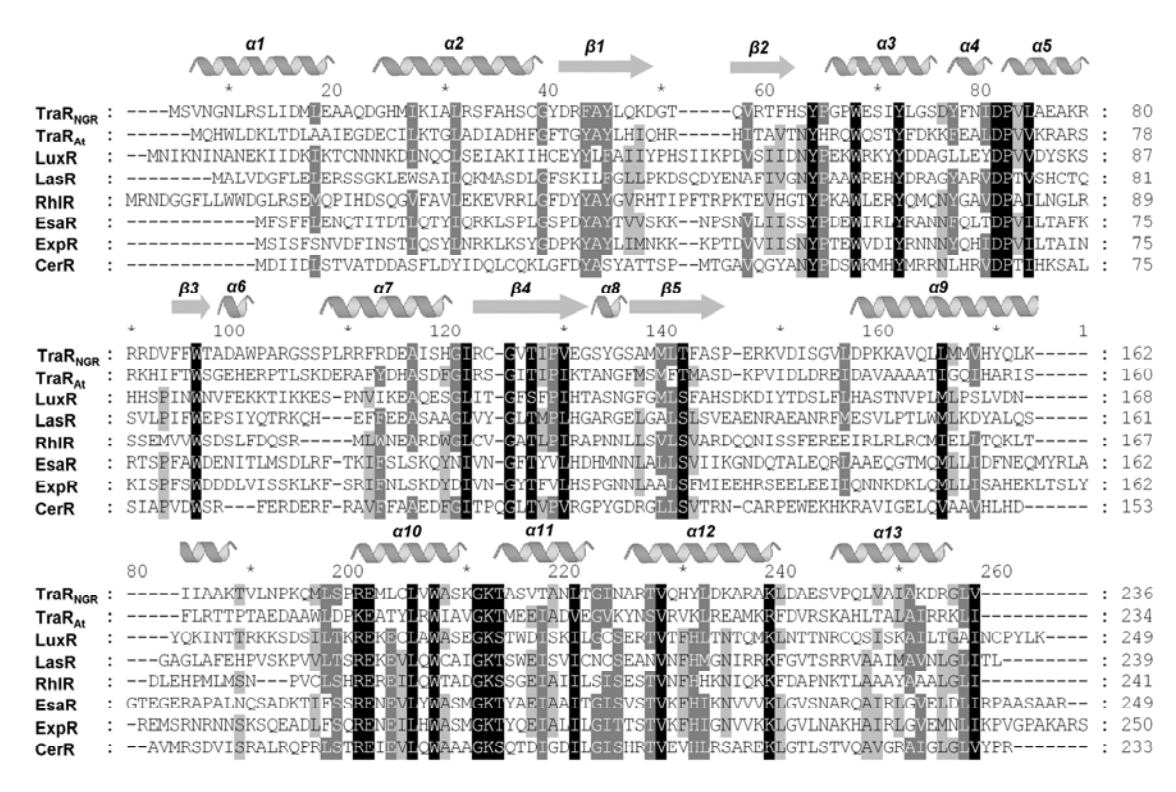
α1 α2 β1 β2 α3 α4 α5
TraR_NGR : ----MSVNGNLRSLIDMLEAAQDGHMIKIALRSFAHSCGYDRFAYLQKDGT-----QVRTFHSYEGFWESIYLGSDYFNIDEVLAEAKR : 80
TraR_At : ------MQHWLDKLTDLAAIEGDECILKTGLADIADHFGFTGYAYLHIQHR-----HITAVTNYHRQWQSTYFDKKGEALDEVVKRARS : 78
LuxR : --MNIKNINANEKIIDKIKTCNNNKDINQQLSEIAKIIHCEYYLFAIIYPHSIIKPDVSIIDNYEEKWRKYYDDAGLLEYDEVVDYSKS : 87
LasR : ---------MALVDGFLELERSSGKLEWSAILQKMASDLGFSKILFGLLPKDSCDYENAFIVGNYEAAWREHYDRAGYARVDEVTVSHCTQ : 81
RhlR : MRNDGGFLLWWDGLRSEMQPIHDSQGVFAVLEKEVRRLGFDYYAYGVRHTIPFTRPKTEVHGTYEKAWLERYQMCNYGAVDEAILNGLR : 89
EsaR : ------------MFSFFLENQTITDTLQTYIQRKLSPLGSPDYAYTVVSKK--NPSNVLIISSYGFDEMIRLYRANNFQLTDFVILTAFK : 75
ExpR : ------------MSISFSNVDFINSTIQSYLNRKLKSYGDPKYAYLIMNKK--KPTDVVIISNYETEWVDIYRNNNMQHIDPVILTAIN : 75
CerR : ------------MDIIDLSTVATDDASFLDYIDQLCQKLGFDYASYATTSP--MTGAVQGYANYFDSWKMHYMRRNLHRVDFTIHKSAL : 75
β3 α6 α7 β4 α8 β5 α9
RRDVFFWTADAWPARGSSPLRRFRDEAISHGIRC-GVTIPVEGSYGSAMLLTFASP-ERKVDISGVLDPKKAVQLLMMVHYQLK----- : 162
TraR_At : RKHIFTWSGEHERPTLSKDERAFYDHASDEGIRS-GITIPIKTANGFMSVSFTMASD-KPVIDLDREIDAVAAAATIGQIHARIS----- : 160
LuxR : HHSPIINANVFEKKTIKKES-PNVIKEAQESGLIT-GFSFPIHTASNGFGMLSFAHSDKDIYTDSLFLHASTNVPLMLPSLVDN------ : 168
LasR : SVLPIFWEPSIYQTRKQH---EFEEEASAAGLVY-GLTVPLHGARGELGAFSLSVEAENRAEANRFVESVLPTLWMLKDYALQS----- : 161
RhlR : SSEMVVASDSLFDQSR-----MLANEARDWGLCV-GATLPIRAPNNLLSVFSVARDQQNISSFEREEIRLRLRCMIELLTQKLT----- : 167
EsaR : RTSPFAADENITLMSDLRF-TKIESSLSKQYNIVN-GFTYVLHDHMNNLALLSVIIKGNDQTALEQRLAAEQGTMQMLLIDFNEQMYRLA : 162
ExpR : KISPFSQDDDLVISSKLKF-SRIQNLSKDYDIVN-GYQFVLHSPGNNLAALSFMIEEHRSEELEEIIQNNKDKLQMLLISAHEKLTSLY : 162
CerR : SIAPVDSR---FERDERF-RAVQFAAEDFGITPQGLTVPVRGPYGDRGLLSVTRN-CARPEWEKHKRAVIGELQVAAVHLHD------ : 153
α10 α11 α12 α13
TraR_NGR : -----IIAAKTVLNPKQMLSFREMLGLVWASKGKTASVTANLTGINARTVQHYLDKARAKLDAESVPQLVAIAKDRGIV---------- : 236
TraR_At : -----FLRTTPTAEDAAWLDEKEATYLRWIAVGKTMEEIADVEGVKYNSVRVKLREAMKRFDVRSKAHLTALAIRRKLI---------- : 234
LuxR : ----YQKINTTRKKSDSILTKREKEGLAWASEGKSTWDISKILGCSERTVTFHLTNTQMKLNTTNRCQSISKAILTGAINCPYLK----- : 249
LasR : ---GAGLAFEHPVSKPVVLTSREKEVLQWCAIGKTSWEISVICNCSEANVNFHMGNIRRKFGVTSRRVAAIMAVNLGIITL--------- : 239
RhlR : --DLEHPMLMSN---PVCLSHRERPILQWTADGKSSGEIAILLSISESTVNFHHKNIQKKFDAPNKTLAAAYQAALGLI---------- : 241
EsaR : GTEGERAPALNQSADKTTFSSRENPVLYWASMGKTYAEIAAILGISVSTVKFHIKNVVVKLGVSNARQAIRLGVELDIIRPAASAAR-- : 249
ExpR : -REMSRNRNNSKSQEADLFSQRENPILHWASMGKTYQEIAAILGITTSTVKFHIGNVVVKLGVLNAKHAIRLGVEMNIIKPVGPAKARS : 250
CerR : --AVMRSDVISRALRQFRLSTREIEVLQWAAAGKSQTDIGDILGISHRTVEVHIRSARDKLGTLSTVQAVGRAIGLGIVYPR------- : 233