Query for confounders

http://epigraphdb.org/confounder/

(cf:Gwas)-[r1:MR]->
(exposure:Gwas {trait: "Crohn's disease"})-[r2:MR]->
(outcome:Gwas {trait: "Inflammatory bowel disease"})
<-[r3:MR]-(cf:Gwas)
Query for confounders

http://epigraphdb.org/confounder/

```
(cf:Gwas)->[r1:MR]->
(exposure:Gwas {trait: "Crohn's disease"})->[r2:MR]->
(outcome:Gwas {trait: "Inflammatory bowel disease"})
<-[r3:MR]-(cf:Gwas)
```
Outcome phenotype: Crohn's disease
Any REST API client (httpie, curl, requests, postman, ...)

R package devtools::install("MRCIEU/epigraphdb-r")

R is a collaborative project with many contributors. Type 'contributors()' for more info.
Type 'citation()' on how to cite R or R packages.
Type 'demo()' for some demos, 'help()' for an HTML interface to help.
Type 'q()' to quit R.

epigraphdb::mr(exposure="Crohn's disease")

# A tibble: 31 x 12
## (1/1)

<table>
<thead>
<tr>
<th>exposure_id</th>
<th>outcome_id</th>
<th>exposure_name</th>
<th>outcome_id</th>
<th>outcome_name</th>
<th>estimate</th>
<th>se</th>
<th>ci_low</th>
<th>ci_upp</th>
<th>df</th>
<th>p</th>
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</thead>
<tbody>
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<td>1</td>
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<td>Crohn's dis.</td>
<td>31</td>
<td>Inflammatory</td>
<td>0.746</td>
<td>2.74e-5</td>
<td>5.36e-163</td>
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<td>5.62e-1</td>
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<td>Ulcerative</td>
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<td>32</td>
<td>Ulcerative</td>
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<td>2.02e-1</td>
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<td>Crohn's dis.</td>
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</tr>
</tbody>
</table>

Return information related to Mendelian Randomisation

Arguments: "optional": ("exposure": "Exposure name", "outcome": "Outcome name"),

Examples:

Get MR evidence between exposure trait Overweight and outcome trait Body mass index:

```
> get_mr(exposure = "Overweight", outcome = "Body mass index")

```

Get MR evidence of exposure trait Overweight:

```
> get_mr(exposure = "Overweight")
```
Web application: http://epigraphdb.org
API: http://api.epigraphdb.org
documentation: http://docs.epigraphdb.org
R package: https://github.com/MRCIEU/epigraphdb-r