILGTVAVILNCHHQGARSVRAVNEDSQPECQITGDRPVIKINNTLWESNTAAAFLNRKSQFLYTTGK

>SEQUENCE\_36|MEDIUM

MKKMFMAVLFALASVNAMAADCAKGKIEFSKYNENDTFTVKVAGKEYWTSRWNLQPLLQSAQLTGMTVTIKSSTHHHHHH

>SEQUENCE\_37|LOW

MKKTAIAIAVALAGFATVAQAGAPVPVDENDEGLQRALQFAIAEYNRASNDKYSSRVVRVISAKRQLVSGIKYILQVEIGRTTCPKSSGDLQSCEFHDEPELAKYTTCTFVVYSIPWLNQIKLLESKCQGGGGGMSPILGYWKIKGLVQPTRLLLETLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGSPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLSHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVSFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPK

>SEQUENCE\_38||HIGH

MASRTLSGALALAAAATAVLAAPATVAHRSPPGTKDVTAVLFEWDYVSVAKECTSTLGPAGYGYVQVSPPAEHIQGSQWWTSYQPVSYKIAGRLGDRAAFRSMVNTCHAAGVKVVVDTVINHMSAGSGTGTGGSSYTKYDYPGLYSAPDFDDCTAEITDYQDRWNVQHCELVGLADLDTGEEYVRQTIAGYMNDLLSLGVDGFRIDAATHIPAEDLANIKSRLSNPNAYWKQEVIYGAGEPPKPGEYTGTGDVQEFRYAYDLKRVFTQEHLAYLKNYGEDWGYLSSTTAGVFVDNHDTERNGSTLNYKNDATYTLANVFMLAWPYGAPDINSGYEWSDPDAGPPDGGHVDACWQNGWKCQHKWPEIASMVAFRNATRGEPVTDWWDDGADAIAFGRGSKGFVAINHESATVQRTYQTSLPAGTYCDVQSNTTVTVDSAGRFTAALGPDTALALHNGRTSC

>SEQUENCE\_39|MEDIUM

MKKTAIAIAVALAGFATVAQAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQAQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRVLAGNPAKHDLDIKPTVISHRLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNALASPGSGGDLGEAIREQPEQARLALTLAAAESERFVRQGTGNDEAGAANADVVSLTCPVAAGECAGPADSGDALLERNYPTGAEFLGDGGDVSFSTRGTQNWTVERLLQAHRQLEERGYVFVGYHGTFLEAAQSIVFGGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTSLTLAAPEAAGEVERLIGHPLPLRLDAITGPEEEGGRLTILGWPLAERTVVIPSAIPTDPRNVGGDLDPSSIPDKEQAISALPDYASQPGKPPREDLK

>SEQUENCE\_40|MEDIUM

MDPSRKLFASILIGALLGIGAPPSAHAGADDVVDSSKSFVMENFSSYHGTKPGYVDSIQKGIQKPKSGTQGNTDDDWKEFYSTDNKYDAAGYSVDNENPLSGKAGGVVKVTYPGLTKVLALKVDNAETIKKELGLSLTEPLMEQVGTEEFIKRFGDGASRVVLSLPFAEGSSSVETINNWEQAKALSVELEINFETRGKRGQDAMYEYMAQACAGNRVRRSPGIRNHGHSCFLCEIVIRSQFHTTYEPEAGPIKNKMSESPNKTVSEEKAKQYLEEFHQTALEHPELSELKTVTGTNPVFAGANYAAWAVNVAQVIDSETADNLEKTTAALSILPGIGSVMGIADGAVHHNTEEIVAQSIALSSLMVAQAIPLVGELVDIGFAAYNFVESIINLFQVVHNSYNRPAYSPGHKTQPFLHDGYAVSWNTVEDSIIRTGFQGESGHDIKITAENTPLPIAGVLLPTIPGKLDVNKSKTHISVNGRKIRMRCRAIDGDVTFCRPKSPVYVGNGVHAAAASYSMEHFRWGKPV

>SEQUENCE\_41|MEDIUM

MKQSTIALALLPLLFTPVTKANSDSECPLSHDGYCLHDGVCMYIEALDKYACNCVVGYIGERCQYRDLKWWELR

>SEQUENCE\_42|HIGH

MLSPKLSLLALLVGGLCTTSAFAMQMPKTIQIKNGEKVKPTFSQQEYANRQSKLRTYLAQNNIDAAVFTSYHNINYYSDFLYCSFGRPYALVVTQEAVVSISANIDGGQPWRRTVGTDNIIYTDWQRDNYFVAIQQALPKAGRIGIEFDHLNLMNRDKLASRYPQAELVDIAAPCMRMRMIKSAEEHAIIRQGARVADIGGAAVVEALRDQVPEYEVALHATQAMVREIARTYPDSELMDTWTWFQSGINTDGAHNPVTSRKVNKGDILSLNCFPMIAGYYTALERTLFLDHCSDEHLRLWEVNVKVHEAGLELVKPGMRSSDIALQLNEIFLEHDLLQYRTFGYGHSFGTLSHYYGREAGLELREDIDTVLEPGMVVSIEPMIMLPEGLPGAGGYREHDILIVNEHGSENITKFPYGPEHNIIKK

>SEQUENCE\_43|MEDIUM

MKKTAIAIAVALAGFATVAQADAPEEEDHVLVLRKSNFAEALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKLKAEGSEIRLAKVDATEESDLAQQYGVRGYPTIKFFRNGDTASPKEYTAGREADDIVNWLKKRTGPAATTLPDGAAAESLVESSEVAVIGFFKDVESDSAKQFLQAAEAIDDIPFGITSNSDVFSKYQLDKDGVVLFKKFDEGRNNFEGEVTKENLLDFIKHNQLPLVIEFTEQTAPKIFGGEIKTHILLFLPKSVSDYDGKLSNFKTAAESFKGKILFIFIDSDHTDNQRILEFFGLKKEECPAVRLITLEEEMTKYKPESEELTAERITEFCHRFLEGKIKPHLMSQELPEDWDKQPVKVLVGKNFEDVAFDEKKNVFVEFYAPWCGHCKQLAPIWDKLGETYKDHENIVIAKMDSTANEVEAVKVHSFPTLKFFPASADRTVIDYNGERTLDGFKKFLESGGQDGAGDDDDLEDLEEAEEPDMEEDDDQKAVKDEL

>SEQUENCE\_44|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGLVQAGGSLRLSCAASGRTFNTLSMGWFRQAPGKEREFVAAVSRSGGSTYYADSVKGRFTVSRDNAKKTVYLQMNSLKPEDTAVYYCAAAATKSNTTAYRLSFDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_45|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGLVQAGGSLRLSCAASGRTFSMYRMGWFRQAPGKEREFVAVITRNGSSTYYADSVKGRFTISRDNAKKTVYLQMNSLKPEDTALYYCAATSGSSYLDAAHVYDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_46|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGLVQPGGSLRLSCAASGRTLSSYIVAWFRQPPGKEREFVAGIISRRGGNSAYVESVKGRFTISRDNAKKTVYLQMNSLKPEDTAVYYCAADGSVAGWGRRSVSVSSYDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_47|MEDIUM

MKKTAIAIAVALAGFATVAQAQVQLVESGGGLAQAGGSLRLSCAASGRTFSMDPMAWFRQPPGKEREFVAAGSSTGRTTYYADSVKGRFTISRDNAKKTVYLQMNSLKPEDTAVYYCAAAPYGANWYRDEYDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_48|MEDIUM

MKKTAIAIAVALAGFATVAQAQVQLVESGGGLVQAGGSLRLSCAASIRSFSNRNMGWFRQPPGKEREFVAGISWGGGSTRYADSVKGRFTISRDNAKKTVYLQMNSLKPEDTAVYYCAAEFGHNIATSSDEYDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_49|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGLVQAGGSLRLSCAASERTFSRYPVAWFRQAPGAEREFVAVISSTGTSTYYADSVKGRFTISRDNAKVTVYLQMNNLKREDTAVYFCAVNSQRTRLQDPNEYDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_50|MEDIUM

MKKTAIAIAVALAGFATVAQAQVQLVESGGGLVQPGGSLRLSCAASGNIFSINTMGWYRQAPGKQLELVAAITSGGTTSYTDSVEGRFTISRDNAKNAVYLQMNSLKAEDTAVYYCNTVKVVGGRLDNPDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_51|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGLVQPGGSLRLSCAASGRTASGYGMGWFRQAPGKEREFVAAISRSGAGTLNADFVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCVARPTKVDRDYATRREMYNYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_52|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGSVQAGGSLRLSCAASGRDFSTLAMGWFRQAPGKEREFVATINWSGGTTHYADSVKGRFTISRDNAKNTVYLQMGSLKPEDTAVYYCGRSKYAAGALTRAYDYNYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_53|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGLVQAGGSLRLSCSASGSIFSINDMGWYRRAPGKRRELVAAITSGGIPNYADSVKGRFTISRDNAKNTGYLQMNSLKPEDTAVYYCAAQFGTVAAALRRHEYDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_54|MEDIUM

MKKTAIAIAVALAGFATVAQAQVKLEESGGGLVQAGGSLRLSCSASGRTFSSGVMGWFRQAPGKQRELVAAITTGGSTSYTDSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNSVAVVGGVIKSPDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_55|MEDIUM

MKKTAIAIAVALAGFATVAQAQVQLVESGGGSVQAGGSLRLSCAASGLSRYAMAWFRQGTGKEREFVASTNWSSGNTPYADSVKGRFIISRDNAKNTVYLQMNSLKPGDTAIYYCAARKLDVPSRYSQHYDYWGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_56|MEDIUM

MKKTAIAIAVALAGFATVAQAQVQLVESGGDLVQAGGSLRLSCAASGSISRISTMGWYRQAPGKQRELVATISTGGTTNYAESVKGRFTVSRDNAKNTMYLQMNSLKPEDTAVYYCAAGWKVVRGSLEYEYSGQGTQVTVSSEQKLISEEDLHHHHHH

>SEQUENCE\_57|HIGH

MKYLLPTAAAGLLLLAAQPAMAHHLGGAKQAGNVQVKLQESGTELAKPGAAVKMSCKASGYTFTDYWMHWVKQRPGQGLEWIGYINPNTAYTDYNQKFKDKATLTADKSSSTAYMQLRSLTSEDSAVYYCAKKTTQTTWGFPFPFWGQGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPKSMAMSVGERVTLSCKASENVDSFVSWYQQKPGQSPKLLIYGASNRYTGVPDRFAGSGSGRDFTLTISSVQAEDLADYHCGQNYRYPLTFGAGTKLEIKREGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNALASPGSGGDLGEAIREQPEQARLALTLAAAESERFVRQGTGNDEAGAASADVVSLTCPVAAGECAGPADSGDALLERNYPTGAEFLGDGGDVSFSTRGTQNWTVERLLQAHRQLEERGYVFVGYHGTFLEAAQSIVFGGVRARSQDLDAIWRGFYIAGDPELAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTGLTLAAPEAAGEVERLIGHPLPLRLDAITGPEEEGGRLETILGWPLAERTVVIPSAIPTDPRNVGGDLDPSSIPDKEQAISALPDYASQPGKPPREDLK

>SEQUENCE\_58|MEDIUM

MANNNDLFQASRRRFLAQLGGLTVAGMLGPSLLTPRRATAAQAXXXXRKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFGYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK

>SEQUENCE\_59|MEDIUM

MGLGKKLSSAVAASFMSLTISLPGVQAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSQSIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF

>SEQUENCE\_60|MEDIUM

MKNRNRMIVNCVTASLMYYSSLPALAQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAAKTGKRKRSQMLFRGRRASQ

>SEQUENCE\_61|LOW

MKNRNRMIVNCVTASLMYYSSLPALAAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

>SEQUENCE\_62|MEDIUM

MKKTAIAIAVALAGFATVAQAFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF

>SEQUENCE\_63|HIGH

MKKKLLALALLALLFNGAQAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFDCWEPVQEGSEQKLISEEDLNSHHHHHH

>SEQUENCE\_64|MEDIUM

MAPSGKSTLLLLFLLLCLPSWNAGACYCQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAAKTGKRKRSQMLFRGRRASQ

>SEQUENCE\_65|MEDIUM

MKYLLPTAAAGLLLLAAQPAMAMDIGINSMLIVTQTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVEELKPTPEGDLEILLQKWENGECAQKKIIAEKTKIPAVFKIDALNENKVLVLDTDYKKYLLFCMENSAEPEQSLACQCLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQCHILEHHHHHH

>SEQUENCE\_66|HIGH

MDPRTTPAPGHPARGARTALRTTLAAAAATLVVGATVVLPAQAASSGPAGCQVLWGVNQWNTGFTANVTVKNTSSAPVDGWTLTFSFPSGQQVTQAWSSTVTQSGSAVTVRNAPWNGSIPAGGTAQFGFNGSHTGTNAAPTAFSLNGTPCTVG

>SEQUENCE\_67|LOW

MKKKNIYSIRKLGVGIASVTLGTLLISGGVTPAANAVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDAQAPKVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDAQAPKMAYRPSETLCGGELVDTLQFVCGDRGFYFSRPASRVSRRSRGIVEECCFRSCDLALLETYCATPAKSE

>SEQUENCE\_68|LOW

MKKTAIAIAVALAGFATVAQADIELTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTAA

>SEQUENCE\_69|HIGH

MMKFTVVAAALLLLGAVRADIELTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTAA

>SEQUENCE\_70|LOW

MRFSTTLATAATLFFTASQVSADIELTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTAA

>SEQUENCE\_71|MEDIUM

MQYKKTLVASALAATTLADIELTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTAA

>SEQUENCE\_72|LOW

MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGGEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTKYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCVRLLPKRTATLHYYIDVWGKGTLVTVSSGSEQKLISEEDLNSHHHHHH

>SEQUENCE\_73|LOW

MKYLLPTAAAGLLLLAAQPAMAQVQLQQSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSSEEGEFSEAREDMAALEKGQIVLTQSPAIMSASPGEKVTMTCSASSSVSYMNWYQQKSGTSPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEAEDAATYYCQQWSSNPFTFGSGTKLEINGSEQKLISEEDLNSHHHHHH

>SEQUENCE\_74|LOW

MKKTAIAIAVALAGFATVAQAAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHTKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFDCWEPVQE

>SEQUENCE\_75|MEDIUM

MKKTAIAIAVALAGFATVAQASSSFDKGKYKKGDDASYFEPTGPYLMVNVTGVDGKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVIEKK

>SEQUENCE\_76|MEDIUM

MKQSTIALALLPLLFTPVTKAMTESTTDPARQNLDPTSPAPATSFPQDRGCPYHPPAGYAPLREGRPLSRVTLFDGRPVWAVTGHALARRLLADPRLSTDRSHPDFPVPAERFAGAQRRRVALLGVDDPEHNTQRRMLIPTFSVKRIGALRPRIQETVDRLLDAMERQGPPAELVSAFALPVPSMVICALLGVPYADHAFFEERSQRLLRGPGADDVNRARDELEEYLGALIDRKRAEPGDGLLDELIHRDHPDGPVDREQLVAFAVILLIAGHETTANMISLGTFTLLSHPEQLAALRAGGTSTAVVVEELLRFLSIAEGLQRLATEDMEVDGATIRKGEGVVFSTSLINRDADVFPRAETLDWDRPARHHLAFGFGVHQCLGQNLARAELDIAMRTLFERLPGLRLAVPAHEIRHKPGDTIQGLLDLPVAW

>SEQUENCE\_77|LOW

MFKFKKKFLVGLTAAFMSISMFSATASATPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP

>SEQUENCE\_78|HIGH

MFKFKKKFLVGLTAAFMSISMFSATASAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRVTGLDFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLPQTSGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQLDVSPEC

>SEQUENCE\_79|HIGH

MKKTAIAIAVALAGFATVAQAMHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYSTEVVALSRLQGSLQDMLWQLDLSPGC

>SEQUENCE\_80|LOW

MKYLLPTAAAGLLLLAAQPAMAMTPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQPDPNSSSVDKLAAALEHHHHHH

>SEQUENCE\_81|HIGH

MFKFKKKFLVGLTAAFMSISMFSATASALQRTPEMPVLENRAAQGDITAPGGARRLTGDQTAALRDSLSDKPAKNIILLIGDGMGDSEITAARNYAEGAGGFFKGIDALPLTGQYTHYALNKKTGKPDYVTDSAASATAWSTGVKTYNGALGVDIHEKDHPTILEMAKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPSATSEKCPGNALEKGGKGSITEQLLNARADVTLGGGAKTFAETATAGEWQGKTLREQAQARGYQLVSDAASLNSVTEANQQKPLLGLFADGNMPVRWLGPKATYHGNIDKPAVTCTPNPQRNDSVPTLAQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAANPCGQIGETVDLDEAVQRALEFAKKEGNTLVIVTADHAHASQIVAPDTKAPGLTQALNTKDGAVMVMSYGNSEEDSQEHTGSQLRIAAYGPHAANVVGLTDQTDLFYTMKAALGLK

>SEQUENCE\_82|HIGH

MKKTAIVIAVALAGFATVAQAVVYTDCTESGQNLCLCEGSNVCGQGNKCILGSDGEKNQCVTGEGTPKPQSHNDGDFEEIPEEYLQ

>SEQUENCE\_83|HIGH

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQUENCE\_84|HIGH

MKKNIAFLLASMFVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCAA

>SEQUENCE\_85|LOW

MKKNIAFLLASMFVFSIATNAYACMHCSGENYDGKISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCVVGGCVAHPHSWPWQVSLRTRFGMHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHVQEIEVSRLFLEPTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEHHHHHH

>SEQUENCE\_86|MEDIUM

MKQSTIALALLPLLFTPVTKAMPSMYGLPAFVSATELLLAVTVFCLGFWVVRATRTWVPKGLKTPPGPWGLPFIGHMLTVGKNPHLSLTRLSQQYGDVLQIRIGSTPVVVLSGLNTIKQALVRQGDDFKGRPDLYSFTLITNGKSMTFNPDSGPVWAARRRLAQNALKSFSIASDPTSASSCYLEEHVSKEANYLVSKLQKVMAEVGHFDPYKYLVVSVANVICAICFGQRYDHDDQELLSIVNLSNEFGEVTGSGYPADFIPVLRYLPNSSLDAFKDLNDKFYSFMKKLIKEHYRTFEKGHIRDITDSLIEHCQDRKLDENANVQLSDDKVITIVLDLFGAGFDTVTTAISWSLMYLVTNPRVQRKIQEELDTVIGRDRQPRLSDRPQLPYLEAFILETFRHSSFVPFTIPHSTTRDTSLNGFYIPKGCCVFVNQWQVNHDRELWGDPNEFRPERFLTPSGTLDKRLSEKVTLFGLGKRKCIGETIGRSEVFLFLAILLQQIEFKVSPGEKVDMTPTYGLTLKHARCEHFQVQMRSSGPQHLQA

>SEQUENCE\_87|HIGH

MSFKKIIKAFVIMAALVSVQAHAGPQNITDLCAEYHNTQIHTLNDKIFSYTESLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTEAKVEKLCVWNNKTPHAIAAISMAN

>SEQUENCE\_88|MEDIUM

MKKTAIAIAVALAGFATVAQAAPADNTVNIKTFDKVKNAFGDGLSQSAEGTFTFPADVTAVKTIKMFIKNECPNKTCDEWDRYANVYVKNKTTGEWYEIGRFITPYWVGTEKLPRGLEIDVTDFKSLLSGNTELKIYTETWLAKGREYSVDFDIVYGTPDYKYSAVVPVVQYNKSSIDGVPYGKAHTLALKKNIQLPTNTEKAYLRTTISGWGHAKPYDAGSRGCAEWCFRTHTIAINNSNTFQHQLGALGCSANPINNQSPGNWTPDRAGWCPGMAVPTRIDVLNNSLIGSTFSYEYKFQNWTNNGTNGDAFYAISSFVIAKSNTPISAPVVTNHHHHHH

>SEQUENCE\_89|MEDIUM

MKKIWLALAGLVLAFSASAAQYEDGKQYTTLEKPVAGAPQVLEFFSFFCPHCYQFEEVLHISDNVKKKLPEGVKMTKYHVNFMGGDLGKDLTQAWAVAMALGVEDKVTVPLFEGVQKTQTIRSASDIRDVFINAGIKGEEYDAAWNSFVVKSLVAQQEKAAADVQLRGVPAMFVNGKYQLNPQGMDTSNMDVFVQQYADTVKYLSEKKGGGGGRFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN

>SEQUENCE\_90|LOW

MKYLLPTAAAGLLLLAAQPAMASYQGNADCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP

>SEQUENCE\_91|MEDIUM

MKKKNIYSIRKLGVGIASVTLGTLLISGGVTPAANAVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDQSANLLAEAKKLNDAQAPKVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDQSANLLAEAKKLNDAQAPKVDANSSSVPFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN

>SEQUENCE\_92|MEDIUM

MKKKNIYSIRKLGVGIASVTLGTLLISGGVTPAANAAQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQKLNDSQAPKADAQQNNFNKDQQSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPKADNNFNKEQQNAFYEILNMPNLNEEQRNGFIQSLKDDPSQSANLLSEAKKLNESQAPKADNKFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEAKKLNDAQAPKADNKFNKEQQNAFYEILHLPNLTEEQRNGFIQSLKDDPSVSKEILAEAKKLNDAQAPKRPDFCLEPPYTGPAKARIIRYFYNAKAGLCQTFVYGGARAKRNNFKSAEDCMRTCGGA

>SEQUENCE\_93|MEDIUM

MKKTAIAIAVALAGFATVAQAAEFLEAIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSNPKIVKWDRDM

>SEQUENCE\_94|MEDIUM

MKYLLPTAAAGLLLLAAQPAMAMCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGSEQKLISEEDLNSHHHHHH

>SEQUENCE\_95|MEDIUM

MKIKTGARILALSALTTMMFSASALAHMTACTATQQTAAYKTLVSILSESSFSQCSKDSGYSMLTATALPTNAQYKLMCASTACNTMIKKIVALNPPDCDLTVPTSGLVLDVYTYANGFSSKCASLLEHHHHHH

>SEQUENCE\_96|MEDIUM

MKYLLPTAAAGLLLLAAQPAMAHMTACTATQQTAAYKTLVSILSESSFSQCSKDSGYSMLTATALPTNAQYKLMCASTACNTMIKKIVALNPPDCDLTVPTSGLVLDVYTYANGFSSKCASLLEHHHHHH

>SEQUENCE\_97|MEDIUM

MKYLLPTAAAGLLLLAAQPAMAMAAGSRTSLLLAFGLLCLSWLQEGSAFPTIPLSRLFDNAMLRARRLYQLAYDTYQEFEEAYILKEQKYSFLQNPQTSLCFSESIPTPSNRVKTQQKSNLELLRISLLLIQSWLEPVQLLRSVFANSLVYGASDSNVYRHLKDLEEGIQTLMWRLEDGSPRTGQIFNQSYSKFDTKSHNDDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGFLVPRGSLEHHHHHH

>SEQUENCE\_98|MEDIUM

MKIKTGARILALSALTTMMFSASALAKIEEAMGQVDTTKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTATQTSTPSYRITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPLALRCHAWKDKLVYNVLYYRNGKAFKFFHWNSNLTILKTNISHNGTYHCSGMGKHRYTSAGISVTVKELFPAPVLNASVTSPLLEGNLVTLSCETKLLLQRPGLQLYFSFYMGSKTLRGRNTSSEYQILTARREDSGLYWCEAATEDGNVLKRSPELELQVLGLQLPTPVHHHHHH