

Supplementary Material

Supplementary Table S1. UniProt and GenBank accession numbers of the proteins used for phylogenetic analysis

Species	Unique ID	Uniprot ID/NCBI accession No.	AA length	Protein family IPR000907	PLAT/LH2 domain IPR001024	C terminal domain IPR013819
<i>Arabidopsis thaliana</i>	AtLOX1	Q06327	859	20-859	19-162	164-859
	AtLOX2	P38418	896	103-896	73-200	202-896
	AtLOX3	Q9LNR3	919	112-919	84-223	225-919
	AtLOX4	Q9FNX8	926	118-926	90-229	231-926
	AtLOX5	Q9LUW0	886	55-886	33-181	183-886
	AtLOX6	Q9CAG3	917	110-917	80-217	219-917
<i>Cannabis sativa</i>	CsLOX1	XP_030504566.2	860	21-860	18-161	163-860
	CsLOX2	XP_030503376.2	955	116-955	113-256	258-955
	CsLOX3	XP_030509377.2	873	32-873	29-172	174-873
	CsLOX4	XP_030493230.2	859	18-859	15-160	162-859
	CsLOX5	XP_030505305.2	848	34-848	5-149	151-848
	CsLOX6	XP_030506244.2 isoform X1	859	42-859	18-160	162-859
	CsLOX7	XP_030504184.2 isoform X1	871	29-871	21-163	165-871
	CsLOX8	XP_030507302.2	869	51-869	19-161	163-869
	CsLOX9	XP_030506393.2	875	52-875	25-167	169-875
	CsLOX10	XP_030507301.2	868	45-868	18-160	162-868
	CsLOX11	XP_060960325.1	868	45-868	18-160	162-868
	CsLOX12	XP_030503471.2	707	1-707	1-51	54-707
	CsLOX13	XP_030496884.1 isoform X1	935	129-935	54-236	238-935
	CsLOX14	XP_030490813.2	931	125-931	97-236	238-931
	CsLOX15	XP_030504574.2 isoform X1	928	114-928	80-227	229-928
	CsLOX16	XP_030504577.2	926	105-926	78-219	221-926
	CsLOX17	XP_060967000.1	926	105-926	78-219	221-926

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Species	Unique ID	Uniprot ID/NCBI accession No.	AA Length	Protein family IPR000907	PLAT/LH2 domain IPR001024	C terminal domain IPR013819
	CsLOX18	XP_030504576.2	929	129-929	92-232	234-929
	CsLOX19	XP_030504578.2	922	105-922	92-228	230-922
	CsLOX20	XP_060966996.1 isoform X1	716	22-716	-	23-716
	CsLOX21	XP_030504581.2	906	83-906	75-212	214-906
<i>Camelia sinensis</i>	CamLOX1	A8W7J7	861	18-861	17-161	163-861
	CamLOX2	B7TZ47	900	96-900	73-205	207-900
	CamLOX3	C4NZX3	901	98-901	73-206	208-901
	CamLOX4	A0A4S4EJA8	883	98-883	73-206	208-883
	CamLOX5	A0A2S1UFW5	914	79-217	79-217	219-914
	CamLOX6	A0A2S1UFW4	906	107-905	74-210	212-906
	CamLOX7	A0A2S1UFW3	912	98-912	75-214	216-912
	CamLOX8	A0A2S1UFW1	869	20-869	18-160	162-869
	CamLOX9	A0A2S1UFW6	906	58-906	56-198	200-906
	CamLOX10	A0A2S1UFX0	873	25-873	23-167	169-873
	CamLOX11	A0A2S1UFW8	876	54-876	30-156	186-876
<i>Glycine max</i>	GmLOX1	P08170	839	8-839	6-146	148-839
	GmLOX2	P09439	865	20-865	17-176	178-865
	GmLOX3	P09186	857	12-857	10-164	166-857
	GmLOXVB	Q43446	853	49-853	9-160	162-853
	GmLOXVD	P24095	846	53-864	10-172	174-864
<i>Nicotiana attenuata</i>	NaLOX1	A0A1J6IB64	861	20-861	18-164	163-861
	NaLOX2	Q6X5R6	900	90-900	70-204	206-900
	NaLOX3	A0A1J6HUT5	914	106-914	78-217	220-914

Supplementary Table S1. UniProt and GenBank accession numbers of the proteins used for phylogenetic analysis (cont.)

Species	Unique ID	Uniprot ID/NCBI accession No.	AA Length	Protein family IPR000907	PLAT/LH2 domain IPR001024	C terminal domain IPR013819
<i>Oryza sativa</i>	OsLOX1	Q76112	863	41-863	15-159	161-863
	OsLOX2	P29250	870	43-870	15-159	161-870
	OsLOX3	Q0IS17	868	45-868	21-152	154-868
	OsLOX4	Q53RB0	877	49-877	21-166	168-877
	OsLOX5	Q7XV13	899	96-899	66-205	207-899
	OsLOX6	Q8H016	918	108-918	98-219	221-918
	OsLOX7	Q2QNN5	922	101-902	76-203	205-922
	OsLOX8	P38419	924	103-924	88-223	225-924
	OsLOX9	Q84YK8	941	120-941	100-241	242-941
<i>Zea mays</i>	ZmLOX1	A0A3L6FBM0	873	51-873	21-167	169-873
	ZmLOX2	A0A1D6N521	871	51-871	21-167	169-871
	ZmLOX3	Q8W0V2	864	19-864	16-160	162-864
	ZmLOX4	A1XCH9	887	24-887	21-166	166-887
	ZmLOX5	A1XCI0	887	24-887	21-166	168-887
	ZmLOX6	A1XCI7	850	48-850	24-154	156-850
	ZmLOX7	B8XH56	916	107-916	79-218	220-916
	ZmLOX8	A1XCI3	941	110-941	82-221	223-941
	ZmLOX9	A1XCI4	922	116-922	86-226	228-922
	ZmLOX10	A1XCI5	905	103-905	68-209	211-905
	ZmLOX11	A0A8J8Y849	911	109-911	72-213	215-911
<i>Solanum lycopersicon</i>	SlLOX1	Solyc08g014000.2.1	860	18-860	17-160	162-860
	SlLOX2	Solyc01g099190.2.1	858	39-858	17-158	160-858
	SlLOX3	Solyc01g006540.2.1	896	93-896	67-198	200-896
	SlLOX4	Solyc03g122340.2.1	908	102-908	74-213	215-908
	SlLOX5	Solyc01g099160.2.1	862	18-862	17-160	162-862

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Species	Unique ID	Uniprot ID/NCBI	AA Length	Protein family IPR000907	PLAT/LH2 domain IPR001024	C terminal domain IPR013819
	SILOX6	Solyc09g075860.2.1	877	29-877	28-171	173-877
	SILOX7	Solyc01g099200.2.1	841	14-841	10-146	148-841
	SILOX8	Solyc08g029000.2.1	861	19-861	18-161	163-861
	SILOX9	Solyc01g099180.2.1	854	14-854	11-152	154-854
	SILOX10	Solyc12g011040.1.1	892	94-892	70-193	195-892
	SILOX11	Solyc05g014790.2.1	911	82-911	77-215	217-911
	SILOX12	Solyc01g006560.2.1	902	107-902	72-206	208-902
	SILOX13	Solyc01g099210.2.1	863	28-863	26-167	169-863
	SILOX14	Solyc09g075870.1.1	854	30-854	28-170	172-854
<i>Vitis vinifera</i>	VvLOX1	D5FUD8	901	76-901	70-205	207-901
	VvLOX2	F6HZ11	869	29-869	26-169	171-869
	VvLOX3	D5FUD9	859	18-859	16-159	161-859
	VvLOX4	A0A438GMK3	848	45-848	20-151	153-848
	VvLOX5	A0A438JV06	808	55-908	14-131	133-808
	VvLOX6	A0A438KLC1	892	56-892	31-173	175-892
	VvLOX7	F6GUA7	903	78-903	75-210	212-903
	VvLOX8	A0A438ELU2	904	76-904	71-208	210-904
	VvLOX9	A0A438ELV0	836	11-836	3-140	142-836
	VvLOX10	A0A438IAA9	876	105-859	78-210	203-866
	VvLOX11	A0A438I2F2	908	114-908	94-222	224-908
<i>Marchantia polymorpha</i>	MpLOX3	E5RS00	955	126-955	90-229	245-955

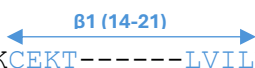
Supplementary Table S2: Key amino acid residues of GmLOX1 and comparison with Cannabis trichome specific LOXs

GmLOX1	Function	9-LOX	13-LOX	Mode of determination	Reference
H499	Fe ligand	Conserved	Conserved	X ray crystallography	Minor et al., 1996; Tomchick et al., 2001
H504	Fe ligand	Conserved	Conserved	X ray crystallography	Minor et al., 1996; Tomchick et al., 2001
H690	Fe ligand	Conserved	Conserved	X ray crystallography	Minor et al., 1996
N694	Fe ligand and second coordination sphere	Conserved	Conserved	X ray crystallography	Minor et al., 1996
I839	Fe ligand	Conserved	Conserved	X ray crystallography	Minor et al., 1996
Q495	Second coordination sphere to Fe	Conserved	Conserved	Mutant studies	Tomchick et al., 2001
Q697	Second coordination sphere to Fe	Conserved	Conserved	Mutant studies	Tomchick et al., 2001
L754	Second coordination and substrate binding	Conserved	Conserved	X ray crystallography	Hu et al., 2019
L553	Substrate binding pocket	Conserved	Conserved	Point mutations	Meyer et al., 2008
L546	Substrate binding pocket	Conserved	Conserved	Point mutations	Li et al., 2018; Hu et al., 2019
T556	Affecting substrate orientation	T (CsLOX1, CsLOX2, CsLOX7) V (CsLOX4)	A (CsLOX15, CsLOX19), T (CsLOX16), I (CsLOX17) S (CsLOX20)	Point mutations	Hornung et al., 1999; Hershelman et al., 2019
F557	Affecting substrate orientation	V	F	Mutation studies	Hornung et al., 1999; Hershelman et al., 2019
W500	Substrate binding	Conserved	Conserved	Point mutations	Ruddat et al., 2004
R707	Substrate positioning, substrate binding	Conserved	Conserved	Point mutations	Ruddat et al., 2004

Supplementary Table S2: Key amino acid residues of GmLOX1 and comparison with Cannabis trichome specific LOXs (cont.)

GmLOX1	Function	9-LOX	13 LOX	Mode of determination	Reference
S749	Surface loop H tunnelling	S (except CsLOX1-A)	A (CsLOx17-L)	Point Mutations	Offenbacher et al., 2017
Y317	Surface loop H tunnelling	F (CsLOX1, CsLOX2, CsLOX4, CsLOX7)	T (CsLOX15, CsLOX19, CsLOX20) A (CsLOX16, CsLOX17)	Point mutations	Offenbacher et al., 2017
A542	Governing the stereospecificity	Conserved	Conserved	X ray crystallography	Youn et al., 2006
H248	Substrate entry strong H bond side chains	Conserved	Conserved	X ray crystallography	Youn et al., 2006
N534	Substrate entry strong H bond side chains	D	T	X ray crystallography	Youn et al., 2006
E256	Strong H bonding -side chains	A (CsLOX1, CsLOX2, CsLOX7), V (CsLOX4)	L (CsLOX15), S (CsLOX16, CsLOX17), a (CsLOX19, CsLOX20)	X ray crystallography	Youn et al., 2006
T259	Substrate entry portal	L (CsLOX1, CsLOX2, CsLOX4, CsLOX7)	V (CsLOX15, CsLOX20), M (CsLOX16) I (CsLOX17), L (CsLOX19)	X ray crystallography	Minor et al., 1996
L541	Substrate entry portal	F (CsLOX1), V (CsLOX2), L (CsLOX7)	L	X ray crystallography	Minor et al., 1996
V237	Cavity entry less bulky groups	N (CsLOX1, CsLOX2, CsLOX4), D (CsLOX7)	D (CsLOX15), A (CsLOX16, CsLOX17), R (CsLOX19), S (CsLOX20)	X ray crystallography	Youn et al., 2006
A254	Cavity entry less bulky groups	F	F	X ray crystallography	Youn et al., 2006
I257	Cavity entry less bulky groups	Y in all, N (CsLOX4)	K (CsLOX15, CsLOX19) R (CsLOX16, CsLOX17)	X ray crystallography	Youn et al., 2006

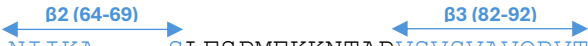
Consensus	MKT TXXLXX	50
GmLOX1	-----	
GmLOX2	-----	
GmLOX3	-----	
GmVLXD	-----	
GmVLXB	-----	
AtLOX1	-----	
CsLOX1	-----	
CsLOX2	-----MLHYRNLNTPSP LLKFGAGVNS-LTSLVFKNSHNSLGFYSENHDR	44
CsLOX3	-----	
CsLOX4	-----	
CsLOX5	-----	
CsLOX6	-----	
CsLOX7	-----	
CsLOX8	-----	
CsLOX9	-----	
CsLOX10	-----	
CsLOX11	-----	
CsLOX12	-----	
CsLOX13	-----MLSLK--PTTTP LNNNPNISGDRSFSSISTATAGKDGD L-RRKTR	42
CsLOX14	----MALAKE--IMCGSIIESTSFSSSASYSKVFLNQNF----R-RNQTR	39

			
CsLOX15	-----MLKPPHQVVQNLK CEKT ----- LVIL NKPFIHGYNGAI-IG-IN		37
CsLOX16	-----MLKPHVQVTSGQT-----SVVLNKPFIHGNYHFQ-SP-FS		33
CsLOX17	-----MLKPHVQVTSGQT-----SVVLNKPFIHGNYHFQ-SP-FS		33
CsLOX19	MKTTEMLVNPTHHSNSSQILYR-----RPPLRKTFVHG L DGAT-SS-FR		42
CsLOX18	-----MLMPQVMNLQTRPIQTTSFSRSFNNNQKSLF L LENNNI--GS-LS		42
CsLOX20	-----		
CsLOX21	-----MLKPQFQKSQTLLN-----SFCNKPLFIHGNNL--SS-FP		33

Consensus	XX	100
GmLOX1	-----	
GmLOX2	-----	
GmLOX3	-----	
GmVLXD	-----	
GmVLXB	-----	
AtLOX1	-----	
CsLOX1	-----	
CsLOX2	VLKSSCLIDLTRSQPLVGGGHCDRREESSISSSGEKMSVRCNTGS-----	89
CsLOX3	-----MGSGS-----	5
CsLOX4	-----	
CsLOX5	-----	
CsLOX6	-----	
CsLOX7	-----	
CsLOX8	-----	
CsLOX9	-----M-----	1
CsLOX10	-----	
CsLOX11	-----	
CsLOX12	-----	

CsLOX13	VAVSG-----SKLRRRGS----VRAAISSGDNKTETVSSNS-----	74
CsLOX14	FLVSPVLPLEQRRRTLHLRKVV-RGPVAAISEDLVRSKAIQPSS-----	82
CsLOX15	SRLFPV-----KPK-----TKRRVASSSSSS-----	58
CsLOX16	LLVP-----SKHTNK-----NN-----VG	47
CsLOX17	LLVP-----SKHTNK-----NN-----VG	47
CsLOX19	ILSLPK-----RHK-----NNRRITCPTSTIRAIS	67
CsLOX18	SISNPN--PLLLVSA-----GNRARVSSSS-----	66
CsLOX20	-----	
CsLOX21	VCII-R--PISLKNN-----NNKIIMKQKN-----	55

Consensus	XX	150
GmLOX1	-----MFSAGHKIKGTVVLMMPKNELEVNP---	24
GmLOX2	-----MFSVPGVSGILNRGGGHKIKGTVVLMRKNVLDNFNSVAD	38
GmLOX3	-----MLGGLLHRGHKIKGTVVLMRKNVLDNFNSVT-	30
GmVLXD	-----MFGIFDKGQKIKGTVVLMMPKNVLDNFNAITS	30
GmVLXB	-----MFPFGHKGQKIKGTMVVMQKNVLDINSIT-	29
AtLOX1	-----MFG-ELRD--LLTGGGNETTTKKVKGTVVLMMKNVLDNFDFNA	40
CsLOX1	-----MLKDIIKAISGDNEEEGKKIRGSVVLMMKNVLDNFDFNA	39
CsLOX2	----HSHNRI-SIEKEDGSGKTTTTKSGGKIKGNVVLMMKNVLDNFDFNA	134
CsLOX3	----SPGITH-KVMQTFCKMDQKEETNHKKIQGEVVLMMKNILDLHDKSA	50
CsLOX4	-----MFGIVKPPSIFGGNKKIKGNVVLMMKNVLDNFDMRN	36
CsLOX5	-----MESGKKIKGVVILTKKNVLPRTNAT	26
CsLOX6	-----MVLNKIMDTLMNNGHGGKKFIGTVVLTNNVIDHSALDR	39
CsLOX7	-----MLL-GKIGDRVSGILNRGDDQKRVKGSVVLMMKNVLEFNPLSA	42
CsLOX8	-----MFI-GK--VVDALSGGNDDKKMINGKVVLSSKNVLEFNPLAT	40
CsLOX9	----LLGKGI-GVDSFTGGLIGGNNGKKIKGSVVLVKKNVLEFNPLAS	46
CsLOX10	-----MNLAKGLVDLTGGLNGKKIKGRVVLAKKNVLEFNPLAA	39
CsLOX11	-----MFLAGKVVDTLGGGLHGKKIKGRVVLAKKNVLEFNPLAA	39
CsLOX12	-----	
CsLOX13	SVPAHQSEDNS-----NGSLKKKKPSKGI EVRAVMTIRKKMKEK----	113
CsLOX14	SSPVESPV-----ESKPVSFKVRAVTVVRNKNKED----	112

			
CsLOX15	-SPGTK---NIIKA---SLFSPMEKKNTARVSVSVAVQVRVTPKFWRFE		99
CsLOX16	VSISHRGKGNIIKASLLGRLVSSKDKTATERVTNVAVQRETAPL----		93
CsLOX17	VSISHGGKGNIIKASLLGRLVSSKDKTATERITVSVVVQRETAPL----		93
CsLOX19	SSPSITDNFQEE-----EEKRESEIEEETIAVKAVVT---VQPTVTGFF		108
CsLOX18	-NHSKRGLFVAPIKAILIGNIINKLTSN----VRLVVT---VLPTLGGVL		108
CsLOX20	-----		
CsLOX21	-----LGLGFNI-----RASLSKDDDIKWIRVRVIVT---VHPTVGGML		91

Consensus	XX	200
GmLOX1	-----DGSVDNLNAFLGR-SVSLQLISATKAD--	51
GmLOX2	LTKGNV----GGLIGTGLNVVGSTLDNLTAFLGR-SVALQLISATKPL--	81
GmLOX3	----SV----GGIIGQGLDLVGSTLDLTLAFLGR-PVSLQLISATKAD--	69
GmVLXD	IGKGGVIDTATGILGQGVSLVGGVIDTATSFLGR-NISMQLISATQTD--	77
GmVLXB	----SV----DGIVGTGLDFLGSALDTV-TFLAS-SISIQQLISATKAD--	67
AtLOX1	-----SFLDRLHEFLGN-KITLRLVSSDVTD-S	66
CsLOX1	-----SILDRFHELVGK-GVSIQLISSVHGD-P	65
CsLOX2	-----SFLDRVHELFGQ-RVSLQLVSAVNGD-P	160
CsLOX3	-----SLLDRIYELFGK-GVSLHLISSVNPH-P	76

CsLOX4	-----GIIDPLSELLGQ-RVSLQLISSVQT-HT	62
CsLOX5	SD-----SVVEPAAADISGQ-EVSLQLVSAVHG---	53
CsLOX7	SV-----NVGSSLLDRVGDFLGN-GISIQLVSGH-----	70
CsLOX8	SV-----NAGSAILDRVVEFLGG-GVSLQLVSGH-----	68
CsLOX9	SV-----NTGTAIFDRFAEFLGS-GVSLQLVSGH-----	74
CsLOX10	SV-----NAGSAIFDRLGEFLGN-GVSLQLVSGH-----	67
CsLOX11	SV-----NAGSAMFDRLGEFLGN-GVSLQLVSGH-----	67
CsLOX12	-----	
CsLOX13	LA-----EKMEDQWEFFVNGIGQ-GIQIQLISEEVDP--	144
CsLOX14	FK-----ETLVKHLDAITDKIGR-NVVLELISTQTDP--	143

CsLOX15	LS-----EKIQDGR ^{β110-114} GLN ^{β4 (119-126)} SLSTELVSTQKDP--	131
CsLOX16	-I-----EKPQSLRDKTNDLGVANFSVELISAQKDP--	124
CsLOX17	-I-----EKPQSLRDKTNDLGVANFSVELISTQKDP--	124
CsLOX19	KS-----LGLDRGLDDIQDLLGK-TFLLELVSADLDP--	139
CsLOX18	TN-----VGIGKGIDDAQDFFGH-SLLIELASAELDLP--	139
CsLOX20	-----	
CsLOX21	SN-----LGLKRGLDDTQDLLGR-SILIQLLSSQLDP--	122

Consensus	XXX	250
GmLOX1	-AHGKGKVGKDTFLEGINT--SLPTLGAGESAFNIHFEWD-GSMGIPGAF	97
GmLOX2	-ANGKGKVGKDTFLEGIIV--SLPTLGAGESAFNIQFEWD-ESMGIPGAF	127
GmLOX3	-ANGKGKLGKATFLEGIIT--SLPTLGAGQSAFKINFEWD-DGSGILGAF	115
GmVLXD	-GSGNGKVGKEVYLEKHLP--TLPTLGARQDAFSIFFEWD-ASFGIPGAF	123
GmVLXB	--GGKGKVGKATNLRGKI---TLPTIGAKEEAYDAQFDWD-SDFGIPGAF	111
AtLOX1	ENGSKGKLGKAAHLEDWIT--TITSLTAGESAFKVTFDYE-TDFGYPGAF	113
CsLOX1	ENGLQGKLGKAAAYLEDWIT--TITPLTAGESAFKVTFDLEDNDIGVAGAF	113
CsLOX2	GNGMRGKLGKEAYLEDWIT--TISPLTAGDSAFDVNFDWD-EKIGVPGAF	207
CsLOX3	EHVDRGSHGNAAYLEKWIT--ANTTITAKETCFNVFFDWE-ESMGIPGAL	123
CsLOX4	GNELKGKLGKESYLENWTNITLFPLLAGESAYSVHFELE-EGFGVPEAF	111
CsLOX5	-NGVKGNVGEPAYLEKLDSY-DISTLSRPDIAFKVAFDKN-ESIGVPGAL	100
CsLOX6	ANGLKGKVGKEACLENEVTS-SLPSLAPGDNAFNVTLDLD-VSVGVP GAL	110
CsLOX7	---SAGKVGKEAHLENWLT--SLPALTPGDSLFRVTFEWD-ESIGVPEAL	114
CsLOX8	---NANKVGKETKLEDWVT--SAPTII PGDSVFKVSFEWD-ESIGVPEAV	112
CsLOX9	---TSGKLSKEAHLENWIT--SLPALTPGDSVFKVTFDWD-ESIGVPEAI	118
CsLOX10	---VAGKVGKETHLENWVT--SLPTLTPGDSVFKVTFDWD-ESIGVPEAI	111
CsLOX11	---TAGKLGKETHLENWVT--SLPTLTPGDSVFKVTFDWD-ESIGVPEAI	111
CsLOX12	-----MGVPPAL	7
CsLOX13	-VTNSGK-SIQSSVRGWL PKPT---NHLHIVEFAANFIVP-KDFGCPGAV	188
CsLOX14	-RTNGPKKSKEAVLRDWSKKVN---VKAERVNYTAEFEVD-SNFGIPGAI	188

CsLOX15	-VTGKER-TVK----GFPKRPDFNIFSSDD ^{β5 (156-163)} VKYEAKFD ^{β6 (172-178)} DIP-KDFGEVGA ^I	174
CsLOX16	-ETGKQRKM-K----CFPESKK-GGKKDKVMNYEAKVDIP-KDFGDVGAV	166
CsLOX17	-ETGKQRKM-K----CFPESKK-GGKEDKVMNYEAKVDIP-KDFGDVGAV	166
CsLOX19	-KTGEEKETVE----GYAHKIGKK--EDGIKYEASFKVP-IKFGHIGAI	180
CsLOX18	-KSGSERKRIK----GYAHKTSLI-DILGKVTYEVDFDIP-KEFGELGAI	182
CsLOX20	-----	
CsLOX21	-KTGLEKKTIN----KYAHRSSLW-N-KEGIQYETDLVDL-ADFGTVGAV	164

Consensus	XX	300
GmLOX1	YIKNYM-QVEFFLKSLTLEAIS-NQGTIRFVCNSWVYNTKLYK---SVRI	142
GmLOX2	YIKNYM-QVEFYLKSLTLEDVP-NQGTIRFVCNSWVYNTKLYK---SVRI	172
GmLOX3	YIKNFM-QTEFFLVSLTLEDIP-NHGSIHFCNSWIYNAKLFK---SDRI	160
GmVLXD	YIKNFM-TDEFFLVSVKLEDIP-NHGTIEFVCNSWVYNFRSYK---KNRI	168
GmVLXB	YIKNYM-QNEFYLKSLILEDIP-NHGTIHFICNSWVYNSKHYK---TDRI	156
AtLOX1	LIRNSH-FSEFLLKSLTLEDVP-GHGRVHYICNSWIYPAKHYT---TDRV	158
CsLOX1	SIRNNH-HSEFYLKTLTLDY-P-DQTRVHFVCNSWVYPAKRYQ---KDRI	157
CsLOX2	IIQNYH-HSEFYLKTLTLDNVP-GHGRIHFVCNSWVYPSDKYH---SPRI	252
CsLOX3	MIKNNH-HSQFFLKTITLKDVP-GHGLVHFVCNSWVYPAHRYK---YDRI	168
CsLOX4	VINNNH-TTEFFLKSLTLEDVP-DQGQVHFVCNSWVYPANHYN---YDRV	156
CsLOX5	IIKNSG-SDEFYVKTITLVDVP-GEHGVHFVCNSWVYPFTKYD---YDRV	145
CsLOX6	IVTNNHATEKFFLKTFTLKDVP-DEGDIHFVCNSWIYPATKYD---YDRV	156
CsLOX7	IIKNNH-LDEFFLKTITLEDVP-GEIVRFICNSWVYPAGRYK---HTRV	159
CsLOX8	IFKNNH-VEELFLKTITLDDVP-GEVVQFICYSWVYSANKYD---YDRV	157
CsLOX9	IFKNNH-LDEFFLKTITLDDVP-AQGVVRFICNSWVYTANKYN---YNRV	163
CsLOX10	IFKNNH-VDEFFLKTITLDDVP-GQGVVRFICNSWVYSARKYN---YDRV	156
CsLOX11	IFKNNH-VDEFFLKTITLDDVP-GQGVVRFICNSWVYSARKYK---YDRV	156
CsLOX12	KITNNN-KDEFLLYITLKYIX-----VKFLCNSWVYPQERYT---YPRV	48
CsLOX13	LVTNLH-GKEFYLLIIVIR--GFDGGPIFFLANTWIHSRNDNP---ESRI	232
CsLOX14	TVTNGH-QKEFFLEAITVE--GLACGPVHFPCNSWVQSKKDHP---AKRI	232

		
CsLOX15	IVE ^{B6} ND ^{B7 (184-192)} -ERE ^{B8 (200-204)} I ^{B9 (223-225)} FLKNII ^{B6} LEDLPSEPS ^{B7 (184-192)} TLEF ^{B8 (200-204)} SCNSWVQSKHDVPTDQHKRV ^{B9 (223-225)}	223
CsLOX16	IIENDF-EREIYMKTISLHYHSSDDKFVNFSCESWVQSKRDVPRDQQLRL	215
CsLOX17	IIENDF-EREIYMKTISLHYHSSDDKFVNFSCESWVQSKRDVPRDQQLRL	215
CsLOX19	LVENEH-HKEMYVSDIVLD--GLSNGPLNIIICGSWVHSKFNNP---EKRI	224
CsLOX18	LVENEH-HKEMFLKDIKIDGEGLLNGPVTINCESWIHSKSQNP---QKRV	228
CsLOX20	-----MIFKICLAKPF---FL---NLLA	17
CsLOX21	LVENEH-HKEMYIKNIVLQ--GFPNGPVNVTCNSWVHSKFDNP---QKRI	208

Consensus	XX	350
GmLOX1	FFANHTYVPSETPA-PLVSYREEELKSLRG-NGTGERKEYDRIYDYDVYN	190
GmLOX2	FFANHTYVPSETPA-ALVGYYEEELKNLRG-DGKGERKEHDRIYDYDVYN	220
GmLOX3	FFANQTYLPSETPA-PLVKYREEELHNLRG-DGTGERKEWERYDYDYDVYN	208
GmVLXD	FFVNDTYLPSATPA-PLLKYRKEELEVLRG-DGTGKRKDFDRIYDYDVYN	216
GmVLXB	FFANNTYLPSETPA-PLVKYREEELKNVRG-DGTGERKEWDRIYDYDVYN	204
AtLOX1	FFSNKTYLPHETPA-TLLKYREEELVSLRG-TGEGELKEWDRVYDYAYYN	206
CsLOX1	FFTNTYLPSETPS-PLLKYREEELLSLRG-NREGELQEWDRVYDYAYYN	205
CsLOX2	FFANKTYLPSETPL-SLRKYREEELANLRG-NGTGERQEWDRIYDYDYYN	300
CsLOX3	FFSNKTYLPCKTPP-LLHHYRQEELKNLRG-NGTGELKEWDRVYDYDYYN	216
CsLOX4	FFRNKTYLPHQTPA-PLIWYREQELVYLRG-NGTGERKDGDRYDYDFYN	204
CsLOX5	FFTNSYLPSETPE-PLRQYRGQELLNLRG-NGTGELQVWDRVYDYAYYN	193
CsLOX6	FFRNKSYLPSETPE-PLRELREQELVNLRG-NGKGERQEWDVYDYAYYN	204
CsLOX7	FFRNKSYLPSATPE-PLLKYRKEELESRLRG-NGKGERKEWDRVYDYDVYN	207
CsLOX8	FFRNKSYLPSATPA-PLLKYRKEELQNLRG-DGKGERKEWDRVYDYDVYN	205
CsLOX9	FFRNKSYIPSATPA-PLLKYRKEELENLRG-NGLGQRKEWDRVYDYDLYN	211
CsLOX10	FFRNKSYLPSATPA-PLLKYRREELQNLRG-DGKGERKEWDRVYDYDVYN	204
CsLOX11	FFRNKSYLPSATPA-PLLKYRKEELQNLRG-NGLGERKEWDRVYDYDVYN	204
CsLOX12	FFTNPYPDPNSERHKLHRLREGELRHLRSENNIGELKEWDRVYDYATYN	98
CsLOX13	IFKNQAYLPSTQTPA-GLKDLRREDLLSIRG-NGKGQRKLHDRIYDYDVYN	280

CsLOX14	FFSNKPYPSETPA-GLKVLREKELKILRG-NGKGVRKLSDRIDYDFDVYN	280
CsLOX15	⁸⁹ FFSNKCYLPSQTPS-GIKELRKIALENLRG-DGKGERKKNERVYDYDVYN	271
CsLOX16	FFSDKSYLPSQTPS-GLKELRNEELKRLRG-NGKGERKEYERVYDYDVYN	263
CsLOX17	FFSDKSYLPSQTPS-GLKELRNEELKRLRG-NGKGERKEYERVYDYDVYN	263
CsLOX19	FFTSKSYLPSQTPS-GLRRLRDEELVKLRG-NGEGERKHIDRIYDYDVYN	272
CsLOX18	FFTNKSFLPSNTPS-GLKKLREEDLKSLRG-NGEGQRKKHERIYDYDVYN	276
CsLOX20	LSSTLSYLPCETPS-GVRKLREEDLKNVRG-NGEGERKRFERIYDYDVYN	65
CsLOX21	FFTNKSYLPSQTPS-GLRRLREEELETLRG-NGRGERKFFERIYDYDVYN	256
Consensus	DJXXXXXXXXXXJGGXXXXXPXRRXRTGRXXXXXXXXXXXXXXXXXXXX	400
GmLOX1	DLGNPDKSEKLARPVLGGSSSTFPYPRRGRTGRGPTVTDPNTEKQG-----	235
GmLOX2	DLGNPDHGENFARPILGGSSSTHPYPRRGRTGRYPTRKDKQNSEKPG-----	265
GmLOX3	DLGDPDKGENHARPVLGGNDTFPYPRRGRTGRKPTRKDPNSESRS-----	253
GmVLXD	DLGNPDGGD--PRPILGGSSIYPYPRRVRTGRERTRTDPNSEKPG-----	259
GmVLXB	DLGDPDKGEKYARPVLGGG-ALPYPRRGRTGRGKTRKDPNSEKPG-----	248
AtLOX1	DLGVPPKN---PRPVLGGTQEYPYPRRGRTGRKPTKEDPQTESRL-----	248
CsLOX1	DLANPDKGPEYARPVLGGSSSEYPYPRRGRTGRPPTKTDPNTE SRL-----	250
CsLOX2	DLGNPDKGAKYARPVLGGSPQYPYPRRGRTGRKRTDTRNTETRL-----	345
CsLOX3	DLGKPNK-PKYARPVLGGSEEHYPYPRRGRTGRKKYKKYPEIETRL-----	260
CsLOX4	DLGNPDKGEKHVRPILGGTSEYPYPRRGRTGRPPTKTDPNSES RD-----	249
CsLOX5	DLGNPDKSPKLARQTLGGSSNFPYPRRGRTGRPPTQTDPNCE SRL-----	238
CsLOX6	DLGNPDKGQDYVRQILGGSSDFPYPRRGRTGRPPTETDANI ESSM-----	249
CsLOX7	DLGDPDKGSKYVRQTLGGSSSEFPYPRRGRTGRAPNRTPKTESRLKRVNL	257
CsLOX8	DLGEPDKGEDFARKILGGNSEFPYPRRGRTGRPPTKTDPKIESRLKAVNL	255
CsLOX9	DLGEPDKGRNFSRKTLLGGNSEFPYPRRGRTGRPTTKSDSRTESRLKQVNL	261
CsLOX10	DLGEPDKGSNFVRKILGGNSEFPYPRRGRTGRASTKTDSTSESRLKQVNI	254
CsLOX11	DLGEPDKGSNFVRKTLGGNSEFPYPRRGRTGRAPTCTDSTSESRLKQVNI	254
CsLOX12	DLGN-----NRPILGGK-DLPYPRRGRTGRPLTHDGHERPDK-----	135
CsLOX13	DLGKPEN-KDLARPVIGGE-KRPYPRRCRTGRPPSKSDPLSETRI-----	323
CsLOX14	DLGNPDKSTELARPKLGGK-EIPYPRRCRTGRLPDTDLQAESRI-----	324
CsLOX15	DLGQPDNNDLKR PVLGGSKFEFPYPRRCRTGRPPTETDPLSESRI-----	316
CsLOX16	DLGDPDKTSDLTRPVLGGG-QRPYPRRCRTGRPPAKTDLSSSESRS-----	307
CsLOX17	DLGVDPKSSDLTRPVLGGP-QHPYPRRCRTGRPQTKTDLSSSESRS-----	307
CsLOX19	DIGDPDRKFKL SRPVLGGE-ERPYPRRCRTGRPPCESDTLAEKRS-----	316
CsLOX18	DLGSPDLMSDLKR PVLGGK-EHPYPRRCRTGRHPSRSDPKTESRL-----	320
CsLOX20	DLGNPDKSHDLKR PVLGGK-ERPYPRRCRTGRPRTKTDVPVSEQNS-----	109
CsLOX21	DLGDPDKSEDLKR PVLGGK-NRPFPRRCRTGRPPTQRDPLSEQPS-----	300
Consensus	XXXXXXXXXXXXXXPRDEXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXX	450
GmLOX1	-----EVFYVPRDENLGHLLKSKDALEIGTKSLSQIVQPAFES-AFD	275
GmLOX2	-----EVYVPRDENFGHLKSSDFLAYGIKSLSQYVLP AFES-VFD	304
GmLOX3	-----NDVYLP RDEAFGHLKSSDFLT YGLKSVSQNVLP LLQS-AFD	293
GmVLXD	-----EVYVPRDENFGHLKSSDFLT YGIKSLSHDVIPLFKSAIFQ	299
GmVLXB	-----DFVYLP RDEAFGHLKSSDFLAYGIKSVAQDVLPVLT D-AFD	288
AtLOX1	----PITSSLDIYVPRDERFGHLKMSDFLAYALKAIAQFIQPALEA---V	291
CsLOX1	----PILMSLNIIYVPRDERFGHLKMSDFLAYALKSVAQVIKPELES---K	293
CsLOX2	----NLALSLNIYAPRDERFGHLKLADFLAYALKSIGQFLKPEIED---L	388
CsLOX3	----PL-LNLDIYVPRDERFGHVKFSDFLAYALKSLVQVLIPELKY---L	302
CsLOX4	----IDLLNLNFYIPRDERFGHLKMSDFLVNTLKSVALI IKPAIES---L	292

CsLOX5	----DIKKS LT IYVPRDEQFNHVKMSDFLAYGLLSIAQAIKPALES---	Y	281
CsLOX6	----SLITSLNVYVPRDERFGHVKMADFLGYGLKSLAQGIFPALES---	Y	292
CsLOX7	MKPLDPLEALDIYVPRDERFGHLKMSDFLAYGLKSLSQSIKPALEH---	Y	304
CsLOX8	TKPLDPVESLDIYVPRDERFGHLKMSDFLAYAIKALSHAVVPALKH---	F	302
CsLOX9	MNPLDPVESLDIYVPRDERFGHLKMSDFLAYGIKSLTQAIIPALKH---	Y	308
CsLOX10	MKPLDPIESLDIYVPRDERFGHLKMSDFLAYAIKSLSQAIIPALKH---	F	301
CsLOX11	MKPLDPIESLDIYVPRDERFGHLKMSDFLAYAIKSLSQAIIPALKH---	F	301
CsLOX12	-----NQVIYI PR DEQINHLKTEPPSSD--TVAKIITTLSED---	D	172
CsLOX13	-----EKHPVYVPRDET FEE IKQNTFSAGRLKALLHNLIPSIAA---	S	364
CsLOX14	-----EKPFPLYVPRDEQFEESKQASFSFGRLKAVLHNLIPSLKA---	S	365

CsLOX15	-----SDFYVPRDEEFAEVKQSNFSLKT VYSVIH AVIPILRQ---	V	354
CsLOX16	-----DKAFYVPRDETFAEVKQSDFGSRMQALAKTLLPFLEN---	N	346
CsLOX17	-----KTAFYVPRDETFAEVKQNDFASRRIALGIKSLIPFLES---	N	346
CsLOX19	-----GRFYVPRDECFSEIKQLTFSAKTLYSVLHALSPSLAN---	V	354
CsLOX18	-----SSDVLFI PR DENFSEIKQMTFGAKTLFSVMHALVPSLEG---	L	361
CsLOX20	-----ASVYVPRDEAFSEIKQITFSANTVYSGLHALVPSLQT---	A	147
CsLOX21	-----RTIYVPRDET FSE IKQLTFQAKTIYSGLHALVPSLQT---	V	338

Consensus	XX		500
GmLOX1	LKSTPIEFHSFQDVHDLYEGGIKLPRD---VI--STIIPLPVIKE----		315
GmLOX2	LNFTPNFEFDSFQDVRDLHEGGIKLPTE---VI--STIMPLPVVKE----		344
GmLOX3	LNFTPREFDSFDEVHGLYSGGIKLPTD---II--SKISPLPVLKE----		333
GmVLXD	LRVTSSEFESFEDVRSLYEGGIKLPTD---IL--SQISPLPALKE----		339
GmVLXB	GNLLSLDFDNFAEVRKLYEGGVTLPTN---FL--SNITPIPIIKE----		328
AtLOX1	FDDTPKEFDSFEDVLKIYEEGIDLPNQALIDSI--VKNIPLLEMLKE----		335
CsLOX1	FDNTPSEFDSFQDVLNMYDGGIELPKG-LVDDI--RENIPAEMLEKE----		336
CsLOX2	FNSTPNFEFDSIDDVFKLYEGGVDPVEG-LLKSV--RDNIPAEMLEKE----		431
CsLOX3	TNKT FNE FDSFKQVLELYDDEAKKPKGHTLSKI--RECVPCCELLRE----		346
CsLOX4	FDRTPAEFDSFKDVL SLY EGGFPLPLT-VFETI--SKNVPLETLKD----		335
CsLOX5	FDETPGEFDSFQDVL DLY KGGGLKLPKE-VVDNI--KKDVPSEMLEE----		324
CsLOX6	FGETPGEFSSFEVYDLYKGGGLKLPPT-VVDNI--EKNVPAELLQE----		335
CsLOX7	FDQTRNEFDNFQEVYDLYEGGFKLPTA-VLDTI--RKTVPFNMLKE----		347
CsLOX8	FDETPNFE DKFQ EVHEL YEGGLE LPTK-VFDKI--RKAVPDDMLKE----		345
CsLOX9	FDQTRNEFDNFQEVLDLYEGGGLKLPKS-VLDNI--RKNVPFDLLKE----		351
CsLOX10	FDETRNEFDSFKEIEDLYEGGGLKLP TS -VLSTI--RNNVPVDLFRE----		344
CsLOX11	FDQTRNEFDSFKEIDDLYEGGGLKLP TS -VLNTI--RNNVPVDLFRE----		344
CsLOX12	TVLDDNY YRSF REVLALFQGT-----		193
CsLOX13	LSSSDISFNCFTDIDKLYNDGFFLKDEDQNEVS-----FTFPVMGKF		406
CsLOX14	FSAENQEFSGFADIDNLYSEGILLKLG VQE ELL-----KKLPLN		404

CsLOX15	LI--DENFPYFTA IDVLY DEGIKIP SNAE KSLI-----QT I KNVNAR		394
CsLOX16	MF--DEKFPNFTDIDKMFKEGYEITDKSISGDKSLKEMLLLHVGTKLHSS		394
CsLOX17	MF--DEKFPNFTDIDKMFKEGYEITDKSISGDKSIKEMLALHVGTKLYSS		394
CsLOX19	MADKDLGFPYLTALDALFSKGVDLPTIGT-E-----GFLRKVMPR		393
CsLOX18	LV-DKEGFPYFTAIDTLFDEGIKIPPNHHNK-----SLLKSALPR		400
CsLOX20	LLNPSLGFPYFRAIDSLFDGGLKLPPTKIEQ-----GILRNVLP		187
CsLOX21	LTDSSLGFPYFRAIDSLFDNGLKLPSTN-Q-----GLLKNILPR		377

Consensus	XXXXXXXXXXXXXXXXXXXXXDXEFXRZXXAGXXPXXJXXX	550
GmLOX1	--LYRTDGQHILKFPQPHVVQ-VSQSAWMTDEEFAREMIAGVNPCVIRGL	362
GmLOX2	--LFRTDGEQVLKFPPPHVIQ-VSKSAWMTDEEFAREMVAGVNPCVIRGL	391
GmLOX3	--IFRTDGEQALKFPPPKVIQ-VSKSAWMTDEEFAREMLAGVNPNIIRCL	380
GmVLXD	--IFRTDGENVLQFPPPHVAK-VSKSGWMTDEEFAREVIAGVNPVIRRL	386
GmVLXB	--LFRTDGEQFLKYPPPKVMQ-VDKSAWMTDEEFARETIAGLNPVVIKII	375
AtLOX1	--IFRTDGQKFLKFPVPQVIK-EDKTAWRTDEEFAREMLAGLNPVVIQLL	382
CsLOX1	--IFRTDGERLLKYPLPQVLK-ESRSAWRTDEEFAREMLAGVNPVSISSL	383
CsLOX2	--IFRTDGERFLKFPVPQVIK-ENKTAWDTDEEFAREMLAGINPVMIHRL	478
CsLOX3	--ILR-QEEGFRKLMPDVIK-EDNSAWRTDEEFGREMLAGVNPVIIRRL	392
CsLOX4	--LFRADGTRFLKYPMPHVIK-EDKAAWMTDEEFGREMLAGVNPVIRRL	382
CsLOX5	--IFHIEAGQFIKYPLPHVIK-EDTSAWRTDEEFGREMVAGVNPVIRRL	371
CsLOX6	--MFKIDRGQFLKYPPPHVIK-ENKSGWRTDEEFGREMVAGVNPVIRRL	382
CsLOX7	--LFRTDGEQFLRFPVPHVIK-VDKSAWRTDAEFGREMLAGVHPVIAIRRL	394
CsLOX8	--LLRSDGEKFLEFMPDVIK-ESKSAWRTDEEFGREMLAGVHPVLIASL	392
CsLOX9	--MFRTDGEQFLKFPPLPHVIK-EDKSAWRTDEEFGREMVAGVHPVLIIRRL	398
CsLOX10	--LLRTDGEQFLKFPMPAVIK-ESKSAWRTDEEFGREMVAGVHPILIRRL	391
CsLOX11	--ILRTDGEQFLKFPMPAVIK-ESKSAWRTDEEFGREMVAGVHPILIRRL	391
CsLOX12	-----GLPVPGVIEAGDENAWRDDEEFGREMIAGVHPVHIRLL	231
CsLOX13	MKQVMSVQERLFKYDPAVIR-RDRFSWLRDNEFARQCLAGVNPVSIELL	455
CsLOX14	LVTRIQQNKGILKYDTPKIIS-KDKFAWLRDDEFARQAIAGVNPVSIERM	453

	α6 (401-405)	α7 (425-432)	β10 (438-442)	
CsLOX15	IYKTVS DADD LQFQQPPTMD-KDKFFWFRD EEFCRQTI AGLNP CCIELV	443		
CsLOX16	VLVAESLVDNVIKFKQPPTAD-MDKFFWFRDEEFARQTIAGLNPCCQLQV	443		
CsLOX17	VLVAESLVDNVIKFKQPPTAD-MDKFFWFRDEEFARQTIAGLNPCCQLQV	443		
CsLOX19	VVKTMDSGKDVLRFEPETIN-RDKLFWFRDEEFARQTLAGLNPCSIIRLI	442		
CsLOX18	LVKAASDVDDVLQFVPEPMD-RDKFFWLRDEEFGRQTLAGLNPHGIQLV	449		
CsLOX20	LIKTVKDANDALQFEIPDTLD-RDKFFWFRDEEFGRQTLAGLNPPCCIQLV	236		
CsLOX21	LVKTVSDANEALQFEIPEPMD-RDKFFWFRDEEFGRQTLAGLNPPYSIQLV	426		

Consensus	XXX PXXS LBXXXXGXXXXXJXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX	600
GmLOX1	EEFPKSNLDPAIYGDQSSKITADSL--DLD--GY-TMDEALGSRRLFML	407
GmLOX2	QEFPPKSNLDPTIYGEQTSKITADAL--DLD--GY-TVDEALASRRLFML	436
GmLOX3	KEFPKSKLDSQVYGDHTSQITKEHLEPNLE--GL-TVDEAIQNKRLFLL	427
GmVLXD	QEFPPKSTLDPTLYGDQTSTITKEQLEINMG--GV-TVEEALSTQRLFIL	433
GmVLXB	EEFPLSSKLDTQAYGDHTCIITKEHLEPNLG--GL-TVEQAIQNKKLFIL	422
AtLOX1	KEFPKSKLDSQVYGDHTSQITKEHLEPNLE--GL-TVDEAIQNKRLFLL	427
CsLOX1	QEFPPASKLDKNYGDQTSTITEEHKNNLD--GL-TVNEALEKNKLFIL	430
CsLOX2	QEFPPKSKLDPKVYGDHTSKITKNYIEHNLD--GL-SVDEAIRNNKVFIL	525
CsLOX3	EVFPVSTLDATQYQKQDSTIIEEHIEAYMN--GL-TVSEAIQNKLFIL	439
CsLOX4	QEFPPKSKLDPKSIYGNQTSNITESHIINNLD--GL-SVNEALEQNKLIL	429
CsLOX5	EEFPPTSKLNPQVYGNQTSKITEEHILNHLNLD--GL-VVHEALKSKRLFIL	418
CsLOX6	EEFPKSKLDPKVYGDQTSKIIEDHIQSNLD--GL-GVFEALNNNKLFIL	429
CsLOX7	EEFPASKLDPKVYGDQTSKITEDHIEKNLE--GL-SVYEALYTNKLFIL	441
CsLOX8	KEFPPTSKLDPKLYGDHTSKITKEHIQNYLE--GL-DVDTALNQNKLFIL	439
CsLOX9	EEFPPTSKLDPKLYGDHTSTITEDHIKNSLE--GL-GVFEALFQNKLFIL	445
CsLOX10	NEFPASKLDPKLYGDQTSTITEEHIQNYLD--GL-DVSTALSQNRLYIL	438
CsLOX11	NEFPASKLDPGLYGDQTSTITEEHIQNYLD--GL-DVSTALNQNKLFIL	438
CsLOX12	KKFPKSKLDRKYGQDSRISEDDIIEKMLE--DFSSVEKAIEQKRLFIL	279
CsLOX13	KEFPILSKLDPKLYGAPESAITKELLEQEL---GGMSVEKAIEDKKLFIL	502

CsLOX14 TVFPPVSKLDPEIYGPQESALKDEHILGHL---NGMTVQQALDEKKLFMV 500

α8 (466-475)
α9 (481-486)
β11 (491-494)

CsLOX15 KEWPLKSELDPSTIYGPPEISKITTELVKFKVYGYNNINEALKEKRLFML 493
 CsLOX16 TEWPLKSELDPSTIYGPQESKITTEIVEQQLKAYDYT-LLDARREKKLYLL 492
 CsLOX17 TEWPLKSELDPSTIYGPQESKITTEIVEQQLKAYDYT-LHDARREKKLYLL 492
 CsLOX19 TEWPIKSKLDPVIYGPQESSITEEMINQEIG--GIMKVDEAIKQKKLFIL 490
 CsLOX18 TEWPLKSKLDPNVYGSAESAITKEIIDKEIK--GFMTVEEAIEQKKLFML 497
 CsLOX20 KEWPLKSKLDPEIYGPAESAITAELIEREIK--GFMTIDEAINEKKLFIL 284
 CsLOX21 TEWPMKSKLDPEIYGPPESAITTELIEREIK--GFMTLDEAMREKKLFIL 474

Consensus XXXDXXXPXXXXXXXXXXXXXXXXXXRXRXXXXXXXXXXXXLXPXXIEXXPXXXX 650

GmLOX1 DYHDI FMPYVRQINQLNSAKTYATRTILFLREDGTLKFPVAIELSLPHSAG 457
 GmLOX2 DYHDV FMPYIRRINQT-YAKAYATRTILFLRENGTLKFPVAIELSLPHPAG 485
 GmLOX3 GHHD PIMPYLRRINAT-STKAYATRTILFLKNDGTLRPLAIELSLPHPQG 476
 GmVLXD DYQDA FIPYLTRINSLPTAKAYATRTILFLKDDGTLKPLAIELSKPHPDG 483
 GmVLXB DHDY LIPYLRKINAN-TTKTYATRTIFFLKNDGTLTPLAIELSKPHPDG 471
 AtLOX1 DHHD TLMPYLGRVNTT-TTKTYASRTLLFLKDDGTLKPLVIELSLPHPNG 478
 CsLOX1 NHHD MLFPYLRRINST-SSKIYATRTLLFLKNDGTLKPLAIELSLPHPDG 479
 CsLOX2 DHHD TLIPFLRRINAT-NTKIYATRTIIFLQKDGTLLKPLAIELSLPHPGG 574
 CsLOX3 DHHD SLMPFLTINST-DSKIYATRTLLLLQDDGTLKPLAIELSLPHPQG 488
 CsLOX4 DHHD SFMPFVRRVNDTTSSKIYATRTLLFLTNDGTLKPLAIELSLPHPNG 479
 CsLOX5 DLHD AFMPYLRRINTT-PTKTYATRTLLFLKDDGTLKPLAIELSLPHPKG 467
 CsLOX6 DHHD SFMPYLRRINST-LTKTYASRTLLFLKDDGTLKPLAIELSLPHPNG 478
 CsLOX7 DHHD SFMPYLTRINST-ATKTYASRTLLLLKNDGTLKPLAIELSLPHPKG 490
 CsLOX8 DHHD SFIPYMRINTT-LTKAYATRTILFLTKDGTLLKPIAIELSLPHQDG 488
 CsLOX9 DHHD SYIPYLRRINST-SSKAYATRTLVLFTSEGTLLKFPVAIELSLPHPNG 494
 CsLOX10 DHHD SFIPYLRRINTT-PTKAYATRTLLFLANDGTLRPIAIELSLPHPDG 487
 CsLOX11 DHHD SFIPYLRRINTT-PTKAYATRTLLFLANDGTLRPIAIELSLPHPDG 487
 CsLOX12 DHHD TFMPYLKRINKT-STKAYATRTILFLTKEEKLMPVAIELSLPKDGP 328
 CsLOX13 DYHD MLLPFIERMNSLPGRKAYASRTVFFYTKSGVLKPLVIELSLPPSSS 552
 CsLOX14 DYHD IFLPFLDKINSLDGRRTYATRTIYFLSPQGTLLKFPVAIELSLPQTGP 550

β11
β12 (517-523)
β13 (529-537)

CsLOX15 DYHDVLLPYVSKVRELENKTLVGSRTLFFLTPYGTLLFLAIELTRPPMDG 543
 CsLOX16 DYHDVLLPYVSKVRKLEKRTLYGSRTLFFLTPYGTLLMPMAIELTRPPMDG 542
 CsLOX17 DYHDVLLPYVSKVRKLEKRTLYGSRTLFFLTPYGTLLMPMAIELTRPPMDG 542
 CsLOX19 DYHDL LLLPFVHQVRELKGTTLVGSRTVFFLNPDPGTLRPLAIELTRPPHLD 540
 CsLOX18 DYMD LLLPFVEKVRELEGTTLVGSRALFFLTEEGTLRPLAIELTRPQMDD 547
 CsLOX20 DYHDL LLLPYVKKVREIEGTTLVGSRTLFFLTDGTLRPLAIELTRPPMDG 334
 CsLOX21 DYHDL LLLPYVKKVREIKGTTLVGSRTLFFLTLGTLRPLAIELTRPPMDG 524

Consensus XXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXDXXXHQXXXHWXXTH 700

GmLOX1 DLSAAVSQVVLPAKEGVES---TIWLLAKAYVIVNDSQYHQLMSHWLNTH 504
 GmLOX2 DLSGAVSQVILPAKEGVES---TIWLLAKAYVVVNDSCYHQLMSHWLNTH 532
 GmLOX3 DQSGAFSQVFLPADEGVES---SIWLLAKAYVVVNDSCYHQLVSHWLNTH 523
 GmVLXD DNLGPESIVVLPATEGVDS---TIWLLAKAHVIVNDSGYHQLVSHWLNTH 530
 GmVLXB EEYGPVSEVYVPSSEGVEA---YIWLLAKAYVVVNDACYHQIISHWLNTH 518
 AtLOX1 DKFGAVSEVYTPG-EGVYD---SLWQLAKAFVGVNDSGNHQLISHWMQTH 524
 CsLOX1 DQFGVVSQVFTPTKEGVES---HIWQLAKAYAAVNDSGVHQLISHWLNTH 526
 CsLOX2 DHFGCISKVYTPADKGVGD---SLWQLAKAYVNVNDSGYHQLISHWLKTH 621

CsLOX3	YEHGAVSKVFTPEEKGIGE---TIWQLAKAYVAVNDSGYHQLISHWLNTH	535
CsLOX4	DALGAVSKICTPAEQGVES---TIWQLSKAYVTVNDYGHHQLVSHWLNTH	526
CsLOX5	DIYGSVSKVYTPAENGVEN---TIWQLAKAYVAVNDSGYHQLISHWLHTH	514
CsLOX6	DQYGAVSKVYTPSKEGVES---AIWELAKAYVAVNDSGYHQLISHWLNTH	525
CsLOX7	DQFGAVSKVYTPAEEGVGA---TIWQLAKAYAAVNDSGYHQLISHWLNTH	537
CsLOX8	DEHGAVSKVYTPTEEGVEG---TIWQLAKAYVAVNDVCYHQVYSHWLKTH	535
CsLOX9	DEFGVVSQVYTPAEEGVG---TIWQLAKAYA AVTDSGYHQLISHWLNTH	541
CsLOX10	DEFGVVSQVYTPSEDGVDG---TIWQLAKAYA AVNDSGYHQLNSHWLNT	534
CsLOX11	DEFGVVSQVYTPSEDGVDG---TIWQLAKAYA AVNDSGYHQLNSHWLNT	534
CsLOX12	DENGADSTVFTPPCDNNDPHKYATWQLAKGYVAVNDSGYHQLYSHWLKTH	378
CsLOX13	SL-ESNKTVYTH---GHDATTHWIKWLAKAHVCSNDAGVHQLVNHWLRTH	598
CsLOX14	SS--RSKRVTTP---PVDATSNWVWQLAKAHVCTNDAGVHQLVNHWLRTH	595

	B14 (549-550) α10 (560-586)	
CsLOX15	KP-QW-KEVYTPM--NWHSTDLWLWRLAKAHVLAHDSGVHQLVSHWLRT	589
CsLOX16	KP-QW-KEVYTPN-SNWHSTDIWLWKLAKAHVLAHDAGVHQLVSHWLRT	589
CsLOX17	KP-QW-KEVYTPN-SNWHSTDIWLWKLAKAHVLAHDATVHQLVSHWLRT	589
CsLOX19	SP-RW-NQVFSP---CWHSTGVWLWRLAKVHVAHDSGYHQLVCHWLKTH	585
CsLOX18	KP-QW-KQVFTP---TWNATGDWLWRLAKAHVLAHDSGVHQLVSHWLRT	592
CsLOX20	KP-QW-KEVFTP---SWHATAVWLWRFKAHVLAHDSGYHQLVSHWLRT	379
CsLOX21	KP-QW-KEVFSP---SWHATGVWLWRFKAHALAHDSGYHQLVSHWLRT	569

Consensus	XXXEPXXJXXRXSXXHPXXLLXPHXRXXXXJNXXARXXLXXXXGXXE	750
GmLOX1	AAMEPFVIATHRHLSVLHPIYKLLTPHYRNNMNINALARQSLINANGIIE	554
GmLOX2	AVIEPFIIATNRHLSALHPIYKLLTPHYRDTMNINALARQSLINADGIIE	582
GmLOX3	AVVEPFIIATNRHLSVHPIYKLLHPHYRDTMNINGLARLSLVNDGGVIE	573
GmVLXD	AVMEPFIAIATNRHLSVLHPIYKLLYPHYRDTININGLARQSLINADGIIE	580
GmVLXB	AVVEPFVIATNRHLSVHPIYKLLFPHYRDTMNINSLARKSLVNADGIIE	568
AtLOX1	ASIEPFVIATNRQLSVLHPVFKLLEPHFRDTMNINALARQILINGGGIFE	574
CsLOX1	AAIEPFVIATNRQLSVLHPHKLQPHFRDTMNINAFARQILINAGGILE	576
CsLOX2	AAIEPFVIATNRQLSVVHPHKLQPHFRDTMNLNAVARQILINAGGALE	671
CsLOX3	AVIEPFIIATNRQLSVLHPIYKLLHPHYRDTMNINALARQTLINAGGILE	585
CsLOX4	AVAEPFVLATNRQLSVLHPHKLQPHFRDTMNINALARQLLVNGGGIIE	576
CsLOX5	AVIEPFVIVTNRQLSVVHPHKLQPHFRDTMNINSLARQALINADGPLE	564
CsLOX6	AVIEPFVIATNRQLSALHPIHKLQPHFRDTMNINALARQTLINAGGILE	575
CsLOX7	AVIEPFVIATNRQLSVLHPIYKLLQPHYRDTMNINALARQTLINAEIGILE	587
CsLOX8	CVSEPFVIATNRQLSVLHPHKLQPHFRDTMNINALARQTLINADGLVE	585
CsLOX9	AVIEPFVIATNRQLSALHPIYKLLQPHYRDTMNINALARQSLVSVDGVIE	591
CsLOX10	AVIEPFVIATNRQLSALHPIYKLLHPHYRDTMNINALARQSLVSADGIIE	584
CsLOX11	AVIEPFVIATNRQLSALHPIYKLLHPHYRDTMNINALARQSLVSADGIIE	584
CsLOX12	AVIEPFVIATNRQLSVIHPIYKLLHPHFRGTMSINARARTILVNADGTIE	428
CsLOX13	ACMEPYIIATHRQLSSMHPVYVLLHPHMYRTLEINALARQSLINGGGIIE	648
CsLOX14	ASLEPFILSAHRQMSAMHPIYKLLDHPHMYRTLEINALARQNLINADGVIE	645

		
CsLOX15	CAVEPYIIATNRQLSAMHPIHRLIKPHFRYTMEINALARESLINAGGIIE	639
CsLOX16	CCVEPYVIATNRQLSAMHPINRLLQPHLRYTMEINALARNTLINAGGVIE	639
CsLOX17	CCVEPYVIATNRQLSAMHPINRLLQPHLRYTMEINALARNILISAGGIIE	639
CsLOX19	SITEPYVIATNRQLSIMHPVHRLHLPHFRYTMEINALAREALINADGTIE	635
CsLOX18	CVTEPYIIATKRQLSAMHPIFRLLHHPHFRYTMEINALARQLLINSNGIIE	642
CsLOX20	CATEPYIIATNRQLSVMHPIYRLLHHPHFRYTMEINALAREALVNAGGIIE	429

CsLOX21	CVTEPYIIAANRQLSVIHPIYRLLHPHFRTMEINALAREALVNAGGIIE	619
Consensus	XXXXXXXXXXEXXXXYXXXWXXXXXXXXXXLXXRXXXXXXXXXXXXXXXXXX	800
GmLOX1	TTFLPSKYSVEMSSAVYK-NWVF TDQALPADLIKRGVAIKDPSTPHGVRL	603
GmLOX2	KSFLPSKHSVEMSSAVYK-NWVF TDQALPADLIKRGVAIKDPSAPHGLRL	631
GmLOX3	QTFLWGRYSVEMSAVYK-DWVF TDQALPADLIKRGMAIEDPSCPHGIRL	622
GmVLXD	KSFLPGKYSIEMSSSVYK-NWVF TDQALPADLVKRGLAIEDPSAPHGLRL	629
GmVLXB	KTFLWGRYSLEMSAVIYK-DWVF TDQALPNDLVKRGVAVKDPSAPHGVRL	617
AtLOX1	ITVFPSKYAMEMSSFIYKNHWF TPDQALPAELKKRGMAVEDPEAPHGLRL	624
CsLOX1	FTVFPAKYAMEMSSAVYK-NWVFPEQALPEELMKRGMAVKDSSAPHGLRL	625
CsLOX2	ATVFPGRYCMEMTSASYK-EWTFPGQALPVDLIKRGVAVEDENSPHGLRL	720
CsLOX3	MTVFPGKYAMEMSAVIYK-NWVF TDHALPADLLKRGVAVEDSSGPHGLKL	634
CsLOX4	SVVFPGKYSMEISSAAYK-NWNLAEQAH PADLIKRGVAVEDPSSPHGVRL	625
CsLOX5	LTVFPRKYSMEMSAVIYK-DWVFPEQALPADLLKRGVAIKDPNSPHGLRL	613
CsLOX6	ITVFPGKYAMEMSAVYK-NWIFPEQALPAELLLKRGVAVEDPNSPHGLRL	624
CsLOX7	STVFPGKYALEMSAVYK-NWVFTEQALPADLLKRGMAVKDPNSPHGLRL	636
CsLOX8	LAFFQGYAMESSSLIYK-DWVFTEQALPTDLLKRGVAVKDENSPHGLRL	634
CsLOX9	STFLPGKYAMELSAVYK-DWVF TDQALPADLLKRGIAEKDVNAPHGLRL	640
CsLOX10	STFFQGKFALESSAIYK-DWKLTEQALPADLLKRGVAVKDQNSPHGVRL	633
CsLOX11	STFFQGQFALESSAIYK-DWKFT EQALPADLLKRGVAVKDKNSPHGLRL	633
CsLOX12	SVFFQGYAMESSSAVYKNNWAFNKQGLPADLIQRGLVDEKTKKPCEL--	476
CsLOX13	ASFSPGKYAMELSSAAYESQWRFDMEALPADLLRRGMAVEDPSMPCGVKL	698
CsLOX14	ACFTAGRYGMEISAAAYKSMWRFDQENLPADLVRRGMAVPDPTQPHGVKV	695

CsLOX15	TAFAPGKYSMELSSVMYDKQWRFDLQALPADLIHRRMAVEDKDSEHGVRV	689
CsLOX16	STFAPGKYCLELSSVIYDKQWRFDLQGLPADLVHRGMAVEDETCEHGLRL	689
CsLOX17	SIFAPGKYCLELSSVIYDKQWRFDLQGLPADLIHRGMAVEDETCEHGLRL	689
CsLOX19	TAFSPGKYSVELSSVAYDKEWRFDLQALPADLIDRGMAVEDPNSPHGLKL	685
CsLOX18	STFSPGKFSMEISSAAYDKLWRFDHEALPADLISRGIATEDPDSPHGLKL	692
CsLOX20	SSFSPGKYSMELCADAYDQIWRFDLEALPADLINRGMAVEDPSAPHGLKL	479
CsLOX21	SSFSPGKYANELCADAYDKQWRFDQQALPADLIKRGMAVEDSSAPHGLKL	669

Consensus	XXXBYPXXDGLXXWXXXXXWVXXYXXXXYXXXXXXXXXXDXEJQXXXXEX	850
GmLOX1	LIEDYPYAADGLEIWAAIKTWVQEYVPLYAR-DDDVKN DSELQHWKKEA	652
GmLOX2	LIEDYPYAVDGLEIWAAIKTWVQEYVSLYAR-DDDVKPDSELQQWWKKEA	680
GmLOX3	VIEDYPYAVDGLEIWD AIKTWVHEYVFLYKS-DDTLREDPELQACWKEL	671
GmVLXD	VIEDYPYAVDGLEIWD AIKTWVHEYVSLYPT-DAAVQQDTELQAWWKEA	678
GmVLXB	LIEDYPYASDGLEIWD AIKSWVEEYVSFYYS-DEELQKDPELQAWWKEL	666
AtLOX1	RIKDYPYAVDGLEVWYAIESWVRDYIFLFYKI-EEDIQTDTELQAWWKEV	673
CsLOX1	LIQDYPYGV DGLEIWIYA IKTWVEDYCSFYKYT-DEAIQKDSELQSWWKEV	674
CsLOX2	LIDDYPFAVDGLEIWSAIKTWVKDYCSLYKYT-DKMVQEDYELQSWWKEL	769
CsLOX3	LIEDYPFAVDGLEIWSAIHTWVTEYCNIYYET-DKMVKEDTELQSWWTEV	683
CsLOX4	LIEDYPYAVDGLEIWAAMKNWVQEYCSFYYS-DEIVQNDKELQAWWKEL	674
CsLOX5	LIEDYPYAVDGLEIWSAIHSWVEEYCSYYYKT-DDIIQKDSELQAWWKEL	662
CsLOX6	LIEDYPYAVDGLEIWSAIKSWVEEYCSFYKYT-DDIVQKDCELQAWWKEL	673
CsLOX7	LIEDYPFAADGLEIWSAIKSWVEEYCSFYKYA-DDTVQNDSELQAWWKEV	685
CsLOX8	LIEDYPYAVDGLEIWFAINS WKEYCSYYYKT-DDTIQNDTEIQAWWKEI	683
CsLOX9	LIEDYPYAVDGLEIWSAIKAWKEYCSHYYSN-DASVQRDTELQAWWKEV	689
CsLOX10	LIEDYPYAVDGLEIWSAIKTWVKEYCSFYKYT-DATVQKDTELQAWWKEV	682
CsLOX11	LIEDYPYAVDGLEIWSAINTWVKEYCSFYKYT-DATVQKDTELQAWWKEV	682

CsLOX12	-VKNYPYAVDGLLEIWNAINKWVKEYCDIYYKGEDKKVQNDKEIQNWWEI	525
CsLOX13	VIEDYPYAADGLLVWSAIKEWVESYVEHHYVE-PNSVRTDVELQAWWDEI	747
CsLOX14	VIEDYPYANDGLLIWGAIVENWVSTYVNRYPN-SSVVCNDLELQNWYSES	744

CsLOX15	IIEDYPYANDGLLIWSSIKQWVTDYVNHYYPISSEVERDEELQAWWTEI	738
CsLOX16	TIDDYPYANDGLLIWDAIKEWVTEYVKHYIAN-SSEVESDEELQEWWEI	738
CsLOX17	TIEDYPYANDGLLIWDAIKEWVSEYINHYIAN-SSEIESDEELQEWWEI	738
CsLOX19	TIEDYPYANDGLIMWDSIKEWVTDYINHYYPK-ASLVESDQELQAWWTEI	734
CsLOX18	NIEDYPFANDGLLIWDALKQWVTSYVNHYYS-SSQVELDEELQSWWTEI	741
CsLOX20	TIEDYPFANDGLVLWDIIKQWVTDYVNYYYPE-PTLIESDLELQSWWTEI	528
CsLOX21	TIEDYPFANDGLALWDIIKQWVTDYVNYYYPE-QTLIESDLELQSWWTEI	718

Consensus	XXXGHXDXXXXXXWXXXXTXXXLXXXXXXXXXWXXSXXHAXXNFGQYXXXX	900
GmLOX1	VEKGHGDLDKDKPWWPKLQTLLEDLVEVCLIIWIASALHAAVNFGQYPYGG	702
GmLOX2	VEKGHGDLDKDKPWWPKLQTIEELVEICTIIWTASALHAAVNFGQYPYGG	730
GmLOX3	VEVGHGDKKNEPWWPKMQTREELVEACAIITWASALHAAVNFGQYPYGG	721
GmVLXD	VEKGHGDLDKDKPWWPKMQTTEDLIQSCSIIVWTASALHAAVNFGQYPYGG	728
GmVLXB	VEVGHGDLKDKPWWQKMQTREELVEASATLIWIASALHAAVNFGQYPYGG	716
AtLOX1	REEGHGDKKSEPWWPKMQTREELVESCTIIWVASALHAAVNFGQYPVAG	723
CsLOX1	REEGHGDKKNEPWWPKMQTRQELIDSCCTIIWIASALHAAVNFGQYPYAG	724
CsLOX2	REEGHGDKKDEPWWPEMQTREDLIETCTIIWIASALHAAVNFGQYPYGG	819
CsLOX3	RIEGHGDKKKEPWWPKMETISELINSCTIIWIASALHAAVNFGQYPYAG	733
CsLOX4	REVGHGDLKDKSWWPSMQTREELVETCTTAIWTTSALHAAVNFGQYPYGG	724
CsLOX5	VEVGHGDKKNEPWWPKMQTRGELVESCATVIWIASALHAAVNFGQYPYAG	712
CsLOX6	REVGHGDKKDELWNNKMQTREELIDSCCTIMIWIWIASALHAAVNFGQYPYAG	723
CsLOX7	RDVGHGDKKDESWWPKMLTREELVESCTIIWISSALHAAVNFGQYPYAG	735
CsLOX8	REVGHGDKKDETWWPQMOTIEELVESCTTIWISSALHAAVNFGQYAYEG	733
CsLOX9	REVGHGDKKDETWWPKMKTREELVESCTILIWISSALHAAVNFGQYSFTG	739
CsLOX10	REVGHGDKKHEAWWPKMQTREELVESCTTLIWISSALHAAVNFGQYSFTG	732
CsLOX11	REVGHGDKKHEAWWPKMQTREELVESCTTLIWISSALHAAVNFGQYSFTG	732
CsLOX12	KEVGHGDKKEYDGWPEMKTIFNELVESCTIIWISSALHAAVNFGQYSFAA	575
CsLOX13	KNKGHYDKRNEPWWPKLETQKQLSGVLTTIIWIASGQHAANFGQYPFGG	797
CsLOX14	INVGHADVRNASWWPKLETPEDLTSLITTLIWLASAQHAALNFGQYPYGG	794

CsLOX15	RTVGHADKKDAPGWPDLKTQQLDIDIVTNMAWTAHHAAVNFGQYAYAG	788
CsLOX16	RTVGHADKKE--GWPDLKTREDLIDIVTNIAWIASGHHAAVNFGQYAFSA	786
CsLOX17	RTVGHADKKE--GWPDLKTREDLIDIVTNIAWIASGHHAAVNFGQYAFSA	786
CsLOX19	RTVGHADKKDEPWWPVLNTPKDLIEILTTLWVTSGYHAAVNFGQYTYGG	784
CsLOX18	RTVGHEDKKDEPWWPTLETPEDLIQILTTIVWVTSGHHAAVNFGQYTYAG	791
CsLOX20	RTVGHGDKKDEPWWPILKTPNDLVQIITTIVWVTSGHHAAVNFGQYTYAG	578
CsLOX21	RTVGHGDKKDEPWWPLLKTPNDLIGIVTTIVWVTSGHHASVNFGQYTYAG	768

Consensus	XXXNRXXXXRXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	950
GmLOX1	LIMNRPTASRRLLEKGG---TPEYEEMINNHEKAYLRTITSKLPTLISL	748
GmLOX2	FILNRPTSSRRLLEKGG---TPEYEEMVKSHQKAYLRTITSKFQTLVDL	776
GmLOX3	LILNRPTLSRRFMPEKGG---SAEYEELRKNPQKAYLKTITPKFQTLIDL	767
GmVLXD	LILNRPTLARRFIPAEG---TPEYDEMVKNPQKAYLRTITPKFETLIDL	774
GmVLXB	LILNRPTISRRFMPEKGG---SPEYDALAKNPEKEFLKTITGKKETLIDL	762
AtLOX1	YLPNRPTISRQYMPKEN---TPEFEELEKNPDKVFLKTITAQLQTLLGI	769

CsLOX1	YLPNRPTLSRRFMPEKG---- <td>770</td>	770
CsLOX2	FPPNRPSMSRRFIPEEG---- <td>865</td>	865
CsLOX3	YLPNRPTVSRRFMPEPG---- <td>779</td>	779
CsLOX4	YIPNRPTISRRLMPEEG---- <td>770</td>	770
CsLOX5	YSPNRPTVSRQFMPVQG---- <td>758</td>	758
CsLOX6	FLPNRPTLSRRFMPEKG---- <td>769</td>	769
CsLOX7	YLPNRPTVSRRFMPEEG---- <td>781</td>	781
CsLOX8	FLLNRPTLSREFMPEKG---- <td>779</td>	779
CsLOX9	YLPNRPTLSRRFMPEEG---- <td>785</td>	785
CsLOX10	YLPNRPTLSRRFMPEEG---- <td>778</td>	778
CsLOX11	YLPNRPTLSRRFMPEEG---- <td>778</td>	778
CsLOX12	FYPNRPTLSRQFMPMGG---- <td>618</td>	618
CsLOX13	YVPNRPTLLRKLIPHED---- <td>843</td>	843
CsLOX14	YVPNRPLMRRLIPEEN----DPEYATFVADPQKYFLLALPSVLQSTKFM	840

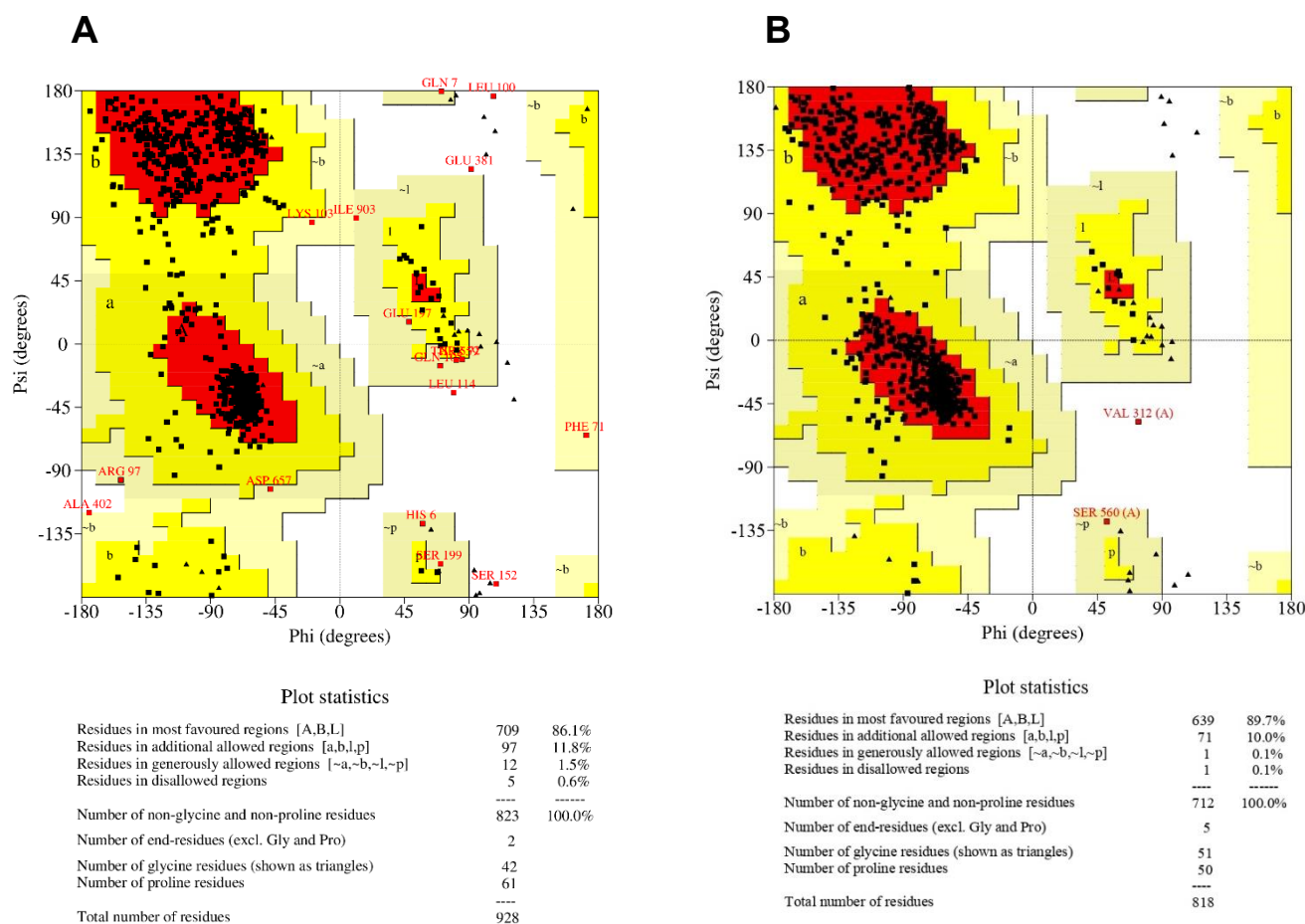
CsLOX15	YFPNRPTITRTVMPSEEKEYNLDAWKHFKNSPEDALLKCLPTQLQAGLVV	838
CsLOX16	YFPNRPSLTRTNMPSEEKESKPEVWKAFFKANPEDTILKCFPSQLQAAKNM	836
CsLOX17	YFPNRPPVTRTNMPSEEKESKPEVWKAFFKANPEDTILKCFPSQREAAALNM	836
CsLOX19	YFPNRPTIARTKMPTEDPD--EEEWKSFVKKPESALLKCFPSQLQATRVM	832
CsLOX18	YFPNRATIARTNVPTEDPT--DEEWKYFIDKPEGTLLQCLPSKLQAAKVM	839
CsLOX20	YFPNRPTIARINVPTEDAS--DEFLEKFWAKPEEALMQCFPSQIQATTVM	626
CsLOX21	YFPNRPTIARTNMPTEDAS--EEVLEKFWAKPEEALMQCFPSQIQATTVM	816

Consensus	XXXXXLSXHXHXXEYJGXXXXXXXXXXWXXXXXXXXXXFXXXXXXXXXXJXXXX	1000
GmLOX1	SVIEILSTHASDEVYLGQRDN--PHWTSDSKALQAFQKFGNKLKEIEEKL	796
GmLOX2	SVIEILSRHASDEVYLGQRDN--PHWTSDSKALQAFQKFGNKLKEIEEKL	824
GmLOX3	SVIEILSRHASDEVYLGQRDN--PNWTSDTTRALEAFKRFGNKLQAIENKL	815
GmVLXD	SVIEILSRHASDEIYLGRET--PNWTTDKKALEAFKRFGSKLTGIEGKI	822
GmVLXB	TIIEILSRHASDEFYLGQRDG-GDYWTS DAGPLEAFKRFGKNLEEIEEKL	811
AtLOX1	SLIEILSTHSSDEVYLGQRDS--KEWAAEKEALEAFEFKFGKVEIEEKNI	817
CsLOX1	ALIEILSRHASDEVYLGQRDT--PQWTS DTAPLEAFDRFGKKLAEIEEKI	818
CsLOX2	SLVEILSRHSSDEVYLGQRDT--PEWTTDKAEKAFEFKFGNKLREIELKI	913
CsLOX3	SLIEVLSRHTGDEIYLGQRDT--MKWMTDDEEALKAFTRFGDRLREIENRI	827
CsLOX4	SIIEVLSKHASDEVYLGERE---EKWTAEAEPLQAFERFGRRLSEIEDGI	817
CsLOX5	SLIEILSRHTSDEVYLGQTD--PEWTAEVDTLQAFERFGRKLDVIGNRI	806
CsLOX6	SLIEVLSRHTSDEVYLGQRDT--PEWTSEGHSLQAFERFGRKKLIQIEDNI	817
CsLOX7	SLIEILSRHASDEVYLGQRDY--DDWTAEAGPLQAFERFGRKLAQIEDKM	829
CsLOX8	SLVEILSRHASDEIYLGQREN--PDWTSES DPLQAFERFGRKKLSEIEDKI	827
CsLOX9	ALVEVLSRHASDEVYLGQREN--PDWTL DAGPLQAFDKFGRKLVQIEDAI	833
CsLOX10	SLVEILSRHASDELYLGQREN--PDWTAEAEPLNAFERFGTKLAQIEDRI	826
CsLOX11	SLVEILSRHASDELYLGQREN--PDWTAEAEPLNAFERFGTKLAQIEDRI	826
CsLOX12	YLIAQLSSHESDEVYLGKNED--VDWTS DKKALDAFKKFQTQLRAIEDDI	666
CsLOX13	AVQDTLSTHSAD EYLGQVNPLHHTWNTNDQIILKIFSKYSAQLEEIDKII	893
CsLOX14	AVVDTLSTHSPDEEYIGERQQ-PSIWSGDPEIVEAFYEFSAQVKNIEKEI	889

CsLOX15	AVLDVLSSTHSPDEEYLGDKM--EPSWGSNLVIAEAFNRFNKRMNEIESII	886
CsLOX16	AALDLLSTHASDEEYLGHHV--ESAWKEDSKILDSFKKFQQRRIKQIEDII	884
CsLOX17	LALDLLSTHASDEEYLGHHV--ESAWKDDSKIFESFKKFQQRRIKKIEDII	884
CsLOX19	AVLDILSNHSPDEEYLGDKM--EKAWADDPVIAKAFERFNGRLKVLLEGII	880

CsLOX18	AVLNVLSTHSPEEEYLGEAL--EPSWGDDTYIKATFEQFSGRLKEIEGII	887
CsLOX20	AVLDILSNHSPDEEYLGEKI--EPSWEEDDVIAAFAFERFQGRLEKEGII	674
CsLOX21	AVLDILSNHSPDEEYLGENI--EPSWEENDVIAAFAFERFNGRLKELEGII	864
Consensus	XXXNXBXXXXXNRXGXXXXXXYLXXXXXXXXXXGXXXXGXPXSXSI	1047
GmLOX1	VRRNNDPSLQGNRLGPVQLPYTLLYPSSE----EGLTFRGIPNSISI	839
GmLOX2	ARKNNDQSL-SNRLGPVQLPYTLLHPNS-----EGLTCRGIPNSISI	865
GmLOX3	SERNNDEKL-RNRCGPVQMPYTL LLPSSK----EGLTFRGIPNSISI	857
GmVLXD	NARNSDPSL-RNRTGPVQLPYTLLHRSSE----EGLTFKGIPNSISI	864
GmVLXB	IEKNNDETL-RNRYGPAKMPYTL LYPSSE----EGLTFRGIPNSISI	853
AtLOX1	DERNDDETL-KNRTGLVKMPYTL LFPSSSE----GGVTGRGIPNSVSI	859
CsLOX1	MNMNNDDEKL-KNRVGPVKVPYTL LYPTSD----EGLTGKGIPNSVSI	860
CsLOX2	EKMNKDQKL-KNRVGPVKMPYTL LYPSSE----GGLTGKGIPNSVSI	955
CsLOX3	TEMNSNGKW-KNRVGPVKLPYTL LY PNTSGHPNEGLTGKGIPNSISI	873
CsLOX4	VKRNDATL-KNRYGLVKFPYNLLI PNGE----IGIAAKGIPNSISI	859
CsLOX5	MSRNTDPNL-KNRVGPVKFPYTL LYPTSG----KGLTSKGIPNSVSI	848
CsLOX6	MRRNNDVNL-KNRVGPIKFPYTL LHPTSE----KGV TAMGIPNSVSI	859
CsLOX7	MSKNKDTNL-KNRAGPVNFPYTL LH PNGE----EGLSAKGIPNSISI	871
CsLOX8	TSRNKDRNM-KNRVGPI SF PYTL LMPNGE----EGLSAKGIPNSISI	869
CsLOX9	VRRNNDLNM-KNRAGPVKFPYGL LIPTSD----QGLTGRGIPNSISI	875
CsLOX10	ASRNKDTNM-KNRAGPVNFEYGL LMPSSSE----QGLTARGIPNSISI	868
CsLOX11	ASRNKDTNM-KNRAGPVNFEYGL LMPSSSE----QGLTARGIPNSISI	868
CsLOX12	TTKNQNHE--KNRCGPIQFPYTL LFPTSE----PGITAKGIPNSISI	707
CsLOX13	NKRNKDNRL-KNRSGAGVPPYEL LLPTSG----PGVTGRGIPNSISI	935
CsLOX14	ERRNNDPSL-RNRCGAGVLPYEL LAPSSSE----PGVTCRGVPNSVSI	931
	α20 →	
CsLOX15	NEKNDNENL-RNRHGAGILSYELLKPFSE----PGVTNKGIPYSISI	928
CsLOX16	DERNDDENL-KNRHGAGILPYEFLKPFSE----EGITNKGVPYSISI	926
CsLOX17	DERNDDENL-KNRHGAGILPYEFLKPFSE----KGITNKGVPYSISI	926
CsLOX19	DEKNENPNL-RNRNGAGI I PYELLKPFST----PGVTGKGVPYSISI	922
CsLOX18	DERNGNQEL-RNRNGAGI APYELLKPSSE----PGVTGMGVPYSISI	929
CsLOX20	DGRNTNKDL-KNRCGVGVPYQL LKPFSE----PGVTSKGVYPYSISI	716
CsLOX21	DERNTNKNL-RNRCGVGVPYQL LKPFSE----PGVTSKGVYPYSISI	906

Supplementary Figure S1: Amino acid sequence alignment of *Cannabis sativa* lipoxygenase (CsLOX) with soybean (*Glycine max*) wild type GmLOX1, GmLOX3, GmVLXB, GmVLXD, *Arabidopsis thaliana* AtLOX1, and. Conserved residues are highlighted in ash. Predicted secondary structural elements of CsLOX15 are highlighted in colours, β-sheets-blue, α-helix-green above the corresponding sequence. Accession numbers and uniprot IDs are provided in supplementary table1.



Supplementary Figure S2: Ramachandran plots for **(A)** CsLOX15 protein model and **(B)** GmLOX1. The putative structure of CsLOX15 obtained from Phyre2 (Kelley et al., 2015) was analysed using PROCHECK in SAVES v6.1¹.

¹ <https://saves.mbi.ucla.edu/>