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(54) Benævnelse: Protein- eller glycoproteinfragment

(57) Sammendrag:

Fragment af et protein eller af et glycoprotein indkodet af en åben læseramme fra RNA-sekvensen fra LAV_{EU}-virus og svarende til fig. 7A-7J eller af RNA-sekvensen fra LAV_{MAL}-virus og svarende til fig. 8A-8I, hvilket fragment er et immunogent epitopbærende peptid, der genkendes fra antistoffer af LAS-patientsera.

10 PATENTKRAV

1. Fragment af et protein eller af et glycoprotein indkodet af en åben læseramme fra RNA-sekvensen fra LAV_{ELI}-virus og svarende til fig. 7A-7J eller af RNA-sekvensen fra LAV_{MAL}-virus og svarende til fig. 8A-8I, hvilket fragment er et immunogent epitopbærende peptid,
 15 der genkendes fra antistoffer af LAS-patientsera.
2. Fragment af et protein eller af et glycoprotein ifølge krav 1, hvilket fragment er et immunogent peptid med LAV_{MAL}- eller LAV_{ELI}-Env-sekvenser som beskrevet i fig. 3E-3F, i hvilket der er mindst én aminosyresubstitution ved én eller flere af stillingerne 8, 9, 90, 102,
 20 131, 133, 140, 156, 172, 177, 179, 185, 188, 192, 198, 207, 209, 290, 305, 308, 323, 333, 335, 337, 341, 342, 353, 356, 359, 363, 404, 428, 440, 457, 461, 477, 483, 484, 486, 538, 555, 641, 652, 656, 660, 663, 694, 740, 733, 799, 854, 856, 862 og 875, i forhold til Env-sekvenserne fra LAV_{BRU} og LAV_{ARV2}, hvor de immunogene peptider binder til antistoffer fra LAS-patientsera.
- 25 3. Fragment af et protein eller af et glycoprotein ifølge krav 2, kendetegnet ved, at peptidet omfatter mindst én af nedenstående konserverede sekvenser: stillinger 37-130, 211-289, 488-830, 490-620, 531-877 og 680-700 fra Env som vist i fig. 3E-3F.
- 30 4. Fragment af et protein eller af et glycoprotein ifølge et hvilket som helst af kravene 1-3 med en størrelse, der er mindre end 250 aminosyrerester eller mindre end 150 aminosyrerester.
5. Fragment af et protein eller af et glycoprotein ifølge krav 4 med en størrelse, der ligger
 35 på mellem 5 og 150 aminosyrerester.
6. Polypeptid omfattende aminosyresekvensen af et fragment af et protein eller af et glycoprotein ifølge et hvilket som helst af kravene 1-5.

7. Polypeptid ifølge krav 6, hvilket polypeptid er kovalent koblet til et fysiologisk acceptabelt og ikke-toksisk bærermolekyle for at forbedre dets *in vivo*-immunogene karakter.
8. Polypeptid ifølge krav 6, hvilket polypeptid omfatter aminosyresekvensen fra p25-peptidet, mellem resterne 138-385 i gag-proteinet fra LAV_{ELI}- eller LAV_{MAL}-viruser, som beskrevet i fig. 3A.
9. Polypeptid ifølge krav 6, hvilket polypeptid omfatter aminosyresekvensen fra p13-peptidet, mellem resterne 385-519 i gag-proteinet fra LAV_{ELI}- eller LAV_{MAL}-viruser, som beskrevet i fig. 3A.
10. Polypeptid ifølge krav 6, hvilket polypeptid omfatter en specifik LAV_{ELI}-epitop og bindes til antistoffer fra LAS-patientsera, hvilken LAV_{ELI}-epitop ikke reagerer med antistoffer rettet mod specifikke epitoper af HIV_{BRU}, HIV_{ARV-2} og HIV_{MAL}.
11. Polypeptid ifølge krav 6, hvilket polypeptid omfatter en specifik LAV_{ELI}-epitop og binder til antistoffer fra LAS-patientsera, hvilken LAV_{ELI}-epitop ikke reagerer med antistoffer rettet mod specifikke epitoper af HIV_{BRU} og HIV_{ARV-2}.
12. Polypeptid ifølge krav 6, hvilket polypeptid omfatter en specifik LAV_{MAL}-epitop og binder til antistoffer fra LAS-patientsera, hvilken LAV_{MAL}-epitop ikke reagerer med antistoffer rettet mod specifikke epitoper af HIV_{BRU}, HIV_{ARV-2} og HIV_{ELI}.
13. Polypeptid ifølge krav 6, hvilket polypeptid omfatter en specifik LAV_{MAL}-epitop og binder til antistoffer fra LAS-patientsera, hvilken LAV_{MAL}-epitop ikke reagerer med antistoffer rettet mod specifikke epitoper af HIV_{BRU} og HIV_{ARV-2}.
14. Fragmenter eller polypeptider ifølge et hvilket som helst af kravene 1-13 dannet ved kemisk spaltning.
15. Fragmenter eller polypeptider ifølge et hvilket som helst af kravene 1-13 dannet ved ekspression af en rekombinant DNA.
16. Fragmenter eller polypeptider ifølge et hvilket som helst af kravene 1-13 dannet ved kemisk syntese.
17. Oligomerer af fragmenter eller polypeptider ifølge et hvilket som helst af kravene 1-13, især oligomerer fra 2 til 10 monomerer.

18. Nukleinsyre, der koder for et fragment af et protein eller af et glycoprotein ifølge et hvilket som helst af kravene 1-5.
19. Rekombinant DNA, der indkoder et polypeptid ifølge et hvilket som helst af kravene 6-13.
20. Rekombinant vektor omfattende en nukleinsyre eller en rekombinant DNA ifølge krav 18 eller 19.
21. Mikroorganismer transformeret med en vektor ifølge krav 20.
22. Celler transformeret med en vektor ifølge krav 20, især eukaryote celler.
23. Celler ifølge krav 22, hvilke celler er gærceller eller pattedyrceller, fortrinsvis lymfocytter.
24. Immunogene præparater omfattende mindst ét polypeptid eller fragment ifølge et hvilket som helst af kravene 1-13.
25. Fremgangsmåde til fremstilling af et epitopbærende polypeptid ifølge krav 1-13, hvilken fremgangsmåde omfatter:
- indsættelse af en nukleinsyre, der koder for et epitopbærende polypeptid ifølge et hvilket som helst af kravene 1-13, i en vektor, hvilken nukleinsyre eksprimeres under regulering af en egnet promotor eller replikon;
 - transformering af en egnet vært med denne vektor; og
 - isolering og rensning af det således vundne epitopbærende polypeptid.
26. Fremgangsmåde ifølge krav 25, hvor det epitopbærende polypeptid isoleres og renses ved elektroforese.
27. Fremgangsmåde til fremstilling af antistoffer, der er specifikke for fragmenter af polypeptider ifølge et hvilket som helst af kravene 1-13, hvilken fremgangsmåde omfatter:
- kondensering af miltceller, der i forvejen er immuniseret med fragmenter eller polypeptider ifølge et hvilket som helst af kravene 1-13, med relevante myelomaceller;
 - udvælgelse af de resulterende hybridoma-producerende antistoffer med specificitet for disse fragmenter eller polypeptider; og
 - isolering af disse antistoffer, der er specifikke for fragmenter eller polypeptider.

FIG. 1 A

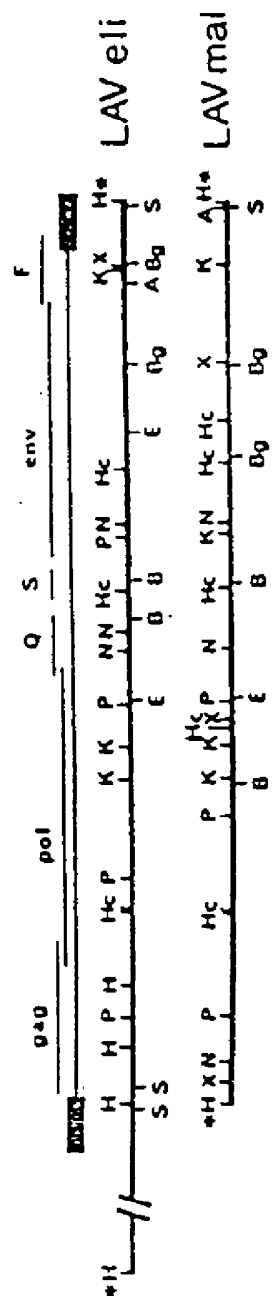


FIG. 1B

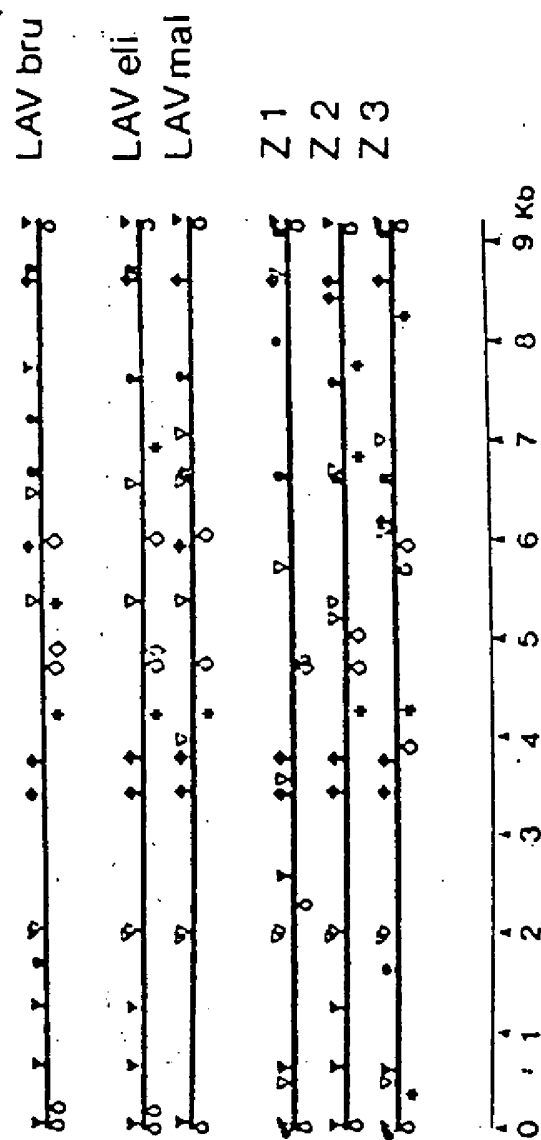


FIG. 2

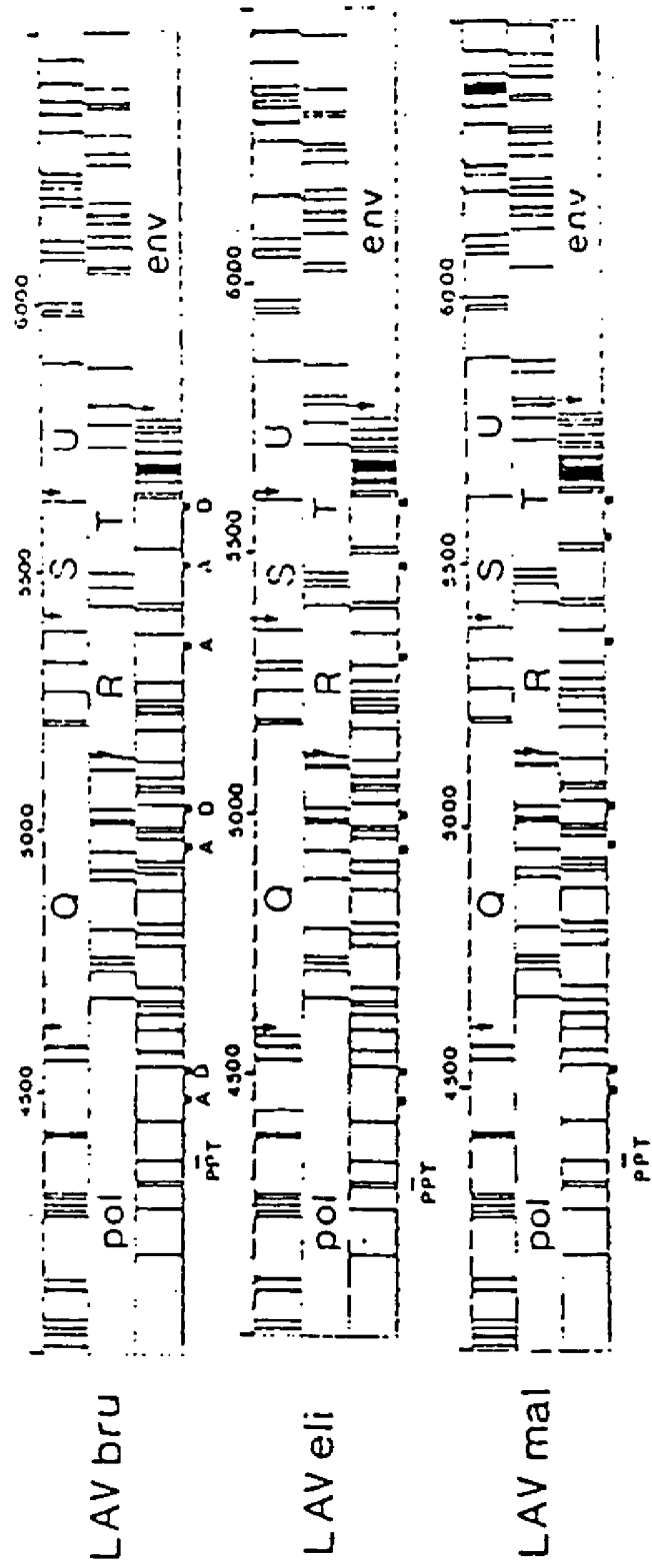


FIG. 3A

Cell
66

GAG

LAV BRU	10	20	30	40	50	60	70	80
ARV 2	HCARASVLSG	GELDRUEKIR	LAPGCKKKYK	LKHIVASRE	LERFAVNPCL	LETSEGCQRI	LCQLQPSLQT	CSEELRSLYN
LAV HAL	K A	K A	R L	L	C	Q	HE	ST K IK
LAV ELI	K K	K K	R R	Y L	Y L	K I	AI	T
LAV BRU	90	100	110	120	130	140	150	160
ARV 2	TVATLYCVHQ	RIEIKDTNEA	LKIFEEQNK	SKKAQAAA	-----DTCH	SSQVSNPI	VQHIQCQMVH	QAISPTINA
LAV HAL	DV	DV	E	-----AAC	N	L	L	L
LAV ELI	K C DV	E H	I	RQ T	AQAAAA	KH S	A I	L
LAV BRU	170	180	190	200	210	220	230	240
ARV 2	WVKVVEENAF	SPEVIFHFA	LSEGATPQDL	HTHMLTVCC	QAANQLKRET	INEEAAEUDK	VHPVMACHIA	PCQMRPRCS
LAV HAL	I	I	M I	D	D	D	L	P
LAV ELI	I	I	M I	D	D	D	L	P
LAV BRU	250	260	270	280	290	300	310	320
ARV 2	DIAGTTSTLQ	EQIGCHTHNP	PIPVGLIYKR	WILGLNKLIV	RHYSPTSILD	IRQCPKEPR	DYVDRFIKTL	RAEQASQEVK
LAV HAL	A S	S S	D	V	V	V	T	T
LAV ELI	A S	S S	D	V	V	V	T	T
LAV BRU	330	340	350	360	370	380	390	400
ARV 2	KUNTEILLVQ	HANPDCKTIL	KALCPAATLE	ENHTACQCVG	CPCHUKARVLA	ZAHSQVTHS	ATIMHQAGNF	RNQRKIVKCF
LAV HAL	C	Q	C	S	S	A T A	KG - RI	KGP I
LAV ELI	C	Q	C	S	S	A T A	KG - RI	KGP I
LAV BRU	410	420	430	440	450	460	470	480
ARV 2	HCGKEGHIAN	HCRAPFKKGC	WKCCKEGHQN	KDCTERQAHF	LCKIMPSTYK	RPCNFLOSRP	EPTAPFLQS	RPEPTAPPEL
LAV HAL	L	K	R	L	R	H	-----A	-----A
LAV ELI	L	K	R	L	R	H	-----A	-----A
LAV BRU	490	500	510	520	530	540	550	560
ARV 2	SFRSCVETTT	PSQKQEPIDK	ELYPLTSLRS	LPGNDPSSQ	-----A	-----A	-----A	-----A
LAV HAL	F E K	QK	A K	QL	L	-----A	-----A	-----A
LAV ELI	GF E IK-	QK	A K	QL	L	-----A	-----A	-----A

Central region : Q

LAV BRU 10 20 30 40 50 60 70 80
 HENRWQVHIV WQVDRNRIRAT WKSLSVKHNNY VSCKARGWYF RHNYESPMPR ISSEVHIPLC DARLVITTYW GLHTGERDWH
 ARV 2 I K K I T V K K
 LAV MAL K H K K K R K V VR Q K E
 LAV ELI K K HA E K E

LAV BRU 90 100 110 120 130 140 150 160
 LCQCVSIEUR KKRYSTQVDP ELADQLINLY YFDCFSDSAI RKALLCHIVS PRCEYQAGUN KVCSLQYLAL AALITPKKIK
 ARV 2 A K G H E KN I YR D T A TR
 LAV MAL H Q L D C H E Q I I T A TR
 LAV ELI R R C H E I D T A Q

LAV BRU 170 180 190
 PPLPSVTKLT EDRUNKPQKT KCHRGSHTHN GH
 ARV 2 K Q R
 LAV MAL R Q R
 LAV ELI R

R

LAV BRU 10 20 30 40 50 60 70 80
 HEQAPEDQCP QREPHNEUTL ELLEELKNEA VNUFPRIULN GLCQHIYETY GDTVAGVEAI INILQLLFI HFNIGCHSR
 ARV 2 Y R Q S Y S Q
 LAV MAL A Y A A E V Q
 LAV ELI A Y A S S Q

LAV BRU 90
 IGVYQNRAR -NGASRS
 ARV 2 II R
 LAV MAL I R - S
 LAV ELI IIR - S

S (tat)

LAV BRU 10 20 30 40 50 60 70
 HEPVDPRLRP WKNPGSQPT ACTTCYCKKC CFHCQVCFTT XALGISYGRK KRPQRNRPQ CSQTHQVSLS KQ
 ARV 2 N R UN YA R C D A
 LAV MAL D N H R P NK Y H I C H A DP P E
 LAV ELI D N H R P NK H Y P LH C C A PIP

FIG. 3B

FIG. 3C

POL

LAV BRU	10	20	30	40	50	60	70	80
ARV 2	FFREDLAFQ	GKAREFSSEQ	TRANSTPSS	EQTRANSPTR	RELQVWGRDH	NSLSZACADR	QCTVSFHFPPQ	ITLVQRPLVT
LAV HAL	H P	P	-----S	-----S	R G -	KT T E	I S	V
LAV ELI	H P	G L P K	-----S	-----S	R -	P KT E		A
LAV BRU	90	100	110	120	130	140	150	160
ARV 2	IKIGCQLKEA	LLDTGADDIV	LEEMSLPGRW	KPKHLCGICG	FIKVRQYDQI	LIEICGHNKAI	CTVLVGPFPV	NIICGNLLTQ
LAV HAL	R		N K		PV	K	I	M
LAV ELI	VRV		IN K		P	Q		
LAV BRU	170	180	190	200	210	220	230	240
ARV 2	IGCTLNFPIS	PIETVPVKLK	PGHDGPKVKQ	UPLTEKIKK	LVEICTENEX	ECKISKICPE	NPYNTPVFAI	KKKDSTKVRK
LAV HAL			R		T KD	L		I
LAV ELI					T D	R		
LAV BRU	250	260	270	280	290	300	310	320
ARV 2	LVDFRELNR	TQDFMEVQLG	IPHPAGLKKK	KSVTVLVDVGD	AYFSVPLDED	FRKYTAFTIP	SINNETFCIR	YQVWVLPQGV
LAV HAL	K				K			
LAV ELI								
LAV BRU	330	340	350	360	370	380	390	400
ARV 2	KGSPAIFQSS	HTXILEPFRK	QNPDIIVIVQY	HDDLYVGSOL	EICQUNTKIE	ELRQULLRUG	LTPDKKHQK	EPFFLWNGYE
LAV HAL			T K E			E K F		
LAV ELI			EN			K E F R		
LAV BRU	410	420	430	440	450	460	470	480
ARV 2	LHPDKWTVQP	IVLPEKDSWT	VNDIQKLCKK	LNWASQIYFG	IKVHQLCKLL	RGTKALTEVI	PLTEEALEEL	AENREILKEP
LAV HAL	H		A		K			
LAV ELI	S K E	Q D E	N ER		K	A	DIV A	
LAV BRU	490	500	510	520	530	540	550	560
ARV 2	VHCVYYDPSK	DLIAETIQKQ	QCQWTYQIVQ	EPFKHLKTKK	YARTGANTH	DVKQLTEAVQ	KITTESIVIV	CKTPKFKLP1
LAV HAL	E	V			H	VS		I
LAV ELI			H	QY	IXS	A	R S	R R

FIG. 3D

LAV BRU	570	580	590	600	610	620	630	640
ARV 2	QKEIWEIWT	EYUQATWIPE	WEFVNTPPV	KLWYQLEKEP	IVGAEIIFYVD	GAASRETKLG	KAGYVINKRG	QKVVILLITTT
LAV HAL	A H				N		D	SIA
LAV ELI	A			T		N K	D	S E
					I	N	D	P
LAV BRU	650	660	670	680	690	700	710	720
ARV 2	HQKTELQAIN	LALQDSGLEV	MIYVDSQYAL	GIQQAQPDXS	ESELVHQILE	QIIKKKKVYL	AWVPANKGIC	GHEQVOKLVS
LAV HAL					S			
LAV ELI	K	S			I	Q D	S	
LAV BRU	730	740	750	760	770	780	790	800
ARV 2	AGIRKVLFLD	GIDKRAQDENE	KYHSNURANA	SDPHLPFYVA	KEIVASCDXC	QLKGEAHICQ	VDCSPGIVQL	DCTHLECKVI
LAV HAL	S	E						I
LAV ELI	Q	E	N	I				I
LAV BRU	810	820	830	840	850	860	870	880
ARV 2	LVAVNVASCY	IEAEVIPAET	CQETATVFLK	LACRNPVKTI	HTDHGSHFIS	ITVKAACWNA	GIXQEFCIPY	NPQSQGVVES
LAV HAL	I		I	VV	AA	N		
LAV ELI				VV	AA			
LAV BRU	890	900	910	920	930	940	950	960
ARV 2	HNKELKKIIC	QVRDQAENLK	TAVQMAVPIH	NFXRKGCGIC	YSAGERIVDI	LATDIQTKEL	QKQITKIQNF	RVYYRDSRDP
LAV HAL	N				I M			KK
LAV ELI		E		RR	I		I	U
LAV BRU	970	980	990	1000	1010			
ARV 2	LVKGPAKLLV	KGECAVVIQD	NSDIKVVPAR	KAKIIRDYCK	QMACDDCVAS	RQDED		
LAV HAL	I				G C			
LAV ELI	I		K	V				

ENV
 LAV BRU
 ARV 2
 LAV MAL
 LAV ELI

10
 DRVR---EKY QHLVRGKXU GTHLLGILNI CSATEKLVUT VYGVGVVKE ATTLFCASD AKAYDIEVRN VVATHACVPT
 K GTRRN
 REIQRN NV ---H H T IA D
 ARGIERND MW K ---I T ADM

20
 ---L H
 ---H H T IA D
 ---I T ADM

30
 SP

40
 OMP

50
 60
 70
 80

90
 DPHPPQEVVLV NVTFENFUMK NDNVEQNHED IISLVQSLK PCVKLTPLCV SLKCTDL-GN AITNSSNMN SSSGENHME-
 C
 IE E C N Q
 IA E

100
 110
 120
 130
 140
 150
 160

170
 KCEIKHCSFN ISTSIRCKVQ KEVAFYKLD IIPIDNDTIS ---YLTIS CNTSVITQAC PKVSFEPIPI MYCAPACFAL
 T D I H L RH VV AS T TNYTH R IH R T D
 V TPVGS D R - T N LVQ DSDN ---S R IN A
 ---H VT VLKD K QV L R V SSI -NSTN R IN A

180
 190
 200
 210
 220
 230
 240

250
 LKCHNKTFNG TGPCTHVSIV QCTHICIRPVV STQLLLNGSL AEEVIVISA HFTDHAKTII VQLHQSVIEM CTRPHUNHTR
 K
 D X EI K K
 RD K

260
 270
 280
 290
 300
 310
 320

330
 SIKIQGPCR AFVTIGK-IG NHRQAHCHIS RAKVNATLKQ IASKLREQFC NNKT-IIPKQ SSCGDPEIVT HSFHCGCEFF
 Y -- H Y AI DI K Q M E VK -V N M R
 G HF-- Q LY T I-V DI R Y T M ETE DK Q V V GSLL- - K NS T R
 RTP -- L Q SLY TRS-AS IIC Q SK Q V R GTLL- - I K P T

340
 350
 360
 370
 380
 390
 400

410
 YCNSTQLFNS TWFNSTVSTE CSNNTGSDT IYLPCHIKQF INHNQEVCKA NYAPPISCQI ACSSNITGLL LYRDCGHN--
 T N ---RLM HTEG K M I I C S
 TSK Q NCARL- - S STGS I KT A V N L I USSD
 TSG NI A MNI TES NSTNTM Q I K VAGH- I ZRN L I --

420
 430
 440
 450
 460
 470
 480

490
 HUCSEIFRPG CGDHRDHURS ELYKYKVVKI EPLGVAPTKA KRRVVQREKR AVGI-CALFL CFLCAACSTH GARSHILTVQ
 T DT V I
 SDN TL R
 STN T Q

500
 510
 520
 530
 540
 550
 560

TMP

V L
 A L
 V

FIG. 3E

FIG. 3F

LAV BRU 570 580 590 600 610 620 630 640
 ARQLLSCTIVQ QQNHLNATE AQNHLLQITV WGIKQLQARI LAVERYLKDQ QLLGIVGCSG KLICTTAVPV MASUSHKSLE
 ARV 2
 LAV MAL
 LAV ELI

LAV BRU 650 660 670 680 690 700 710 720
 QIUHHNTVKE WDREINMYTS LINSLESQ NQQRKEQEL LEIDKMASLV HUFNITHVLV YIKIFIMIVG CLVGLRIVFA
 ARV 2
 LAV MAL
 LAV ELI

LAV BRU 730 740 750 760 770 780 790 800
 VLSIVNRVQ CYSPLSFQTH LPTPRCP-DR PEGIEECCE NDRDSIRLV NCSLALINDD LNSLCFSYH RLKOLLIVT
 ARV 2
 LAV MAL
 LAV ELI

LAV BRU 810 820 830 840 850 860 870
 RIVELLGRG VEALKYUHL LQYUSQELKN SAVSLLNATA IAVAGCTDER IEVVQGAERA IRHIPRIRIQ GLERILL
 ARV 2
 LAV MAL
 LAV ELI

F

LAV BRU 10 20 30 40 50 60 70 80
 .MGCKWSKSSV VGMPTVBERM H----RAEPA ADGVGAASH- ----DLEKUC AITSSNTAAT HAACAVLEAQ EE-EZVGFPV
 ARV 2
 LAV MAL
 LAV ELI

LAV BRU 90 100 110 120 130 140 150 160
 TPQVPLRPHT YKAAVDLSNF LKEXGGLGL INSQRQDIL DLVIYHTQCY FPDVQNYTPG PCVRYPLTFG WCYKLVPEP
 ARV 2
 LAV MAL
 LAV ELI

LAV BRU 170 180 190 200 210
 DKVEEANKGE MTSLSHPVSL HCHDDPEREV LEWRFDLSRLA FHNVARELHP EYFANC
 ARV 2
 LAV MAL
 LAV ELI

FIG. 4A

A	LAVbru vs.	GAG		POL		ENV					
						Total	OMP		TMP		
A	HTLV-3 USA	512 0/0	0.8	1015 0/0	1.3	856 5/0	1.4	507 5/0	1.6	349 0/0	1.1
		502 12/2	3.4	1003 12/0	3.1	855 17/11	13.0	505 17/10	14.3	350 0/1	11.2
	LAVeli Zaire	500 13/1	9.8	1002 13/0	5.5	853 22/14	20.7	504 22/14	25.3	349 0/0	13.8
		505 14/7	12.0	1002 13/0	7.7	859 13/11	21.7	509 13/10	26.4	350 0/1	14.9
B	LAVeli vs.										
		LAVmal	505 1/6	10.8	1002 0/0	8.4	859 13/11	19.8	509 8/13	23.6	350 0/1

FIG. 4B

A LAVbru vs.	orf F		central region				
			orf Q	orf R	orf S		
HTLV-3 USA	206 0/0	1.5	192 0/0	0	80 0/0	nd	2.5
ARV-2 USA	210 0/4	12.6	192 0/0	97 0/1	81 0/1	9.4	15.0
LAVeli Zaire	206 1/1	19.4	192 0/0	96 0/0	80 0/0	11.5	27.5
LAVmal Zaire	209 2/5	27.0	192 0/0	96 0/0	80 0/0	10.4	23.8
B LAVeli vs.							
LAVmal	208 3/6	22.5	192 0/0	12.0	96 0/0	6.3	11.3

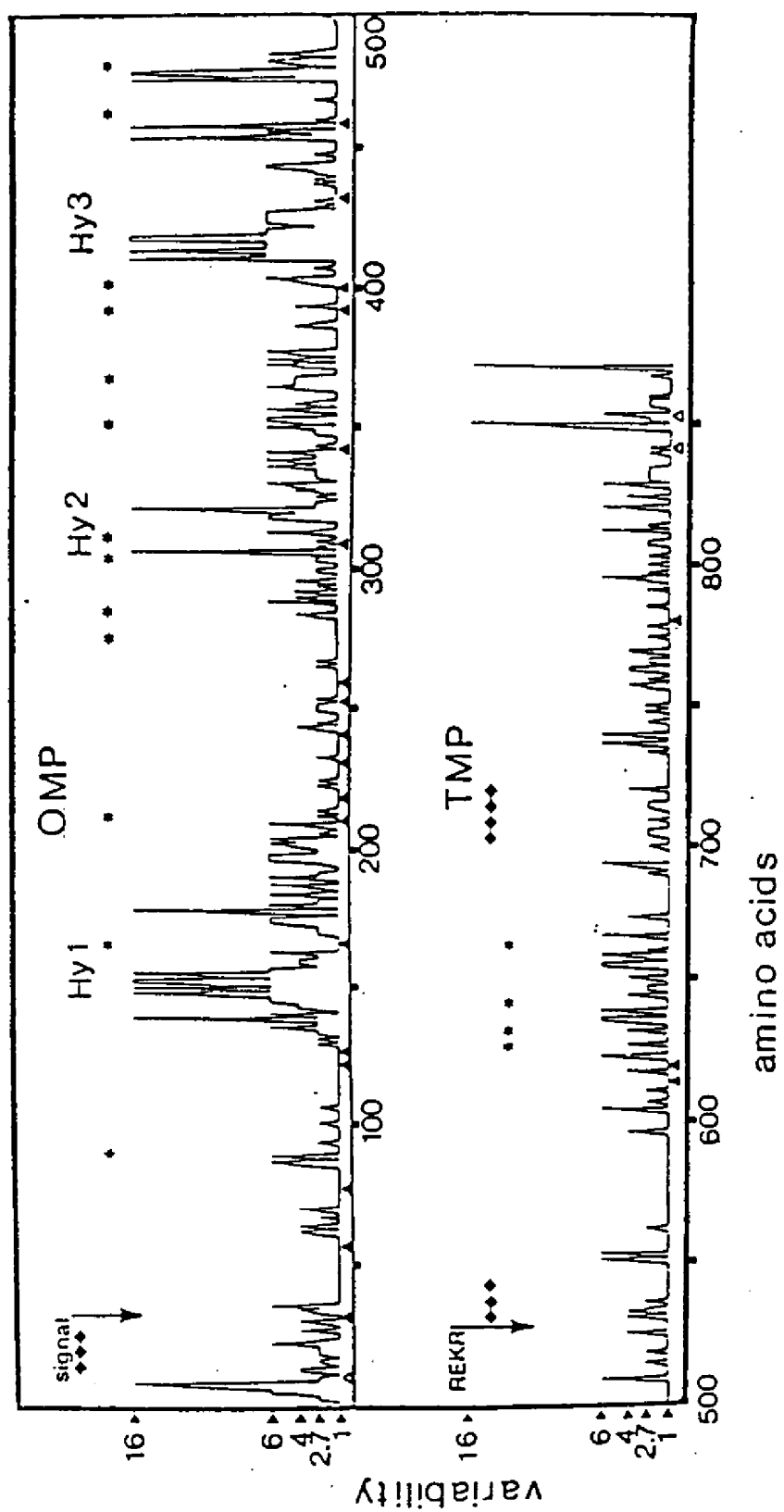


FIG. 5

02.

[illegible]

Q	H	L	N	M	A	166	ACC	116	C1C
Q	R	M	M	M	G			M	M
Q	H	M	M	A	166	ACC		ATB	ATB
Q	H	M	M	M	G			I	M
Q	H	M	M	A	166	ACC		ACC	ATB

L	X	C	T	D	L	G	A	T	N	T	N	S	S	M	I	N	S	S	S	G	C	M	N	M	C	X	G	C	A	G	A	A	160	
TA	AA	TC	ACT	GAT	TTC	-	GGG	AA	CC	ACT	AA	ACC	AA	ACT	AGT	ACC	AA	ACT	AGT	AGT	ACC	GGG	CAA	ATC	ATC	ATC	GGC	-	AAA	CGA	GAG	ATA		
L	U	C	T	D	L	G	K	A	T	N	T	H	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
TA	AA	TC	ACT	GAT	TTC	-	GGG	AA	CC	ACT	AA	ACC	AA	ACT	AGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
L	H	C	T	N	V	M	G	T	A	V	N	G	T	N	A	G	S	N	R	T	N	A	L	L	K	M	C	I	V	G	C	A	160	
TA	AA	TC	ACT	GAT	TTC	-	GGG	AA	CC	ACT	AA	ACC	AA	ACT	AGT	AGT	ACC	AA	ACT	AGT	AGT	ACC	GGG	CAA	ATC	ATC	ATC	GGC	-	AAA	CGA	GAG	ATA	
L	A	N	C	T	S	D	C	-	L	M	N	M	G	C	T	A	G	N	T	V	T	T	I	C	A	G	-	-	-	-	-	-	-	-
TA	AA	TC	ACT	GAT	TTC	-	GGG	AA	CC	ACT	AA	ACC	AA	ACT	AGT	AGT	ACC	AA	ACT	AGT	AGT	ACC	GGG	CAA	ATC	ATC	ATC	GGC	-	AAA	CGA	GAG	ATA	

[illegible][illegible]

n10										n70										n20																													
M	S	I	O	L	F	M	S	I	M	S	I	E	G	S	M	H	I	E	G	S	D	I	M	S	I	O	L	F	M	S	I	M	S	I	E	G	S	M	H	I	E	G	S	D	I				
I	ANT	TCA	ACA	CTG	TTT	ANT	AGT	ACT	TGG	TTT	ANT	AGT	ACT	TGG	TTT	ANT	AGT	ACT	TGG	TTT	ANT	AGT	ACT	TGG	I	ANT	TCA	ACA	CTG	TTT	ANT	AGT	ACT	TGG	TTT	ANT	AGT	ACT	TGG	TTT	ANT	AGT	ACT	TGG	TTT	ANT	AGT	ACT	TGG
M	I	I	O	L	F	M	M	I	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	I	I	O	L	F	M	M	I	M	M	M	M	M	M	M	M	M	M	M	M	M					
T	ANT	ACA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	-	-	-	-	-	-	-	-	-	-	-	-	T	ANT	ACA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	-	-	-	-	-	-	-	-	-	-	-	-						
H	I	S	K	L	F	M	S	I	M	D	M	G	A	R	L	S	M	S	I	E	G	S	H	I	S	K	L	F	M	S	I	M	D	M	G	A	R	L	S	M	S	I	E	G	S				
T	ANT	ACA	TCA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	TAC	ACA	ACT	ACA	CTA	-	-	ACT	ANT	ACC	ACA	TCA	ACT	T	ANT	ACA	TCA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	TAC	ACA	ACT	ACA	CTA	-	-	ACT	ANT	ACC	ACA	TCA	ACT		
M	T	ANT	ACA	TCA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	ANT	ACA	TCA	TGG	ANT	I	S	A	D	M	M	I	M	T	ANT	ACA	TCA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	ANT	ACA	TCA	TGG	ANT	I	S	A	D	M	M	I		
T	ANT	ACA	TCA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	ANT	ACA	TCA	TGG	ANT	I	S	A	D	M	M	I	T	ANT	ACA	TCA	ACA	CTG	TTF	ANT	ANT	ACA	TGG	ANT	ACA	TCA	TGG	ANT	I	S	A	D	M	M	I				

[illegible]

LAV.ELI

→R
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1400

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1600

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1700

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2000

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2100

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2200

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3400

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3500

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3600

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3700

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3800

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3900

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4200

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4300

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5500

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5600

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5800

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5900

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6100

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6200

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6300

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6400

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LAV.MAL

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 5300
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 5400
 ArgAsnGlySerSerArgSer
 MetAspProValAspProAsnLeuGluProTrpAsnHisProGlySerGlnProArg
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 ThrProCysAsnLysCysTyrCysLysLysCysCysTyrHisCysGlnMetCysPheIle
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 5500
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 GlnGlyAsnGlnAlaHisGlnAspProLeuProGluGln
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 5600
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 5700
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 5900
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 6000
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 6100

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6200

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6300

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6400

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6500

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6600

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6700

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6800

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6900

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7000

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7200

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7300

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7400

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7500

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7600

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7700

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7800

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7900

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8000

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8100

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8200

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8500

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8700

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9000

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