A Role for KH Domain Proteins (Sam68-like Mammalian Proteins and Quaking Proteins) in the Post-transcriptional Regulation of HIV Replication*

Received for publication, July 19, 2001, and in revised form, November 30, 2001

T. Raghavendar Reddy¶¶¶, Modem Suhasini¶¶, Weidong Xu¶¶, Lan-yu Yeh†, Jian-Ping Yang‡, Jiang Wu**, Karen Artzt***, and Flossie Wong-Staal†

From the ¶Department of Immunology and Microbiology, Wayne State University, Detroit, Michigan 48201, the †Department of Medicine, University of California, San Diego, La Jolla, California 92033, and the **Institute for Cellular and Molecular Biology, Section of Molecular Genetics and Microbiology, University of Texas at Austin, Austin, Texas 78721

Overexpression of Sam68 functionally substitutes for, as well as synergizes with, human immunodeficiency virus type 1 (HIV-1) Rev in RRE (Rev response element)-mediated gene expression and virus replication. In addition, COOH-terminal deletion and/or point mutants of Sam68 exhibit a transdominant negative phenotype for HIV replication. Sam68 is a member of KH domain family that includes SLM-1, SLM-2 (Sam68 like mammalian); and QKI-5, QKI-6, and QKI-7 (mouse quaking proteins). The objective of this study was to examine the effects of these KH family proteins on RRE- and CTE (constitutive transport element of type-D retrovirus)-mediated transactivation. We now report that SLM-1 and SLM-2 proteins, which are the closest relatives of Sam68, marginally enhanced RRE-mediated transactivation, while QK isoforms that are distant relatives of Sam68 had no effect. Interestingly, these proteins still enhanced the effect of Rev in RRE-mediated gene expression. The increase in chimpanoolphenolic acetyltransferase activity was also reflected at the levels of cytoplasmic RRE-chloramphenicol acetyltransferase mRNAs, indicating that Sam68 and KH proteins may have been involved in the stability or export of unspliced RNA. The increase in Rev activity was sensitive to leptomycin B, but not to olomoucine, indicating that the effect of SLM-1, SLM-2, QKI-5, QKI-6, and QKI-7 is exerted through a CRM-1-dependent mRNA export pathway. Thus, KH family proteins play an important role in the post-transcriptional regulation of HIV.

The Rev protein of human immunodeficiency virus (HIV) facilitates the nuclear export of unspliced or singly spliced viral mRNA (1). Rev has been shown to be a shuttle protein (2), comprised of a basic, nuclear localization sequence (3) and a leucine-rich nuclear export sequence (4). The basic domain also constitutes an RNA-binding domain that specifically interacts with the cognate target sequence, RRE. Substitutions of leucine residues within nuclear export sequence yielded a mutant Rev protein (RevM10) with a dominant negative phenotype (3). RevM10 has been shown to confer human CD4 cells with antiviral resistance in cell culture (5) and preferential survival in HIV-1-infected patients (6, 7). Recently, the Rev-nuclear export sequence was shown to bind the nuclear export receptor CRM-1, a member of the importin-β family (8). This interaction is functionally relevant, since leptomycin B (LMB), a drug that disrupts the complex formation of Rev, CRM-1, and RanGTP, also inhibits the nuclear export of Rev-nuclear export sequence conjugates (8). CRM-1 probably bridges the indirect interaction of Rev with members of the nucleoporin family (9) such as CAN/Nup214 proteins (10). Additional cellular proteins that bind Rev (11–15) and/or RRE (16, 17) have been identified, which either positively or negatively modulate Rev activity. Recently, one such cellular protein that functionally substitutes for Rev has been identified as Sam68 (18). Sam68 binds to RRE in vitro and in vivo, and functionally replaces as well as synergizes with HIV-1 Rev in RRE-mediated gene expression and virus replication (18). Sam68 mutants deleted in the carboxyl terminus show a dominant negative phenotype in HIV replication (18). Furthermore, a single amino acid (P439R) substitution in the COOH-terminal domain of Sam68 also confers a transdominant negative phenotype (19). Overexpression of Sam68 also activated CTE-regulated HIV gag gene expression in human cells as well as in quail cells in the presence of human Tap (20).

Sam68 is a target of the e-Src tyrosine kinase (21, 22). It contains an hnRNP-K homology domain (KH domain) (23) that mediates RNA binding and protein-protein interaction (24). The KH domain has also been reported in several RNA-binding proteins such as GRP33 (25), fragile X mental retardation gene (FMR-1) (26), and the Caenorhabditis elegans germ line-specific tumor suppressor GLD-1 (27), and as recently reported, other proteins such as SLM-1, SLM-2 (28), QKI-5, QKI-6, and QKI-7 (29, 30). In this study, we have investigated the role of KH proteins in the post-transcriptional regulation of HIV replication. Here, we report that KH proteins (SLM-1, SLM-2, QKI-5, QKI-6, and QKI-7), that have partial homology with Sam68 failed to transactivate RRE-directed reporter gene expression independent of Rev, but are able to enhance Rev transactivation on RRE. These effects were sensitive to LMB,
but insensitive to olomoucine. Our results provide the first direct evidence that other members of KH proteins are also involved in post-transcriptional regulation of HIV gene expression.

**EXPERIMENTAL PROCEDURES**

**Construction of Plasmids—**The construction of Sam68 expression plasmid were described previously (18). pSLM-1 and pSLM-2 were generated by cloning the coding region of EcoRI fragment of 1.1 and 18.2 clones (28) into the cognate sites of pcDNA6.1 vector (Invitrogen). The mammalian expression constructs pcDNA3-QKI-5, QKI-6, and QKI-7 were generated by inserting the corresponding region of QKI isoforms in vector pcDNA3.1 using HindIII and BamHI sites. The bacterial expression plasmid pET28-QKI and purification of QKI-5 and QKI-6 was described previously (30). Dr. Michael Malim (University of Pennsylvania, Philadelphia, PA) generously provided the Rev mutant expression plasmids (31).

**Cells, Transfections, and Chloramphenicol Acetyltransferase (CAT) Assays—**The 293T, HeLa, and COS cells were maintained in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum. In general, between 1 and 3 μg of DNA was transfected into (1 × 10⁶) 293T cells using FuGENE 6 (Roche Molecular Biochemicals) according to the manufacturers protocols. To normalize the transfection efficiencies, 1 μg of pcDNA-Lac Z expression vector was used as an internal control. pcDNA3 plasmid was used to equalize the amount of DNA for each transfection. For treatment with soluble inhibitors, 18 h after transfection, cells were incubated in medium containing 2 mM LMB, and/or 75 μM olomoucine. Forty-eight hours post-transfection, cells were harvested, washed with phosphate-buffered saline, and then re-suspended in 50–100 μl of 0.25 mM Tris, pH 7.8. The cell extracts, CAT assays, and separation of reaction products were performed as previously described (18). Fold of trans-activation was quantified by scintillation counting of the products separated from the reaction.

**Northern Analysis—**We have fractionated the nuclear and cytoplasmic fractions as described by Maniatis (32). Using Ultraspec™ (Biotecx Laboratories, Inc.) reagent, total or fractionated RNA was extracted from the 293T cells transfected with different plasmids shown in Figs. 2 and 5 by FuGENE 6 as described previously (19). Approximately 20 μg of RNA was separated on 1% agarose formaldehyde gels by electrophoresis and blotted onto nitrocellulose filters. The filters were hybridized with ³²P-labeled CAT cDNA and detected by autoradiography. Blots were re-hybridized with control ChoA DNA. Ribosomal RNA (28 S and 18 S) was also used to assess the integrity of the RNA and for RNA loading controls (data not shown).

In **In Vitro Transcription and RNA Gel Mobility Shift Assay—**Plasmid pRRE was constructed by inserting PCR-amplified HIV-1 (HXB-2) RRE sequence into HindIII and BamHI cloning site of pcDNA3 (Invitrogen). [³²P]UTP-labeled RRE RNA were synthesized by in vitro transcription with T7 RNA polymerase according to the protocols (Promega) using BamH1 linearized pRRE plasmid as template. RNA-protein binding were carried out at room temperature in a total volume of 30 μl in the binding buffer containing 60 mM NaCl, 12 mM Hepes (pH 7.9), 12 mM dithiothreitol, and 50 units of RNasin. Typically, 1 × 10⁶ cpm of ³²P-labeled RNA and 100 ng of protein were used. The binding reaction was allowed to proceed for 15 min at room temperature and then the mixture was electrophoresed on a 4.5% nondenaturing PAGE and then subjected directly to autoradiography.

**Co-immunoprecipitation Assay—**293T cells (6 well dish) were co-transfected with pCMV128 (1 μg) alone and with wild-type and/or mutant pRev (3 μg). Forty-eight hours later, cell extracts were prepared by lysing the cells in 1 ml of 0.65% Nonidet P-40 lysis buffer (150 mM NaCl, 10 mM Tris-HCl, pH 7.8, 1 mM MgCl₂, 0.65% Nonidet P-40). For the detection of RNA free interaction, cell extracts were treated with 10 μg of RNase per ml for 30 min at 37 °C. Cell lysates were precleared with normal rabbit serum by incubating overnight with 20 μl of normal rabbit serum-conjugated agaroase beads at 4 °C. The resultant lysate from the cells co-transfected with pCMV128 and pRev was divided into four parts. Each part was mixed with 40 μl of protein A- and G-agarose beads plus 10 μl of anti-QKI-5, QKI-6, Rev, and/or normal rabbit IgG. After incubating at 4 °C overnight, the beads were washed 2 times with lysis buffer and immunoprecipitates were suspended in SDS buffer, boiled for 5 min, and analyzed by Western blot using Rev antibody.

**P24 Antigen Capture Assay—**293T cells were co-transfected with CTE-gag expression vector (33) with KH proteins and/or HIV-1 rev(−) proviral DNA (34) and KH proteins expressing vectors plus Rev expression vector. Forty-eight hours post-transfection, cell-free supernatants were collected and subjected to p24 antigen assay (Coulter).

**RESULTS**

**Effects of KH Proteins on RRE- and CTE-mediated Reporter Gene Expression—**We have previously demonstrated that overexpression of Sam68 functionally substitutes for, as well as synergizes with HIV-1 Rev in RRE-mediated gene expression and virus replication. Amino acid sequence alignment suggests that SLM-1, SLM-2 (28), QKI-5, QKI-6, and QKI-7 (29, 30) have partial homology with Sam68 and belong to the KH domain family (Fig. 1). Because of the sequence homology among these proteins, we have investigated the role of KH proteins in the post-transcriptional regulation of HIV replication. To explore a potential role of KH family proteins in RRE- and CTE-mediated transactivation, we examined the effect of exogenously expressed SLM-1, SLM-2, QKI-5, QKI-6, and QKI-7 under the control of the CMV promoter on a RRE-regulated reporter gene expression in transient co-transfection assays. As shown in Fig. 2A, Sam68, SLM-1, and SLM-2 induced 5-, 2.5-, and 1.7-fold of RRE-mediated CAT reporter gene expression, respectively, while Rev expression yielded a 10-fold increase in these studies (Fig. 2B). In contrast, QKI-5, QKI-6, and QKI-7 did not trans-activate RRE-mediated gene expression. We next investigated whether an increased CAT activity was also reflected at the levels of RRE-CAT mRNAs. We isolated total RNA from 293T cells transfected with the plasmids shown in Fig. 2A and performed Northern analysis using CAT gene as a probe. Northern blot analysis demonstrated (Fig. 2B) that an increase of RRE-CAT mRNA (5- and 3-fold) was observed from the cells co-transfected with Sam68 and SLM-1 but not SLM-2, QKI-5, QKI-6, and QKI-7 expression plasmids. Thus, the increase in mRNA levels (Fig. 2B) was comparable with the CAT activity shown in Fig. 2A. These results suggest that Sam68 may be involved in the stability and/or export of mRNAs.

We previously reported that Sam68 also efficiently activated HIV-gag expression from a CTE-reporter gene (20). To assess the effect of other KH proteins on CTE-mediated gene expression, we co-transfected expression vectors for these proteins with CTE-gag reporter gene (33) and measured the p24 antigen expression in cell-free supernatants 48 h post-transfection. As a positive control, we used Sam68. Here, we demonstrate that Sam68, but not other KH proteins, significantly enhanced CTE-mediated gag expression (Fig. 3). These results suggest that among the KH proteins tested, only Sam68 efficiently activated RRE and CTE-mediated reporter gene expression.

**Effects of KH Proteins on Rev Activation of RRE—**To determine whether these KH proteins also enhance Rev activation of RRE-directed CAT reporter gene expression, we co-transfected expression vectors for these proteins with CTE-gag reporter gene (33) and measured the p24 antigen expression in cell-free supernatants 48 h post-transfection. As a positive control, we used Sam68. Here, we demonstrate that Sam68, but not other KH proteins, significantly enhanced CTE-mediated gag expression (Fig. 3). These results suggest that among the KH proteins tested, only Sam68 efficiently activated RRE and CTE-mediated reporter gene expression.

**Effects of KH Proteins on RRE- and CTE-mediated Reporter Gene Expression—**We have previously demonstrated that overexpression of Sam68 functionally substitutes for, as well as synergizes with HIV-1 Rev in RRE-mediated gene expression and virus replication. Amino acid sequence alignment suggests that SLM-1, SLM-2 (28), QKI-5, QKI-6, and QKI-7 (29, 30) have partial homology with Sam68 and belong to the KH domain family (Fig. 1). Because of the sequence homology among these proteins, we have investigated the role of KH proteins in the post-transcriptional regulation of HIV replication. To explore a potential role of KH family proteins in RRE- and CTE-mediated transactivation, we examined the effect of exogenously expressed SLM-1, SLM-2, QKI-5, QKI-6, and QKI-7 under the control of the CMV promoter on a RRE-regulated reporter gene expression in transient co-transfection assays. As shown in Fig. 2A, Sam68, SLM-1, and SLM-2 induced 5-, 2.5-, and 1.7-fold of RRE-mediated CAT reporter gene expression, respectively, while Rev expression yielded a 10-fold increase in these studies (Fig. 2B). In contrast, QKI-5, QKI-6, and QKI-7 did not trans-activate RRE-mediated gene expression. We next investigated whether an increased CAT activity was also reflected at the levels of RRE-CAT mRNAs. We isolated total RNA from 293T cells transfected with the plasmids shown in Fig. 2A and performed Northern analysis using CAT gene as a probe. Northern blot analysis demonstrated (Fig. 2B) that an increase of RRE-CAT mRNA (5- and 3-fold) was observed from the cells co-transfected with Sam68 and SLM-1 but not SLM-2, QKI-5, QKI-6, and QKI-7 expression plasmids. Thus, the increase in mRNA levels (Fig. 2B) was comparable with the CAT activity shown in Fig. 2A. These results suggest that Sam68 may be involved in the stability and/or export of mRNAs.

We previously reported that Sam68 also efficiently activated HIV-gag expression from a CTE-reporter gene (20). To assess the effect of other KH proteins on CTE-mediated gene expression, we co-transfected expression vectors for these proteins with CTE-gag reporter gene (33) and measured the p24 antigen expression in cell-free supernatants 48 h post-transfection. As a positive control, we used Sam68. Here, we demonstrate that Sam68, but not other KH proteins, significantly enhanced CTE-mediated gag expression (Fig. 3). These results suggest that among the KH proteins tested, only Sam68 efficiently activated RRE and CTE-mediated reporter gene expression.**
spliced CAT mRNA into the cytoplasm (Fig. 5, A and B). Thus, the increase in CAT activities of KH proteins and Rev correlated with the RNA levels shown in Fig. 5. This effect of the KH proteins was also apparent in a virus rescue assay. We co-transfected 293T cells with a rev(H11002) proviral DNA plasmid (34), various KH domain protein expression vectors and a Rev expression vector, and measured the expression of p24 antigen in the cell-free supernatants. Expression of Rev alone yielded 18 ng/ml p24 expression, while co-expression of KH proteins and Rev resulted in 2–3.5-fold (36 to 67 ng/ml) of p24 antigen expression increase over Rev (Fig. 6). These results indicate that KH proteins enhance Rev activation of RRE-directed gene expression in the context of a provirus.

Effects of KH Proteins on RRE-mediated Gene Expression in Various Cells—To determine whether the effect of KH family proteins is specific to 293T cells, we co-transfected various expression plasmids into COS and HeLa cells and investigated the consequence of overexpressed KH proteins on RRE-mediated CAT gene expression (Table I). Sam68 enhanced RRE-mediated CAT gene expression independently of Rev in these
cell lines while QK proteins had no effect (data not shown). However, all KH proteins tested enhanced Rev activation of RRE-mediated reporter gene expression in COS and HeLa cells, consistent with the results with 293T cells. These results suggest that the effects of KH proteins on RRE-mediated gene expression are not cell-type specific.

**Interaction of KH Proteins with RRE and Rev**—Since unlike Sam68, the other KH proteins tested did not enhance RRE-directed reporter gene expression in COS and HeLa cells, consistent with the results with 293T cells. These results suggest that the effects of KH proteins on RRE-mediated gene expression are not cell-type specific.

**Interaction of KH Proteins with RRE and Rev**—Since unlike Sam68, the other KH proteins tested did not enhance RRE-directed reporter gene expression in COS and HeLa cells, consistent with the results with 293T cells. These results suggest that the effects of KH proteins on RRE-mediated gene expression are not cell-type specific.

**Interaction of KH Proteins with RRE and Rev**—Since unlike Sam68, the other KH proteins tested did not enhance RRE-directed reporter gene expression in COS and HeLa cells, consistent with the results with 293T cells. These results suggest that the effects of KH proteins on RRE-mediated gene expression are not cell-type specific.

**Interaction of KH Proteins with RRE and Rev**—Since unlike Sam68, the other KH proteins tested did not enhance RRE-directed reporter gene expression in COS and HeLa cells, consistent with the results with 293T cells. These results suggest that the effects of KH proteins on RRE-mediated gene expression are not cell-type specific.

**Interaction of KH Proteins with RRE and Rev**—Since unlike Sam68, the other KH proteins tested did not enhance RRE-directed reporter gene expression in COS and HeLa cells, consistent with the results with 293T cells. These results suggest that the effects of KH proteins on RRE-mediated gene expression are not cell-type specific.
Rev, but not M21, co-immunoprecipitated with QKI-5 (Fig. 8B). All Rev mutant proteins were expressed at comparable levels, as detected by anti-Rev antibodies (Fig. 8C). To determine the functional relevance of these interactions, 293T cells were co-transfected with Rev and wild-type and mutant Rev constructs with or without QKI-5 expression vectors. Forty-eight hours post-transfection, cell extracts were made and subjected to CAT assays as described previously (18). The CAT activity presented here is representative of two independent experiments.

| Plasmids              | Relative CAT activity |
|-----------------------|-----------------------|
|                       | HeLa  | COS  |
| RRE-CAT reporter      |       |      |
| Alone                 | 1     | 1    |
| Sam68                 | 5     | 6    |
| Rev                   | 13    | 11   |
| Rev + Sam68           | 42    | 45   |
| Rev + SLM-1           | 24    | 23   |
| Rev + SLM-2           | 26    | 26   |
| Rev + QKI-5           | 28    | 21   |
| Rev + QKI-6           | 25    | 25   |
| Rev + QKI-7           | 38    | 40   |

Rev and QKI-5 co-immunoprecipitated with QKI-5 (Fig. 8B). All Rev mutant proteins were expressed at comparable levels, as detected by anti-Rev antibodies (Fig. 8C). To determine the functional relevance of these interactions, 293T cells were co-transfected with RRE-CAT and wild-type and mutant Rev constructs with or without QKI-5 expression vectors. Forty-eight hours post-transfection, cell extracts were made and subjected to CAT assays as described previously (18). M18 and M20, but not M21, were functional in activating RRE-mediated CAT gene expression. As shown above, QKI-5 only interacted with functional Rev (M18, M20, and wild type) but not the nonfunctional M21 mutant. In addition, they only increased RRE-mediated CAT gene expression in the presence of wild-type Rev or functional Rev mutants (Fig. 8D). Taken together, these results strongly suggest that the in vivo interaction of QKI-5 and Rev is specific and functionally relevant.

The Effect of KH Proteins on Rev Activation Is hCRM-1 Dependent—Previously, we demonstrated that the activation of RRE RNA by Sam68, in contrast to Rev, was hCRM-1 independent (18), since it was resistant to LMB treatment. Furthermore, we showed that Sam68, but not Rev, was inhibited by olomoucine, an inhibitor of Cdc2 kinase (35). To determine whether the increase in Rev activation by KH proteins is still mediated by hCRM-1, we assessed the effect of LMB and olomoucine on these activities. LMB inhibited 50 to 58% of the activity of Rev in the presence or absence of KH proteins. In contrast, olomoucine did not have any effect on these activities (Table I). As a positive control, we have used Sam68 and Rev. These results suggest that the non-Sam68 KH proteins only enhanced the CRM-1-dependent, Rev-mediated RNA export pathway.

**DISCUSSION**

Sam68 is a member of the KH domain family proteins that include SLM-1, SLM-2 (28), and mouse quaking genes QKI-5, QKI-6, and QKI-7 (36). Although most of the biochemical and molecular analyses of these genes have been carried out, the role of these genes in vivo has not yet been defined. We now extend our earlier studies on the effects of Sam68 on RRE-mediated gene expression and HIV replication to these additional members of the KH domain protein family.

We demonstrate here that, unlike Sam68, the other KH proteins tested failed to significantly activate RRE-directed reporter gene expression in the absence of Rev (Fig. 2A). Sequence alignment of these proteins suggests that SLM-1 and SLM-2 are more related to Sam68 than QKI-5, QKI-6, and QKI-7, with the greatest homology in the GSG and KH domain, and lesser homology in the COOH-terminal region (Fig. 1A). Furthermore, Sam68 and SLM-1 but not SLM-2 are the substrates for c-Src kinase (28), and the heterodimerization ability of SLM-1 with Sam68 is greater than SLM-2 (28). Our results showed that SLM-1 is more efficient than SLM-2 in transactivating RRE-mediated gene expression (Fig. 2) and both are far less active than Sam68. The COOH-terminal domains of QKI-5, QKI-6, and QKI-7 proteins have no sequence homology...
activation of RRE-mediated gene expression in two different assay systems (Fig. 4 and 6). This enhancement may be mediated by interaction between Rev and the KH domain proteins, since QKI-5 and QKI-6 proteins do not bind RRE RNA in vitro, but complex with Rev in vivo (Figs. 7 and 8). Similarly, SLM-2, which is more closely related to Sam68 than the QK proteins, also failed to bind RRE RNA (data not shown) and marginally activated RRE-mediated gene expression independently of Rev (Fig. 2A). The increases in CAT activity also correlated with increases in cytoplasmic CAT mRNAs (Figs. 4 and 5). These results suggest that these proteins are involved in increasing the stability or export of unspliced mRNAs, rather than their translational efficiency. In fact, QKI-6 was reported to act as a translational repressor (38).

LMB, a drug that interferes with the CRM-1-dependent nuclear export pathways, inhibits Rev but not Sam68 activation of RRE-dependent gene expression (18). In contrast, olomoucine, an inhibitor of Cdc2 kinase, specifically inhibits Sam68, but not Rev activation (18). Our data presented here showed that the increase in Rev activity due to the non-Sam68 KH proteins was inhibited by LMB to the same extent as Rev itself, and not at all inhibited by olomoucine (Table II). These results suggest that phosphorylation of KH proteins by Cdc2 kinase is not important for the observed enhancing effect of Rev function.

Sam68, SLM-1, SLM-2, and QKI-5 are predominantly nuclear proteins (39), while QKI-6 and QKI-7 are mostly cytoplasmic. Furthermore, QKI-5 was shown to shuttle between the nucleus and cytoplasm (30). Although Sam68 does not seem to be a shuttle protein, it has been reported to re-localize to the cytoplasm of cells infected with poliovirus (40). Recently, it was reported that insulin stimulation promotes the re-localization of Sam68 from the nucleus to the cytoplasm (41). Since the KH proteins can interact with each other (24, 28) as well as Rev in vivo (Fig. 7), it is conceivable that they can traffic between the nucleus and cytoplasm through a piggy-back mechanism. Alternatively, different KH proteins might co-operate with Rev in the two cellular compartments at different stages of nuclear export. In light of these findings, it would be of interest to determine whether the functional domains are interchangeable among the KH proteins, and if the COOH-terminal domain mutants of the other KH proteins also exhibit transdominant negative phenotype for HIV replication. Additionally, it would be important to determine which of the nuclear pore proteins associate with Sam68 or other KH proteins and play a role in the export of HIV mRNA.

Acknowledgments—We thank Dr. Stephane Richard for SLM-1 and SLM-2 expression vectors, Dr. Michael Malim for Rev antibodies and Rev mutant plasmids, and Dr. Minoru Yoshida for LMB. We also thank Dr. Thomas Holland for helpful suggestions and Dr. Keshamouni Venkateshwar for assistance in preparing the manuscript.
A Role for KH Domain Proteins (Sam68-like Mammalian Proteins and Quaking Proteins) in the Post-transcriptional Regulation of HIV Replication
T. Raghavendar Reddy, Mode Suhasini, Weidong Xu, Lan-yu Yeh, Jian-Ping Yang, Jiang Wu, Karen Artzt and Flossie Wong-Staal

J. Biol. Chem. 2002, 277:5778-5784.
doi: 10.1074/jbc.M106836200 originally published online December 7, 2001

Access the most updated version of this article at doi: 10.1074/jbc.M106836200

Alerts:
• When this article is cited
• When a correction for this article is posted

Click here to choose from all of JBC's e-mail alerts

This article cites 40 references, 22 of which can be accessed free at http://www.jbc.org/content/277/8/5778.full.html#ref-list-1