An Adenosine 3':5'-Monophosphate-Adenosine Binding Protein from Mouse Liver

PURIFICATION AND PARTIAL CHARACTERIZATION*

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A cyclic AMP-adenosine binding protein from mouse liver has been purified to apparent homogeneity as judged by polyacrylamide gel electrophoresis in the absence and presence of sodium dodecyl sulfate and by analytical ultracentrifugation. The binding protein had a Stokes radius of 48 Å based on gel chromatography. Both the purified binding protein and the binding activity in fresh cytosol sedimented as 9 S on sucrose gradient centrifugation. The homogeneous protein had a sedimentation coefficient ($s_{20,w}$) of 8.8 x 10⁻¹³ s, as calculated from sedimentation velocity experiments. By use of the Stokes radius and $s_{20,w}$, the molecular weight was calculated to be 180,000. The protein was composed of polypeptides having the same molecular weight of 45,000 as judged by sodium dodecyl sulfate-polyacrylamide gel electrophoresis, and thus appeared to consist of four subunits of equal size. The isoelectric point, $pI = 5.7$.

The binding capacity for cyclic AMP increased by preincubating the receptor protein in the presence of Mg²⁺ ATP. This process, tentatively termed activation, was studied in some detail and was shown not to be accompanied by dissociation, aggregation, or phosphorylation of the binding protein.

Cyclic AMP was bound to the protein with an apparent dissociation constant ($K_d$) of $1.5 \times 10^{-7}$ M. The binding of cyclic AMP was competitively inhibited by adenosine, AMP, ADP, and ATP whose inhibition constants were $8 \times 10^{-7}$ M, $1.2 \times 10^{-6}$ M, $1.5 \times 10^{-6}$ M, and higher than $5 \times 10^{-6}$ M respectively.

A hyperbolic Scatchard plot was obtained for the binding of adenosine to the activated binding protein, indicating more than one site for adenosine. The binding of adenosine to the site with the highest affinity ($K_d = 2 \times 10^{-7}$ M) for this nucleoside was not suppressed by excess cyclic AMP and was thus different from the aforementioned cyclic AMP binding site.

Cyclic GMP, GMP, guanosine, cyclic IMP, IMP, and inosine did not inhibit the binding of either cyclic AMP or adenosine.

The binding protein had no cyclic AMP phosphodiesterase, adenosine deaminase, phosphofructokinase, or protein kinase activities, nor does it inhibit the catalytic subunit of the cyclic AMP-dependent protein kinase.

Cyclic AMP probably exerts its effects by interacting with intracellular proteins. Much interest has been devoted to the binding of cyclic AMP to the regulatory subunit of cyclic AMP-dependent protein kinase (ATP: protein phosphotransferase EC 2.7.1.37) (1-4; for review, see ref. 5). Cyclic AMP receptors not related to protein kinase have recently been described in various eukaryotes (6-8).

We have reported the existence in mouse liver of a cyclic AMP binding protein not related to cyclic AMP-dependent protein kinase. The cyclic AMP binding sites were activated by treatment with Mg²⁺ ATP (9). Here we describe the purification of this protein to apparent homogeneity and present some characteristics of the purified binding protein.

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The abbreviation used is, Hepes, N-2-hydroxyethylpiperazine N'-2-ethanesulfonic acid. SDS, sodium dodecyl sulfate.
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study the binding of ligands to the protein, the experimental conditions must be such that only minor changes in activation occur during the incubation. These demands were met by performing the incubation at 30°C in the presence of 20% glycerol, conditions found to preserve the degree of activation. However, during the purification procedure, measurement of binding activity in separate fractions was performed at 30°C for 1 h i.e. under nonequilibrium conditions. The measurement of cyclic AMP binding activity was conducted in the presence of 10 mM MgCl2 and KCl at 30°C. In this way, cyclic AMP binding activity could be detected without prior treatment of the binding protein with Mg2+ ATP. Therefore, two incubation conditions were used.

1. For studies of binding kinetics the samples and various concentrations of cyclic AMP (0.54 Ci/mmol) or [3H]adenosine (1.42 Ci/mmol) were incubated at 0°C for 18 h in 15 mM Hepes buffer, pH 7.5, containing 20% glycerol and 10 mM 2-mercaptoethanol.

2. To measure the cyclic AMP or adenosine binding activity during the purification procedure, samples of 20 ml from the fractions were incubated in the presence of 10 mM cyclic AMP (0.54 Ci/mmol), 150 mM KCl, and 10 mM magnesium acetate in 15 mM Hepes buffer, pH 7.0 or 10 mM MgCl2, and 100 mM 2-mercaptoethanol.

All incubations were performed in a volume of 120 ml and were stopped by pipetting an aliquot of 100 ml into 5 ml of ice-cold 80% saturated ammonium sulfate containing 100 mM unlabeled cyclic AMP or adenosine. After blending on a Vortex mixer, the protein was allowed to precipitate for 1 h at 0°C and then was collected by suction through Millipore filters (HAWP, 0.45 pm). The precipitate was dissolved in 1 ml 1% SDS and 7 ml of Diluene (Packard) added.

The background radioactivity was independent of the amount of protein in the sample. It was proportional to the amount of radioactive activity passing through the filter; i.e. about 0.35% of the cyclic [3H]AMP or [3H]adenosine applied was retained on the filters in the absence of binding protein.

To exclude the possibility that radioactive ligand was bound or trapped during or after precipitation, 50 ml of 20 mM [3H]labeled ligand was mixed with the ammonium sulfate (2 ml), and then 50 ml of receptor protein (1 mg/ml) was added. The retention of radioactivity by the Millipore filters was not above background.

The following experiments were conducted to measure that ligand (cyclic AMP or adenosine) was not released from the binding protein during or after precipitation. The binding protein (0.5 mg/ml) was incubated for 1 h at 30°C in the presence of 10 mM cyclic AMP (0.54 Ci/mmol), 150 mM KCl and 10 mM MgCl2 in Buffer A or 10 mM [3H]adenosine in Buffer A. An aliquot of 400 ml was applied to a Sephadex G-25 column (0.9 15 cm) equilibrated with 15 mM Hepes buffer, pH 7.5, and eluted with the same buffer. Fractions of 0.3 ml were collected and 20-ml aliquots counted (Fig. 1, inset). After the column had been calibrated, new incubations of binding protein with cyclic [3H]AMP or [3H]adenosine were performed. The fractions, eluted in a position corresponding to the material excluded from the column (Fractions 15 to 18, Fig. 1), were pooled (1.2 ml). Samples of 100 ml were counted directly or added immediately to ice-cold 80% ammonium sulfate as described. Precipitation was allowed to proceed for the time indicated on the abscissa of Fig. 1, the precipitate collected on Millipore filters and the radioactivity measured. The experimental results (for both cyclic [3H]AMP and [3H]adenosine) presented in Fig. 1, show that almost total recovery of the radioactivity excluded by Sephadex G-25 was obtained with the ammonium sulfate precipitation Millipore filtration technique. No carrier protein was necessary to give quantitative recovery of protein-bound radioactive ligand, even with dilute solutions.

The radioactivity bound to the protein, excluded from the Sephadex G-25 column (see above), was identified as cyclic [3H]AMP or [3H]adenosine by thin layer chromatography when the receptor protein was incubated with cyclic [3H]AMP or [3H]adenosine, respectively.

Using the ammonium sulfate precipitation Millipore filtration technique as reference, 5 to 25% of cyclic [3H]AMP and about 75% of [3H]adenosine bound (to both activated and unactivated receptor protein) was recovered by the following method. Aliquots (100 ml) from the incubation mixture were added to and mixed with 3 ml of ice-cold 10 mM sodium phosphate buffer, pH 6.0, and after 1 min, filtered through Millipore filters and washed three times with 3 ml of the same buffer. When 15 mM Hepes buffer, pH 7.5, was used, low recovery (2 to 10%) was obtained for both cyclic AMP and adenosine.

The buffer passing through the filters was collected and immediately mixed with 3 times its volume of 100% saturated ice-cold ammonium sulfate (containing unlabeled ligand). After 1 h at 0°C, the mixture was filtered and the radioactivity measured as described. About 20% of the [3H]adenosine-receptor complex was recovered when the reaction mixture was added to and filtered washed in 10 mM sodium phosphate, pH = 6.0. (Low and variable recovery (2 to 20%) of cyclic [3H]AMP was obtained under these conditions.) In this way, 50 to 85% of both [3H]adenosine and cyclic [3H]AMP bound could be recovered when the buffer was 15 mM Hepes, pH = 7.5.

These experiments suggest that at pH = 6.0 about 75% of the binding protein was retained on the Millipore filter. Adenosine was bound to the protein whereas cyclic AMP was rapidly released. At pH = 7.5, both adenosine and cyclic AMP were bound to the receptor protein, but the receptor protein passed through the filter.

Assay for Enzyme Activity—Protein kinase activity was assayed essentially as described (11) by determining the amount of phosphate incorporated into histone (0.67 mg/ml) or casein (5 mg/ml) from [γ-32P]ATP (13)

Phosphodiesterase activity was measured by determining the hydrolysis of 10 mM cyclic [3H]AMP in the presence of 10 mM magnesium acetate, 160 mM KCl in Buffer A. The reaction was run for 1 h at 30°C and was stopped by heating. Cyclic [3H]AMP was separated from its reaction products by thin layer chromatography (System A). The cyclic AMP, AMP, and adenosine zones were cut out and counted by liquid scintillation.

Adenosine deaminase activity was measured by following the change of absorbance at 260 nm resulting from the conversion of adenosine to inosine (12) or by determination of the conversion of [3H]adenosine to [3H]inosine by thin layer chromatography (System C).

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FIG. 1. Separation of the free and protein-bound radioactive ligand by Sephadex G-25 filtration and recovery of the excluded radioactivity after ammonium sulfate precipitation and collection of the protein on Millipore filters. Experimental details are given in the text. Inset shows binding of [3H]adenosine (•—•) or cyclic [3H]AMP (O—O) to the receptor protein as determined by Sephadex G-25 chromatography. In separate experiments the effluent corresponding to Fractions 15 to 18 were pooled and equal portions (100 ml) were counted directly or allowed to precipitate in 80% ammonium sulfate for the time indicated on the abscissa. [3H]Adenosine and cyclic [3H]AMP (O—O) recovered after ammonium sulfate precipitation and filtration through Millipore filters as percent of counts per min counted directly, is plotted against time of precipitation.
Phosphofructokinase activity was determined as described by Massey and Deal (13). The reaction was started by adding sample to be tested (5 to 40 µl) or 20 µl of fructose 6-phosphate (0.1 m) to 500 µl of 50 mM Tris/HCl, pH 8.0, containing 5 mM MgCl₂, 50 mM KCl, 50 mM 2-mercaptoethanol, 1 mg of aldolase, 0.5 mg of glycerol phosphate dehydrogenase:triosephosphate isomerase mixture (10:1), 20 mM NADH, 2 mM ATP, and if the reaction was initiated by addition of enzyme, 4 mM fructose 6-phosphate.

Preparation of Free Catalytic and Regulatory Subunit of Cyclic AMP-dependent Protein Kinase—Protein kinase (isoenzyme PK I) from mouse liver was prepared through DEAE-cellulose chromatography as described (11). The holoenzyme was incubated for 2 h at 0° in the presence of 800 mM KCl, 0.1% bovine serum albumin in Buffer A, and 500 µl of the incubate was applied to a Sephadex G-150 column (0.9 x 40 cm) equilibrated with the same buffer. Fractions of 0.3 ml were collected and assayed for cyclic AMP binding activity and protein kinase activity as described in legend to Fig. 4. The protein kinase activity, independent of cyclic AMP, eluted well behind the cyclic AMP binding activity, indicating dissociation of the holoenzyme into the free catalytic and the regulatory subunits.

Polyacrylamide Gel Electrophoresis—Polyacrylamide gel electrophoresis of the native binding protein was performed at different pH and gel concentrations (5%, 7.5%, and 9%) and 3% cross-linking in tubes (75 x 5 mm). The protein (5 to 80 µg) was applied to the gel in 50 mM Tricine, pH 8.0. The electrophoresis proceeded at 4° for 1 to 4 h (depending on the gel concentration) at 1/4 to 1 mA per gel. The following buffer systems were used: A, 20 mM phosphate buffer, pH 7.0; B, 15 mM Tris/phosphate, pH 7.8; C, 15 mM Tris/glycine, pH 8.9. The gels were stained in Coomassie blue and destained in 7% acetic acid.

Polyacrylamide gel electrophoresis in the presence of sodium decyl sulfate was performed according to the method of Weber et al. (14) using 10 µg of protein per tube. The electrophoresis was run in tubes (75 x 5 mm) for 4 h using 5 µA per gel. Gel concentration was 7.5%. The electrophoretic mobility of the denatured receptor was compared to that of the following standard proteins: Bovine serum albumin (Mr ~ 69,000), catalase (Mr ~ 232,000), human γ-globulin heavy chain (Mr ~ 50,000), ovalbumin (Mr ~ 43,000), glyceraldehyde-3-phosphate dehydrogenase (Mr ~ 36,000), chymotrypsinogen a (Mr ~ 25,700), human γ-globulin light chain (Mr ~ 23,500).

Isoelectric Focusing—This was carried out by using a 110-ml column (LKB Instrument). The amount of carrier ampholyte used, with the voltage was increased and maintained at 700 V. The duration of hemoglobin (4.5 S) was used as an internal marker, and human γ-globulin light chain (Mr ~ 23,500) was measured during centrifugation using a split-beam photoelectric densitometer. Blue dextran was used to determine the void volume. The gels were stained in Coomassie blue and destained in 7% acetic acid.

RESULTS

Purification

All steps were carried out at 0–4°.

Step I: Preparation of Tissue Extract—Mice of the NMRI strain were killed by cervical dislocation and their livers were rapidly removed and put into liquid N₂, where they were kept until use. Frozen livers (400 g) were thawed, finely minced with scissors, and homogenized (1/4 w/v) with three strokes at 465 rpm in a Teflon glass homogenizer in 15 mM Tris/HCl buffer, pH 7.6, containing 10 mM EDTA, 5 mM 2-mercaptoethanol, and 0.25 mM sucrose (Buffer B). The homogenate was centrifuged for 40 min at 20,000 x gav.

Step II: Polyethylene Glycol Fractionation—Polyethylene glycol 6000 (130 g) was slowly added to 1080 ml of supernatant solution from Step I and dissolved under constant stirring for 1 h. The solution was then centrifuged for 40 min at 20,000 x gav. The pellet, containing no adenosine binding activity, was discarded, and 194 g of polyethylene glycol was added to the supernatant. After centrifugation (20,000 x gav for 40 min), the pellet so obtained was dissolved in 400 ml of 10 mM Tris/HCl, pH 7.5, 4 mM EDTA, and 5 mM 2-mercaptoethanol (Buffer C).

Step III: DEAE-cellulose (DE 52) Chromatography—The solution obtained from Step II was applied to a DEAE-cellulose (DE 52) column (2.4 x 31 cm) equilibrated with Buffer C, and the column was washed with the same buffer. Fractions of 20 ml were collected. The cyclic AMP-adenosine binding activity eluted as a sharp peak after washing with about 500 ml of buffer (Fig. 2).

Step IV: Ammonium Sulfate Fractionation—Fractions 32 to 40 (Fig. 2) were pooled (160 ml). Ammonium sulfate fractionation (33 to 60%) was performed by slowly adding solid ammonium sulfate with stirring in the solution. The precipitates were collected by centrifugation for 40 min at 20,000 x gav.

Step V: Sephadex G-150 Chromatography—The ammonium sulfate precipitate from Step IV was dissolved in 7 ml of Buffer A and applied to a Sephadex G-150 column (2.6 x 90 cm) equilibrated with the same buffer. Fractions of 7 ml were collected. The cyclic AMP-adenosine binding activity eluted as a sharp symmetrical peak and the fractions containing the main activity (70%) were pooled (35 ml).

Step VI: Isoelectric Focusing—This was performed as described under “Materials and Methods.” The solution from Step V (35 ml) was diluted in the middle three-fifths of the sucrose gradient. After completion of the focusing, 2-ml fractions were collected and assayed for adenosine and cyclic AMP binding activity (Fig. 5). Fractions 17 to 29 were pooled (12 ml) and concentrated by ammonium sulfate precipitation. The precipitate was dissolved in 2 ml of Buffer A and desalted by passage through a Sephadex G-25 column (0.9 x 9 cm) equilibrated with Buffer B.
with a linear gradient from 0 to 300 mM KCl (data not shown).

the native binding protein at various gel concentrations and in

ration after Step IV eluted as a peak well behind the cyclic

column (Step V). The ultraviolet absorbing contaminants after

acrylamide gel electrophoresis) sedimented in the 4 to 7.5 S

protein was obtained.

use.

formed as described under "Materials and Methods." Samples

of 20 ~1 from each fraction were subjected to polyacrylamide

various steps were impossible to obtain because crude prepara-

ations contained appreciable amounts of adenosine deaminase

and cyclic AMP binding protein associated with protein ki-

nase. The fact that the binding properties may change widely

depending on the pretreatment of the binding protein (see

below) made it difficult to make comparable quantization of

the binding protein during different steps in the purification

procedure.

About 80% of the cyclic AMP-dependent protein kinase was

recovered in the pellet obtained between 0 and 11 g of poly-

ethylene glycol/100 ml. The fraction (11 to 24 g of polyethylene
glycol/100 ml) containing the main adenosine binding activity

was applied to the DEAE-cellulose column from which it was

eluted with start buffer, (Fig. 2) whereas the small amount of

protein kinase left in the preparation after Step II was eluted

with a linear gradient from 0 to 300 mM KCl (data not shown).

The amount of adenosine deaminase detected in the prepa-

ration after Step IV eluted as a peak well behind the cyclic

AMP-adenosine binding activity on the Sephadex G-150 col-

umn (Step V). The ultraviolet absorbing contaminants after

Step V focused essentially as two main peaks between pH 6

and 8 (Fig. 3). The cyclic AMP-adenosine binding protein was

90% pure after Step VI as judged by analytical ultracentrifuga-

tion, and the contaminants (three to four bands on poly-

crylamide gel electrophoresis) sedimented in the 4 to 7.5 S

region of the sucrose gradient (Step VII).

From 400 g of liver about 30 mg of homogeneous binding

protein was obtained.

Homogeneity

Purity was checked by polyacrylamide gel electrophoresis of

the native binding protein at various gel concentrations and in

brated with the same buffer.

Step VII: Sucrose Gradient Centrifugation—This was per-

formed as described under "Materials and Methods." Samples

of 20 ~1 from each fraction were subjected to polyacrylamide
gel electrophoresis in 9% gel at pH 8.9. Fractions 5 to 8 (Fig.

4A) giving one single band, were pooled and concentrated by

ammonium sulfate precipitation and desalted by passage

through a Sephadex G-25 column (0.9

x

9 cm) equilibrated

with Buffer A. The preparation was stored in liquid N2 until

use.

Notes on Recovery and Purification

Data on the recovery of the binding protein through the

various steps were impossible to obtain because crude prepara-

tions contained appreciable amounts of adenosine deaminase

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region of the sucrose gradient (Step VII).

From 400 g of liver about 30 mg of homogeneous binding

protein was obtained.

Homogeneity

Purity was checked by polyacrylamide gel electrophoresis of

the native binding protein at various gel concentrations and in

different buffer systems as described under "Materials and

Methods." A sharp single band was observed. Fig. 5, A and B

show the gel electrophoresis at alkaline pH. A single band was

observed on SDS-polyacrylamide gel electrophoresis (Fig. 5C).
The purified protein sedimented as a single boundary on ana-

tlytical ultracentrifugation, indicating a high degree of purity

(data not shown).

Stability

The receptor protein was stable for months when stored in

liquid N2. Repeated freezing and thawing did not affect the

binding characteristics. The protein was stable for at least 3

weeks at 4 in 10 mM Hepes buffer, pH 7.0. The binding

capacity for adenosine and cyclic AMP decreased after incu-

bating the receptor in the presence of pronase, indicating its

protein nature.
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B

FIG. 5. Polyacrylamide gel electrophoresis. Native binding protein (Step VII) was subjected to electrophoresis in polyacrylamide gel (9%) using alkaline buffer (pH = 8.9). A, 5 µg of protein; B, 50 µg of protein; C, sodium dodecyl sulfate-polyacrylamide gel electrophoresis of cyclic AMP-adenosine binding protein performed as described under "Materials and Methods" using 10 µg of protein.

Physical Properties

The isoelectric point was at pI = 5.7 as determined in four separate experiments (Fig. 3).

The binding protein eluted from a Sephadex G-200 column corresponding to a Stokes radius of about 48 Å (Fig. 6) and sedimented as 9 S on sucrose gradient centrifugation (Fig. 4A).

The molecular size as determined by either of these methods was independent of the ionic strength (150 or 600 mM KCl or NaCl was included in the buffer during the experiments) and protein concentration (varied in the range 0.1 to 11 mg/ml). The presence of 10% glycerol did not affect the elution or sedimentation behavior (relative to marker proteins).

Untreated binding protein and binding protein activated by treatment with Mg²⁺ATP (as described in legend to Fig. 7) were subjected to sucrose gradient centrifugation. The degree of activation of the binding protein was checked in these experiments after completion of the centrifugation to exclude the possibility of inactivation. No difference in the sedimentation behavior was detected when the unactivated and the activated binding protein were compared.

Fig. 4B shows the sedimentation of the binding protein in freshly prepared cytosol, indicating that the 9 S form is not a result of proteolysis during purification. (For comparison, the cyclic AMP binding activity associated with protein kinase activity is also shown in the figure.)

The pure binding protein was subjected to analytical ultracentrifugation as described under "Materials and Methods." The data from the sedimentation velocity experiments were plotted as time versus logarithm of distance from center of rotation. The linear plot obtained was consistent with a sedimentation coefficient \( s_{20,w} \) of 8.8 \( \times 10^{-13} \) s.

From the equation \( M_s = 6 \pi \eta N S a/(1 - \eta \rho) \) where \( \eta \) = viscosity of medium, \( \rho \) = density of medium, and \( N = Avogadro's number, the molecular weight (\( M_s \)) could be calculated by use of the experimentally determined Stokes radius (\( a \)) and \( s_{20,w} \). Assuming a partial specific volume (\( \nu \)) of 0.70 cm³/g, the molecular weight was calculated to be 180,000.

The mobility of the protein compared to that of standards on SDS-polyacrylamide gel electrophoresis as described under "Materials and Methods" indicated that the binding protein is composed of polypeptides with the same molecular weight of 45,000.
Preliminary Studies on the Activation of the Binding Protein by Mg\(^{2+}\)ATP

The untreated purified protein bound adenosine with apparently low affinity and high capacity (dashed line, Fig. 8). The amount of cyclic AMP bound, with an apparent dissociation constant of \(1 \times 10^{-7}\) to \(3 \times 10^{-7}\) M, was 2 to 10% of the adenosine binding capacity (data not shown).

An increase in binding capacity for cyclic AMP after preincubation in the presence of \(Mg^{2+}\)ATP and a monovalent cation (K\(^+\)) was confirmed on the purified binding protein. As most of the binding kinetic data presented in this work are based on experiments performed on binding protein treated with \(Mg^{2+}\)ATP, this process, tentatively termed activation, was studied in some detail.

The binding protein was preincubated in the presence of \(Mg^{2+}\)ATP and KCl for increasing periods of time (Fig. 7). ATP was separated from the binding protein by Sephadex G-25 filtration. (High concentrations of ATP interfered with the binding studies which might be expected as ATP competes with cyclic AMP for the site specific for this nucleotide, as shown in the following paragraph.) After Sephadex G-25 filtration, the binding protein was appropriately diluted and incubated in the presence of radioactive ligand. The incubation was performed at 0° in 15 mM Hepes buffer, pH 7.5 containing 20% glycerol, conditions found to preserve the degree of activation as judged by stability of the binding properties with respect to time. Equilibrium of the binding reaction was reached within 12 h of incubation. The amount of cyclic AMP and adenosine bound was linear with respect to concentration of the total radioactive ligand was bound.

The binding capacity for cyclic AMP increased in a time-dependent manner upon activation (Fig. 7, inset). The affinity for cyclic AMP (apparent \(K_d = 1.5 \times 10^{-7}\) M) was independent of the degree of activation (Fig. 7). These results indicate that activation made more sites available for cyclic AMP. Activation did not increase the total binding capacity for adenosine, but high affinity sites for adenosine appeared (Fig. 8).

The possibility existed that ATP was decomposed during the preincubation and that activation was effected by the decomposition products. Binding protein was preincubated in the presence of \([\text{PH}]\text{ATP}\) (13 mCi/mmol) under the conditions described in the legend to Fig. 7 and samples from the preincubation were subjected to thin layer chromatography (System B). Less than 3% of the total ATP was converted to ADP and nondetectable amounts to AMP and adenosine. The binding protein was not activated when preincubated in the presence of phosphate or pyrophosphate (1, 10, and 150 mM of the sodium salts) instead of ATP. ADP and AMP were apparently poor activators (9).

To check if the activation process was accompanied by a phosphorylation of the binding protein, the latter (3 mg/ml) was incubated in the presence of 6 mM \(\gamma\text{-}[\text{32P}]\text{ATP}\) (2.5 mCi/mmol), 150 mM KCl, and 10 mM magnesium acetate for 30 min at 30°. Samples of 30 \(\mu\)l were applied to a Sephadex G-25 column (0.45 x 6 cm) equilibrated with 15 mM Hepes buffer, pH 7.5, containing 20% glycerol. Radioactivity was excluded from the gel clearly separated from free ATP, indicating association of radioactive \(\gamma\text{-}[\text{32P}]\text{ATP}\) with the protein. The excluded radioactivity was pooled (150 \(\mu\)l) and 25 \(\mu\)l (about 8000 cpm) subjected to SDS-polyacrylamide gel electrophoresis as described under "Materials and Methods." The gel was sliced and counted. No radioactivity could be detected corresponding to the protein band. Furthermore, when 100 \(\mu\)l of the excluded radioactivity was spotted on Whatman filters and washed in 5% ice-cold trichloroacetic acid as described for assay of protein kinase activity (11), no incorporation of \(\text{32P}\) could be detected. These results indicate that activation was not accompanied by phosphorylation, but that ATP bound to the receptor protein. Furthermore, about 50% of the \(\gamma\text{-}[\text{32P}]\text{ATP}\) bound was removed by filtration through a column containing charcoal, which supports the suggestion that \(\text{32P}\) was not covalently bound.

There was a correlation between the degree of activation of cyclic AMP binding sites and the concentration of ATP present during the activation. The results obtained with the partly purified binding protein (9) were confirmed using the homogeneous receptor. The binding capacity for cyclic AMP increased between \(5 \times 10^{-4}\) M and \(10^{-2}\) M ATP. Studies on the activation by adenine derivatives other than ATP met with the problem that these derivatives, being potent inhibitors to cyclic AMP binding, cause serious interference with the subsequent measurement of cyclic AMP bound to the receptor.

We have tried to correlate the degree of activation with the amount of ATP bound to the receptor protein. When ATP was partly removed (50%) by treatment with charcoal prior to incubation in the presence of cyclic \([\text{H}]\text{AMP}\), the binding capacity for cyclic AMP did not decrease. Thus, there was no relation between ATP binding and the degree of activation as judged by cyclic AMP binding. The extension of these studies were hampered by a low apparent affinity for ATP under the conditions of activation. Furthermore by preincubating in the presence of \(\gamma\text{-}[\text{32P}]\text{ATP}\), it was possible to demonstrate that more than 95% of the ATP bound was dissociated from the receptor protein during incubation (18 h at 0°) in the presence of \(\text{H}\)-labeled ligand.

Specificity of Cyclic AMP Binding Site

The double reciprocal plot of the data presented in Fig. 9, was consistent with adenosine, AMP, ADP, and ATP competi-

![Scatchard plot for the binding of \([\text{H}]\text{adenosine}\) (1.42 Ci/mmole) to nonactivated binding protein and to the activated protein, in the absence and presence of cyclic AMP. Cyclic AMP-adenosine binding protein was activated for 30 min and desalted on a Sephadex G-25 column as described in legend to Fig. 7. The binding of \([\text{H}]\text{adenosine}\) was measured at 40 \(\mu\)g of protein/ml incubate. Data on \([\text{H}]\text{adenosine}\) binding to the nonactivated receptor (\(\Delta\cdots\Delta\)), activated receptor in the absence (\(\bullet\)) or presence (\(\circ\)) of 100 \(\muM\) cyclic AMP are shown.](image-url)
tively inhibited the binding of cyclic \(^{3}H\)AMP to the activated receptor protein indicating that these adenine derivatives were bound to the same site as cyclic AMP. Adenine did not compete for this site. The inhibition constant (\(K_I\)) calculated from the equation (19):

\[
K_I = \frac{K_{cyclic\ AMP}(I)}{v_{max}(cyclic\ AMP) - (I)(cyclic\ AMP) + K_{cyclic\ AMP}}
\]

where \(v\) = amount of cyclic AMP bound and \((I)\) = concentration of competing molecule, was about \(8 \times 10^{-9}\) M for adenine, \(1.2 \times 10^{-8}\) M for AMP, \(1.5 \times 10^{-8}\) M for ADP, and higher than \(5 \times 10^{-8}\) M for ATP. The inhibition constant for unlabeled cyclic AMP was \(1.5 \times 10^{-7}\) M. Cyclic GMP, GMP, guanosine, cyclic IMP, IMP, and inosine did not inhibit the binding of cyclic \(^{3}H\)AMP.

**Binding of Adenosine to Activated Receptor Protein**

A Scatchard plot for the binding of \(^{3}H\)adenosine to the binding protein activated as described in the legend to Fig. 7, was hyperbolic (Fig. 8), indicating the existence of more than one site binding adenosine. The part of the curve with the steepest slope corresponded to a dissociation constant of about \(2 \times 10^{-7}\) M. To test the specificity of the high affinity site, the binding at 0.1 \(\mu\)M \(^{3}H\)adenosine was measured in the presence of increasing concentrations of inhibitors (Table I). Under the experimental conditions described, only about 50% of the binding could be suppressed by cyclic AMP which was the most effective inhibitor. This could be interpreted as competition between cyclic AMP and adenosine for only a part of the adenosine binding sites. This interpretation was supported by studies on binding of adenosine in the presence of a concentration of cyclic AMP (100 \(\mu\)M) high enough to saturate the cyclic AMP site. Under these conditions the steepest part of the Scatchard plot for adenosine binding showed the same slope as in the absence of cyclic AMP, whereas the part corresponding to low affinity was suppressed by cyclic AMP (Fig. 8, filled symbols). This might represent inhibition of the binding of adenosine to the site shown preferentially to bind cyclic AMP.

To test the specificity of the high affinity binding for adenosine not suppressed by cyclic AMP, the binding of \(^{3}H\)adenosine at a concentration of 0.1 \(\mu\)M was measured in the presence of 100 \(\mu\)M unlabeled cyclic AMP and possible (as judged from the results presented in Table I) inhibitors of adenosine binding (adenine, AMP, ADP, and ATP). The binding of adenosine to the high affinity site was inhibited by adenine and to a slight degree by AMP, whereas ADP and ATP were ineffective (Table II).

**Table I**

**Effect of purine derivatives on the binding of \(^{3}H\)adenosine**

The binding of \(^{3}H\)adenosine to the activated receptor protein (activated as described in legend to Fig. 7) was measured in the presence of various purine derivatives at concentrations indicated in the table. The concentrations were 0.1 \(\mu\)M and 40 \(\mu\)g/ml for \(^{3}H\)adenosine and receptor protein respectively.

<table>
<thead>
<tr>
<th>Additions</th>
<th>(\mu)M</th>
<th>(^{3}H)Adenosine bound per ml of incubate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td></td>
<td>100%</td>
</tr>
<tr>
<td>Adenosine</td>
<td>10</td>
<td>23.3</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>2.2</td>
</tr>
<tr>
<td>Cyclic AMP</td>
<td>4</td>
<td>12.2</td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>10.7</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>10.6</td>
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<td>4</td>
<td>19.0</td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>18.5</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>12.5</td>
</tr>
<tr>
<td>AMP</td>
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</tr>
<tr>
<td></td>
<td>10</td>
<td>10.6</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>9.2</td>
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<tr>
<td>ADP</td>
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<td>17.0</td>
</tr>
<tr>
<td></td>
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<td>12.8</td>
</tr>
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<td></td>
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<tr>
<td>Guanosine</td>
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<td>29.0</td>
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<tr>
<td>GMP</td>
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<tr>
<td>Cyclic GMP</td>
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<td>21.2</td>
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<tr>
<td>Inosine</td>
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<td>22.3</td>
</tr>
<tr>
<td>IMP</td>
<td>50</td>
<td>20.0</td>
</tr>
<tr>
<td>Cyclic IMP</td>
<td>50</td>
<td>24.2</td>
</tr>
</tbody>
</table>

**Table II**

**Specificity of the high affinity adenosine binding not suppressed by cyclic AMP**

Receptor protein was activated as described in the legend to Fig. 7 except that the concentration of binding protein was 4 mg/ml and the preincubation was allowed to proceed for 60 min at 30°. Measurement of \(^{3}H\)adenosine binding was performed at 80 \(\mu\)g binding protein per ml and 0.1 \(\mu\)M \(^{3}H\)adenosine. In addition to 100 \(\mu\)M cyclic AMP present in all incubations, various adenine derivatives (at concentrations indicated in the table) were added. The binding of \(^{3}H\)adenosine with only 100 \(\mu\)M cyclic AMP and buffer (control) was taken as 100%.

<table>
<thead>
<tr>
<th>Additions</th>
<th>(\mu)M</th>
<th>(^{3}H)Adenosine bound</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td></td>
<td>100%</td>
</tr>
<tr>
<td>Adenosine</td>
<td>5</td>
<td>15.4</td>
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<td>1.4</td>
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<tr>
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<tr>
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<td>ADP</td>
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<td></td>
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<td>107</td>
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<tr>
<td>ATP</td>
<td>5</td>
<td>102.4</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>102.4</td>
</tr>
</tbody>
</table>
Cyclic AMP-adenosine Binding Protein from Mouse Liver

**Table III**

<table>
<thead>
<tr>
<th>Regulatory subunit or cyclic AMP-adenosine binding protein</th>
<th>pmol of phosphate incorporated</th>
<th>Ratio</th>
</tr>
</thead>
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<tr>
<td>Free-catalytic and regulatory subunits from cyclic AMP-dependent protein kinase</td>
<td>- Cyclic AMP</td>
<td>- Cyclic AMP</td>
</tr>
<tr>
<td>Buffer control</td>
<td>430</td>
<td>370</td>
</tr>
<tr>
<td>Regulatory subunit</td>
<td>172</td>
<td>453</td>
</tr>
<tr>
<td>Cyclic AMP-adenosine binding protein</td>
<td>0.5 mg/ml</td>
<td>380</td>
</tr>
<tr>
<td></td>
<td>1.2 mg/ml</td>
<td>365</td>
</tr>
<tr>
<td></td>
<td>2.3 mg/ml</td>
<td>470</td>
</tr>
</tbody>
</table>

**Test for Enzymic Properties**

The pure preparation of binding protein had no adenosine deaminase or cyclic AMP phosphodiesterase activity. Under conditions optimal for photophosphatase activity catalyzed by cyclic AMP-dependent protein kinase or casein kinase, neither the unactivated nor the activated binding protein phosphorylated casein (5 mg/ml) or histone (0.7 mg/ml) to any significant extent.

The photophosphatase activity of the free catalytic subunit of cyclic AMP-dependent protein kinase has been shown to be inhibited by the addition of the regulatory subunit from the same enzyme (20) and Table III. The cyclic AMP-adenosine binding protein did not inhibit the protein kinase activity of the free catalytic subunit of cyclic AMP-dependent protein kinase (PK I) under conditions (in the presence of Mn2+ATP) where recombination with the free regulatory subunit occurred (Table III). These results serve to differentiate the cyclic AMP-adenosine binding protein from the regulatory subunit of cyclic AMP-dependent protein kinase.

As phosphofructokinase has been shown to bind cyclic AMP with about the same affinity for this nucleotide as the binding protein described by us (19, 21), it should be noted that neither the unactivated nor activated form of the binding protein had any phosphofructokinase activity, and neither form inhibited the phosphofructokinase from rabbit skeletal muscle added to the assay mixture.

**Discussion**

This paper reports the existence of a cyclic AMP-adenosine binding protein in mouse liver. The binding protein was purified to apparent homogeneity as judged by polyacrylamide gel electrophoresis in the absence and presence of sodium dodecyl sulfate and by analytical ultracentrifugation. The binding protein appears to be tetrameric with a molecular weight of 180,000. The molecular size seems to be independent of ionic strength and concentration of protein. The same molecular form was detected in freshly prepared, crude liver extract. This indicates structural stability of the cyclic AMP-adenosine binding protein.

Measurement of the binding activity involved ammonium sulfate precipitation of the binding protein and collection of the precipitate on Millipore filters. Experiments presented indicate that this method gives a true estimate of the amount of protein-bound ligand. The method can be performed under conditions preserving the degree of activation and is less laborious than the gel filtration technique (22) and equilibrium dialysis.

The binding of cyclic AMP to the regulatory subunit of protein kinase can be measured by the Millipore filtration technique described by Gilman (22). It was of interest to investigate whether the binding of cyclic AMP and adenosine to the cyclic AMP-adenosine binding protein could be detected by a similar method not involving ammonium sulfate precipitation. When the assay of Gilman was adopted, 75% of the adenosine binding activity was detected. Cyclic AMP seemed to be rapidly liberated from the binding protein under these conditions (sodium phosphate buffer, pH 6.0). When 15 mm Hepes, pH = 7.5, was used instead of the phosphate buffer, low recovery was obtained for both cyclic [3H]AMP and [3H]adenosine bound to the receptor protein. The reason seemed to be poor retention of the binding protein on the Millipore filter. The following observations support this explanation. The ligand-receptor complex was recovered in the buffer passing through the filter. Both cyclic AMP and adenosine bind to the receptor molecule under similar conditions as judged by the gel filtration technique (Fig. 1).

An increased capacity for cyclic AMP binding after preincubation of a crude preparation of the binding protein in the presence of Mg2+ATP has been presented in a recent communication (23). In the present work it was demonstrated that treatment with Mg2+ATP activated a high affinity site for adenosine, and an increased capacity for cyclic AMP binding after such treatment was confirmed on the pure binding protein. Thus, activation is not affected by a contaminating factor. Recently, autophosphorylation of cyclic AMP-dependent protein kinase with subsequent changes in binding properties of the regulatory subunit has been reported (24-26). Our results indicate that autophosphorylation is not the mechanism of activation of the cyclic AMP-adenosine binding protein from mouse liver. Furthermore, sucrose gradient centrifugation did not reveal changes in sedimentation behavior upon activation. Thus, dissociation or aggregation does not accompany activation of the binding protein.

As radioactive ATP was eluted from Sephadex G-25 columns after preincubation with the binding protein, ATP probably binds to the protein under conditions of activation. Experiments presented suggest that no direct relation exists between binding of ATP and activation, as partial removal of ATP did not decrease the binding capacity for cyclic AMP. ATP seems to competitively inhibit the binding of cyclic [3H]AMP to the binding protein (Fig. 9). This may indicate binding of ATP to the cyclic AMP binding site. Whether ATP interaction with this or another site is a prerequisite to activation remains to be established.

Studies on the activation of the cyclic AMP-adenosine binding protein showed that its binding properties can change widely. If the ratio of cyclic AMP to adenosine binding capacity is taken as a measurement of activation, this varies between 0.05 and 1. Assuming that the binding protein is

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This text is a part of the Journal of Biological Chemistry, published by the American Society for Biochemistry and Molecular Biology (ASBMB). The content is a contribution to the understanding of cyclic AMP-adenosine binding proteins in mouse liver, detailing their purification, properties, and interactions with regulatory subunits under varying conditions.
subjected to similar changes in binding properties in the cell, one may speculate whether this protein modulates the effects of cyclic AMP. Studies on the mutual interactions of binding sites under conditions approaching those believed to exist in the cell, may give some insight into the functional role of activation.

Binding studies on the activated receptor protein indicate that cyclic AMP binds (with an apparent dissociation constant of $1.5 \times 10^{-7}$ M) to one main site (Figs. 7 and 9). Assuming that the inhibition constant ($K_i$) is the same as the dissociation constant ($K_d$) for one particular inhibitor of cyclic AMP binding, one might expect that adenosine binds to the cyclic AMP binding site with a $K_i$ 4 to 5 times higher than that for cyclic AMP. Competition studies (Table I) suggest heterogeneity of adenosine binding sites, only part of the adenosine binding was inhibited by cyclic AMP. A Scatchard plot for adenosine binding in the absence and presence of 100 µM cyclic AMP (Fig. 8) showed suppression of the part of the curve corresponding to low affinity ($K_d$ about $10^{-9}$ M) binding of adenosine. These data were interpreted as adenosine binding to at least both the cyclic AMP site and to a site with high specificity for this adenine derivative. The high specificity of the adenosine binding site points to the possibility of adenosine as a modulator of intracellular effects of cyclic AMP. The binding kinetic studies presented here do not exclude the possibility that part of the inhibition of cyclic AMP binding effected by adenosine may be explained by altered affinity for cyclic AMP when the adenosine binding site is occupied.

Recently, the existence of two types of cyclic AMP binding sites, one of which had a $K_d$ of $1.6 \times 10^{-7}$ M, has been reported in cells of Dictyostelium discoideum (37). These findings, together with a report on ATP activation of cyclic AMP receptors in the same species (38), should be taken into account when the possibility of activation of cyclic AMP receptors in intact mammalian cells is considered.

Several workers have reported on the existence in eukaryotic cells of cyclic AMP binding factors not related to protein kinase (6–8). These factors have one or all of the following characteristics. The dissociation coefficient is about 9 S (6–8); the dissociation constant for cyclic AMP is about $2 \times 10^{-4}$ M (7, 8); adenosine derivatives compete for the cyclic AMP site (7, 8). Specific adenosine binding activity has been described in rat liver (29). These reports, together with the observation that cyclic AMP-adenosine binding proteins are present in bovine adrenal cortex, human renal cortex, and human renal cell carcinoma, indicate that the cyclic AMP-adenosine binding proteins are widely distributed.

The adenosine-cyclic AMP binding factors purified to homogeneity from rabbit erythrocytes by Yuh and Tao (7) have similar binding properties to the binding protein described by us. The binding factors from rabbit erythrocytes were suggested to be pentamers and of higher molecular weight (240,000) than the cyclic AMP-adenosine binding protein from mouse liver. The factors from rabbit erythrocytes bound more adenosine than cyclic AMP with a ratio of 3 to 8 (7, 39). The authors commented upon the low binding capacity for cyclic AMP (about 0.44 molecule of cyclic AMP was bound to each molecule of receptor). The possibility that a large population of the proteins might be in an inactive form and the possible requirement for cofactors for optimal binding were in fact discussed. For comparison, it could be mentioned that about 2 molecules of cyclic AMP were bound to 1 molecule of binding protein from mouse liver when the receptor was treated with Mg²⁺ATP as described in legend to Fig. 7.

The functional role of the cyclic AMP-adenosine binding protein is unknown. Increasing evidence is accumulating suggesting that cyclic AMP and adenosine metabolism in mammalian cells is interrelated (31–36). Adenosine has been proposed as a metabolic and physiological regulator (34, 37–39). The interaction of adenosine with its intracellular receptor sites may mediate some of its metabolic effects.

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Cyclic AMP-adenosine Binding Protein from Mouse Liver

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