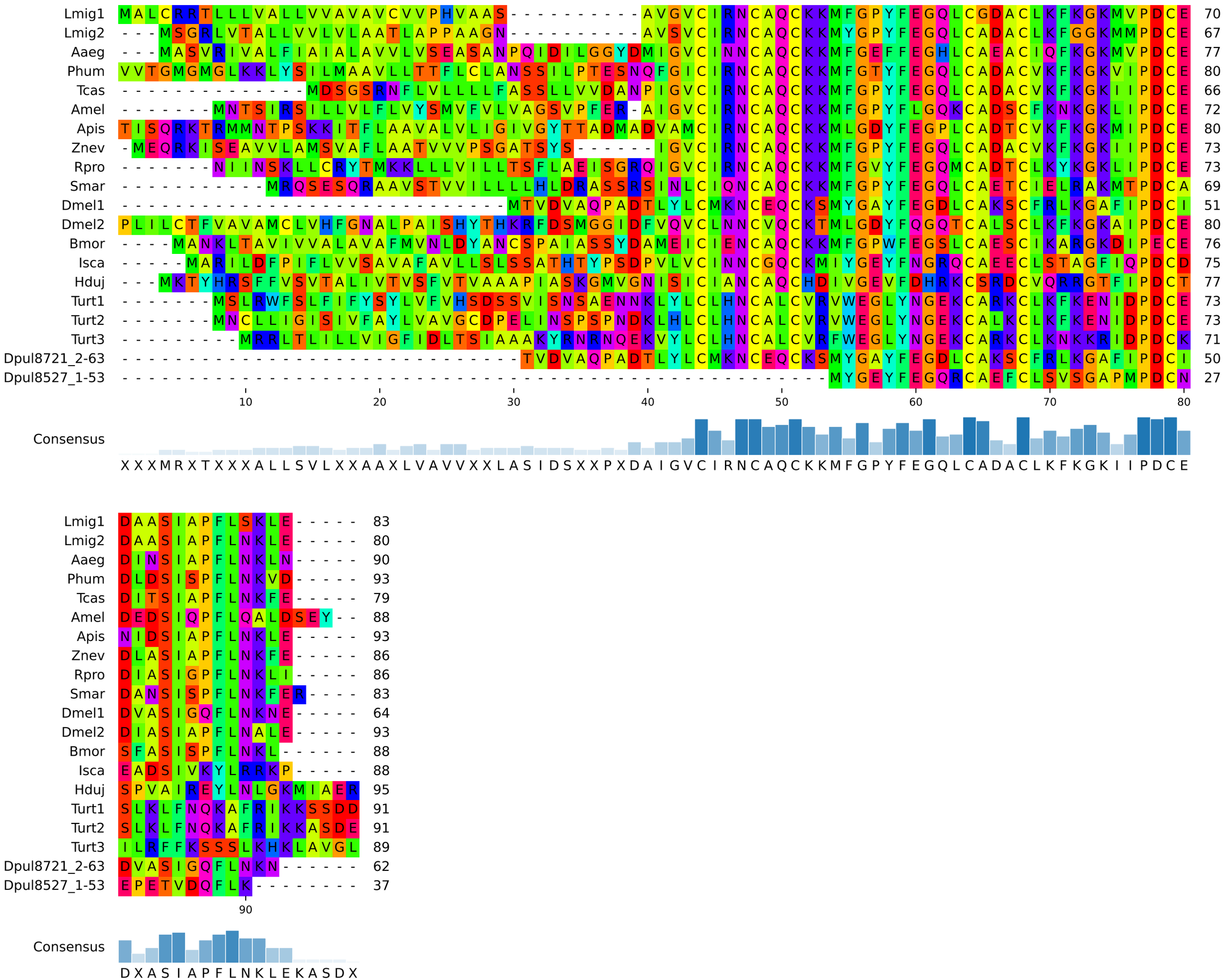
Lmig1 MALCRRTLLLVALLVVAVAVCVVPHVAAS----------AVGVCIRNCAQCKKMFGPYFEGQLCGDACLKFKGKMVPDCE 70
Lmig2 ---MSGRLVTALLVVLVLAATLAPPAAGN----------AVSVCIRNCAQCKKMYGPYFEGQLCADACLKFGGKMMPDCE 67
Aaeg ---MASVRIVALFIAIALAVVLVSEASANPQIDILGGYDMIGVCINNCAQCKKMFGEFFEGHLCAEACIQFKGKMVPDCE 77
Phum VVTGMGMGLKKLYSILMAAVLLTTFLCLANSSILPTESNQFGICIRNCAQCKKMFGTYFEGQLCADACVKFKGKVIPDCE 80
Tcas ----------MDSGSRNFLVLLLLFASSLLVVDANPIGVCIRNCAQCKKMFGPYFEGQLCADACVKFKGKIIPDCE 66
Amel -------MNTSIRSILLVLFLVYSMVFVLVAGSVPFER-AIGVCIRNCAQCKKMFGPYFLGQKCADSCFKNKGKLIPDCE 72
Apis TISQRKTRMMNTPSKKITFLAAVALVLIGIVGYTTADMADVAMCIRNCAQCKKMLGDYFEGPLCADTCVKFKGKMIPDCE 80
Znev -MEQRKISEAVVLAMSVAFLAATVVVPSGATSYS------IGVCIRNCAQCKKMFGPYFEGQLCADACVKFKGKIIPDCE 73
Rpro -------NIINSKLLCRYTMKKLLLVILLTSFLAEISGRQIGVCIRNCAQCKKMFGVYFEGQMCADTCLKYKGKLIPDCE 73
Smar ----------MRQSESQRAAVSTVVILLLLHLDRASSRSINLCIQNCAQCKKMFGPYFEGQLCAETCIELRAKMTPDCA 69
Dmel1 ----------MTVDVAQPADTLYLCMKNCEQCKSMYGAYFEGDLCAKSCFRLKGAFIPDCI 51
Dmel2 PLILCTFVAVAMCLVHFGNALPAISHYTHKRFDSMGGIDFVQVCLNNCVQCKTMLGDYFQGQTCALSCLKFKGKAIPDCE 80
Bmor ----MANKLTAVIVVALAVAFMVNLDYANCSPAIASSYDAMEICIENCAQCKKMFGPWFEGSLCAESCIKARGKDIPECE 76
Isca -----MARILDFPIFLVVSAVAFAVLLSLSSATHTYPSDPVLVCINNCGQCKMIYGEYFNGRQCAEECLSTAGFIQPDCD 75
Hduj ---MKTYHRSFFVSVTALIVTVSFVTVAAAPIASKGMVGNISICIANCAQCHDIVGEVFDHRKCSRDCVQRRGTFIPDCT 77
Turt1 -------MSLRWFSLFIFYSYLVFVHSDSSVISNSAENNKLYLCLHNCALCVRVWEGLYNGEKCARKCLKFKENIDPDCE 73
Turt2 -------MNCLLIGISIVFAYLVAVGCDPELINSPSPNDKLHLCLHNCALCVRVWEGLYNGEKCALKCLKFKENIDPDCE 73
Turt3 ---------MRRLTLILLVIGFIDLTSIAAAKYRNRNQEKVYLCLHNCALCVRFWEGLYNGEKCARKCLKNKKRIDPDCK 71
Dpul8721_2-63 ----------TVDVAQPADTLYLCMKNCEQCKSMYGAYFEGDLCAKSCFRLKGAFIPDCI 50
Dpul8527_1-53 ----------MYGEYFEGQRCAEFCLSVSGAPMPDCN 27
10 20 30 40 50 60 70 80
Consensus
XXXMRXTXXXALLSVLXXAAXLVAVVXXLASIDSXXPXDAIGVCIRNCAQCKKMFGPYFEGQLCADACLKFKGKIIPDCE
Lmig1 DAASIAPFLSKLE----- 83
Lmig2 DAASIAPFLNKLE----- 80
Aaeg DINSIAPFLNKLN----- 90
Phum DLDSISPFLNKVD----- 93
Tcas DITSIAPFLNKFE----- 79
Amel DEDSIQPFLQALDSEY-- 88
Apis NIDSIAPFLNKLE----- 93
Znev DLASIAPFLNKFE----- 86
Rpro DIASIGPFLNKLI----- 86
Smar DANSISPFLNKFER---- 83
Dmel1 DVASIGQFLNKNE----- 64
Dmel2 DIASIAPFLNALE----- 93
Bmor SFASISPFLNKL------ 88
Isca EADSIVKYLRRKP----- 88
Hduj SPVAIREYLNLGKMIAER 95
Turt1 SLKLFNQKAFRIKKSSDD 91
Turt2 SLKLFNQKAFRIKKASDE 91
Turt3 ILRFFKSSSLKHKLAVGL 89
Dpul8721_2-63 DVASIGQFLNKN------ 62
Dpul8527_1-53 EPETVDQFLK-------- 37
90
Consensus
DXASIAPFLNKLEKASDX