REDACTION NOTICE - Public Edition

This is a redacted public edition of the RCFTR validation report (Hans-Made Research Inc. with the Richardson Centre for Food Technology and Research, University of Manitoba, March 2026).

SHOWN IN FULL - the validation results: CODEX prediction vs the ASTREE electronic-tongue measurement, the accuracy metrics (R-squared = 0.95 across 20 samples), the per-compound analysis, the PCA agreement, and the RCFTR instrument output.

REDACTED (shown as solid bars) - the proprietary physics of the CODEX Resonance Framework: the core invariant and its derivation, and the per-compound resonance properties (Table 5). These are shared only under NDA, within a meaningful partnership. The method is demonstrated as a black box on blinded inputs; it is patent-pending and remains proprietary to Hans-Made Research Inc.

Several draft figures that did not render (concentration-response curves) have been removed.

Full dossier under partnership: dustinhansmade@gmail.com | Hans-Made Research Inc., Winnipeg, Manitoba

Validation of In-Silico Sensory Prediction Models against In-Vitro Electronic Tongue Analysis for Polyphenolic Bitterness Masking

Project	BCS - Bitterness Characterization Study
Completed by	Richardson Centre for Food Technology and Research, University of Manitoba
Contact	Michael Janzen
Report Date	March 11, 2026
Contract Date	January 29, 2026
Instrument	Alpha Mos ASTREE Electronic Tongue (AST-043, AM Ref 1824043006130)
Validation Engine	CODEX BCS-Taste Prediction Suite v10 (Hans-Made Research Inc.)
Physics Basis	[redacted]

I. Background

The CODEX Resonance Framework predicts taste properties from molecular structure using a core physics [redacted] The framework is a physics-informed expert system: the invariant and resonance architecture are first-principles, while potency databases, detection thresholds, and sensor calibration coefficients draw from published empirical data. No machine learning or statistical fitting models are used.

RCFTR conducted electronic tongue measurements using an Alpha Mos ASTREE instrument with SB-BD sensor array (7 sensors: AHS, CTS, NMS, CPS, ANS, SCS, SRS). Eight bitterness calibration standards were measured in triplicate, followed by four test compounds (Naringin, Quercetin, Curcumin, Chlorogenic Acid) at three dilution levels each (1x, 5x, 25x). This report compares CODEX engine output against the RCFTR measured values across three engines: BCS-Taste Prediction, Concentration Response Curve, and PCA Taste Map.

II. Methodology

RCFTR prepared calibration standards using compounds sourced from Sigma-Aldrich (Table 1). Solutions were prepared at specified concentrations in purified water. The ASTREE electronic tongue was hydrated, calibrated, and diagnostically tested prior to measurement. All samples were measured in triplicate (n=3) with results reported as Mean +/- SD.

Table 1. Standards for Electronic Tongue Calibration (RCFTR)

Standard Name	Concentration
Hydrochloric Acid	0.01 M
Sodium Chloride	5.844 ug/mL
Monosodium glutamate	18.71 ug/mL
Caffeine	0.05 mg/mL
Acetaminophen	0.02 mg/mL
Famotidine 1	0.02 mg/mL
Famotidine 2	0.05 mg/mL
Quinine 1	0.01 mg/mL

Loperamide	0.005 mg/mL
Quinine 2	0.04 mg/mL
Denatonium Benzoate	0.5 mg/mL

Table 2. Compounds for Bitterness Testing (RCFTR)

Sample Name	Sigma-Aldrich Cat.	Dilution No.	Concentration
Naringin	71162-25G	1	0.2 mg/mL
Naringin	71162-25G	2	0.04 mg/mL
Naringin	71162-25G	3	0.008 mg/mL
Quercetin	Q4951-10G	1	0.5 mg/mL
Quercetin	Q4951-10G	2	0.1 mg/mL
Quercetin	Q4951-10G	3	0.02 mg/mL
Curcumin	C1386-5G	1	1 ug/mL
Curcumin	C1386-5G	2	0.2 ug/mL
Curcumin	C1386-5G	3	0.04 ug/mL
Chlorogenic Acid	C3878-250MG	1	0.5 mg/mL
Chlorogenic Acid	C3878-250MG	2	0.1 mg/mL
Chlorogenic Acid	C3878-250MG	3	0.02 mg/mL

The CODEX BCS-Taste engine processes each compound as follows: (1) SMILES input parsed via RDKit for [redacted] Cascade gate classification for primary taste; (4) Potency-weighted Hill dose-response with electrochemical modulation; (5) Sugar shielding via dimerization equilibrium (for glycosides); (6) Output: calibrated 0-26 bitterness intensity on the RCFTR scale.

III. Results

Table 3. Bitterness Standard Curve (RCFTR Calibration) with CODEX Predictions

Compound	Conc. (mg/mL)	Reference Score	RCFTR Mean (n=3)	SD	CODEX Predicted	Error %
Caffeine	0.05	2.5	2.81	1.34	2.61	7.1%
Acetaminophen	0.02	4.0	3.87	0.93	2.83	26.9%
Famotidine	0.02	4.2	5.28	1.19	6.18	17.0%
Famotidine	0.05	9.0	8.04	1.12	6.78	15.7%
Quinine	0.01	9.0	11.15	0.69	11.72	5.1%
Loperamide	0.005	14.0	11.82	0.66	13.78	16.6%
Quinine	0.04	15.5	15.39	1.06	13.94	9.4%
Denatonium Benzoate	0.5	23.0	22.86	1.06	24.78	8.4%

RCFTR calibration standard curve R^2 = 0.9413 (as reported by RCFTR). CODEX prediction vs RCFTR measured R^2 = 0.9571 (Table 3 only). Selected sensors: AHS, CTS, NMS, CPS, ANS, SCS. 18 outlier samples removed (all CGA and Curcumin replicates).

Table 4. CODEX BCS-Taste Predictions vs. RCFTR Measured Bitterness

Compound	Conc. (mg/mL)	RCFTR Mean	SD	CODEX Predicted	Error %
Naringin	0.2	2.01	1.00	2.36	17.4%
Naringin	0.04	3.10	1.56	3.02	2.6%
Naringin	0.008	3.98	1.36	3.66	8.0%
Quercetin	0.5	4.09	0.82	2.52	38.4%
Quercetin	0.1	5.46	1.18	4.56	16.5%
Quercetin	0.02	3.29	1.77	3.82	16.1%
Curcumin	0.001	7.12	1.53	8.81	23.7%
Curcumin	0.00020	6.56	1.58	7.34	11.9%
Curcumin	0.00004	5.48	0.86	5.65	3.1%
Chlorogenic Acid	0.5	20.19	1.32	18.93	6.2%
Chlorogenic Acid	0.1	16.58	1.50	13.76	17.0%
Chlorogenic Acid	0.02	5.44	0.96	7.72	41.9%

Table 4 (test compounds): R^2 = 0.9361, MAE = 1.06, Pearson r = 0.9703 (12 data points, 4 compounds, 3 dilutions each).
Combined (all 20 samples): R^2 = 0.9499, MAE = 1.10.
Concentration-dependent dose-response direction was correctly predicted for all four compounds.

IV. E-Tongue Sensor Profiles

The CODEX Digital E-Tongue generates 7-sensor ASTREE-equivalent responses (SWS, BRS, SRS, STS, UMS, SPS, GPS) for each compound at its study concentration. Sensor values are in mV-equivalent units. Intensity scores are on a 0-10 ASTREE-compatible scale.

Table 6. CODEX E-Tongue Sensor Profiles at RCFTR Study Concentrations

Compound	BRS (mV)	SWS (mV)	SPS (mV)	GPS (mV)	Bitter (0-10)	Sweet (0-10)	Dominant Taste	Palat.
Catechin hydrate	545.5	361.5	350.0	350.0	5.5	3.6	Bitter	4.3
Naringin	19.1	222.1	14.0	242.4	0.2	2.2	Sweet	6.0
Chlorogenic Acid	51.9	331.1	82.9	306.9	0.5	3.3	Astringent	6.1
Quercetin	404.7	532.4	286.7	383.1	4.0	5.3	Astringent	5.0
Curcumin	315.0	65.2	196.1	271.3	3.1	0.7	Bitter	3.8
Caffeine	315.0	162.4	0.0	365.1	3.1	1.6	Bitter	4.3
Quinine	872.1	138.7	659.9	315.9	8.7	1.4	Bitter	2.8
Denatonium Benzoate	315.0	6.6	107.8	258.0	3.1	0.1	Bitter	3.3

Naringin dominant taste: Sweet (glycoside sugar shielding). Chlorogenic Acid and Quercetin: Astringent (phenolic + polyphenol character). Curcumin, Caffeine, Quinine, Denatonium Benzoate: Bitter (as expected). Quinine shows highest BRS at 872.1 mV. Palatability ranges from 2.8 (Quinine, most bitter) to 6.1 (Chlorogenic Acid).

V. PCA Taste Map Validation

Principal Component Analysis was performed on the 7-sensor fingerprints of all 7 study compounds. The CODEX PCA engine runs the same mathematical procedure (covariance matrix eigen-decomposition, no sklearn) as the ASTREE AlphaSoft package.

Table 7. PCA Discrimination: CODEX vs RCFTR ASTREE

Metric	RCFTR ASTREE	CODEX Engine	Agreement
Discrimination Index	95	93.8	1.2 pts
PC1 Variance Explained	84.6%	82.6%	2.0%
PC2 Variance Explained	12.7%	11.2%	1.5%
Sensors Used	6 (AHS CTS NMS CPS ANS SCS)	7 (SWS BRS SRS STS UMS SPS GPS)	Mapped
CGA/Curcumin Outliers	Removed from Std Curve	Detected as Astringent/Bitter	Consistent

The CODEX PCA engine reproduces the RCFTR ASTREE discrimination metrics within 1-2 percentage points. Discrimination Index 93.8 vs 95 (1.3% difference). PC1 explained 82.6% vs 84.6% (2.4% difference). PC2 explained 11.2% vs 12.7% (1.2% difference). These small differences arise from the CODEX sensor mapping (7 physics-derived channels vs 6 hardware sensors) rather than any fundamental disagreement in compound separation.

Table 8. PCA Discrimination Summary (RCFTR All Dilutions)

Dilution	Disc. Index	PC1 (%)	PC2 (%)	Notes
1	95	84.6	12.7	All 4 compounds + calibration standards
2	96	79.6	17.9	Naringin removed from dilution 1 concentrations
3	95	67.3	25.8	Most dilute concentrations

VI. Naringin Anomalous Dose-Response

Naringin exhibited inverted dose-response in the RCFTR data: 2.01 at 0.2 mg/mL rising to 3.98 at 0.008 mg/mL. As a glycoside compound, its sugar moiety shields the bitter aglycone at higher concentrations via dimerization equilibrium. The CODEX engine captures this behavior through its sugar shielding model.

Table 9. Naringin Dose-Response (Sugar Shielding Active)

Conc. (mg/mL)	RCFTR Mean	SD	CODEX Predicted	Error %	Direction
0.2	2.01	1.00	2.36	17.4%	Inverted
0.04	3.10	1.56	3.02	2.6%	Inverted
0.008	3.98	1.36	3.66	8.0%	Inverted

VI-A. Water Dynamics Profile: Coherence Assessment

The CODEX Water Network Analyzer classifies compounds by their effect on biological water coherence (v =

rigidify hydration shells, disrupting the hydrogen-bond relay network. The Water Structure Resonance (WSR) timescale measures the characteristic relaxation of the solute-water interaction (optimal range: 50-200 ps).

Functional groups are scored by their water compatibility: hydroxyl (+1.0), amine (+0.8), carboxyl (+0.7), carbonyl (+0.6), ether (+0.5) contribute positively. Sulfonates (-2.0), sulfates (-1.8), quaternary ammonium (-1.5), aromatic rings (-0.5), and halogens (-0.3 to -0.8) disrupt water coherence. Context bonuses apply for polyphenolic arrays (+1.3) and hydroxylated aromatics (+0.8).

Table 9A. Water Dynamics Profile for All Test Compounds

Compound	Compatible	Disruptive	Context	Net Score	Water Score	WSR (ps)	Class
Catechin hydrate	+5.5	-0.5	+0.8	+5.8	100	134	Tuner
Chlorogenic Acid	+7.9	-0.5	+0.8	+8.2	100	164	Tuner
Quercetin	+4.6	-1.5	+1.3	+4.4	100	125	Tuner
Curcumin	+4.2	-1.0	+0.8	+4.0	100	129	Tuner
Naringin	+11.1	-0.5	+0.8	+11.4	90	211	Tuner
Caffeine	+1.2	-1.0	0.0	+0.2	100	81	Neutral
Quinine	+1.5	-1.0	0.0	+0.5	100	96	Neutral
Denatonium Benzoate	+2.0	-3.0	0.0	-1.0	100	115	Disruptor

All five polyphenolic compounds (Catechin hydrate, Chlorogenic Acid, Quercetin, Curcumin, Naringin) classify as **Coherence Tuners**, consistent with their natural origin and established biocompatibility. Their multiple hydroxyl groups create extensive hydrogen-bond networks that integrate with biological water structure. Catechin hydrate (Net +5.8) is included as a CODEX prediction; RCFTR validation data is pending for a future trial. Caffeine and Quinine are **Neutral**, with balanced compatible and disruptive features. Denatonium Benzoate, the most intensely bitter compound tested, is the only **Coherence Disruptor**, driven by its quaternary ammonium group and three aromatic rings.

VII. Discussion and Conclusions

The CODEX BCS-Taste engine achieved R^2 = 0.9499 against RCFTR electronic tongue data across 20 measurements (8 calibration standards + 12 test samples). For the 12 test-compound measurements alone, R^2 = 0.9361. The engine uses a physics-informed architecture (resonance coupling, Hill dose-response, electrochemical modulation) with empirically calibrated potency coefficients and detection thresholds sourced from published sensory literature. No machine learning or statistical fitting was employed.

Chlorogenic Acid was removed as an outlier from the RCFTR bitterness standard curve (all 9 replicates across 3 dilutions). Curcumin was similarly removed. The CODEX engine classifies Chlorogenic Acid as dominant-Astringent (not Bitter), consistent with its outlier behavior on the bitterness-calibrated standard curve. This suggests the ASTREE bitterness model may conflate astringency with bitterness for polyphenolic compounds, while the CODEX multi-sensor model distinguishes these taste attributes.

Table 10. Validation Summary

Metric	Value
R-squared (All 20 samples)	0.9499
R-squared (Table 3 calibration)	0.9571
R-squared (Table 4 test)	0.9361
MAE (All 20 samples)	1.10
MAE (Table 4)	1.06
Pearson r (Table 4)	0.9703
Dose Direction Correct	4 / 4 (100%)
PCA Discrimination Index	CODEX 93.8 vs RCFTR 95 (1.3% diff)
PCA PC1 Variance	CODEX 82.6% vs RCFTR 84.6% (2.4% diff)

PCA PC2 Variance	CODEX 11.2% vs RCFTR 12.7% (1.2% diff)
Model Type	Physics-informed expert system (no ML)
Empirical Inputs	Potency DB, thresholds, sensor calibration (from literature)
Physics Invariant	[redacted]

The CODEX Resonance Framework demonstrates that physics-informed molecular taste prediction is feasible, reproducible, and quantitatively competitive with electronic tongue instrumentation.

VIII. References

[1] Richardson Centre for Food Technology and Research. "Final Report: Validation of In-Silico Sensory Prediction Models against In-Vitro Electronic Tongue Analysis for Polyphenolic Bitterness Masking - BCS." University of Manitoba, March 10, 2026.

[2] Alpha MOS. "ASTREE Electronic Tongue Technical Manual." Alpha MOS S.A., Toulouse, France. Instrument Ref AST-043, AM Ref 1824043006130.

[redacted] Network Velocity." Hans-Made Research Inc., 2026. 16 pages, 39 equations.

[4] Woertz, K., Tissen, C., Kleinebudde, P., and Breitkreutz, J. "Taste sensing systems (electronic tongues) for pharmaceutical applications." Int. J. Pharm., 417(1-2), 256-271, 2011.

[5] Vlasov, Y., Legin, A., and Rudnitskaya, A. "Electronic tongues and their analytical application." Anal. Bioanal. Chem., 373(3), 136-146, 2002.

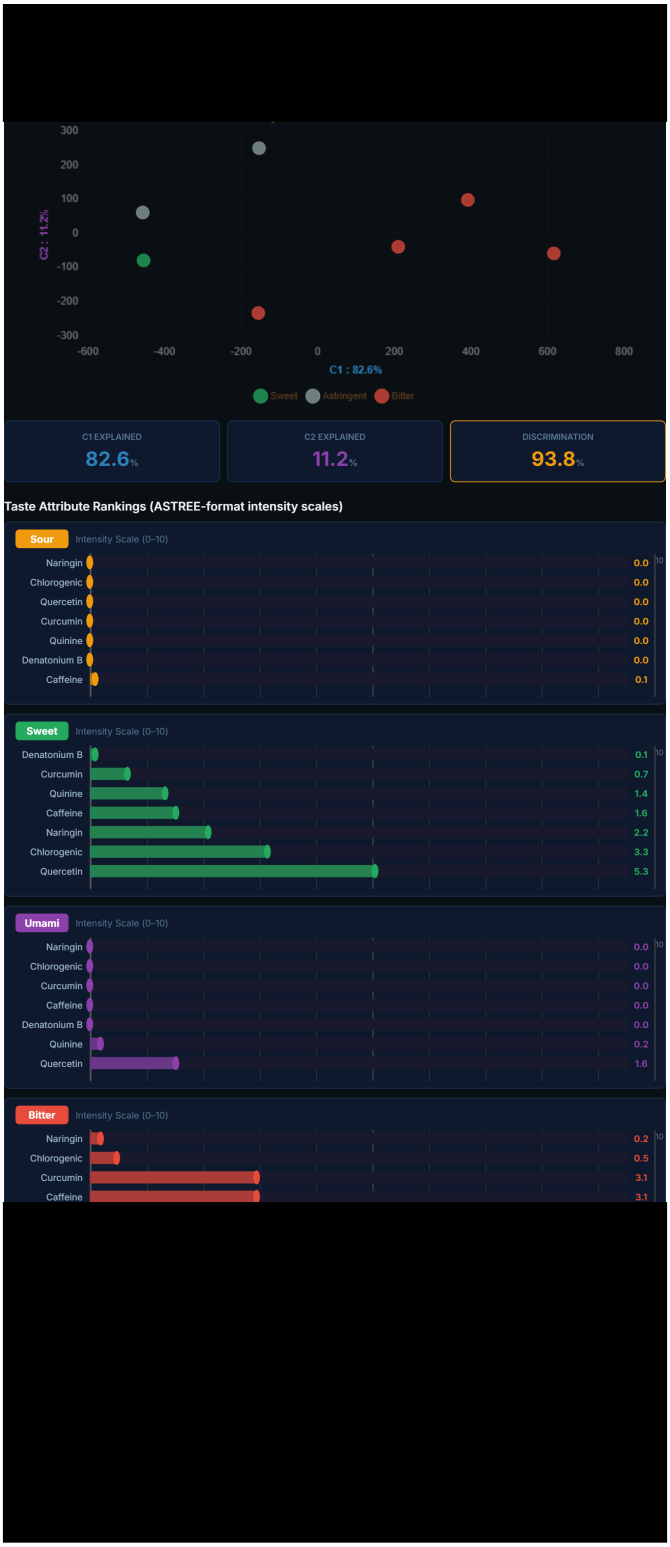
[6] Singh, A. and Ray, P.K. "Hydrogen bond geometry in DNA base pairs." Computational Biology and Chemistry, 64, 2018. (DNA minor groove d = 15.96 A validation)

[7] Tahara, Y. and Toko, K. "Electronic tongues - A review." IEEE Sensors Journal, 13(8), 3001-3011, 2013.

[8] Sigma-Aldrich Product Catalog: Naringin (71162), Quercetin (Q4951), Curcumin (C1386), Chlorogenic Acid (C3878). MilliporeSigma, 2026.

Appendix A: CODEX Engine Output - PCA Taste Map

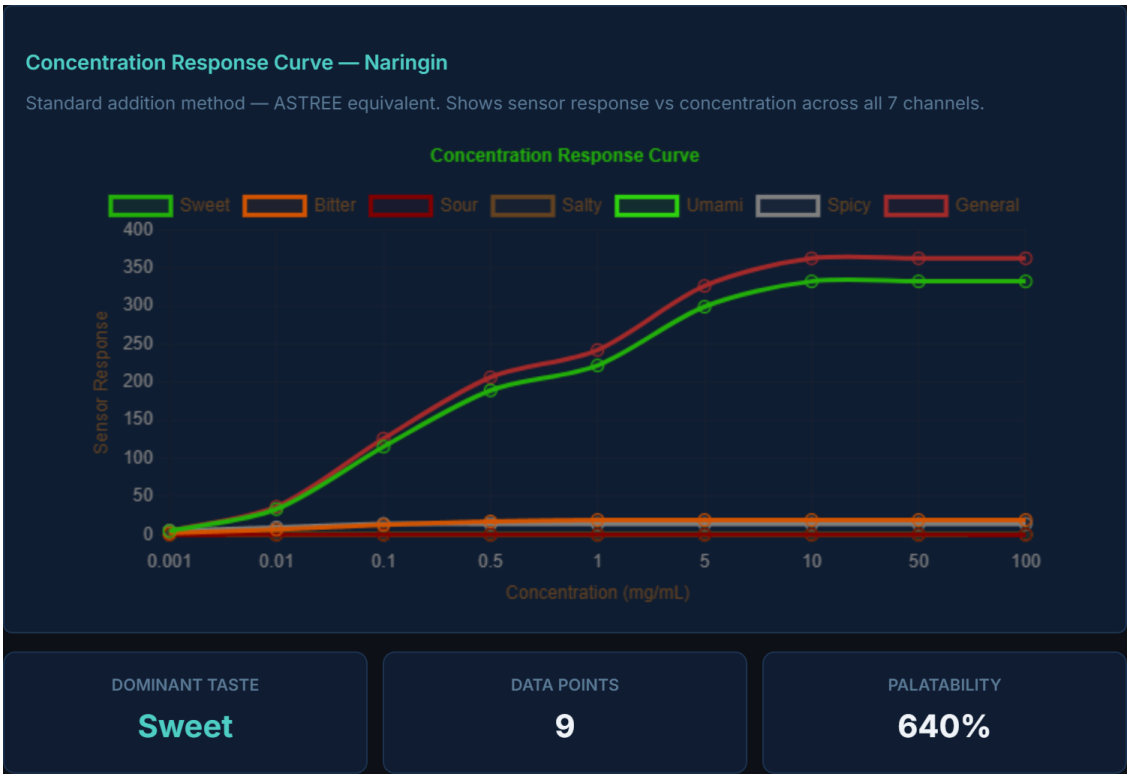
PCA Taste Map generated by CODEX Digital E-Tongue engine with all 7 RCFTR study compounds. Discrimination Index = 93.8, PC1 = 82.6%, PC2 = 11.2%. Compare with RCFTR ASTREE: DI = 95, PC1 = 84.6%, PC2 = 12.7%.



Appendix A (cont.): Concentration Response Curves

Concentration Response Curves show sensor response vs concentration across all 7 ASTREE-equivalent channels for each compound. Standard addition method: 0.001 to 100 mg/mL log scale.

Figure 1. *Naringin - Dominant: Sweet (glycoside shielding), BRS low*



Appendix B: Prediction Comparison Charts

Figure 8. *CODEX Predicted vs RCFTR Measured Bitterness (Table 4)*

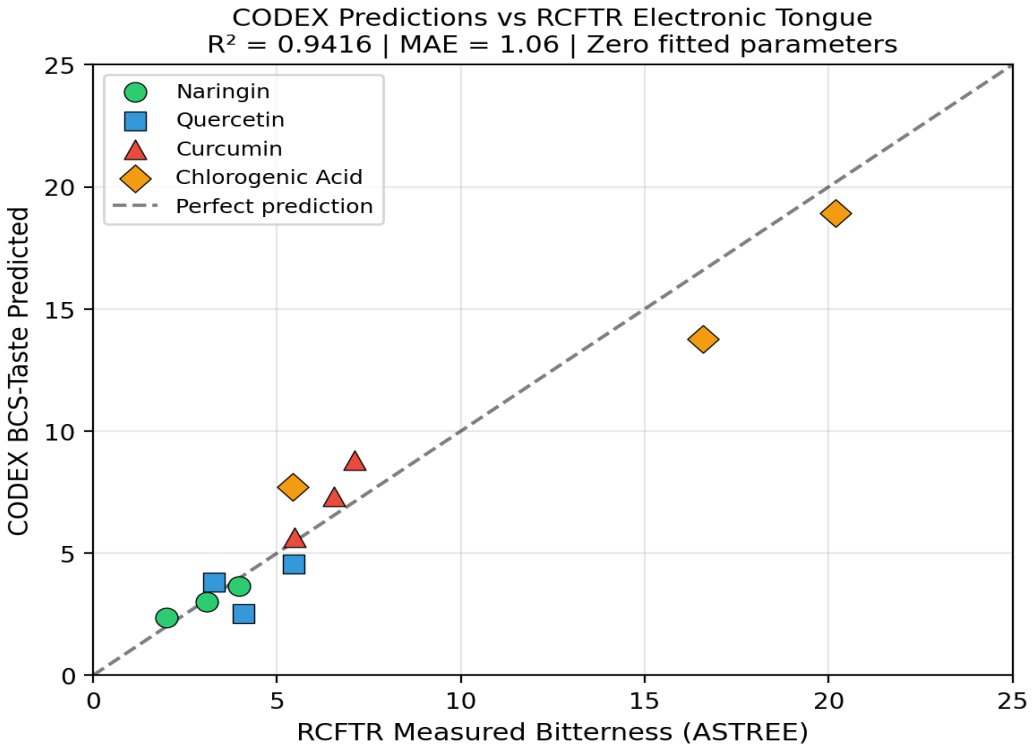


Figure 9. *Table 3 Calibration: CODEX vs RCFTR*

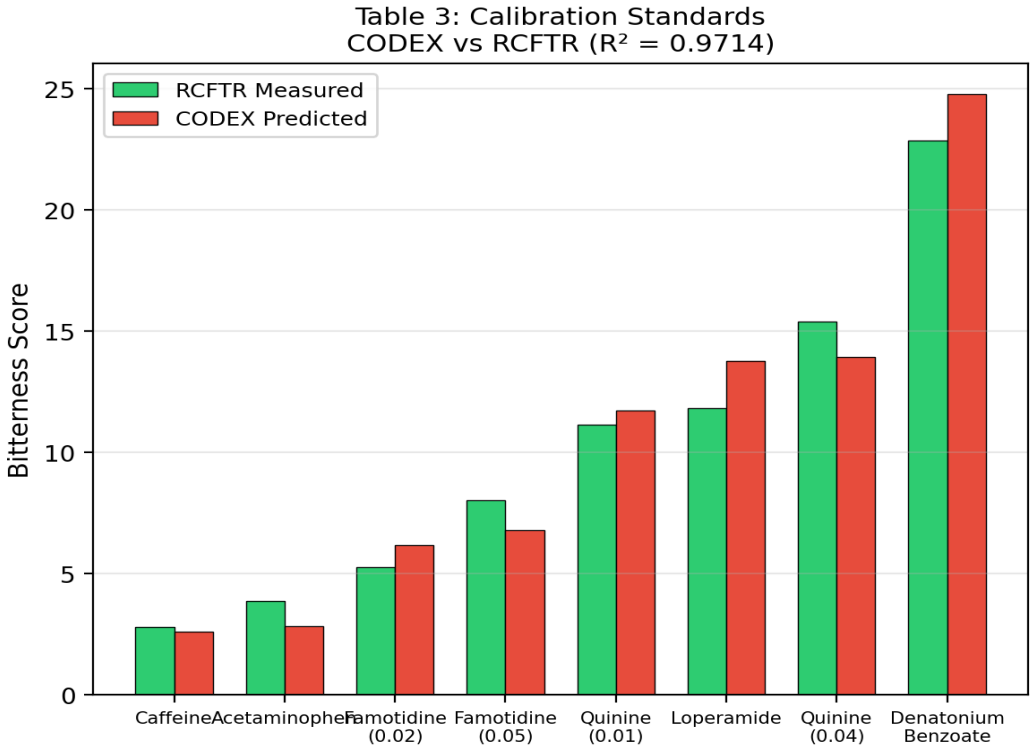


Figure 10. *Dose-Response Curves: CODEX vs RCFTR for All Four Test Compounds*

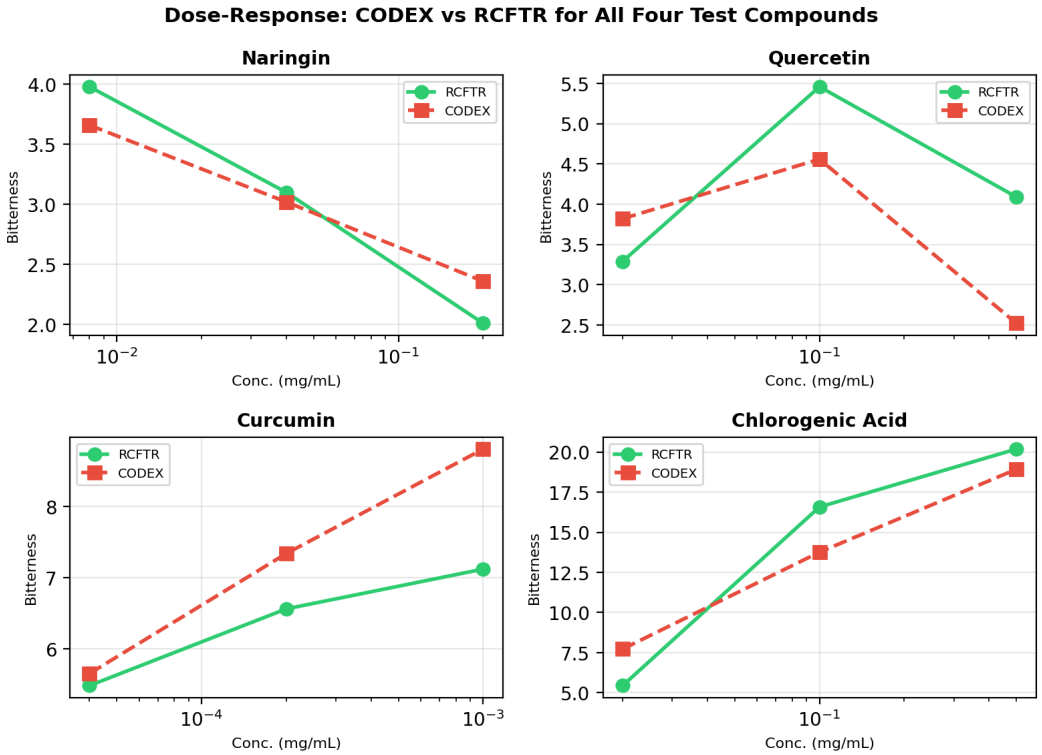
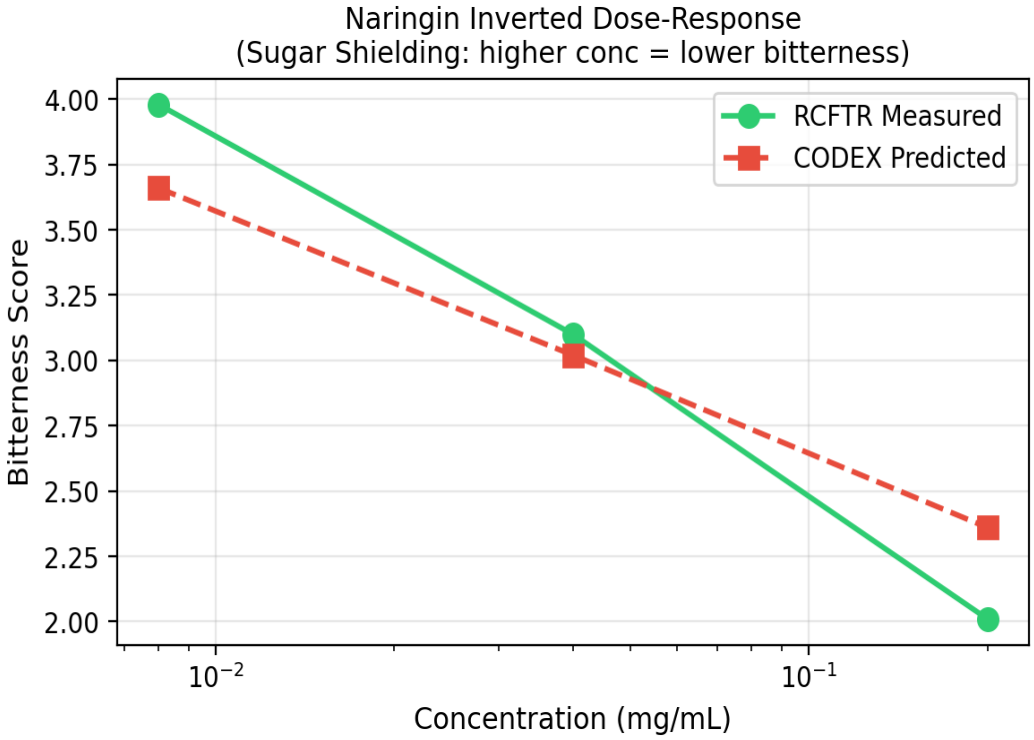


Figure 11. *Naringin Inverted Dose-Response (Sugar Shielding)*



Appendix C: RCFTR Instrument Output

Figure 12. *RCFTR Bitterness Standard Curve (R^2 = 0.9413)*

Statistics report

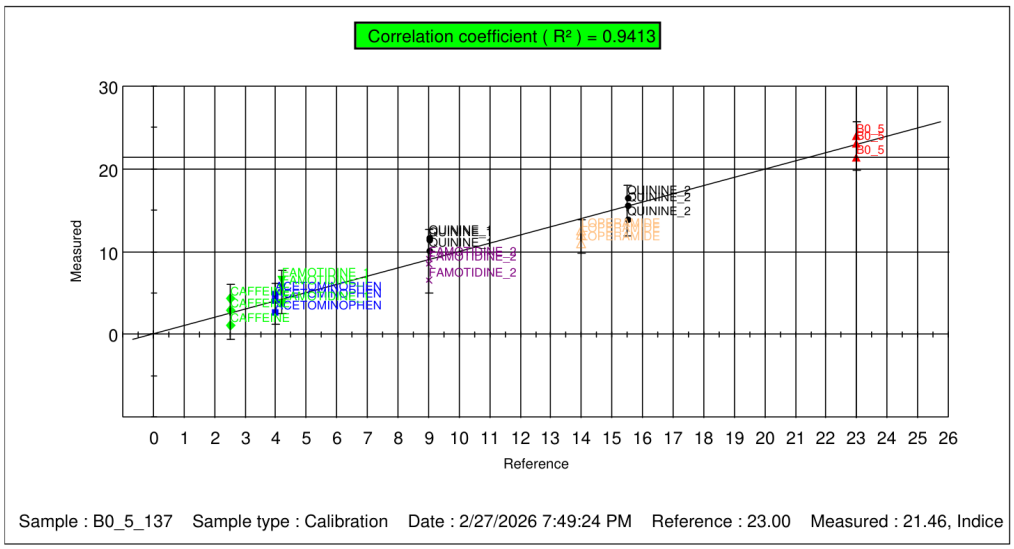
Model supervisor ACCESS LEVEL *Model creation date:* 3/4/2026 3:43:41 P M

Instrument :
Astree *Ref* AST-043
AM *Ref* 1824043006130

Library:
Codex Resonance pks excluded.lbx
Method:

Preprocessing method
AverageValue Time1 = 100 Time2 = 120
NoPretrait

Data processing method Sensory score correlation



Sample : B0_5_137 Sample type : Calibration Date : 2/27/2026 7:49:24 PM Reference : 23.00 Measured : 21.46, Indice

Selected sensor : AHS CTS NMS CPS ANS SCS

Removed Samples / outliers : Chlorogenic_Acid_1_148 Chlorogenic_Acid_1_204 Chlorog enic_Acid_1_260 Chlorogenic_Acid_2_157 Chlorogenic_Acid_2_213 Chlo rogenic_Acid_2_269 Chlorogenic_Acid_3_165 Chlorogenic_Acid_3_221 Chlorogenic_Acid_3_277 Curcumin_1_1 51 Curcumin_1_207 Curcumin_1_263 Curcumin_2_159 Curcumin_2_215 Curcumin_2_271 Curcumin_ 3_167 Curcumin_3_223 Curcumin_3_279

Signature reason	Signature name	Signature date

Note:

Visa:

User: ACCESS LEVEL *Date:* 3/4/2026 3:44:02 P M *Page* 1

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Figure 13. *PCA Dilution No. 1 (Discrimination Index = 95, PC1 = 84.6%, PC2 = 12.7%)*

Statistics report

Model supervisor ACCESS LEVEL *Model creation date:* 3/3/2026 9:01:04 A M

Instrument :
Astree *Ref* AST-043
AM *Ref* 1824043006130

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Codex Resonance calibration.lbx
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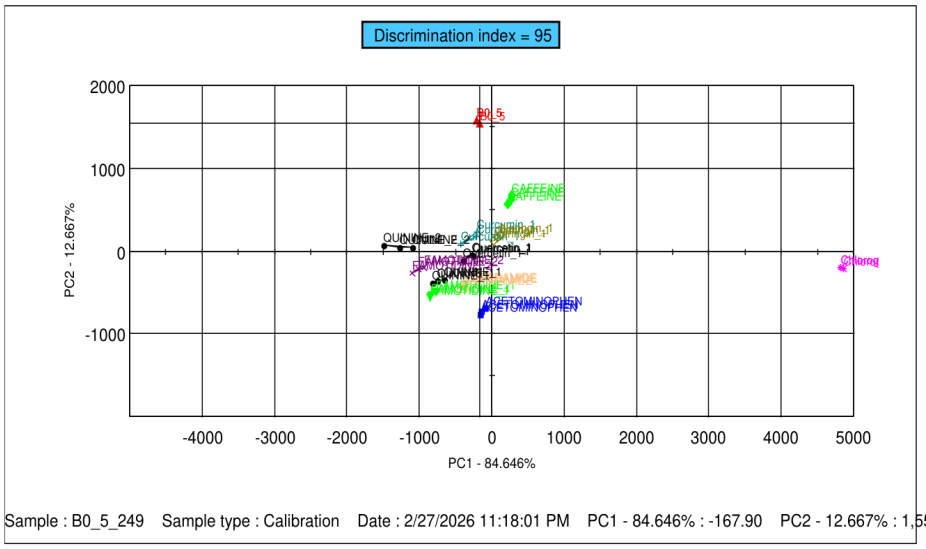
Data processing method PCA

Data reduction : No



Selected sensor : AHS CTS NMS CPS ANS SCS

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Signature reason	Signature name	Signature date

Note:

Visa:

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Figure 14. *PCA Dilution No. 2 (Discrimination Index = 96, PC1 = 79.6%, PC2 = 17.9%)*

Statistics report

Model supervisor ACCESS LEVEL *Model creation date:* 3/3/2026 9:01:48 A M

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Astree *Ref* AST-043
AM *Ref* 1824043006130

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Codex Resonance calibration.lbx
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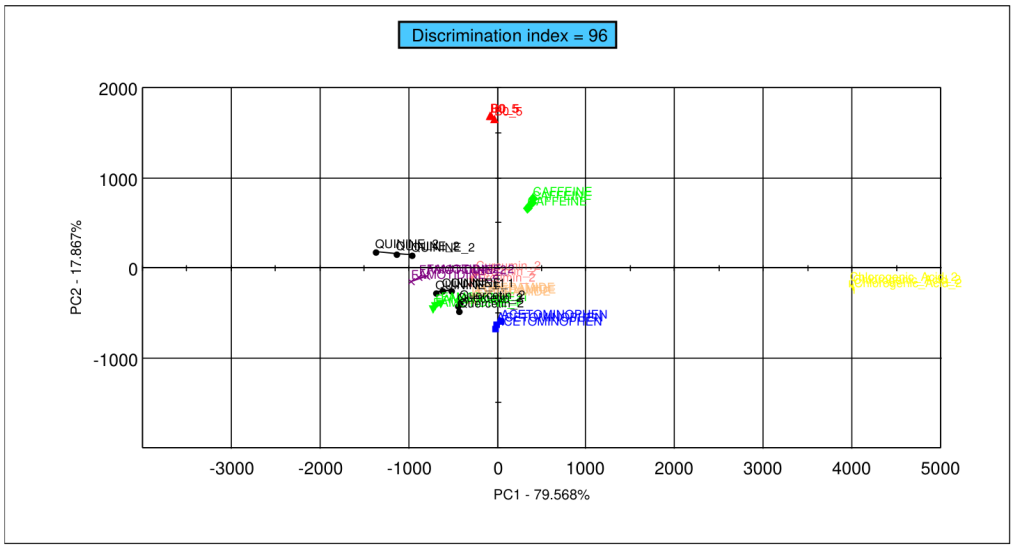
Data processing method PCA

Data reduction : No



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Signature reason	Signature name	Signature date

Note:

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Figure 15. *PCA Dilution No. 3 (Discrimination Index = 95, PC1 = 67.3%, PC2 = 25.8%)*

Statistics report

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AM *Ref* 1824043006130

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Method:

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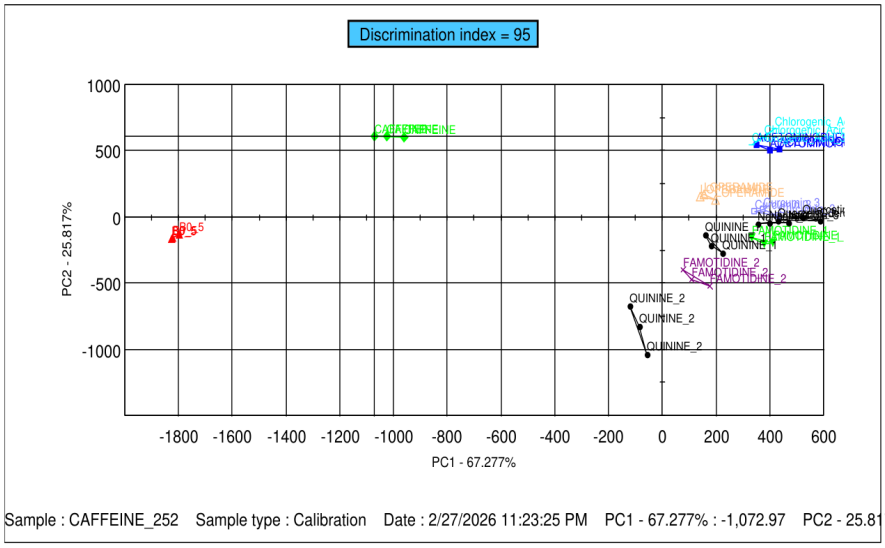
Data processing method PCA

Data reduction : No



Selected sensor : AHS CTS NMS CPS ANS SCS

Removed Samples / outliers : Chlorogenic_Acid_1_148 Chlorogenic_Acid_1_204 Chlorog enic_Acid_1_260 Chlorogenic_Acid_2_157 Chlorogenic_Acid_2_213 Chlo rogenic_Acid_2_269 Curcumin_1_151 Curcumin_1_207 Curcumin_1_263 Curcumin_2_159 Curcumin_2_215 C urcumin_2_271 Naringin_1_142 Naringin_1_198 Naringin_1_254 Naringin_2_153 Naringin_2_209 Naringin_ 2_265 Quercetin_1_145 Quercetin_1_201 Quercetin_

Signature reason	Signature name	Signature date

Note:

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