This is a rat monoclonal antibody raised against bacterially expressed murine GATA-1.

Members of the GATA family share a conserved zinc finger DNA-binding domain and are capable of binding the WGATAR consensus sequence. GATA-1 is erythroid-specific and is responsible for the regulated transcription of erythroid genes. It is an essential component in the generation of the erythroid lineage.
Immunoprecipitation of K562 nuclear extract with sc-266 antibody efficiently enriches a protein of molecular weight of GATA1 (46KD).
Western blot analysis of immunoprecipitated proteins from K562 nuclear extracts detected using anti-GATA1 (sc266) antibody from Santa Cruz Biotechnology. Expected protein band 47KD.

Input: Input lysate, Sup: Supernatant from IP, IP: Immunoprecipitated fraction from 07-729, IgG: Control Immunoprecipitation using IgG.

IgG: Control Immunoprecipitation using IgG.
Fig. 1: GATA motif enrichment

<table>
<thead>
<tr>
<th>GATA motif enrichment (log 2)</th>
<th>4.6723</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell line</td>
<td>K562</td>
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</tbody>
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Fig. 2: Motif enrichment sequence and position weight matrix for the highly enriched GATA motif
Calculations were done by Alan Boyle using a collection of known motifs. Table 1 shows the fold-enrichments and fraction of peaks which contain the motif. The motif which produced the largest value for each criterion is shown in Table 1. Note that while the maximally enriched motifs may differ from the motif with the highest enrichment p-values and the most represented motif, the motifs are highly similar (Figure 1) and thus all values are similar between motifs. Motifs were identified using a matching stringency corresponding to 4-6 (6mer). Peaks identified by IDR (1% cutoff) were used in the analysis and +/-50bp from peak centers were considered. Background consisting of UCSC and all gencode v7 exons (including non-protein coding genes) were excluded from the analysis. Comparison to shuffle motifs were used to correct for compositional bias. Enrichment is the corrected # of motifs in ChIP peaks/corrected # of motifs in DNaseI peaks. The current ENCODE standard calls for >4 fold enrichment and >10% motif representation for this criteria to be used for validation. The K562 C-Fos dataset presented here exceed these thresholds and sc-266 is considered validated.