Mutations in Retroviral Genes Associated with Drug Resistance

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Introduction

Drug resistance is the inevitable consequence of incomplete suppression of HIV replication. The rapid replication rate of HIV and its inherent genetic variation have led to the identification of many HIV variants that exhibit altered drug susceptibility. The growing number of drug resistance mutations listed in this revised table stands as a testimony to the genetic flexibility of HIV. This table, updated in early 2001, lists 200 HIV-1 mutation/drug combinations, of which 179 occur in protease, 1 in integrase, 296 in RT, and 131 in Env. Although the tables are quite comprehensive, the reader should be reminded that the mutations described are predominantly found in clade B virus and not in other HIV genotypes. The revised table also includes drug resistance mutations that have been identified for SIV and FIV.

In the table the phrase "Enzyme resist" refers to inhibition assays done just with a mutated enzyme. Instead of introducing the mutations into a virus and testing the susceptibility of the mutant virus to a drug, researchers introduce the mutation(s) into the enzyme and determine their effect by running enzyme activity assays. This type of susceptibility testing does not take into account changes in other viral proteins (like Gag) that would also help confer resistance, which is the reason for distinguishing enzyme resistance from whole virus resistance. In the "Amino Acid Change" column a + means amino acids have been inserted into the sequence, while a Δ indicates a deletion. In the "Class of Drug" column the abbreviation MN stands for "Multiple Nucleoside" and refers to resistance to combinations of nucleoside RTIs. Other abbreviations used in the table are listed in a separate Abbreviations Table on page 415.

All of the information contained in these printed tables and other useful tools are available at our new Web site: `http://resdb.lanl.gov/Resist_DB`.

Acknowledgments

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Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
M 41 L	ATG⟶TTG/CTG	NRTI	AZT (zidovudine)	?	Y	4		M41L/T215Y: 60–70-fold; M41L/D67N/K70R/T215Y: 180-fold.	Larder89, Larder91, Kellam92
E 44 A	GAA⟶GCA	NRTI	3TC (lamivudine)	N	Y			Seen in NRTI-experienced patients but not in antiretroviral naïve patients.	Montes02
E 44 D	GAA⟶GAC	NNRTI	AZT (zidovudine) + 3TC (lamivudine)	N	Y	1.0		Confers moderate levels of resistance to 3TC (4 to 50-fold) when present in an AZT-resistant genetic background without diminishing AZT resistance.	Hertogs00
A 62 V	GCC⟶GTC	MN		N	Y	Nil		A62V alone has no effect, but in combination with mutations at 75, 77, 116, 151 causes multi NRTI resistance.	Iversen96, Shirasaka95
I 63 M	ATA⟶ATG	NNRTI	BHAP U-90152 (delavirdine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to delavirdine with respect to WT	Pelemans01
I 63 M	ATA⟶ATG	NNRTI	BI-RG-587 (nevirapine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 23-fold resistant to nevirapine with respect to WT	Pelemans01
I 63 M	ATA⟶ATG	NNRTI	GW 420867X	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 8-fold resistant to GW 420867X with respect to WT	Pelemans01
I 63 M	ATA⟶ATG	NNRTI	HBY 097	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 5-fold resistant to HBY 097 with respect to WT	Pelemans01

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I 63 M	ATA→ATG	NNRTI	I-EBU (emivirine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 7-fold resistant to emivirine with respect to WT	Pelemans01
I 63 M	ATA→ATG	NNRTI	UC-781	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to UC-781 with respect to WT	Pelemans01
K 65 R	AAA→AGA	NRTI	1592U89 (abacavir)	Y	N	3		K65R/L74V: 3.6-fold; K65R/M184V: 7-fold; K65R/L74V/M184V: 10.2-fold	Tisdale97
K 65 R	AAA→AGA	NRTI	ddC (zalcitabine)	Y	Y	4–10			Zhang94, Gu94
K 65 R	AAA→AGA	NRTI	ddI (didanosine)	Y	Y	4–10	ddC; PMEA; 3TC5	Infrequently observed in patients receiving ddI or ddC	Zhang94
K 65 R	AAA→AGA	NRTI	dOTC	Y	?			K65R/M184V: 4.2-fold.	Rando99
K 65 R	AAA→AGA	NRTI	DXG	Y	?	8	other dioxolane derivatives	Reverses AZT resistance in D67N/K70R/T215Y/K219Q background	Mellors96
K 65 R	AAA→AGA	NRTI	PMEA (adefovir)	Y	N	10–25			Gu95, Foli96
K 65 R	AAA→AGA	NRTI	PMPA (tenofovir)	Y	?	3.5			Cherrington97
Δ67	deletion	MN	AZT (zidovudine) + ddI (didanosine)	N	Y	AZT: 1.2, ddI: 3.8, ddC:18.0		Δ67/T69G/AZT resistance mutations: 445-fold AZT resistance. When NNRTI resistance mutations are also added, AZT resistance increases to 1,813-fold.	Imamichi00a, Imamichi00b, Imamichi01
D 67 E	GAC→GAG	MN		N	Y				Larder99
D 67 G	GAC→GGC	MN		N	Y				Larder99
D 67 G	GAC→GAG	NNRTI	(-)dOTFC	Y	?	4.5	(-)dOTFC: 5.2-fold		Richard00
D 67 N	GAC→AAC	NRTI	AZT (zidovudine)	Y	Y			D67N/K70R/T215Y/K219Q: 120-fold; M41L/D67N/K70R/T215Y: 180-fold.	Larder89, Larder91, Kellam92
D 67 S	GAC→AAC	MN		N	Y				Larder99

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S 68 G	AGT→GGT	MN		?	Y			Frequently associated with other multi-ddN resistance mutations V75I, F77L, F116Y and Q151M.	Schmit98
S 68 N	AGT→AAT	MN		N	Y				Larder99
S 68 N	AGT→AAT	MN		N	Y				Larder99
S 68 S + GGG	AGT→AAT	MN		N	Y				Larder99
S 68 S + SS	AGT→AAT	MN		N	Y				Larder99
S 68 S + SSG	AGT→AAT	MN		N	Y				Larder99
S 68 S + ST	AGT→AAT	MN		N	Y				Larder99
S 68 S + SV	AGT→AAT	MN		N	Y				Larder99
S 68 Y	AGT→TAT	MN		N	Y				Larder99
T 69 A	ACT→GCT	MN	3TC (lamivudine) + d4T (stavudine)	?	Y			Seen in one patient on 3TC + d4T combination therapy.	Lawrence99
T 69 A + SG	ACT→GCT + AGT GGT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC, 3TC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 D	ACT→GAT	MN	AZT (zidovudine) + 3TC (lamivudine)	?	Y			Seen in one patient on AZT + 3TC combination therapy.	Lawrence99
T 69 D	ACT→GAT	NRTI	ddC (zalcitabine)	N	Y	5			Fitzgibbon92
T 69 G	ACT→GGT	NNRTI	AZT (zidovudine) + ddI (didanosine)	N	Y	AZT: 1.5, ddC: 11.0, ddI: 10.0		Δ67/T69G/AZT resistance mutations: 445-fold AZT resistance. When NNRTI resistance mutations are also added, AZT resistance increases to 1,813-fold.	Imamichi00a, Imamichi00b, Imamichi01
T 69 N	ACT→AAT	MN	3TC (lamivudine) + d4T (stavudine)	?	Y			Seen in two patients on 3TC + d4T combination therapy.	Lawrence99
T 69 S + AG	ACT→AAT	MN		N	Y				Larder99
T 69 S + EA	ACT→AGT + AGA GCA	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC, 3TC and PMEA.		Seen in heavily treated patients.	Winters98

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Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
T 69 S + EE	ACT⟶AGT + AGA GCA	MN		N	Y				Larder99
T 69 S + RA	ACT⟶AGT + AGA GCA	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC, 3TC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + SA	ACT⟶AGC + AGC GCT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + SA	ACT⟶TCT + AGT GCT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + SA	ACT⟶AGT + AGC GCT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC, 3TC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + SG	ACT⟶AGT + AGT GGT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + SG	ACT⟶AGT + AGT GGT	NNRTI	ddI (didanosine) + hydroxyurea	?	Y			Seen in one patient.	DeAntoni97
T 69 S + SS	ACT⟶TCT + AGC TCT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC, 3TC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + SS	ACT⟶TCT + AGT TCT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC, 3TC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + SS	ACT⟶AGT + AGT AGT	NNRTI	ddI (didanosine) + hydroxyurea	?	Y			Seen in one patient.	DeAntoni97

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
T 69 S + TS	ACT→TCT + ACC TCT	MN		?	Y	Confers >4-fold resistance to: AZT, ddI, ddC, 3TC and PMEA.		Seen in heavily treated patients.	Winters98
T 69 S + VG	ACT→TCT + ACC TCT	MN		N	Y				Larder99
K 70 E	AAA→GAA	NRTI	PMEA (adefovir)	Y	Y	9	3TC (7); PFA: 2-fold hypersusceptibility		Cherrington96, Mulato97
K 70 R	AAA→AGA	NRTI	AZT (zidovudine)	Y	Y			D67N/K70R/T215Y/K219Q: 120-fold	Larder89, Larder91, Kellam92
K 70 S	AAA→AGA	MN	ddI (didanosine) + d4T (stavudine)	?	Y			Seen in one patient on ddC + d4T combination therapy.	
L 74 I	TTA→ATA	NNRTI	HBY 097	Y	?				Kleim96
L 74 V	TTA→GTA	NRTI	1592U89 (abacavir)	Y	N	4		K65R/L74V: 3.6-fold; K65R/L74V/M184V: 10.2-fold	Tisdale97
L 74 V	TTA→GTA	NRTI	ddI (didanosine)	N	Y	5–10	ddC (4)	Can reverse effect of T215Y AZT resistance mutation	StClair91
L 74 V	TTA→GTA	NRTI	DXG	Y	?	4			Mellors96
L 74 V	TTA→GTA	NNRTI	HBY 097	Y	?				Kleim96
V 75 I	GTA→ATA	MN		N	Y	Nil		V75I alone has no effect, but in combination with mutations at 62, 77, 116, 151 causes multi NRTI resistance.	Iversen96, Shirasaka95
V 75 I	GTA→TTA	NNRTI	HBY 097	Y	?			Compensates for negative effect of G190E mutation on RT activity	Kleim96
V 75 L	GTA→TTA	NNRTI	HBY 097	Y	?				Kleim96
V 75 M	GTA→ATG	MN	ddC (zalcitabine) + d4T (stavudine)	?	Y			Seen in one patient on ddC + d4T combination therapy.	Lawrence99
V 75 T	GTA→ACA	NRTI	d4T (stavudine)	Y	Y	7	ddI; ddC; d4C; (-)-FTC	Observed with d4T selection in vitro, rarely in patients receiving d4T	Lacey94, Schinazi96
F 77 L	TTC→CTC	MN		N	Y	Nil		F77L alone has no effect, but in combination with mutations at 62, 75, 116, 151 causes multi NRTI resistance.	Iversen96, Shirasaka95

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Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
W 88 G	TGG→GGG	PARTI	PFA (foscarnet)	Y	Y	5	Hypersusceptibility to AZT	Observed after selection with AZT and PFA; suppresses effects of AZT mutations	Mellors95, Tachedjian95, Tachedjian96
W 88 S	TGG→TCG	PARTI	PFA (foscarnet)	N	Y	2–4	Wild-type susceptibility to AZT.	Partially suppresses effects of AZT resistance mutations	Mellors95, Tachedjian95, Tachedjian96
E 89 G	GAA→GGA	PARTI	PFA (foscarnet)	Y	N	14		Isolated by screening RT clones for ddGTP resistance	Prasad91
E 89 K	GAA→GGA	PARTI	PFA (foscarnet)	Y	N	> 16		Suppresses effects of AZT resistance mutations	Tachedjian95, Tachedjian96
L 92 I	TTA→ATA	PARTI	PFA (foscarnet)	Y	N	8		Partially suppresses effects of AZT resistance mutations	Tachedjian95, Tachedjian96
A 98 G	GCA→GGA	NNRTI	BI-RG-587 (nevirapine)	N	Y				Richman94
A 98 G	GCA→GGA	NNRTI	L-697,661	N	Y	8			Byrnes93
L 100 I	TTA→ATA	NNRTI	BHAP U-88204E	Y	?				Balzarini93d, Vasudevachari92
L 100 I	TTA→ATA	NNRTI	BI-RG-587 (nevirapine)	N	Y				Richman93
L 100 I	TTA→ATA	NNRTI	DMP-266 (efavirenz)	Y	?	8–11		Combinations of mutations needed for high-level resistance; L100I/V108I: 1,000-fold; L100I/V179D/Y181C: 1,000-fold	Young95, Winslow96
L 100 I	TTA→ATA	NNRTI	DMP-266 (efavirenz)	Y	Y				Bacheler00
L 100 I	TTA→ATA	NNRTI	L-697,661	Y	N	2			Byrnes93
L 100 I	TTA→ATA	NNRTI	TIBO R82150	Y	?	> 100		Suppresses effects of AZT resistance mutations	Mellors93, Balzarini93c, Byrnes93a
L 100 I	TTA→ATA	NNRTI	TIBO R82913	Y	?			Found in combination with E138K	Larder92
L 100 I	TTA→ATA	NNRTI	UC-68	Y	?	70			Balzarini95
L 100 I	TTA→ATA	NNRTI	UC-70	Y	?	758			Buckheit95a
L 100 I	TTA→ATA	NNRTI	UC-781	Y	?	20		Activity of UC-781 versus L100I, K103N, V106A, E138K, Y181C and Y188L reduced by 2-, 7-, 1.5-, 1.5-, 5- and 150-fold, respectively, compared to wild type	Balzarini96a, Balzarini96b
L 100 I	TTA→ATA	NNRTI	UC-84	Y	?	> 40, > 33			Buckheit95a, Buckheit95b

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K 101 E	AAA→GAA	NNRTI	8-Chloro-TIBO (tivirapine)	?	Y				Moeremans95
K 101 E	AAA→GAA	NNRTI	ADAMII	Y	?	30		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
K 101 E	AAA→GAA	MN	AZT (zidovudine) + BHAP U-87201E (atevirdine)	?	Y			Seen in one patient on atevirdine + AZT combination therapy. Found in association with K103N.	Demeter98
K 101 E	AAA→GAA	NNRTI	DMP-266 (efavirenz)	Y	?	1,000			Young95
K 101 E	AAA→GAA	NNRTI	DMP-266 (efavirenz)	Y	Y				Bacheler00
K 101 E	AAA→GAA	NNRTI	L-697,661	N	Y	8			Byrnes93
K 101 E	AAA→GAA	NNRTI	UC-10	Y	?	12		K101E/Y181C: 200-fold	Buckheit95a, Buckheit97
K 101 E	AAA→GAA	NNRTI	UC-38	Y	N			K101E/G190E: > 100-fold	Balzarini95a, Balzarini95
K 101 E	AAA→GAA	NNRTI	UC-57	Y	?			K101E/Y181C: 58-fold	Buckheit95a
K 101 E	AAA→GAA	NNRTI	UC-781	Y	?	7	UC040 (18); Nevirapine (15)	V108I/Y181C: 55-fold; K101E/V108I/Y181C: 500-fold.	Buckheit97
K 101 I	AAA→ATA	NNRTI	UC-16	Y	N	10		K101I/G141E: 10-fold	Balzarini95
K 101 Q	AAA→CAA	NNRTI	DMP-266 (efavirenz)	N	Y				Bacheler00
K 101 Q	AAA→CAA	NNRTI	LY-300046 HCl (trovirdine)	Y	?			Found in combination with V108I	Zhang95, Vrang93
K 103 E	AAA→GAA	NRTI	BHAP U-87201E (atevirdine)	?	Y			Found in association with Y181C in one patient on monotherapy. K103E, K103N and Y181C observed with monotherapy.	Demeter98
K 103 N	AAA→AAC	NNRTI	8-Chloro-TIBO (tivirapine)	?	Y				Moeremans95
K 103 N	AAA→AAC	NNRTI	ADAMII	Y	?	>28		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
K 103 N	AAA→AAC	NNRTI	α-APA (loviride)	Y	Y				Staszewski96a

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K 103 N	AAA→AAC	NRTI	BHAP U-87201E (atevirdine)	?	Y			Found in association with Y181C in several patients on monotherapy. Also seen in patients on ATV + AZT combination therapy.	Demeter98
K 103 N	AAA→AAC	NNRTI	BHAP U-90152 (delavirdine)	?	Y			K103N/Y181C seen separately and in combination in patients	Demeter95
K 103 N	AAA→AAC	NNRTI	BI-RG-587 (nevirapine)	N	Y				Richman93
K 103 N	AAA→AAC	NNRTI	DMP-266 (efavirenz)	Y	Y	67		Predominant mutation in vivo	Winslow96
K 103 N	AAA→AAC	NNRTI	DMP-266 (efavirenz)	Y	Y				Bacheler00
K 103 N	AAA→AAC	NRTI	GW 420867X	Y	?				Kleim99
K 103 N	AAA→AAC	NNRTI	I-EBU (emivirine)	Y	?			Predominant mutation in vivo	Seki95
K 103 N	AAA→AAC	NNRTI	L-697,593	Y	?	20		K103N/Y181C: > 1,000-fold	Nunberg91
K 103 N	AAA→AAC	NNRTI	L-697,661	Y	Y	8		K103N and Y181C most common with monotherapy	Byrnes93, Saag93
K 103 N	AAA→AAC	NNRTI	TIBO R82913	Y	?	> 100		K103N/Y181C: > 1,000-fold	Balzarini93d
K 103 N	AAA→AAC	NNRTI	UC-10	Y	N	5			Balzarini95
K 103 N	AAA→AAC	NNRTI	UC-81	Y	?				Balzarini95, Yang97
K 103 Q	AAA→CAA	NNRTI	L-697,661	N	Y	8			Saag93
K 103 R	AAA→AGA	NNRTI	I-EBU (emivirine)	Y	Y				BorrotoEsoda97
K 103 R	AAA→AGA	NNRTI	LY-300046 HCl (trovirdine)	Y	?		Nevirapine; 9-chloro-TIBO	K103R/V179D: 500-fold; Found in combination with V179D or Y181C	Zhang95, Vrang93
K 103 T	AAA→ACA	NNRTI	BHAP U-90152 (delavirdine)	?	Y				Demeter95
K 103 T	AAA→ACA	NRTI	S-1153	Y	?				Fujiwara98
K 103 T	AAA→ACA	NNRTI	UC-42	Y	N	100			Balzarini95
V 106 A	GTA→GCA	NNRTI	ADAMII	Y	?	7.13		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
V 106 A	GTA→GCA	NNRTI	BHAP U-88204E	Y	?				Vasudevachari92
V 106 A	GTA→GCA	NNRTI	BI-RG-587 (nevirapine)	Y	Y	100		No effect on AZT resistance	Richman94, Larder92, Richman93, Balzarini93d
V 106 A	GTA→GCA	NNRTI	E-EBU-dM	Y	?				Balzarini93
V 106 A	GTA→GCA	NRTI	GW 420867X	Y	?			V106A/Y181C: 400-fold resistance	Kleim99

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V 106 A	GTA→GCA	NRTI	S-1153	Y	?	4.5		V106A + F227L: 387-fold	Fujiwara98
V 106 A	GTA→GCA	NNRTI	S-2720 (Quinoxaline)	Y	?			P225H follows V106A. Also seen with L101I and Y181C. Double and triple mutants highly resistant to other NNRTI's, including MKC442	Pelemans97
V 106 A	GTA→GCA	NNRTI	TIBO R82913	Y	?	100			Larder92
V 106 A	GTA→GCA	NNRTI	UC-69	Y	?			V106A/V181C: 166-fold	Buckheit95a
V 106 A	GTA→GCA	NNRTI	UC-82	Y	?	13		Activity of UC-82 versus L100I, K103N, V106A, E138K, Y181C and Y188L reduced by 2-, 6-, 1.5-, 2-, 4- and 200-fold, respectively, compared to wild type	Balzarini96b, Balzarini96a
V 106 I	GTA→ATA	NNRTI	HBY 097					Appears under lowered drug concentration selection	Kleim97
V 108 I	GTA→ATA	NNRTI	ADAMII	Y	?	6.74		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
V 108 I	GTA→ATA	NNRTI	α-APA (loviride)	Y	?				Staszewski96a
V 108 I	GTA→ATA	NNRTI	BI-RG-587 (nevirapine)	N	Y				Richman93
V 108 I	GTA→ATA	NNRTI	DMP-266 (efavirenz)	Y	?			L100I/V108I: 1,000-fold	Winslow96
V 108 I	GTA→ATA	NNRTI	DMP-266 (efavirenz)	Y	Y				Bacheler00
V 108 I	GTA→GCA	NNRTI	I-EBU (emivirine)	Y	?				Seki95
V 108 I	GTA→GCA	NNRTI	L-697,661	Y	Y	4			Byrnes93
V 108 I	GTA→ATA	NNRTI	LY-300046 HCl (trovirdine)	Y	?			Found in combination with K101Q	Zhang95
V 108 I	GTT→GAT	NNRTI	TIBO R82913	N	Y	> 100	R82150 (> 100)		Vandamme94a
V 108 I	GTA→ATA	NNRTI	UC-781	Y	?		V108I/Y181C: 55 fold. K101E/V108I/Y181C: 500 fold.		Buckheit97
Y 115 F	TAT→TTT	NRTI	1592U89 (abacavir)	Y	N	2		K65R/L74V and/or Y115F with M184V: 10 fold; L74V/Y115F/M184V: 11-fold	Tisdale97

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
F 116 Y	TTT→TAT	MN		N	Y	Nil		F116Y alone has no effect, but in combination with mutations at 62, 75, 77, 151 causes multi NRTI resistance.	Iversen96, Shirasaka95
V 118 I	GTT→ATT	MN	AZT (zidovudine) + 3TC (lamivudine)	N	Y	2.0		Confers moderate levels of resistance to 3TC (4 to 50-fold) when present in an AZT-resistant genetic background without diminishing AZT resistance.	Hertogs00
P 119 S	CCC→TCC	NRTI	F-ddA (lodenosine)	Y	?	4.6		Found with V179D and/or L214F, which are possibly compensatory	Tanaka97
I 135 L	ATA→AAA	NNRTI		N	Y	Nil		Mutation identified by logistic regression analysis. I135L/L283I: 5.0-fold Delavirdine resistance, 4.2-fold Nevirapine resistance, 4.1-fold Efavirenze resistance.	Brown00
I 135 M	ATA→ATG	NNRTI		N	Y	Nil		Mutation identified by logistic regression analysis. I135L/L283I: 4.0-fold Delavirdine resistance, 4.5-fold Nevirapine resistance, 3.2-fold Efavirenze resistance.	Brown00
I 135 T	ATA→ACA	NNRTI		N	Y	Nil		Mutation identified by logistic regression analysis. I135L/L283I: 3.4-fold Nevirapine resistance.	Brown00
E 138 A	GAG→GCG	NNRTI	TSAO	N	Y			Mutation reducing susceptibility to TSAO in TSAO therapy naive patients.	VanLaethem00
E 138 K	GAG→AAG	NNRTI	I-EBU (emivirine)	Y	N			Obtained in the concomitant presence of low 3TC concentrations	Balzarini96c
E 138 K	GAG→AAG	NNRTI	TIBO R82913	Y	?			Found in combination with L100I	Balzarini93c
E 138 K	GAG→AAG	NNRTI	TSAO	Y	?	> 100		E138A (GAG to GCG) in TSAO-naive patients confers TSAO viral resistance	Balzarini93a, Balzarini93b, Vandamme96

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
E 138 K	GAG→AAG	NNRTI	UC-82	Y	?	5		Activity of UC-82 versus L100I, K103N, V106A, E138K, Y181C and Y188L reduced by 2-, 6-, 1.5-, 2-, 4- and 200-fold, respectively, compared to wild type	Balzarini96b, Balzarini96a
E 138 K	GAG→AAG	NNRTI	UC-84	Y	?	> 100	TSAOs		Balzarini95, Balzarini95b
T 139 I	ACA→ATA	NNRTI	ADAMII	Y	?	38		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
T 139 I	ACA→ATA	NNRTI	Calanolide A	Y	?	> 70	Not other NNRTIs		Buckheit95c
G 141 E	GGG→GAG	NNRTI	UC-16	Y	N			K101I/G141E: 10-fold	Balzarini95
Q 151 M	CAG→ATG	MN		N	Y	AZT: 10; ddI/ ddC: 5		Pivotal multi nucleoside RTI resistance mutation (first to occur), found in association with combinations of four other mutations: A62V/V75I/F77L/F116Y/ Q151M: AZT 190-fold; ddI 50-fold; ddC 20-fold; d4T > 10-fold	Iversen96, Shirasaka95, Schmit96
S 156 A	TCA→GCA	PARTI	PFA (foscarnet)	Y	N	4.5			Tachedjian95
P 157 S	CCA→TCA	NNRTI	3TC (lamivudine)			5		Mutation increases susceptibility to AZT and PMPA	Smith99
Q 161 L	CAA→CTA	PARTI	PFA (foscarnet)	Y	Y	5		Q161L/H208Y: 9-fold; Q161L/H208Y suppresses effects of AZT mutations	Mellors95
V 179 D	GTT→GAT	NNRTI	ADAMII	Y	?	28		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
V 179 D	GTT→GAT	NNRTI	DMP-266 (efavirenz)	Y	?			L100I/V179D/Y181C: 1,000-fold	Winslow96
V 179 D	GTT→GAT	NNRTI	L-697,661	N	Y	4			Byrnes93
V 179 D	GTT→GAT	NNRTI	LY-300046 HCl (trovirdine)	Y	?			Found in combination with K103R or Y181C; V179D/Y181C: > 1,000-fold	Zhang95

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
V 179 D	GTT→GAT	NNRTI	QM96521	Y	?	10	Other TDD derivative: 15–140-fold; 8-chloro-TIBO: 10-fold		Witvrouw98
V 179 D	GTT→GAT	NNRTI	TIBO R82913	N	Y	20	R82150 (20)		Vandamme94
V 179 D	GTT→GAT	NNRTI	UC-10	Y	?	16			Balzarini95, Balzarini96a
V 179 E	GTT→GAG	NNRTI	L-697,661	N	Y	8			Byrnes93
Y 181 C	TAT→TGT	NNRTI	1737	Y	?	20		Y181C also confers resistance to numerous other tetrahydronaphthalene derivatives.	Hara97
Y 181 C	TAT→TGT	NNRTI	ADAMII	Y	?	>28		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
Y 181 C	TAT→TGT	NNRTI	α-APA (loviride)	Y	?				deBethune93
Y 181 C	TAT→TGT	NNRTI	α-APA (loviride)	?	Y				Staszewski96
Y 181 C	TAT→TGT	NNRTI	BHAP U-87201E (atevirdine)	N	Y			K103E, K103N and Y181C observed with monotherapy	Demeter95, Demeter98
Y 181 C	TAT→TGT	NNRTI	BHAP U-88204E	Y	?				Vasudevachari92
Y 181 C	TAT→TGT	NNRTI	BHAP U-90152 (delavirdine)	?	Y			K103N/Y181C seen separately and in combination in vivo	Demeter95
Y 181 C	TAT→TGT	NNRTI	BI-RG-587 (nevirapine)	Y	Y	> 100	Other NNRTIs	Can suppress effects of AZT mutations	Richman94, Richman91, Mellors92
Y 181 C	TAT→TGT	NNRTI	BM+51.0836	Y	?				Maass93
Y 181 C	TAT→TGT	NNRTI	DMP-266 (efavirenz)	Y	?	4		L100I/V179D/Y181C: 1,000-fold; uncommon in vivo	Winslow96, Young95
Y 181 C	TAT→TGT	NNRTI	E-BPTU	Y	?	160	Other NNRTIs		Buckheit95c
Y 181 C	TAT→TGT	NNRTI	E-EBU	Y	?				Balzarini93
Y 181 C	TAT→TGT	NNRTI	E-EPSeU	Y	?	> 50		Y188C confers greater resistance than Y181C	Nguyen94
Y 181 C	TAT→TGT	NNRTI	E-EPU	Y	?	> 95		Y188C confers greater resistance than Y181C	Nguyen94
Y 181 C	TAT→TGT	NRTI	GW 420867X	Y	?			V106A/Y181C: 400-fold resistance	Kleim99

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
Y 181 C	TAT→TGT	NNRTI	I-EBU (emivirine)	?	Y				BorrotoEsoda97
Y 181 C	TAT→TGT	NNRTI	L-697,593	Y	?	> 100		K103N/Y181C: > 1,000-fold	Nunberg91
Y 181 C	TAT→TGT	NNRTI	L-697,661	Y	Y	> 30		K103N and Y181C most common with monotherapy	Byrnes93, Saag93
Y 181 C	TAT→TGT	NNRTI	LY-300046 HCl (trovirdine)	Y	?		Nevirapine; 9-chloro-TIBO	V179D/Y181C: > 1,000-fold; Found in combination with K103R or V179D	Zhang95, Vrang93
Y 181 C	TAT→TGT	NNRTI	TIBO R82913	Y	?	> 100		K103N/Y181C: > 1,000-fold	Larder92
Y 181 C	TAT→TGT	NNRTI	UC-10	Y	?	6		K101E/Y181C: 200-fold	Buckheit95a
Y 181 C	TAT→TGT	NNRTI	UC-32	Y	?	38			Buckheit95a
Y 181 C	TAT→TGT	NNRTI	UC-38	Y	?	8–149	Other NNRTIs		Buckheit95a
Y 181 C	TAT→TGT	NNRTI	UC-57	Y	?			K101E/Y181C: 58-fold	Buckheit95a
Y 181 C	TAT→TGT	NNRTI	UC-68	Y	?	5			Buckheit95a
Y 181 C	TAT→TGT	NNRTI	UC-69	Y	?			V106A/V181C: 166-fold	Buckheit95a
Y 181 C	TAT→TGT	NNRTI	UC-781	Y	?	13		V108/Y181C: 55 fold; K101E/V108I/ Y181C: 500 fold. 42	Balzarini98, Buckheit97
Y 181 C	TAT→TGT	NNRTI	UC-80	Y	?	18			Buckheit95a
Y 181 C	TAT→TGT	NNRTI	UC-81	Y	?	53			Balzarini95, Yang97
Y 181 C	TAT→TGT	NNRTI	UC-84	Y	?	> 118			Buckheit95a
Y 181 I	TGT→ATT	NNRTI	BHAP U-88204E	Y	Y			Appeared after treatment of Y181C-mutated virus with BHAP; high-level resistance to BHAP, nevirapine and TIBO; observed in one nevirapine-treated patient	Balzarini94
Y 181 I	TGT→ATT	NNRTI	BI-RG-587 (nevirapine)	N	Y	High-level		Observed in one patient	Shaw94
Y 181 I	TAT→ATT	NNRTI	I-EBU (emivirine)	Y	N	1,000			Balzarini96c
M 184 I	ATG→ATA	NRTI	3TC (lamivudine)	Y	Y			M184V and M184I can suppress effects of AZT resistance mutations	Schinazi93, Tisdale93, Gao93
M 184 I	ATG→ATA	NNRTI	QYL-685	Y	?	9	QYL-609	Additional passage of virus did not select M184V	Yoshimura99a
M 184 T	ATG→ACG	NRTI	3TC (lamivudine)	Y	?			Reduced replication capacity and RT activity	Larder95, Keulen96

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
M 184 V	ATG→GTG	NRTI	1592U89 (abacavir)	Y	N	3		K65R/L74V and/or Y115F with M184V: 10-fold; K65R/M184V: 8-fold; L74V/M184V: 9-fold resistance; L74V/Y115F/M184V: 11-fold	Tisdale97
M 184 V	ATG→GTG	NRTI	3TC (lamivudine)	Y	Y	>100	ddI; ddC; (-)-FTC	M184V and M184I can suppress effects of AZT resistance mutations; GTA seen in cell culture	Schinazi93, Tisdale93, Gao93
M 184 V	ATG→GTG	NRTI	ddC (zalcitabine)	Y	Y	2–5			Gu92
M 184 V	ATG→GTG	NRTI	ddI (didanosine)	Y	Y	2–5		Rarely observed in patients receiving ddI	Gu92
M 184 V	ATG→GTG	NRTI	dOTC	Y	?			K65R/M184V: 4.2-fold.	Rando99
M 184 V	ATG→GTG	NRTI	(-)dOTC	Y	?	nil			Rando99
M 184 V	ATG→GTG	NRTI	(+)dOTC	Y	?				Rando99
M 184 V	ATG→GTG	NNRTI	(-)dOTFC	Y	?	13			Richard00
M 184 V	ATG→GTG	NNRTI	(-)dOTFC	Y	?	>15.0			Richard00
M 184 V	ATG→GTG	NRTI	(-)-FTC (emtricitabine)	Y	?	> 100		M184V can suppress effects of AZT mutations	Schinazi93, Tisdale93
M 184 V	ATG→GTG	NRTI	L-FddC	Y	?	> 100			Schinazi95
Y 188 C	TAT→TGT	NNRTI	ADAMII	Y	?	6.07		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
Y 188 C	TAT→TGT	NNRTI	BI-RG-587 (nevirapine)	N	Y				Richman93
Y 188 C	TAT→TGT	NNRTI	E-EPSeU	Y	?	> 250		Y188C is the predominant mutation for E-EPSeU; Y188C confers greater resistance than Y181C	Nguyen94
Y 188 C	TAT→TGT	NNRTI	E-EPU	Y	?	> 250		Y188C confers greater resistance than Y181C	Nguyen94
Y 188 C	TAT→TGT	NNRTI	HEPT	Y	?				Balzarini93

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
Y 188 H	TAT→CAT	NNRTI	ADAMII	Y	?	>128		Not selected for in vitro, resistance determined against a panel of mutants. Viruses with the L100I mutation show an enhanced sensitivity to ADAMII.	Cushman98
Y 188 H	TAT→CAT	MN	AZT (zidovudine) + BHAP U-87201E (atevirdine)	?	Y			Found in two patients on atevirdine + AZT combination therapy.	Demeter98
Y 188 H	TAT→CAT	NNRTI	DMP-266 (efavirenz)	N	Y				Bacheler00
Y 188 H	TAT→CAT	NNRTI	TIBO R82913	Y	?				Balzarini93c
Y 188 H/L	TAT→CAT/CTT	NNRTI	α-APA (loviride)	?	Y				Staszewski96
Y 188 L	TAT→TTA	NNRTI	DMP-266 (efavirenz)	Y	?	1,000			Winslow96
Y 188 L	TAT	NNRTI	DMP-266 (efavirenz)		Y				Bacheler00
Y 188 L	TAT→TTA	NNRTI	TIBO R82913	N	Y				Vandamme94
V 189 I	GTA→ATA	NNRTI	BHAP U-90152 (delavirdine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to delavirdine with respect to WT	Pelemans01
V 189 I	GTA→ATA	NNRTI	BI-RG-587 (nevirapine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 23-fold resistant to nevirapine with respect to WT	Pelemans01
V 189 I	GTA→ATA	NNRTI	GW 420867X	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 8-fold resistant to GW 420867X with respect to WT	Pelemans01
V 189 I	GTA→ATA	NNRTI	HBY 097	Y	?	2	Other NNRTIs (2–6)		Kleim96

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
V 189 I	GTA→ATA	NNRTI	HBY 097	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 5-fold resistant to HBY 097 with respect to WT	Pelemans01
V 189 I	GTA→ATA	NNRTI	I-EBU (emivirine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 7-fold resistant to emivirine with respect to WT	Pelemans01
V 189 I	GTA→ATA	NNRTI	UC-781	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to UC-781 with respect to WT	Pelemans01
G 190 A	GGA→GCA	NNRTI	α-APA (loviride)	?	Y				Moeremans95
G 190 A	GGA→GCA	NNRTI	BI-RG-587 (nevirapine)	N	Y				Richman94
G 190 A	GGA→GCA	NNRTI	DMP-266 (efavirenz)	N	Y				Bacheler00
G 190 E	GGA→GAA	NNRTI	AAP-BHAP (U-104489)	Y	?	>100		T139I/G190E/T200A/L214F: >100. Additional mutations possibly restore the replication capacity of the G190E mutant	Olmsted96
G 190 E	GGA→GAA	NNRTI	DMP-266 (efavirenz)	N	Y				Bacheler00
G 190 E	GGA→GAA	NRTI	GW 420867X	Y	?				Kleim99
G 190 E	GGA→GAA	NNRTI	HBY 097	Y	?		Other NNRTIs	Reduces enzymatic activity of RT and viral replication competency	Kleim95
G 190 E	GGA→GAA	NNRTI	S-2720 (Quinoxaline)	Y	?				Kleim93
G 190 E	GGA→GAA	NNRTI	UC-38	Y	N			K101E/G190E: > 100-fold; cross resistance to: TSAO-m3T, Nev, TIBO R82913, BHAP U88204; susceptible to L697,661	Balzarini95a
G 190 Q	GGA→CAA	NNRTI	HBY 097	Y	?		Other NNRTIs	Appears exclusively in connection with V179D	Kleim96

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
G 190 S	GGA→TCA	NNRTI	DMP-266 (efavirenz)	N	Y				Bacheler00
G 190 T	GGA→ACA	NNRTI	HBY 097	Y	?			Appears during selection with low drug concentrations.	Kleim97
H 208 Y	CAT→TAT	MN	AZT (zidovudine) + 3TC (lamivudine)	?	Y			Polymorphism facilitating AZT+3TC dual resistance	Kemp98
H 208 Y	CAT→TAT	PARTI	PFA (foscarnet)	Y	Y	2		Q161L/H208Y: 9-fold; increased susceptibility to AZT 100-fold), nevirapine (20-fold) and TIBO R82150 (30-fold); Q161L/H208Y suppresses effects of AZT mutations	Mellors95
L 210 W	TTG→TGG	NRTI	AZT (zidovudine)	Y	Y			210W/215Y: 42-fold 41L/210W/215Y: 49-fold 41L/67N/70R/210W/215Y: 366-fold Mutation arises after prolonged AZT therapy.	Gurusinghe95, Harrigan96, Hooker96
R 211 K	AGG→AAG	MN	AZT (zidovudine) + 3TC (lamivudine)	?	Y			Polymorphism facilitating AZT+3TC dual resistance in association with M184V and other AZT resistance mutations.	Kemp98
F 214 L	TTT→CTT	MN	AZT (zidovudine) + 3TC (lamivudine)	?	Y			Polymorphism facilitating AZT+3TC dual resistance in association with M184V and other AZT resistance mutations.	Stuyver97
T 215 F	ACC→TTC	NRTI	AZT (zidovudine)	?	Y			K67N/K70R/T215Y/K219Q: 120-fold	Larder89, Larder91, Kellam92
T 215 Y	ACC→TAC	NRTI	AZT (zidovudine)	Y	Y			M41L/T215Y: 60–70-fold; K67N/K70R/T215Y/K219Q: 120-fold. Effect of T215Y is reversed by a ddI mutation (L74V), NNRTI mutations (L100I;Y181C) or (-)-FTC/3TC mutations (M184I/V)	Larder891, Larder91, Kellam92
Y 215 C	TTC→TGC	NRTI	ddC (zalcitabine)	N	Y	4		Arises on background of T215Y AZT resistance	Slade93
K 219 E	AAA→GAA	NRTI	AZT (zidovudine)	Y	N				Larder89, Larder91, Kellam92
K 219 Q	AAA→CAA	NRTI	AZT (zidovudine)	?	Y			K67N/K70R/T215Y/K219Q: 120-fold	Larder89, Larder91, Kellam92
K 219 R	AAA→AGA	MN	3TC (lamivudine) + d4T (stavudine)	?	Y			Seen in two patient on 3TC + d4T combination therapy.	Lawrence99

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
K 219 R	AAA→AGA	MN	AZT (zidovudine) + 3TC (lamivudine)	?	Y			Seen in two patient on AZT + 3TC combination therapy.	Lawrence99
K 219 W	AAA→TGG	MN	ddC (zalcitabine) + d4T (stavudine)	?	Y			Seen in one patient on ddC + d4T combination therapy.	Lawrence99
P 225 H	CCT→CAT	NNRTI	DMP-266 (efavirenz)	N	Y				Bacheler00
P 225 H	CCT→CAT	NNRTI	S-2720 (Quinoxaline)	Y	?	4.0	MKC-442 (5.7); HBY-097 (4.0); UC-781 (3.7)	P225H follows V106A. Also seen with L101I and Y181C. Double and triple mutants highly resistant to other NNRTI's, including MKC442. The presence of P225H in a V106A backgrough restores sensitivity to BHAP U-90152.	Pelemans97, Pelemans98
F 227 L	TTA→CTC	NRTI	S-1153	Y	?	nil		V106A + F227L: 387-fold. This mutation confers hypersensitivity to delavirdine.	Fujiwara98
F 227 L	TTA→CTC	NNRTI	UC-781	Y	?			V106A/F227L: 10-fold. Found with V106A, K101I, Y181C and L100I. Appears in a V106A background following dose-escalating UC-781 treatment.	Balzarini98
W 229 Y	TGG→TAC	NNRTI	BHAP U-90152 (delavirdine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to delavirdine with respect to WT	Pelemans01
W 229 Y	TGG→TAC	NNRTI	BI-RG-587 (nevirapine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 23-fold resistant to nevirapine with respect to WT	Pelemans01

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
W 229 Y	TGG→TAC	NNRTI	GW 420867X	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 8-fold resistant to GW 420867X with respect to WT	Pelemans01
W 229 Y	TGG→TAC	NNRTI	HBY 097	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 5-fold resistant to HBY 097 with respect to WT	Pelemans01
W 229 Y	TGG→TAC	NNRTI	I-EBU (emivirine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 7-fold resistant to emivirine with respect to WT	Pelemans01
W 229 Y	TGG→TAC	NNRTI	UC-781	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to UC-781 with respect to WT	Pelemans01
V 233 E	GAA→GTA	NNRTI	AZT (zidovudine) + BHAP U-87201E (atevirdine)	N	Y			Seen in 1 patient. K101E, Y188H and K238T also seen in patients on ATV/AZT combination therapy.	Demeter98
L 234 I	CTC→ATC	NRTI	S-1153	Y	?	22		This mutation confers hypersensitivity to Loviride.	Fujiwara98
P 236 L	CCT→CTT	NNRTI	BHAP U-87201E (atevirdine)	Y	N				Dueweke93
P 236 L	CCT→CTT	NNRTI	BHAP U-90152 (delavirdine)	Y	Y			Sensitizes RT 10-fold to nevirapine, TIBO R82913 and L-697,661	Dueweke93
P 236 L	CCT→CTT	NNRTI	HEPT	Y	?				Buckheit95c
K 238 T	AAA→ACA	MN	AZT (zidovudine) + BHAP U-87201E (atevirdine)	N	Y			Seen in 1 patient. K101E, K103N, Y188H, and V233E also observed with ATV/AZT combination therapy.	Demeter98

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
K 238 T	AAA→ACA	MN	AZT (zidovudine) + BHAP U-87201E (atevirdine)	N	Y			Seen in 1 patient. K101E, K103N, Y188H and E233V also seen in patients on ATV/AZT combination therapy.	Demeter98
L 283 I	CTT→ACT	NNRTI		N	Y	Nil		Mutation identified by logistic regression analysis. Confers resistance to Delavirdine, Nevirapine, and Efavirenze in conjunction with mutations at codon 135.	Brown00
G 333 D	GGC→GAC	MN	AZT (zidovudine) + 3TC (lamivudine)	Y	Y			Facilitates dual resistance to AZT+3TC in association with M184V and standard AZT resistance mutations.	Kemp98
G 333 D	GGC→GAC	MN	AZT (zidovudine) + 3TC (lamivudine) + 1592U89 (abacavir)	?	Y				Caride00
G 333 E	GGC→GAG	MN	AZT (zidovudine) + 3TC (lamivudine)	Y	Y			Facilitates dual resistance to AZT+3TC in association with M184V and standard AZT resistance mutations.	Kemp98
G 333 E	GGC→GAG	MN	AZT (zidovudine) + 3TC (lamivudine) + 1592U89 (abacavir)	?	Y				Caride00
T 386 I	ACT→ATT	MN	AZT (zidovudine) + 3TC (lamivudine) + 1592U89 (abacavir)	?	Y			Abrogates M184V suppression of L210W and L210W/G333D/E	Caride00
E 396 G	GAA→GGA	NNRTI	BHAP U-90152 (delavirdine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to delavirdine with respect to WT	Pelemans01
E 396 G	GAA→GGA	NNRTI	BI-RG-587 (nevirapine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 23-fold resistant to nevirapine with respect to WT	Pelemans01

Mutations in HIV RT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
E 396 G	GAA→GGA	NNRTI	GW 420867X	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 8-fold resistant to GW 420867X with respect to WT	Pelemans01
E 396 G	GAA→GGA	NNRTI	HBY 097	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 5-fold resistant to HBY 097 with respect to WT	Pelemans01
E 396 G	GAA→GGA	NNRTI	I-EBU (emivirine)	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 7-fold resistant to emivirine with respect to WT	Pelemans01
E 396 G	GAA→GGA	NNRTI	UC-781	Y	N			Compensatory mutation restoring replication competence to W229Y mutant. I63M/V189I/W229Y/E396G mutant 2.5-fold resistant to UC-781 with respect to WT	Pelemans01

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
R 8 K	CGA→AAA	PI	A-77003	Y	?	10		R8K/M46I/G48V: 20-fold	Ho94, Tisdale94
R 8 Q	CGA→CAA	PI	A-77003	Y	?	10		M46I improves replication competency of R8Q mutant	Ho94, Kaplan94
L 10 F	CTC→TTC	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	I84V/L10F/M46I: 4 fold, I84V/L10F/M46I/T91S: 12 fold, I84V/L10F/M46I/T91S/V32I/I47V: 46 fold, Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98
L 10 F	CTC→TTC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
L 10 F	CTC→TTC	PI	BILA 2185 BS	Y	?		BILA 1906 BS (360)	L10F/L23I/V32I/M46I/I47V/I54M/A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′, A to V (GCT to CTT) at P2′).	Croteau97
L 10 F	CTC→TTC	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
L 10 F	CTC→TTC	PI	DMP 450	Y	?			Probably compensatory	Otto95, Winslow95
L 10 F	CTC→TTC	PI	DMP-323					L10F/V82A: 2-fold; L10F/K45I/I84V: 50-fold	King95

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
L 10 F	CTC→TTC	PI	JE-2147	Y	?		KNI-272: 7-fold; Ritonavir: 9-fold	L10F/I47V/I84V: 19-fold. L10F/M46I/I47V/I84V: 28-fold. >50 passages required for isolation of resistant virus.	Yoshimura99
L 10 F	CTC→TTC	PI	SC-55389A	Y	?	2.8	Not SC-52151	N88S/L10F: 25-fold	Potts94, Pillay96, Smidt97
L 10 F	CTC→TTC	PI	VB 11,328	Y	?			L10F/I84V: 8-fold	Partaledis95
L 10 F	CTC→TTC	PI	VX-478 (amprenavir)	Y	?				Tisdale96
L 10 I	CTC→ATC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
L 10 I	CTC→ATC	PI	MK-639 (indinavir)	?	Y				Condra96
L 10 I	CTC→ATC	PI	Ro 31–8959 (saquinavir)		Y			Found in combination with G48V in vivo.	Schapiro96
L 10 R	CTC→CGC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
L 10 R	CTC→CGC	PI	MK-639 (indinavir)	N	Y		XM-323 (15)	L10R/M46I/L63P/V82T: 4-fold; L10R/M46I/L63P/V82T/I84V: 8-fold	Condra96, Condra95
L 10 V	CTC→GTC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
L 10 V	CTC→GTC	PI	MK-639 (indinavir)	?	Y		A-80987 (4)		Condra96, Condra95
L 10 Y	CTC→TAC	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
I 15 V	CTC→TAC	PI	PNU-140690 (tipranavir)	?	Y				Rusconi00
G 16 E	GGG→GAG	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98
K 20 M	AAG→ATG	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
K 20 M	AAG→ATG	PI	AG1343 (nelfinavir)	?	Y			Seen in two patients following a switch from saquinavir. Associated with reduced susceptibility to both saquinavir and nelfinavir.	Lawrence99
K 20 M	AAG→ATG	PI	MK-639 (indinavir)	?	Y		VX-478 (8)		Condra96
K 20 R	AAG→AGG	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
K 20 R	AAG→AGG	PI	ABT-538 (ritonavir)	N	Y			K20R/M36I/I54V/V82A: 41-fold	Molla96
K 20 R	AAG→AGG	PI	MK-639 (indinavir)	?	Y		Ro-31–8959 (8);		Condra96

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
L 23 I	CTA→ATA	PI	BILA 2185 BS	Y	?		Ro-31–8959 (50); L-735,524 (80); BILA 1906 BS (360)	L10F/L23I/V32I/M46I/I47V/I54M/ A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′, A to V (GCT to CTT) at P2′).	Croteau97, Doyon96
L 24 I	TTA→ATA	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
L 24 I	TTA→ATA	PI	MK-639 (indinavir)	?	Y		SC-52151 (8)		Condra96, Condra95
L 24 V	TTA→GTA	PI	SC-52151 (telinavir)	Y	?	10–20	SC55389A	L24V/G48V/A71V/V75I/P81T: 1000-fold	Potts94, Pillay96
D 30 N	GAT→AAT	PI	AG1343 (nelfinavir)	Y	Y			D30N/A71V: 7-fold; D30N and N88D are most common in vivo after 24 weeks of therapy; they do not cause cross-resistance to other protease inhibitors	Patick96, Patick97
V 32 I	GTA→ATA	PI	A-77003	Y	?	7 (enzyme resist.)		V32I appears first; progression to V32I/ M46V and V32I//M46V/A71V/V82A occurs even in the absence of drug	Kaplan94
V 32 I	GTA→ATA	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	I84V/L10F/M46I/T91S/V32I/I47V: 46 fold, Passage 17 virus: I84V/L10F/ M46I/T91S/V32I/I47V/V47A/G16E/ H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98
V 32 I	GTA→ATA	PI	ABT-538 (ritonavir)	Y	?	40		V32I and V82I are synergistic mutations yielding 20-fold enzyme resistance	Molla96

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
V 32 I	GTA→ATA	PI	BILA 1906 BS	Y	?			V32I/A71V: 3-fold; V32I/M46I,L/A71V/I84V: 5-fold; V32I/M46I,L/A71V/I84A: 520-fold. 32I/46L/71V/84A are functionally impaired. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′)	Lamarre94, Croteau97
V 32 I	GTA→ATA	PI	BILA 2011 (palinavir)	Y	?	1200	BILA 1906 (1400)	Other mutations found in p1/p6 cleavage site	Lamarre95
V 32 I	GTA→ATA	PI	BILA 2185 BS	Y	?		BILA 1906 (360)	L10F/L23I/V32I/M46I/I47V/I54M/A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′, A to V (GCT to CTT) at P2′).	Croteau97
V 32 I	GTA→ATA	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
V 32 I	GTA→ATA	PI	KNI-272	Y	?	2		V32I/M46I/I84V: 37-fold; V32I/L33F/K45I/F53L/A71V/I84V/L89M: 130-fold	Gulnik95
V 32 I	GTA→ATA	PI	MK-639 (indinavir)	Y	Y			V32I/M46L/V82A: 3-fold; V32I/M46L/A71V/V82A: 14-fold	Condra96, Condra95
L 33 F	TTA→TTC	PI	ABT-538 (ritonavir)	N	Y			M36I/I54V/A71V/V82I: 8-fold; K20R/M36I/I54V/V82A: 41-fold. In vivo, V82A/F/T/S occurs first, often followed by changes at 54,71 and 36	Molla96
L 33 F	TTA→TTC	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
E 35 D	TTA→TTC	PI	PNU-140690 (tipranavir)	?	Y			Seen in 60% of patients receiving Tipranavir therapy.	Rusconi00

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
M 36 I	ATG→ATA	PI	ABT-538 (ritonavir)	N	Y			In vivo, V82 occurs first, often followed by changes at 54, 71 and 36	Molla96
M 36 I	ATG→ATA	PI	AG1343 (nelfinavir)		Y				Patick96
N 37 D	ATG→ATA	PI	PNU-140690 (tipranavir)	?	Y			Seen in 30% of patients receiving Tipranavir therapy.	Rusconi00
R 41 K	ATG→ATA	PI	PNU-140690 (tipranavir)	?	Y			Seen in 20% of patients receiving Tipranavir therapy.	Rusconi00
K 45 I	AAA→ATA	PI	DMP-323					L10F/K45I/I84V: 50-fold	Tisdale94
M 46 F	ATG→TTC	PI	A-77003	Y	?	4 (enzyme resist.)		Seen with V82A	Kaplan94
M 46 I	ATG→ATA	PI	A-77003	Y	?			No effect on susceptibility but improves replication competency of R8Q mutant; R8K/M46I/G48V: 20-fold	Ho94, Kaplan94
M 46 I	ATG→ATA	PI	ABT-378 (lopinavir)	Y			Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	I84V/L10F/M46I: 4 fold, I84V/L10F/M46I/T91S: 12 fold, I84V/L10F/M46I/T91S/V32I/I47V: 46 fold, Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98
M 46 I	ATG→ATA	PI	ABT-538 (ritonavir)	Y	Y			M46I/L63P/A71V/V82F/I84V: 27-fold	Molla96
M 46 I	ATG→ATA	PI	AG1343 (nelfinavir)	Y	Y				Patick96
M 46 I	ATG→ATA	PI	BILA 1906 BS	Y	?		L 735,524 (60)	V32I/A71V: 3-fold; V32I/M46I,L/A71V/I84V: 5-fold; V32I/M46I,L/A71V/I84A: 520-fold. V32I/M46L/A71V/I84A is functionally impaired. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′)	Croteau97, Doyon96, Lamarre94, Lamarre95

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
M 46 I	ATG→ATA	PI	BILA 2185 BS	Y	?		BILA 1906 (360)	L10F/L23I/V32I/M46I/I47V/I54M/A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′, A to V (GCT to CTT) at P2′).	Croteau97
M 46 I	ATG→ATA	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
M 46 I	ATG→ATA	PI	DMP 450	Y	?			Probably compensatory	Otto95, Winslow95
M 46 I	ATG→ATA	PI	JE-2147	Y	?		KNI-272: 7-fold; Ritonavir: 9-fold	L10F/M46I/I47V/I84V: 28-fold. >50 passages required for isolation of resistant virus.	Yoshimura99
M 46 I	ATG→ATA	PI	MK-639 (indinavir)	N	Y			M46I/L63P/V82T: 4-fold; L10R/M46I/L63P/V82T: 4-fold; L10R/M46I/L63P/V82T/I84V: 8-fold	Condra96, Condra95
M 46 I	ATG→ATA	PI	VB 11,328	Y	?			I50V/M46I/I47V: 20-fold	Tisdale94, Partaledis95
M 46 I	ATG→ATA	PI	VX-478 (amprenavir)	Y	?	Nil			Partaledis95
M 46 L	ATG→TTC	PI	A-77003	Y	?	2–3 (enzyme resist.)			Kaplan94
M 46 L	ATG→TTG	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
M 46 L	ATG→TTG	PI	BILA 1906 BS	Y	?			Associated p1/p6 cleavage site mutation (L to F (CTT to TTT) at P1′)	Croteau97, Doyon96, Lamarre94, Lamarre95
M 46 L	ATG→CTG	PI	DMP-323	Y	?			V82A/M46L: 7-fold; V82A/M46L/L97V: 11-fold	King95

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
M 46 L	ATG→TTG	PI	MK-639 (indinavir)	Y	Y			V32I/M46L/A71V/V82A: 14-fold; V32I/M46L/V82A: 3-fold	Tisdale94
M 46 V	ATG→GTG	PI	A-77003	Y	?			V32I appears first; progression to V32I/M46V and V32I/M46V/A71V/V82A occurs even in the absence of drug.	Tisdale94
I 47 V	ATA→GTA	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	I84V/L10F/M46I/T91S/V32I/I47V: 46 fold, Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98
I 47 V	ATA→CTA	PI	BILA 2185 BS	Y	?		BILA 1906 (360)	L10F/L23I/V32I/M46I/I47V/I54M/A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′, A to V (GCT to CTT) at P2′).	Croteau97
I 47 V	ATA→CTA	PI	JE-2147	Y	?		KNI-272: 7-fold; Ritonavir: 9-fold	L10F/I47V/I84V: 19-fold. L10F/M46I/I47V/I84V: 28-fold. >50 passages required for isolation of resistant virus.	Yoshimura99
I 47 V	ATA→CTA	PI	VB 11,328	Y	?			I50V/M46I/I47V: 20-fold	Partaledis95
I 47 V	ATA→CTA	PI	VX-478 (amprenavir)	Y	?	Nil			Partaledis95
V 47 A	GTA→TAT	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	I84V/L10F/M46I/T91S/V32I/I47V: 46 fold, Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98
G 48 V	GGG→GTG	PI	A-77003	Y	?			R8K/M46I/G48V: 20-fold; G48V/I82T: 100-fold	Borman95
G 48 V	GGG→GTG	PI	MK-639 (indinavir)	?	Y				Vasudevachari96

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
G 48 V	GGG→GTG	PI	MP-167	Y	?	20	MP-134(5) SC-52151(16) Ro31–8959(5) (Fold increase in IC90s).	L10F/G48V: 20-fold	Mo96
G 48 V	GGG→GTG	PI	Ro 31–8959 (saquinavir)	Y	Y			Found in comb. with L10I in vivo; G48V/I84V/L90M: 30-fold; G48V/L90M: >100-fold enzyme resistance; G48V/L90M/I54V: > 50-fold (subtype B or O)	Jacobsen94, Eberle95
G 48 V	GGG→GTG	PI	SC-52151 (telinavir)	Y	?		Ro 31–8959	G48V/V82A, G48V/L63P/V82A or I54T: 10- to 20-fold; L24V/G48V/A71V/V75I/P81T: 1000-fold	Potts94, Pillay96
I 50 L	ATT→CTT	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
I 50 V	ATT→GTT	PI	VB 11,328	Y	?	3		I50V/M46I/I47V: 20-fold	Tisdale94, Partaledis95
I 50 V	ATT→GTT	PI	VX-478 (amprenavir)	Y	?	3			Partaledis95, Rao96
G 52 S	GGT→AGT	PI	AG1343 (nelfinavir)	?	Y			D30N/G52S: 93-fold	Patick98
F 53 L	TTT→?	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
I 54 L	ATC→CTC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
I 54 M	ATT→ATG	PI	BILA 2185 BS	Y	?		BILA 1906 (360)	L10F/L23I/V32I/M46I/I47V/I54M/A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′; A to V (GCT to CTT) at P2′).	Croteau97
I 54 T	ATC→ACC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
I 54 V	ATC→GTC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
I 54 V	ATC→GTC	PI	ABT-538 (ritonavir)	N	Y			I54V/V82T: 9-fold; K20R/M36I/I54V/V82A: 41-fold; M36I/I54V/A71V/V82T: 8-fold; I54V/A71V/V82A/L90N: 7-fold; In vivo, V82A/F/T/S occurs first, followed by changes at 54, 71 and 36	Molla96
I 54 V	ATC→GTC	PI	MK-639 (indinavir)	?	Y				Lamarre94
I 54 V	ATA→GTA	PI	Ro 31–8959 (saquinavir)	Y				In subtype O and B	Jacobsen94, Eberle95
K 55 R	AAA→AGA	PI	AG1343 (nelfinavir)	?	Y			Seen in one patient following a switch from saquinavir. Associated with reduced susceptibility to both saquinavir and nelfinavir.	Lawrence99

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
R 57 K	AGA→AAA	PI	AG1343 (nelfinavir)	?	Y			Seen in one patient following a switch from saquinavir. Associated with reduced susceptibility to both saquinavir and nelfinavir.	Lawrence99
D 60 E	GAT→GAA	PI	DMP 450	Y	?			Probably compensatory	Otto95, Winslow95
D 60 E	GAT→GAA	PI	PNU-140690 (tipranavir)	?	Y			Seen in 30% of patients receiving Tipranavir therapy.	Rusconi00
L 63 P	CTC→CCC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
L 63 P	CTC→CCC	PI	AG1343 (nelfinavir)	?	Y			D30N/M36I/L63P: 60-fold	Patick98
L 63 P	CTC→CCC	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
L 63 P	CTC→CCC	PI	MK-639 (indinavir)	N	Y			M46I/L63P/V82T: 4-fold; L10R/M46I/L63P/V82T/I84V: 8-fold; L10R/M46I/L63P/V82T: 4-fold	Condra96, Condra95
H 69 Y	CAT→TAT	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
A 71 I	GCT→ATT	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
A 71 L	GCT→CTC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
A 71 T	GCT→ACT	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
A 71 T	GCT→ACT	PI	BMS 186318	Y	?			A71T/V82A: 15-fold	Patick95, Rose94
A 71 T	GCT→ACT	PI	MK-639 (indinavir)	?	Y				Condra96, Condra95
A 71 T	GCT→ACT	PI	PNU-140690 (tipranavir)	?	Y				Rusconi00
A 71 V	GCT→GTT	PI	A-77003	Y	?			V32I appears first; progression to V32I/M46V and V32I/M46V/A71V/V82A occurs even in the absence of drug; M46I/L63P/A71V/V82F/I84V: 27-fold	Tisdale94, King95

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
A 71 V	GCT→GTC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
A 71 V	GCT→GTT	PI	ABT-538 (ritonavir)	Y	Y				Molla96
A 71 V	GCT→GTT	PI	AG1343 (nelfinavir)	Y	?	5		D30N/A71V: 7-fold; M46I/L63P/A71V/I84V: 30-fold	Patick98
A 71 V	GCT→GTT	PI	BILA 1906 BS	Y	?			V32I/A71V: 3-fold; V32I/M46I,L/A71V/I84V: 5-fold; V32I/M46I,L/A71V/I84A: 520-fold. 32I/46L/71V/84A are functionally impaired. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′)	Croteau97, Doyon96, Lamarre94, Lamarre95
A 71 V	GCT→GTT	PI	BILA 2011 (palinavir)	Y	?		BILA 2185: 30-fold		Lamarre94
A 71 V	GCT→GTT	PI	BILA 2185 BS	Y	?		BILA 1906 (360)	L10F/L23I/V32I/M46I/I47V/I54M/A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′; A to V (GCT to CTT) at P2′).	Croteau97
A 71 V	GCT→GTT	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
A 71 V	GCT→GTT	PI	MK-639 (indinavir)	Y	Y			V32I/M46L/A71V/V82A: 14-fold	Tisdale94
A 71 V	GCT→GTT	PI	SC-52151 (telinavir)	Y	?		Not L-735,524	A71V/V75I/P81T: 20- to 30-fold; L24V/G48V/A71V/V75I/P81T: 1000-fold; N88D or I11V/M46I/F53L/A71V/N88D:10- to 20-fold	Potts94, Pillay96

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
G 73 S	GGT→AGT	PI	AG1343 (nelfinavir)	?	Y			Seen in two patients following a switch from saquinavir. Associated with reduced susceptibility to both saquinavir and nelfinavir.	Lawrence99
G 73 S	GGT→GCT	PI	MK-639 (indinavir)	?	Y			Emerges following a switch from saquinavir to indinavir.	Dulioust97
V 75 I	GTA→ATA	PI	SC-52151 (telinavir)	Y	?			L24V/G48V/A71V/V75I/P81T: 1000-fold; A71V/V75I/P81T: 20- to 30-fold; L24V/G48V/A71V/V75I/P81T: 1000-fold	Potts94, Pillay96
V 77 I	GTA→ATA	PI	AG1343 (nelfinavir)	Y	Y				Patick98
P 81 T	CCT→ACT	PI	SC-52151 (telinavir)	Y	?			A71V/V75I/P81T: 20- to 30-fold; L24V/G48V/A71V/V75I/P81T: 1000-fold	Potts94, Pillay96
I 82 T	ATC→ACC	PI	A-77003	Y	?			G48V/I82T: 100-fold 82T was derived from in vitro passage of 82I)	Swanstrom94
V 82 A	GTC→GCC	PI	A-77003	Y	?			Rare; seen with M46F; V32I appears first; progression to V32I/M46V and V32I//M46V/A71V/V82A occurs even in the absence of drug	Tisdale94, Borman95, Swanstrom94
V 82 A	GTC→GCC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
V 82 A	GTC→GCC	PI	ABT-538 (ritonavir)	N	Y	2		In vivo, V82 occurs first, often followed by changes at I54, A71 and M36	Molla96
V 82 A	GTC→GCC	PI	AG1343 (nelfinavir)	?	Y				Lawrence99
V 82 A	GTC→GCC	PI	BMS 186318	Y	?		A-77003 (4)	A71T/V82A: 15-fold	Patick95, Rose94

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
V 82 A	GTC→GCC	PI	DMP-323	Y	?			V82A/M46L: 7-fold; V82A/M46L/L97V: 11-fold; L10F/V82A: 2-fold; ; V82A/L97V: 3-fold	King95
V 82 A	GTC→GCC	PI	MK-639 (indinavir)	Y	Y			V32I/M46L/V82A: 3-fold; V32I/M46L/A71V/V82A: 14-fold	Condra96, Condra95
V 82 A	GTC→GCC	PI	P9941	Y	?	6–8			Otto93
V 82 A	GTC→GCC	PI	Ro 31–8959 (saquinavir)	?	Y			Follows G48V during saquinavir therapy or after a switch to nelfinavir or indinavir.	Winters97, Eastman97, Schapiro97
V 82 A	GTC→GCC	PI	SC-52151 (telinavir)	Y	?			G48V/V82A, G48V/L63P/V82A or I54T: 10- to 20-fold	Potts94, Pillay96
V 82 A	GTC→GCC	PI	SKF108922	Y	?				Shao95
V 82 F	GTC→TTC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
V 82 F	GTC→TTC	PI	ABT-538 (ritonavir)	Y	Y			V82F/I84V: 8- to 10-fold; M46I/L63P/A71V/V82F/I84V: 27-fold	Molla96
V 82 F	GTC→TTC	PI	DMP-323	Y	?			V82F/I84V: 92-fold	King95
V 82 F	GTC→TTC	PI	MK-639 (indinavir)	?	Y				Partaledis94
V 82 I	GTC→ATC	PI	A-77003	Y	?			No resistance alone but V32I and V82I are synergistic mutations yielding 20-fold enzyme resistance 82T was derived from in vitro passage of 82I)	Kaplan94
V 82 I	GTC→ATC	PI	DMP-323	Y	?	< 2			King95
V 82 S	GTC→TCC	PI	ABT-538 (ritonavir)	N	Y	6		In vivo, V82 occurs first, often followed by changes at I54, A71 and M36	Molla96

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
V 82 T	GTC→ACC	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
V 82 T	GTC→ACC	PI	ABT-538 (ritonavir)	N	Y	3		In vivo, V82 occurs first, often followed by changes at I54, A71 and M36; V82T has reduced replication efficacy in natural background	Molla96
V 82 T	GTC→ACC	PI	MK-639 (indinavir)	N	Y			M46I/L63P/V82T: 4-fold; L10R/M46I/L63P/V82T: 4-fold; L10R/M46I/L63P/V82T/I84V: 8-fold	Condra96, Condra95
V 82 T	GTC→ACC	PI	SKF108842	Y	?				Shao95
V 82 T	GTC→ACC	PI	SKF108922	Y	?				Shao95
I 84 A	ATA→GCA	PI	BILA 1906 BS	Y	?		BILA 2185 BS (200)	V32I/A71V: 3-fold; V32I/M46I,L/A71V/I84V: 5-fold; V32I/M46I,L/A71V/I84A: 520-fold. 32I/46L/71V/84A are functionally impaired. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′))	Croteau97, Doyon96, Lamarre94, Lamarre95
I 84 A	ATG→ATA	PI	BILA 2011 (palinavir)	Y	?		Ro 31–8959 (400);	I84A is the most common mutation	Lamarre94
I 84 V	ATA→GTA	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	I84V/L10F/M46I: 4 fold, I84V/L10F/M46I/T91S: 12 fold, I84V/L10F/M46I/T91S/V32I/I47V: 46 fold, Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
I 84 V	ATA→GTA	PI	ABT-538 (ritonavir)	Y	Y			M46I/L63P/A71V/V82F/I84V: 27-fold; V82F/I84V: 8- to 10-fold; M46I/L63P/A71V/V82F/I84V: 27-fold	Molla96
I 84 V	ATA→GTA	PI	AG1343 (nelfinavir)		?			M46I/L63P/A71V/I84V: 30-fold	Patick96
I 84 V	ATA→GTA	PI	BILA 1906 BS	Y	?		BILA 2185 BS(200)	V32I/A71V: 3-fold; V32I/M46I,L / A71V/I84V: 5-fold; V32I/M46I,L/ A71V/I84A: 520-fold. 32I/46L/71V/ 84A are functionally impaired. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′)	Croteau97, Doyon96, Lamarre94, Lamarre95
I 84 V	ATA→GTA	PI	BILA 2185 BS	Y	?		BILA 1906 BS(360)	L10F/L23I/V32I/M46I/I47V/I54M/ A71V/I84V: 1,500-fold. Associated Gag mutations: p1/p6 cleavage site (L to F (CTT to TTT at P1′); p7/p1 cleavage site (Q to R (CAG to CGG) at P3′, A to V (GCT to CTT) at P2′).	Croteau97
I 84 V	ATA→GTA	PI	BMS 232632	Y	?			Minor resistance mutation for BMS-232632.	Gong99
I 84 V	ATA→GTA	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/ N88S: 93-fold., V32I/M46I/I84V/ L89M: 96-fold.	Gong00
I 84 V	ATA→GTA	PI	DMP 450	Y	?				Otto95, Winslow95
I 84 V	ATA→GTA	PI	DMP-323	Y	?	12	P9941; not A-77003 or Ro 31–8959	V82F/I84V: 92-fold; L10F/K45I/I84V: 50-fold	Tisdale94, King95
I 84 V	ATA→GTA	PI	JE-2147	Y	?		KNI-272: 7-fold; Ritonavir: 9-fold	L10F/I47V/I84V: 19-fold. L10F/M46I/ I47V/I84V: 28-fold. >50 passages required for isolation of resistant virus.	Yoshimura99
I 84 V	ATA→GTA	PI	MK-639 (indinavir)	N	Y			G48V/I84V/L90M: 30-fold; L10R/ M46I/L63P/V82T/I84V: 8-fold	Condra96, Condra95

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
I 84 V	ATA→GTA	PI	MP-134	Y	?	10	MP-167(5) ABT-538(10) MK-639(8) SC-52151(8) Ro31–895(2) (IC90 data)		Mo96
I 84 V	ATA→GTA	PI	Ro 31–8959 (saquinavir)	Y	?				Tisdale94
I 84 V	ATA→GTA	PI	RPI-312	Y	?	5			el-Farrash94
I 84 V	ATA→GTA	PI	SKF108842	Y	?				Shao95
I 84 V	ATA→GTA	PI	VB 11,328	Y	?			L10F/I84V: 8-fold	Partaledis95
I 84 V	ATA→GTA	PI	VX-478 (amprenavir)	Y	?				Partaledis95
N 88 D	AAT→GAT	PI	AG1343 (nelfinavir)	Y	Y			D30N and N88D are most common in vivo after 24 weeks of therapy; they do not cause cross-resistance to other protease inhibitors.	Patick96
N 88 D	AAT→GAT	PI	SC-52151 (telinavir)	Y	?			N88D compensatory, no resistance alone	Potts94, Pillay96
N 88 S	AAT→AGT	PI	BMS 232632	Y	?			Major resistance mutation for BMS-232632.	Gong99
N 88 S	AAT→AGT	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00
N 88 S	AAT→AGT	PI	SC-55389A	Y	?	20	L735,524 (3); not SC-52151	N88S/L10F: 25	Smidt97
N 88 S	AAT→AGT	PI	VX-478 (amprenavir)	Y	Y			Confers >2.5-fold hypersusceptibility to Amprenavir.	Ziermann00
L 89 M	AAT→AGT	PI	BMS 232632	Y	?			V32L/L33F/M46I/A71V/I84V/N88S: 183-fold., L10Y,F/I50L/L63P/A71V/N88S: 93-fold., V32I/M46I/I84V/L89M: 96-fold.	Gong00

Mutations in HIV PROTEASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
L 90 M	TTG→ATG	PI	ABT-378 (lopinavir)	N	Y			In conjunction with other mutations, susceptibility to lopinavir was reduced by mutations at positions 82,54,10,63,71 and 84 by 4–10-fold, K20M/R by >20-fold and F53L by >40-fold. IC50 of lopinavir against isolates with 0–3 mutations was 0.8-fold higher	Kempf01
L 90 M	TTG→ATG	PI	ABT-538 (ritonavir)	N	Y			82A/54V/I/71V/90L/M: 7-fold	Molla96
L 90 M	TTG→ATG	PI	AG1343 (nelfinavir)	N	Y			Rare in patients	Patick96
L 90 M	TTG→ATG	PI	MK-639 (indinavir)	?	Y				Condra96
L 90 M	TTG→ATG	PI	Ro 31–8959 (saquinavir)	Y	Y			G48V/L90M: >100-fold enzyme resistance; double mutant rare in vivo; L90M most common in vivo; G48V/I84V/L90M: 30-fold	Jacobsen94
T 91 S	ACT→TCT	PI	ABT-378 (lopinavir)	Y	?		Passage 17 virus: ritonavir, 21-fold; saquinavir, 4-fold	I84V/L10F/M46I/T91S: 12 fold, I84V/L10F/M46I/T91S/V32I/I47V: 46 fold, Passage 17 virus: I84V/L10F/M46I/T91S/V32I/I47V/V47A/G16E/H69Y: 338 fold (in presence of p7/p1 (AN/F to VN/F) cleavage-site mutation and p1/p6 (F/L to F/F) cleavage-site mutation).	Carrillo98
L 97 V	TTA→GTA	PI	DMP-323	Y	?			No resistance alone; V82A/L97V: 3-fold; V82A/M46L/L97V: 11-fold	King95

Mutations in HIV INTEGRASE that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
G 140 S	GGC→AGC	II	L-Chicoric Acid	Y	?	156-fold		Mutation located in the catalytic core of integrase. Mildly attentuates virus growth.	King98

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
R 22 A	AGG→AGA	F/BI	RPR103611	Y	?				Labrosse97
G 36 S	GGT→AGT	F/BI	T20 (pentafuside)	Y	?			Both G36S and V38M mutations must be present to confer resistance.	Rimsky98
V 38 M	GTG→ATG	F/BI	T20 (pentafuside)	Y	?			Both G36S and V38M mutations must be present to confer resistance.	Rimsky98
I 84 S	ATC→AGC	F/BI	RPR103611	Y	?				Labrosse97
L 91 H	ATC→AGC	F/BI	RPR103611	Y	?				Labrosse00
N 106 K	AAT→AAG	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98
S 113 N	AGT→AAT	F/BI	DS (Dextran sulphate)	Y	?			S113N/S134N/K269E/Q278E/N293D/N323S/R387I: 250-fold; 113 is in the V1 loop region	Este96a, Este97
S 134 N	AGC→AAC	F/BI	DS (Dextran sulphate)	Y	?			V2 loop region; S113N/S134N/K269E/Q278E/N293D/N323S/R387I: 250-fold	Este97, Este96a
S 134 N	AGC→AAC	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98
F 145 L	TTC→TTA	F/BI	JM-3100	Y	?			Combination of mutations: 2- to 100-fold	DeVreese96, DeVreese96a
F 145 L	TTC→TTA	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98
N 188 K	AAT→AAA	F/BI	Siamycin I	Y	?			N188K/G332E/N351D/A550T/N633D/L762S: 9-fold	Lin96
I 228 V	ATA→GTA	F/BI	JM-2763	Y	?			Combination of mutations	DeVreese96a
G 237 R	ATA→GTA	F/BI	IC9564 (emivirine)	Y	?				Holz-Smith01
F 245 I	TTC→ATC	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98
R 252 K	TTC→ATC	F/BI	IC9564 (emivirine)	Y	?				Holz-Smith01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
K 269 E	AAA→GAA	F/BI	DS (Dextran sulphate)	Y	?			V3 loop region; S113N/S134N/K269E/ Q278E/N293D/N323S/R387I: 250-fold	Este97, Este96a
N 269 E	AAC→GAA	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/ 288V/293D/364–367Deletion/387T: 15-fold.	Schols98
N 269 K	AAC→?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 269 K	AAC→?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 269 K	AAC→?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
N 269 K	AAC⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
N 269 K	AAC⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 269 K	AAC⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 270 S	AAT⟶AGT	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
R 272 T	AGA⟶ACA	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
S 274 del	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
S 274 del	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
S 274 del	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
S 274 del	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
S 274 del	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
S 274 del	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
S 274 R	AGT⟶AGA	F/BI	JM-2763	Y	?			Combination of mutations: 95- to 792-fold	DeVreese96, DeVreese96a
S 274 R	AGT⟶AGA	F/BI	JM-3100	Y	?	DS (> 7 to 6,667)			DeVreese96, DeVreese96a
I 275 del	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 275 del	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 275 del	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
I 275 del	?→?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
I 275 del	?→?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 275 del	?→?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 278 H	CAG→CAT	F/BI	DS (Dextran sulphate)	Y	?			V3 loop region; S113N/S134N/K269E/Q278E/N293D/N323S/R387I: 250-fold	Este97, Este96a
Q 278 H	CAG→CAT	F/BI	JM-2763	Y	?				DeVreese96, DeVreese96a
Q 278 H	CAG→CAC	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
Q 278 H	CAG→CAT	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
Q 278 T	CAG→ACG	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 278 T	CAG→ACG	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 278 T	CAG→ACG	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 278 T	CAG→ACG	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
Q 278 T	CAG→ACG	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 278 T	CAG→ACG	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
R 279 K	?→?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
R 279 K	?→?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
R 279 K	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
R 279 K	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
R 279 K	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
R 279 K	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
A 284 V	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
A 284 V	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
A 284 V	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
A 284 V	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
A 284 V	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
A 284 V	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
F 285 L	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
F 285 L	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
F 285 L	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
F 285 L	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
F 285 L	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
F 285 L	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
V 286 Y	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
V 286 Y	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
V 286 Y	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
V 286 Y	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
V 286 Y	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
V 286 Y	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 288 T	ATA⟶ACA	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 288 T	ATA⟶ACA	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
I 288 T	ATA→ACA	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 288 T	ATA→ACA	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
I 288 T	ATA→ACA	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 288 T	ATA→ACA	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
I 288 V	ATA→GTA	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
I 288 V	ATA→GTC	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
ins 290 T	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
ins 290 T	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
ins 290 T	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
ins 290 T	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
ins 290 T	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
ins 290 T	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
K 290 E	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
K 290 E	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
K 290 E	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
K 290 E	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
K 290 E	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
K 290 E	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
N 293 D	AAT→GAT	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 293 D	AAT→GAT	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 293 D	AAT→GAT	F/BI	DS (Dextran sulphate)	Y	?			V3 loop region; S113N/S134N/K269E/ Q278E/N293D/N323S/R387I: 250-fold	Este97, Este96a
N 293 D	AAT→GAT	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 293 D	AAT→GAT	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/ 288V/293D/364–367Deletion/387T: 15-fold.	Schols98

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
N 293 D	AAT→GAT	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
N 293 D	AAT→GAT	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 293 D	AAT→GAT	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
N 293 H	AAT→CAT	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
M 294 I	?→?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
M 294 I	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
M 294 I	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
M 294 I	?⟶?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
M 294 I	?⟶?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
M 294 I	?⟶?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 296 K	?⟶?	F/BI	ALX40–4C	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 145-fold cross-resistant to ALX40–4C. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 296 K	?⟶?	F/BI	AMD3100	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 15-fold cross-resistant to AMD3100. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 296 K	?⟶?	F/BI	SDF-1	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 26-fold cross-resistant to SDF-1. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
Q 296 K	?→?	F/BI	T134	Y	N			In vitro selected virus (p145 of HIV-1NL4–3, contains mutations N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275 in V3 loop of gp120) 15-fold resistant to T134. Role of each mutation not confirmed by site	Kanbara01
Q 296 K	?→?	F/BI	T140	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 21-fold cross-resistant to T140. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
Q 296 K	?→?	F/BI	vMIP-II	Y	N			T134-resistant virus (selected in vitro, contains N269K, Q278T, R279K, A284V, F285L, V286Y, I288T, K290E, N293D, M294I, and Q296K; 290Tins, D274–275) 42-fold cross-resistant to vMIP II. Role of each mutation not confirmed by site-directed mutagenesis.	Kanbara01
A 297 T	GCA→ACA	F/BI	JM-2763	Y	?				DeVreese96, DeVreese96a
A 297 T	GCA→ACA	F/BI	JM-3100	Y	?				Este97, Este96a
N 323 S	AAT→AGT	F/BI	DS (Dextran sulphate)	Y	?			C3 region; S113N/S134N/K269E/ Q278E/N293D/N323S/R387I: 250-fold	Este97, Este96a
G 332 E	GGA→GAA	F/BI	Siamycin I	Y	?			N188K/G332E/N351D/A550T/N633D/ L762S: 9-fold	Lin96
N 351 D	AAT→GAT	F/BI	Siamycin I	Y	?			N188K/G332E/N351D/A550T/N633D/ L762S: 9-fold	Lin96
P 385 L	CCA→CTA	F/BI	JM-2763	Y	?				DeVreese96, DeVreese96a
P 385 L	CCA→CTA	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a

Mutations in HIV ENV that confer drug resistance, ordered by position.

Amino Acid Change			Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
R	387	I	AGA→ACA	F/BI	DS (Dextran sulphate)	Y	?			CD4 binding region; S113N/S134N/K269E/Q278E/N293D/N323S/R387I: 250-fold	Este97, Este96a
R	387	T	AGA→ACA	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98
Q	410	E	CAA→GAA	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
S	433	P	TCC→CCC	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
V	457	I	GTA→ATA	F/BI	JM-3100	Y	?				DeVreese96, DeVreese96a
A	550	T	GCC→ACC	F/BI	Siamycin I	Y	?			N188K/G332E/N351D/A550T/N633D/L762S: 9-fold	Lin96
N	633	D	AAT→GAT	F/BI	Siamycin I	Y	?			N188K/G332E/N351D/A550T/N633D/L762S: 9-fold	Lin96
L	762	S	TTG→TCG	F/BI	Siamycin I	Y	?			N188K/G332E/N351D/A550T/N633D/L762S: 9-fold	Lin96
FNSTW	364–368		Deletion	F/BI	SDF-1α	Y	?		SDF-1β: 15-fold; AMB2763: 3-fold.	106K/134N/145L/245I/269E/278H/288V/293D/364–367Deletion/387T: 15-fold.	Schols98

Mutations in SIVRT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
K 65 R	AAA→AGA	F/BI	PMPA (tenofovir)	?	Y	5	3TC (80); ddI; ddC; d4T; PMEA	K65R appears first, followed by N69S and I118V. Observed changes at N69S and I118V do not result in increased resistance.	VanRompay96, Cherrington96a, VanRompay97a
Q 151 M	CAG→ATG	F/BI	AZT (zidovudine)	?	Y	>100	ddI; ddC; d4T; 3TC		VanRompay97
M 184 V	ATG→GTG	F/BI	(-)-FTC (emtricitabine)	Y	?				Schinazi95

Mutations in FIVRT that confer drug resistance, ordered by position.

Amino Acid Change	Codon Change	Drug Class	Compound	In vitro	In vivo	-Fold -resist	Cross-resist (-fold)	Comments	Refs
D 3 H	GAT→CAT	FIV NRTI	ddC (zalcitabine)	Y	?	4	ddI; PFA		Medlin96, Zhu96
V 47 I	GTA→ATA	FIV NRTI	d4T (stavudine)	Y	?	4–6	PFA (>50); AZT; ddI; PMEA		Smith96
P 156 S	CCA→TCA	FIV NRTI	3TC (lamivudine)	Y	?	7	AZT (4), AZT + 3TC (6)		Smith98
M 183 T	ATG→ACG	FIV NRTI	(-)-FTC (emtricitabine)	Y	?	10	ddC	Corresponds to 184 in HIV; M183V recombinant displays 10-fold resistance to 3TC or (-)-FTC.	Smith97

Abbreviations used in tables

Amino acids

A	alanine
C	cysteine
D	aspartate
E	glutamate
F	phenyalanine
G	glycine
H	histidine
I	isoleucine
K	lysine
L	leucine
M	methionine
N	asparagine
P	proline
Q	glutamine
R	arginine
S	serine
T	threonine
V	valine
W	tryptophan
Y	tyrosine

Drug class

F/BI	Fusion/Binding Inhibitor
II	Integrase Inhibitor
MN	Multiple Nucleoside
NRTI	Nucleoside Reverse Transcriptase Inhibitor
NNRTI	HIV-1 Specific Nonnucleoside RT Inhibitor
PI	Protease Inhibitor
PARTI	Pyrophosphate Analogue RTI
SIV RTI	SIV Nucleoside RTI

Compounds

Compound	Other Names (Company)	Chemical Name or Description
1737		Tetrahydronapthalene lignan derivative
(-)-dOTC	BCH-10652	(-)-2′-deoxy-3′-oxa-4′-thiocytidine
(-)-dOTFC		(-)-2′-deoxy-3′-oxa-4′-thio-5-fluorocytidine
(-)-FTC	Emtricitabine, Coviracil (Triangle Pharmaceuticals)	(-)-(2*R*,5*S*)-5-fluoro-1-[2-(hydroxymethyl)-1,3-oxathiolan-5-yl]cytosine
(+)-dOTC		(+)-2′-deoxy-3′-oxa-4′-thiocytidine
(+)-dOTFC		(+)-2′-deoxy-3′-oxa-4′-thio-5-fluorocytidine
1592U89	Abacavir, Ziagen (Glaxo Wellcome)	(1*S*,4*R*)-4-[2-amino-6-cyclopropyl-amino)-9H-purin-9-yl]-2-cyclopentene-1-methanol succinate
3TC	(-)-BCH-189, Lamivudine, Epivir (Glaxo Wellcome)	(-)-β-L-2′,3′-dideoxy-3′-thiacytidine
8-chloro-TIBO	RO91767, R86183, tivirapine	(+)-(*S*)-4,5,6,7-Tetrahydro-8-chloro-5-methyl-6-(3-methyl-2-butenyl)imidazol[4,5,1-jk][1,4]benzodiazepine
A-77003	C2 symmetry-based protease inhibitor (Abbott)	2PyridCH2NCH3CO-Val-NHCH(Bz)]CHOHCHOH
AAP-BHAP	U-104489 (Pharmacia & Upjohn)	1-[(5-Methanesulfonamidoindol-2-yl)carbonyl]-4-[N-ethyl-N-[3-(1,1-dimethyl)amino]-2-pyridinyl]amino]piperidine
ABT-378	Aluviran, Lopinavir (Abbott)	N-[(1S,3S,4S)-4-[[2,6-dimethylphenoxy)acetyl]amino]-3-hydroxy-5-phenyl-1-(phenylmethyl)pentyl]tetrahydro-α-(1-methylethyl)-2-oxo-1(2H)-pyrimidineacetamide
ABT-538	Ritonovir, Norvir (Abbott)	10-Hydroxy-2-methyl-5-(1-methylethyl)-1-[2-(1-methylethyl)-4-thiazolyl]-3,6-dioxo-8,11-bis(phenylmethyl)-2,4,7,12-tetraazatridecan-13-oic acid, 5-thiazolylmethyl ester

Abbreviations (cont)

Compounds (cont)

ADAMII		Methyl 3′,3″-dichloro-4′,4″-dimethoxy-5′,5″-bis(methoxycarbonyl)-6,6-diphenyl-5-hexenoate
AG1343	Nelfinavir, Viracept (Agouron)	(3*S*,4a*S*,8a*S*)-N-tert-Butyl-2-[(2*R*,3*R*)-3-(3,2-cresotamido)-2-hydroxy-4-(phenylthio)butyl]decahydro-3-isoquinoline-carboxamide monomethanesulfonate
ALX40-4C		a polypeptide of nine d-Arg residues
AMD3100		octahydrochloride dihydrate of 1,19-[1,4-phenylene-bis-(methylene)]-bis-1,4,8,11-tetra-azacyclotetradecane
AZT	zidovudine (Glaxo Wellcome)	3′-azido-3′-deoxythymidine
BHAP U-87201E	Atevirdine (Pharmacia Upjohn)	1-[(5-Methyoxyindol-2-yl)carbonyl]-4-[3-(ethylamino)-2-pyridyl]piperazine
BHAP U-88204E		1-(Indolyl-2-carbonyl)-4-[3-[(1-methylethyl)amino]pyridyl-piperazine
BHAP U-90152	Delavirdine, Rescriptor (Pharmacia Upjohn)	1-(5-Methanesulphonamido)-1H-indol-2-yl-carbonyl)-4-[3-(isopropylamino)-2-pyridinyl]piperazine
BHAP U-90153		bisheteroarylpiperidinyl derivative
BHAP U-90154		bisheteroarylpiperidinyl derivative
BHAP U-90155		bisheteroarylpiperidinyl derivative
BILA 1906 BS	(Bio-Mega/Boehringer Ingelheim)	N-{1*S*-[[[3-[2*S*-(1,1-dimethylethyl)amino]carbonyl-4*R*-]3-pyridinylmethyl)thio]-1-piperidinyl]-2*R*-hydroxy-1*S*-(phenylmethyl)propyl]amino]carbonyl]-2-methylpropyl}-2-quinolinecarboxamide
BILA 2011	Palinavir (Bio-Mega/Boehringer Ingelheim)	N-{1*S*-[[[3-[2*S*-(1,1-dimethylethyl)amino]carbonyl]-4*R*-[4-pyridinylmethyl)oxy]-1-piperidinyl]-2*R*-hydroxy-1*S*-(phenylmethyl)propyl]amino]carbonyl]-2-methylpropyl}-2-quinolinecarboxamide
BILA 2185 BS	(Bio-Mega/Boehringer Ingelheim)	N-(1,1-dimethylethyl)-1-[2*S*-[[2-2,6-dimethyphenoxy)-1-oxoethyl]amino]-2*R*-hydroxy-4-phenylbutyl]4*R*-pyridinylthio)-2-piperidine-carboxamide
BI-RG-587	Nevaripine, Viramune (Boehringer Ingleheim)	11-Cyclopropyl-4-methyl-5,11-dihydro-6H-dipyrido[3,2-b:2′,3′-e]-[1,4]diazepin-6-one
BM+51.0836		thiazolo-isoindolinone derivative
BMS 186318	(Bristol-Myers Squibb)	[1*S*-[1*R**,2*S**(2*S**,3*R**)]]-[3-[[3-[[(1,1-Dimethylethoxy)-carbonyl]amino]-2-hydroxy-4-[4-[2-(4-morpholinyl)-2-oxoethoxy]phenyl]butyl]amino]-2-hydroxy-1-(phenylmethyl)propyl]carbamic Acid, 1,1-dimethylethyl-ester
BMS 232632		azapeptide protease inhibitor
Calanolide A	NSC675451	a dipyranocoumarin
d4T	Stavudine, Zerit (Bristol-Myers Squibb)	2′,3′-didehydro-3′-deoxythymidine
ddC	Zalcitabine, Hivid (Roche)	2′,3′-dideoxycytidine
ddI	Didanosine, Videx (Bristol-Myers Squibb)	2′,3′-dideoxyinosine
DMP-266	Efavirenze, Sustiva (Dupont Merck)	(-)-6-Chloro-4-cyclopropylethynyl-4-trifluoromethyl-1,4,-dihydro-2H-3,1-benzoxazin-one
DMP-323	XM-323 (Dupont Merck)	[4*R*-(4-α,5-α,6-β,7-β)]-hexahydro-5,6-dihydroxy-1,3-bis[(4-hydroxymethyl)phenyl]methyl]-4,7-bis(phenylmethyl)-2H-1,3-diazepin-2-one

Abbreviations (cont)

Compounds (cont)

DMP-450	(Avid Therapeutics)	[4*R*-(4-α,5-α,6-β,7-β)]-hexahydro-5,6-bis(hydroxy)-1,3-bis(3-amino)phenyl]methyl)-4,7-bis(phenylmethyl)-2H-1,3-diazepin-2-onebismesylate
DS		dextran sulfate
DXG	(-)-β-dioxolane-G	(-)-(2*R*,4*R*)-9-[2-(Hydroxymethyl)-1,3-dioxolan-4-yl]guanine
E-BPTU	NSC 648400	1-benzyloxymethyl-5-ethyl-6-(2-pyridylthio)uracil
EBU-dM		5-ethyl-1-ethoxymethyl-6-(3,5-dimethylbenzyl)uracil
E-EBU		5-ethyl-1-ethoxymethyl-6-benzyluracil
E-EPSeU		1-(ethoxymethyl)-(6-phenylselenyl)-5-ethyluracil
E-EPU		1-(ethoxymethyl)-(6-phenyl-thio)-5-ethyluracil
F-ddA	Lodenosine	2′-fluoro-2′,3′-dideoxyadenosine
GW420867X		S-3-ethyl-6-fluoro-4-isopropoxycarbonyl-3,4-dihydro-quinoxalin-2(1H)-one
HBY 097		(*S*)-4-isopropoxycarbonyl-6-methoxy-3-(methylthio-methyl)-3,4-dihydroquinoxalin-2(1H)-thione
HEPT		1-[(2-hydroxyethoxy)methyl]6-(phenylthio)thymine
IC9564	Betulinic acid derivative	4*S*-[8-(28 betuliniyl) aminooctanoylamino]-3*R*-hydroxy-6-methylheptanoic acid
I-EBU	MKC-442, emivirine, coactinon (Triangle Pharmaceuticals)	6-benzyl-1-ethoxymethyl-5-isopropyluracil (I-EBU, Triangle Pharmaceuticals/
JE-2147		an allophenylnorstatine-containing dipeptide protease inhibitor
JM-2763	(Johnson Matthey)	1,10-(1,3-propanediyl)-bis-1,4,8,11-tetraazacyclo-tetradecane
JM-3100	SID791 (Johnson Matthey)	1,10-[1,4-phenylenebis-(methylene)]bis-(1,4,8,11-tetraazacyclotetradecane)octahydrochloride dihydrate
KNI-272	Kynostatin 272	(2*S*,3*S*)-3-amino-2-hydroxy-4-phenylbutyric acid-containing tripeptide
L-697,593		5-ethyl-6-methyl-3-(2-phthalimido-ethyl)pyridin-2(1H)-one
L-697,661		3-[(-4,7-dichloro-1,3-benzoxazol-2-yl)methyl]amino-5-ethyl-6-methylpyridin-2(1H)-one
L-Chicoric acid		[S-(*R**,*R**)]-2,3-Bis[[3-(3,4-dihydroxyphenyl)-1-oxo-2-propenyl]oxy]butanedioic acid
L-FddC		(-)-β-L-5-fluoro-2′,3′-dideoxy-cytidine
LY-300046 HCl	Trovirdine (Lilly/Medivir/Abbott)	N-[2-(2-pyridylethyl)-N′-[2-(5-bromopyridyl)thiourea,hydrochloride
MK-639	Indinavir, Crixivan, L-735,524 (Merck)	[1(1*S*,2*R*),5(*S*)]-2,3,5-Trideoxy-N-(2,3-dihydro-2-hydroxy-1H-inden-1-yl)-5-[2-[[(1,1-dimethylethyl)amino]carbonyl]-4-(3-pyridinylmethyl)-1-piperazinyl]-2-(phenylmethyl)-D-erythro-pentonamide sulfate
MP-134		C2 symmetry-based protease inhibitor
P9941	(Dupont Merck)	[2-pyridylacetyl-IIePheAla-y(CHOH)]$_2$
PFA	Foscarnat (Astra)	phosphonoformate
PMEA	(Gilead Sciences)	9-(2 phosphonylmethoxyethyl)adenine
PMPA	(Gilead Sciences)	(*R*)-9-(2-phosphonyl-methoxypropyl)adenine
PNU-140690	Tipranavir, U-140690 (Pharmacia & Upjohn)	(6*R*)-3-(1*R*)-1-[3-([Trifluoromethyl)(2-pyridyl)]sulfonylamino)-phenyl]propyl-4-hydroxy-6-(2-phenylethyl)-6-propyl-5,6-dihydro-2H-pyran-2-one

Abbreviations (cont)

Compounds (cont)

QM96521		1,1,3-trioxo-2H,4H-thieno[2,4-3][1,2,4]thiadiazine derivative (TTD)
QYL-685		methylenecyclopropane nucleoside analog with a phenylphosphoralaninate moiety
Ro 31-8959	Saquinavir, Invirase, Fortovase (Roche)	N(1)-[3-[3-[[(1,1-dimethylethyl)amino]carbonyl]octahydro-2(1H)-isoquinolinyl]-2-hydroxy-1-(phenylmethyl)propyl]-2-[(2-quinolinylcarbonyl)amino]-,[3*S*-[2[1*R**(*R**),2*S**],3α,4aβ,8aβ]]-, monomethanesulfonate
RPI-312		1-[(3*S*)-3-(n-alpha-benzyloxycarbonyl)-l-asparginyl)-amino-2-hydroxy-4-phenyl-butyryl]-n-tert-butyl-l-proline amide (peptidyl protease inhibitor)
RPR103611		a triterpene betulinic acid derivative
S-1153		5-(3,5-dichlorophenyl)thio-4-isopropyl-1-(4-pyridyl)methyl-1Himidazol-2-yl methyl carbamate
S-2720		6-chloro-3,3-dimethyl-4-(isopropenyl-oxycarbonyl)-3,4-dihydroquinoxalin-2(1H)thione
SC-52151	Telinavir	N-tert-butyl-N′-isobutyl-N′-[2(*R*)-hydroxy-4-phenyl-3(*S*)-[4-amino-1,4-dioxo-2(*S*)-(2-quinolinylcarboxamido)butyl-amino]butyl]urea
SC-55389A	(Searle)	hydroxyethyl-urea isostere protease inhibitor
SDF-1		Stromal derived factor 1
SDF-1α		Stromal cell-derived factor 1α
Siamycin I		21-residue tricyclic peptide
SKF108842		protease inhibitor
T134		[Tyr5,12, Lys7]-polyphemusin II-derivative with amino acid sequence R-R-W-C-Y-R-K-DK-P-Y-R-Ci-C-R-COOH
T140		[Tyr5,12, Lys7]-polyphemusin II-derivative
T20	DP-178, Pentafuside (Trimeris)	Ac-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-NH2
TIBO R82150	(Janssen)	(+)-(5*S*)-4,5,6,7-tetrahydro-5-methyl-6-(3-methyl-2-butenyl)-imidazo[4,5,1-jk][1,4]-benzodiazepin-2(1H)-thione
TIBO R82913	(Janssen)	(+)-(5*S*)-4,5,6,7,-tetrahydro-9-chloro-5-methyl-6-(3-methyl-2-butenyl)-imidazo-[4,5,1-jk]-[1,4]benzo-diazepin-2(1it H)-thione
TSAO		[2′,5′-bis-O-(tert-butyldimethylsilyl)-3′-spiro-5″-(4″-amino-1″,2″-oxathiole-2″,2″-dioxide)]-β-D-pentofuranosyl derivative
UC-10	NSC 645129 (Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-16	(Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-32	NSC 645542 (Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-38	NSC 629243 (Uniroyal Chemical Co)	4-chloro-3-(isopropoxycarbonyl)phenylcarbamothioic acid, O-isopropyl ester
UC-42	(Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-57	NSC 647014 (Uniroyal Chemical Co)	thiocarboxanilide derivative

Abbreviations (cont)

Compounds (cont)

UC-68	NSC 638532 (Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-69	NSC 646989 (Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-70	NSC 638534 (Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-781	(Uniroyal Chemical Co)	N-[4-chloro-3-(3-methyl-2-butenyloxy)phenyl]-2-methyl-3-furancarbothioamide
UC-80	NSC 639475 (Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-81	NSC 615727 (Uniroyal Chemical Co)	thiocarboxanilide derivative
UC-82	(Uniroyal Chemical Co)	N-[4-chloro-3-(3-methyl-2-butenyloxy)phenyl]-2-methyl-3-thiophenecarbothioamide
UC-84	NSC 615985 (Uniroyal Chemical Co)	thiocarboxanilide derivative
VB 11,328	(Vertex)	Carbamic acid, [3-[[(4-methoxyphenyl)sulfonyl](cyclopentyl-methyl)amino]-2-hydroxy-1-(phenylmethyl)propyl]-,tetrahydro-3-furanyl ester
vMIP-II		viral macrophage inflammatory protein II
VX-478	141W94, Amprenavir, Agenerase	Carbamic acid, ((1*S*,2*R*)-3-(((4-aminophenyl)sulfonyl)(2-methylpropyl)amino)-2-hydroxy-1-(phenylmethyl)propyl)-,(3*S*)-tetrahydro-3-furanyl ester
α-APA	R18893, loviride analog	(+)-2,6-Dichloro-α-[(2-acetyl-5-methylphenyl)amino]benzamide

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