Method summary (v1.0)

Design
Rows are built as a four-stage chain:
molecular_event -> acute_synaptic_effect -> circuit_level_signature -> expected_readout.

Workflow
1. Selected high-yield neurobiochemistry domains relevant to synaptic and circuit function.
2. Encoded one distinct event per row with a stable event_id.
3. Assigned the primary cellular/anatomical compartment for localization.
4. Wrote non-diagnostic translational context for clinical relevance.
5. Added evidence tier and citation key for traceability.
6. Applied teaching level tags for curricular scaffolding.

Quality checks
- Unique event_id values
- All required columns populated
- Consistent sentence-level formatting
- No patient-level identifiers
- Citation keys resolved against citation_map.csv

Scope
This dataset is for educational and research communication.
It is not intended for diagnosis or treatment guidance.