

On mirror symmetry, CSB and anti-hydrogen states in natural atom H.¹

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Abstract

Molecular band spectra reveal a left-right symmetry for atoms (Van Hooydonk, Spectrochim. Acta A, 2000, 56, 2273). Intra-atomic left-right symmetry points to anti-atom states and, to make sense, this must also show in line spectra. H Lyman ns^{1/2} singlets show a mirror plane at quantum number $n_0 = 1/2\pi$. Symmetry breaking oscillator $(1 - 1/2\pi/n)^2$ means that some of these n-states are anti-hydrogenic. This view runs ahead of CERN's AD-project on antihydrogen.

A final validation of QED is not yet possible. QED cannot cope with classical chiral symmetry breaking (CSB) effects known from the 19th century. In 2000, we found that molecular band spectra suggest an atomic left-right symmetry [1]. If true, this only makes sense if this symmetry is also visible in atomic line spectra. So we decided to reanalyze the H Lyman ns^{1/2} series with precise data. Kelly's data [2], though useful, have an error of 3 MHz. Erickson [3] claims a better precision with QED calculations, but these lack a classical CSB effect. To test CPT with the CERN AD artificial antihydrogen project [4], data must be as precise as possible. Only H 1s2s is now accurate within parts in 10¹⁴-10¹⁵, an error of order 10 Hz [5].

Not constant running Rydbergs $R_H(n)$

$$R_H(n) = -E_{nH} \cdot n^2 \quad (1)$$

reflect errors in Bohr theory. The values for Lyman ns^{1/2}-singlets in Table 1 are plotted versus 1/n in

Fig. 1. A parabola appears (inconsistent with Dirac theory, due to the Lamb shift). A 2nd order fit

$$R_H(n) = 4.36747232754714/n^2 - 5.5556171802571/n + 109,677.585534983 \text{ cm}^{-1} \quad (2)$$

produces a harmonic Rydberg of

$$R_{H(\text{harm})} = 109,679.3522824 \text{ cm}^{-1} \quad (3)$$

different from series limit E_{1H} in Table 1.

Internal anchor (3) is disregarded by NIST, despite its important classical meaning. Strangely enough

$$n_0 = 1.572273... \approx 1/2\pi \quad (4)$$

is the n-value where the extremum appears. This is close to the generic angle $1/2\pi$ for mirror planes. For these singlets, a true CSB oscillator, hidden in QED theory, appears:

$$(1 - 1/2\pi/n)^2 \quad (5)$$

Table 1 $-E_{nH}$ [3] and $R_H(n)$ for Lyman ns singlets

n	$-E_{nH}$ [3]	$R_H(n)$
1	109678,7737040000	109678,773704000
2	27419,8178352300	109679,271340920
3	12186,5502372100	109678,952134890
4	6854,9188453940	109678,701526304
5	4387,1408809200	109678,522023000
6	3046,6219504100	109678,390214760
7	2238,3324513070	109678,290114043
8	1713,7220591550	109678,211785920
9	1354,0512214330	109678,148936073
10	1096,7809744220	109678,097442200
11	906,4302025320	109678,054506372
12	761,6529039910	109678,018174704
13	648,9821718410	109677,987041129
14	559,5814289189	109677,960068104
15	487,4574954578	109677,936478005
16	428,4293581016	109677,915674010
17	379,5082947805	109677,897191565
18	338,5119773555	109677,880663182
19	303,8168027574	109677,865795421
20	274,1946308763	109677,852350520

Fit (2) is consistent with QED and with data [2] but (4) and (5) lead to mirror symmetry. The only left-right symmetry imaginable within an atom is atom-antiatom symmetry, and this we already found for atoms in a molecule [1].

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Now, (2)-(5) leave a choice between CSB and QED.

The accuracy of closed classical CSB theory must be comparable with that of open complex QED theory [6].

A harmony obeying π/n agrees with the de Broglie equation and since $\alpha/2\pi \approx 2m_e/M_p$, scale factor π is like fine structure constant over recoil [6].

In CSB, H is not a 2- but a 4-fermion system [6]. H symmetry is broken with $1 \pm m_e/m_H$ (m_H is hydrogen, m_e electron mass). Baryon mass in a reduced mass for a *bound* electron in atom H is 1,836.1526675 m_e (proton mass) for hydrogenic ns-singlets, it is 1,838.1526675 m_e for anti-hydrogenic ns-singlets [6]. The value of $1+2m_e/M_p=1.001089$ is consistent with the observed *free* electron anomaly.

CSB points to different scaling in world and anti-world. Lamb shifts provide the finer details of intra-atomic chiral symmetry breaking.

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Fig. 1 $R_H(n)$ versus $1/n$ for H Lyman ns singlets

