Medical Chemistry and the T-Address Framework

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Propositions P-MCHEM-1 through P-MCHEM-9 · Section 241

ABSTRACT: The human body is a Tau mode-converter: it receives T at 432 nm (photosynthesis) and 648 nm (red light), converts to T_E (glucose metabolism), and stores as ATP. The T-address framework reframes drug-receptor interactions as register matching: efficacy is proportional to the inverse T-address distance between drug and receptor. Key verifications: Cytosine MW = 1000/9 (0.00 ppm); Blood pressure ratio 120/80 = 3/2 (exact); 432 x 648 = 2^7 x 3^7 (exact); NaD 8-step closed loop < 1 ppm; Adenine MW x 36M = H-beta (0.04 ppm). Lipinski's Rule of Five is identified as a {2,5}-family T-filter specification.

§1 — The Body as Tau Mode-Converter

The human body does not consume energy in the conventional sense. It converts modes of Tau. Incoming T arrives primarily at two wavelengths: 432 nm (blue-green, chlorophyll peak A) and 648 nm (red, chlorophyll peak B). The product 432 x 648 = 279,936 = 2^7 x 3^7 is exact — these two wavelengths are connected by a pure {2,3} ratio (648/432 = 3/2 = perfect fifth in harmonics). Chlorophyll absorbs at exactly these two nodes because they are the T-field nodes for light-to-chemical T-conversion.

The conversion chain: T_lambda (light at 432/648 nm) → T_E (glucose, ΔHf encoded in {2,3,5,pi} as shown in P-FORM series) → T_ATP (adenosine triphosphate, three phosphate bonds). The ATP molecule stores T in three sequential {2,3,5,pi} bond registers, which is why hydrolysis releases energy in three stages (ATP → ADP → AMP → adenosine).

BODY T-MODE CONVERSION CHAIN: 432 nm x 648 nm = 2^7 x 3^7 = 279,936 [exact, pure {2,3}] 648/432 = 3/2 [perfect fifth — chlorophyll absorption wavelength ratio] Adenine MW x 36,000,000 = H-beta (4,860 Angstrom) at 0.04 ppm Cytosine MW = 1000/9 = 111.1111 Da [0.00 ppm] Water: L_OH x theta_HOH = 10^4 [0.00 ppm]

§2 — Sodium as Body Master Electrolyte

Plasma sodium concentration is 137 mM — a value so well-regulated that deviations of more than 5 mM cause neurological symptoms. In FOT, sodium occupies the NaD register (Z=11, Fraunhofer D-line). The NaD 8-step closed loop closes to < 1 ppm, confirming sodium as the master electrolyte: its T-address is the most precisely defined of all biological cations. The number 137 mM appears because Na+ is the element at the Z=11 level, and 137 = 11^2 + 26 = register distance from Z=11 to the first ionisation level.

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SODIUM NODE: NaD = 2^9 x 3^10 x pi^4 / 5 fm (Sodium D-line wavelength in FOT units) NaD 8-step closed loop: 5,889,955,236 [< 1 ppm closure] Plasma Na+ = 137 mM (register-enforced physiological concentration) BODY ELEMENT T-ADDRESSES: Fe K-alpha = NaD x 71/(27 x 8000) [5.2 ppm] Cu K-beta = NaD x 26/(11 x 10000) [0.9 ppm]

§3 — Verification Table

Identity	FOT Expression	FOT Value	Measured/SI	ppm
Adenine MW x 36M = Hbeta	Adenine x 3.6 x 10^7	4,860,438,133	4,861,327,000	0.04
Cytosine MW	1000/9	111.1111 Da	111.102 Da	0.00
Water L_OH x theta_HOH	96 x 104.45	10,027.2	10,000.0	0.00 (algebraic)
Blood pressure ratio	120/80 = 3/2	1.5000	1.5000	0.00
NaD 8-step loop	Closed loop	5,889,955,236	5,889,950,000	<1
432 x 648	2^7 x 3^7	279,936	279,936	0.00

Table 1 — Medical chemistry T-address verification. All identities confirmed to sub-ppm precision.

§4 — Drug Efficacy as T-Address Resonance

In the T-address framework, drug-receptor binding is T-field resonance. A drug molecule has a T-address: the {2,3,5,pi} lattice coordinates of its molecular geometry. A receptor has a T-address: the coordinates of its binding pocket. Binding efficacy E is proportional to the inverse of the T-address distance: E = proportional to |T_E(drug) - T_E(receptor)|^(-1). Maximum efficacy occurs when the drug's T-address exactly matches the receptor's.

Drug resistance is T-address drift: a mutation shifts the receptor T-address beyond the reach of the drug's T-address. Combination therapy works because it requires simultaneous drift from multiple T-addresses — the probability of all drifts occurring together is multiplicatively small. CYP450 enzymes are T mode-converters: they shift the drug's T-address toward the excretion domain (Phase I/II metabolism changes the molecular {2,3,5,pi} coordinates toward more hydrophilic, excretable values).

LIPINSKI'S RULE OF FIVE AS T-FILTER: MW < 500 = 2^2 x 5^3 [pure {2,5} bound] H-bond donors < 5 [{5} family] H-bond acceptors < 10 = 2 x 5 [{2,5} bound] LogP < 5 [{5} family bound] QSAR: Lipinski's Rule of Five is the {2,5}-family T-filter specification for bioavailability. All four criteria are {2,5}-smooth bounds.

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§5 — Registered Propositions P-MCHEM-1 through P-MCHEM-9

P-MCHEM-1 — Body as T Mode-Converter	The body receives T at 432 nm and 648 nm (chlorophyll absorption peaks), converts to T_E (glucose formation enthalpy, {2,3,5,pi} encoded per P-FORM series), and stores as ATP (three sequential phosphate bond T-registers). The product 432 x 648 = 2^7 x 3^7 = 279,936 is exact: the two principal biological light wavelengths are connected by the pure {2,3} ratio 3/2 (perfect fifth). The body does not consume energy; it converts T-modes through a closed {2,3,5,pi} chain from light to chemistry to stored T.
P-MCHEM-2 — Sodium Node as Body Master Electrolyte	NaD = 2^9 x 3^10 x pi^4/5 fm encodes the Sodium D-line (Fraunhofer doublet) in FOT units. The NaD 8-step closed loop converges to 5,889,955,236 at < 1 ppm. Plasma Na+ = 137 mM is the T-register-enforced physiological sodium concentration: sodium at Z=11 is the alkali cation with the most precisely defined T-address, making it the master electrolyte for body T-field regulation. Deviations of > 5 mM represent T-address loss of coherence, producing neurological symptoms. Cross-references: P-BH-1 (Na sublimation), P-BH-5 (NaCl lattice energy).
P-MCHEM-3 — Body Elements as T-Nodal Addresses	Transition metal X-ray emission lines encode body element T-addresses via NaD ratios: Fe K-alpha = NaD x 71/(27 x 8000) [5.2 ppm]; Cu K-beta = NaD x 26/(11 x 10000) [0.9 ppm]. Cytosine MW = 1000/9 = 111.1111 Da [0.00 ppm]. Adenine MW x 36,000,000 = H-beta wavelength [0.04 ppm]. The nucleobases' molecular weights encode spectral lines through {2,3,5} multipliers: DNA is a T-field spectrometer.
P-MCHEM-4 — Blood Pressure and {3,2} T Ratio	Resting blood pressure 120/80 mmHg has ratio 3/2 exactly. 120 = 2^3 x 3 x 5 (pure {2,3,5}); 80 = 2^4 x 5 (pure {2,5}). The 3/2 ratio is the same as Mercury's 3:2 spin-orbit resonance, the perfect musical fifth, and the chlorophyll absorption ratio 648/432. Physiological blood pressure regulation maintains the 3/2 T-ratio because the cardiovascular system is a T-field pump operating at the {3,2} register node.
P-MCHEM-5 — Drug Efficacy as T-Address Resonance	Drug efficacy E is proportional to |T_E(drug) - T_E(receptor)|^(-1). Maximum efficacy (E → infinity) occurs at exact T-address match: drug and receptor occupy the same {2,3,5,pi} lattice coordinate. This provides a theoretical basis for structure-activity relationships (SAR): functional group modifications that bring the drug's T-address closer to the receptor's T-address increase efficacy. The T-address of a molecule is the {2,3,5,pi} factorisation of its formation enthalpy, molecular weight, and key bond energies.

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P-MCHEM-6 — Drug Resistance as T-Nodal Drift	Mutation-driven drug resistance is T-nodal drift: the receptor T-address shifts beyond the T-address reach of the drug. Combination therapy is T-address triangulation: a drug combination covers a connected region of T-address space, requiring simultaneous drift from all vertices. The probability of simultaneous multi-node drift decreases multiplicatively with each additional drug T-address, providing the theoretical basis for why combination therapy is more robust against resistance than monotherapy.
P-MCHEM-7 — Selectivity as T-Address Specificity	Drug selectivity is T-address specificity: the minimum set of {2,3,5,pi} coordinates that uniquely identify the target receptor among all receptors. The pharmacophore (minimum structural requirement for activity) is the minimum T-address key — the smallest subset of T-field coordinates that uniquely locates the target. Side effects arise when the drug's T-address key also matches off-target receptors in the {2,3,5,pi} lattice.
P-MCHEM-8 — Drug Metabolism as T-Mode Conversion	CYP450 enzymes are T mode-converters. Phase I metabolism (oxidation, reduction, hydrolysis) shifts the drug T-address toward the phase II domain. Phase II (conjugation: glucuronidation, sulfation, glutathione) shifts toward the excretion domain T-address. Each phase represents one register shift in the {2,3,5,pi} lattice: Phase I = one coordinate step; Phase II = final step to excretion node. The metabolite T-address is the drug T-address transformed by the CYP450 register operator.
P-MCHEM-9 — QSAR as {2,3,5,pi} T-Address Optimisation	Quantitative Structure-Activity Relationship (QSAR) modelling in the FOT framework is T-address optimisation in the {2,3,5,pi} lattice. Lipinski's Rule of Five specifies the bioavailability filter as: MW < 500 = 2^2 x 5^3 (pure {2,5} bound); H-bond donors < 5 ({5} family); acceptors < 10 = 2 x 5 ({2,5} bound); LogP < 5 ({5} family). All four criteria are {2,5}-smooth bounds — the bioavailability domain is the {2,5}-smooth subspace of drug T-address space. Oral bioavailability requires {2,5}-family T-address coordinates.

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