

Centre for AIDS Reagents.

Data Sheet

NAME: HIV-1 B Gag Peptides

REPOSITORY REFERENCE: ARP7114.1-84

SIZE: 11-19 mers

SPECIAL CHARACTERISTICS: Series of peptides comprising the Gag region. Peptides are 11-19 amino acids in length. Most peptides are >80% pure. Peptides that are difficult to solubilize can almost always be dissolved in DMSO. Once a peptide is in solution, the DMSO can be slowly diluted with aqueous medium. Care must be taken to ensure that the peptide does not begin to precipitate out of solution.

REGION OF HOMOLOGY: HIV-1 Gag (see Legend for sequence homology)

PRESENTATION: 1mg

ACKNOWLEDGEMENTS: Publications should acknowledge the donor of the reagent and the Programme EVA Centre for AIDS Reagents. Suggested wording can be found on our website at <http://www.nibsc.ac.uk/spotlight/aidsreagent/index.html> in the "Acknowledgements" section. Please also ensure that you send us a copy of any papers resulting from work using reagents acquired through CFAR (this can be electronically or as a paper copy)

Repository Reference	Amino Acid Sequence	Size	
ARP7114.1	MGARASVLSGGEL	13mer	
ARP7114.2	ASVLSGGELDRWEKI	15mer	(4aa gap)
ARP7114.3	GELDRWEKIRLRPGGKKKY	19mer	(6aa gap)
ARP7114.4	WEKIRLRPGGKK	12mer	(5aa gap)
ARP7114.5	RPGGKKKYKCLKHIVW	15mer	(6aa gap)
ARP7114.6	KYKCLKHIVWASREL	14mer	(6aa gap)
ARP7114.7	HIVWASRELERFAVNPGLL	19mer	(5aa gap)
ARP7114.8	VWASRELERFA	11mer	(2aa gap)
ARP7114.9	LERFAVNPGLLETSEGCR	18mer	(6aa gap)
ARP7114.10	NPGLLETSEGC	11mer	(6aa gap)
ARP7114.11	SEGCRQILGQLQPSLQT	17mer	(7aa gap)
ARP7114.12	LGQLQPSLQTGSEELRSLY	19mer	(7aa gap)

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ARP7114.13	PSLQTGSEELRSLYNTV	17mer	(5aa gap)
ARP7114.14	EELRSLYNTVATLY	14mer	(7aa gap)
ARP7114.15	SLYNTVATLYCVH	13mer	(4aa gap)
ARP7114.16	ATLYCVHQRIEVKDTKEAL	19mer	(6aa gap)
ARP7114.17	QRIEVKDTKEALEKI	15mer	(7aa gap)
ARP7114.18	TKEALEKIEEEQNKSCKKA	19mer	(7aa gap)
ARP7114.19	IEEEQNKSCKKAQQAAADT	19mer	(7aa gap)
ARP7114.20	SKKKAQQAAADTGNSSQV	18mer	(7aa gap)
ARP7114.21	AAADTGNSSQVSQNY	15mer	(7aa gap)
ARP7114.22	QVSQNYPIVQNLQGQMV	17mer	(9aa gap)
ARP7114.23	NYPIVQNLQGQMVHQAIISP	19mer	(4aa gap)
ARP7114.24	VQNLQGQMVHQAIISPRTL	18mer	(4aa gap)
ARP7114.25	QMVHQAIISPRTLNAW	15mer	(6aa gap)
ARP7114.26	QAISPRTLNAWVKVY	14mer	(4aa gap)
ARP7114.27	NAWVKVYEEKAFSPEV	16mer	(8aa gap)
ARP7114.28	VKVYEEKAFSPEVIP	15mer	(3aa gap)
ARP7114.29	EEEKAFSPEVIPMF	13mer	(4aa gap)
ARP7114.30	KAFSPEVIPMFSALS	15mer	(2aa gap)
ARP7114.31	VIPMFSALSEGATPQDL	17mer	(6aa gap)
ARP7114.32	LSEGATPQDLNTMLNTV	17mer	(7aa gap)
ARP7114.33	TPQDLNTMLNTVGGHQAAM	19mer	(5aa gap)
ARP7114.34	TMLNTVGGHQAAMQMLK	17mer	(6aa gap)
ARP7114.35	GHQAAMQMLKETINEEAA	18mer	(7aa gap)
ARP7114.36	AMQMLKETINEEAAEW	16mer	(4aa gap)
ARP7114.37	ETINEEAAEWDRLHPV	16mer	(6aa gap)
ARP7114.38	EEAAEWDRLHPVHAGPIA	18mer	(4aa gap)
ARP7114.39	LHPVHAGPIAPGQMREP	17mer	(8aa gap)
ARP7114.40	GPIAPGQMREPRGSDIAGT	19mer	(6aa gap)
ARP7114.41	REPRGSDIAGTTSTLQEIQI	19mer	(8aa gap)
ARP7114.42	GSDIAGTTSTLQEIQIGWM	18mer	(4aa gap)
ARP7114.43	STLQEIQIGWMTNPPIPV	18mer	(8aa gap)
ARP7114.44	GWMTNPPIPVGEIYKRW	18mer	(7aa gap)
ARP7114.45	PIIPVGEIYKRWIIL	15mer	(6aa gap)
ARP7114.46	IYKRWIILGLNKIV	14mer	(7aa gap)
ARP7114.47	KRWIILGLNKIVRMYS	17mer	(2aa gap)
ARP7114.48	GLNKIVRMYSPTSIL	15mer	(6aa gap)
ARP7114.49	MYSPTSILDIRQGPKPEP	17mer	(7aa gap)
ARP7114.50	DIRQGPKPEFRDYVDRFYK	19mer	(8aa gap)
ARP7114.51	QGPKPEFRDYVDRF	14mer	(3aa gap)
ARP7114.52	FRDYVDRFYKTLRA	14mer	(6aa gap)
ARP7114.53	YVDRFYKTLRAEQASQEV	18mer	(3aa gap)
ARP7114.54	KTLRAEQASQEVKNWMT	17mer	(6aa gap)
ARP7114.55	QASQEVKNWMTETLLV	16mer	(6aa gap)
ARP7114.56	VKNWMTETLLVQANPDC	18mer	(5aa gap)
ARP7114.57	TLLVQANPDCCKTIL	15mer	(7aa gap)
ARP7114.58	NANPDCCKTILKAL	13mer	(5aa gap)
ARP7114.59	KTILKALGPAATLEEMMTA	19mer	(6aa gap)
ARP7114.60	GPAATLEEMMTACQGVGGP	19mer	(7aa gap)
ARP7114.61	ATLEEMMTACQGV	13mer	(3aa gap)
ARP7114.62	TACQGVGGPGHKARVLA	17mer	(7aa gap)
ARP7114.63	GGPGHKARVLAEAMSQV	17mer	(6aa gap)
ARP7114.64	VLAEAMSQVNTSATIMMQR	19mer	(8aa gap)
ARP7114.65	SQVNTSATIMMQRGNFR	17mer	(6aa gap)
ARP7114.66	SATIMMQRGNFRNQRKTV	18mer	(5aa gap)

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ARP7114.67	QRGNFRNQRKTVKCFNC	17mer	(6aa gap)
ARP7114.68	RNQRKTVKCFNCGKEGHI	18mer	(5aa gap)
ARP7114.69	VKCFNCGKEGHIA	13mer	(6aa gap)
ARP7114.70	KEGHIA <u>K</u> NCRAPRKK	15mer	(7aa gap)
ARP7114.71	CRAPRKKGCWKCGKEGHQM	19mer	(8aa gap)
ARP7114.72	KGCWKCGKEGHQMKDCTER	19mer	(6aa gap)
ARP7114.73	KEGHQMKDCTERQANFL	17mer	(7aa gap)
ARP7114.74	KDCTERQANFLGKI	14mer	(6aa gap)
ARP7114.75	RQANFLGKIWPSHKGR	16mer	(5aa gap)
ARP7114.76	KIWPSHKGRPGNFL <u>Q</u> S <u>R</u>	17mer	(7aa gap)
ARP7114.77	KGRPGNFL <u>Q</u> S <u>R</u> PEPTAPP	18mer	(6aa gap)
ARP7114.78	FLQSRPEPTAPPEESF	16mer	(6aa gap)
ARP7114.79	EPTAPPEESFRFGREETTP	19mer	(6aa gap)
ARP7114.80	ESFRFGREETTP <u>S</u> Q <u>Q</u> EPI	19mer	(7aa gap)
ARP7114.81	ETTP <u>S</u> Q <u>Q</u> EPI <u>D</u> KEL <u>Y</u> PL	19mer	(7aa gap)
ARP7114.82	QEPIDKEL <u>Y</u> PLAS <u>L</u> R <u>S</u> L	17mer	(8aa gap)
ARP7114.83	KEL <u>Y</u> PLAS <u>L</u> R <u>S</u> L <u>F</u> G <u>N</u> D <u>P</u>	17mer	(5aa gap)
ARP7114.84	LYPLAS <u>L</u> R <u>S</u> L <u>F</u> G <u>N</u> D <u>P</u> S <u>S</u> Q	18mer	(2aa gap)

Legend:

- Red:** Peptide specific for consensus B and SF2
- Green:** Peptide specific for consensus B with 1 aa change for SF2 (aa change: bold green underlined)
- Blue:** Peptide common for all the tested sequences
- Tangerine:** Peptide common for consensus sequences (B and C) but with 2 aa changes for SF2 (aa changes: bold red underlined)
- Brown:** peptide specific for consensus B only (aa changes with SF2: bold red underlined)
- Violet:** Peptide specific for consensus B and SF2 with 1 aa change for consensus C (aa change: bold violet underlined)

p17 (aa 1-132): **ARP7114.1-22** (9 red, 5 green, 3 blue, 2 tangerine, 2 brown, 1 violet)

p24 (aa 133-363): **ARP7114.23-62** (5 red, 2 green, 16 blue, 15 violet)

p2, p7, p1, p6 (aa 364-500): **ARP7114.63-84** (10 red, 6 blue, 3 brown, 3 violet)