

Amino Acid Sequence of Ranibizumab/Bevacizumab Fab Heavy Chain

	10	20	30	40	50	60
→V _H	EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNWRQAPGKGLEWVGWINTYTCEPTY					
	-----T-N-----					
	70	80	90	100	110	120
	AA DFKRR FTFSLDTSKSTAYLQMNSLRAEDTAVYYCAKYPYYYGTSHWYFDVWGQCTLV					
			Y-site		G-site	
	-----H-S-----					
	130	140	150	160	170	180
→C _H	VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL					
				G-site		
	190	200	210	220	230	
	QSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHL					

Amino Acid Sequence of Ranibizumab/Bevacizumab Fab Light Chain

	10	20	30	40	50	60
→V _L	DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIIYFTSSLHSGVPS					
	-----M-----					
	70	80	90	100	110	120
	RFSGSGSGTDFTLTISSLQPEDFATYYCQGYSTVPWTFQGGTKVEIKRTVAAPSVFIFPP					
			Y-site	G-site		
	-----→C _L -----					
	130	140	150	160	170	180
	SDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT					
				G-site		
	190	200	210			
	LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC					
			G-site			

FIG. 1

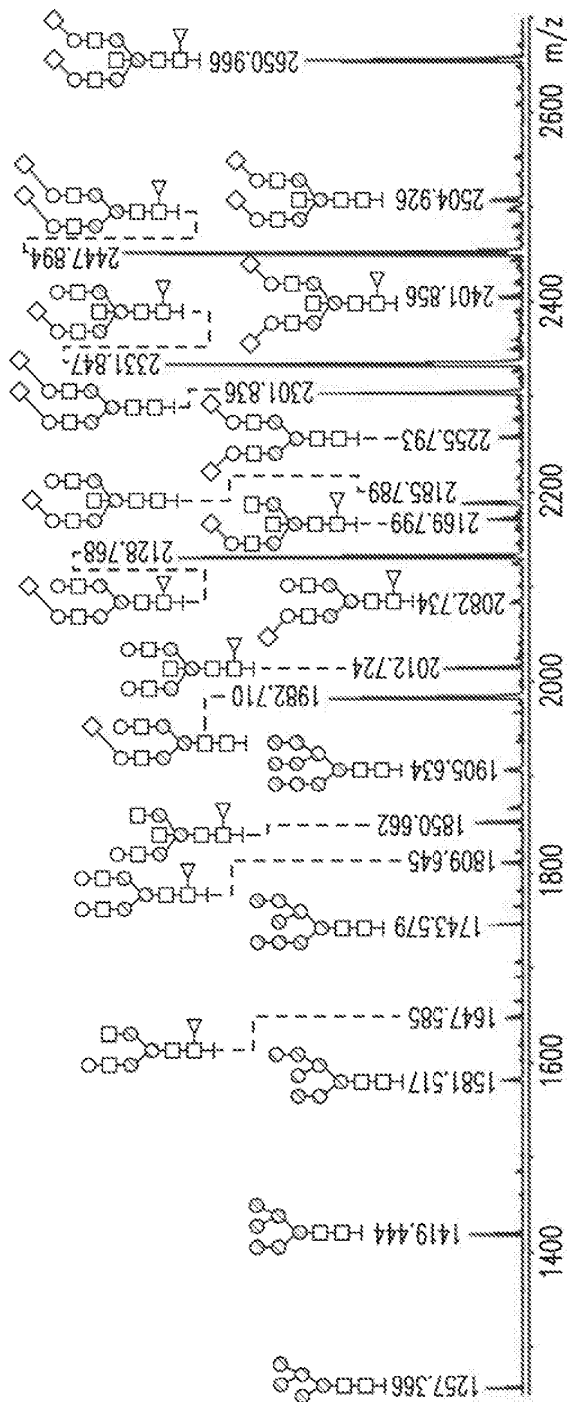


FIG. 2

Amino Acid Sequence of Hyperglycosylated Ranibizumab/Bevacizumab Fab Heavy Chain

10	20	30	40	50	60
→V _H					
EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNWVRQAPGKLEWVGWINTYTGPTY					
-----T-N-----					
70	80	90	100	110	120
AADEKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAKYPYYGTSHWYFDVWGQGTNVT					
			Y-site		G-site
-----H-S-----L-----					
130	140	150	160	170	180
→C _H					
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALITSGVHTFPAVL					
-----G-site-----					
190	200	210	220	230	
QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHL					

Amino Acid Sequence of Hyperglycosylated Ranibizumab/Bevacizumab Fab Light Chain

10	20	30	40	50	60
→V _L					
DIQLTQSPSSLSASVGDRTITCSASQDISNYLNWYQQKPGKAPKVLIIYFTSSLHSGVPS					
-----M-----					
70	80	90	100	110	120
RFGSGSGTDFTLTISSLQPEDFATYYCQGYSTVPWTFGGTKKVEIKRTVAAPSFIFFP					
			Y-site	G-site	→C _L

130	140	150	160	170	180
SDEQLKSGTASVCLLNFPYFREAKVQWKVDNALQSGNSNIESVTEQDSKDYSLSSLT					
			G-site		
-----Q-----					
190	200	210			
LSKADYEKHKVYACQNVTHQGLSSPVTKSFNRGEC					
			G-site		
-----E-----					

FIG. 3

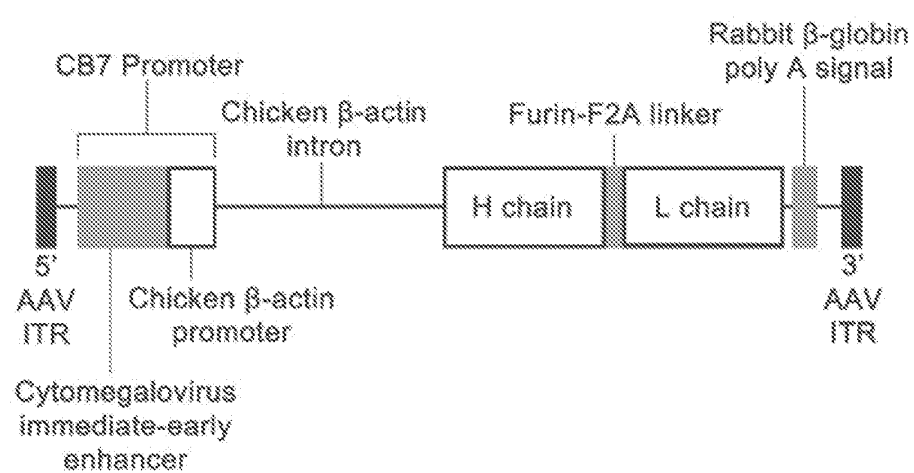


FIG. 4

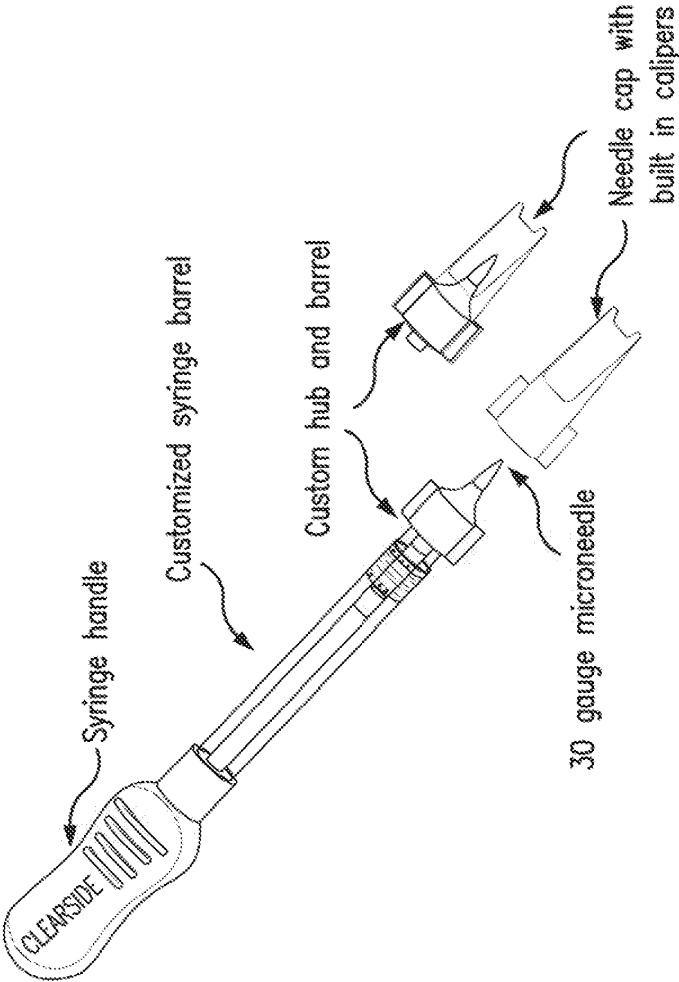


FIG. 5

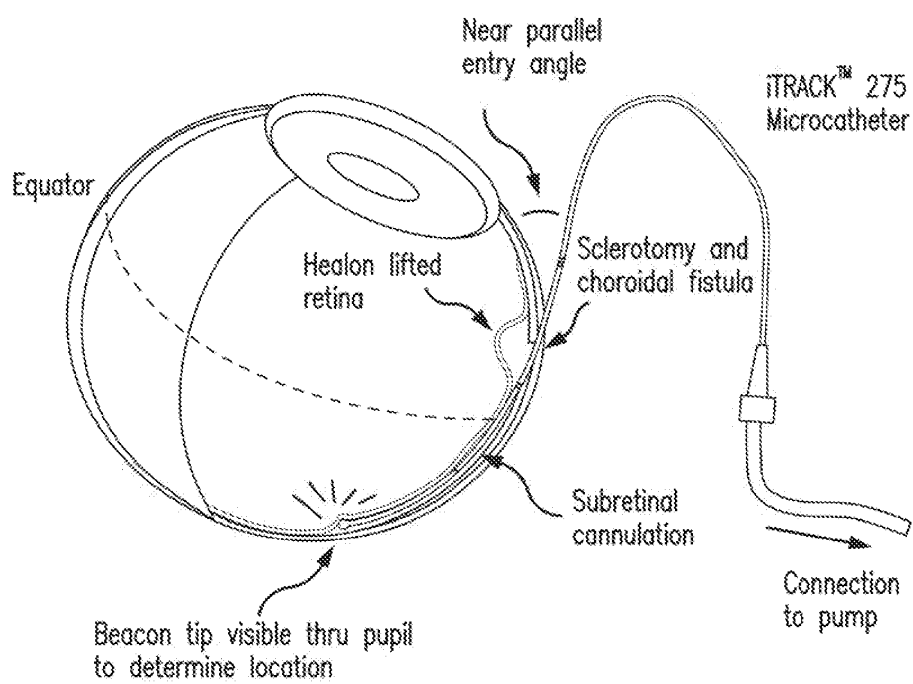


FIG. 6

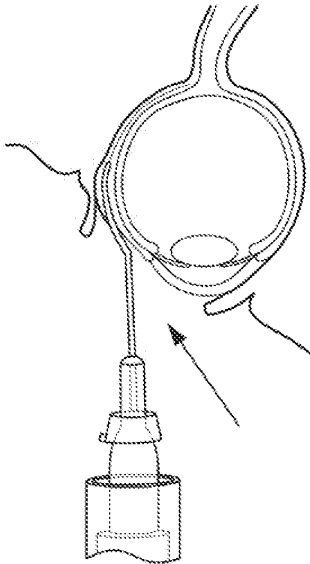


FIG. 7B

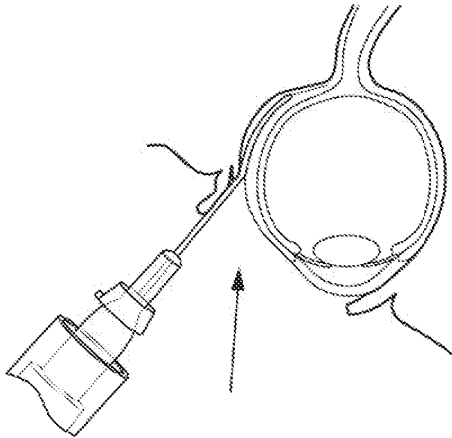


FIG. 7D

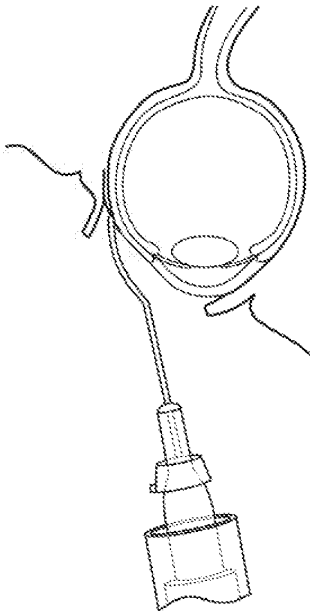


FIG. 7A

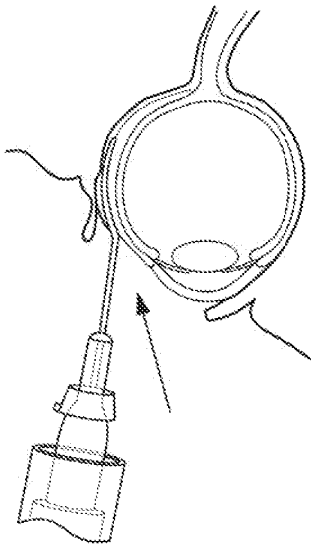


FIG. 7C

VP1₁₋₇₃₆→

AAV1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQCKQDDGRGLVLPGYKYLGPFFNGLD 60
 AAV2 MAADGYLPDWLEDNLSEGIROWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFFNGLD 60
 AAV3-3 MAADGYLPDWLEDNLSEGIREWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPFGNGLD 60
 AAV4-4 -MTDGYLPDWLEDNLSEGIREWALKPGAPKPKANQQHQDNARGLVLPGYKYLGPFGNGLD 59
 AV5 MSFVDHPPDWLEE-VGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGPFGNGLD 59
 AAV6 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQCKQDDGRGLVLPGYKYLGPFFNGLD 60
 AAV7 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQCKQDNGRGLVLPGYKYLGPFFNGLD 60
 AAV8 MAADGYLPDWLEDNLSEGIREWALKPGAPKPKANQCKQDDGRGLVLPGYKYLGPFFNGLD 60
 hu31 MAADGYLPDWLEDNLSEGIROWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFGNGLD 60
 hu32 MAADGYLPDWLEDNLSEGIROWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFGNGLD 60
 AAV9 MAADGYLPDWLEDNLSEGIREWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPFGNGLD 60
 SUBS -STVDHP-----ETVG--V-QFLK-QA-P-K---PAERKK-DG-----N----F-----
 MF L D E V P QS
 G Q R

AAV1 KGEFVNAADAAALEHDKAYDQQLKAGDNFYLRYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
 AAV2 KGEFVNEADAAALEHDKAYDQQLDSGDNFYLKYNHADADEFQERLKEDTSFGGNLGRAVFQ 120
 AAV3-3 KGEFVNEADAAALEHDKAYDQQLKAGDNFYLKYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
 AAV4-4 KGEFVNAADAAALEHDKAYDQQLKAGDNFYLKYNHADADEFQERLQEDTSFGGNLGRAVFQ 119
 AV5 RGEFVNADEVARCHDSISYNEQLEAGDNFYLKYNHADADEFQERLKADDTSGGNLGRAVFQ 119
 AAV6 KGEFVNAADAAALEHDKAYDQQLKAGDNFYLKYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
 AAV7 KGEFVNAADAAALEHDKAYDQQLKAGDNFYLRYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
 AAV8 KGEFVNAADAAALEHDKAYDQQLQAGDNFYLRYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
 hu31 KGEFVNAADAAALEHDKAYDQQLKAGDNFYLKYNHADADEFQERLKEDTSFGGNLGRAVFQ 120
 hu32 KGEFVNAADAAALEHDKAYDQQLKAGDNFYLKYNHADADEFQERLKEDTSFGGNLGRAVFQ 120
 AAV9 KGEFVNAADAAALEHDKAYDQQLKAGDNFYLKYNHADADEFQERLKEDTSFGGNLGRAVFQ 120
 SUBS R-----E--EV-R---IS-NE--DS-----R-----QK-QD-----K-----
 R R E AG
 Q

VP2₁₃₈→ [HVR1-7]

AAV1 AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTCQQPAKKRLNFGQTGDS 179
 AAV2 AKKRVLEPLGLVEEPVKTAPGKKRPVENSPV-EPDSSSGTSGKACQQPAKKRLNFGQTGDA 179
 AAV3-3 AKKRVLEPLGLVEEAAKTAPGKYGAVDQSPQ-EPDSSSGVGKSCQPAKKRLNFGQTGDS 179
 AAV4-4 AKKRVLEPLGLVEQAGETAPGKKRPLIESPQ-QPDSSSGIGKKGKQPAKKRLVFEDETGA 178
 AV5 AKKRVLEPFGLVEEGAKTAPGKKRIDDRFF-----KRRKARTEEDSKPSTSSDA 168
 AAV6 AKKRVLEPFGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTCQQPAKKRLNFGQTGDS 179
 AAV7 AKKRVLEPLGLVEEGAKTAPAKKRPVESPQSPDSSSGIGKKGKQPAKKRLNFGQTGDS 180
 AAV8 AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQSPDSSSGIGKKGKQPAKKRLNFGQTGDS 180
 hu31 AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSSAGIGKSGSQPAKKRLNFGQTGDT 179
 hu32 AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSSAGIGKSGSQPAKKRLNFGQTGDT 179
 AAV9 AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSSAGIGKSGAQPAKKRLNFGQTGDT 179
 SUBS -----V----F----QGGE---TG-GIDDRF-V-S-----S-T--KKQARTREKSVPEDETGA
 I PV A ALIP Q T V T K E D K STSS S
 E A S
 R A

FIG. 8

VP3₂₀₃→

AAV1 ESVPD-PQPLGEPPATPAAVGPTTMSAGGGAPMADNNEGADGVGNASGNWBCDSTWLGDR 238

AAV2 DSVPD-PQPLGQPPAAPSGGLGTNTMATSSGAPMADNNEGADGVGNSSGNWBCDSTWLGDR 238

AAV3-3 ESVPD-PQPLGEPPAAPTSLGSSNTMASGGGAPMADNNEGADGVGNSSGNWBCDSQWLGD 238

AAV4-4 GDGP-----PQGSTSGAMS--DDSEMRAAAGGAAVEGGQSGADGVGNASGDWHCDSTWSEGH 232

AV5 EAGPSGSSQLQIFAQPASSLGDITMSAGGGGFLGDNNQSGADGVGNASGDWHCDSTWLGDR 226

AAV6 ESVPD-PQPLGEPPATPAAVGPTTMSAGGGAPMADNNEGADGVGNASGNWBCDSTWLGDR 238

AAV7 ESVPD-PQPLGEPPAAPSSVGSGTVAAGGAPMADNNEGADGVGNASGNWBCDSTWLGDR 239

AAV8 ESVPD-PQPLGEPPAAPSGVGPNTMAAGGGAPMADNNEGADGVGSSGNWBCDSTWLGDR 239

hu31 ESVPD-PQPIGEPPAAPSGVGSITMASGGGAPVADNNEGADGVGSSGNWBCDSQWLGD 238

hu32 ESVPD-PQPIGEPPAAPSGVGSITMASGGGAPVADNNEGADGVGSSGNWBCDSQWLGD 238

AAV9 ESVPD-PQPIGEPPAAPSGVGSITMASGGGAPVADNNEGADGVGSSGNWBCDSQWLGD 238

SUBS GDG-S-S-QLQQTSGTMSLDENEVRAAA-GAMGEGGQ-----NA--D-----T-MEGH

DA E S AQPATA AG ST S LV S

I -- DT A

TD

S

VP3

AAV1 VITTSTRTWALPTYNNHLYKQIS-SASTGASNDNHFGYSTPWGYFDENRFCHFSPRDW 297

AAV2 VITTSTRTWALPTYNNHLYKQIS--SQSGASNDNHFGYSTPWGYFDENRFCHFSPRDW 296

AAV3-3 VITTSTRTWALPTYNNHLYKQIS--SQSGASNDNHFGYSTPWGYFDENRFCHFSPRDW 296

AAV4-4 VTTTSTRTWLPTYNHLYKRLG-----ESLQSNNTYNGFSTPWGYFDENRFCHFSPRDW 287

AV5 VVKSTRTWLPLSYNNHLYKREIKS-GSDGGSNANAYFGYSTPWGYFDENRFCHFSPRDW 287

AAV6 VITTSTRTWALPTYNNHLYKQISSAST-GASNDNHFGYSTPWGYFDENRFCHFSPRDW 297

AAV7 VITTSTRTWALPTYNNHLYKQISS-ETAGSTNDNTYFGYSTPWGYFDENRFCHFSPRDW 298

AAV8 VITTSTRTWALPTYNNHLYKQISNGTSGCATNDNTYFGYSTPWGYFDENRFCHFSPRDW 299

hu31 VITTSTRTWALPTYNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDENRFCHFSPRDW 298

hu32 VITTSTRTWALPTYNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDENRFCHFSPRDW 298

AAV9 VITTSTRTWALPTYNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDENRFCHFSPRDW 298

SUBS -T-K-----V--S---Q-RRLGSGSQSDATQA-T-----S-W-----

V E K AATTEGL S H

G V

E A

AAV1 QRLINNNWGFRRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSUSEYQLPYVLGS 357

AAV2 QRLINNNWGFRRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356

AAV3-3 QRLINNNWGFRRPKRLSEKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356

AAV4-4 QRLINNNWGMRRPKAMRVKIFNIQVKEVTSNGETTVANNLTSTVQIFADGSSYELPYVMDA 347

AV5 QRLINNNWGFRRPSLRVXIFNIQVKEVTVDSTTTIANNLTSTVQVFTDDYQLPYVVGW 347

AAV6 QRLINNNWGFRRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSUSEYQLPYVLGS 357

AAV7 QRLINNNWGFRRPKRLSEKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSUSEYQLPYVLGS 358

AAV8 QRLINNNWGFRRPKRLSEKLFNIQVKEVTQNECTXTIANNLTSTVQVFTDSEYQLPYVLGS 359

hu31 QRLINNNWGFRRPKRLNFKLFNIQVKEVTDNNGVKTIANNTSTVQVFTDSDYQLPYVLGS 358

hu32 QRLINNNWGFRRPKRLNFKLFNIQVKEVTDNNGVKTIANNTSTVQVFTDSDYQLPYVLGS 358

AAV9 QRLINNNWGFRRPKRLNFKLFNIQVKEVTDNNGVKTIANNTSTVQVFTDSDYQLPYVLGS 358

SUBS -----M--RAMRV-I-----VQDSTT-----I-I-S-DE-E-----MDA

K S QSE E A S

S

FIG. 8 (continued)

Sheet 10 of 14

HVR4

AAV1 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 414
 AAV2 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 413
 AAV3-3 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 413
 AAV4-4 GQGCCLPPFPADVFMI PQYGYCGLVTGNTSQQQTD:NAFYCLEYFPSSQMLRTGNNFEITY 407
 AV5 GTEGCLPAFFPQVFTLPQYGYATLLNRD-NTENPTESPSSFFCLEYFPSSKMLRTGNNFEITY 406
 AAV6 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 414
 AAV7 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 415
 AAV8 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 416
 hu31 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 415
 hu32 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 415
 AAV9 AHQGCCLPPFPADVFMI PQYGYLTLLNG----SQAVGRSSFYCLEYFPSSQMLRTGNNFTFSY 415
 SUBS GQQ-S--A--PQ--TL-----CG-VND--GNPTD-NA-F-----EIT--
 T N V A T Q Q E T
 R E S

HVR5

AAV1 TFEEVVFHSSSYAHSQSLDRLMNPFLIDQYLYYLNRTO-NQSSSAQNKDILLFSGSPAGMSV 473
 AAV2 TFEDVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTO-TFSETTOSRLQFSQAGASDIRD 472
 AAV3-3 TFEDVVFHSSSYAHSQSLDRLMNPFLIDQYLYYLNRTOQTTSQTTNQSRLFSQAGSPQMSL 473
 AAV4-4 SFEEKVVFHSSMYAHSQSLDRLMNPFLIDQYLYLNRTOQTTSQTTNQSRLFSQAGSPQMSL 467
 AV5 NFEEVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTO-NQSSSAQNKDILLFSGSPAGMSV 473
 AAV6 TFEDVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTO-TFSETTOSRLQFSQAGASDIRD 472
 AAV7 SFEDVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTOQTTSQTTNQSRLFSQAGSPQMSL 473
 AAV8 TFEDVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTO-TFSETTOSRLQFSQAGASDIRD 472
 hu31 EFENVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTOQTTSQTTNQSRLFSQAGSPQMSL 473
 hu32 EFENVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTOQTTSQTTNQSRLFSQAGSPQMSL 473
 AAV9 EFENVVFHSSSYAHSQSLDRLMNPFLIDQYLYLNRTOQTTSQTTNQSRLFSQAGSPQMSL 473
 SUBS T--D-----MF-----A--V----WGFNR-QTNTS--ACTKRTQ-TQGSAAATFSN
 S E QS NSTPT TQMSDVN NKNL QGYRD
 N K V TG Q T AE L YRLR TRI L
 A RG G GS E
 ND

HVR6 HVR7 HVR8

AAV1 QFKNWLPFGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYHLNGRDSLVNPGFAMASHK 528
 AAV2 QSRNWLPFGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYHLNGRDSLVNPGFAMASHK 527
 AAV3-3 QARNWLPFGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYHLNGRDSLVNPGFAMASHK 528
 AAV4-4 FKKNWLPFGPSIKQGGFSTANQNYKIPATGSDSLIKYETHSTLDGRWCALTPOPPMATAG 527
 AV5 TYKNWFPQGMGRTQGNWLGSGVN-----RASVSAFATNRMELEGASYQVFPQPGMTNN 514
 AAV6 QFKNWLPFGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYHLNGRDSLVNPGFAMASHK 528
 AAV7 QAKNWLPFGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYHLNGRDSLVNPGFAMASHK 528
 AAV8 QAKNWLPFGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYHLNGRDSLVNPGFAMASHK 528
 hu31 QGRNYIPGFSYRQQRVSTTVTON-----NNSEFAWPCASSWALNGRDSLVNPGFAMASHK 528
 hu32 QGRNYIPGFSYRQQRVSTTVTON-----NNSEFAWPCASSWALNGRDSLVNPGFAMASHK 528
 AAV9 QGRNYIPGFSYRQQRVSTTVTON-----NNSEFAWPCASSWALNGRDSLVNPGFAMASHK 528
 SUBS FAK-WL---CIKT-GWNLGSGV-----TG-DSLIKYETHST-D-ASYQVF-QTPGMTAG
 TP F MG F K AND RA NYTFATNRME E D ALT VN NN
 K F L KA V P TAG KYN W II I
 Y LD S H E A
 S T

FIG. 8 (continued)

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      -----HVR9-----
AAV1  DDEDEKFFPMSCVMIPOKESA--CASNTALD-NVMITDEEEIKATNPVATERPCTVAVNLPQ 585
AAV2  DDEEKFFPQSCVLIPOKQCS--EKTHVDIE-KVMITDEEEIKATNPVATEQYQSVSTNLQ 584
AAV3-3 DDEEKFFPMHGNLIPOKEGT--TASNAELD-NVMITDEEEIKATNPVATEQYQCTVANWLPQ 585
AAV4-4 PADSKEFS-NSQLIFAGEKQN---CNTATVPG-TLIFTSEELAAATNATDIDMWGNLPQGDQ 583
AV5    LQGSNTYALENTMIFNSQAPNPOTTATYLECNMLITSESETQPVNRVAYNVGQGMATHNQ 574
AAV6  DDKDKFFPMSCVMIPOKESA--CASNTALD-NVMITDEEEIKATNPVATERPCTVAVNLPQ 585
AAV7  DDEDRFFPSSGVLIPOKTCG--TN-KTFLK-NVLMITNEEEIKATNPVATEEYGVSSNLQ 586
AAV8  DDEERFFPENGILIPCKQNA---ARDNADYS-DVMLTSEEEIKATNPVATEEYGVADNLQ 587
hu31  EGEDRFFFLSGSLIPCKQGT--GRDNVDAD-KVMITNEEEIKATNPVATESYGVQVATNHQ 585
hu32  EGEDRFFFLSGSLIPCKQGT--GRDNVDAD-KVMITNEEEIKATNPVATESYGVQVATNHQ 585
AAV9  EGEDRFFFLSGSLIPCKQGT--GRDNVDAD-KVMITNEEEIKATNPVATESYGVQVATNHQ 585
SUBS  LQGSNTYAMENTMIFANPKQN---TNTATVPG-TLIF-S-S-TQPV-ATDYDMW-NLPGGD-
      PADEK S QHQLT SESA EASKAALE-NMLM D RA R NVF TMSN L
      DDK NN V TPS AK KTY L A QG I V N
      S I N EI E S S F
      N Y R D

      -----HVR10-----
AAV1  SSSTDPATGCVHMGALPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLMGGFGLKNPPP 645
AAV2  RGNRQATADVNTQCVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLMGGFGLKHPPP 644
AAV3-3 SSNTAPTGTGVNHGALPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLMGGFGLKHPPP 645
AAV4-4 SNSNLPTVDRLTALCAVPGMVWQNRDIYQGPWAKIPHTDGHFHPSPFLIGGFGLKHPPP 643
AV5    CSTAPATGCTYNLQEIIVPGSVMERDVYLQGPWAKIPETGAHHPSPAMGGFGLKHPPP 634
AAV6  SSSTDPATGCVHVMGALPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLMGGFGLKHPPP 645
AAV7  AANTAAGTQGVNSQCALPGMVWQNRDIYQGPWAKIPHTDGNFHPSPLMGGFGLKHPPP 646
AAV8  QONTAPGCTGVNSQCALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPP 647
hu31  SAQAQAQTCGVVQNGGILPGMVWQDRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPP 645
hu32  SAQAQAQTCGVVQNGGILPGMVWQDRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPP 645
AAV9  SAQAQAQTCGVVQNGGILPGMVWQDRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPP 645
SUBS  RNSNLPTVDRLTALEAV--S--ME--I-----E-GAH-----AI-----L-N---
      ASNTA AIADYHTM V N
      QGTRD QT NH
      Q V L
      V
      S

      -----HVR11-----
AAV1  QILIKNTVPFANPFAEFSATFFASFITQYSTGQVSVIEIWELOKENSRRWNPEVQYTSNY 705
AAV2  QILIKNTVPFANPSTTFSAAKFASFITQYSTGQVSVIEIWELOKENSRRWNPEIQYTSNY 704
AAV3-3 QIMIKNTVPFANPPTTFSPAKFASFITQYSTGQVSVIEIWELOKENSRRWNPEIQYTSNY 705
AAV4-4 QIFIKNTVPFANPATTFSTFVNSFITQYSTGQVSVQIDWEIQKERSKRWNPVQFTSNY 703
AV5    MMLIKNTVPVPGNI-TSFSQVSVSSFITQYSTGQVTVMEWEHLKENSRRWNPEIQYTSNY 693
AAV6  QILIKNTVPFANPFAEFSATKFAFITQYSTGQVSVIEIWELOKENSRRWNPEVQYTSNY 705
AAV7  QILIKNTVPFANPPEVETPAKFASFITQYSTGQVSVIEIWELOKENSRRWNPEIQYTSNF 706
AAV8  QILIKNTVPFADPPTTFNQSKLNSFITQYSTGQVSVIEIWELOKENSRRWNPEIQYTSNY 707
hu31  QILIKNTVPFADPPTAFNKKLNSFITQYSTGQVSVIEIWELOKENSRRWNPEIQYTSNY 705
hu32  QILIKNTVPFADPPTAFNKKLNSFITQYSTGQVSVIEIWELOKENSRRWNPEIQYTSNY 705
AAV9  QILIKNTVPFADPPTAFNKKLNSFITQYSTGQVSVIEIWELOKENSRRWNPEIQYTSNY 705
SUBS  MMM-----G-IAAE-SDVPVS-----QMD--IK--R-----V-N---
      F SET TAA FA
      S PT
      V QS
      S

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FIG. 8 (continued)

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      -----SVRI2-----
AAV1  AKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736 (SEQ ID NO. 41)
AAV2  NKSVMVDCTVDINQVYSEPRPIGTRYLTRNL 736 (SEQ ID NO. 42)
AAV3-3 NKSVMVDCTVDINQVYSEPRPIGTRYLTRNL 736 (SEQ ID NO. 43)
AAV4-4 GQQNSLLWAPDAACKYTEPRAIGTRYLTHHL 734 (SEQ ID NO. 44)
AV5    NDPQFVDFAPDSTGEYRTTRPIGTRYLTRPL 724 (SEQ ID NO. 45)
AAV6  AKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736 (SEQ ID NO. 46)
AAV7  EKQTGVDFAVDSQQGVYSEPRPIGTRYLTRNL 737 (SEQ ID NO. 47)
AAV8  YKSTSVDFAVNTEGVYSEPRPIGTRYLTRNL 738 (SEQ ID NO. 48)
hu31  YKSNVVEFAVSTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO. 49)
hu32  YKSNVVEFAVNTTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO. 50)
AAV9  YKSNVVEFAVNTTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO. 51)
SUBS  GQQVSLWTPDAA-K-RTT-A-----HP--
      NDPQF D   SSN E T               H
      A  TG      NQ L
      E  A        T

```

FIG. 8 (continued)

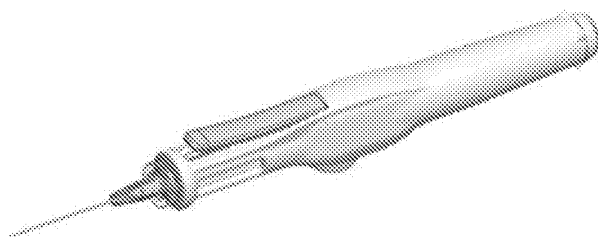


FIG. 9A

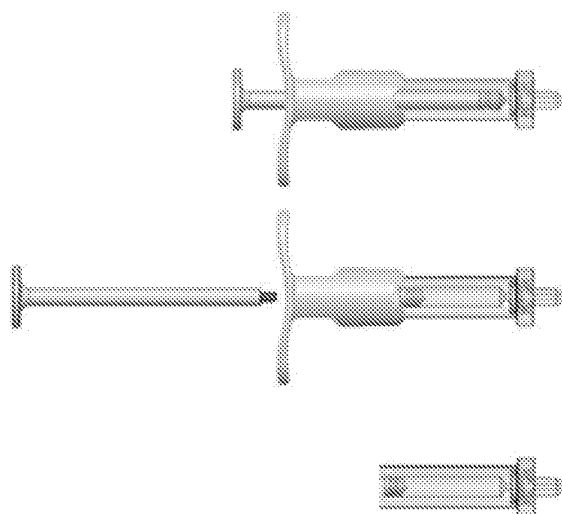


FIG. 9B

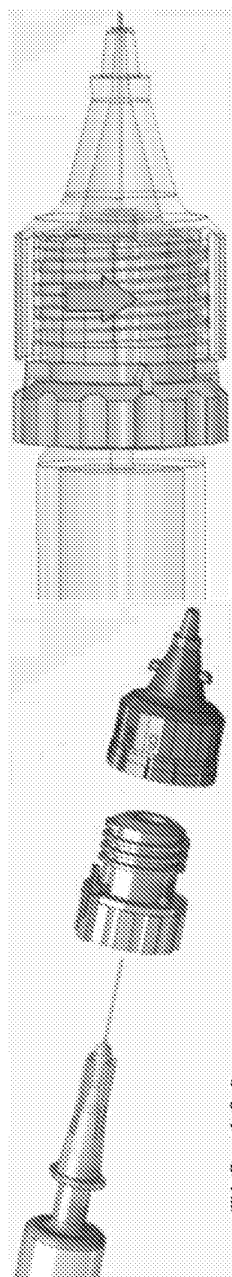


FIG. 10A

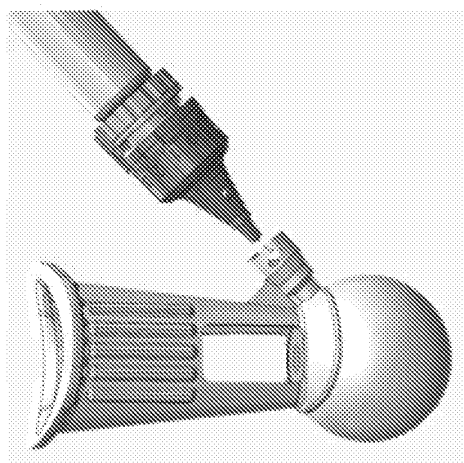


FIG. 10B