**Supplementary Table 1**

**Sup.Table 1: Linear B-cell epitopes from membrane proteins of *Staphylococcus aureus* and *Streptococcus pyogenes***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **S.No.** | **Protein name**  | **BCPred** | **AAPPred** | **ABCpred** |
|  | **20 mer Epitopes**  | **BC score** | **20 mer Epitopes**  | **AAP score** | **16 mer Epitopes**  | **ABC****score** |
| ***Staphylococcus aureus*** |
| 1. | sak | EVSASSSFDKGKYKKGDDASKIEVTYYDKNKKKEETKSFPPTGPYLMVNVTGVDGKGNEL | 10.9970.956 | - | - | LCCCSARESXGNSAKPAKIEVTYYDKNKKKEEASESSTAPHYLCCCSASTAASTAPHYLKINASALDATAYKEFRVVELDDGKGNELLSPHYVEFPYLMVNVTGVDGKGNELESXGNSAKPESVMLKR | 0.860.840.830.800.780.720.700.62 |
| 2. | tst | VDLNTKRTKKSQHTSEGTYIGLYRSSDKTGGYWKITMNDGVHGKDSPLKYGPKFDKKQLA | 0.9820.8720.81 | EKVDLNTKRTKKSQHTSEGTVKVHGKDSPLKYGPKFDKKQEYNTEKPPINIDEIKTIEAETQIHGLYRSSDKTGGYWKIT | 1111 | CSHCKSYNDRMETXINDSPLKYGPKFDKKQLASSTSTAATXICSHCKSRESXGNTSTPESVMNKGSTYQSDLSKKFEYNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRTKEGTYIHFQISGVTNTELCCCSARESXGNTSTPPTPIELPLKVKVHGKDYSSGSDTFTNSEVLDNYWKITMNDGSTYQSDLKQLAISTLDFEIRHQLLSKKFEYNTEKPPINIRSSDKTGGYWKITMNDKVDLNTKRTKKSQHTSNFFIVSPLLLATTATDEVLDNSLGSMRIKNTDESVMNKKLLMNFFIVSSMRIKNTDGSISLIIFGPKFDKKQLAISTLDF | 0.920.910.890.890.890.880.870.860.850.850.850.830.830.820.810.790.770.720.670.670.61 |
| 3 | isdA | AKPNNVKPVQPKPAQPKTPTVNAATEATNATNNQSTQVSQADTRTINVAVEPGYKSLTTKTAKSESNNQAVSDNKSQQTNDNHSTKVVSTDTTKDQTKTQTKHNETPKQASKAKELPKTGHIVVPQINYNHRYTTHLEFE | 10.9980.990.9870.9720.9160.865 | TAKSESNNQAVSDNKSQQTNGADSQQVNAATEATNATNNQVEPGYKSLTTKVHIVVPQINAHTVKTAQTAQEQNKVQTPVKYQSEQRSSAMKKITMGTAS | 11110.925 | VKTAQTAQEQNKVQTPCSARESSTRAINNCTCRTEINASSTAPHYLCCTERMINANTPRTEINALVYIGADSQQVNAATESDASTAAIRNREGLATNHRYTTHLEFEKAIPTTKVVSTDTTKDQTKTQKDVATAKSESNNQAVSTRAINNCTCXGNISDATCXGNISDAPESVMTKDGSSEKSHMDDYMQHPTKTQTAHTVKTAQTAQPTVTTTSKVEDNHSTKTQVSQATSQPINFQVQNKSQQTNKVTKHNETPSQQVNAATEATNATNNNSKYQSEQRSSAMKKIQELATTVVNDNKKADTKVHIVVPQINYNHRYTEPGYKSLTTKVHIVVPKHNETPKQASKAKELPATNNQSTQVSQATSQPDNKKADTRTINVAVEPSSTAPHYLCCCSARESATEATNATNNQSTQVS | 0.940.920.920.920.890.860.860.850.840.830.820.800.790.790.790.780.780.760.760.730.730.700.700.690.670.66 |
| 4 | clfB | DSDSDSDSDSDSDSDSDSGSPTPGPPVDPEPEPEPTPDPESDSDSDSDSDSDSESDSESDTSNTTTTEPASTNETPQPTASVTGNGDVDYSNSNNTMPIAANSQVDNKTTNDANNIATNSSEKNNTIETPQLNTTANDTSLPQSSPQTISNAQGTSKPSVDALPETGDKSENTNATLFDAGNTWVYIKGYQDKIEESSGKTAFDPNQSGNTFMAANFKVTVAEPVVNAADAKGTNVNDKV | 111110.9990.9960.9920.9850.9830.8850.777 | QHQTDALPETGDKSENTNATVPQEANSQVDNKTTNDANNISANVDSTAKTMSTQTSNTTTGSADGDSAVNPVDPTPGPPVPVVNAADAKGTNVNDKVTASNNTIETPQLNTTANDTSDISSSPQTISNAQGTSKPSVRTRDSVTGNGDVDYSNSNNTMPIEPASTNETPQPTAIKDQATAIKSTNGDVVAKATYDILTKTDKIEESSGKVSATDTKLRIFLKTQVIQENIDPATGKDYSIPTPDPEPSPEPDPDSDSDSDDKPNGANISSQIIGVDTASGDSDSDSDSGSDSESDSDSDSSGSDSDSDSDSDSDSDSDSNSGNTFMAANFKVTGQVKSGDSDSDSDSESDSDSDSDSNSDSDSDSDSNSDSESDSDSDSD | 111111111111110.610.240.180.1180.118 | TGEATTTTTNQANTPADSSSDSDSESDSNSDSSGSGDGIDKPVVPEQPCSARESSTRAINNCTCDSDSDSASDSDSGSDSASDSDSDNDSDSDSDSASDSDSASDSDSDNDSPEDSDSDPGSDSGSDSDSDSDSDSDSDSESDSDSDSDSASDSDSDSDSKDDVKATLTMPAYIDPDSDSDSDSDSDSDSDSKELNLNGVTSTAKVPPSSVSAAPKTDDTNVSDPNPNQYKVEFNTPDDQGNVIYTFTDYVNTKDDSTTQDTSTEATPSNNEESAPQSTDASNKDVVNETTSNDTNTVSSVNSPSMSWDNEVAFNNGSGSATTEETPVTGEATTTTDSDSDSDSDSDSDSASGSDSGSDSTSDSGSDSTDYVNTKDDVKATLTMTNVSDTKTSSNTNNGEESDSNSDSESVSNNNVASDSDSGSDSDSSSDSIVVVNGHIDPNSKGDLACTRASSTAPHYLCCCTQSDSASNESKSNDSSEPLPDTGSEDEANTSLDSNSDSGSDSGSDSTSTLTMPAYIDPENVKKTPAQQETTQSSSTNATTKHAIRKKSIGVASVLVASDSDSASDSDSASDSASDSDSASDSDSASDSASDSDSASDSDSASDSTVGIDSGTTVYPHQAGNSPQNSTNAENVSTTQDSTSDSGSDSASDSDSSKSNDSSSVSAAPKTDSVMNMKKKEKHAIRKKLATGIGSTTANKTVLVPNSAVKGDTFKITVPKGDLALRSTLYGYNSNITRAINNCTCXGNCLFATSSNTNNGETSVAQNPNVVPPNSPKNGTNASNGSDSGSDSNSDSGSDSGVTSTAKVPPIMAGDQTFKITVPKELNLNGVTAVAADAPVAGTDITNQGTTVYPHQAGYVKLNYQAVNTSAPRMRAFSLATDASNKDVVNQAVNTSSVNITFPNPNQYKVEFNPENFEDVTNSVNITFKKTGNVTLATGIGSTTANTPATTQSSNTNAEETEATPSNNESAPQSTDLLSSKEADASENSVTQNALIDQQNTSIKVYKVDSESVSNNNVVPPNSPQITTPYIVVVNGHIDPTGNLKPNTDSNALIDQPRMRAFSLAAVAADAPIDPENVKKTGNVTLATGDQVLANGVIDSDGNVTQSSNTNAEELVNQTSGSEDEANTSLIWGLLASPKNGTNASNKNEAKD | 0.930.920.920.920.910.910.910.910.910.910.910.900.900.900.890.890.890.880.880.870.870.860.860.860.860.850.850.850.850.840.830.830.830.830.820.820.820.820.820.820.810.810.800.800.800.790.790.790.780.780.780.780.780.770.770.760.750.750.750.740.730.700.700.690.680.660.520.620.620.620.530.63 |
| 5 |  cna | YTTDINGTTITNKYTPGETSVNAQGKDTTPEGYTKKEDGLDGKATGKTATLNESNNWTHTYVSKDITIKDQIQGGQQLDLTQTNTSDDKVATITSGNKSTNGKAFNHTVHNINANAGIEGVKMTFDDKNGKIQNGDTIKVTVTKNWDDNNNQDGKRPTEININVTGTHSNYYSGPNAITDTIYFKLYKQDDNQNTTPVDKLPKYDEGKKIEYTVTEDHVKKVWDDKDNQDGKRPEKVSVNSTNVTDLTVSPSKIEDGGKTVVKDNQKEIEIKTDANGIANTTKVTWSNLPENDKNGKTIK | 10.9980.9950.9930.9850.9830.9790.960.9560.9460.9420.9270.9230.9050.899 | TPVDKAEIKKLEDGTTKVTWNGTTITNKYTPGETSATVTKNVTGTHSNYYSGPNAITDFEQDGKATGKTATLNESNNWTHKPKDKTPPTKPDHSNKVKPTATITSGNKSTNVTVHKSEAGLPKYDEGKKIEYTVTEDHVKSKIEDGGKTTVKMTFDDKNGPGSKITVDNTKNTIDVTIPQVNNSQAWYQEHGKEEVNGKAQNGDTIKVAWPTSGTVKIEGDKNGKTIKYLVKEVNAQGKDHTVHNINANAGIEGTVKGELFAEFEVQGRNLTQTNTSDDKANGEKVKTLDVTSETNWKYENEKRYVSKDITIKDQIQGGQKMTFDDKNGKIQNGDTIQNG | 11111111111110.9980.9960.2611 | DKTPPTKPDHSNKVKPPGETSATVTKNWDDNNKVTWSNLPENDKNGKTQKEIEIKTDANGIANIAWYQEHGKEEVNGKAFGKKIEYTVTEDHVKDYNGKAFNHTVHNINANAARDISSTNVTDLTVSPDITIKDQIQGGQQLDLGTTITNKYTPGETSATDVTSETNWKYEFKNLPTPEGYTKKEDGLVVTNPSKVDKDDQPKDNKTKSFSINYKTKITNEQQKKSEAGTSSVFYYKTGDGENINDINGPRTEINCYTTDINGTTITNKYTPEDHVKDYTTDINGTTIRESSSPARESXGNCNAEKVWDDKDNQDGKRPEAKEIEKTKDVSAQKVWGGKTTVKMTFDDKNGKPSKIEDGGKTTVKMTFTHTWTGLDEKAKGQQVAAEAMAAEAMSTAACLNGKIQNGDTIKVAWPTTKNWDDNNNQDGKRPTKAEIKKLEDGTTKVTWPTEIKVELYQDGKATGAQGKDTTPEGYTKKEDNAGIEGTVKGELKVLKSDDKVATITSGNKSTNEGTQKVKPTIYFKLYKNQDGKRPTEIKVELYQPTIYFKLYKQDDNQNTGSVVKDNQKEIEIKTDRNLTQTNTSDDKVATIPESVMNKNVLKFMVFITVHNINANAGIEGTVKLNINVTGTHSNYYSGPTVKIEGYSKTVSLTVKEINCNASSTAPHYLCCTITSGNKSTNVTVHKSNGEKVKTLDVTSETNWAPHYLCCCSARESSSPSLTVKGEQVGQAVITPDDNQNTTPVDKAEIKKKFKLSKKDGSVVKDNQTVKGELKVLKQDKDTKKMTFDDKNGKIQNGDTKDNQDGKRPEKVSVNLQGYGSLNSFSINYKTKEKVSVNLLANGEKVKTGGQQLDLSTLNINVTG | 0.960.950.940.930.920.900.900.900.890.880.880.880.870.870.870.870.860.860.860.850.850.850.850.840.840.830.820.820.810.810.810.810.800.780.770.750.750.740.740.740.740.730.730.720.720.720.710.710.690.690.660.660.610.61 |
| ***Streptococcus pyogenes*** |
| 6 | SPy | VMIEKTTKGGQAPVQTEASIIDKVPGVSYDTTSYTVQVHVYVVTEDDYKSEKYTTNVEVSMTKVTYTNSDKGGSNTKTAENIAGNSTEQETSTDKDMTITSTTLTVKKKVSGTGGDRSKDPNTDFTFKIEPDTTVNEDGNYHFTLKDGESIKVTNLPVGV | 0.9990.9840.9720.9720.9530.9320.9170.849 | TTKGGQAPVQTEASIDQLYHSTEQETSTDKDMTITFTNKKVTEDDYKSEKYTTNVEVSPQYTNSDKGGSNTKTAEFDFSEVTEEKIDKVPGVSYDTTSYTDSTTLTVKKKVSGTGGDRSKIPNTDFTFKIEPDTTVNEDGFGLTLKANQYYKASEKVMIE |  11111110.986 | TFKIEPDTTVNEDGNKYVVTEDDYKSEKYTTNTEEKIDKVPGVSYDTTCCSPYGENESSERTYPVSPQDGAVKNIAGNSTTKGGQAPVQTEASIDQGTGGDRSKDFNFGLTLGGSNTKTAEFDFSEVTEQETSTDKDMTITFTNTVVNGAKLTVTKNLDLTTVHGETVVNGAKLTVEASIDQLYHFTLKDGEPMTKVTYTNSDKGGSNVGYKEGSKVPIQFKNSGVALNTPMTKVTYTNSPGVSYDTTSYTVQVHVPGVYYYKVTEEKIDKVTTVNEDGNKFKGVALNKVPIQFKNSLDSTTLTDFEVPTGVAMTVAPYIKSEKYTTNVEVSPQDGGESIKVTNLPVGVDYVNSLDSTTLTVKKKVSGAVKNIAGNSTEQETSTHFTLKDGESIKVTNLPSKDFNFGLTLKANQYY | 0.950.920.900.870.860.850.850.850.840.830.830.830.830.820.810.790.790.790.740.730.710.670.670.620.600.58 |
| 7 | scpA | APQAPAKTADTPATSKATIRTPQPTAVSEEVPSSKETKTPAPDKKPEAKPEQDGSGQTPDPEKDSSGQTPGKTPQKGQPSKPEQDGSGQTPDKKPEAKPEHANGEPYAAISPNGDGNRDYFEKTRWDGKDKDGKVVANGTHTDFDVIVDNTTPEVATSATLSGNAPSETKEPYRLEGAMPDAKKASAATMYVTDKDNTSSLNDPSQVKTLQEKAGKGAGTTKASTRDQLPTTNDKDTNRLSWGLTADGNIKPDIAAPGQDLQKQYETQYPDMTPSERLDLKTKARYQSKEDLEKAKKEHGAYANRGMKEDDFKDVKGKIAKDQLDGDGLQFYALKNNFTATAMVKTDDQQDKEMPVLSTNRGDIDFKDKVANAKKAGAVGNAQSDIKANTVTEDTPVTEQ | 110.9990.9990.9980.9970.9950.9930.9810.9780.9650.9410.9350.9120.8890.8730.8550.840.830.755 | TKPEKDSSGQTPGKTPQKGQNAQSDIKANTVTEDTPVTEQKSKGVSIVTSAGNDSSFGGKETPQPTAVSEEVPSSKETKTLLEGHSNKPEQDGSGQTPDKQEHGTHVSGILSGNAPSETKEQHTDFDVIVDNTTPEVATSRDLNDPSQVKTLQEKAGKGAPRQQGAGAVDAKKASAATMYNDLAPQAPAKTADTPATSKATAMVKTDDQQDKEMPVLSTNAPDKKPEAKPEQDGSGQTPDANGEPYAAISPNGDGNRDYVQYETQYPDMTPSERLDLAKKRTLEKRSSKRALATKASTRDSWGLTADGNIKPDIAAPGQDFEKTRWDGKDKDGKVVANGTPTTNDKDTNRLHLLKLVMTT | 11111111111111110.8720.549 | KVVANGTYTYRVRYTPTVTEDTPVTEQAVETPSGAKEQHTDFDVIVDNYETQYPDMTPSERLDLNGEPYAAISPNGDGNREGHSNKPEQDGSGQTPSSGQTPGKTPQKGQPSTAMVKTDDQQDKEMPVDASESSTREPTCCCSPDKKPETKPEKDSSGQTCCSPYGENESXGNSCPDGSGQTPDKKPETKPEDKVAYYHDYSKDGKTADKKPEAKPEQDGSGQTDGSGQTPDKKPEAKPEGSTRFEKTRWDGKDKDYIHRHANGEPYAAISPGSSYYHEANSDAKDQLSYSPDKQLTETAMVKTDKKPEAKPEQDGSDQAAETMEGATVPLKMSDFKTRWDGKDKDGKVVANSRFSSWGLTADGNIKPAKTADTPATSKATIRDSTRDQLPTTNDKDTNRYRVRYTPISSGAKEQHSIVTSAGNDSSFGGKTTEQAVETPQPTAVSEEELYYQATVQTDKVDGKAGAVDAKKASAATMYVTAVSEEVPSSKETKTPTAVDQEHGTHVSGILSSRTLEKRSSKRALATKYVTDKDNTSSKVHLNNMKEDDFKDVKGKIALIAPSETKEPYRLEGAMPEKAGKGAGTVVAVIDAGKTPQKGQPSRTLEKRSDIKANTVTEDTPVTETDKTKARYQSKEDLEKYQSKEDLEKAKKEHGIANNKYAKLSGTSMSAPTADGNIKPDIAAPGQDLKLVMTTFFFGLVAHIRGDIDFKDKVANAKKADANDLAPQAPAKTADTAYANRGMKEDDFKDVKSPNGDGNRDYVQFQGTDPSQVKTLQEKAGKGAVQTDKVDGKHFALAPKSSKVHLNNVSDKFEVTLVAHIFKTKRQKETKK | 0.970.970.940.940.930.930.920.910.910.900.890.890.880.880.880.870.870.870.860.860.860.840.840.840.840.830.820.810.810.810.810.800.800.790.780.760.760.760.750.750.740.730.730.710.700.680.670.650.650.600.570.56 |
| 8 | hylpL | KADKETVYTKAESKQELDKKKKTNGAGTAAQGIYINSTSGNITSGNENGSAMQLRGSEKAFYVKSDGGFYAKETSQIDGNNLKGGVMTGQLKFKPAATVA | 0.9790.9330.8990.8770.796 | QPTTPNFSSALNITSGNENGSTRGAGVVVYSDNDTSDGPLNGAGTAAQGIYINSTSGTTGKADKETVYTKAESKQELDKKKLKDPTANDHAATKAYVDKAMTGQLKFKPAATVAYSSSTGFETDTGFARAGDGHNRFSDL | 1111111 | AMQAMSTRPHYALRNIATEDSSTREPTCCCSPNPSIGADYDKNAAALSYTKAESKQELDKKLNLCCSPYGENESSERTYPASEPHAGEASSCIATEDPTANDHAATKAYVDKSSTRGAGVVVYSDNDTGGVMTGQLKFKPAATVARAGDGHNRFSDLGYIAVNIDLSSTRGAGVVVYAKETSQIDGNLKLKDTSGTTGKLLRIRNLSDNGAGTAAQGIYINSTSGNLKLKDPTANDHAATDYKGTTNAVNIAMRQPTSGNENGSAMQLRGSEKPNIDGLATKVETAQKPESVMSENIPLRVQFKAYSSSTGGAVNIDLSSGTLKITHENPSIGADYATKVETAQKLQQKADKAALSIDIVKKTNGAGTAQGIYINSTSGTTGKLYNLLTNKPNIDGLATKGSAMQLRGSEKALGTL | 0.910.900.880.880.870.870.850.850.840.840.820.800.800.800.770.760.750.750.730.730.710.690.640.610.610.60 |