

1 **Supplemental information for “Synergism, bifunctionality, and the evolution of a gradual**
2 **sensory trade-off in hummingbird taste receptors”**

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8 **Supplemental Figure 1.** Behavioral responses of wild hummingbirds to different combinations
9 of sugars and amino acids.

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11 **Supplemental Figure 2.** Chimeric dissection of ancestral pairs (AR1 and AR2).

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13 **Supplemental Figure 3.** Tests of positive selection in the hummingbird clade.

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15 **Supplemental Figure 4.** Responses of hummingbird T1R1-T1R3 to carbohydrates and amino
16 acids.

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18 **Supplemental Figure 5.** Synergistic responses of Anna’s hummingbird and saw-billed hermit
19 T1R1-T1R3 receptors to combinations of amino acids and sugars.

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21 **Supplemental Table 1.** Natural history traits of tested hummingbirds.

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23 **Supplemental Table 2.** Normalized ligand responses.

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25 **Supplemental Table 3.** Location of AR2 residues in T1R1 CRD-TMD.

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27 **Supplemental Table 4:** Sample sizes for behavioral trials with wild hummingbirds.

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35 **Supplemental Figure 1.** Behavioral responses of wild hummingbirds to different combinations
36 of sugars and amino acids.

37 **(a-f)** Drinking bout lengths from a wild population of hummingbirds (primarily Anna's and black-
38 chinned hummingbirds) presented with sugars and amino acids. **(a-c)** Responses to
39 simultaneous presentation of 500 mM carbohydrates for **(a)** all birds (all species and sexes), as
40 well as responses separated by species and sex: **(b)** black-chinned males (see Fig. 1c for
41 Anna's males), and **(c)** females (all species). All groups show strong sucrose preferences. **(d)**
42 In the absence of sucrose, fructose (500 mM) is preferred, data from both sexes and all species
43 combined. **(e)** Responses from all birds for trials with amino acid solutions (1.5 M). Tests with
44 three receptor agonists—alanine, serine, and glycine—but not proline (which does not activate
45 the hummingbird receptor, Fig. 1b) elicited longer drinking bouts than paired water controls (see
46 Fig. 1d for Anna's hummingbird males). **(f)** Lower-concentration (500 mM) solutions of serine
47 evoked some long bouts, but the difference between bout lengths compared to water controls
48 was not significant (see Fig. 1e for Anna's hummingbird males). Asterisks denote $p < 0.05$, two-
49 sample Kolmogorov-Smirnov tests; see Supplemental Table 4 for sample sizes.

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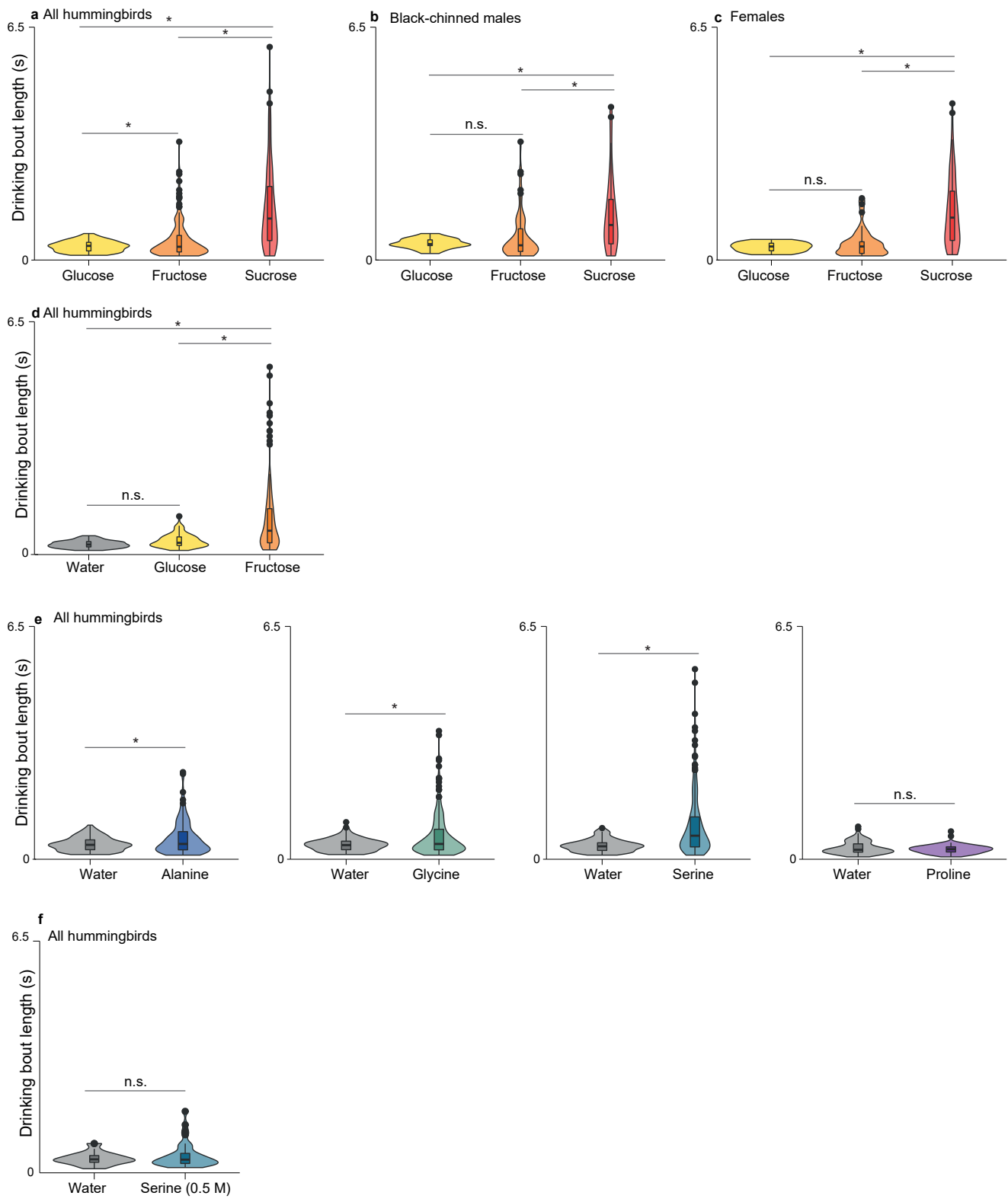
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Supplemental Figure 1

70 **Supplemental Figure 2.** Chimeric dissection of ancestral pairs (AR1 and AR2).
71 **(a)** Schematic of T1R1-T1R3 heterodimer indicating receptor domains, and diagram depicting
72 the sequence identities (as a percentage of sequence length, number of coding differences
73 given in parentheses) between receptors from different species (chicken, chimney swift, black
74 jacobin, Anna's hummingbird) and ancestral nodes (AR1 and AR2). **(b)** Alignment of 19
75 previously-identified residues (Baldwin et al. 2014) with our ancestral receptors and the
76 hummingbirds cloned in this study; 10 of these 19 residues differ between ancestors, and 9
77 (highlighted in yellow) are conserved across the 8 examined hummingbirds. **(c)** Responses of
78 ancestral receptors to sucrose, sucralose, alanine and no-ligand control. AR1 responds only to
79 amino acids, whereas AR2 responds robustly both to sugars as well as amino acids ($n = 6$,
80 mean \pm SE; $*p < 0.05$). Mixed pairs of heterodimers comprising AR1 & AR2 fail to respond
81 strongly to sucrose and sucralose. **(d)** Domain chimeras between AR1 and AR2 demonstrate a
82 critical role of T1R1 CRD+TMD and T1R3 VFT. **(e)** The domain combination underlying
83 songbird sweet taste acquisition (T1R1-VFT and T1R3-CRD-TMD (Toda et al. 2021)) does not
84 evoke a response to sugars or sweeteners in hummingbirds. In hummingbirds, the strongest
85 sucralose responses were observed when both domains were present. **(f)** Dissection of the
86 T1R3 VFT domain reveals highest responses from the second domain quarter, consistent with
87 previous findings (Baldwin et al. 2014). **(g)** When expressed with AR1 T1R1, this second VFT
88 domain quarter does not show any sugar or sweetener response, underscoring the role of the
89 CRD-TM domain of T1R1. **(h)** By examining patterns of conservation and radical change (see
90 Methods), a subset of 5 residues from the second quarter of the VFT were tested with the AR2
91 CRD-TMD chimera; interestingly, responses to sucralose from this smaller residue subset were
92 elevated compared with the responses from the second domain chimera (when both were co-
93 expressed with the CRD-TMD chimera) in f. **(i)** A similar approach to narrow down CRD-TMD
94 residues, from an initial 40 differences between receptor pairs, to 22 (using radical changes) or
95 17 (using BLOSUM62 similarity scores) did not capture the relevant residues, and no response
96 to sucralose was recovered. **(j)** Alignment of a subset of the dissected region of the T1R3
97 domain, showing the five examined residues (yellow highlighting; asterisks indicate residues
98 discussed in Baldwin et al. (2014)). A more extensive chimeric dissection will be required to
99 uncover the full set of necessary and sufficient residues across both T1R1 and T1R3 underlying
100 hummingbird sugar sensing.

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105 **Supplemental Figure 3.** Tests of positive selection in the hummingbird clade.
106 **(a)** Tests of positive selection (aBSREL branch models (Smith et al. 2015)) suggest selection on
107 T1R3 at the base of the hummingbird radiation (red branches: uncorrected p -value < 0.05). **(b)**
108 In free-ratio models (CODEML; PAML v4.8a, (Yang 2007)), T1R3 has higher ratios of non-
109 synonymous to synonymous rates (ω) on many branches compared with T1R1. **(c)** Site-wise ω
110 values from M8 (CODEML) are shown, as well as the location of residues predicted to be under
111 selection by site models implemented in CODEML (orange, BEB sites from M8 (Yang 2005);
112 asterisks indicate $Pr > 0.95$) or in MEME (Murrell et al. 2012) (yellow; $p < 0.05$). Little overlap is
113 seen with sites determined by chimeric dissection (black) with the exception of site 175 (T1R3),
114 and five sites in T1R1 (see Supplemental Table 3).

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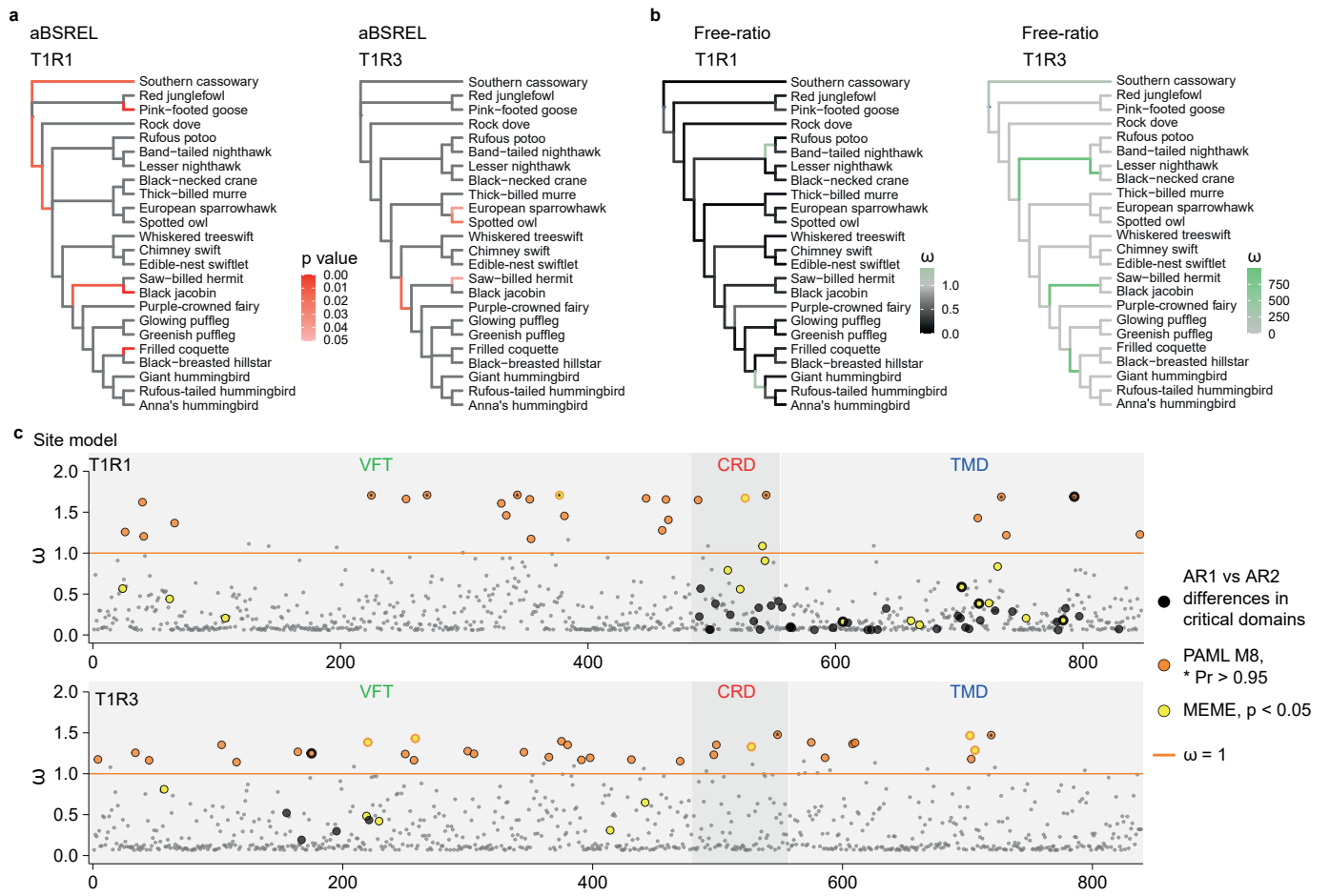
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Supplemental Figure 3

140 **Supplemental Figure 4.** Responses of hummingbird T1R1-T1R3 to carbohydrates and amino
141 acids.

142 **(a)** Bar plots of single ligand plots ($n = 6$, mean \pm SE) for eight hummingbirds, the swift and the
143 two ancestral reconstructions as well as responses from untransfected control cells.
144 Carbohydrates and sucralose are in light orange, amino acids are in light blue and no-ligand
145 controls are shown in gray. Asterisks denote p -values < 0.05 after multiple correction by ligand
146 using the Holm method. **(b)** Phylogenetic PCA (phyloPCA) of log-transformed responses
147 including the swift. **(c)** Hummingbird-wide average; responses are similar to Figure 3a (see also
148 Supplemental Table 2).

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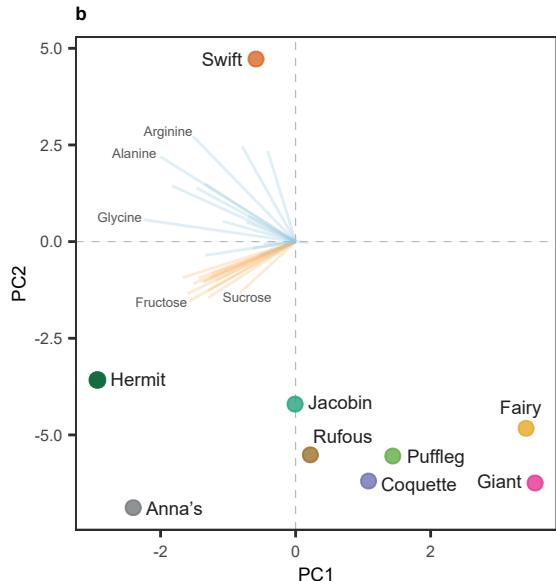
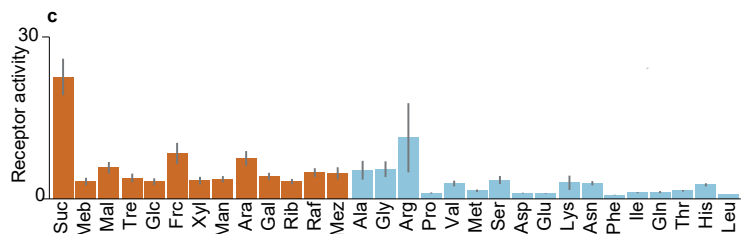
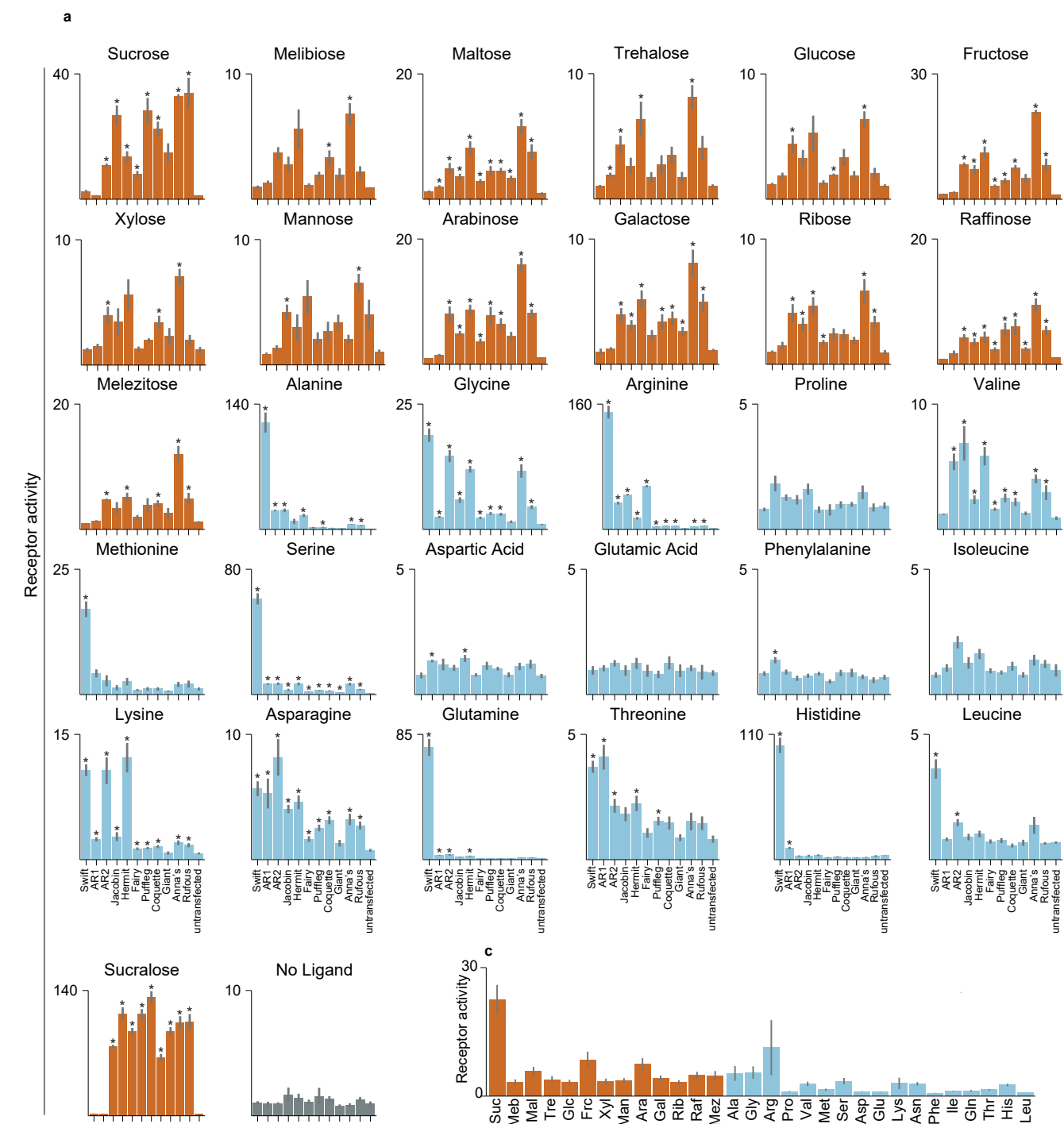
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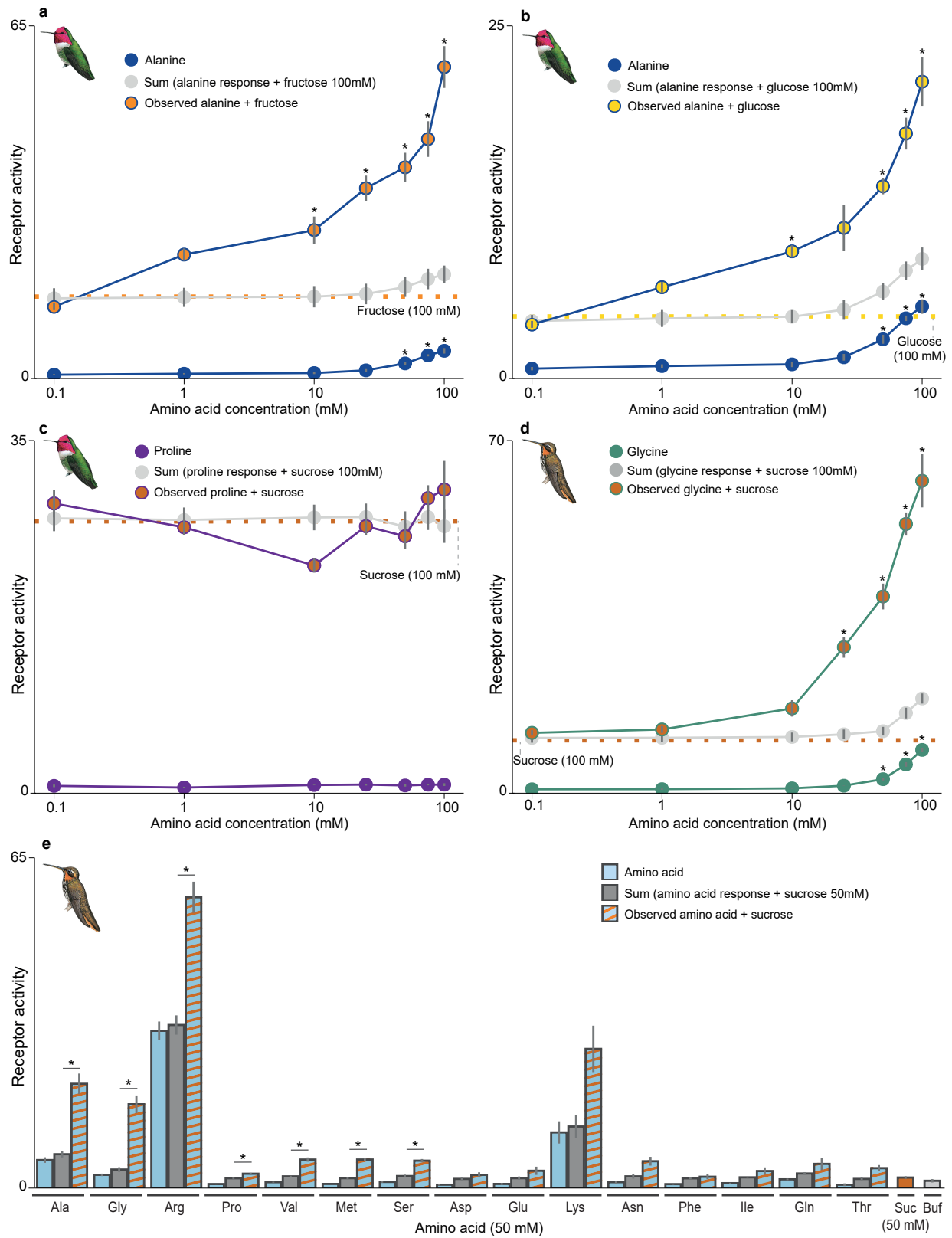


Supplemental Figure 4

176 **Supplemental Figure 5.** Synergistic responses of Anna's hummingbird and saw-billed hermit
177 T1R1-T1R3 receptors to combinations of amino acids and sugars.

178 **(a,b)** Alanine also enhances responses to two monosaccharides (fructose and glucose)
179 commonly found in nectar; observed responses larger than simple additive responses are seen
180 when both sugars are presented in combination with 10 mM alanine (* $p < 0.05$, Welch's two-
181 tailed t -test; mean \pm SE, $n = 4$). The average values for 100 mM fructose and glucose ($n = 6$ for
182 each) are indicated by dashed orange and yellow lines. **(c)** Proline does not enhance responses
183 of the Anna's T1R1-T1R3 receptor when combined with sucrose (* $p < 0.05$, Welch's two-tailed
184 t -test; mean \pm SE, $n = 4$; average value for 100 mM sucrose ($n = 6$) indicated by dashed line).
185 **(d)** Synergy between glycine and sucrose is also observed in responses of the saw-billed
186 hermit, from concentrations of 25 mM onward (* $p < 0.05$, Welch's two-tailed t -test; mean \pm SE, n
187 = 4; average value for 100 mM sucrose ($n = 6$) indicated by dashed line). **(e)** Saw-billed hermit
188 receptors show synergism between 50 mM sucrose and 7 of 15 tested amino acids (blue, amino
189 acid response; striped bar, amino acid + sucrose; gray, estimated additive response; * $p < 0.01$,
190 Welch's two-tailed t -test; mean \pm SE, $n = 4$); no ligand controls ('buf' = buffer) are shown.

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Supplemental Figure 5

213 **Supplemental Table 1.** Natural history traits of tested hummingbirds.
214 Data on the mean weight (g), size (cm), elevation (m), migratory status, range size (km²) and
215 plant families visited (see Methods) are shown for the eight species of hummingbird tested in
216 this study.

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Supplemental Table 1. Natural history traits of tested hummingbirds

Species	Mean weight (g)	Mean size (cm)	Mean elevation (m)	Migratory	Range size (km ²)	Plant families visited (Birds of the World)	Plants visited (Macaulay library)
Black jacobin <i>Florisuga fusca</i>	8	12.5	456.4	Yes (primarily within Brazil)	1,790,000	Euphorbiaceae, Malvaceae, Myrtaceae, Fabaceae, Bromeliaceae	Variety of trees, shrubs, and epiphytes including numerous Fabaceae and Bignoniaceae
Saw-billed hermit <i>Ramphodon naevius</i>	8.2	15	515.5	No	517,000	Bromeliaceae, Costaceae, Fabaceae, Gesneriaceae, Heliconiaceae, Lobeliaceae, Rubiaceae, Malvaceae, Marcgraviaceae, Caricaceae	Shrubs and epiphytes, particularly <i>Heliconia</i> , <i>Costus</i> , <i>Justicia</i> , <i>Centropogon</i> , etc.
Purple crowned fairy <i>Heliostyris barroti</i>	5.47	11	373.9	No	2,200,000	Passifloraceae, Bromeliaceae, Heliconiaceae	Wide variety of plants, but frequently seen at Fabaceae trees
Greenish puffleg <i>Haplophaedia aureliae</i>	5.5	10	1961.7	No	435,000		Small flowering plants, particularly Ericaceae
Friiled coquette <i>Lophornis magnificus</i>	2.66	7.5	561.5	No	3,080,000	Verbenaceae, Ranunculaceae, Rubiaceae, Malvaceae, Leguminosae, Myrtaceae, Acanthaceae, Polemoniaceae, Lamiaceae, Bromeliaceae	Small flowering plants, e.g. <i>Lantana</i> , <i>Stachytarpheta</i> , etc.
Giant hummingbird <i>Patagona gigas</i>	19	21	3066.0	No	3,690,000	Scrophulariaceae, Passifloraceae, Loranthaceae, Myrtaceae, Mutiseae, Solanaceae, Campanulaceae, Bromeliaceae	<i>Puya</i> (and introduced <i>Agave</i>), Cactaceae, variety of other shrubs
Anna's hummingbird <i>Calypte anna</i>	4.5	10	640.6	Yes	1,580,000	Many plant families visited including non-native. Ericaceae, Phrymaceae, Lamiaceae, Plantaginaceae, Onagraceae,	Wide variety, particularly small herbs in the order Lamiales

Ranunculaceae, Thymelaeaceae

Rufous-tailed hummingbird <i>Amazilia tzacatl</i>	5	9	404.4	No	3,770,000	Heliconiaceae, Musaceae, Rubiaceae	Wide variety of trees and shrubs
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260 **Supplemental Table 2.** Normalized ligand responses.

261 All eight hummingbirds responded most strongly to sucralose (Supplemental Figure 4a);
262 therefore, to account for possible differences in transfection efficiency, we divided each
263 species' ligand responses by the respective response to sucralose (Fig. 3a). Relative
264 average responses were consistent in both normalized and non-normalized comparisons.
265 Sucrose elicited the strongest response of all carbohydrates, followed by fructose and
266 arabinose. Across species, sucrose responses were always the highest, and most species
267 responded more to fructose than to arabinose. For amino acids, the hummingbird-wide
268 average response to arginine was higher than to other amino acids in both comparisons
269 (and arginine responses were highest for most species), followed by glycine and alanine. In
270 Anna's hummingbirds, glycine evoked the highest amino acid response.

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Supplemental Table 2. Normalized ligand response

Species	Mean amino acid / mean sucralose																
	<u>Ala</u>	<u>Gly</u>	<u>Arg</u>	<u>Pro</u>	<u>Val</u>	<u>Met</u>	<u>Ser</u>	<u>Asp</u>	<u>Glu</u>	<u>Phe</u>	<u>Ile</u>	<u>Lys</u>	<u>Asn</u>	<u>Gln</u>	<u>Thr</u>	<u>His</u>	<u>Leu</u>
Jacobin	0.08	0.05	0.12	0.01	0.02	0.01	0.03	0.01	0.01	0.01	0.01	0.02	0.04	0.01	0.02	0.03	0.01
Hermit	0.17	0.13	0.58	0.02	0.06	0.03	0.07	0.02	0.01	0.01	0.02	0.13	0.05	0.03	0.02	0.04	0.01
Fairy	0.02	0.02	0.03	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.01
Puffleg	0.02	0.02	0.03	0.01	0.02	0.01	0.02	0.01	0.01	0.00	0.01	0.01	0.02	0.01	0.01	0.02	0.01
Coquette	0.02	0.05	0.07	0.02	0.03	0.02	0.04	0.02	0.02	0.01	0.02	0.02	0.05	0.01	0.02	0.03	0.01
Giant	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.01
Anna's	0.06	0.11	0.03	0.01	0.04	0.02	0.06	0.01	0.01	0.01	0.01	0.02	0.03	0.01	0.01	0.02	0.01
Rufous	0.04	0.04	0.04	0.01	0.03	0.02	0.03	0.01	0.01	0.01	0.01	0.02	0.03	0.01	0.01	0.03	0.01
Grand																	
Mean	0.05	0.05	0.12	0.01	0.03	0.01	0.04	0.01	0.01	0.01	0.01	0.03	0.03	0.01	0.02	0.03	0.01
SE	0.02	0.01	0.06	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Species	Mean sugar / mean sucralose																
	<u>Suc</u>	<u>Meb</u>	<u>Mal</u>	<u>Tre</u>	<u>Glc</u>	<u>Frc</u>	<u>Xyl</u>	<u>Man</u>	<u>Ara</u>	<u>Gal</u>	<u>Rib</u>	<u>Raf</u>	<u>Mez</u>				
Jacobin	0.24	0.02	0.03	0.02	0.03	0.06	0.03	0.03	0.04	0.03	0.03	0.03	0.03				
Hermit	0.14	0.06	0.09	0.07	0.06	0.12	0.06	0.06	0.09	0.05	0.05	0.05	0.05				
Fairy	0.07	0.01	0.02	0.02	0.01	0.03	0.01	0.02	0.03	0.02	0.02	0.02	0.02				
Puffleg	0.21	0.01	0.03	0.02	0.01	0.03	0.01	0.02	0.06	0.03	0.02	0.04	0.03				
Coquette	0.34	0.05	0.07	0.05	0.05	0.12	0.05	0.05	0.10	0.06	0.04	0.09	0.06				
Giant	0.16	0.02	0.04	0.02	0.02	0.05	0.02	0.02	0.05	0.03	0.02	0.03	0.03				
Anna's	0.31	0.07	0.11	0.08	0.06	0.20	0.07	0.06	0.15	0.08	0.06	0.09	0.12				
Rufous	0.32	0.02	0.07	0.04	0.02	0.08	0.02	0.04	0.08	0.05	0.03	0.05	0.05				
Grand																	
Mean	0.23	0.03	0.06	0.04	0.03	0.09	0.03	0.04	0.08	0.04	0.03	0.05	0.05				
SE	0.03	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.00	0.01	0.01				

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303 **Supplemental Table 3.** Location of AR2 residues in T1R1 CRD-TMD.

304 Number of differences (between AR1 and AR2) for each transmembrane helix (TM),
305 extracellular loop (ECL), intracellular loop (ICL) and C-terminus are presented separately.
306 Most differences (standardized by region length) occur in ECL2 and TM7. Predicted selected
307 sites from MEME and CODEML analyses are indicated, as are residues that overlap with
308 sites of known function from other studies.

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Supplemental Table 3. Location of AR2 residues in T1R1 CRD-TMD

Domain	Length	Synonymous sites	Non-synonymous sites	Proportion non-synonymous sites	MEME & PAML sites	Known functional sites
CRD	68	57	11	0.16		#491 sugars (Toda et al. 2021) #548 thaumatin (Masuda et al. 2013)
TM1	24	20	4	0.17		
ICL1	13	12	1	0.08		
TM2	21	18	3	0.14	#606 MEME	
ECL1	5	5	0	0.00		
TM3	34	30	4	0.12		#626 sugars (Toda et al. 2021) and cyclamate (Jiang et al. 2005), #641 sugars (Toda et al. 2021)
ICL2	14	14	0	0.00		
TM4	26	25	1	0.04		
ECL2	19	14	5	0.26	#702 MEME	
TM5	29	26	3	0.10	#716 MEME	
ICL3	2	2	0	0.00		
TM6	28	27	1	0.04		#743 monosodium glutamate (Dang et al. 2019)
ECL3	7	7	0	0.00		
TM7	26	20	6	0.23	#784 MEME #793 PAML(M8)	#784 lactisol (Xu et al. 2004), #786 methional (Toda et al. 2018)
C-terminus	25	24	1	0.04		
SUM	341	301	40	0.12		

327 **Supplemental Table 4:** Sample sizes for behavioral trials with wild hummingbirds.
328 Top: number of visits (all species and both sexes, pooled and shown separately) to feeders
329 containing carbohydrates or water. Occasional visits by Allen’s hummingbirds are included in
330 the “all-birds” column. Bottom: number of visits (all birds, and Anna’s hummingbird males
331 shown separately) to feeders containing water or amino acids (trials were repeated 2 – 4
332 times and visits were pooled).

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Supplemental Table 4. Sample sizes for behavioral trials with wild hummingbirds

Carbohydrates				
	All birds	Anna's males	Black-chinned males	Females
Sucrose	138	24	28	78
Fructose	144	45	63	34
Glucose	59	14	16	28
All birds				
Fructose	164			
Glucose	59			
Water	57			
Amino acids				
	All birds		Anna's males	
	Amino acid	Water	Amino acid	Water
Alanine (1.5M)	98	114	34	50
Glycine (1.5M)	223	110	42	31
Serine (1.5M)	185	79	65	26
Proline (1.5M)	62	74	25	32
	All birds		Anna's males	
Serine (500 mM)	36	28	22	14

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