

表皮生长因子受体在肿瘤发生中的作用及机制

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表皮生长因子受体 (epidermal growth factor receptor, EGFR)

Isolation of a Mouse Submaxillary Gland Protein Accelerating Incisor Eruption and Eyelid Opening in the New-born Animal*

STANLEY COHEN†

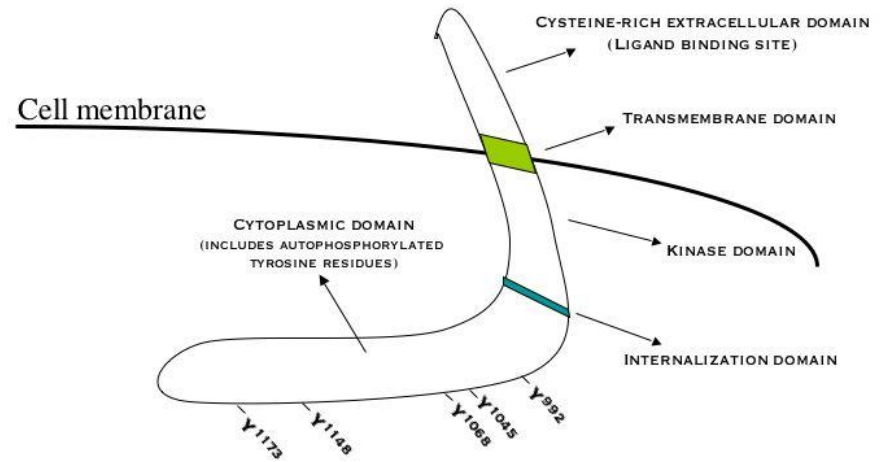
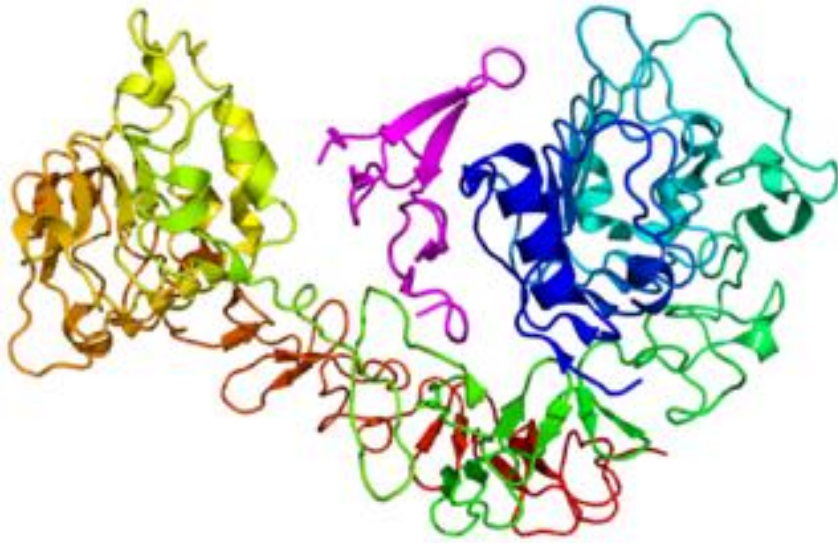
From the Department of Biochemistry, Vanderbilt University School of Medicine, Nashville 5, Tennessee

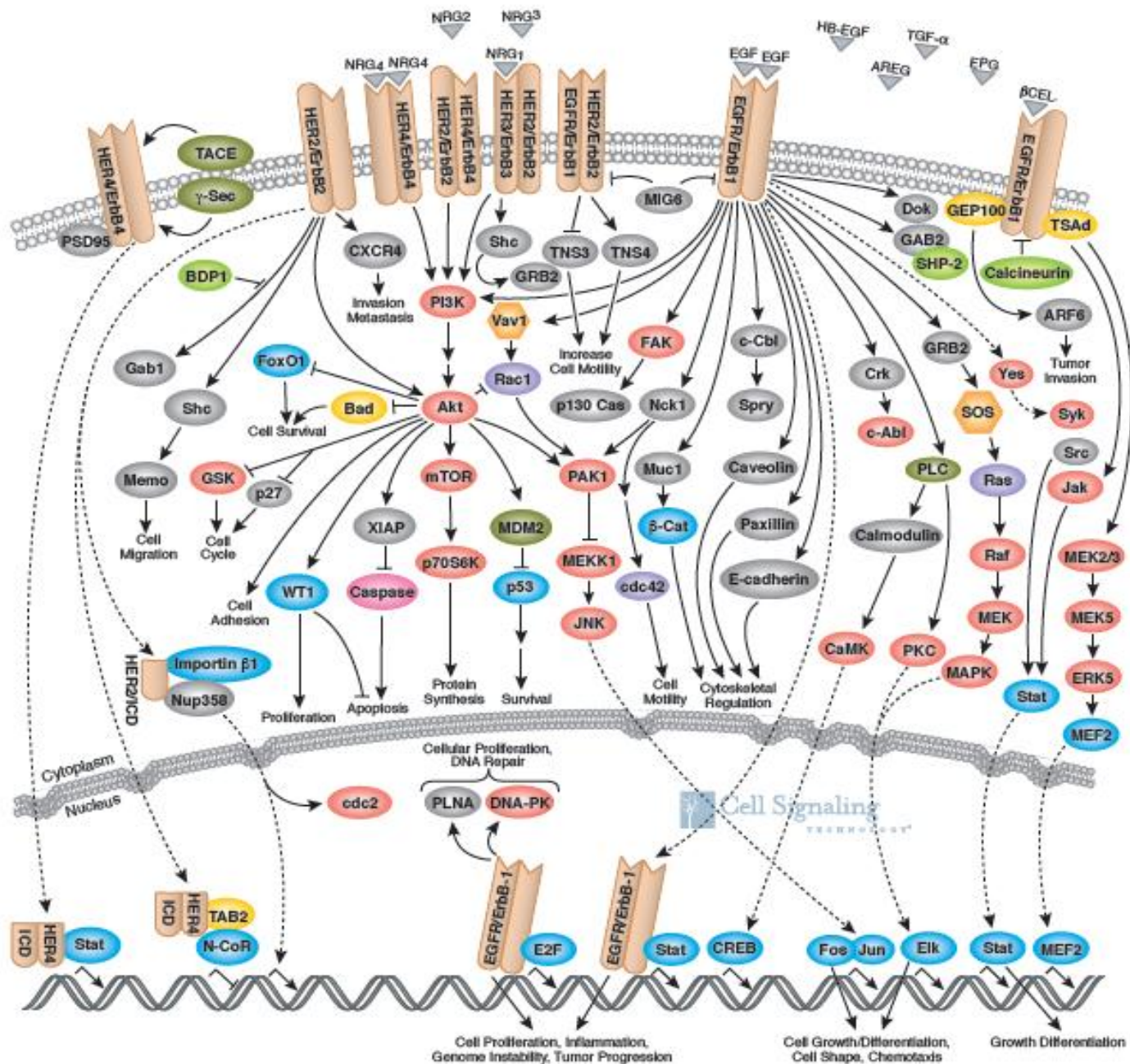
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1986

Physiology or Medicine

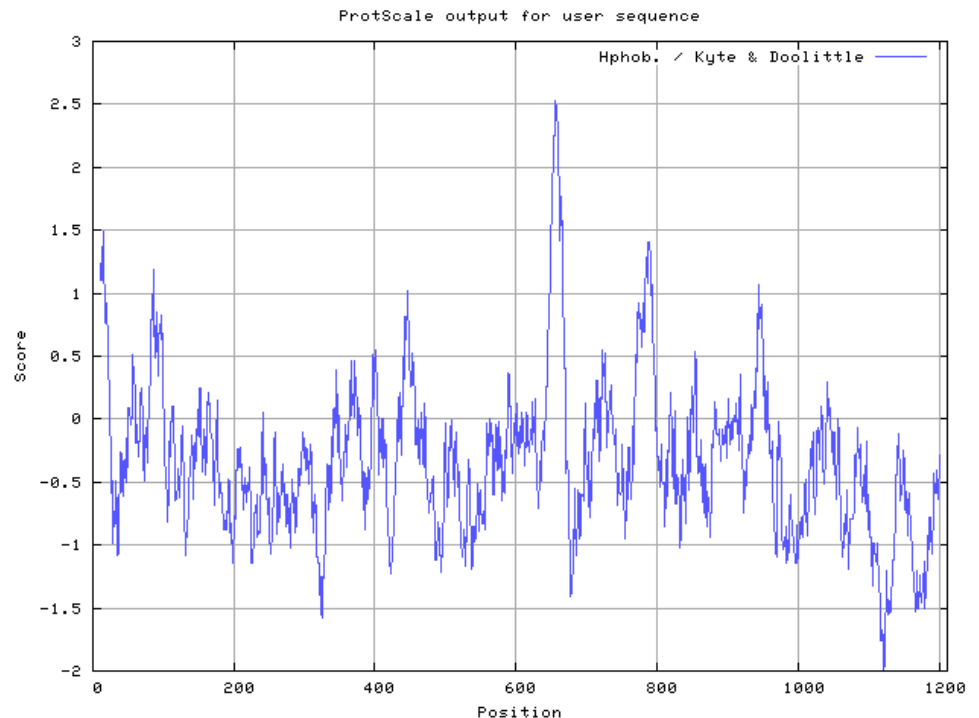




预测跨膜结构（疏水结构）

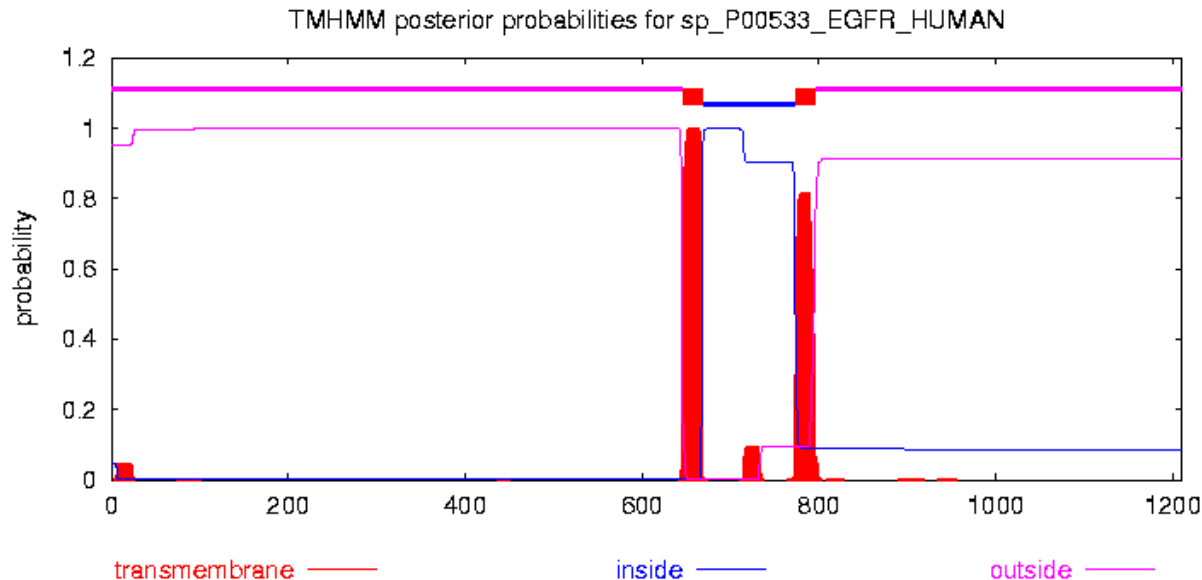
进入ExPASy的网站：

<http://expasy.org/tools/protscale.html>，选择
Hphob. / Kyte & Doolittle。将氨基酸序列输入



预测跨膜结构

- 使用TMHMM网站可预测蛋白的胞内区域和胞外区域:
- # sp_P00533_EGFR_HUMAN Length: 1210# sp_P00533_EGFR_HUMAN Number of predicted TMHs: 2# sp_P00533_EGFR_HUMAN Exp number of AAs in TMHs: 42.29864# sp_P00533_EGFR_HUMAN Exp number, first 60 AAs: 0.88712# sp_P00533_EGFR_HUMAN Total prob of N-in: 0.04662sp_P00533_EGFR_HUMAN TMHMM2.0 outside
1 645sp_P00533_EGFR_HUMAN TMHMM2.0 TMhelix 646
668sp_P00533_EGFR_HUMAN TMHMM2.0 inside 669
772sp_P00533_EGFR_HUMAN TMHMM2.0 TMhelix 773
795sp_P00533_EGFR_HUMAN TMHMM2.0 outside 796 1210

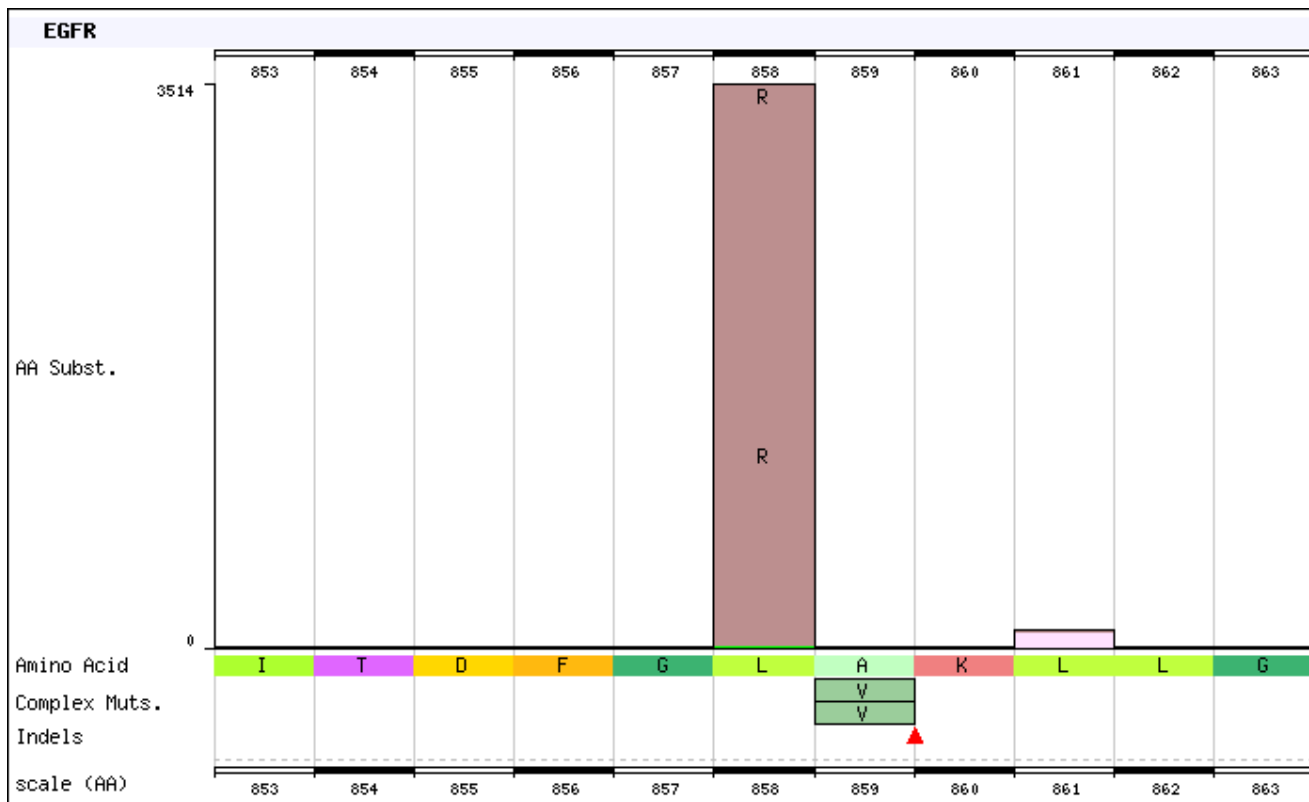


预测重复结构

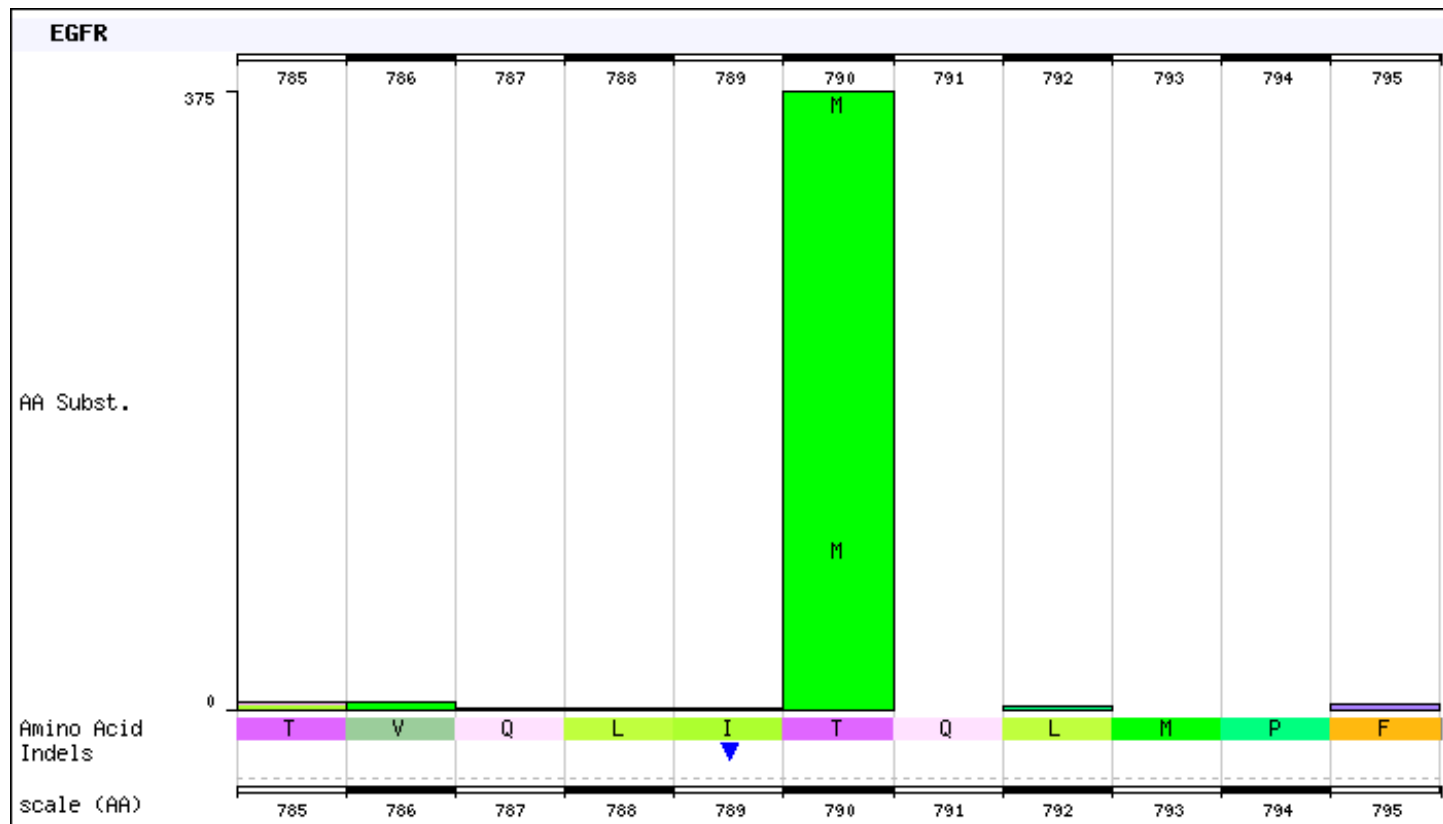
- 无重复结构

- COSMIC网站
- [Catalogue of Somatic Mutations in Cancer - COSMIC](#)
- www.sanger.ac.uk/genetics/CGP/cosmic
- 找出EGFR在癌细胞里的突变位点，分析这些突变为什么会引起癌症。
- 分别由三个位点在癌症中突变频率较高

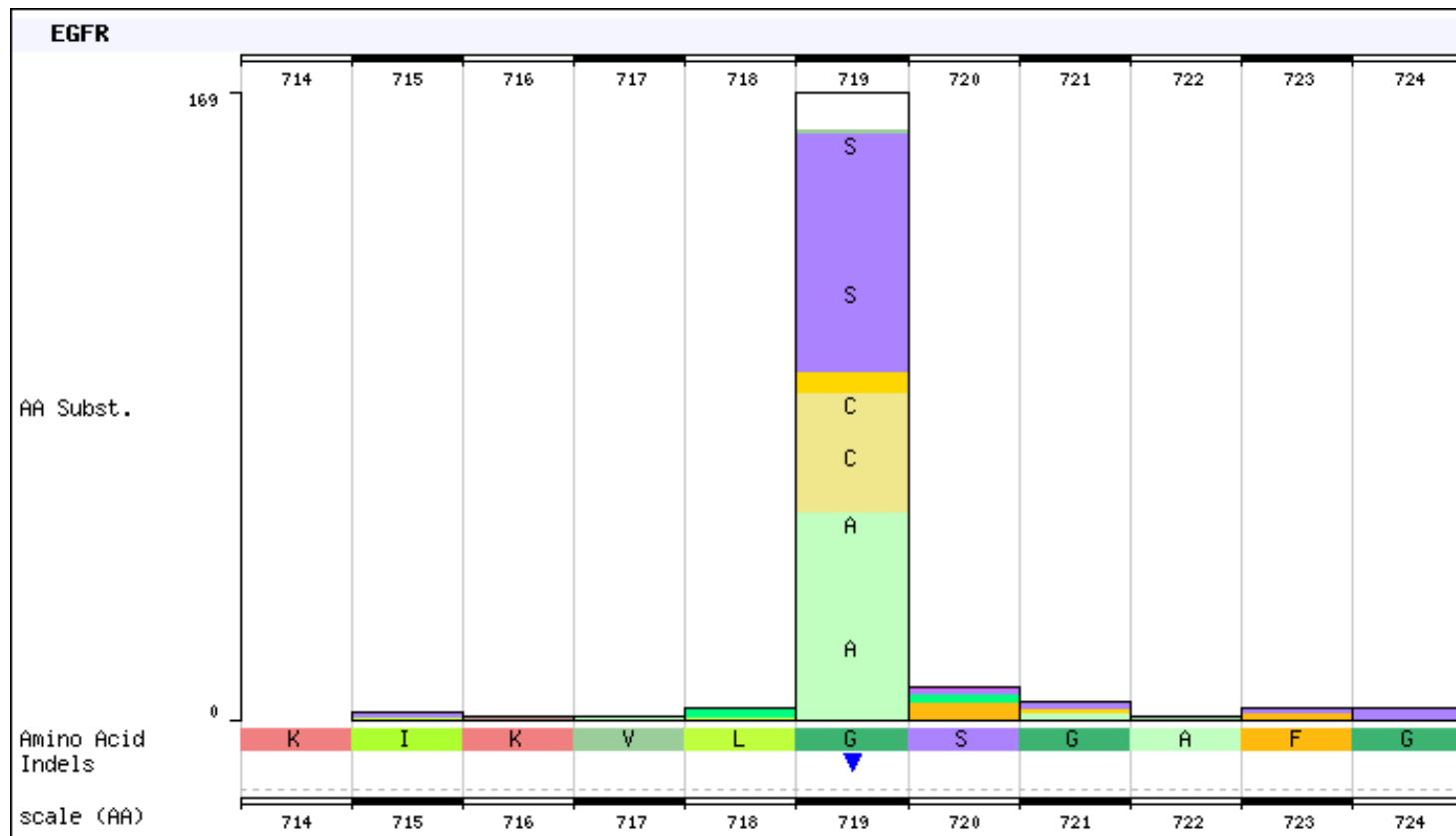
- 858 L->R、



- 790 T->M



- 719 G->SCA

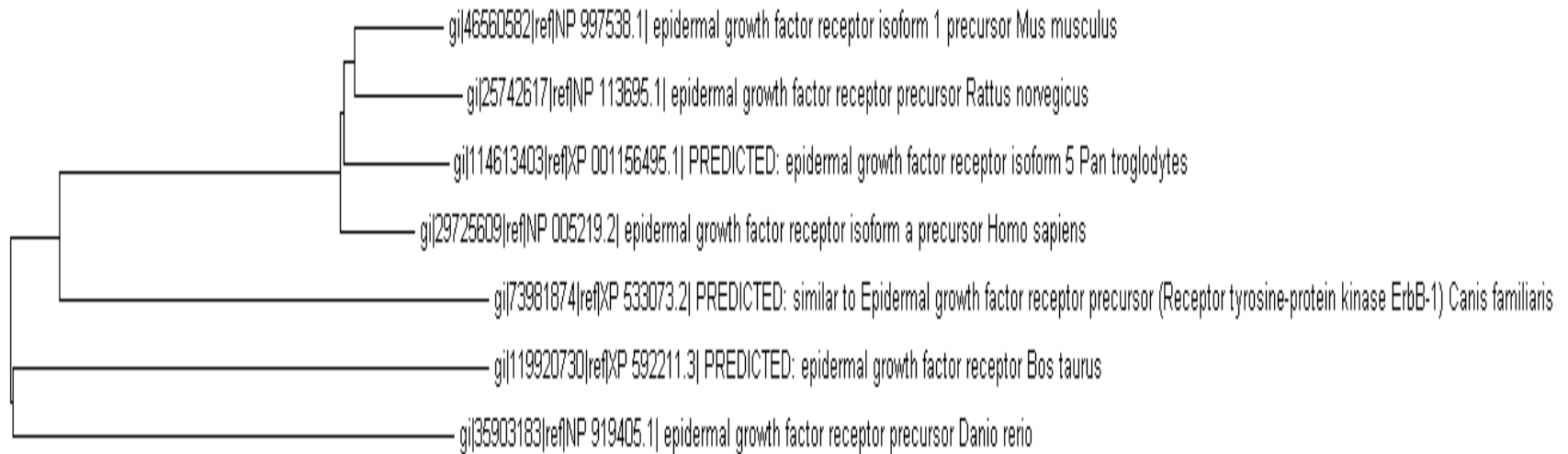


EGFR 6个物种比较保守

Protein Acc.	Gene	Organism
NP_005219.2	EGFR	H.sapiens
XP_001156495.1	EGFR	P.troglodytes
XP_533073.2	EGFR	C.lupus
XP_592211.3	EGFR	B.taurus
NP_997538.1	Egfr	M.musculus
NP_113695.1	Egfr	R.norvegicus
NP_919405.1	egfra	D.erio

P_033073.2	1183	FGCLLDVFRKKNIDSSGQLLNVCQIANGDVTLEKRLVRSGLAARVTL	1232
P_592211.3	772	FGCLLDVFRKKNIDSSGQLLNVCQIANGDVTLEKRLVRSGLAARVTL	821
P_997538.1	707	FGCLLDVFRKKNIDSSGQLLNVCQIANGDVTLEKRLVRSGLAARVTL	756
P_113695.1	716	FGCLLDVFRKKNIDSSGQLLNVCQIANGDVTLEKRLVRSGLAARVTL	765
P_919405.1	704	FGCLLDVFRKKNIDSSGQLLNVCQIANGDVTLEKRLVRSGLAARVTL	753
P_000219.2	840	VNTFQRVWITDFGLAKLGAEEKKFAAGGNVPIFIRGALSILKRAVTTGQ	894
P_001156495.1	802	VNTFQRVWITDFGLAKLGAEEKKFAAGGNVPIFIRGALSILKRAVTTGQ	851
P_533073.2	1233	VNTFQRVWITDFGLAKLGAEEKKFAAGGNVPIFIRGALSILKRAVTTGQ	1282
P_592211.3	822	VNTFQRVWITDFGLAKLGAEEKKFAAGGNVPIFIRGALSILKRAVTTGQ	871
P_997538.1	847	VNTFQRVWITDFGLAKLGAEEKKFAAGGNVPIFIRGALSILKRAVTTGQ	898
P_113695.1	846	VNTFQRVWITDFGLAKLGAEEKKFAAGGNVPIFIRGALSILKRAVTTGQ	895
P_919405.1	844	VNTFQRVWITDFGLAKLGAEEKKFAAGGNVPIFIRGALSILKRAVTTGQ	893
P_000219.2	890	SDVNSGVTVWEIATFGSKFDGSPASESSILEKGERLQPPPCIDIVY	941
P_001156495.1	912	SDVNSGVTVWEIATFGSKFDGSPASESSILEKGERLQPPPCIDIVY	964
P_533073.2	1283	SDVNSGVTVWEIATFGSKFDGSPASESSILEKGERLQPPPCIDIVY	1332
P_592211.3	870	SDVNSGVTVWEIATFGSKFDGSPASESSILEKGERLQPPPCIDIVY	921
P_997538.1	897	SDVNSGVTVWEIATFGSKFDGSPASESSILEKGERLQPPPCIDIVY	948
P_113695.1	898	SDVNSGVTVWEIATFGSKFDGSPASESSILEKGERLQPPPCIDIVY	949
P_919405.1	894	SDVNSGVTVWEIATFGSKFDGSPASESSILEKGERLQPPPCIDIVY	945
P_000219.2	840	NINIVYCNIDADRFRFRFLIIEFSFGARDPQRULVIQGRPHMLPSPFD	894
P_001156495.1	802	NINIVYCNIDADRFRFRFLIIEFSFGARDPQRULVIQGRPHMLPSPFD	851
P_533073.2	1333	NINIVYCNIDADRFRFRFLIIEFSFGARDPQRULVIQGRPHMLPSPFD	1382
P_592211.3	822	NINIVYCNIDADRFRFRFLIIEFSFGARDPQRULVIQGRPHMLPSPFD	871
P_997538.1	847	NINIVYCNIDADRFRFRFLIIEFSFGARDPQRULVIQGRPHMLPSPFD	898
P_113695.1	848	NINIVYCNIDADRFRFRFLIIEFSFGARDPQRULVIQGRPHMLPSPFD	895
P_919405.1	844	NINIVYCNIDADRFRFRFLIIEFSFGARDPQRULVIQGRPHMLPSPFD	893
P_000219.2	890	SNTFVALAEDKEDIDVYDADEVLPQQGFFSSPSSSRPILLSGLSATSNV	1044
P_001156495.1	1012	SNTFVALAEDKEDIDVYDADEVLPQQGFFSSPSSSRPILLSGLSATSNV	1061
P_533073.2	1383	SNTFVALAEDKEDIDVYDADEVLPQQGFFSSPSSSRPILLSGLSATSNV	1432
P_592211.3	970	SNTFVALAEDKEDIDVYDADEVLPQQGFFSSPSSSRPILLSGLSATSNV	1021
P_997538.1	997	SNTFVALAEDKEDIDVYDADEVLPQQGFFSSPSSSRPILLSGLSATSNV	1048
P_113695.1	998	SNTFVALAEDKEDIDVYDADEVLPQQGFFSSPSSSRPILLSGLSATSNV	1049
P_919405.1	994	SNTFVALAEDKEDIDVYDADEVLPQQGFFSSPSSSRPILLSGLSATSNV	1042
P_000219.2	1040	STVACIDRNLQSCPTKEDAFLQRVSSDPTGALTESSDITFLPVP---E	1091
P_001156495.1	1002	STVACIDRNLQSCPTKEDAFLQRVSSDPTGALTESSDITFLPVP---E	1053
P_533073.2	1433	STVACIDRNLQSCPTKEDAFLQRVSSDPTGALTESSDITFLPVP---E	1477
P_592211.3	1022	PTVTCIDRNLQSCPTKEDAFLQRVSSDPTGALTESSDITFLPVP---E	1071
P_997538.1	1047	STVACIDRNLQSCPTKEDAFLQRVSSDPTGALTESSDITFLPVP---E	1098
P_113695.1	1048	STVACIDRNLQSCPTKEDAFLQRVSSDPTGALTESSDITFLPVP---E	1099
P_919405.1	1043	STVACIDRNLQSCPTKEDAFLQRVSSDPTGALTESSDITFLPVP---E	1094
P_000219.2	1092	VINGVFRPAGGVQRFVYKQPLFAPAPGPRVQDPSSTAYVSPVEYLN-	1140
P_001156495.1	1109	VINGVFRPAGGVQRFVYKQPLFAPAPGPRVQDPSSTAYVSPVEYLN-	1157
P_533073.2	1478	VINGVFRPAGGVQRFVYKQPLFAPAPGPRVQDPSSTAYVSPVEYLN-	1528
P_592211.3	1087	VYNGVFRPAGGVQRFVYKQPLFAPAPGPRVQDPSSTAYVSPVEYLN-	1135
P_997538.1	1092	VYNGVFRPAGGVQRFVYKQPLFAPAPGPRVQDPSSTAYVSPVEYLN-	1140
P_113695.1	1091	VINGVFRPAGGVQRFVYKQPLFAPAPGPRVQDPSSTAYVSPVEYLN-	1139
P_919405.1	1088	VNGV-----ESSNINPVVQ--QV--RSPFRTLLSSPALGTEE+EYLNQ	1138
P_000219.2	1141	--TVQPTCVHSTFDSPAMAGKSSQIQLNIPVQDQFFFKKANPQGIFF	1188
P_001156495.1	1108	--TVQPTCVHSTFDSPAMAGKSSQIQLNIPVQDQFFFKKANPQGIFF	1159
P_533073.2	1527	--T-RPTCVHSLVLDSPSLVQKARQIQLNIPVQDQFFFKKANPQGIFF	1573
P_592211.3	1116	--TSPACVHSTFDSPAMAGKSSQIQLNIPVQDQFFFKKANPQGIFF	1165
P_997538.1	1141	--TAQPTCLEGGTDSALMIDKSSQIQLNIPVQDQFFFKKANPQGIFF	1188
P_113695.1	1140	--TAQPTCLEGGTDSALMIDKSSQIQLNIPVQDQFFFKKANPQGIFF	1187
P_919405.1	1137	FKSPAPAVYVYLNSTHTLLSTKFFSKNIPVQDQFFPKLNTHTSK	1178
P_000219.2	1189	GSTAEHAEYLRYAPSSSEFSGA	1210
P_001156495.1	1208	GSTAEHAEYLRYAPSSSEFSGA	1237
P_533073.2	1574	GPAAEHAEYLRYAPSSSEFSGA	1595
P_592211.3	1104	GPAAEHAEYLRYAPSSSEFSGA	1125
P_997538.1	1189	GPTAEHAEYLRYAPSSSEFSGA	1210
P_113695.1	1188	GPTAEHAEYLRYAPSSSEFSGA	1209
P_919405.1	1177	LPAAGHEYLGLVY-----	1191

6个物种比较保守序列进化



0.2

ErbB 蛋白家族保守结构域

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      . ** * : . . : * ** : . * . * : *      * * * . * * * : *
581 DGPHCVSSCPHGVLG--AMGPIYKYFDVQNECRPCHEMCTQSCWGPQLQDCL----GQT    633 P21860 ERBB3_HUMAN
585 DGFNCEVKECPDGLQG--ANSFIFKYADPDRECHPCHEMCTQSCWGPSTSHDCIYFPWTGHS    642 Q15303 ERBB4_HUMAN
587 DGPHCVKTCFAGVMGENNTL-VWKYADAGFVCHLCHENCTYSCITGPGLEGCP-----    637 P00533 EGFR_HUMAN
592 DPPFCVARCPSGVKFDLSYMPINKFVDEEGSAQCPCPINCTHSCVLDLDDKGCPC-----    643 P04626 ERBB2_HUMAN
      * * * * * * * * :      : : : * * * * * * * * . . . *
634 LVLIGKTHLTMALTVINGLWVIFMMLGGFTFLVWRGR-RIQNWRAMRRVLERGESIEPLDP    692 P21860 ERBB3_HUMAN
643 TLQKHARTPLIAAGVIGGLFLFVLVIGLTFPAVVRK-RSIKGGALRRFLLET-ELVEPLTP    700 Q15303 ERBB4_HUMAN
638 TNG--FKIPSIATGMGALLLLLLLVALGIGLPMRR-RHIVKRTLRLLQERELVEPLTP    694 P00533 EGFR_HUMAN
644 REQRASPLTISIISAVG-ILLVVLGVVFGILIKRQQKIRKRYIMRLLQETELVEPLTP    702 P04626 ERBB2_HUMAN
      : . . : : : : : : : : : : : : : * : : * * : * : * * * *
699 S-EKANVKLARIFKETEELRKLKVLGSGVFGTVHKGWVPEGESIKIPVCIKIVIEDKSGRQ    751 P21860 ERBB3_HUMAN
701 SGTAFNQQLRILKETEELKRVKVLGSGAGFTVYKGINVPEGETVKIPVAIKILNETTGPR    760 Q15303 ERBB4_HUMAN
695 SGTAFNQALLRILKETEELKRVKVLGSGAGFTVYKGLNIPEGEKVKIPVAIKELREATSPK    754 P00533 EGFR_HUMAN
703 SGAMFNQAQMRILKETEELRKLKVLGSGAGFTVYKGINIPDGENVKIPVAIKVLENTSEK    762 P04626 ERBB2_HUMAN
      * * * * * * * * : : * * * * * * * * * * * * * * * * * * * * : : : :
752 SFQAVTDMLAIGSLDHAHIVRLLGLCPGSSLQVLTQVLPGLSLLDHTVQHRGALGQLL    811 P21860 ERBB3_HUMAN
761 ANVEFMDEALIMASMDHPHLVRLGLVCLSPITQLVLTQLMFGSCLEPVHEHKNVIGSQLL    820 Q15303 ERBB4_HUMAN
755 ANVEILDEAYVMAQVSNFVHCRLLGLICLTSTVQLITQLMFGSCLLDPVREHKNVIGSQYL    814 P00533 EGFR_HUMAN
763 ANVEILDEAYVMAQVSGPVVSRLLGLICLTSTVQLVLTQLMFGSCLLDHTVRENTRGLGQLL    822 P04626 ERBB2_HUMAN
      : . . * . : : : : : : * * * * * * * * : : * * * * * * * * : : * * *
812 LNWCVQIAGKGMVYLEEHGMVHRDLAARVLLKSPSQVQVADFGVADLLPDDWQQLLYSEA    871 P21860 ERBB3_HUMAN
821 LNWCVQIAGKGMVYLEERRLVHRDLAARVLLKSPFNHVKITDFGLARLLGSEKENVADGG    880 Q15303 ERBB4_HUMAN
815 LNWCVQIAGKGMVYLEDRLVHRDLAARVLLKSPQVQVADFGVADLLPDDWQQLLYSEA    874 P00533 EGFR_HUMAN
823 LNWCVQIAGKGMVYLEDVLRVHRDLAARVLLKSPFNHVKITDFGLARLLDIDETETHADGG    882 P04626 ERBB2_HUMAN
      * * * * * * * * * * : * * * * * * * * * * * * * * * * * * * * * * : : :
872 KVIKGMMALESILRRRPTHQSDVNSYGVTVWELMTFGAEFYAGLRLAEVPDLLEKGERLA    931 P21860 ERBB3_HUMAN
881 KVIKGMMALESILRRRPTHQSDVNSYGVTVWELMTFGAEFYAGLRLAEVPDLLEKGERLB    940 Q15303 ERBB4_HUMAN
875 KVIKGMMALESILRRRPTHQSDVNSYGVTVWELMTFGAEFYAGLRLAEVPDLLEKGERLB    934 P00533 EGFR_HUMAN
883 KVIKGMMALESILRRRPTHQSDVNSYGVTVWELMTFGAEFYAGLRLAEVPDLLEKGERLB    942 P04626 ERBB2_HUMAN
      * * * * * * * * * * : * * * * * * * * * * * * * * * * * * * * * *
932 QPFICTIDVVMV/KCNMIDENIRPTFWELANEPTFMARDPPRYLVHKGESGPGIAPGPE    991 P21860 ERBB3_HUMAN
941 QPFICTIDVVMV/KCNMIDADSRPKFHELAEEFARMARDPQRYLVIQGDDR-MKLPSPN    999 Q15303 ERBB4_HUMAN
935 QPFICTIDVVMV/KCNMIDADSRPKFHELIIEFSARMARDPQRYLVIQGDEEMHLPSS-PT    993 P00533 EGFR_HUMAN
943 QPFICTIDVVMV/KCNMIDSECRPFRELIVSEFSARMARDPQRYLVIQ-NEDLGPAS-PL    1000 P04626 ERBB2_HUMAN
      * * * * * * * * * * : * * * * * * * * * * * * * * * * * * * * * *
992 FHGLTWKLEEVELEPELDDLDLEAEEDNLATTTLGSALSFLVGTLNKPRGSSQSLSPS    1051 P21860 ERBB3_HUMAN
1000 DSKFQNLDEEDLEDDMMADEEVLVQAFNIPFPIYTSRARIDS---NR---SEIGHSP    1053 Q15303 ERBB4_HUMAN
994 DSNFYRALMDEEDMDVDAEYVLIQ-----QGFFS--    1025 P00533 EGFR_HUMAN
1001 DSTFYRALLEDDMDVDAEYVLIQ-----QGFFCPD    1024 P04626 ERBB2_HUMAN
      : . . : : : : : * : * : * :
1052 SGVFMVQGNLGECSQESAVGSSSERCFRVSFLHFMFRGLASESSEGHVITGSEAELOEK    1111 P21860 ERBB3_HUMAN
1054 FAYTFMS-GNQFVYRGGFFAAGQGVSVFYRAPTSTIPEAFVAQ-----GATAEIFDD    1104 Q15303 ERBB4_HUMAN
1026 -----SPSTS-----RTPLLS-----LSATEN--NS    1045 P00533 EGFR_HUMAN
1035 FAPGAGGMVHHRHSRSTREGGDLTLGLEPSEEEAFRSPLAPS-----EGAGSDVFDG    1088 P04626 ERBB2_HUMAN
      : : : : :
1112 VMCRSRSRSRSPFRPGDSAYHSQPHSLITFVPLSPGLEEEDVNGVMPDTHLKGTFP    1171 P21860 ERBB3_HUMAN
1105 SOCNGTLRKFVAPHVQEDSS--TQRNSADPTVFAFERSFAGLEEDGVMTP--MRDWP-    1158 Q15303 ERBB4_HUMAN
1046 TVACIDRNLGQSCPIKEDSF--LQRNSEDPTGALTEDS----IDDTFLPVFE--YINQS-    1096 P00533 EGFR_HUMAN
1059 DLGMGAAGLQLSPTHDSPF--LQRNSEDPTVFLFSETDGVVAPLTCSPQFE--YVNQPD    1144 P04626 ERBB2_HUMAN
      : : : * * * * * * * * * * * * * * * * * * * * * *

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重复序列比对 比较保守

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59 VMGNLEIVLIGHNADLSFLQWIREVTGVVLMAMNEFSTLPLENLRVVRGTQVYDGKFAIF 118 P21860 ERBB3_HUMAN
59 VMGNLEITSIEHWRLDSFLRSVREVTGVVLMALNQFVYLPLENLRIRIGTKLYEDRYALA 118 Q15303 ERBB4_HUMAN
61 VLGNLEITYVQWVYDLSFLKTIQEVAGVYLIALNTVERIPLFNLIQIIRGMYVENSVALA 120 P00533 EGFR_HUMAN
56 VQGNLEILYLFTHASLSPFDIQEVQGVYLIHNVVRFVPLQLRIVRGTQLFEDRYALA 115 P04626 ERBB2_HUMAN
* * * * *
119 VMLNVT-----NSSHALRQLRLTQLTEILSGVYIEKNDKLCHEMTIDWRDIVRD 169 P21860 ERBB3_HUMAN
119 IFLNVR-----DGNFQLQLGLKHLTEILNGVYVQDKFLCYADITHQDIVRN 169 Q15303 ERBB4_HUMAN
121 VLNVT-----NHTGLKELPMNQLQELHSGVYFSPNFPALCVESIQWRDIVRS 170 P00533 EGFR_HUMAN
116 VLDNGDPLNMTTFTVTSFGGLRELQLRSLTEILKSGVLIQRNPLQCYQDTILWQDIFPK 175 P04626 ERBB2_HUMAN
* * * * *
170 ---RDAEIVKMGNSRCPCEVCKG-RCWGPGEEDCQLTRTICAPQNGHCYGFNPMQ 225 P21860 ERBB3_HUMAN
170 WPFNLLVTVNGSSGCGRCHK3CTG-RCWGPTEHRCQTLTRTVCAEQCDGRCYGPFVSD 225 Q15303 ERBB4_HUMAN
171 DPLSNMMDPQNHLSGCGKDPFCGNGSGAGEENCQKLTILICACQCSGRCYGFVSD 230 P00533 EGFR_HUMAN
176 NNQLALTLDITNRSRACHFCSPMCKGSRGWESSEDCQLTRTVCAAGCA-RCWGFPLTD 234 P04626 ERBB2_HUMAN
* * * * *
226 CCHDECAGGCGSPQDTCDFACRHNDSGACVFRCPQLVNVKLTQLLEFNHTVYQYGVV 285 P21860 ERBB3_HUMAN
229 CCHRECAGGCGSPKDTDFACRHNDSGACVTCQCFQVFNFTFQLLEHNWAKYITGAF 288 Q15303 ERBB4_HUMAN
281 CCHQCAGGCTGFRSDCLVCRFRDEATCKDTCPPLMNFPTVQMDNPFKGYFPGAT 290 P00533 EGFR_HUMAN
285 CCHQCAGGCTGFRSDCLVCRFRDEATCKDTCPPLMNFPTVQMDNPFKGYFPGAT 294 P04626 ERBB2_HUMAN
* * * * *
286 CVASCPHFVVDQT-SCVRACPFRMEVD-KNGLKMCPEQSGLCFACESTGSGSRF--Q 341 P21860 ERBB3_HUMAN
289 CVKCPHFVVDSS-SCVRACPSSMEVE-ENGKMKKPCCTDICFACDSTGSLMSAQ 346 Q15303 ERBB4_HUMAN
291 CVKCPHFVVDSS-ITDSSCVRACADSTHEM-EDGVKCKKCGSPCKKVCWIGTGEFMDL 349 P00533 EGFR_HUMAN
295 CVTACFINVLSIDVSGSCLVCLRNQVTAEDGTQKCKKSPCARVYGLGMDHLREVR 354 P04626 ERBB2_HUMAN
* * * * *
342 TVDSNIDGFNCTKILGNLDFLITGLNGDFMHHKIPALDSEKLVFRTVREITGVLMIQS 401 P21860 ERBB3_HUMAN
347 TVDSNIDGFNCTKINGMLFLFVIGHGDFVNAIEADSEKLVFRTVREITGVLMIQS 406 Q15303 ERBB4_HUMAN
350 SIMATNIKHFQNTSISGDLHLFVAFRGDSPTHTPFLD-LELDILKTVREITGVLMIQS 409 P00533 EGFR_HUMAN
355 NTSANIQEFAGCKNIFGSLALFESFDGDPASNTAFIQPEQLQVFETLEITGVLYISA 414 P04626 ERBB2_HUMAN
* * * * *
402 WPFHMNFVFMNLTITGGRLYNGFSLIMGQNVVLSLGRSLKEISAGRIYISANRQ 461 P21860 ERBB3_HUMAN
407 WPFMNTDFVFMNLTITGGRLYVLS-GLSLLILKQGITSLQFSLKEISAGRIYITDSEN 465 Q15303 ERBB4_HUMAN
410 WFNRTDLHAFENLIRGTVHSGQPSLAVS-NITSLGRLSLKEISAGRIYISGNHN 468 P00533 EGFR_HUMAN
415 WFDLFDPLSPQVLQVIRGRLHNGAYSLTQGLGSMGLRLSLELGGSLALIHNTH 473 P04626 ERBB2_HUMAN
* * * * *
462 LCYHSLNWKVLRGPTTEERLDIKHNRFRRCVAEGK/CDPLCSGGCGSPGQCLSCR 521 P21860 ERBB3_HUMAN
466 LCYHTINWTLFES-TINQRIVIRDNKRAENCTAEGM/CNHLCSDDGCGSPGQCLSCR 524 Q15303 ERBB4_HUMAN
469 LCYHTINWTKLES-TSGKTKLISNRSNCAATGQ/CHALCSPEGCGSPFRDQVSCR 527 P00533 EGFR_HUMAN
474 LCPVHTVFDQVLR-NFQALLHTANRFEDECVSEGLACHQLCARGHCWSPGPTQVNCIS 532 P04626 ERBB2_HUMAN
* * * * *
522 NYRGGV/CVTHCNFLNGEPRFAHEAECFSPHFECQPMEG-TAICNGSGSDTCAQCAFR 580 P21860 ERBB3_HUMAN
525 RFSRGRICIESCHLYDGEFREFENSGICVECDQCEQMEDGLLICHGSPGDMCTKSHFK 584 Q15303 ERBB4_HUMAN
528 NYRSGREC/DACHLLEGESEFREFENSECIQCHPECLPQAM-NITCTGSGSDMCTCAHY 586 P00533 EGFR_HUMAN
533 QLRGQCEVEECRVLQGLFREVYNARHCLPCHPECPQNG-SVTCFGEADQVACAHYK 591 P04626 ERBB2_HUMAN
* * * * *
581 DGPHCVS8CPHVLG--AMGPIYKYPDVQNECRBCHENCTQCGKPELQDCL----GQT 633 P21860 ERBB3_HUMAN
585 DGPHCVTKCPDGLQ--ANSIFPKYADFDRECHPCHPCTQCGNGPTSHDCIYVFWTGH 642 Q15303 ERBB4_HUMAN
587 DGPHCVTKCPAGVGENVTL-VWYADAGH/VCHLHPACTVGTCTGPGLEGCP----- 637 P00533 EGFR_HUMAN
592 DFPFCVACRSPGVKEDLSYMFIMKPFDEEGACQPCPINCTHSCVLDLDDWGPC----- 643 P04626 ERBB2_HUMAN
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