



BLAST Results

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Job title: NP_705927.1 reverse transcriptase [Human immunodeficiency virus...]

RID [YM01ZCD001R](#) (Expires on 10-21 21:55 pm)

Query ID Icl|Query_333722
Description NP_705927.1 reverse transcriptase [Human immunodeficiency virus 1]
Molecule type amino acid
Query Length 560

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR-excluding environmental samples from WGS projects
Program BLASTP 2.7.0+ [Citation](#)

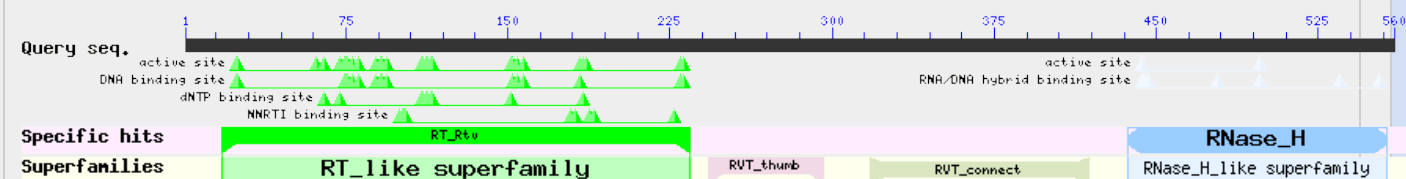
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Graphic Summary

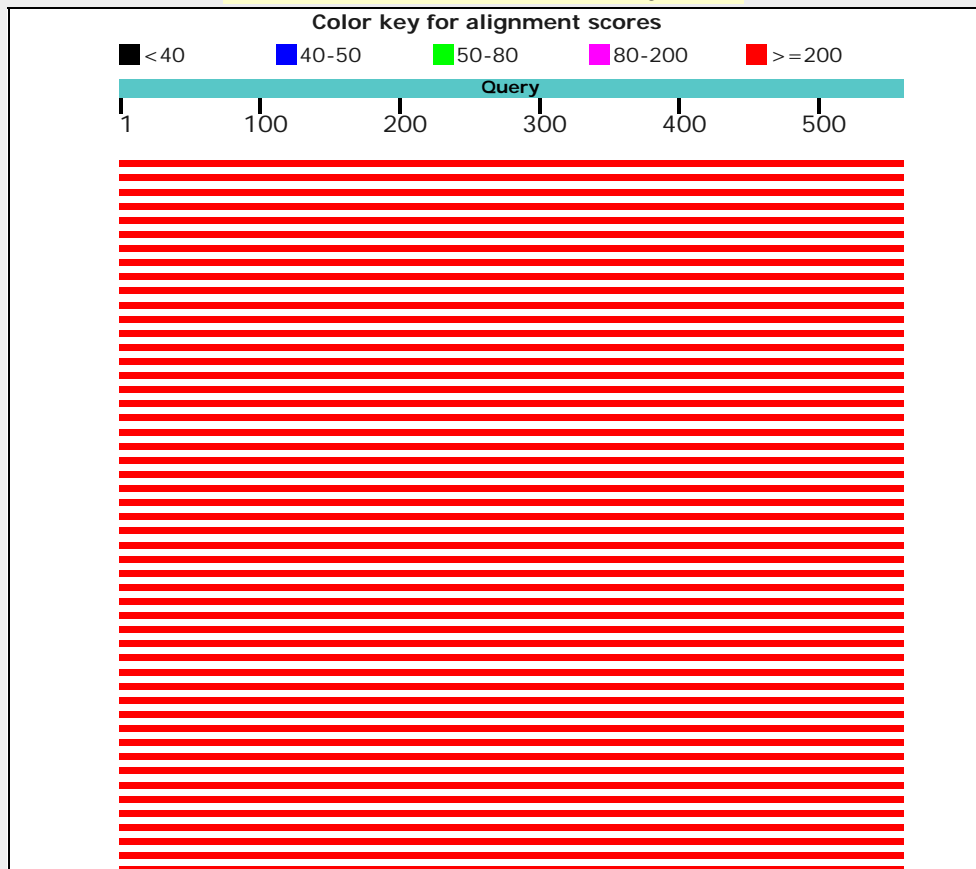
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Distribution of the top 100 Blast Hits on 100 subject sequences

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Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

Alignments	Download	GenPept	Graphics	Distance tree of results	Multiple alignment							
						Description	Max score	Total score	Query cover	E value	Ident	Accession
						Gag-Pol [Human immunodeficiency virus 1]	1149	1149	100%	0.0	100%	NP_057849.4
						RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=M	1142	1142	100%	0.0	99%	P03367.3
						pol protein [synthetic HIV-1]	1142	1142	100%	0.0	100%	APS90951.1
						Pol [Human immunodeficiency virus 1]	1142	1142	100%	0.0	100%	NP_789740.1
						RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=M	1139	1139	100%	0.0	99%	P03366.3
						pol protein [Human immunodeficiency virus 1]	1138	1138	100%	0.0	99%	ABM63566.1
						Chain A. Hiv Reverse Transcriptase In Complex With Inhibitor 7e (Nnrti)	1136	1136	100%	0.0	100%	2RF2_A
						reverse transcriptase [Human immunodeficiency virus 1]	1136	1136	100%	0.0	100%	NP_705927.1
						Chain A. Hiv-1 Rt With Pyridone Non-Nucleoside Inhibitor	1136	1136	100%	0.0	100%	3FFI_A
						pol gene	1136	1136	100%	0.0	99%	1103299E
						Chain A. Novel Indazole Nrtis Created Using Molecular Template Hybridization Based On Crys	1136	1136	100%	0.0	100%	2JLE_A
						Pol [Human immunodeficiency virus 1]	1135	1135	100%	0.0	99%	BAA12997.1
						Chain A. Hiv-1 Rt With Pyridazinone Non-Nucleoside Inhibitor	1135	1135	100%	0.0	100%	3DI6_A
						Chain A. Crystal Structure Of Hiv Rt In Complex With Bilr0355bs	1135	1135	100%	0.0	100%	4KV8_A
						Chain A. Hiv Reverse Transcriptase K103n Mutant In Complex With Inhibitor R8d	1134	1134	100%	0.0	99%	3DRS_A
						pol protein [Human immunodeficiency virus 1]	1134	1134	100%	0.0	99%	AIJ50269.1
						RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=M	1134	1134	100%	0.0	98%	P04587.3
						pol polyprotein (NH2-terminus uncertain) [Human immunodeficiency virus 1]	1134	1134	100%	0.0	99%	AAB59867.1
						Chain A. Hiv-1 K103n Reverse Transcriptase In Complex With Tmc125	1134	1134	100%	0.0	99%	3MED_A
						Chain A. Hiv Reverse Transcriptase Y181c Mutant In Complex With Inhibitor R8e	1134	1134	100%	0.0	99%	3DRR_A
						HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate LAV-1a)	1134	1134	100%	0.0	99%	GNVWLV
						reverse transcriptase/RNaseH [Human immunodeficiency virus 1]	1133	1133	100%	0.0	99%	AAA93161.1
						Chain A. Hiv-1 Reverse Transcriptase Y188I Mutant In Complex With Inhibitor Gsk560	1133	1133	100%	0.0	99%	2YNF_A
						pol polyprotein [Human immunodeficiency virus 1]	1132	1132	100%	0.0	99%	AAA44198.1
						Chain A. Hiv-1 Reverse Transcriptase	1131	1131	100%	0.0	99%	1REV_A
						Chain A. Crystal Structure Of L100i Mutant Hiv-1 Reverse Transcriptase In Complex With Uc-78	1131	1131	100%	0.0	99%	1S1T_A
						Chain A. Crystal Structure Of V108i Mutant Hiv-1 Reverse Transcriptase In Complex With Nevira	1131	1131	100%	0.0	99%	1S1X_A
						Chain A. Crystal Structure Of V106a Mutant Hiv-1 Reverse Transcriptase In Complex With Uc-78	1130	1130	100%	0.0	99%	1S1W_A
						Pol [Human immunodeficiency virus 1]	1130	1130	100%	0.0	99%	BAA12989.1
						Chain A. Crystal Structure Of M184v Mutant Hiv-1 Reverse Transcriptase In Complex With Nevir	1129	1129	100%	0.0	99%	1LWC_A
						pol protein [synthetic construct]	1129	1129	100%	0.0	99%	AAS59072.1
						Chain A. Crystal Structure Of Hiv-1 K103n Mutant Reverse Transcriptase In Complex With Gw56	1129	1129	100%	0.0	99%	3DM2_A
						Chain A. Hiv-1 Reverse Transcriptase In Complex With Dna	1129	1129	100%	0.0	99%	3KJV_A
						Chain A. Crystal Structure Of T215y Mutant Hiv-1 Reverse Transcriptase In Complex With Nevir	1129	1129	100%	0.0	99%	1LW0_A
						Chain A. Crystal Structure Of Y188c Mutant Hiv-1 Reverse Transcriptase	1129	1129	100%	0.0	99%	1JLE_A
						Chain A. Crystal Structure Of Y188c Mutant Hiv-1 Reverse Transcriptase In Complex With Nevir	1128	1128	100%	0.0	99%	1JLF_A
						Chain A. Crystal Structure Of Y181c Mutant Hiv-1 Reverse Transcriptase In Complex With Dmp-	1128	1128	100%	0.0	99%	1JKH_A
						pol protein [Simian immunodeficiency virus]	1128	1128	100%	0.0	98%	AGV34093.1

Chain A, Crystal Structure Of M41IT215Y MUTANT HIV-1 Reverse Transcriptase (Rtmn) In Cor	1127	1127	100%	0.0	99%	1LWE_A
Chain A, Crystal Structure Of Hiv-1 V106a And Y181c Mutant Reverse Transcriptase In Comple	1127	1127	100%	0.0	99%	3DMJ_A
RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=IV	1127	1127	100%	0.0	98%	P35963.3
pol protein [Human immunodeficiency virus 1]	1127	1127	100%	0.0	99%	AFD54422.1
pol polyprotein [Human immunodeficiency virus 1]	1126	1126	100%	0.0	98%	AAA44653.1
Chain A, The Structure Of Unliganded Reverse Transcriptase From The Human Immunodeficien	1126	1126	100%	0.0	99%	1HMV_A
pol protein [Simian immunodeficiency virus]	1126	1126	100%	0.0	98%	AGV33869.1
Chain A, Structures Of Hiv-1 Rt And Rna-dna Complex Reveal A Unique Rt Conformation And S	1126	1126	100%	0.0	99%	4B3O_A
pol protein [Human immunodeficiency virus 1]	1126	1126	100%	0.0	99%	AFD54424.1
pol protein [Human immunodeficiency virus 1]	1125	1125	100%	0.0	99%	ADM25290.1
reverse transcriptase/RNaseH [Human immunodeficiency virus 1]	1125	1125	100%	0.0	99%	AAA93165.1
Chain A, Wild Type Hiv-1 Reverse Transcriptase In Complex With Efavirenz	1125	1125	100%	0.0	99%	1IKW_A
pol protein [Simian immunodeficiency virus]	1125	1125	100%	0.0	98%	AGV34097.1
Chain A, Azt Drug Resistant Hiv-1 Reverse Transcriptase Complexed With 1051u91	1124	1124	100%	0.0	99%	1RT3_A
Chain A, Structures Of Hiv-1 Rt And Rna-dna Complex Reveal A Unique Rt Conformation And S	1124	1124	100%	0.0	99%	4B3Q_A
reverse transcriptase/RNaseH [Human immunodeficiency virus 1]	1123	1123	100%	0.0	99%	AAA93162.1
Chain A, Structures Of Hiv-1 Rt And Rna-dna Complex Reveal A Unique Rt Conformation And S	1123	1123	100%	0.0	99%	4B3P_A
Chain A, Crystal Structure Of A Mutant Hiv-1 Reverse Transcriptase (rtmq+m184v: M41I/d67n/k)	1123	1123	100%	0.0	99%	1LWF_A
reverse transcriptase, RT [human immunodeficiency virus type 1 HIV-1, zidovudine (AZT)-sensit	1123	1123	99%	0.0	99%	AAB24839.1
Chain A, K103n Mutant Hiv-1 Reverse Transcriptase In Complex With Efavirenz	1122	1122	100%	0.0	99%	1IKV_A
Chain A, Crystal Structures Of Hiv-1 Reverse Transcriptase Complexes With Thiocarbamate No	1122	1122	99%	0.0	99%	2VG5_A
Chain A, Crystal Structure Of Human Immunodeficiency Virus Type 1 Reverse Transcriptase (Rt	1122	1122	100%	0.0	99%	1S6P_A
pol protein [Human immunodeficiency virus 1]	1122	1122	100%	0.0	97%	AOW43127.1
pol protein [Simian immunodeficiency virus]	1122	1122	100%	0.0	98%	AGV34223.1
pol protein [Simian immunodeficiency virus]	1121	1121	100%	0.0	98%	AGV34189.1
Chain A, Hiv-1 Reverse Transcriptase In Complex With The Inhibitor Msc204	1121	1121	99%	0.0	99%	1EET_A
pol protein [Human immunodeficiency virus 1]	1121	1121	100%	0.0	98%	AGG76245.1
pol protein [Human immunodeficiency virus 1]	1120	1120	100%	0.0	97%	AFI39022.1
Chain A, Human Immunodeficiency Virus Type 1	1120	1120	100%	0.0	99%	1HPZ_A
Chain A, Structure Of Hiv-1 Reverse Transcriptase In A Complex With The Nonnucleoside Inhibi	1120	1120	99%	0.0	99%	1HNI_A
pol polyprotein [Human immunodeficiency virus 1]	1119	1119	100%	0.0	97%	AAA86247.1
RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=IV	1118	1118	100%	0.0	97%	P03369.3
Chain A, Structural Basis Of Asymmetry In The Human Immunodeficiency Virus Type 1 Reverse	1118	1118	99%	0.0	99%	3HVT_A
pol protein [Human immunodeficiency virus 1]	1118	1118	100%	0.0	97%	ADC96546.1
pol protein [Human immunodeficiency virus 1]	1118	1118	100%	0.0	98%	AGG76244.1
pol polyprotein [Human immunodeficiency virus 1]	1118	1118	100%	0.0	97%	AAC32294.1
pol polyprotein [HIV-1 vector pMN4/LSDQgtu]	1118	1118	100%	0.0	97%	BBA21940.1
pol protein [Human immunodeficiency virus 1]	1118	1118	100%	0.0	98%	ADC96559.1
Chain A, Crystal Structure Of 3tc-Resistant M184i Mutant Of Hiv-1 Reverse Transcriptase	1118	1118	99%	0.0	99%	1QE1_A
Chain A, Crystal Structure Of K103n/y181c Mutant Hiv-1 Reverse Transcriptase (rt) In Complex	1117	1117	99%	0.0	99%	5FDL_A
Chain A, Hiv-1 Reverse Transcriptase Crosslinked To Post- Translocation Aztmp-Terminated Dr	1117	1117	99%	0.0	99%	1N5Y_A
Chain A, Tyr 181 Cys Hiv-1 Rt8-CI Tibo	1117	1117	99%	0.0	99%	1UWB_A
RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=IV	1117	1117	100%	0.0	97%	P20875.3
pol protein [Human immunodeficiency virus 1]	1116	1116	100%	0.0	97%	AQY59216.1
pol protein [Human immunodeficiency virus 1]	1116	1116	100%	0.0	97%	ALE27619.1
pol protein [Human immunodeficiency virus 1]	1116	1116	100%	0.0	97%	AAG16819.1
pol protein [Human immunodeficiency virus 1]	1116	1116	100%	0.0	97%	AAX32977.1
Chain A, Human Immunodeficiency Virus Type 1	1116	1116	99%	0.0	99%	1DLO_A

Chain A. K65r Mutant Hiv-1 Reverse Transcriptase Cross-Linked To Ds-Dna And Complexed W	1116	1116	99%	0.0	99%	3JSM_A
pol protein [Human immunodeficiency virus 1]	1116	1116	100%	0.0	97%	AOW43385.1
pol protein [Human immunodeficiency virus 1]	1116	1116	100%	0.0	97%	AOW43126.1
pol polyprotein [Human immunodeficiency virus 1]	1116	1116	100%	0.0	97%	AAC68851.1
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	AFI39013.1
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	ALP13083.1
reverse transcriptase [Human immunodeficiency virus 1]	1115	1115	100%	0.0	98%	AAC55950.1
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	ADC96552.1
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	AGG77703.1
Chain A. Human Immunodeficiency Virus Type 1 Reverse Transcriptase Complexed With A 33-F	1115	1115	98%	0.0	99%	1HVU_A
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	AGG77792.1
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	AFI39049.1
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	AOW43154.1
pol protein [Human immunodeficiency virus 1]	1115	1115	100%	0.0	97%	ANW11238.1

Alignments

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Gag-Pol [Human immunodeficiency virus 1]
 Sequence ID: [NP_057849.4](#) Length: 1435 Number of Matches: 1
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Range 1: 588 to 1147 [GenPept](#) [Graphics](#)
Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1149 bits(2971)	0.0	Compositional matrix adjust.	560/560(100%)	560/560(100%)	0/560(0%)

Query	1	PISPIETVPVKLPGMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV	60
Sbjct	588	PISPIETVPVKLPGMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV	647

Query	61	FAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL	120
Sbjct	648 <th>FAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL</th> <td>707</td>	FAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL	707

Query	121	DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGWKGSPIFQSSMTKILEPFRKQNPDI	180
Sbjct	708	DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGWKGSPIFQSSMTKILEPFRKQNPDI	767

Query	181	YQYMDLLVVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWT	240
Sbjct	768	YQYMDLLVVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWT	827

Query	241	VQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGIKVRQLCKLLRGTKALTEVIPLTEAAE	300
Sbjct	828	VQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGIKVRQLCKLLRGTKALTEVIPLTEAAE	887

Query	301	LELAENREILKEPVHGVYDPSKDLIAEIQKQGQGWTYQIYQEPFNKLTGKYARMRGA	360
Sbjct	888	LELAENREILKEPVHGVYDPSKDLIAEIQKQGQGWTYQIYQEPFNKLTGKYARMRGA	947

Query	361	HTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWTEYQATWIPEWFEVNT	420
Sbjct	948	HTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWTEYQATWIPEWFEVNT	1007

Query	421	PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVVTLDTTNQT	480
Sbjct	1008	PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVVTLDTTNQT	1067

Query	481	AIYLALQDSGLEVNIVTDSQYALGIIQAQPDQSESELVNQIIIEQLIKKEKVYLAWVPAHK	540
Sbjct	1068	AIYLALQDSGLEVNIVTDSQYALGIIQAQPDQSESELVNQIIIEQLIKKEKVYLAWVPAHK	1127

Query	541	GIGGNEQVDKLVLSAGIRKVL	560
Sbjct	1128	GIGGNEQVDKLVLSAGIRKVL	1147

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RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=Matrix protein p17; Short=MA; Contains: RecName: Full=Capsid protein p24; Short=CA; Contains: RecName: Full=Spacer peptide 1; Short=SP1; AltName: Full=p2; Contains: RecName: Full=Nucleocapsid protein p7; Short=NC; Contains: RecName: Full=Transframe peptide; Short=TF; Contains: RecName: Full=p6-pol; Short=p6*; Contains: RecName: Full=Protease;

AltName: Full=PR; AltName: Full=Retropepsin; Contains: RecName: Full=Reverse transcriptase/ribonuclease H; AltName: Full=Exoribonuclease H; AltName: Full=p66 RT; Contains: RecName: Full=p51 RT; Contains: RecName: Full=p15; Contains: RecName: Full=Integrase; Short=IN

Sequence ID: [P03367.3](#) Length: 1447 Number of Matches: 1

Related Information

Range 1: 600 to 1159		GenPept	Graphics	Next Match	Previous Match
Score	Expect	Method	Identities	Positives	Gaps
1142 bits(2954)	0.0	Compositional matrix adjust.	556/560(99%)	559/560(99%)	0/560(0%)
Query 1		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			60
Sbjct 600		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			659
Query 61		FAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			120
Sbjct 660		FAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			719
Query 121		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGKWSGPAIFQSSMTKILEPFRKQNPDI			180
Sbjct 720		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGKWSGPAIFQSSMTKILEPFRKQNPDI			779
Query 181		YQYMDLLYVGSdleIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWMGYELHPDKWT			240
Sbjct 780		YQYMDLLYVGSdleIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWMGYELHPDKWT			839
Query 241		VQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGKVRQLCKLLRGTKALTEVIPLTEEAE			300
Sbjct 840		VQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGKVRQLCKLLRGTKALTEVIPLTEEAE			899
Query 301		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFKNLTKGYARMRGA			360
Sbjct 900		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFKNLTKGYARMRGA			959
Query 361		HTNDVKQLTEAVQKITTESIIVGKTPKFKLPIQKETWETWTEYQATWIPPEWVFNTP			420
Sbjct 960		HTNDVKQLTEAVQKITTESIIVGKTPKFKLPIQKETWETWTEYQATWIPPEWVFNTP			1019
Query 421		PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVTVLTDTTNQKTELQ			480
Sbjct 1020		PLVKLWYQLEKEPIVGAETFYVDGAASRETKLGKAGYVTVNRGRQKVTVLTDTTNQKTELQ			1079
Query 481		AIYLALQDSGLEVNIIVTDSQYALGIIQAQPDQSESELVNQIIIEQLIKKEKVYLAWVPAHK			540
Sbjct 1080		AIHLALQDSGLEVNIIVTDSQYALGIIQAQPDQSESELVNQIIIEQLIKKEKVYLAWVPAHK			1139
Query 541		GIGGNEQVDKLVASAGIRKVL 560			
Sbjct 1140		GIGGNEQVDKLVASAGIRKVL 1159			

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pol protein, partial [synthetic HIV-1]

Sequence ID: [APS90951.1](#) Length: 1003 Number of Matches: 1

Related Information

Range 1: 156 to 715		GenPept	Graphics	Next Match	Previous Match
Score	Expect	Method	Identities	Positives	Gaps
1142 bits(2954)	0.0	Compositional matrix adjust.	560/560(100%)	560/560(100%)	0/560(0%)
Query 1		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			60
Sbjct 156		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			215
Query 61		FAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			120
Sbjct 216		FAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			275
Query 121		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGKWSGPAIFQSSMTKILEPFRKQNPDI			180
Sbjct 276		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGKWSGPAIFQSSMTKILEPFRKQNPDI			335
Query 181		YQYMDLLYVGSdleIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWMGYELHPDKWT			240
Sbjct 336		YQYMDLLYVGSdleIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWMGYELHPDKWT			395
Query 241		VQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGKVRQLCKLLRGTKALTEVIPLTEEAE			300
Sbjct 396		VQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGKVRQLCKLLRGTKALTEVIPLTEEAE			455
Query 301		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFKNLTKGYARMRGA			360
Sbjct 456		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFKNLTKGYARMRGA			515
Query 361		HTNDVKQLTEAVQKITTESIIVGKTPKFKLPIQKETWETWTEYQATWIPPEWVFNTP			420
Sbjct 516		HTNDVKQLTEAVQKITTESIIVGKTPKFKLPIQKETWETWTEYQATWIPPEWVFNTP			575
Query 421		PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVTVLTDTTNQKTELQ			480
Sbjct 576		PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVTVLTDTTNQKTELQ			635
Query 481		AIYLALQDSGLEVNIIVTDSQYALGIIQAQPDQSESELVNQIIIEQLIKKEKVYLAWVPAHK			540
Sbjct 636		AIYLALQDSGLEVNIIVTDSQYALGIIQAQPDQSESELVNQIIIEQLIKKEKVYLAWVPAHK			695
Query 541		GIGGNEQVDKLVASAGIRKVL 560			
		GIGGNEQVDKLVASAGIRKVL			

Sbjct 696 GIGGNEQVDKLVASGIRKVL 715

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Pol [Human immunodeficiency virus 1]

Sequence ID: [NP_789740.1](#) Length: 995 Number of Matches: 1

Related Information

[Gene](#) - associated gene details

Range 1: 148 to 707		GenPept	Graphics	Next Match	Previous Match
Score	Expect	Method	Identities	Positives	Gaps
1142 bits(2954)	0.0	Compositional matrix adjust.	560/560(100%)	560/560(100%)	0/560(0%)
Query 1		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			60
Sbjct 148		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			207
Query 61		FAIKKDDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			120
Sbjct 208		FAIKKDDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			267
Query 121		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGWKGSPIAFQSSMTKILEPFRKQNPDI			180
Sbjct 268		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGWKGSPIAFQSSMTKILEPFRKQNPDI			327
Query 181		YQYMDLTVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWNGYELHPDKWT			240
Sbjct 328		YQYMDLTVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWNGYELHPDKWT			387
Query 241		VQPIVLPKDSWTVNDIQKLVGKLNWASQIYPGKIVRQLCKLLRGTALTEVIPLTEEA			300
Sbjct 388		VQPIVLPKDSWTVNDIQKLVGKLNWASQIYPGKIVRQLCKLLRGTALTEVIPLTEEA			447
Query 301		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFNKLTGKYARMRGA			360
Sbjct 448		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFNKLTGKYARMRGA			507
Query 361		HTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWTEYQATWIPEWEFVNT			420
Sbjct 508		HTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWTEYQATWIPEWEFVNT			567
Query 421		PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVVTLTDTTQKTELQ			480
Sbjct 568		PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVVTLTDTTQKTELQ			627
Query 481		AIYALQDSGLEVNIIVTDSQYALGIIQAQPDQSESELVNIIEQLIKKEKVVYLAWPAAH			540
Sbjct 628		AIYALQDSGLEVNIIVTDSQYALGIIQAQPDQSESELVNIIEQLIKKEKVVYLAWPAAH			687
Query 541		GIGGNEQVDKLVASGIRKVL 560			
Sbjct 688		GIGGNEQVDKLVASGIRKVL 707			

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RecName: Full=Gag-Pol polyprotein; AltName: Full=Pr160Gag-Pol; Contains: RecName: Full=Matrix protein p17; Short=MA; Contains: RecName: Full=Capsid protein p24; Short=CA; Contains: RecName: Full=Spacer peptide 1; Short=SP1; AltName: Full=p2; Contains: RecName: Full=Nucleocapsid protein p7; Short=NC; Contains: RecName: Full=Transframe peptide; Short=TF; Contains: RecName: Full=p6-pol; Short=p6*; Contains: RecName: Full=Protease; AltName: Full=PR; AltName: Full=Retropepsin; Contains: RecName: Full=Reverse transcriptase/ribonuclease H; AltName: Full=Exoribonuclease H; AltName: Full=p66 RT; Contains: RecName: Full=p51 RT; Contains: RecName: Full=p15; Contains: RecName: Full=Integrase; Short=IN

Sequence ID: [P03366.3](#) Length: 1447 Number of Matches: 1

Related Information

Range 1: 600 to 1159		GenPept	Graphics	Next Match	Previous Match
Score	Expect	Method	Identities	Positives	Gaps
1139 bits(2947)	0.0	Compositional matrix adjust.	554/560(99%)	559/560(99%)	0/560(0%)
Query 1		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			60
Sbjct 600		PISPIETVPVKLKPMDGPKVKQWPLTEEEKIKALVEICTEMEKEGKISKIGPENPYNTPV			659
Query 61		FAIKKDDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			120
Sbjct 660		FAIKKDDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKSVTVLDVGDAYFSVPL			719
Query 121		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGWKGSPIAFQSSMTKILEPFRKQNPDI			180
Sbjct 720		DEDFRKYTAFTIPISINNETPGIRYQYNVLPQGWKGSPIAFQSSMTKILEPFRKQNPDI			779
Query 181		YQYMDLTVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWNGYELHPDKWT			240
Sbjct 780		YQYMDLTVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPFLWNGYELHPDKWT			839
Query 241		VQPIVLPKDSWTVNDIQKLVGKLNWASQIYPGKIVRQLCKLLRGTALTEVIPLTEEA			300
Sbjct 840		VQPIVLPKDSWTVNDIQKLVGKLNWASQIYPGKIVRQLCKLLRGTALTEVIPLTEEA			899
Query 301		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFNKLTGKYARMRGA			360
Sbjct 900		LELAENREILKEPVHGVYDPSKDLIAEIQKQGGQWYQIYQEPFNKLTGKYARMRGA			959
Query 361		HTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWTEYQATWIPEWEFVNT			420
Sbjct 1000		HTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWTEYQATWIPEWEFVNT			1059

Sbjct	960	HTNDVKQLTEAVQKITTESIIVGKTPKFKLPIQKETWETWTEYWQATWIPEWEFVNTP	1019
Query	421	PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTNRGRQKVVTLDTTNQKTELO	480
Sbjct	1020	PLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYVTN+GRQKV LT+TTNQKTELO	1079
Query	481	AIYLALQDSGLEVNIVTDSQYALGIIQAQPDQSESELVNQIIIEQLIKKEKVYLAWVPAHK	540
Sbjct	1080	AIYLALQDSGLEVNIVTDSQYALGIIQAQPD+SESELVNQIIIEQLIKKEKVYLAWVPAHK	1139
Query	541	GIGGNEQVDKLVSAGIRKVL	560
Sbjct	1140	GIGGNEQVDKLVSAGIRK+L	
Sbjct	1140	GIGGNEQVDKLVSAGIRKIL	1159

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