acidic

basic

Ser stretches

other stretches

GRAS region

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>PrSCR

MAACIAMNTRFRGGDASGEEVFVVGETDSNNSMIIPASEGENRRKRTGMELNGPLFRRINPSESSDYGQIKW
NNLSSGLRESQSPVPLASAAGWQYPSSATVDSVSHRISAPSRTPGLGLANSVLSGESNGQPFNGAYSNMPFF
QNSNMERQVSDSCSQWNKWGSVVQPEVGLGCDGTGQQLSSLNAVQTMDEAAAAVWVDGMIKDLMMQSSPNVS
MAQIIQSLQEIALYNPHIASVLEYRLRSLGQSELGLAGNTQIGRDQNVGMNVSSDGRGFKRSMDQSDHHRRD
MNSQQQIMVDWKSIGANPDSARRSARASQLDDDENRLIDNIHGRGLDVDDQRLRRGNDDLRLRIQSTESHDI
QREHQPDSALKLYLDSSGYDQTSWASSKDQFSETAFMANQSMWVQPRQPDNNSQPPVLSLQHQANEDDPLRV
APSNDNYITMNRRINTNSNQDPSVNQTPQQQGPSDITASDEEGLHLLALLLQCAEAVSADNFEEANTILPQI
TELSTPYGNSVQRVAAYFAEAMSARLVSSCIGMYSPLPPIHMSQSQKIVNAFQVFNGISPFVKFSHFTANQA
IQEAFEREQRVHIIDLDIMQGLQWPGLFHILASRPGGPPHVRITGLGTSLEALEATGKRLSDFAHTLNLPFE
FHPVADKVGKLDPERLKVNRGDALAVHWLHHSLYDVTGSDTNTLRLLQRLSPKVITVVEQDLSHGGSFLSRF
VEAIHYYSALFDSLGASYPEDSHDRHLVEQQLLSREIKNILAVGGPARTGEVKFDNWRDQLKQTGFKPISLA
GNAATQATLLLGMFPCQGYTLMEENGTLKLGWKGLCLLTASAWRPAHHGLIY
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>PrSCL2

MSMGGVNMNMNMSPWLSAPTAWQHDGLMSFPPGICTDVVGDLCSTTTNSYLSEPNSVLDLSRASMLFSPMEQ
FQDFTQHLHDGIGAKQMPLLGGVEPPAPAFKDNALYHHEALVKKERPPIKEPGVGDGSSAALRSSVFRSPEL
HTFGFESPVSNRNDFVSPDVCTEWMDCLMSDLQPEAIAGNGNAAIASCFDSSNPCESTESSELPNGGSGYRR
HSSEDAAAWQSEFGILGEAFKRSSPTSWTPDTTTEQLLCSSPSADLLSAASSELLSTNSLKGKAALQEQYGG
AAGGGHEFQTLHHRMPNVHQSVCPPKQQLIREPSTPPQKRQQGQQEQDPLKGKREEDPPKPEIDALDRHMQG
QRSDLLHSLLDCAKIVDTEPERAGQSVAYLQRIASHHGDPTQRIASHFADALAKRLSKGIEQKPQFQSSDEC
SKSFEDLTLAYKALNDACPYSKFAQLTGNQAILEAMDKAEKIHIVDFGIVQGVQWAALLHAFATRPGGKPHK
IKITGIPAPTLGQNPTSSLLATGKRLTEFAKLLDLEFEFCPVSKHMSEVELSTLKIEQDECIAVNFMLQLYN
LLGDSPEPLVKILKLAHALSPKVVTLGEYEAHLNACQFQVRFRNALEYFSAFFESMEPNMARDSAERLNVEK
HFFAEKIMGIVAFEGAERKIRLEGRDQWRIVMESAGFKFTNLSHYARSQARILLYNYCEAYSLDESSGFLSL
AWQNRPLLTVSAWCCC
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>PtSCL5

MAESEECNGGYESLLDWLDIGDESSSMDPFINGDSCPIADQDHEDFWEAALPTMDIQSETQFVMEPSFSSND
SVAPAAQKGDAESFWVEPPVNDVEDSPKITKKRKRARVSGESTKGKLWNVFENNAASPHTGESLDHGNHCLA
PETKLSSLHGAESDNQLDLEATRNNSNNNNNNSSNSNNKGRSGGRQSSPPNLPKESRWAEQLLNPCAVAIAN
NNIVRIQHLIWVLHDLASISGDANHRLAAHGLRAFTAKIMHPGASLPCSEFLSADPKLFHKALXQFHEVSPW
YQLLYTIANKYLLEAFEDQNSKALHVIDIGVSHGIQWPTFMEALARRPAGPPSLLRLTIIADTLGAPFSAGP
PSNDFPNRLKRYAKTLNLDMEVNVIAQPLDSLTREALGVKEDEALAICGQFRLHQLLGEGLDKNEGKDNQLT
SVSPRDKFIKFIKDLNPLVFFLSDNDIDHSSPDFIERFKNSVDHLWRFLDSTSVCFKGRECEERRMVEGEAA
MGLVNNVAYDGASRVERNENHLNWANRVREEGFVCEIPSDKIVDCARAMLRKHDSNWEMRLEDGCISLCWKS
HPVTFCSLWKPCFNEPT
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>PtSCL6

MKGELEIMGINHQADFQISRHAPVLFSEKRMKLEESGQYLVRNEAAALSPQDCFEATGGQIGWILSESSELG
QPSSVGLTAVTCQESNIDVNSIKARQQSLQFADTSDRPDCTRQVQCIIKNSPKLKSLDSKLAFTPQLRSPSM
AATHREWNASTDLNTNRSHYYEELSTAPADQDQSWPLLGVSIAKGLGNLGACHDASCMEQLLLHCSSALENN
DVTLAQQIMWVLNNIASAEGDPNQRVTSCFLRALIARAARMSNSNMLRAMAATTANAHVGDTKRLSVIELAG
FVDLTPWHRFGFSSSNGAIAEAVEGYSVVHILDFGIAHCMQWPTLIDSLSKRPDGPPYIRLTVSCARPPVPP
LLNMSYEELGTRLSNFARSRNVPFEFRAIPPDPSEEFLVLDQLEPSILDIREGEALVINCQFRLHYIPDETA
DQQSSCSSSSCQRDEFLRIIRSFEPTIMTLVDEDSNLTSTSLVSRLKSAFNYLWIPFDALNTFLPRDSKQRQ
QYESDVGYKIENIIAFEGHQRIERLESKAKWTQRMRKACFQSISFSEDTVAEVKAMLDEHAAGWGLKKEEDD
LLLTWKGHNVVFATAWVPSHL
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>PrSCL10

MSLASPCQESMRGDDNSYRTNSWYRGNLSGVPEISRNMGMQYMPGGIGLNLQRGWGNSFRSCSTDLSPKQNG
NFAIDHTSTTGERSAGTLKMIDQRSPISPLSPKGIGSDGLPQTSQSQRLYSSERIQMHDDLIHSSSHNHGSF
NDQVYIHESFPCNNELSRESSICIQSSDGSPLSSQHSQSYSSDSRYFHSAEDAADLVGNAYSGNGQPANLKI
LEEIETALLGPDGDDPLDMDYAYGDHTLNSNSEWSLEALSDFNDFLDQTSNPGYSQINNADSSRVPDNLQQL
TNHGDRNVKEETVNEVNLKIEHFSPSSSDMEKLEIEELGSPQGDVKSLLIECAKAIADGRNADNLIAGLRQV
VNIYGDPLHRLAAYMVEGLVARLHFSGGHIYKTLKCKEPTSSELLSYMHILYEVCPYFKFGYVAANGAIAEA
FKDKDRVHIIDFQIAQGSQWVTLIQAFAARQGGSPHVRITGVDDPQSEYARGQGLNLVGERLSKLAESYQVP
FEFHGLSVFGSDVHAEMLKIRPGEALAVNFPLQLHHMPDESVNTSNHRDRLLRMVKNFSPNVVTLVEQEANT
NTAPFFPRFMETLSYYTAMFESLDVTLPRDSKERVSVEQHCLARDIVNVIACEGDERVERHELFGKWRSRLT
MAGFKSYPLSAHVNSTIKVVLNSYNENYRLIEKDEALYLGWLDRDLIVASAWK
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>PtSCL12

MNGMLSRTSGNSLPPAQLKHQILQSKTSPDQAQKRHCKSSVWQRSRSGGEIEPTSVLDIRSPSPTSTLSSSL
GGSSESAGAVAAVSSGLLCEAVSDGGGGGSGSGGAETLLLESSGKEAFNNGGGSTGSPARWYSNRGGSGNGG
REGFGWRLNNGEQQPGGGGMVEGKSEVKKEDPQQHSRAEEWGSGGGAGTAGGMDDLESMLFESGAAPPDQSL
MRWLLGEIEDPKDLPPPQIKSATSGGSTSAPQFVDPSIEPNFADPGAFAFSNNNLSDVIAPPQHASVPSSFR
PSYATLPNLPQQQFIPPPPPPPPPPPPPFAYNGPMPTPFGPNAYHPEVLFSGPAVYGSNPVQHLGPDFPRFN
MAADPNRNNNNLLFDMPHPPPPKRFGLEHQLWQQTFKQQEYMNMMKPQQQQELLQSLHRRQQFLHQAPPPSP
HHQMRQKAVVNHTFKVGGSGAVADEVHVIVEQLLKAAEAVELGNLDHAQAILARLNQHLSPLGKPLQRAAFY
FKEALASRILNTTATNTGGDNRNATVTGTATSNISSPLDMVHKISAYKSFSEASPLAQFAHFTANQAFLEAL
EGAEAIHIIDFEIGLGGQWASFLQELAVKLGGAPPVRITALGSSASSSLELHLTRDNLCNFAKQLNVPFEFE
LLHFDHIESLTLREREAVAVNLSLLPSTFSSPDSISRLLRLVKNLAPRAVVVVDAETTATAAAASAATTSSA
SFVHHFLEALQFYSFLFDSLDAVNINMDAVHKIEKFLLAPKIDATISSAGAPPWKTLFAAAGFSPVAFSNFT
ETQAEYLIQRLHSRGFEVEKAHAALLLGWQGRPLVSATAWRCGPPP
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```
>PtSCL14

MDPMERAAKVLGSSPGHKNMMGCSSSGVKIEPEIDGLLANAGYTVKASDLAHVAQRLEQLESIMGTVQDPGI
SHLASEAVHYNPSDLAGWIESMFGELNPGADMPVPFGDRGSLIDSSQVHKPIQDDPSLSAMDLALIHEYGLQ
FNGSQASNPQGFSPDSDPSVRCNIFSGPPLRSGDSTTHTNFQARSFSAQSSDEGSSLSSTRLGTAQQSIDNG
AQESGIRVVHLLMGCAEAIQRNNLKVASDLVREIRMTVNSAPCGAMGKVASHFVEALARRICGLNGAESNMS
QADAQSEILYHHFYEVCPYLKFAHFTANQAILEAFEGHGSVHVIDLNLMHGLQWPALIQALALRPGGPPLLR
LTAIGPRQPDGRDVLQEIGMKLAQFAESVNVEFDFRGVMADKLEDIKPWMFQVKPGEVVAVNSVLQLHRLLY
MDAPTGSSPIDVVLKSIGSLRPKIVTVVEHEANHNGPVFLDRFVEALHYYSTMFDSLEACNVLPNSMEKFLA
ELYIQKEICNIVACEGRYRIERHETLSHWRIRLGRAGFRPSHLGSNAFKQARMLLTLFSGEGYTVEENNGSL
TLGWHSRPLIAASAWQGS
```

```
>PtSCl16

MEAGMQGASWFSEHQWDHIFDSPPHVDWDSNTTTTQSVAVEQLDVDLDAIDWLSWHDLIIDDINASSVNNMS
LPADLQAMEEYLMDAELQDDNNNMEEALISSPRKDAIVFQSPIDSTDAITLRHPALIAGDQLVSKSIVTGNT
CSYSVDVDHGSVEYKGLRLIHLLTACAEAMLEGAQDLVEVILCRLRQLVSCTGSTMERVGYYLFDALLHSNV
NSLAHLELNDKTTKEHFLGALKLLHAAYPYIRIPHFTANECILEAVVAVGGGNNVGIHIIDFDIMEGMQWPP
LMETLRNKDDVRHLRITTIKWADDEEDEFLRYSGHTGRWLSEYAASAGIPFWYEKMDLKGVKDILPSQEGEI
VVVNCMWQLPHMLNPRNKSHLLEFLVGAHHLNPVAVTLATGPHGTESDSANFVDSLVNRLKELCAIFDSLEA
GLPEHGLARTMVERIFFGPAMSKRVMSSARGDDRPADTTNSNVVDLPLRCGYEECNISNDNMIYAKYNVLMC
SVSGGCYEVELVGEHRLVLKSGCTPLVWVSTWKSPQLSEFDSLNFLEKN
```

```
>PtSCL21

MVKDKSNDLGGAQNDKSNDVRICTKGQEQQPWGAQKDKRYVFNGNMEQTNLCLEQISVLACVTGDPMQRLAT
YFMEGLAARITKSWPGLYKALNSTHLQPSMADLVSARQVFFTLFPYLKFAFNTVHLTILESMEKEKVVHIID
LDASEAAQWIPLLQSLSRRPGGPPHLKMTGINEKKEVVQQTAAILTEEAERLDIPFQFNQLVTRLDRLTDDM
LAVKTGEAVAISAVLQFHALLAEDQDFDHNFGGGGGGGGGGGGGGGGGGGRVGINRKRPRQSCTTLGDEDLI
LRSMFNMEALVKKEGSVGRPKYSPSEIEAAISSRRPNLEAAGARSNVEEVRNGRRSTIVEGNIERFLRMLRG
LSPKVMVVVEQESNHNGEHLMDRFVEALYYYSAMFDSLESTLPRQSIERVTVEKYLFGKQIHNIVACEGSER
VERHEKLQGWMKRLDRTGFAQLPLGYTTLLHANNLLHTYTSHSYRLLHHEGCLTICWEERPLYSVSAWQSA
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