

Lep_BmorSCP2 (type-1)	73	IPIYVNNNCGSTG	287	QVDVVELHDCFAA	334	NPSGGLIAKGHP	377	LQLGGGMG
Hym_AmelSCP2 (type-1)	77	CPIYVNNNCGSTG	290	DVDVIELHDCFSI	337	NPSGGLISKGHP	380	LQI GGG LG
Dip_DmeISCP2 (type-1)-1	76	IPVYVNNNCGSTG	290	DVQVVELHDCFSA	337	NPSGGLISKGHP	380	LQLGGGLG
Dip_DmeISCP2 (type-1)-2	76	IPVYVNNNCGSTG	290	DVQVVELHDCFSA	337	NPSGGLISKGHP	380	LQLGGGLG
Dip_AgamSCP2 (type-1)	76	IPIYVNNNCGSTG	289	DVDVVELHDCFSA	336	NPSGGLISKGHP	379	LQI GGG LG
Col_AglaSCP2 (type-1)	73	IPIFVNNNCGSTG	286	DVQVVELHDCFSA	333	NPSGGLISKGHP	376	LQI GGG LG
Col_NvesSCP2 (type-1)	73	IPIINVNNNCGSTG	286	DVQVVELHDCFSA	333	NPSGGLISKGHP	376	LQI GGG LG
Col_TcasSCP2 (type-1)	189	IPIFVNNNCGSTG	402	DVQVVELHDCFSA	449	NPSGGLISKGHP	492	LQI GGG LG
Dip_CquiSCP2 (type-1)	76	IPVYVNNNCGSTG	289	DVDVVELHDCFSA	336	NPSGGLISKGHP	379	LQI GGG LG
Hem_ApisSCP2 (type-1)-1	76	IPIYVNNNCGSTG	289	DVNVVELHDCFSA	336	NPSGGLISKGHP	379	LQI GGG LG
Hem_ApisSCP2 (type-1)-2	7	- - - - -	102	DVNVVELHDCFSA	149	NPSGGLISKGHP	171	- - - - -
Hem_ClecSCP2 (type-1)	76	IPIYVNNNCGSTG	289	DVDVVELHDCFSA	336	NPSGGLISKGHP	379	LQI GGG LG
Hem_HhalSCP2 (type-1)	77	IPIYVNNNCGSTG	290	DI DVVELHDCFSA	337	NPSGGLISKGHP	380	LQI GGG LG
Hym_BimpSCP2 (type-1)-2	77	CPIYVNNNCGATG	290	DVDVIELHDCFST	337	NPSGGLISKGHP	380	LQI GGG LG
Hym_BimpSCP2 (type-1)-1	77	CPIYVNNNCGATG	290	DVDVIELHDCFST	337	NPSGGLISKGHP	380	LQI GGG LG
Hym_DallSCP2 (type-1)	77	CPVYVNNNCGATG	290	DVDVVELHDCFSA	337	NPSGGLISKGHP	380	LQI GGG LG
Lep_DpleSCP2 (type-1)	73	IPIYVNNNCGSTG	287	QVDVVELHDCFAT	334	NPSGGLIAKGHP	377	LQLGGGMG
Lep_HmelSCP2 (type-1)	73	IPIYVNNNCGSTG	287	QVDVVELHDCFAA	334	NPSGGLIAKGHP	377	LQLGGGMG
Lep_MsexSCP2 (type-1)	73	IPIYVNNNCGSTG	287	QVDVVELHDCFAA	334	NPSGGLIAKGHP	377	LQLGGGMG
Lep_PxutSCP2 (type-1)-1	73	LPVHNI NNHGATG	286	EVDVVELHDCFSS	333	NPSGGLI AKGNP	376	LQLGGG - A
Lep_PxutSCP2 (type-1)-2	73	IPIYVNNNCGSTG	287	QIDVVELHDCFAA	334	NPSGGLIAKGHP	377	LQLGGGMG
Lep_PxutSCP2 (type-1)-3	5	- PIYVNNNCGSTG	218	EVDVVELHDCFAS	265	NPSGGLIAKGHP	308	LQLGGGMG
Lep_PxylSCP2 (type-1)	73	IPIYVNNNCGSTG	287	QIDVVELHDCFAA	334	NPSGGLIAKGHP	377	LQLGGGMG
Pht_PhumSCP2 (type-1)	76	IPIFVNNNCGSTG	288	DVHVVELHDCFST	335	NPSGGLISKGHP	378	LQI GGG LG
Hsap_SCP2 (type-1)	85	IPIINVNNNCGATG	298	DI DVIELHDCFST	345	NPSGGLISKGHP	388	LQI GGG LG
MtubSCP2 (type-1)	92	IPIVNVNNNCGSTG	303	DFGVIELHDCFSA	350	NPSGGLISKGHP	393	LQI GGG - A
MtubSCP2 (type-2)	84	TPATRHEAACASG	300	DL DGI EVHDCFPS	347	NPSGGLI - - GHP	386	A - EAGG - G
Lep_BmorT1-1	85	KPVLGINRLCGSG	313	DVDLIEINEAFVA	342	NVNGGATALGHP	381	ACI GGGQG
Lep_BmorT1-2	87	KPALGVNRLCGSG	317	DI DLVEINEAFVA	346	NVNGGAIAMGHP	385	ACI GGGQG
Lep_BmorT1-3	85	RPALGVSKACGTG	315	DVDLFEINEAFAS	344	NVNGGALAFGNP	383	SC - GGGQG
Hym_AmeIT1	85	KPSFSLNRLCGSG	315	DI ELIEINEAFGS	344	NVDGGSIALGHP	384	ACI GGGQG
Dip_DmeIT1	85	KPALGINRLCGSG	315	DI DLIEINEAFAA	344	NVNGGAIALGHP	383	ACI GGGQG
Dip_AgamT1-2	85	RPALGVNRLCGSG	315	DI DLFEINEAFGV	344	NLNGGAIALGHP	383	ACI GGGQG
Dip_AgamT1-1	127	RPALGVNRLCGSG	190	D - ALWTLTDSY - -	204	- - - - - - - - P	205	- - - - -
Col_AglaT1-1	73	YILILI - - FITNG	242	- - - - -	246	- - - - - - - - G - -	263	LR - - - - -
Col_AglaT1-2	4	- - - - -	22	DI DLIEINEAFGA	51	NVDGGAIALGHP	90	ACI GGGQG
Col_NvesT1	85	KPALQVNRRLCGSG	315	DM DLIEINEAFGA	344	NVNGGAIALGHP	383	ACI GGGQG
Col_TcasT1	85	RP AFLVNRLCGSG	315	DI DLIEINEAFAA	344	NVDGGAIALGHP	383	ACI GGGQG
Dip_CquiT1	85	KPALGVNRLCGSG	315	DI DLVEINEAFGV	344	NLNGGAIALGHP	383	ACI GGGQG
Hem_ApisT1	84	RHALGVNRLCGSG	314	DI DLVEINEAFGA	343	NVNGGAIALGHP	382	ACI GGGQG
Hem_ClecT1	85	RPALGINRLCGSG	315	DI DLVEINEAFGA	344	NVNGGAIALGHP	383	ACI GGGQG
Hem_HhalT1	85	KPALGVNRLCGSG	316	DI DLIEINEAFGA	345	NP DGGAIALGHP	384	ACI GGGQG
Hym_BimpT1-1	90	KPAFSVNRLCGSG	320	DVELVEINEAFGA	349	NVDGGAIALGHP	389	ACI GGGQG
Hym_BimpT1-2	85	KPAFSVNRLCGSG	315	DVELVEINEAFGA	344	NVDGGAIALGHP	384	ACI GGGQG
Hym_DallT1	85	KPALGVNRLCGSG	315	DI DLVEINEAFGA	344	NVNGGAIALGHP	383	ACI GGGQG
Iso_ZnevT1	85	RP AVAVNRLCGSG	315	DI DLVEINEAFGA	344	NVNGGAIALGHP	383	ACI GGGQG
Lep_DpleT1-1	25	RPALAVNRLCGSG	253	DI DLVEINEAFVA	282	NVNGGATALGHP	321	ACI GGGQG
Lep_DpleT1-2	87	KPALGVNRLCGSG	317	DI DLVEINEAFAA	346	NVNGGAIALGHP	385	ACI GGGLG
Lep_HmelT1	407	KPALGVNRLCGSG	637	DI DLVEINEAFAA	713	SSWGGSLSLGTP	972	LAIAGGTG
Lep_MsexT1-3	21	KPVVSTNLLSGSA	282	DI DLVEI HETNAA	311	NLSGGAIALGHP	336	ICVAGGQG
Lep_MsexT1-1	125	KPVLGINRLCGSG	353	DI DLIEINEAFVA	382	NVNGGATALGHP	411	- - - - -
Lep_MsexT1-2	87	KPALGINRLCGSG	317	DI DLVEINEAFAA	346	NVNGGAIAMGHP	385	ACI GGGQG
Lep_PxutT1-1	85	RPVLGINRLCGSG	313	DI DLVEINEAFVA	342	NVNGGATALGHP	381	ACI GGGQG
Lep_PxutT1-2	85	RPALGVSKACGAG	314	DVEIFEINETTAI	343	NVSGGALALGHP	383	SC - GGGQG
Lep_PxylT1-1	38	KPVLGVNRLCGSG	266	DVDLIEVR - VY - -	288	- - - GGQLSV - HP	329	VC DGGGLG
Lep_PxylT1-2	341	TPALGVNRLCGSG	571	DVDLVEINEAFAA	600	NVSGGAIAMGHP	639	ACI GGGQG
Lep_PxylT1-3	84	RPALVNMACGAG	307	DVDLIEINETFAA	336	NVNGGALAVGHP	375	SC - GGGQG
Lep_PxylT1-4	84	RPALAVNLACGAG	308	GVDLIEINETFAA	337	NVNGGALAVGHP	384	SC - GGGQG
Lep_PxylT1-5	84	RPALGVNLACGAG	308	GVDLIEINETFAA	337	NVNGGALAVGHP	376	SC - GGGQG
Lep_PxylT1-6	84	RPALAVNLACGAG	307	SVDLIEINETFAA	336	NVNGGALAVGHP	365	- - - - -
Lep_PxylT1-7	17	- - - - -	192	DVDLVEINEAFAA	221	NVNGGAIAMGHP	260	ACI GGGQG
Lep_PxylT1-8	9	- - - - - CV - -	76	DVDLVEINEAFAA	105	NVNGGAIAMGHP	144	ACI GGGQG
Lep_PxylT1-9	85	KPVLGVNRLCGSG	313	DVDLIEINEAFCA	342	NVNGGATALGHP	381	ACI GGGMG
Lep_PxylT1-10	43	HPR - - - - - ES	144	DVDLIEINEAFCA	173	NVNGGATALGHP	202	- - - - -
Pht_PhumT1	6	- - - - -	207	DI DLVEINEAFSA	236	NVNGGAVALGHP	275	ACI GGGQG
HsapT1	83	TPALTI NRLCGSG	313	DM DLVEINEAFAP	342	NVNGGAIALGHP	381	ACI GGGQG
Lep_BmorT2	66	TICTTVNKVCASG	295	DVALWEINEAFSV	324	NVHGGAVSLGHP	361	ICN GGG - G
Hym_AmeIT2	66	TICTTVNKVCASG	292	DIALWEINEAFSV	321	NIHGGAVSLGHP	358	ICN GGG - G
Col_AglaT2-2	100	TICTTVNKVCASG	330	EVALWEINEAFSV	359	NVHGGAVSLGHP	396	ICN GGG - G
Col_AglaT2-1	89	TICTTVNKVCASG	319	EVALWEINEAFSV	348	NVHGGAVSLGHP	385	ICN GGG - G
Dip_DmeIT2	100	VCCTTVNKVCSSG	329	DVAMWEINEAFSL	358	NVHGGAVSLGHP	395	ICN GGG - G
Dip_AgamT2	87	TICTTVNKVCSSG	317	DVAMWEINEAFSL	346	NVHGGAVSLGHP	383	ICN GGG - G
Col_NvesT2-1	102	TICTTVNKVCASG	332	DVAMWEINEAFSV	361	NIHGGAVSLGHP	398	ICN GGG - G
Col_NvesT2-2	102	TICTTVNKVCASG	332	DVAMWEINEAFSV	361	NIHGGAVSLGHP	398	ICN GGG - G
Col_TcasT2	101	TICTTVNKVCASG	331	DVALWEINEAFSV	360	NVHGGAVSLGHP	397	ICN GGG - G
Dip_CquiT2	99	TICTTVNKVCSSG	329	DVAMWEINEAFSV	358	NVHGGAVSLGHP	395	ICN GGG - G
Hem_ApisT2	103	TICTTVNKVCASG	333	DIALWEINEAFSV	362	NVHGGAVSLGHP	399	ICN GGG - G
Hem_ClecT2	103	VICTTVNKVCSSG	333	DVALWEINEAFSV	362	NVHGGAVSLGHP	399	ICN GGG - G
Hem_HhalT2	101	VICTTVNKVCASG	331	DVALWEINEAFSV	360	NVHGGAVSLGHP	397	ICN GGG - G
Hym_DallT2-2	102	TICTTVNKVCASG	332	DVALWEINEAFSV	361	NVHGGAVSLGHP	398	ICN GGG - G
Hym_DallT2-1	102	TICTTVNKVCASG	332	DVALWEINEAFSV	361	NVHGGAVSLGHP	398	ICN GGG - G
Hym_DallT2-3	102	TICTTVNKVCASG	332	DVALWEINEAFSV	361	NVHGGAVSLGHP	398	ICN GGG - G
Iso_ZnevT2	99	TICATINNKVCASG	329	DISLWEINEAFSV	358	NVHGGAVSLGHP	395	ICN GGG - G
Hym_BimpT2-2	102	TICTTVNKVCASG	332	DIALWEINEAFSV	361	NIHGGAVSLGHP	398	ICN GGG - G
Hym_BimpT2-1	102	TICTTVNKVCASG	332	DIALWEINEAFSV	361	NIHGGAVSLGHP	398	ICN GGG - G
Lep_DpleT2	112	TICTTVNKVCSSG	342	DIALWEINEAFSV	371	NVHGGGVS LGHP	408	ICN GGG - G
Lep_HmelT2	110	TICTTVNKVCASG	340	DVALWEINEAFSV	369	NVHGGAVSLGHP	406	ICN GGG - G
Lep_MsexT2	66	TICTTVNKVCASG	296	DVALWEINEAFSV	325	NVHGGAVSLGHP	362	ICN GGG - G
Lep_PxutT2-1	111	TICTTVNKVCASG	341	DVALWEINEAFSV	370	NVHGGAVSLGHP	407	ICN GGG - G
Lep_PxutT2-2	88	TICTTVNKVCASG	318	DVALWEINEAFSV	347	NVHGGAVSLGHP	384	ICN GGG - G
Lep_PxylT2	111	TICTTVNKVCSSG	341	EVALWEINEAFSV	370	NVHGGAVSLGHP	407	ICN GGG - G
Pht_PhumT2-2	102	TVCTTVNKVCSSG	330	QIAQWEINEAFSV	359	NKHGGAVSLGHP	396	ICN GGG - G
Pht_PhumT2-1	19	VIASSIN KLCGSG	247	DIHLWEI HETFSL	276	NIHGGGVS MGHP	289	- - - - - G
HsapT2	117	TPCTTVNKVCASG	346	DIAMWEINEAFSL	375	NINGGAVSLGHP	412	ICN GGG - G
MtubT2	75	VPALTI NKMCLSG	306	QLDVVEINEAFAA	335	NVNGGAIALV GHP	374	LC - GGGQG
Hym_AmeICT	81	TPAYLINMLCGSG	313	EVDLFEINEAFAA	342	NINGGAIALGHP	381	LCI GGGMG
Dip_AgamCT	78	VPAYLINMLCGSG	307	EVDLFEINEAFAA	336	NVGGGAIALGHP	375	LCV GGGMG
Dip_DmeICT	79	VPAYGINMLCGSG	308	EVDLYELNEAFAA	337	NVNGGAIALGHP	376	LCI GGGMG
Col_NvesCT	80	VPATTLNMLCGSG	305	DVELYEINEAFAS	334	NVNGGAIALGHP	373	LCI GGGMG
Col_TcasCT	80	VPAYTINMLCGSG	306	DVDLYELNEAFAV	335	NITGGAIALGHP	374	LCI GGGMG
Dip_CquiCT-1	82	APAYLINLLCGSG	311	EVDLFEINEAFAA	340	NVGGGAIALGHP	379	LCV GGGMG
Dip_CquiCT-2	77	- PA - DVDEIL - G	303	EVDLFEINEAFAA	332	NVGGGAIALGHP	371	LCV GGGMG
Hem_ApisCT-6	77	VPAHGINLLCGSG	307	SVDIFELNEAYAA	336	NINGGAISLGHP	375	LCI GGGMG
Hem_ApisCT-2	80	VPAHVINMLCGSG	310	SVDIFELNEAFAA	339	NIYGGAIALGHP	378	LCV GGGMG
Hem_ApisCT-5	80	VPAHGINLLCGSG	310	SVDIFELNEAYAA	339	NINGGAISLGHP	378	LCI GGGMG
Hem_ApisCT-4	98	VPAHGINLLCGSG	329	SVDIFELNEAYAA	357	NVNGGAIALGHP	396	LCI GGGMG
Hem_ApisCT-3	80	VPAHVINMLCGSG	310	SVDIFELNEAFAA	339	NINGGAIALGHP	378	LCV GGGMG
Hem_ApisCT-7	23	- - - - -	186	DI DLVEMTEAFSA	215	NIYGGAIALGHP	254	ACI GGGLG
Hem_ApisCT-1	61	- - - - - CTPL	184	EADTLDLNEAV - -	196	- - - - - SF - -	206	- - - - -
Hem_ClecCT-1	80	VP AFTVNQLCGSG	309	DVDLFEINEAFAA	338	NVSGGAIALGHP	377	LCI GGGMG
Hem_ClecCT-2	79	TPAMTINEVCGSG	299	DI DVIEIEMTEAFAS	328	NLYGGAIALGHP	367	ACI GGGLG
Hem_HhalCT	81	VPAYTINMLCGSG	310	DVDLFEINEAFSA	339	NINGGAISLGHP	378	LCI GGGMG
Hym_BimpCT	81	VPAYTINMLCGSG	311	EVDLFEINEAFAA	340	NINGGAIALGHP	379	LCI GGGMG
Hym_DallCT-2	81	VPAYVINMICGSG	311	EVDLYELNEAFAS	340	NVNGGAIALGHP	379	LCI GGGMG
Hym_DallCT-1	28	TPAFTVSKVCGSG	258	DI DLIEANEAFAA	287	NVNGGAIALGHP	326	LCI GGGQG
Iso_ZnevCT	81	VPAYLVNMLCGSG	311	DVDLFEINEAFAA	340	NICGGAIALGHP	379	LCV GGGMG
Lep_PxylCT	79	VSAITINDVCGSG	290	DVDLFEINEAFAA	319	NVNGGAIALGHP	358	LCI GGGMG
Pht_PhumCT	81	VP AFTVNMLCGSG	311	EVDLFEINEAFAA	340	NVNGGAIALGHP	379	LCI GGGME
HsapCT	83	VP AWSCQMICGSG	314	DVDIFEINEAFAA	343	NI EGGAIALGHP	382	LCI GGGMG
Lep_PxutAB-1	87	IPVSTVNRQCASG	301	DVSYFEINEAFSP	330	NVYGGSIALGHP	371	LCV GG - FG
Lep_PxutAB-2	87	IPVSTVNRQCASG	301	DVSYFEINEAFSP	330	NVYGGSIALGHP	371	LCV GG - FG
HsapAB	114	VPLSTVNRQCSSG	338	DVDIFEINEAFAS	367	NPLGGGVALGHP	408	MC IGG - MG
Lep_BmorTFE	141	TPAHTVTMACISS	385	DI DTWEIHEAFAG	431	NKWGGSLSIGHP	470	ACAAGGGQG
Hym_AmeITFE	117	IPAHTVTMACISS	361	DI GVWEIHEAFAG	407	NAWGGSLSIGHP	446	ACAAGGGQG
Dip_DmeITFE	119	TPAHTVTMACISS	363	DI DSWEIHEAFAG	409	NNWGGSLSIGHP	448	ACAAGGGQG
Dip_AgamTFE-2	27	VGAVTVNRLCGSS	246	DI DLFEINEAFAA	278	NLNGGAIALGHP	423	ACVGGGGQG
Dip_AgamTFE-1	81	TPAHTVTMACISS	325	DI DTWEIHEAFAG	371	NNWGGSLSIGHP	410	ACAAGGGQG
Col_NvesTFE	122	IPAHTVTMACISS	366	DI DWEFHEAFAG	412	NNWGGSLSIGHP	451	ACAAGGGQG
Col_TcasTFE	124	TPAHTVTMACISS	368	DI AVWEFHEAFAG	414	NNWGGSLSIGHP	453	ACAAGGGQG
Dip_CquiTFE	117	TPAHTVTMACISS	361	DI DSWEIHEAFAG	407	NNWGGSLSIGHP	446	ACAAGGGQG
Hem_ApisTFE	119	VP AHTVTMACISS	363	DI DVWEVHEAFAG	409	NKWGGSLSIGHP	448	ACAAGGGQG
Hem_ClecTFE-2	117	TPAHTVTMACISS	382	DI DAWEFHEAFAG	428	NNWGGSLSIGHP	467	ACAAGGGQG
Hem_ClecTFE-1	117	TPAHTVTMACISS	361	DI DAWEFHEAFAG	407	NNWGGSLSIGHP	446	ACAAGGGQG
Hem_HhalTFE	120	TPAHTVTMACISS	364	DI DVWEFHEAFAG	410	NNW		