Supplementary information for "Factors influencing hydrogen peroxide versus water inclusion in molecular crystals"

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CONTENTS

I. EXPERIMENTAL METHODS

A. Cambridge Structural Database searching

Searching for hydrates in the Cambridge Structural Database (November 2018, v.5.40) was conducted using the IsoStar (2018, v2.3) program maintained by the Cambridge Crystallographic Data Centre. As IsoStar subdivides the hydrate crystal structures into bins for each contact group (functional group) based on degree of van der Waals overlap, the modal bin was selected for in-depth geometric analysis using the angle and torsion parameters specified for each functional group in Tables S1-S12. Hydrogen peroxide solvates were identified using the Substructure Search option available through ConQuest (v2.0.0). Given the uncertainty in identifying hydrogen atom positions by X-ray diffraction, interaction distances for each crystal structure were measured as the distances between the heteroatoms participating in the hydrogen bond. Interactions between crystallographically disordered molecules of water or hydrogen peroxide and functional groups of interest were not included in this analysis.

B. Analysis of experimentally determined crystal structures

FIG. S1. Definition of geometric parameters and example crystal structures for measured interactions between water or hydrogen peroxide and various functional groups. All measured values presented in this figure represent dihedral or torsion angles given in degrees.

Figure [S1](#page-2-3) illustrates the angles measured for the six different types of interactions considered here using as examples actual crystals included in the tables. All angles are between heavy atoms. Most $Y-X \cdots$ O angles are bond angles with \cdots denoting the hydrogen bond. Two exceptions are $C-N \cdot \cdot \cdot O$ angles in the carbonyl case and $R-N \cdot \cdot \cdot O$ angle in the nitro case, where these are just angles between three atoms. If more than one $X-Y\cdots$ O are measured, for example, the angles C_1 -N···O, C_2 -N···O, and C_3 -N···O in the case of sp^3 amines, we will use the subscript "short", "medium", and "long" to distinguish the angles, with the subscripts related to the lengths of C-N bonds. The subscripts n in C_n used in Fig. $S1$ are then redundant and will not be used in the tables. Similarly, the subscripts n in angles R_n -N···O in the case of sp² amines in Fig. [S1](#page-2-3) are replaced by subscripts "short" and "long" in the tables. Similar rules apply to dihedral angles $Z-Y-X\cdots$ O. If in most cases the X, Y, or Z atom is the same atom, we used this atom symbol in the tables. If several different atoms appear at these positions at different crystals, such positions are denoted by R. For example, the angle $C_2-C_1-O\cdots O$ in the case of alcohol group is really the angle $N-C-O\cdots O$, but we will use symbol C since in most crystals C appears in the place of N. The sets of angles are in all cases redundant. For example, to determine the position of water's oxygen relative to the sp^3 amino group, if is sufficient to know angles C_1 -N···O and $C_3-N\cdots$ For each particular crystal, the redundant angle is congruent with those of the minimal set. However, for the averages given in the tables, this is usually not true. The non-congruency is not large, e.g., for the $sp³$ amino group it is within the standard deviations (given as values in parentheses in all tables). The choices of angles made in constructing the near-experimental dimer structures are described in Sec. [III.](#page-15-0)

II. TABLES OF INTERACTION GEOMETRIES FOR FUNCTIONAL GROUPS FROM THE CSD SEARCH

A. Alcohol functional groups

TABLE S1. Refcodes and interaction parameters for the subset of crystal structures containing $water \cdot \cdot$ alcohol interactions measured for this study where water is serving as a hydrogen bond acceptor.

Number of Structures: 18 Number of Interactions: 28

Refcode		$\angle(C-O\cdots O)$ (°) $\angle(C-C-O\cdots O)_{short}$ (°) $\angle(C-C-O\cdots O)_{long}$ (°)		$d(O \cdots O)$ (Å)
ACLACT	103.52	82.91	155.97	2.794
$\overline{\text{ACLACT}}$	118.02	97.25	134.23	2.898
ACOQEP	129.26	76.31	167.83	2.741
AXUKAH	121.15	74.80	165.15	2.806
BIGWET	122.45	86.97	156.61	2.820
BIGWET	123.84	116.70	119.10	2.830
BIKCIH10	125.50	120.74	122.38	2.799
BODGEG	111.99	69.97	165.44	2.768
CAMTIU	118.47	70.71	163.78	$2.775\,$
CAMTIU	129.36	95.29	144.95	$2.815\,$
CEQJEO	142.38	85.44	153.04	2.714
CEQJEO	125.33	101.29	138.84	2.876
$\sf CIDRUC$	121.25	65.93	173.39	2.757
CUPSAI	112.92	73.21	165.60	$2.801\,$
CUQGIE	124.18	111.02	127.57	2.682
CUQGIE	98.18	92.92	146.86	2.759
CUQGIE	131.66	103.77	134.59	2.764
CUQGIE	132.23	116.76	121.69	$2.765\,$
DEZHOG	114.91	11.26	168.73	2.628
DEZHOG	118.05	38.06	143.21	2.790
DIDDUQ	111.04	109.47	130.49	2.796
DUWKUD	105.40	16.29	133.62	2.763
DXIFPO	134.30	98.82	136.90	2.776
ELEVOG	113.82	60.33	179.68	2.779
JOWWAT	125.33	92.32	150.17	2.772
JOWWAT	131.83	$115.53\,$	127.51	2.804
KEPYUB	147.56	115.84	120.41	2.758
MOPMOT	113.41	79.39	159.47	2.773
MUSPAT	119.74	67.79	176.98	2.760
OFOQAD	115.57	101.20	137.46	2.697
OWOSOK	116.77	84.08	$153.32\,$	$2.759\,$
PEMTOT	105.37	$110.53\,$	129.49	2.744
$\rm RIWCIK$	132.82	132.82	$139.52\,$	2.798
SOBJID	154.53	106.98	132.13	2.776
Average	120(10)	90(30)	150(20)	2.775(2)

TABLE S2. Refcodes and interaction parameters for the subset of crystal structures containing $water \cdot \cdot$ alcohol interactions measured for this study where water is serving as a hydrogen bond donor.

Number of Structures: 25 Number of Interactions: 34 TABLE S3. Refcodes and interaction parameters for the subset of crystal structures containing hydrogen peroxide \cdots alcohol interactions measured for this study.

Number of Structures: 4 Number of Interactions: 4

B. Carbonyl functional groups

TABLE S4. Refcodes and interaction parameters for the subset of crystal structures containing water \cdots carbonyl (amide) interactions measured for this study.

Number of Structures: 16 Number of Interactions: 22

TABLE S5. Refcodes and interaction parameters for the subset of crystal structures containing hydrogen peroxide··· carbonyl (amide) interactions measured for this study.

Number of Structures: 2 Number of Interactions: 2

C. N-oxide functional groups

Number of Structures: 22 Number of Interactions: 39 TABLE S7. Refcodes and interaction parameters for the subset of crystal structures containing hydrogen peroxide \cdots N-oxide (aliphatic and aromatic) interactions measured for this study.

Number of Structures: 3 Number of Interactions: 5

D. Nitro functional groups

Number of Structures: 10 Number of Interactions: 14

E. $sp³$ nitrogen functional groups

TABLE S9. Refcodes and interaction parameters for the subset of crystal structures containing water \cdots amine interactions measured for this study.

Number of Structures: 22 Number of Interactions: 26

TABLE S10. Refcodes and interaction parameters for the subset of crystal structures containing hydrogen peroxide \cdots amine interactions measured for this study.

Number of Structures: 3 Number of Interactions: 3

F. sp^2 nitrogen functional groups

TABLE S11. Refcodes and interaction parameters for the subset of crystal structures containing water \cdots aromatic nitrogen interactions measured for this study.

Number of Structures: 25 Number of Interactions: 26

TABLE S12. Refcodes and interaction parameters for the subset of crystal structures containing hydrogen peroxide \cdots aromatic nitrogen interactions measured for this study.

Number of Structures: 5 Number of Interactions: 6

G. Summary tables of functional group averages and deviations

TABLE S13. Average interaction distances and angles between oxygen-containing hydrogen bond accepting functional groups and water or hydrogen peroxide. The numbers in parentheses are the standard deviations for the data sets analyzed to calculate the averages.

$O-H \cdots O-H$ (Alcohol)	$d(O \cdots O)$	\angle (C-O \cdots O)	$ \angle$ (C – C – O \cdots O) _{short}	$ \angle (C - C - O \cdots O)_{long} $
$H2O$ Average of Bin Mode	2.775(2)	120(10)	90(30)	150(20)
$H2O2$ Average of CSD	2.75(8)	110(20)	90(20)	140(30)
$O-H \cdots O=C$ (Amide)	$d(O \cdots O)$	\angle (C-N \cdots O)	\angle (C=O \cdots O)	$ \angle(N - C = 0 \cdots 0) $
$H2O$ Average of CSD Organics	2.808(9)	30(20)	130(10)	120(50)
$H2O2$ Average of CSD (COO)	2.72(5)	40(20)	140(10)	120(50)
$O-H \cdots O-N$ (N-oxide)	$d(O \cdots O)$	$\angle(N-O\cdots O)$	$ \angle$ (C – N – O \cdots O) _{short}	$ \angle$ (C – N – O · · · O) _{long}
$H2O$ Average of Bin Mode	2.752(2)	119(9)	60(30)	130(30)
H_2O_2 Average of CSD	2.70(1)	125(9)	70(20)	140(40)
$O-H \cdots O_2-N$ (Nitro)	$d(O \cdots O)$	\angle (R-N \cdots O)	$\angle(N-O\cdots O)$	$ \angle(R-N-O\cdots O) $
$H2O$ Average of Bin Mode	2.889(9)	140(30)	120(20)	130(50)
$H2O2$ Refcode: AZACIP	3.037	152.02	127.95	167.69

TABLE S14. Average interaction distances and angles between nitrogen-containing hydrogen bond accepting functional groups and water or hydrogen peroxide. The numbers in parentheses are the standard deviations for the data sets analyzed to calculate the averages.

III. NEAR-EXPERIMENTAL DIMER CONFIGURATIONS

The coordinates of oxygen atoms in water or hydrogen peroxide were fixed with respect to model molecules by using the distance, a bond angle, and a dihedral angle given in Tables [S13](#page-14-1) and $S14$. For all dimers, except the ones involving $sp³$ nitrogen, the redundant angles that were not used are: $|\angle(C - C - O \cdots O)_{short}|$, $\angle(C - N \cdots O)$, $|\angle(C - N - O \cdots O)_{short}|$, ∠(R – N · · · O), and ∠(R-N · · · O)_{long} in alcohol, carbonyl, N-oxide, nitro, and sp² nitrogen cases, respectively. The redundant angles were not used, but we checked that their values in the model systems are within the standard deviation given in Tables [S13](#page-14-1) and [S14.](#page-14-2) In case of the sp³ nitrogen, we have kept the \angle (C-N···O)_{long} angle at its averaged experimental value and rotated the $N \cdots$ O hydrogen bond until the two other angles had values within the experimental uncertainties. The values of these angles used in our calculations are 94° (106°) for ∠(H-N···O)_{short} and 111[°] (108[°]) for ∠(H-N···O)_{med} for the water (hydrogen peroxide) dimer. In case of alcohol functional group, the leftmost carbon atoms in the dihedral angles $|\angle$ (C – C – O · · · O)_{short} and $|\angle$ (C – C – O · · · O)_{long} were replaced by hydrogens bonded to the carbon in methanol. Similarly, in case of sp^3 nitrogen functional group, the carbon atoms in the angles \angle (C-N···O)_{short} and \angle (C-N···O)_{med} were replaced by hydrogens bonded to the nitrogen in methylamine. After the position of the oxygen atom was established, the orientation of water or hydrogen peroxide was found by minimizing the interaction energies given by the appropriate PES with respect to the rotation around space-fixed x, y, and z axes to get near-experimental dimer configurations.

IV. GENERATION OF POTENTIAL ENERGY SURFACES AND FIRST-PRINCIPLES METHODOLOGY

The autoPES software package [\[1\]](#page-23-1) was used to generate potential energy surfaces for the dimers under consideration. Monomers were assumed rigid in all calculations. The process is divided into five parts: asymptotic calculations, generation of grid points of close-range dimer configurations, calculation of interaction energies at close-range grid points, fitting an analytic functional form to the data, and finally evaluation of the quality of the fit and iterative improvement. Each step is described in detail in Ref. [1.](#page-23-1) A brief outline is given below. The overall computational cost and the number of close-range grid points are reduced by using asymptotic calculations. Asymptotic expansion is used in the region where the charge overlap effects can be neglected, which is about 1.5 times the radial van der Waals minimum intermonomer separation for a given orientation. Multipole expansion located at the center of mass (COM) of monomers [\[2,](#page-23-2) [3\]](#page-23-3) is used to calculate the interaction energy of the dimers at asymptotic separations. The coefficients of the expansion are computed from monomer's charge distributions and static and frequency-dependent density susceptibilities (FDDS). In order to connect seamlessly with the close-range calculations, the same basis set and level of theory is used for calculating monomer properties as in the close-range calculations. A set of 12,000 dimer grid points was used for calculating interaction energies in the asymptotic region. A guided Monte Carlo procedure was used for generating close-range grid points, with higher concentration of grid points in energetically relevant regions such as minima. The interaction energy at each of these close-range points was computed using the SAPT(DFT) method at the level specified in the main text. A set of six coordinates, the distance between the monomer's COMs and five Euler angles describing the relative angular orientation of the monomers, are used to describe the grid points. However, the functional form of the fit uses only atom-atom distances r_{ab} where atom $a(b)$ belongs to monomer A(B). After calculating interaction energies in the asymptotic and close-range regions, the energies are fit with the following functional form of the potential:

$$
V = V_{\text{elst}} + V_{\text{exp}} + V_{\text{asymp}}^{(2)} = \sum_{a \in A, b \in B} u_{ab}(r_{ab}) = \sum_{a \in A, b \in B} \left[u_{\text{elst},ab}(r_{ab}) + u_{\text{exp},ab}(r_{ab}) + u_{\text{asymp},ab}^{(2)}(r_{ab}) \right]
$$
\n(1)

The atom-atom functions are of the form

$$
u_{\text{elst},ab}(r_{ab}) = f_1(\delta_1^{ab}, r_{ab}) \frac{q_a q_b}{r_{ab}}
$$

$$
u_{\text{exp},ab}(r_{ab}) = \left[1 + \sum_{i=1}^2 a_i^{ab}(r_{ab})^i\right] e^{\alpha^{ab} - \beta^{ab}r_{ab}} + \frac{A_{12}^{ab}}{(r_{ab})^{12}}
$$

$$
u_{\text{asymp},ab}^{(2)}(r_{ab}) = - \sum_{n=6,8} f_n(\delta_n^{ab}, r_{ab}) \frac{C_n^{ab}}{(r_{ab})^n},
$$
 (2)

where f_n are Tang-Toennies damping functions [\[4\]](#page-23-4)

$$
f_n(\delta_n^{ab}, r_{ab}) = 1 - e^{-\delta r} \sum_{m=0}^n \frac{(\delta r)^m}{m!}.
$$
 (3)

The distributed induction plus dispersion coefficients C_n^{ab} and the partial charges q_x were fit to the asymptotic-expansion COM-COM interaction energies at long-range grid points. These are kept unchanged in the subsequent fitting stage in order to make sure the PES behaves correctly in the asymptotic region. The remaining parameters: α^{ab} , β^{ab} , δ^{ab}_n , a_i^{ab} , and behaves correctly in the asymptotic region. The remaining parameters, α , β , α_n , a_i , and A_{12}^{ab} , were fit to energies calculated at short-range grid points. To ensure correct repulsive behavior at very close range, coefficients A_{12}^{ab} are constrained to be positive. Geometric combination rule is used for C_n^{ab} parameters such that C_n^{ab} is expressed through the atomic parameters C_n^a and C_n^b . Similarly, arithmetic combination rule is used for parameters α^{ab} and β^{ab} . For details of this fitting stage, see Ref. [1,](#page-23-1) Sec. VI. The quality of the PES was evaluated after the fitting stage using two criteria, and additional iterations were performed if necessary. The first criterion ensures correct repulsive behavior such that there are no 'holes' in the PES at very-close range. If holes are found then additional grid points are added at appropriate configurations, and the potential is refit. The procedure is repeated until there is a barrier of at least 15 kcal/mol for each orientation of the monomer. The second criterion evaluates the accuracy of the PES by comparing the root mean square error (RMSE) of the 85% of the total grid points called the fitting (training) set with the remaining 15% of the total grid points called the test set. If the RMSE of the test set is greater by a factor of 1.2 than that of the fitting set, then a PES is considered to be not converged. Additional grid points are added at close-range and the procedure is repeated until the above two criteria are satisfied. In the final fitting stage, the test set was not used and the PES was fit to all the available data.

The interaction energies were computed using symmetry adapted perturbation theory (SAPT)[\[3\]](#page-23-3) based on density functional theory (DFT) description of monomers, denoted as $SAPT(DFT)$ and developed in Refs. [5](#page-23-5)[–13,](#page-23-6) in the density fitting version [\[9,](#page-23-7) [14,](#page-23-8) [15\]](#page-23-9). The ORCA[\[16,](#page-23-10) [17\]](#page-23-11) electronic structure package was used for performing monomer DFT calculations with the PBE functional $\left[18\right]$ including the gradient-regulated asymptotic correction (GRAC)[\[19,](#page-24-1) [20\]](#page-24-2). The ionization potential of each monomer, required for GRAC, was computed using separate DFT calculations with the PBE functional. The augmented correlation-consistent double-zeta (aug-cc-pVDZ) basis set $[21]$ together with the corresponding correlation-energy fitted auxiliary bases from Ref. [22](#page-24-4) were used in all cases. We have applied the monomer-centered 'plus' basis set (MC⁺BS) form with midbond functions, see Ref. [23.](#page-24-5) Midbond function exponents and placement are as described in Ref. [24,](#page-24-6) with the midbond auxiliary basis set from Ref. [15.](#page-23-9) The SAPT2016 system of codes [\[25\]](#page-24-7) was used in calculations. For all dimers, the $\delta E_{\text{int,resp}}^{\text{HF}}$ correction [\[26,](#page-24-8) [27\]](#page-24-9), which accounts mostly for induction and exchange-induction effects beyond second order, was added to the SAPT(DFT) interaction energy, see the main text. The accuracy of the SAPT(DFT) interaction energies for most systems increases by including $\delta E_{\text{int,resp}}^{\text{HF}}$ terms, but its use increases the associated computational cost by about 60%. Based on the magnitude of the electric dipole moments of the monomers and the induction component of the interaction energy, autoPES determines if $\delta E_{\rm int,resp}^{\rm HF}$ should be included for a given dimer, see Ref. [1.](#page-23-1) $E_{\rm ind}^{(2)}$ was computed from coupled Kohn Sham (CKS) FDDSs at zero frequency. The exchange-induction energy, $E^{(2)}_{\text{exch-ind}}$, was also computed at the CKS level, i.e., from the CKS FDDS amplitudes. The dispersion energy, $E_{\text{disp}}^{(2)}$, was computed from frequency-dependent CKS FDDSs. Fast dispersion method, developed in Ref. [28,](#page-24-10) was used to compute this term. When this approach is used, the exchange counterpart, $E^{(2)}_{\text{exch-disp}}$, can be computed only in the uncoupled form. It was then scaled to approximate the CKS value as described in Ref. [12.](#page-23-12)

The V_{elst} term in Eq. [\(1\)](#page-16-1) was fitted to the asymptotic values of $E_{\text{elst}}^{(1)}$, and was damped

(using close-range values of $E_{\text{elst}}^{(1)}$) to ensure correct behavior of this component at shortranges. The coefficients C_n^{ab} in $V_{\text{asymp}}^{(2)}$ were fit to the sum of the COM-COM asymptotic expansions of $E_{\text{ind}}^{(2)}$ and $E_{\text{disp}}^{(2)}$. The damping factors were fit to $E_{\text{indx}} + E_{\text{dispx}}^{(2)}$ computed at close range. Finally, the exponential term, $V_{\rm exp}$, was fit to $E_{\rm int} - V_{\rm elst} - V_{\rm asym}$. It mainly reproduces the sum of exchange components of E_{int} .

V. SAPT COMPONENTS AT GLOBAL MINIMA OF PESS FOR WATER AND HYDROGEN PEROXIDE INTERACTING WITH MODEL MOLECULES

The global energy minimum geometries for each heterodimer interaction are presented in Figure 2 of the main text, while Figure [S2](#page-18-1) displays interaction energies, hydrogen bond distances, and SAPT components. In general, the small molecules considered were found

FIG. S2. (a) Interaction energy comparison for model molecules interacting with water or hydrogen peroxide at the global minima of the PESs. Top to bottom: water and hydrogen peroxide dimers of imidazole, methylamine, nitromethane, pyridine-N-oxide, formamide, and methanol; (b) hydrogen bond distances (defined as distances between the two heavy atoms forming the hydrogen bond) at the global minima, where double bars represents doubly hydrogen bonded systems; (c) analysis of the components of SAPT energies for the global minimum of the PESs.

to form more favorable hydrogen bonding interactions with hydrogen peroxide than water. Specifically, the dimers containing hydrogen peroxide have more favorable interaction energies by 1.3, 1.1, 1.2, 0.8, 2.2, and 3.3 kcal/mol for methanol, formamide, pyridine-N-oxide, nitromethane, methylamine, and imidazole than the water counterparts. These energy differences predict that sp^3 amine and sp^2 nitrogen functional groups will show the strongest selectivities for hydrogen peroxide over water interaction. The trend in relative interaction strength between hydrogen peroxide and water-containing heterodimers is generally consistent with the shorter interaction distances between hydrogen peroxide and the model molecules, Figure S2(b). The correlation between the differences of hydrogen bond distances and differences in interaction energies are presented in Fig. S3. Methylamine was found to

FIG. S3. Correlation between differences of hydrogen bond distances $\Delta d = d_{\text{H}_2\text{O}} - d_{\text{H}_2\text{O}_2}$ and differences of interaction energies $\Delta E_{\text{int}} = E_{\text{int},H_2O} - E_{\text{int},H_2O_2}$. Values for PES minima are in blue and near-experimental geometries are in red. The numbering is as follows: $1 =$ alcohol, $2 =$ carbonyl, $3 = N$ -oxide, $4 = \text{nit}$, $5 = sp^3$, and $6 = sp^2$ functional groups.

show the most dramatic difference in hydrogen bonding distance (0.156 Å) shorter with hydrogen peroxide) and formamide shows the least difference (0.041 Å) shorter with hydrogen peroxide). In all singly-bound (only one hydrogen bond present in the PES minimum geometry) cases, water and hydrogen peroxide are hydrogen bond donors. In the doubly-bound (two hydrogen bonds present in the PES minimum geometry) cases, the shorter and presumably stronger bonds are also of this character. The secondary hydrogen bonds, indicated by sky blue and purple colored bars in Figure S2(b), are donated by the model molecules. The secondary hydrogen bond distances are shorter and therefore presumably stronger for heterodimers containing water.

The components of the interaction energies are shown in Figure $S_2(c)$. As the intermolecular distance between monomers shortens, both the attractive and repulsive components increase in magnitude. This relationship explains the correlation between Figure S2(b) and Figure S2(c), i.e., shorter (primary) bonds roughly correlate with larger magnitudes of components. For all dimers, all of the components are larger in magnitude for hydrogen peroxide-containing dimers than for those containing water. For most heterodimers, the magnitude of the exchange interaction is approximately that of the electrostatic contribution (i.e., the $E_{\text{exch}}^{(1)}$ component nearly cancels the $E_{\text{elst}}^{(1)}$ component). For this reason, the interaction energy more closely reflects the sum of the induction and dispersion components, emphasizing the importance of including the latter contributions for accurately determining the geometry at the global energy minimum.

VI. COMPARISON OF SAPT AND PES ENERGIES AT NEAR-EXPERIMENTAL GEOMETRIES AND PES GLOBAL MINIMUM GEOMETRIES

Table [S15](#page-21-0) gives the SAPT and PES interaction energies at the PESs global minimum and at near-experimental geometries, while Table [S16](#page-22-0) gives the information of PESs developed in this study. In particular, the latter table gives root mean square errors (RMSEs) of the PESs for $E_{\text{int}} < 0$. As seen in Table [S15,](#page-21-0) at the global minimum geometries the fits are very accurate, with deviations much smaller than the RMSEs for $E_{\text{int}} < 0$ and all percentage errors smaller than 7.7% (in 83% of cases smaller than 3%). This is expected since the global minimum region is the most sampled and weighted region of the PES. At near-experimental geometries, in 50% of cases the deviations are below RMSEs and in 25% of cases are within 0.3 kcal/mol of RMSEs. There are three cases: both water and hydrogen peroxide interacting with N-oxide and water interacting with N sp³, where accuracy of the fit is poor, with deviations up to 5 times the RMSE. The existence of the regions in configuration space where accuracy is poor is the effect of using the default setting of autoPES for sampling of dimer configurations, which are chosen to minimize the costs of PES developments. As seen in Table [S16,](#page-22-0) the number of grid points ranges between 382 and 1335, whereas other methods of fitting 6-dimensional surfaces use tens of thousands of grid points. In applications to crystal structure predictions, the initial autoPES fit is improved using the dimer configurations extracted from polymorphs generated using the initial fit. This procedure was not needed here since the PESs were used in a very limited way: only to determine the coordinates of dimers that are not fixed by average experimental geometries given in Table [S13.](#page-14-1) All the interaction energies given in the main text and in the SI are from SAPT(DFT) ab initio calculations.

TABLE S15. Comparison of SAPT and PES energies at global minimum and near-experimental geometries. E_{int} and V are defined in main text, $\Delta = E_{\text{int}}$ - V, and % deviation = $|\Delta/E_{\text{int}}| \times$ $100\%.$

		$E_{\rm int}$	V	Δ	$%$ deviation	
At global minimum geometries						
$O-H \cdots O-H$ (Alcohol)	H_2O	-4.43	-4.35	-0.08	1.8	
	H_2O_2	-5.71	-5.81	0.10	1.8	
$O-H \cdots O=C$ (Amide)	H_2O	-7.72	-7.58	-0.14	1.8	
	H_2O_2	-8.84	-8.75	-0.09	1.0	
$O-H \cdots O-N$ (N-oxide)	H_2O	-7.87	-8.05	0.18	2.3	
	H_2O_2	-9.06	-9.15	0.09	1.0	
$O-H \cdots O_2-N$ (Nitro)	H_2O	-4.74	-4.61	-0.13	2.7	
	H_2O_2	-5.57	-5.74	0.17	3.1	
$O-H \cdots N$ (sp ³)	H_2O	-5.57	-5.14	-0.43	7.7	
	H_2O_2	-7.74	-7.71	-0.03	0.4	
$O-H \cdots N$ (sp ²)	H_2O	-6.72	-6.34	-0.38	5.7	
	H_2O_2	-10.06	-10.07	0.01	0.1	
At near-experimental geometries						
$O-H \cdots O-H$ (Alcohol)	H_2O	-2.34	-2.39	0.05	2.1	
	H_2O_2	-3.25	-3.61	0.36	11.1	
$O-H \cdots O=C$ (Amide)	H ₂ O	-4.29	-4.96	0.67	15.6	
	H_2O_2	-5.29	-5.28	-0.01	0.2	
$O-H \cdots O-N$ (N-oxide)	H_2O	-4.74	-5.85	1.11	23.4	
	H_2O_2	-5.83	-7.44	1.61	27.6	
$O-H \cdots O_2-N$ (Nitro)	H ₂ O	-1.90	-1.89	-0.01	0.5	
	H_2O_2	-3.54	-3.39	-0.15	4.2	
$O-H \cdots N$ (sp ³)	H_2O	-5.90	-4.01	-1.89	32.0	
	H_2O_2	-6.57	-7.10	0.53	8.1	
$O-H \cdots N$ (sp ²)	H_2O	-5.71	-5.63	-0.08	1.4	
	H_2O_2	-7.85	-8.66	0.81	10.3	

		$N_{\rm grid}$	$N_{\rm FP}$	$N_{\rm grid}/N_{\rm FP}$	$N_{\rm min}$	RMSE $(E_{\text{int}} < 0)$
$O-H \cdots O-H$ (Alcohol)	H_2O	382	40	9.6	3	0.27(166)
	H_2O_2	482	54	8.9	6	0.39(246)
$O-H \cdots O=C$ (Amide)	H ₂ O	422	40	10.6	$\overline{2}$	0.37(188)
	H_2O_2	845	54	15.7	7	0.39(305)
$O-H \cdots O-N$ (N-oxide)	H ₂ O	830	76	10.9	6	0.43(413)
	H_2O_2	1265	128	9.9	17	0.39(694)
$O-H \cdots O_2-N$ (Nitro)	H_2O	421	46	9.2	$\overline{4}$	0.28(204)
	H_2O_2	568	62	9.2	4	0.28(264)
$O-H \cdots N$ (sp ³)	H ₂ O	404	46	8.8		0.40(177)
	H_2O_2	1092	62	17.6	8	0.44(532)
$O-H \cdots N$ (sp ²)	H_2O	674	58	11.6	$\overline{2}$	0.50(313)
	H_2O_2	1334	98	13.6	9	0.64(697)

TABLE S16. RMSEs (in kcal/mol) of PESs evaluated at close-range grid points with number of grid points given in parentheses. Here, N_{grid} : total number of grid points, N_{FP} : number of free parameters of the PES, and $N_{\rm min}$: number of detected minima of the PES.

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