GPT4 aided biomaterials research use case: stabilization of selenium nanoparticles with proteins

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Recent advancements in LLMs based on various transformer architectures such as BERT and GPT family models, brought many new possibilities for application in scientific research. The specific architecture and broad knowledge of these models give them the ability to understand concepts, to plan and solve different kinds of problems, including various chemistry - related tasks.

We evaluated a case of GPT4 performance for recommending proteins suitable for the stabilization of selenium nanoparticles (SeNPs). SeNPs exhibit diverse beneficial bioactivities, including antioxidant, antibacterial, and anticancer properties.

Stabilization of SeNPs with suitable proteins may be an effective approach to improve their bioactivities.

Methods

- **◆Prompt engineering:**
- ►GPT4 turbo preview
- Open Al playground and API
- **Python 3.10 virtual environment**

◆Data:

- Science parse AllenAl
- Research articles PDFs
- Review articles PDFs
- UniProt API for protein records
- Chemistry knowledge assessment:
- Chemistry knowledge and reasoning SeNp synthesis and stabilization methods
- Synthesis text classification
- Information extraction to tabular data **JSON** format

◆Protein knowledge:

- Properties and functions of proteins
- >Amino acid sequence recognition
- amino acid sequences Comparing (failed)
- > Propose proteins with desired bioactivites after examples provided



github.com/ zorankiki/ gpt4_for_SeNp _research







Classification prompt example

Extraction prompt example





BSA UniProt ID Test

Conclusion

The study demonstrates the successful application of advanced transformer architecture models like GPT4 in addressing relatively complex tasks in materials research. Despite GPT4 capabilities being largely dependent on the quality and size of training data, utilization of strategically designed and optimized prompts significantly improves it's performance in many cases. Although models can not perform well some "trivial" tasks, such as find longest common substring between two (or more) protein sequences, it has a great potential in research design and planing.

> LLMs, what was that?



Results

- Chemistry knowledge assessment
- Classification task accuracy 96%

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▶Synthesis	information	extraction	task

	pos	neg
neg	9	275
pos	10	2

[BSA, Chitosan]

[tea protein]

[Spray drying]



Protein stabilizers extraction task from reviews – proteins that interacts with Se



Se

molecule	freq	desc	molecule	freq	desc	molecule	freq	desc	molecule	freq	desc	molecule	freq	desc
bsa	4	None	glutathione peroxidase	2	None	sparc	1	secreted protein and rich in cysteine	selenocysteine	1	None	cytochrome c4	1	None
lysozyme	3	None	insulin	2	None	pacap-derived peptide dbayl	1	pituitary adenylate catalase activating peptide	selenos	1	None	dio2	1	selenoprotein
transferrin	3	None	chitosan	2	polysacharide	eadf4(k16)	1	positively charged spider silk protein eADF4(k16)	reductase protein	1	None	selenon	1	None
mushroom polysaccharide protein complex	2	None	selenok	1	None	horseradish peroxidase	1	None	polysaccharide and protein complex of edible m	1	None	selenof	1	None
human serum albumin	2	None	keratin	1	None	hsp-70	1	heat shock protein	thioredoxin reductase	1	None	selenot	1	None
silk fibroin	2	None	streptavidin	1	None	psp	1	polysaccharide- protein	selenomethionine	1	None	selenom	1	None
cytochrome c3	2	None	ox26	1	monoclonal antibodies antitransferin recepotor	selenoproteins	1	None	sef a	1	Sef A protein	rgdfc	1	RGDfC (cyclic peptide)

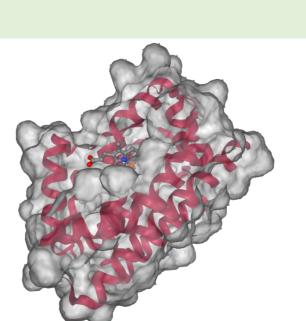
Examples of recommended proteins by model



Seleno protein

MSRB

HO-1

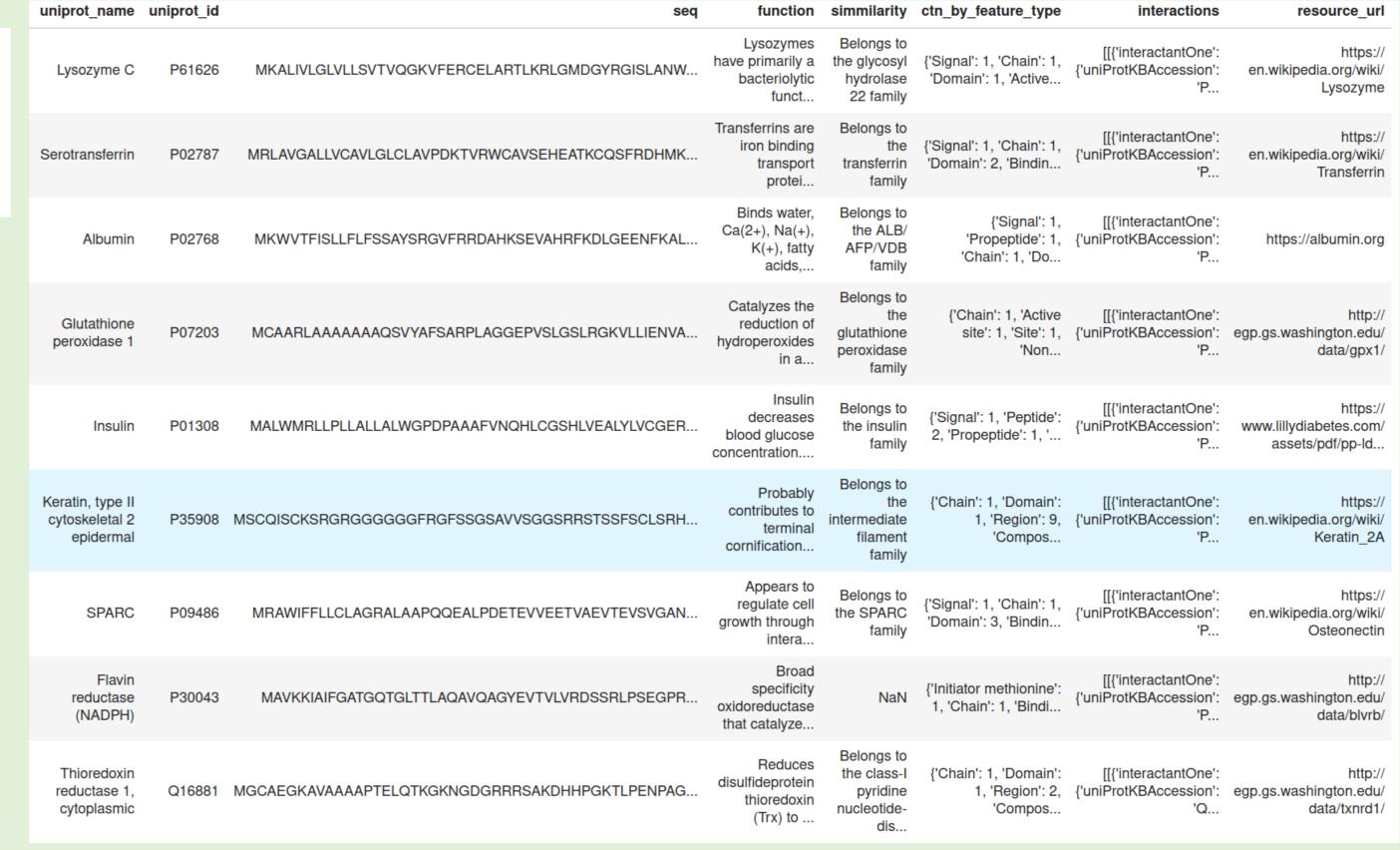


who you are: you are research scientist, expert in biochemistry. # your task: propose human proteins that interact with Selenium (Se) which have: a) anti-inflammatory; b) anti-apoptotic and c) anti-cancer role. You will get data of human proteins known to interact with Se. Propose proteins that are not listed in data that have stated roles (a, b, c, or combination of two or all together). # data format example: {'uniprot_name': {0: 'protein_0', 1: 'protein_1', ...}, {'uniprot_id': {0: 'ID_protein_0', 1: 'ID_protein_1', ...},

'seq': {0: 'seq_protein_0', 1: 'seq_protein_1', ...}, ...} # data fields and explanation: 'uniprot_name' - name of protein in UniProt DB; 'uniprot_id' - id in UniProt DB; 'seq' - amino acid sequence of protein, 'function' - description of protein function in human body, 'simmilarity' - protein family, 'ctn_by_feature_type' - protein features like binding sites, helices, etc; 'resource_url' - external url usually Wikipedia entry.

Human proteins stabilizers examples data to prompt





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