

LIBRA-WA: a web application for ligand binding site detection and protein function recognition

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1 SUPPLEMENTARY METHODOLOGY

1.1 Clusterization of ligands according to their mutual similarity

The ligands stored in LIBRA-WA's binding sites database have been clustered according to their mutual similarity, as computed by an automatic procedure that was meant to compare their SMILES representation. For this purpose, the SMILES information was retrieved from the Protein Data Bank in Europe⁰ via a corresponding crawling mechanism, and a similarity threshold (set to 0.7 after a fine-tuning process) was placed for generating the clusters. The actual similarity score was computed by using a combination of Levenshtein and Jaccard distances applied to the SMILES strings. The clusters' semantics is as follows: each ligand has been placed into a cluster so that its similarity score with all of the other members of the cluster is above or equal the given threshold; the ligand with the highest average similarity score with the other members of the cluster has been dubbed the "core" ligand of such a cluster. Each ligand is thus present within one cluster at most. Clusters can be freely browsed by LIBRA-WA users via their corresponding web page, where the ligands making up each cluster are shown.

1.2 Extension and refinements of the alignment output and the scoring mechanism

Results produced by LIBRA-WA have been enriched with respect to LIBRA with additional information and a new scoring mechanism. Specifically, each binding site alignment record displayed within the results of an alignment process now features the information related to the cluster the corresponding ligand falls into (if any), including the core ligand of the cluster, its total size and the number of records within the result page whose ligand falls into that cluster. Alternatively, if the ligand from the record is not included in any cluster, the ligands from other records that are most similar to the considered ligand are shown. Along with the cluster information, a new, refined score mechanism has been implemented to rank more accurately the alignment records. This new score (S_{new}) combines the contributions given by the aligned binding site's clique size (C , corresponding to the number of matching residues between the input protein and the target binding site), RMSD value (R) and the relative size of the cluster containing the ligand (K), each normalized according to the following formulas:

$$C_n = \frac{C - C_{min}}{C_{max} - C_{min}} \quad (1)$$

$$R_n = \frac{1 - (R - R_{min})}{R_{max} - R_{min}} \quad (2)$$

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⁰ <http://www.ebi.ac.uk/pdbe-srv/pdbechem/>

$$K_n = \frac{K - K_{min}}{K_{max} - K_{min}} \quad (3)$$

where min and max indicate the minimum and maximum value of the respective parameter observed in the considered alignment records.

These normalized values are then weighted and linearly combined according to the following formula:

$$S_{new} = w_c * C_n + w_r * R_n + w_k * K_n \quad (4)$$

where $w_c = 0.5$, $w_r = 0.3$ and $w_k = 0.2$. According to its respective value for S_{new} , each alignment record shows a "Confidence" indicator for the quality of the alignment itself, ranging from "green" ($S_{new} \geq 0.7$), to "yellow" ($0.4 \leq S_{new} < 0.7$), up to "red" ($S_{new} < 0.4$).

1.3 Identification of ligand binding sites across different protein subunits

As a result of the extensive experimentation carried out on LIBRA (Viet Hung *et al.*, 2015), a number of cases were detected where the program could not identify the correct ligand binding site for the input protein, due to the fact that such a site included residues belonging to different protein subunits or "chains". As a matter of fact, the original algorithm was able to identify only binding sites whose residues belonged to the same chain. In order to overcome this weakness of the application, a mechanism has been devised for identifying binding sites across different chains, by considering, for each residue of a given chain, its neighbours from different chains within a distance threshold. Since a naive iterative approach for performing this computation would obviously degrade the efficiency of the algorithm, residues have been thus indexed via a kind of n -dimensional indexes called KD-Trees, by using the three-dimensional coordinates of their geometric center as their index key. Then, the identification of their neighbours was only a matter of computing the respective Euclidean distances between residues belonging to different chains by applying an efficient nearest-neighbour algorithm, as implemented by (Levy *et al.*, 2015). This resulted in an extremely fast computation that leaves the original performance of LIBRA's algorithm virtually unaffected, while increasing its accuracy for such critical cases.

1.4 Additional features and improvements to user experience

Aside from the scientific advancements mentioned in the previous paragraphs, whose purpose was to improve the effectiveness of the alignment process, LIBRA-WA provides the users with an improved user experience and additional features as described below.

1.4.1 User account and personal panel As a web application (sharing the same architectural framework of (Atzeni *et al.*, 2011a,b; Toti *et al.*, 2012)), LIBRA-WA can be freely accessed and used by any web user without

Bioinformatics's Recognition Panel

Recognize the function of a given protein			Display ligand clusters	Delete selected results				
<input type="checkbox"/>	Id	Creation date	Status	Completion level	Completion date	Results	Export?	Delete?
<input type="checkbox"/>	144	2016-05-30 16:23:22.0	Completed	100%	2016-06-01 07:42:41.0	Show	Export	Delete
<input type="checkbox"/>	143	2016-05-30 16:23:17.0	Completed	100%	2016-06-01 02:31:35.0	Show	Export	Delete
<input type="checkbox"/>	142	2016-05-30 16:23:15.0	Completed	100%	2016-06-01 02:23:14.0	Show	Export	Delete
<input type="checkbox"/>	141	2016-05-30 16:23:13.0	Completed	100%	2016-06-01	Input parameters	Export	Delete
<input type="checkbox"/>	140	2016-05-30 16:23:10.0	Completed	100%	2016-06-01	Input protein: 4ake.pdb	Export	Delete
<input type="checkbox"/>	139	2016-05-30 16:23:08.0	Completed	100%	2016-06-01	Input database: Ligand binding sites	Export	Delete
<input type="checkbox"/>	138	2016-05-30 16:23:06.0	Completed	100%	2016-05-31	Minimum percentage of similar residues: 70	Export	Delete
<input type="checkbox"/>	137	2016-05-30 16:23:03.0	Completed	100%	2016-05-31	Minimum motif size: 5	Export	Delete
<input type="checkbox"/>	136	2016-05-30 16:22:50.0	Completed	100%	2016-05-31	Maximum alignment RMSD (Å): 2.5	Export	Delete
<input type="checkbox"/>	135	2016-05-30 16:22:45.0	Completed	100%	2016-05-31	Inter-residues distance similarity threshold (Å): 1.5	Export	Delete
<input type="checkbox"/>	134	2016-05-30 16:22:44.0	Completed	100%	2016-05-31 07:25:08.0	Check steric clashes: No	Export	Delete
<input type="checkbox"/>	133	2016-05-30 16:22:38.0	Completed	100%	2016-05-31 05:40:34.0	Chain check: Yes	Export	Delete
<input type="checkbox"/>	132	2016-05-30 16:22:35.0	Completed	100%	2016-05-31 05:05:59.0	Maximum distance for chain check (Å): 20	Export	Delete
<input type="checkbox"/>	131	2016-05-30 16:22:33.0	Completed	100%	2016-05-31 04:44:29.0	Structure level: Backbone and side chain	Export	Delete
<input type="checkbox"/>	130	2016-05-30 16:22:31.0	Completed	100%	2016-05-31 04:04:23.0	Conservation measure: Residue identity	Export	Delete
<input type="checkbox"/>	129	2016-05-30 16:22:28.0	Completed	100%	2016-05-31 03:32:27.0	Show	Export	Delete
<input type="checkbox"/>	128	2016-05-30 16:22:27.0	Completed	100%	2016-05-31 03:03:57.0	Show	Export	Delete
<input type="checkbox"/>	127	2016-05-30 16:22:21.0	Completed	100%	2016-05-31 01:39:35.0	Show	Export	Delete
<input type="checkbox"/>	126	2016-05-30 16:22:16.0	Completed	100%	2016-05-30 21:41:04.0	Show	Export	Delete
<input type="checkbox"/>	125	2016-05-30 16:22:02.0	Completed	100%	2016-05-30 16:28:39.0	Show	Export	Delete

First | 1 2 3 4 5 6 7 | Last

Recognize the function of a given protein			Display ligand clusters	Delete selected results			
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Fig. 1. Screenshot of a user's personal panel in LIBRA-WA, where recognition jobs scheduled, running or completed are shown. For the user's convenience, hovering the mouse over a recognition job displays a summary of the input parameters used when launching it, as shown in the case of the third result from the top. Once available, each result can be browsed in greater detail ("Show"), exported in the LIBRA/LIBRA+ .alg desktop file format ("Export") or deleted altogether ("Delete"). From this panel, a user can access the page where recognitions can be launched ("Recognize the function of a given protein"), as well as browse the ligand clusters generated from the currently available database ("Display ligand clusters").

the need for setting up a personal account; users can start and schedule multiple recognition jobs as they see fit. Optionally, LIBRA-WA allows users to also create a personal workspace on the server by providing a valid e-mail address and selecting a personal password. Once their registration is confirmed via the e-mail sent by the system, they can access their personal panel (as shown in Figure 1). Recognition jobs started by users are automatically placed by the system into its centralized queue and executed in a First-In-First-Out (FIFO) fashion. At the present time, each user can execute only one job at a time while having an unlimited number of scheduled jobs in the queue. Recognition jobs can be launched against a number of pre-compiled databases, including: a manually curated ligand binding sites database, dating back to 2015, with more than 173,000 entries; an unsupervised ligand binding site database, last updated in Q4 2017, including more than 200,000 entries; and a database of active sites derived from the Catalytic Site Atlas (Furnham, 2014) (~1000 entries) that can be used for the prediction of the catalytic activity of an input protein. Registered users can also edit their personal information and log-in credentials via the corresponding page. Each result can be individually analyzed via a corresponding

panel showing the alignments produced by the recognition job, as displayed in Figure 2. This panel provides the user with the functionalities to sort the results as needed (by score, clique size, RMSD, protein, ligand, etc.) and filter them by protein, ligand and "core ligand" of a cluster. Besides, the user can display three-dimensional representations of the aligned proteins, check referenced literature for the proteins featured in the database, as well as export the results as described below.

1.4.2 Backward compatibility with LIBRA desktop application and introduction of LIBRA+ The results produced by LIBRA-WA can be easily exported as LIBRA recognition files (.alg) for offline viewing via the desktop application. Additionally, a new version of the desktop application, called LIBRA+, has been released in order to include and display the clusters information and the new scoring mechanism for each of the recognition files: such information is also retroactively available for results produced with the previous version of the desktop application when opened with LIBRA+.

Recognition result for 1ESC (id: 260) (1)

[Export .alg file](#)

[--Back to Recognition Panel](#)

Filters

Known protein:

Ligand:

Ligand in cluster:

(3)

(2) Input database: **Ligand binding sites**

Minimum percentage of similar residues: **70**

Minimum motif size: **5**

Maximum alignment RMSD (Å): **2.5**

Inter-residues distance similarity threshold (Å): **1.5**

Check steric clashes: **No**

Chain check: **Yes**


Structure level: **Backbone and side chain**

Conservation measure: **Residue identity**

Known protein	Ligand	Input residues	Known residues	Binding site	Site size	Conservation	Clique size	RMSD	Cluster	Combined Score	Superimpose	Active site context	Info	Confic
ESTERASE	DEP	ASP 13 A TYR 186 A PRO 128 A LEU 127 A LEU 126 A PHE 110 A ALA 67 A GLY 65 A CYS 64 A PHE 19 A TYR 15 A HIS 283 A ASN 106 A GLY 105 A GLY 66 A SER 14 A	ASP 13 A TYR 186 A PRO 128 A LEU 127 A LEU 126 A PHE 110 A ALA 67 A GLY 65 A CYS 64 A PHE 19 A TYR 15 A HIS 283 A ASN 106 A GLY 105 A GLY 66 A SER 14 A	ASP 13 A SER 14 A GLY 66 A GLY 105 A HIS 283 A	6	1.0	16	0.467	Cluster C11 Size: 2 Matches: 3	0.8	Open Jmol	Open Jmol	Info	
ESTERASE ESTA	C8E	SER 14 A ILE 291 A	SER 14 X LEU 297 X	SER 14 X ASN 147	5	0.46	11	1.251	Cluster 12P Size: 60 Matches: 17	0.62	Open Jmol	Open Jmol	Info	
ESTERASE					9			0.254	Cluster VXA Size: 3 Matches: 1	0.45	Open Jmol	Open Jmol	Info	
ACETYL YLAN E ERASE T2A					6			0.638	Cluster 11A Size: 47 Matches: 14	0.41	Open Jmol	Open Jmol	Info	
ARYLES RASE		GLY 65 A HIS 283 A ASN 106 A	GLY 49 A HIS 187 A ASN 90 A	SER 10 A GLY 50 A ASN 90 A	6			0.908	Cluster 11A Size: 47 Matches: 14	0.38	Open Jmol	Open Jmol	Info	

JMol - Alignment id: 1 - 1esc-1ESE - Supe...

localhost:8080/LIBRAWA/getJmol.do?resultId=234&i=1esc&k=1ESE&



(5)

Fig. 2. Screenshot of the panel showing the detailed results for a recognition job. (1) The input protein's PDB code is reported and the possibility of exporting the results in LIBRA+ .alg file format is provided. (2) The values of the input parameters used for the given execution are recapped. (3) Filters are in place for the user's convenience when browsing the results obtained; results can be filtered by known protein, ligand and "core" ligand of a cluster. (4) The results are shown in a table which can be re-ordered as needed by clicking on each column's header. Further information is displayed by hovering the mouse over the known protein and ligand, such as the known protein's PDB ID and ligand's full name, respectively, as well as over the "Cluster" information, where all the records falling into the same clusters are shown (as depicted in the screenshot). For each record, via the Jmol HTML 5 plug-in, three-dimensional representations can be visualized, either showing (i) the input protein with its aligned residues highlighted, upon which the corresponding active site from the known protein is superimposed by means of roto-translations of its residues (as exemplified in the screenshot), or (ii) the known protein where the residues from its binding/active site are highlighted instead. Additional information on the aligned protein from each record, including a reference and PubMed ID of the related literature describing the protein's structure, can be found by clicking on "Info", which opens a corresponding pop-up window. Coloured circles in the right side of results panel represent the "Confidence" indicator as detailed in the text, with green circles characterizing high-confidence results.

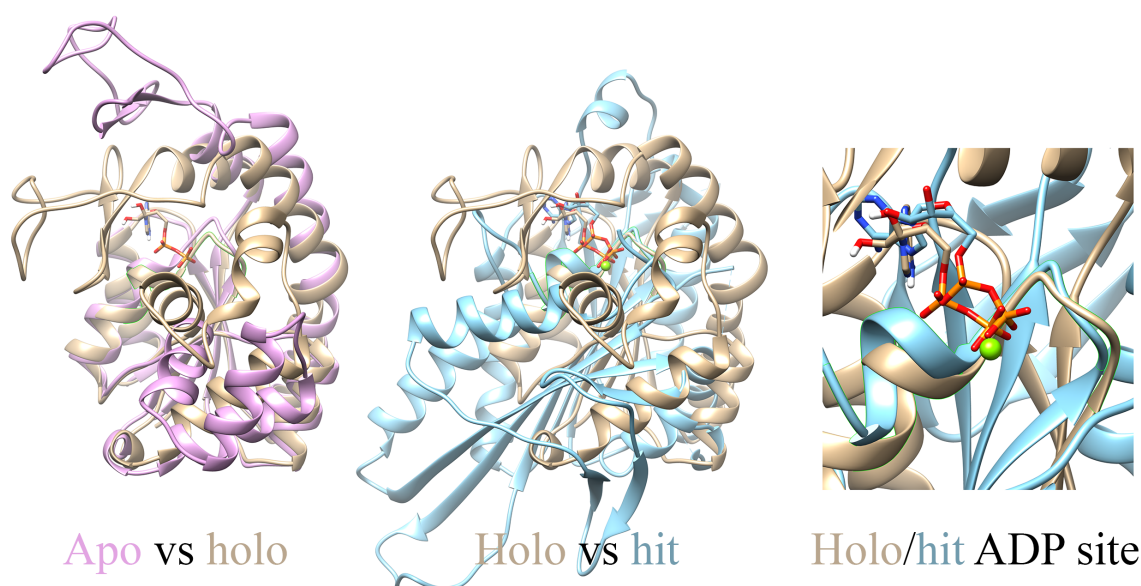


Fig. 3. Left panel. Superimposition of the *E. coli* adenylate kinase in the apo (PDB code 4AKE) and the holo ADP-bound (PDB code 2ECK) form. Note the large conformational change occurring upon ADP binding. Central panel. Superimposition of the ADP-bound structures of the *E. coli* adenylate kinase and the human kinesin-8 motor domain (PDB code 3LRE). Note the lack of structural similarity between the two proteins, paralleled by a lack of significant sequence identity (see text for details). Right panel. Detail of the ADP binding site of the two proteins. Note the good superimposition of the ADP molecules and the local structural similarity of a portion of the α helix and the connected loop hosting the ADP binding site in both proteins (circled in red).

2 SUPPLEMENTARY RESULTS

The effectiveness of LIBRA-WA, and in particular the performance improvement with respect to LIBRA due to the novel scoring mechanism, has been evaluated using the LigaSite set of 373 apo-proteins as a test set. As shown in Table 1 LIBRA-WA finds the biologically relevant ligand/binding site in ~96% of the cases. More importantly, the correct ligand/binding site ranks first in almost all of these cases. In detail, the correct hit is a substrate/substrate analog in 35% of the cases, a specific inhibitor in 16% of the cases, a product/product analog in 13% of the cases, a cofactor/cofactor analog in 13% of the cases, a specific ligand other than the above mentioned categories in 15% of the cases and a transition state analog/reaction intermediate in 3% of the cases. It must be remarked that this performance is in many cases independent from the sequence/structure similarity between the input protein and the holo protein from which the known binding site has been extracted. As already mentioned in the main text, one example of this performance is *E. coli* adenylate kinase (apoprotein PDB code 4AKE) which, upon ADP binding undergoes a large conformational change. As a consequence, LIBRA-WA does not identify the ADP binding site of the corresponding holo protein (PDB code 2ECK) as a correct match. Nonetheless, it correctly identifies the ADP binding site in the input apo protein by virtue of the local, structural similarity with the ADP binding site of the human kinesin-8 motor domain (PDB code 3LRE) which shares a mere 11% sequence identity with the *E. coli* adenylate kinase and practically no significant similarity in the overall protein topology (Figure 3). This observation suggests the possibility to exploit the ligand binding sites database, developed to be used with LIBRA-WA, to analyze if there are common, local structural determinants which govern the binding of specific ligands to different proteins, a possibility which will be explored as one of

the future perspectives of this work. Detailed results of the tests performed on the LigaSite set are reported in Table 1. Even removing from the database the holo-proteins present in the LigaSite set, the application still performs fairly well. In fact, LIBRA-WA still identifies a biologically relevant ligand in 88% of the cases, with the correct ligand ranking first in 80% of the cases (Table 4).

For comparative purposes, LIBRA-WA, SiteSeer (Laskowski *et al.*, 2005a,b) and the COACH meta-server (Yang *et al.*, 2013; Roy *et al.*, 2012; Brylinski and Skolnick, 2008; Capra *et al.*, 2009) have been tested on a set of 30 apo-proteins randomly chosen from LigaSite. As it can be seen from Table 2, LIBRA-WA finds a correct solution in 97% of the cases (29 out of 30) as opposed to a success rate of 87% for SiteSeer and 90% for COACH meta-server. Particularly interesting is LIBRA-WA's performance in comparison to COACH meta-server as the latter incorporates the results of several different sequence-based and structure-based algorithms (TM-Site, S-Site, COFACTOR, FINDSITE and ConCavity), while LIBRA-WA is, by design, exclusively structure-based; incidentally, COACH meta-server was ranked as the best method in the weekly CAMEO ligand Binding Site Prediction Experiments (Haas *et al.*, 2013). This observation has prompted a more extensive comparison of LIBRA-WA's performance with respect to COACH. For this purpose, COACH's performance has been evaluated on the entire LigaSite test set. The results, shown in Table 3, indicate that COACH performs slightly better than LIBRA-WA as it finds a biologically relevant ligand in 98% of the cases (versus the 96% success rate of LIBRA-WA). However, the correct result found by COACH ranks first only in 90% of the cases (versus the 94% performance of LIBRA-WA). This is a very good result for LIBRA-WA, given its exclusively structure-based approach and the presence of only small molecules and ions in its database, as opposed to COACH's

database which contains also peptides and nucleic acids. In the light of these extensive tests, it can be stated that LIBRA-WA achieves a performance which is comparable to that of the COACH meta-server.

Table 1: LIBRA-WA's ligand/binding site recognition performance on the LigoSite non-redundant dataset containing 373 apo-proteins for which a corresponding holo structure is available (Desailly *et al.*, 2008). APO and HOLO Protein ID are the PDB codes of the corresponding three-dimensional structures. Ligand ID is the ligand name abbreviation used in the Protein Data Bank.

APO Protein ID	HOLO Protein ID	Ligand ID	Rank	rmsd (Å)	Ligand details
180L	186L	N4B	1 st	0.485	Specific ligand analog
1A4U	1B2L	NDC	1 st	0.664	Cofactor analog
1ADE	1HOP	GCP	1 st	1.023	Substrate analog
1AK1	1C9E	MP1	1 st	0.89	Substrate analog
1AKZ	3FCK	FCK	1 st	0.593	Specific inhibitor
1ARB	4NSV	2OY	1 st	0.324	Specific inhibitor
1ARL	3FVL	BHK	1 st	0.533	Specific inhibitor
1B8E	3UEX	STE	1 st	0.791	Specific ligand
1B8P	1B8U	NAD	1 st	0.558	Cofactor
1BD9	2B7A	OPE	1 st	0.648	Natural ligand analog
1BK7	1UCD	U5P	1 st	0.456	Reaction product
1BKZ	4UW6	VV7	1 st	0.512	Natural ligand
1BQC	2MAN	MAN	1 st	0.545	Reaction product
1BY1	1DAG	ACP	1 st	0.857	Substrate analog
1C48	1CQF	GAL	1 st	0.69	Natural ligand
1C5H	2B46	XYP	1 st	0.434	Reaction product
1CEO	1CEN	BGC	1 st	0.672	Substrate analog
1CEX	1OXM	TC4	1 st	0.484	Covalent inhibitor
1CPJ	2DC7	042	1 st	0.654	Covalent inhibitor
1CRW	2B4R	NAD	1 st	0.729	Cofactor
1CWY	1ESW	ACR	1 st	0.543	Specific inhibitor
1DCO	1DCP	HBI	1 st	0.713	Cofactor analog
1DHN	2NM3	MPU	1 st	0.622	Substrate analog
1DQ0	4P9W	R3M	1 st	0.726	Specific ligand analog
1DUP	1DUD	DUD	1 st	0.402	Substrate analog
1E4F	4A2B	AGS	1 st	0.817	Substrate analog
1E5L	1ESQ	NDP	1 st	0.887	Cofactor
1E8Y	3L13	JZW	1 st	0.582	Specific inhibitor
1EDQ	1X6N	AO3	1 st	0.444	Specific inhibitor
1EPA	1EPB	REA	1 st	0.711	Natural ligand
1EWZ	2WGI	PNM	1 st	0.936	Specific inhibitor
1EY0	1A2T	THP	1 st	0.937	Specific inhibitor
1EZI	1EYR	CDP	1 st	0.847	Substrate analog
1F14	1F17	NAI	1 st	0.409	Cofactor
1F1S	2BRP	SIE	1 st	0.509	Specific inhibitor
1F2V	1I1H	COJ	1 st	0.665	Reaction product
1F41	1DVS	STL	1 st	0.593	Specific inhibitor
1F5Z	4IMF	SI3	1 st	0.723	Substrate
1FCQ	1FCV	NAG	1 st	0.7	Substrate fragment
1FGB	1JQY	A32	1 st	0.883	Specific inhibitor
1FO9	2APC	UDM	1 st	0.863	Substrate analog
1FSF	1HOR	AGP	1 st	0.673	Specific inhibitor
1FTF	1FTH	A3P	1 st	0.64	Reaction product
1FTR	2FHJ	MFN	1 st	0.558	Cofactor
1FWL	1H72	ANP	1 st	0.66	Substrate analog
1G40	1RID	IDS	1 st	1.783	Natural ligand

1G4E	1G4S	TPS	1 st	0.428	Reaction product
1G95	1G97	UD1	1 st	0.879	Reaction product
1GBS	1LSP	BUL	1 st	0.716	Specific inhibitor
1GCE	1GA0	DVR	1 st	0.604	Specific inhibitor
1GFS	1FXS	NAP	1 st	0.524	Reaction product
1GOU	1GOY	3GP	1 st	1.017	Substrate analog
1GSH	1GSA	GSH	1 st	0.773	Reaction product
1GWK	1W8U	BMA	1 st	1.254	Natural ligand
1GY0	1OG1	TAD	1 st	0.57	Substrate analog
1HK9	3QO3	ATP	1 st	0.362	Natural ligand
1HKA	3UDV	JIC	1 st	0.592	Substrate analog
1HM5	4QFH	G6P	1 st	1.003	Reaction product
1HNK	1HNJ	MLC	1 st	0.8	Substrate
1HO1	1HO4	PXP	1 st	0.482	Reaction product
1I7N	1I7L	ATP	1 st	1.263	Endogenous ligand
1IAD	1QJI	PKF	1 st	0.575	Specific inhibitor
1ILV	1J9K	WO4	1 st	0.817	Specific inhibitor
1INL	1JQ3	AAT	1 st	0.309	Substrate analog
1J85	1MXI	SAH	1 st	0.686	Cofactor
1J8S	1J8R	GLA	1 st	0.179	Endogenous ligand
1JCF	1JCG	ANP	1 st	0.528	Substrate analog
1JKS	1IG1	ANP	1 st	0.568	Substrate analog
1JXO	1JXM	MPD	1 st	0.434	Non-specific ligand
1JYK	1JYL	CDC	1 st	0.701	Reaction product
1K0M	1K0N	GSH	1 st	0.87	Substrate
1K3O	4HJ2	LZ6	1 st	0.66	Substrate analog
1K6A	1B30	XYP	1 st	0.449	Reaction product
1KAM	1KAQ	DND	1 st	1.517	Substrate
1KF5	1QHC	PUA	1 st	0.802	Reaction product
1KHD	1KGZ	PRP	1 st	0.932	Substrate
1KN9	1B12	1PN	1 st	0.677	Specific inhibitor
1KPA	1KPE	ADW	1 st	0.457	Substrate analog
1KWB	1EIR	BPY	1 st	0.406	Substrate
1L7D	1XLT	NAD	1 st	1.049	Substrate
1LBV	1LBZ	FBP	1 st	0.801	Substrate
1LCI	3RIX	923	1 st	0.695	Specific Inhibitor
1LF4	1LF3	EH5	1 st	0.541	Specific Inhibitor
1LTU	1LTZ	HBI	1 st	0.412	Cofactor
1MIZ	1MB9	ATP	1 st	0.753	Substrate
1MKB	4KEH	1r3	1 st	0.59	Substrate analog
1MMI	3QSB	743	1 st	0.555	Specific inhibitor
1MR7	1KK4	ACO	1 st	0.544	Substrate
1MTZ	1MU0	PHK	1 st	0.632	Specific inhibitor
1MWK	4A61	ANP	1 st	0.985	Substrate analog
1MZL	1FK4	STE	1 st	0.697	Natural ligand
1N05	1N07	FMN	1 st	1.144	Reaction intermediate
1NDB	2H3P	ACO	1 st	0.559	Substrate
1NON	1XZ8	5GP	1 st	0.439	Substrate analog
1NXM	2IXL	TRH	1 st	0.684	Substrate analog
1O24	1KQ4	FAD	1 st	0.501	Cofactor
1OEM	3EAX	LZP	1 st	0.827	Specific inhibitor

1OFP	1OF6	DTY	1 st	0.906	Specific inhibitor
1OGH	1PKJ	DUT	1 st	0.575	Substrate
1OGL	2YB0	DUR	1 st	0.82	Substrate analog
1OGM	1OGO	GLC	1 st	0.503	Reaction product
1OJQ	1OJZ	NAD	1 st	0.877	Cofactor
1OLZ	3OL2	NAG	1 st	0.524	Sugar chain
1OOI	2GTE	VA	1 st	0.532	Natural ligand
1OPY	3OWY	EQU	1 st	0.698	Transition state analog
1OXT	1OXV	ANP	1 st	0.534	Reaction product
1P1X	1JCJ	HPD	1 st	0.418	Reaction intermediate
1P5H	1T3Z	CAO	1 st	0.838	Substrate analog
1P74	3PHJ	DHK	1 st	1.024	Reaction product
1PDB	1BOZ	NDP	1 st	0.938	Cofactor
1PNG	1PNF	NDG	1 st	0.458	Substrate analog
1Q52	1Q51	CAA	1 st	0.81	Substrate analog
1Q7M	1Q8J	C2F	1 st	0.744	Substrate analog
1QCZ	2FWP	ICR	1 st	0.685	Substrate
1QID	1H23	E12	1 st	0.322	Specific inhibitor
1QTO	1JIF	BLM	1 st	0.703	Natural ligand
1QTR	1X2B	STX	1 st	0.415	Specific inhibitor
1R0M	1XPY	NLQ	1 st	0.398	Substrate
1R12	3ZWP	AVU	1 st	0.601	Substrate analog
1R29	4CP3	RBT	1 st	0.761	Specific inhibitor
1R15	2HV9	SFG	1 st	0.301	Specific inhibitor
1RIQ	3HXQ	ASA	1 st	0.873	Substrate analog
1RJ1	2CJ7	IOD	1 st	0.105	Non-specific ligand
1RKM	2RKM	LYS	4 th	1.029	Specific ligand
1RZV	1RZU	ADP	1 st	0.655	Reaction product analog
1S2L	1S2D	AR4	1 st	0.396	Substrate analog
1S7K	1S7L	COA	1 st	0.861	Reaction product
1SGK	1DDT	APU	1 st	0.561	Substrate analog
1SGZ	3I25	MV7	1 st	0.657	Specific inhibitor
1SJY	1S23	GNP	1 st	0.121	Product analog
1SNT	1VCU	DAN	1 st	0.938	Specific inhibitor
1SQG	1SQF	SAM	1 st	0.723	Cofactor
1SUL					No significant results
1SWH	3WZP	ZOF	1 st	0.715	Specific ligand analog
1TGN	1C2F	BAH	1 st	0.887	Specific inhibitor
1THV	4TVT	NA	2 nd	0.162	Non-specific ligand
1TIB	1GT6	OLA	1 st	0.874	Reaction product
1TJE	1TKY	A3S	1 st	0.346	Substrate analog
1TJV	1TJW	AS1	1 st	0.834	Substrate analog
1TVN	4A3H	DCB	1 st	1.021	Substrate analog
1TW0	1TXC	2AN	1 st	0.671	Non-specific ligand
1TYF	2FZS	CMQ	1 st	0.508	Specific inhibitor
1TYV	3TH0	PZU	1 st	0.632	Natural ligand analog
1TZV	1TZX	CIT	1 st	0.987	Specific ligand analog
1U0T	1Y3I	NAD	1 st	1.315	Substrate
1U7U	1U7Z	PMT	1 st	0.83	Substrate analog
1UAJ	1P9P	SAH	1 st	0.701	Substrate analog
1UBI	4WZP	SEP	1 st	1.045	Specific ligand
1UF4	1UF5	CDT	1 st	0.287	Substrate

1ULU	2WYV	NAD	1 st	0.444	Cofactor
1UMF	1UM0	FMN	1 st	0.465	Cofactor
1UXZ	1UZ0	BGC	1 st	0.337	Specific ligand
1UYL	3T0Z	ATP	1 st	0.934	Substrate
1V0S	2ZE9	PD7	1 st	0.335	Reaction product
1V6Z	2CX8	SAH	1 st	0.626	Cofactor analog
1V77	2CZV	ACY	1 st	0.357	Non-specific ligand
1VFJ	1V9O	ADP	1 st	0.643	Specific ligand
1VIC	1H7H	CDP	1 st	1.172	Substrate analog
1VJU	3DWR	0PA	1 st	0.671	Substrate analog
1VPN	1VPS	SIA	1 st	0.62	Specific ligand
1W9A	4QVB	F42	1 st	0.741	Cofactor
1WJG	2Z08	ATP	1 st	0.987	Specific ligand
1WNY	1WNZ	2VA	1 st	0.6	Substrate analog
1WOS	1WOP	FFO	1 st	0.551	Substrate analog
1WS9	2D29	FAD	1 st	0.327	Cofactor
1WTJ	2CWF	NDP	1 st	0.457	Cofactor
1WXF	1EE1	ATP	1 st	0.556	Substrate analog
1X56	1X55	NSS	1 st	0.713	Substrate analog
1X70	1X7P	SAM	1 st	0.534	Cofactor
1X8F	1X6U	DO8	1 st	0.457	Reaction product
1XIX	1P4N	UMA	1 st	0.225	Substrate
1XK7	1XA4	COA	1 st	0.569	Substrate analog
1XO6	1XNY	191	1 st	0.548	Substrate
1XQO	1XQP	8HG	1 st	0.575	Substrate analog
1XW2	2B4F	XYP	1 st	0.381	Reaction product
1Y2Q	3PD2	A3S	1 st	0.817	Substrate analog
1Y2T	20FD	NGA	1 st	0.896	Endogenous ligand
1YBT	1YBU	APC	1 st	1.21	Substrate analog
1YVY	1YTM	ATP	1 st	0.994	Substrate
1Z7G	4RAB	3L3	1 st	0.872	Specific inhibitor
1ZAH	3TU9	5MM	1 st	0.319	Specific inhibitor
1ZCU	1ZDF	UPG	1 st	0.305	Substrate
1ZNW	1ZNX	5GP	1 st	0.279	Substrate
1ZTY	1ZU0	CBS	1 st	0.815	Natural ligand
1ZUH	3MUF	ADP	1 st	1.294	Reaction product
2A6Z					No significant results
2A8F	1LRI	CLR	1 st	0.897	Specific ligand
2AD1	1BO6	VO4	2 nd	0.713	Transition state analog
2AHF	2AHG	UCD	1 st	0.617	Substrate
2AHU	2AHV	COA	1 st	0.862	Cofactor
2AMJ	2B3D	FAD	1 st	0.449	Cofactor
2B0J	3F46	I2C	1 st	0.68	Cofactor
2B6P	1YMG	BNG	1 st	0.152	Non-specific ligand
2B78	3LDF	SAH	1 st	0.405	Cofactor
2B98	2B99	RDL	1 st	0.53	Substrate analog inhibitor
2BGT	1J39	UPG	1 st	0.96	Substrate
2BJW	2C96	ATP	1 st	0.593	Substrate
2BOE	2BOD	BGC	1 st	0.267	Reaction product
2C61	3B2Q	ATP	1 st	0.592	Reaction product
2C7I	2ARU	ATP	1 st	0.555	Substrate
2CAR	2J4E				No significant results

2CHS	1COM	PRE	1 st	0.599	Reaction product
2CI3	2CI1	KOR	1 st	0.654	Specific inhibitor
2CWK	2DY9	ADP	1 st	0.678	Substrate
2CX5	2Z0X	5CA	1 st	0.717	Substrate analog
2D59	2D5A	COA	1 st	0.681	Natural ligand
2DHQ	3N76	CA2	1 st	0.515	Specific inhibitor
2DJ6	2DTT	H4B	1 st	0.84	Substrate analog
2DKA	2DKC	16G	1 st	0.814	Substrate
2DPS	2DPT	PUY	1 st	0.532	Substrate analog
2DQW	1EYE	PMM	1 st	0.982	Substrate analog
2E0C	2E5M	NAP	1 st	0.722	Substrate
2E0K	2E0N	SAH	1 st	0.721	Cofactor
2E10	1WQW	BT5	1 st	0.409	Substrate analog
2E1V	2E1T	MLC	1 st	0.449	Substrate
2E3S	2E3O	16C	1 st	0.739	Substrate
2ECR	2ED4	FAD	1 st	0.556	Substrate
2EX0	2IIQ	C5P	1 st	0.583	Substrate analog
2F82	2FA0	HMG	1 st	0.713	Reaction product
2F9T	2F9W	PAU	1 st	0.565	Substrate
2FK7	3HA7	B32	1 st	0.49	Specific inhibitor
2FP8	2V91	S55	1 st	0.691	Substrate
2FSF	2FSH	ANP	1 st	0.51	Substrate analog
2G67	2G25	TZK	1 st	0.775	Reaction intermediate analog
2G95	3G8E	IS1	1 st	0.88	Specific inhibitor
2GFV	2GFX	PMN	1 st	0.414	Specific inhibitor
2GG4	1RF6	S3P	1 st	1.113	Substrate
2GQV	2P4T	NAP	4 th	0.86	Cofactor
2GSF	4P5Z	Q7M	1 st	0.924	Specific inhibitor
2GT2	2GT4	GDD	1 st	0.623	Substrate
2GUB	4QDW	LAI	1 st	0.696	Reaction intermediate
2GWX	3GWX	EPA	1 st	0.776	Natural ligand
2GYY	2GZ1	NAP	1 st	0.709	Cofactor
2H2Z	2A5K	AZP	1 st	0.74	Inhibitor
2HBJ	2HBL	AMP	1 st	0.423	Reaction product
2HIV	2HIX	ATP	1 st	0.988	Substrate
2HK0	3VNL	TAG	1 st	0.357	Substrate
2HVM	1LLO	AMI	1 st	0.304	Specific inhibitor
2HY7	2Q6V	UDP	1 st	0.966	Substrate analog/reaction product
2HZR	2HZQ	STR	1 st	0.589	Natural ligand
2I4L	2I4M	PSD	1 st	0.644	Substrate
2IOB	3A2Y	TS5	1 st	0.882	Substrate
2IRU	2IRX	GTP	1 st	1.127	Substrate
2J71	2J72	GLC	10 th	1.18	Natural ligand
2J8N	3DR8	ACO	1 st	0.836	Cofactor
2JBR	2JBS	FMN	1 st	0.608	Substrate
2NWD	4XAD	3ZW	1 st	0.722	Substrate analog
2NXC	3CJT	SAM	1 st	0.374	Cofactor
2O9P	2Z1S	CTT	1 st	0.403	Substrate
2OAM	2OA1	FAD	1 st	0.587	Cofactor
2OPT	3B6A	ZCT	1 st	0.959	Specific inhibitor
2OU1	4JGX	PLM	1 st	2.203	Natural ligand
2OVE	2OVD	DAO	1 st	0.695	Specific ligand

2PAW	4HHY	15R	1 st	0.694	Specific inhibitor
2PFK	1PFK	ADP	1 st	1.001	Reaction product
2PKF	4OIG	AGS	1 st	0.471	Substrate analog
2PPN	1BL4	AP1	1 st	0.916	Specific ligand
2Q5R	2JGV	ADP	1 st	0.762	Reaction product
2Q6Z	1R3Q	ACP	1 st	0.796	Reaction product
2QBV	2W1A	TSA	1 st	1.193	Transition state analog
2QDK	1RXU	THM	1 st	0.595	Reaction product analog
2QEV	2QEO	LNR	1 st	0.412	Natural ligand
2QSU	2QTG	MTH	1 st	0.574	Substrate analog
2QVL	2QV7	ADP	1 st	0.518	Reaction product
2QYS	2QW8	NAP	1 st	0.432	Cofactor
2R60	2R68	SUP	1 st	0.24	Reaction product
2RG7	1AIJ	BPH	5 th	2.363	Endogenous ligand analog
2RJD	3P8H	P8H	1 st	0.248	Specific inhibitor
2SGA	2QAA	TYR	1 st	0.559	Reaction intermediate
2SIL	2SIM	DAN	1 st	0.179	Specific inhibitor
2TS1	3TS1	TYA	1 st	0.41	Reaction intermediate
2UYO	2UYQ	SAM	1 st	0.57	Cofactor
2V78	2VAR	ANP	1 st	0.494	Substrate
2VFB	2VFC	COA	1 st	0.686	Cofactor
2VFY	2VFK	AMP	1 st	0.904	Natural ligand
2VQ4	4BFN	GLC	2 nd	0.731	Natural ligand
2VUA	2VU9	GAL	1 st	0.197	Natural ligand
2WN4	2WN6	NDP	1 st	0.768	Cofactor
2WVH	3OE1	TDL	1 st	0.457	Reaction intermediate
2WZT	2WZM	NA7	1 st	0.928	Cofactor analog
2X5S	2X5Z	GDD	1 st	0.829	Reaction product
2YWB	1GPM	AMP	1 st	1.03	Product analog
2YXF	1LDS	NA	10 th	0.9	Non-specific ligand
2YYA	2YW2	ATP	1 st	0.833	Substrate
2YYT	2YYU	C5P	1 st	0.481	Product analog
2YZG	2YZN	ANP	1 st	0.944	Substrate analog
2ZBS	1S9Q	OHT	1 st	1.022	Natural ligand analog
2ZCG	2ZA1	OMP	1 st	0.767	Substrate
2ZCO	3ADZ	PS7	1 st	0.8	Reaction intermediate
2ZGL	2ZGM	LAT	1 st	0.398	Natural ligand analog
2ZHY	2ZHZ	ATP	1 st	0.707	Substrate
2ZJ8	2ZJA	ACP	1 st	0.717	Substrate analog
2ZTY	3ZZ9	G83	1 st	0.645	Specific inhibitor
3A0Y	3A0T	ADP	1 st	0.991	Reaction product
3A5Q	1CHW	HXC	1 st	0.849	Substrate analog
3AAP	3AAR	ANP	1 st	0.793	Specific inhibitor
3ADO	3ADP	NAI	1 st	0.632	Cofactor
3APP	1PPM	0P1	1 st	0.66	Specific inhibitor
3B3G	2Y1W	SFG	1 st	1.05	Cofactor analog
3BA1	3BAZ	NAP	1 st	0.583	Cofactor
3BLM	1GHP	PNM	1 st	0.481	Reaction intermediate
3BTV	3BTS	NAD	1 st	0.827	Specific ligand (activator)
3BUE	3CAG	ARG	1 st	0.855	Natural ligand
3BYL	3BYN	RAF	1 st	0.762	Substrate analog
3C2E	3C2V	PHT	1 st	0.725	Specific inhibitor

3C8N	3B4Y	F42	1 st	0.656	Cofactor
3CAF	1E0O	SGN	1 st	1.313	Specific ligand
3CB6	3CB5	B3P	30 th	0.735	Non-specific ligand
3CGZ	3CGY	RDC	1 st	0.849	Specific inhibitor
3COU	2XSQ	IMP	1 st	0.497	Reaction product
3CQ1					No significant results
3CRM	3CRQ	DPO	1 st	0.502	Reaction product
3CSR	3CSZ	NAG	1 st	0.249	Substrate analog
3CTB	11LH	SRL	1 st	0.816	Specific agonist
3D0O	3D4P	NAD	1 st	0.603	Cofactor
3D95	3CWK	REA	1 st	0.683	Endogenous ligand
3DRD	3DOD	PLP	1 st	0.954	Cofactor
3DRE	3JU6	ANP	1 st	1.295	Substrate analog
3DUL	3DUW	SAH	1 st	1.374	Cofactor
3E1S	2EWV	ADP	11 th	1.859	Substrate analog
3E5B	3POX	ICT	1 st	0.786	Substrate
3EIZ	3E1Y	POP	1 st	1.051	Substrate
3EK6	2BND	UDP	1 st	1.04	Reaction product
3ETF	3EFV	NAD	1 st	0.362	Cofactor
3EX9	3B4P	3B4	1 st	0.528	Substrate analog
3EXR	3EXS	5RP	1 st	0.574	Product analog
3FIL	3FIK	NAP	1 st	0.592	Cofactor
3F6F	3GH6	GSH	1 st	0.217	Substrate
3FTD	2ZBR	SFG	1 st	1.578	Cofactor analog
3FV6	3FWS	ANP	1 st	1.079	Natural ligand analog
3G1S	3G1F	2OM	1 st	0.785	Substrate analog
3GBT	3LL3	ATP	1 st	0.711	Substrate
3GD0	3GD9	BGC	1 st	0.527	Substrate/product analog
3GLK	3GID	S1A	1 st	0.483	Specific ligand
3GPG	3GPO	APR	1 st	0.58	Specific ligand
3GQH	3GQK	ATP	1 st	1.385	Specific ligand
3GSZ	3BR9	DEY	1 st	0.547	Specific inhibitor
3H2G	1GKK	SEP	2 nd	0.806	Specific ligand
3H38	3H39	ATP	1 st	0.883	Substrate
3H49	3IN1	ADP	1 st	0.624	Reaction product
3H71	2YA6	DAN	1 st	0.604	Specific inhibitor
3HBH	2DKV	MES	1 st	0.938	Substrate mimic
3HIS	3HIV	C2X	1 st	0.613	Transition state analog
3HJ4	3HIY	UTP	1 st	0.874	Substrate
3HNX	3HP8	SUC	1 st	0.546	Specific ligand
3I0C	3V0N	3GW	1 st	0.831	Specific inhibitor
3I3I	1QLL	TDA	1 st	0.688	Specific inhibitor
3I8S	3WIC	GNP	1 st	1.196	Substrate analog
3IK8	4TYO	39X	1 st	0.419	Specific inhibitor
3ILY					No significant results
3ITY	3ITV	PSJ	1 st	0.523	Substrate
3IUJ	3IVM	ZPR	1 st	0.955	Specific inhibitor
3JYL	3JYN	NDP	1 st	0.641	Cofactor
3K0M	4J5A	67Z	1 st	0.637	Specific inhibitor
3KAJ	3KAL	HGS	1 st	0.633	Reaction product
3KDH	3NJ0	PYV	1 st	0.368	Natural ligand mimic

3KJE	3KJG	ADP	1 st	1.123	Reaction product
3KJT	4IKM	TYI	1 st	0.866	Modified amino acid
3KP7	4EJW	SRY	1 st	0.969	Specific inhibitor
3KR9	3KU1	SAM	1 st	0.752	Cofactor
3KX7	3KVU	ACO	1 st	0.867	Cofactor
3LIG	3LIH	RAF	1 st	0.331	Substrate
3LOI	3LZZ	GDP	1 st	0.641	Specific ligand
3LXZ	3PR8	GSH	1 st	0.209	Substrate
3M4D	3M4E	BCD	1 st	0.428	Natural ligand
3N6J	1ECQ	DXG	1 st	0.636	Substrate analog
3NK6	3NK7	SAM	1 st	0.766	Cofactor
3PTE	1IKG	REX	1 st	0.49	Substrate fragment
3SSW	1ZT9	TRP	1 st	0.577	Specific ligand
3VZT	3VZU	ANP	1 st	0.381	Specific ligand
4AKE	3LR3	ADP	1 st	1.273	Reaction product
4PGM	1E59	VO3	1 st	1.009	Specific inhibitor
4PTI	1YLC	ABA	1 st	1.003	Modified amino acid

Table 2: Comparison of LIBRA-WA, SiteSeer and COACH on their respective ligand/binding site recognition performance, applied on a set of ligand-free proteins randomly chosen from the LigASite. Please note that only the first result provided by each respective system is reported. Wrong results (wrong target protein, ligand not biologically relevant or no results) are highlighted in bold font. Superscript notes for ligands correspond to the following descriptions: 1: Substrate analog; 2: Reaction product; 3: Covalent inhibitor; 4: Cofactor; 5: Specific inhibitor; 6: Substrate; 7: Reaction product analog; 8: Natural ligand analog; 9: Cofactor analog; 10: Reaction intermediate; 11: Natural ligand; 12: Non-specific ligand.

PDB code	Experimental function and LigA-Site ligand	Predicted function (PDB code) and ligand (ligand ID)		
		LIBRA-WA	SiteSeer	COACH server
1AK1	Ferrochelatase N-methylmesoporphyrin	Ferrochelatase (1C9E) N-methylmesoporphyrin (MP1) ¹	Ferrochelatase (1C9E) N-methylmesoporphyrin (MP1) ¹	Ferrochelatase (2HRE) Protoporphyrin IX (PP9) ⁶
1BK7	Ribonuclease MC1 Uridine-5'-monophosphate	Ribonuclease MC1 (1UCD) Uridine-5'-monophosphate (U5P) ²	Ribonuclease NW (1IYB) Guanosine-5'-monophosphate (5GP) ²	Ribonuclease NW (1IYB) Guanosine-5'-monophosphate (5GP) ²
1CEX	Cutinase Butyl-phosphinic acid 2,3-bis-butylcarbamoyloxy-propyl ester group	Cutinase (1OXM) Butyl-phosphinic acid 2,3-bis-butylcarbamoyloxy-propyl ester (TC4) ³	Cutinase (1XZM) N-undecanylphosphonate methyl ester group (DPE) ³	Cutinase (1XZM) N-undecanylphosphonate methyl ester group (DPE) ³
1CRW	D-Glyceraldehyde-3-phosphate dehydrogenase Nicotinamide-adenine-dinucleotide	Glyceraldehyde-3-phosphate dehydrogenase (2B4R) Nicotinamide-adenine-dinucleotide (NAD) ⁴	D-Glyceraldehyde-3-phosphate dehydrogenase (1DSS) Sulfate ion (SO4)¹²	Glyceraldehyde-3-phosphate dehydrogenase (4WNC) Nicotinamide-adenine-dinucleotide (NAD) ⁴
1EDQ	Chitinase A Allosamizoline	Chitinase A mutant W167A (1X6N) Allosamidin (AO3) ⁵	Chitinase A mutant W167A (1X6N) Allosamidin (AO3) ⁵	Chitinase 1 (3WL1) N-acetyl-D-glucosamine (NAG) ²
1EWZ	Beta-Lactamase OXA-10 (1R)-2-(1-carboxy-2-hydroxy-2-methyl-propyl)-5,5-dimethyl-thiazolidine-4-carboxylic acid	OXA-10 (2WG1) Open form - penicillin g (PNM) ⁵	OXA-10 (1FOF) Cobalt (II) ion (Co) ¹¹	Beta-lactamase OXA-24 8 (3FZC) (2S,3R)-4-(2-aminoethylcarbamoyloxy)-2-[(2-methanoylindolizin-3-yl)amino]-3-methyl-3-sulfinobutanoic acid (MXF) ⁵
1GOU	Ribonuclease Guanosine-3'-monophosphate	Ribonuclease bi (1GOY) Guanosine-3'-monophosphate (3GP) ¹	Ribonuclease bi (1GOY) Sulfate ion (SO4)¹²	Ribonuclease bi (1GOY) Guanosine 3'-monophosphate (3GP) ¹
1MR7	Streptogramin A Acetyltransferase Acetyl-coenzyme A	Vat(D) (1KK4) Acetyl coenzyme A (ACO) ⁶	Vat(D) (1KK4) Acetyl coenzyme A (ACO) ⁶	Hexapeptide-repeat containing-acetyltransferase (3NZ2) Acetyl-coenzyme A (ACO) ⁶
1MTZ	Proline iminopeptidase 3-amino-1-chloro-4-phenylbutanol-2-yl	Tricorn interacting factor F1 (1MU0) (2R,3S)-3-amino-1-chloro-4-phenylbutan-2-ol (PHK) ⁵	Tricorn F1-mutant e245q (1XRR) Proline (PRO) ¹	Gamma lactamase (1HL7) 3a,4,7,7a-tetrahydro-benzo [1,3] dioxol-2- one (BD1)¹²

1NDB	Carnitine acetyltransferase Coenzyme A	Carnitine acetyltransferase (2H3P) Acetyl coenzyme A (ACO) ⁶	No results	Carnitine acetyltransferase isoform 2 (1S5O) Carnitine (152) ⁶
1ROM	N-acylamino acid racemase N-2-acetyl-L-glutamine	N-acylamino acid racemase (1XPY) N 2 -acetyl-L-glutamine (NLQ) ⁶	Nacylamino acid racemase (2FKR) N 2 -acetyl-L-glutamine (NLQ) ⁶	Mandelate racemase/muonate lactonizing enzyme family pro- tein (3TOY) Calcium ion (Ca) ¹²
1RZV	Glycogen synthase 1 Adenosine-5'-diphosphate	Glycogen synthase (1RZU) Adenosine-5'-diphosphate (ADP) ⁷	Glycogen synthase (1RZU) Adenosine-5'-diphosphate (ADP) ⁷	Glycogen synthase (3GUH) 1,5-anhydrosorbitol (ASO) ¹
1SGZ	Beta-secretase Beta-secretase inhibitor	Beta-secretase 1 (3I25) N-[(2S,3S,5R)-1-(3,5- difluorophenoxy)-3-hydroxy- 5-(2-methoxyethoxy)-6- [[[(2S)-3-methyl-1-oxo-1- (phenylmethylamino)butan-2- yl]amino]-6-oxo-hexan-2-yl]-5- (methyl-methylsulfonyl-amino)-n'- [(1R)-1-phenylethyl]benzene-1,3- dicarboxamide (MV7) ⁵	Beta secretase (2OHQ) Glycerol (GOL) ¹²	Beta-secretase 1 (2FDP) N1-((2S,3S,5R)-3-amino- 6-(4-fluorophenylamino)- 5-methyl-6-oxo-1-phenylhexan-2- yl)-n3,n3- dipropylisophthalamide (FRP) ⁵
1TIB	Lipase Diundecyl phosphatidyl choline	Lipase (1GT6) Oleic acid (OLA) ²	Triglyceride lipase (4TGL) Diethyl phosphonate (DEP) ³	Lipase (1GT6) Oleic acid (OLA) ²
1TVN	Cellulase Cellobiose	Endoglucanase cel5a (4A3H) 2,4-dinitrophenyl-2-deoxy- 2-fluoro-beta-D-cellobioside (DCB) ¹	Endoglucanase cel5g (1TVP) 4-(2-hydroxyethyl)-1-piperazine ethanesulfonic acid (EPE) ¹²	Endoglucanase D (3NDZ) Cellotriose (CT3) ¹
1V0S	Phospholipase D 2-(butyryloxy)-1- [(tetrahydroxyphosphoranyl)oxy] methyl ethyl butyrate	Phospholipase D (2ZE9) (2r)-3-(phosphonoxy)propane- 1,2-diyl diheptanoate (PD7) ²	Phospholipase D (1U52) 1,2-didecanoyl- <i>sn</i> -glycero- 3-phosphoethanolamine (PEX) ⁶	Phospholipase D (1V0R) Tungstate (VI) ion (WO5) ⁵
1Y2Q	Threonyl-tRNA synthetase Serine-3'-aminoadenosine	Threonyl-tRNA synthetase (3PD2) Serine-3'-aminoadenosine (A3S) ¹	Threonyl-tRNA synthetase (2HL0) Serine-3'-aminoadenosine (A3S) ¹	Threonyl-tRNA synthetase (4RR6) Serine-3'-aminoadenosine (A3S) ¹
1ZUH	Shikimate kinase Shikimate-3-phosphate	Shikimate kinase (3MUF) Adenosine-5'-diphosphate (ADP) ²	Shikimate kinase (1ZUI) Trihydroxycyclohex-1- ene-1-carboxylic acid (SKM) ⁶	APS kinase domain of the PAPS synthetase 1 (2OFW) Adenosine-5'-phosphosulfate (ADX) ⁶
2CHS	Chorismate mutase Prephenic acid	Chorismate mutase (1COM) Prephenic acid (PRE) ²	Chorismate mutase (1COM) Prephenic acid (PRE) ²	Chorismate mutase (1COM) Prephenic acid (PRE) ²
2DPS	Leucyl/phenylalanyl-tRNA-protein transferase Puromycin	Leucyl/phenylalanyl-tRNA-protein transferase (2DPT) Puromycin (PUY) ¹	Leucyl/phenylalanyl-tRNA-protein transferase (2DPT) Puromycin (PUY) ¹	Leucyl/phenylalanyl-tRNA-protein transferase (2Z3O) Phenylalanine (PHE) ⁶
2GT2	GDP-mannose mannosyl hydrolase Guanosine-5'-diphosphate	GDP-mannose mannosyl hydrolase (2GT4) Guanosine-5'-diphosphate-alpha- d-mannose (GDD) ⁶	GDP-mannose mannosyl hydrolase (2I8T) Guanosine-5'-diphosphate-alpha- d-mannose (GDD) ⁶	GDP-mannose mannosyl hydrolase (2GT4) Guanosine-5'-diphosphate-alpha- d-mannose (GDD) ⁶
2O9P	Beta-glucosidase B Cellotetraose	Beta-glucosidase B (2Z1S) Beta-D-glucopyranosyl-(1- >4)-beta-D-glucopyranosyl-(1- >4)-beta-D-glucopyranosyl- (1->4)-beta-D-glucopyranose (CTT) ⁶	Beta-glucosidase B (2JIE) 2-deoxy-2-fluoro-alpha-D- glucopyranose (G2F) ⁷	Beta-glucosidase A (1OIM) Moranoline (NOJ) ⁵
2SIL	Sialidase 2-deoxy-2,3-dehydro-N-acetyl- neuraminic acid	Neuraminidase (2SIM) 2-deoxy-2,3-dehydro-N- acetyl-neuraminic acid (DAN) ⁵	Neuraminidase (1SIL) 2-deoxy-2,3-dehydro-N- acetyl-neuraminic acid (DAN) ⁵	Trans-sialidase (2AH2) 3-fluorosialic acid (FSI) ⁵
2V78	Fruktokinase Adenosine monophosphate	2-keto-3-deoxygluconate kinase (2VAR) Phosphoaminophosphonic acid-adenylate ester (ANP) ⁶	2-keto-3-deoxygluconate kinase (2DCN) Trihydroxy-5- [(phosphonatoxy)methyl] tetrahydrofuran-2-carboxylic acid (CKP) ⁷	Ketohexokinase (3QAI) N 8 -(cyclopropylmethyl)-2- (2,6-diazaspiro[3.3]hept-2-yl)- n 4 -[2-(methylsulfanyl)phenyl] pyrimido[5,4-d]pyrimidine-4,8- diamine (XNN) ⁵
2VQ4	Glucoamylase A Glucose	Acyl carrier protein (3EJB) Heptyl 1-thiohexopyranoside (HTG) ⁸	No results	Glucoamylase A (2V8L) Alpha-D-glucose (GLC) ¹¹

2WZT	Aldo-ketoreductase (2R,3R,4R,5R)-5-(6-amino-9H-purin-9-yl)-3-hydroxy-4-(phosphonoxy)-tetrahydrofuran-2-yl]-methyl [(2R,3S,4S)-3,4-dihydroxytetrahydrofuran-2-yl]-methyl diphosphate	Aldo-keto reductase (2WZM) [(2R,3R,4R,5R)-5-(6-amino-9H-purin-9-yl)-3-hydroxy-4-(phosphonoxy)-tetrahydrofuran-2-yl]-methyl [(2R,3S,4S)-3,4-dihydroxytetrahydrofuran-2-yl]-methyl dihydrogen diphosphate (NA7) ⁹	Aldose reductase (1AZ2) NADP nicotinamide-adenine-dinucleotide phosphate (NAP) ⁴	Yvgn protein (3D3F) NADPH (NDP) ⁴
3BLM	Beta-lactamase N-(1-carboxy-2-hydroxy-4-oxo-butyl)-N-(3-oxo-cispropenyl)-amine	Beta-lactamase (1GHP) Open form - penicillin g (PNM) ¹⁰	Beta-lactamase (1BLC) N-(2-hydroxy-4-oxo-butyl)-N-(3-oxo-transpropenyl)amine (TEM)	Beta-lactamase (4XUZ) (3R,6S)-2-hydroxy-3-[(thiophen-2-ylacetyl)amino]-1,2-oxaborinan-6-ylacetic acid (4D6) ⁵
3D0O	L-lactate dehydrogenase 1 Nicotinamide-adenine-dinucleotide	Lactate dehydrogenase (3D4P) Nicotinamide-adenine-dinucleotide (NAD) ⁴	Lactate dehydrogenase (1LDN) Oxamic acid (OXM) ⁵	Malate dehydrogenase (1UXJ) Nicotinamide-adenine-dinucleotide (NAD) ⁴
3GSZ	RNA-directed RNA polymerase 2-(3-bromophenyl)-6-[(2-hydroxymethyl)-amino]-1H-benzo[de]isoquinoline-1,3(2H)-dione	RNA polymerase (3BR9) (2r)-2-(3-[5-hydroxy-2-(3-methylbutyl)-3-oxo-6-thiophen-2-yl-2,3-dihydropyridazin-4-yl]-1,1-dioxido-2h-1,2,4-benzothiadiazin-7-yloxy)propanamide (DEY) ⁵	RNA polymerase (1YVX) 3-[isopropyl(4-methylbenzoyl)amino]-5-phenylthiophene-2-carboxylic acid (IPC) ⁵	RNA-directed RNA polymerase (3CSO) (11S)-10-acetyl-11-[4-(benzyloxy)-3-chlorophenyl]-3,3-dimethyl-2,3,4,5,10,11-hexahydro-1h-dibenzo[b,e][1,4]diazepin-1-one (XNI) ⁵
3I0C	ABO glycosyltransferase D-galactose	Fucosylgalactoside alpha N-acetylgalactosaminyltransferase (3V0N) 5-(5-formylthiophen-2-yl)uridine-5'(2-(acetylamino)-2-deoxy-alpha-D-galactosyl)-diphosphate (3GW) ⁵	Galactosyltransferase (1ZIZ) Beta-D-galactose (GAL) ⁶	Histo-blood group abo system transferase (5C1H) Octyl 3-deoxy-2-O-(6-deoxy-alpha-L-galactopyranosyl)-beta-D-xylo-hexopyranoside (DA8) ⁵

Table 3: COACH's ligand/binding site recognition performance on the LigaSite non-redundant dataset containing 373 apo-proteins for which a corresponding holo structure is available (Desailly *et al.*, 2008). APO and HOLO Protein ID are the PDB codes of the corresponding three-dimensional structures. Ligand ID is the ligand name abbreviation used in the Protein Data Bank. Ligand type indicates the nature of the ligand: organic (O) or ion (I).

APO Protein ID	HOLO Protein ID	Ligand ID	Rank	Ligand details	Ligand type
180L	3GUM	PXY	1 st	Substrate analog	O
1A4U	2BD0	NAP	1 st	Cofactor analog	O
1ADE	1GIN	GDP	1 st	Cofactor	O
1AK1	2HRE	PP9	1 st	Substrate	O
1AKZ	3EUG	GOL	1 st	Natural ligand	O
1ARB	3E0N	ARM	1 st	Specific inhibitor	O
1ARL	3WC7	EF1	1 st	Specific inhibitor	O
1B8E	1GX9	REA	1 st	Specific ligand	O
1B8P	4PLT	NAI	1 st	Cofactor	O
1BD9	1B7A	OPE	1 st	Natural ligand analog	O
1BK7	1IYB	5GP	1 st	Reaction product	O
1BKZ	4BLJ	70B	1 st	Natural ligand analog	O
1BQC	5D9M	GLC	1 st	Substrate	O
1BYI	4WOP	CTP	1 st	substrate	O
1C48	1CQF	GLA	1 st	Natural ligand	O
1C5H	1H4G	FXP	1 st	Specific inhibitor	O
1CEO	1CEN	BGC	1 st	Substrate analog	O
1CEX	1XZM	DPE	1 st	Covalent inhibitor	O
1CPJ	2XU1	424	1 st	Specific inhibitor	O
1CRW	4WNC	NAD	1 st	Cofactor	O
1CWY	1ESW	ACR	1 st	Specific inhibitor	O
1DCO	1DCP	HBI	1 st	Cofactor analog	O
1DHN	2NM2	NEU	1 st	Substrate analog	O
1DQ0	3U4X	XMM	1 st	Natural ligand analog	O
1DUP	1SEH	UMP	1 st	Reaction product	O
1E4F	4PL7	ATP	1 st	Substrate	O
1E5L	3ABI	NAD	1 st	Cofactor	O
1E8Y	3QK0	QK0	1 st	Specific inhibitor	O
1EDQ	3WL1	NAG	1 st	Reaction product	O
1EPA	1EPB	REA	1 st	Natural ligand	O
1EWZ	3FZC	MXF	1 st	Inhibitor	O
1EY0	1A2T	THP	1 st	Specific inhibitor	O
1EZI	3K8D	CTP	1 st	Substrate	O
1F14	4DYD	NAD	1 st	Cofactor	O
1F1S	1OJM	GCD	1 st	Reaction product	O
1F2V	1I1H	COJ	1 st	Reaction product	O
1F41	4IK7	IMN	1 st	Specific ligand	O
1F5Z	4OE7	GXP	1 st	Product analog	O
1FCQ	1FCV	NAG	1 st	Substrate fragment	O
1FGB	1EEI	GAA	1 st	Specific inhibitor	O
1FO9	2AM3	UPG	1 st	Substrate analog	O
1FSF	1HOR	AGP	1 st	Specific inhibitor	O
1FTF	2WDS	COA	1 st	Substrate	O
1FTR	2FHJ	MFN	1 st	Cofactor	O
1FWL	1H73	ANP	1 st	Substrate analog	O

1G40	1Y8E	SVR	1 st	Specific inhibitor	O
1G4E	1G4T	FTP	1 st	Reaction product	O
1G95	1HM9	UD1	1 st	Reaction product	O
1GBS	4CFP	AMV	1 st	Substrate analog	O
1GCE	3O88	BSH	1 st	Specific inhibitor	O
1GFS	3ICP	NAD	1 st	Cofactor	O
1GOU	1GOY	3GP	1 st	Substrate analog	O
1GSH	1GSA	ADP	1 st	Reaction product	O
1GWK	1GWL	BMA	1 st	Natural ligand	O
1GY0	1OG1	TAD	1 st	Substrate analog	O
1HK9	4Y91	NUC	1 st	Natural ligand	O
1HKA	1RAO	HH2	1 st	Product analog	O
1HM5	3Q7I	6GP	1 st	Reaction product	O
1HNK	1HND	COA	1 st	Reaction product	O
1HO1	1M5W	DXP	3 rd	Substrate	O
1I7N	1I7L	ATP	1 st	Endogenous ligand	O
1IAD	1QJJ	Peptide	1 st	Inhibitor	O
1ILV	2V4O	PO4	1 st	Reaction product	I
1INL	2O0L	S4M	1 st	Substrate analog	O
1J85	4PZK	SAH	1 st	Cofactor	O
1J8S	1J8R	GAL	1 st	Natural ligand	O
1JCF	4PKG	ATP	1 st	Substrate	O
1JKS	3NAY	MP6	1 st	Inhibitor	O
1JXO	3WP0	Peptide	1 st	Specific ligand	O
1JYK	4ZDQ	CTP	2 nd	Substrate	O
1K0M	1EV9	GST	1 st	Substrate analog	O
1K3O	3VPQ	GSH	1 st	Substrate	O
1K6A	5D4Y	XYP	1 st	Substrate	O
1KAM	1K4M	NAD	1 st	Substrate	O
1KF5	1JVU	C2P	1 st	Reaction product	O
1KHD	3R88	PRP	1 st	Substrate	O
1KN9	1B12	1PN	1 st	Specific inhibitor	O
1KPA	1RZY	5AS	1 st	Substrate analog	O
1KWB	1EIR	BPY	1 st	Substrate	O
1L7D	1L7E	NAI	1 st	Reaction product	O
1LBV	1NV6	PI	1 st	Reaction product	I
1LCI	2D1S	SLU	1 st	Reaction intermediate analog	O
1LF4	3APR	Peptide	1 st	Inhibitor	O
1LTU	1KW0	BH4	1 st	Cofactor	O
1M1Z	1JGT	APC	1 st	Substrate analog	O
1MKB	4KEH	1R3	1 st	Substrate analog	O
1MMI	1D1E	Peptide	1 st	Specific inhibitor	O
1MR7	3NZ2	ACO	1 st	Substrate	O
1MTZ	1XQX	PCS	2 nd	Specific inhibitor	O
1MWK	3KVG	ANP	1 st	Substrate analog	O
1MZL	1UVC	STE	1 st	Natural ligand	O
1N05	1N07	FMN	1 st	Reaction product	O
1NDB	1S5O	152	1 st	Substrate	O
1NON	4P83	U5P	1 st	Specific ligand	O
1NXM	2IXC	TRH	1 st	Substrate analog	O
1O24	3HZG	FAD	1 st	Cofactor	O
1OEM	2CNH	IZB	1 st	Specific inhibitor	O

1OFP	4UMB	0V5	1 st	Specific inhibitor	O
1OGH	3TPS	DUP	1 st	Substrate analog	O
1OGL	1CJE	DUN	1 st	Substrate analog	O
1OGM	1OGO	GLC	1 st	Reaction product	O
1OJQ	1GZF	NAD	1 st	Cofactor	O
1OLZ	4GZ8	CA	1 st	Specific ligand	I
1OOI	2GTE	VA	1 st	Natural ligand	O
1OPY	2INX	FFP	2 nd	Transition state analog	O
1OXT	1OXU	ADP	1 st	Reaction product	O
1P1X	1UB3	HPD	1 st	Reaction product	O
1P5H	2GCE	SFC	1 st	Substrate analog	O
1P74	3PGJ	SKM	1 st	Substrate	O
1PDB	3CL9	MTX	1 st	Inhibitor	O
1PNG	1PNF	NDG	1 st	Substrate analog	O
1Q52	4I42	IHA	1 st	Product analog	O
1Q7M	2YCK	THG	1 st	Substrate	O
1QCZ	2ATE	NIA	1 st	Substrate analog	O
1QID	5EHN	5NZ	1 st	Specific inhibitor	O
1QTO	5CJB	52G	1 st	Specific ligand	O
1QTR	1XRR	Pro	10 th	Substrate	O
1R0M	1SJC	SMG	2 nd	Substrate	O
1R12	4F46	DVN	1 st	Substrate analog	O
1R29	1R2B	Peptide	1 st	Natural ligand	O
1R15	1R14	SAM	1 st	Substrate	O
1RIQ	2ZZG	A5A	1 st	Substrate analog	O
1RJ1	3OIB	IOD	2 nd	Non-specific ligand	I
1RK M	1B0H	Peptide	1 st	Specific ligand	O
1RZV	3GUH	ASO	1 st	Substrate analog	O
1S2L	1S2G	3D1	1 st	Substrate	O
1S7K	4LXY	ACO	1 st	Substrate	O
1SGK	1DDT	APU	1 st	Substrate analog	O
1SGZ	2FDP	FRP	1 st	Inhibitor	O
1SJY	2A8P	MN	1 st	Cofactor	I
1SNT	1F25	DAN	1 st	Specific inhibitor	O
1SQG	3M6V	SAM	1 st	COFACTOR	O
1SUL	1Z22	GDP	1 st	Specific ligand	O
1SWH	4CPH	LH4	1 st	Specific ligand analog	O
1TGN	4Z6A	0Z6	1 st	Specific inhibitor	O
1THV	4TVT	ASC	3 rd	Natural ligand	I
1TIB	1GT6	OLA	1 st	Reaction product	O
1TJE	1TKE	SER	1 st	Substrate analog	O
1TJV	2E9F	ARG	1 st	Reaction product	O
1TVN	3NDZ	CT3	1 st	Substrate analog	O
1TW0	1TXC	2AN	1 st	Non-specific ligand	O
1TYF	4U0G	ZIL	1 st	Substrate analog	O
1TYV	1TYU	TYV	2 nd	Natural ligand	O
1TZV	3R2C	NUC	1 st	Natural ligand	O
1U0T	1Z0U	NAP	1 st	Reaction product	O
1U7U	1U7W	CTP	1 st	Substrate	O
1UAJ	4YVK	SFG	1 st	Substrate analog	O
1UBI	2D3G	Peptide	1 st	Specific ligand	O

1UF4	1UF5	CDT	1 st	Substrate	O
1ULU	1VL8	NAP	1 st	Cofactor	O
1UMF	1QXO	FMN	1 st	Cofactor	O
1UXZ	1UYX	BGC	1 st	Specific ligand	O
1UYL	4YKQ	4EO	1 st	Inhibitor	O
1V0S	1V0R	WO5	1 st	Inhibitor	I
1V6Z	2CX8	SAH	1 st	Cofactor	O
1V77				No significant results	
1VFJ	2XUL	ATP	1 st	Specific ligand	O
1VIC	2XWL	CTP	1 st	Substrate	O
1VJU	3DWR	OPA	1 st	Substrate analog	O
1VPN	3BWR	SIA	1 st	Specific ligand	O
1W9A	2AQ6	PLP	1 st	Reaction product	O
1WJG	3HGM	ATP	1 st	Specific ligand	O
1WNY	1WK8	VMS	1 st	Substrate analog	O
1WOS	1WOO	THG	1 st	Substrate	O
1WS9	2JIF	FAD	1 st	Cofactor	O
1WTJ	1V9N	NDP	1 st	Cofactor	O
1WXF	2PZ8	APC	1 st	Substrate analog	O
1X56	3A5Y	KAA	1 st	Substrate analog	O
1X7O	1X7P	SAM	1 st	Cofactor	O
1X8F	3UND	PEP	1 st	Substrate	O
1XIX	1P4N	Peptide	1 st	Substrate	O
1XK7	1T3Z	CAO	1 st	Substrate analog	O
1XO6	3TV5	RCP	1 st	Inhibitor	O
1XQO	1XQP	8HG	1 st	Substrate analog	O
1XW2	1WU5	XYP	2 nd	Reaction product	O
1Y2Q	4RR6	A3S	1 st	Substrate analog	O
1Y2T	4Z2S	NDG	1 st	Endogenous ligand analog	O
1YBT	4WP8	ZDA	1 st	inhibitor	O
1YVY	2GMV	PEP	1 st	Reaction product	O
1Z7G	1HMP	5GP	1 st	Reaction product	O
1ZAH	3TU9	5MM	1 st	Specific inhibitor	O
1ZCU	3T7O	UPG	1 st	Substrate	O
1ZNW	1ZNX	5GP	1 st	Substrate	O
1ZTY	1ZU0	CBS	7 th	Natural ligand	O
1ZUH	2IYR	SKM	2 nd	Substrate	O
2A6Z	1N47	TNR	1 st	Specific ligand	O
2A8F	2AIB	ERG	1 st	Specific ligand	O
2AD1	1LS6	A3P	1 st	Reaction product	O
2AHF	2AHG	UCD	1 st	Substrate	O
2AHU	2AHV	COA	1 st	Cofactor	O
2AMJ	4FGJ	FAD	1 st	Cofactor	O
2B0J	3F46	I2C	1 st	Cofactor	O
2B6P	2EVU	GOL	1 st	Non-specific ligand	O
2B78	3VSE	SAH	1 st	Cofactor	O
2B98	2C9D	PHR	1 st	Inhibitor	O
2BGT	1IXY	UDP	1 st	Reaction product	O
2BJW	4LZZ	08T	1 st	Substrate analog	O
2BOE	2BOG	SGC	1 st	inhibitor	O
2C61	3OAA	ANP	1 st	Reaction product analog	O
2C7I	3A7R	LAQ	1 st	Reaction intermediate	O

2CAR	3S86	IMP	1 st	Reaction product	O
2CHS	1COM	PRE	1 st	Reaction product	O
2CI3	1LXY	CYR	1 st	Reaction product	O
2CWK	1F3F	D4T	1 st	Substrate analog	O
2CX5	2Z0X	5CA	1 st	Substrate analog	O
2D59	4XYL	COA	1 st	Substrate	O
2DHQ	2BT4	CA2	1 st	Specific inhibitor	O
2DJ6	3QNA	BIO	1 st	Substrate	O
2DKA	2DKD	PO4	1 st	Substrate	I
2DPS	2Z3O	PHE	1 st	Substrate	O
2DQW	3TZF	HH2	1 st	Substrate analog	O
2E0C	4AJ3	NAP	1 st	Substrate	O
2E0K	2E0N	SAH	1 st	Cofactor	O
2E10	2DTI	BT5	1 st	Reaction intermediate	O
2E1V	2E1T	MLC	1 st	Substrate	O
2E3S	2E3O	16C	1 st	Substrate	O
2ECR	2R6V	FMN	1 st	Substrate	O
2EX0	2ZWI	C5P	1 st	Substrate analog	O
2F82	5HWQ	CAA	1 st	Substrate	O
2F9T	5B8H	PAU	1 st	Substrate	O
2FK7	1KPG	SAH	1 st	Cofactor	O
2FP8	2V91	S55	2 nd	Substrate	O
2FSF	2FSH	ANP	1 st	Substrate analog	O
2G67	2QTC	TDK	1 st	Reaction intermediate analog	O
2G95	2H3D	NMN	1 st	Reaction product	O
2GFV	2BYZ	DAO	1 st	Substrate analog	O
2GG4	2GGA	S3P	1 st	Substrate	O
2GQV	2P4T	NAP	1 st	Cofactor	O
2GSF	4HYH	1AM	1 st	Specific inhibitor	O
2GT2	2GT4	GDD	1 st	Substrate	O
2GUB	1S5N	XYL	1 st	Inhibitor	O
2GWX	3V18	13M	4 th	Natural ligand analog	O
2GYY	1DSS	NAD	1 st	Cofactor	O
2H2Z	2A5I	AZP	1 st	Inhibitor	O
2HBJ	1ZBH	MG	1 st	Cofactor	I
2HIV	2HIX	ATP	1 st	Substrate	O
2HK0	2HK1	FUD	1 st	Substrate	O
2HVM	1FFR	NAG	1 st	Substrate	O
2HY7	2Q6V	UDP	1 st	Substrate analog/reaction product	O
2HZR	2HZQ	STR	1 st	Natural ligand	O
2I4L	2J3L	P5A	1 st	Reaction intermediate analog	O
2IOB	2IO9	GSH	1 st	Substrate	O
2IRU	3PKY	UTP	1 st	Substrate	O
2J71	2J72	GLC	1 st	Natural ligand	O
2J8N	2CY2	ACO	1 st	Cofactor	O
2JBR	3PFD	FDA	1 st	Cofactor	O
2NWD	1BB5	CTO	1 st	Inhibitor	O
2NXC	3CJT	SAM	1 st	Cofactor	O
2O9P	1OIM	NOJ	1 st	Inhibitor	O
2OAM	3E1T	FAD	1 st	Cofactor	O
2OPT	3B6A	ZCT	1 st	Specific inhibitor	O
2OU1	1L6L	BOG	10 th	Natural ligand analog	O

2OVE	2OVD	DAO	1 st	Specific ligand	O
2PAW	4ZZZ	FSU	1 st	Specific inhibitor	O
2PFK	2F48	FBP	1 st	Reaction product	O
2PKF	4O1G	AGS	1 st	Substrate analog	O
2PPN	1BL4	AP1	1 st	Specific ligand	O
2Q5R	2JG1	ANP	1 st	Cofactor analog	O
2Q6Z	1R3Q	ICP	1 st	Reaction product	O
2QBV	5CKX	TSA	1 st	Transition state analog	O
2QDK	1RXU	THM	1 st	Substrate analog	O
2QEV	2QEH	SRO	1 st	Specific ligand	O
2QSU	3DP9	BIG	1 st	Substrate analog	O
2QVL	2QV7	ADP	1 st	Reaction product	O
2QYS	3C1O	NAP	1 st	Cofactor	O
2R60	3S27	FRU	1 st	Substrate	O
2RG7	2R7A	HEM	1 st	Specific ligand	O
2RJD	3H6Z	Peptide	3 rd	Specific ligand	O
2SGA	3NCL	CCZ	1 st	Specific inhibitor	O
2SIL	2AH2	FSI	1 st	Inhibitor	O
2TS1	3TZL	TRP	1 st	Substrate analog	O
2UYO	1RJD	SAM	1 st	Cofactor	O
2V78	3QAI	XNN	1 st	Inhibitor	O
2VFB	4B55	P18	1 st	Specific inhibitor	O
2VFY	2VFK	AMP	1 st	Specific ligand	O
2VQ4	2V8L	GLC	1 st	Natural ligand	O
2VUA	3RSJ	GAL	1 st	Specific ligand	O
2WN4	1GIR	NDP	1 st	Substrate	O
2WVH	2VBI	TPP	1 st	Cofactor	O
2WZT	3D3F	NDP	1 st	Cofactor	O
2X5S	2PA4	UPG	1 st	Product analog	O
2YWB	2YWB	AMP	1 st	Product analog	O
2YXF	4RA3	TFX	2 nd	Non-specific ligand	O
2YYA	3RV3	ADP	1 st	Reaction product	O
2YYT	4MUZ	BMP	1 st	Specific inhibitor	O
2YZG	1EZ1	ANP	1 st	Substrate analog	O
2ZBS	5DKS	5C6	1 st	Specific ligand	O
2ZCG	4MUZ	BMP	1 st	Specific inhibitor	O
2ZCO	3WEH	PS7	1 st	Reaction intermediate	O
2ZGL	2R0H	CTO	1 st	Natural ligand	O
2ZHY	3KE5	ATP	1 st	Substrate	O
2ZJ8	4F93	ATP	1 st	Substrate	O
2ZTY	3ZZD	G85	1 st	Specific inhibitor	O
3A0Y	3TZ5	ADP	1 st	Reaction product	O
3A5Q	2D52	COA	1 st	Substrate	O
3AAP	3CJA	ANP	1 st	Specific inhibitor	O
3ADO	4OM8	NAD	1 st	Cofactor	O
3APP	3K5C	OBI	1 st	Specific inhibitor	O
3B3G	2FYT	SAH	1 st	Cofactor	O
3BA1	4NJO	NAD	1 st	Cofactor analog	O
3BLM	4XUZ	4D6	1 st	inhibitor	O
3BTV	3NTQ	NAD	1 st	Specific ligand	O
3BUE	2ZfZ	ARG	1 st	Natural ligand	O
3BYL	1W2T	SUC	1 st	Substrate	O

3C2E	1QPQ	NTM	1 st	Substrate	O
3C8N	3B4Y	F42	1 st	Cofactor	O
3CAF	3CU1	SCR	2 nd	Specific ligand	O
3CB6				No significant results	
3CGZ	4PL9	ADP	1 st	Reaction product	O
3COU	2A8S	GTP	2 nd	Substrate analog	O
3CQ1	3CQ3	MG	1 st	Non-specific ligand	I
3CRM	2ZE7	DST	2 nd	Substrate analog	O
3CSR	3CT5	NAG	1 st	Substrate analog	O
3CTB	4OK1	198	1 st	Specific agonist	O
3D0O	1UXJ	NAD	1 st	Cofactor	O
3D95	1FE3	OLA	1 st	Ligand analog	O
3DRD	4ATP	PLP	1 st	Cofactor	O
3DRE	4V7N	ADP	1 st	Reaction product	O
3DUL	5FHQ	SAM	1 st	Cofactor	O
3E1S	4C30	ANP	1 st	Substrate analog	O
3E5B	2HJP	PPR	1 st	Substrate analog	O
3EIZ	2AU9	MG	1 st	Specific ligand	I
3EK6	2J4L	UTP	1 st	Specific inhibitor	O
3ETF	4I8P	NAD	1 st	Cofactor	O
3EX9	3JUM	AOD	2 nd	Reaction intermediate analog	O
3EXR	1XBZ	LX1	1 st	Reaction product	O
3F1L	1VL8	NAP	1 st	Cofactor	O
3F6F	2IMI	GSH	1 st	Substrate	O
3FTD	4GC9	SAM	1 st	Cofactor	O
3FV6	4QFG	AMP	1 st	Natural ligand analog	O
3G1S	3VE7	BMP	1 st	Specific inhibitor	O
3GBT	1BWF	GOL	1 st	Substrate analog	O
3GD0	3GD9	BCG	1 st	Substrate/product analog	O
3GLK	3OUZ	ADP	1 st	Reaction product	O
3GPG	3GQO	APR	1 st	Specific ligand	O
3GQH	3SUC	ATP	1 st	Specific ligand	O
3GSZ	3CSO	XNI	1 st	Inhibitor	O
3H2G	2XLC	DEP	1 st	Specific inhibitor	O
3H38	1MIY	CTP	1 st	Substrate	O
3H49	3QAI	XNN	1 st	Specific inhibitor	O
3H71	2YA7	ZMR	1 st	Specific inhibitor	O
3HBH	3HBD	MXE	1 st	Substrate mimic	O
3HIS	1MRG	ADN	1 st	Substrate analog	O
3HJ4	2Q0D	ATP	1 st	Substrate analog	O
3HNX	3HP8	SUC	1 st	Specific ligand	O
3I0C	5C1H	DA8	1 st	Inhibitor	O
3I3I	1KQU	BR4	1 st	Substrate analog	O
3I8S	4R98	GNH	1 st	Substrate analog	O
3IK8	3IKD	J9Z	1 st	Specific inhibitor	O
3ILY	3ROF	Peptide	8 th	Substrate mimic	O
3ITY	3ITL	LRH	1 st	Reaction product	O
3IUJ	1O6F	PRO	1 st	Substrate analog	O
3JYL	1H2B	NAJ	1 st	Cofactor	O
3K0M	2POY	Peptide	1 st	Specific ligand	O
3KAJ	3KAL	HGS	1 st	Reaction product	O
3KDH	3NMV	PYV	1 st	Natural ligand analog	O

3KJE	1G3R	ACP	1 st	Substrate analog	O
3KJT	5HZ7	MLR	1 st	Natural ligand analog	O
3KP7	4EJW	SRY	1 st	Specific inhibitor	O
3KR9	3KU1	SAM	1 st	Cofactor	O
3KX7	3KVU	ACO	2 nd	Substrate analog	O
3LIG	3PIJ	FRU	1 st	Substrate mimic	O
3LOI	3LZZ	GDP	2 nd	Specific ligand	O
3LXZ	4IS0	GDS	1 st	Substrate analog	O
3M4D	3M4E	BCD	2 nd	Natural ligand	O
3N6J	1ECQ	MG	1 st	Specific ligand	I
3NK6	3NK7	SAM	1 st	Cofactor	O
3PTE	3O88	BSH	1 st	Specific inhibitor	O
3SSW	1JHG	TRP	1 st	Specific ligand	O
3VZT	3A2S	SUC	4 th	Specific ligand	O
4AKE	4EDH	ADP	1 st	Reaction Product	O
4PGM	2IKQ	PO4	1 st	Reaction product	O
4PTI	3LDJ	SCR	2 nd	Specific ligand analog	O

Table 4: Table 4: LIBRA-WA's ligand/binding site recognition performance excluding from the ligand binding sites database the holo proteins present in the LigaSite non-redundant dataset (Dessailly *et al.*, 2008). APO and HOLO Protein ID are the PDB codes of the corresponding three-dimensional structures. Ligand ID is the ligand name abbreviation used in the Protein Data Bank.

APO Protein ID	HOLO Protein ID	Ligand ID	Rank	Ligand details
180L	186L	N4B	1 st	Specific ligand analog
1A4U	1MG5	NAI	1 st	Cofactor
1ADE	2V40	GDP	1 st	Substrate
1AK1	1C9E	MP1	1 st	Substrate analog
1AKZ	2C53	DUR	5 th	Substrate analog
1ARB	4NSV	2OY	1 st	Specific inhibitor
1ARL	3FVL	BHK	1 st	Specific inhibitor
1B8E	3NQ3	DKA	2 nd	Substrate analog
1B8P	1BMD	NAD	1 st	Cofactor
1BD9	2B7A	OPE	1 st	Natural ligand analog
1BK7	1UCA	U2P	1 st	Reaction product
1BKZ	4UW6	VV7	1 st	Natural ligand
1BQC	2MAN	MAN	1 st	Reaction product
1BYI	3QXS	NAP	3 rd	Substrate analog
1C48	1BOS	GLA	1 st	Natural ligand
1C5H	2B46	XYP	1 st	Reaction product
1CEO	3AOF	BMA	1 st	Substrate
1CEX	1XZL	HEE	1 st	Covalent inhibitor
1CPJ	2DC7	042	1 st	Covalent inhibitor
1CRW	2B4R	NAD	1 st	Cofactor
1CWY	2OWC	ACR	1 st	Specific inhibitor
1DCO	2V6T	H2B	3 rd	Substrate-like ligand
1DHN	1RRY	204	1 st	Inhibitor
1DQ0	4P9W	R3M	1 st	Specific ligand analog
1DUP	1SYL	DUT	1 st	Substrate analog
1E4F	4A2B	AGS	1 st	Substrate analog

1E5L	2QG4	NAD	135 th	Cofactor
1E8Y	3L13	JZW	1 st	Specific inhibitor
1EDQ	1X6N	AO3	1 st	Specific inhibitor
1EPA	2RA6	ETY	1 st	Ligand analog
1EWZ	2WGI	PNM	1 st	Specific inhibitor
1EY0	1A2T	THP	1 st	Specific inhibitor
1EZI	1QWJ	NCC	1 st	Reaction product
1F14	1F0Y	NAI	1 st	Cofactor
1F1S	2BRP	SIE	1 st	Specific inhibitor
1F2V	4AU1	P8X	1 st	Reaction intermediate
1F41	1DVS	STL	1 st	Specific inhibitor
1F5Z	4IMF	SI3	1 st	Substrate
1FCQ	2ATM	MES	1 st	Substrate analog
1FGB	1JQY	A32	1 st	Specific inhibitor
1FO9	2APC	UDM	1 st	Substrate analog
1FSF	1NE7	AGP	1 st	Specific inhibitor
1FTF	3HYK	A3P	1 st	Reaction product
1FTR				No significant results
1FWL	3BY5	NAI	2 nd	Substrate analog
1G40	1Y8E	SVR	9 th	Competitive inhibitor
1G4E	1G4S	TPS	1 st	Reaction product
1G95	2W0W	LZS	1 st	Inhibitor
1GBS	154L	NAG	2 nd	Substrate analog
1GCE	1LLB	PCN	1 st	Inhibitor
1GFS	1E6U	NAP	1 st	Reaction product
1GOU	1GMP	2GP	1 st	Substrate analog
1GSH	3R5X	ATP	1 st	Cofactor
1GWK	1W8U	BMA	1 st	Natural ligand
1GY0	1OG4	NAI	1 st	Cofactor
1HK9	3QO3	ATP	1 st	Natural ligand
1HKA	3ILJ	APC	2 nd	Inhibitor
1HM5	4QFH	G6P	1 st	Reaction product
1HNK	4NHD	COEA	1 st	Product
1HO1	3F4N	PXP	1 st	Reaction product
1I7N	1AUX	AGS	1 st	Ligand analog
1IAD	1QJJ	HOA	1 st	Inhibitor
1ILV	2E6B	WO4	5 th	Specific inhibitor
1INL	2O0L	S4M	1 st	Substrate analog
1J85	4JAL	SAH	1 st	Cofactor
1J8S				No significant results
1JCF	4CZJ	ANP	1 st	Substrate analog
1JKS	3ZXT	ACP	1 st	Substrate analog
1JXO				No significant results
1JYK	2O63	UDP	20 th	Substrate analog
1K0M	4K0N	MAL	38 th	Natural ligand mimic
1K3O	4HJ2	LZ6	1 st	Substrate analog
1K6A	1B30	XYP	1 st	Reaction product
1KAM	1YUM	NCN	1 st	Cofactor
1KF5	1R5C	CPA	1 st	Substrate analog
1KHD	1ZXY	PRP	1 st	Substrate
1KN9	1B12	IPN	1 st	Specific inhibitor

1KPA	3RHN	5GP	1 st	Substrate
1KWB	1EIR	BPY	1 st	Substrate
1L7D	1NM5	NAD	1 st	Substrate
1LBV	1LBY	F6P	1 st	Product
1LC1	1BA3	MBR	1 st	Inhibitor
1LF4	1LF2	R37	1 st	Inhibitor
1LTU	1DMW	HBI	1 st	Cofactor
1M1Z	3SEZ	ATP	1 st	Substrate
1MKB	4KEH	1r3	1 st	Substrate analog
1MMI	3QSB	743	1 st	Specific inhibitor
1MR7	4HUR	ACO	1 st	Substrate
1MTZ	1XRQ	LEU	1 st	Substrate
1MWK	4A61	ANP	1 st	Substrate analog
1MZL	1UVC	STE	1 st	Natural ligand
1N05	1NB9	RBF	1 st	Substrate
1NDB	2H3P	ACO	1 st	Substrate
1NON	4P86	5GP	1 st	Substrate analog
1NXM	1DZT	ATY	1 st	Substrate analog
1O24	4KAT	FDA	1 st	Cofactor
1OEM	2QBP	527	1 st	Inhibitor
1OFP	1OF6	DTY	1 st	Specific inhibitor
1OGH	3TPS	DUP	4 th	Substrate analog
1OGL	2YB0	DUR	1 st	Substrate analog
1OGM	3WWG	BGC	1 st	Substrate analog
1OJQ				No significant results
1OLZ				No significant results
1OOI	3B88	ETE	1 st	Substrate analog
1OPY	3OWY	EQU	1 st	Transition state analog
1OXT	3C4J	AGS	1 st	Nucleotide analogs
1PIX	1JCJ	HPD	1 st	Reaction intermediate
1P5H	1T3Z	CAO	1 st	Substrate analog
1P74	3PHJ	DHK	1 st	Reaction product
1PDB	1BOZ	NDP	1 st	Cofactor
1PNG	3PMS	GOL	1 st	Non-specific ligand
1Q52	4QII	2NE	1 st	Substrate analog
1Q7M	2E7F	2CF	1 st	Substrate analog
1QCZ	2FWP	ICR	1 st	Substrate
1QID	1H23	E12	1 st	Specific inhibitor
1QTO	4IAG	GOL	1 st	Non-specific ligand
1QTR	1MU0	PHK	22 nd	Inhibitor
1R0M	1SJB	OSB	1 st	Product
1R12	3ZWP	AVU	1 st	Substrate analog
1R29	4CP3	RBT	1 st	Specific inhibitor
1R15	3BGV	SAH	1 st	Reaction product
1RIQ	3HXQ	A5A	1 st	Substrate analog
1RJ1	2CJ7	IOD	1 st	Non-specific ligand
1RKM				No significant results
1RZV	3CX4	GLC	1 st	Substrate
1S2L	1S2D	AR4	1 st	Substrate analog
1S7K				No significant results
1SGK	1DTP	APU	1 st	Substrate analog
1SGZ	3I25	MV7	1 st	Specific inhibitor

1SJY	1SOI	SM	1 st	Non-specific ligand
1SNT	2F25	DAN	1 st	Inhibitor
1SQG	4FP9	SAM	1 st	Cofactor
1SUL				No significant results
1SWH	3WZP	ZOF	1 st	Specific ligand analog
1TGN	1C2F	BAH	1 st	Specific inhibitor
1THV	4TVT	NA	2 nd	Non-specific ligand
1TIB	1GT6	OLA	1 st	Reaction product
1TJE	1TKE	SER	1 st	Substrate analog
1TJV	1DCN	AS1	1 st	Substrate analog
1TVN	4A3H	DCB	1 st	Substrate analog
1TW0	2QIM	ZEA	3 rd	Non-specific ligand
1TYF	1TG6	FME	113 th	Reaction product
1TYV	3TH0	PZU	1 st	Natural ligand analog
1TZV				No significant results
1U0T	4DY6	A22	1 st	Substrate analog
1U7U				No significant results
1UAJ	1P9P	SAH	1 st	Substrate analog
1UBI	4WZP	SEP	1 st	Specific ligand
1UF4	1UF5	CDT	1 st	Substrate
1ULU	2QIO	NAD	1 st	Cofactor
1UMF				No significant results
1UXZ	1W9W	BGC	1 st	Specific ligand
1UYL	3T0Z	ATP	1 st	Substrate
1V0S	2ZE9	PD7	1 st	Reaction product
1V6Z	3KW2	ADN	3 rd	Substrate analog
1V77				No significant results
1VFJ	4CNZ	ADP	1 st	Specific ligand
1VIC	1H7H	CDP	1 st	Substrate analog
1VJU				No significant results
1VPN	1SIE	SIA	1 st	Specific ligand
1W9A	4QVB	F42	1 st	Cofactor
1WJG	3QTB	D5M	1 st	Reaction product analog
1WNY	1WK8	VMS	1 st	Substrate analog
1WOS	3AOI	C2F	1 st	Reaction product analog
1WS9	2DVL	FAD	1 st	Cofactor
1WTJ				No significant results
1WXF	1EE1	ATP	1 st	Substrate analog
1X56	2XTI	NB8	1 st	Substrate analog
1X7O	1ZJR	GOL	40 th	Substrate analog
1X8F	2NXH	PEP	1 st	Substrate
1XIX				No significant results
1XK7	1XA4	COA	1 st	Substrate analog
1XO6	3IB9	BTN		Substrate
1XQO				No significant results
1XW2	2B4F	XYP	1 st	Reaction product
1Y2Q	3PD2	A3S	1 st	Substrate analog
1Y2T	2OFD	NGA	1 st	Endogenous ligand
1YBT	1WC1	TAT	61 st	Substrate analog
1YVY	1AQ2	ATP	1 st	Substrate
1Z7G	4RAB	3L3	1 st	Specific inhibitor
1ZAH	3MMT	2FP	1 st	Substrate
1ZCU	1LL2	UPG	1 st	Substrate

1ZNW	2F3T	LGP	1 st	Substrate analog
1ZTY				No significant results
1ZUH	1ZUI	SKM	1 st	Substrate
2A6Z				No significant results
2A8F	1LRI	CLR	1 st	Specific ligand
2AD1	1B06	VO4	2 nd	Transition state analog
2AHF	2FUZ	MPD	1 st	Non-specific ligand
2AHU				No significant results
2AMJ	3RPE	FAD	1 st	Cofactor
2B0J	3F46	I2C	1 st	Cofactor
2B6P	2B6O	MC3	1 st	Specific ligand analog
2B78	3VSE	SAH	1 st	Cofactor
2B98				No significant results
2BGT	1NZF	GOL	1 st	Substrate analog
2BJW	2VII	AMP	1 st	Substrate analog
2BOE	2BOD	BGC	1 st	Reaction product
2C61	3B2Q	ATP	1 st	Reaction product
2C7I	3R07	MPD	1 st	Substrate analog
2CAR				No significant results
2CHS	3ZP7	ISJ	1 st	Substrate
2CI3	2CI1	KOR	1 st	Specific inhibitor
2CWK	2HVD	ADP	1 st	Substrate
2CX5				No significant results
2D59	3Q9N	COA	1 st	Natural ligand
2DHQ	3N76	CA2	1 st	Specific inhibitor
2DJ6	1Y13	BIO	1 st	Substrate
2DKA	3UW2	ZN	93 rd	Inhibitor
2DPS	2Z3P	LEU	1 st	Substrate
2DQW	1EYE	PMM	1 st	Substrate analog
2E0C	1XKD	NAP	1 st	Substrate
2E0K	1S4D	GOL	6 th	Substrate analog
2E10	1WQW	BT5	1 st	Substrate analog
2E1V	2XR7	MLC	5 th	Substrate
2E3S	2Z9Z	DDR	1 st	Substrate
2ECR	1RZ1	NAD	1 st	Cofactor
2EX0	3S44	FN5	1 st	Substrate analog
2F82	2WYA	HMG	1 st	Reaction product
2F9T	3BF3	PAZ	1 st	Reaction product
2FK7	1KP1	SAH	1 st	Cofactor
2FP8	2V91	S55	1 st	Substrate
2FSF	3BXZ	ADP	1 st	Reaction product
2G67	3AI7	TPP	1 st	Reaction intermediate
2G95	4M6Q	20T	1 st	Specific inhibitor
2GFV	4C70	TLJ	1 st	Inhibitor
2GG4	1RF6	S3P	1 st	Substrate
2GQV	2P4T	NAP	4 th	Cofactor
2GSF	4P5Z	Q7M	1 st	Specific inhibitor
2GT2	2GT4	GDD	1 st	Substrate
2GUB	4QDW	LAI	1 st	Reaction intermediate
2GWX	3GWX	EPA	1 st	Natural ligand
2GYY	4R3N	NAP	1 st	Cofactor
2H2Z	2A5K	AZP	1 st	Inhibitor

2HBJ	2HBK	MN	1 st	Cofactor
2HIV	4EQ5	AMP	1 st	Reaction product
2HK0	3VNL	TAG	1 st	Substrate
2HVM	1KQY	NAG	1 st	Substrate
2HY7				No significant results
2HZR	40SD	PLM	1 st	Natural ligand analog
2I4L	2J3L	P5A	1 st	Substrate analog
2IOB	3A2Y	TS5	1 st	Substrate
2IRU	2FAR	DTP	1 st	Substrate analog
2J71				No significant results
2J8N	3DR8	ACO	1 st	Cofactor
2JBR				No significant results
2NWD	4XAD	3ZW	1 st	Substrate analog
2NXC	3CJT	SAM	1 st	Cofactor
2O9P	2JIE	G2F	1 st	Product analog
2OAM	2APG	FAD	1 st	Cofactor
2OPT				No significant results
2OU1	4JGX	PLM	1 st	Natural ligand
2OVE	1EPB	REA	1 st	Natural ligand analog
2PAW	4HHY	15R	1 st	Specific inhibitor
2PFK	4XYK	ADP	1 st	Reaction product
2PKF	4O1G	AGS	1 st	Substrate analog
2PPN	1BL4	AP1	1 st	Specific ligand
2Q5R	2JG1	ANP	1 st	Substrate analog
2Q6Z	1R3Q	ACP	1 st	Reaction product
2QBV	2VKL	MLT	1 st	Product analog
2QDK	1RXU	THM	1 st	Reaction product analog
2QEV	2QEO	LNR	1 st	Natural ligand
2QSU	2H8G	ADE	1 st	Reaction product
2QVL	4WER	AMP	1 st	Reaction product analog
2QYS	2QW8	NAP	1 st	Cofactor
2R60	2R66	F6P	1 st	Substrate
2RG7	1AIJ	BPH	55 th	Endogenous ligand analog
2RJD	3P8H	P8H	1 st	Specific inhibitor
2SGA	2QAA	TYR	1 st	Reaction intermediate
2SIL	1N1T	DAN	1 st	Specific inhibitor
2TS1	1VBM	YSA	1 st	Substrate analog
2UYO				No significant results
2V78	2DCN	ADP	1 st	Reaction product
2VFB	4NV7	COA	1 st	Cofactor
2VFY	4YEZ	A2P	13 th	Specific ligand analog
2VQ4	4BFN	GLC	2 nd	Natural ligand
2VUA	3RSJ	GAL	7 th	Natural ligand
2WN4	2WN6	NDP	1 st	Cofactor
2WVH	3OE1	TDL	1 st	Reaction intermediate
2WZT	1S2C	FLF	9 th	Specific inhibitor
2X5S	2X65	M1P	1 st	Substrate
2YWB	1GPM	AMP	1 st	Product analog
2YXF	1LDS	NA	10 th	Non-specific ligand
2YYA	2XD4	ADP	1 st	Substrate analog
2YYT	2CZF	XMP	1 st	Product analog

2YZG	4L1K	ANP	1 st	Substrate analog
2ZBS	1S9Q	OHT	1 st	Natural ligand analog
2ZCG	3MWA	UFT	1 st	Covalent inhibitor
2ZCO	3ADZ	PS7	1 st	Reaction intermediate
2ZGL	2ZGO	LAT	1 st	Natural ligand analog
2ZHY	3KE5	ATP	1 st	Substrate
2ZJ8	2I4I	AMP	2 nd	Specific ligand
2ZTY	3ZZ9	G83	1 st	Specific inhibitor
3A0Y	1Y8O	ADP	38 th	Reaction product
3A5Q	1CHW	HXC	1 st	Substrate analog
3AAP	4BR7	AU1	1 st	Specific inhibitor
3ADO	3F3S	NAD	1 st	Cofactor
3APP	1PPM	OP1	1 st	Specific inhibitor
3B3G	2Y1W	SFG	1 st	Cofactor analog
3BA1	2DBQ	NAP	1 st	Cofactor
3BLM	1GHP	PNM	1 st	Reaction intermediate
3BTV				No significant results
3BUE	2ZFZ	ARG	1 st	Natural ligand
3BYL	1PT2	SUC	1 st	Substrate
3C2E	3C2R	PHT	1 st	Specific inhibitor
3C8N	4ICC	MLY	6 th	Non-specific ligand
3CAF	1E0O	SGN	1 st	Specific ligand
3CB6				No significant results
3CGZ	2GR7	C8E	1 st	Specific inhibitor mimic
3COU	2A8S	GTP	1 st	Substrate analog
3CQ1				No significant results
3CRM	3CRQ	DPO	1 st	Reaction product
3CSR				No significant results
3CTB	1ILH	SRL	1 st	Specific agonist
3D0O	1LDN	NAD	1 st	Cofactor
3D95	1CBQ	RE9	1 st	Natural ligand analog
3DRD	3DOD	PLP	1 st	Cofactor
3DRE	3JU6	ANP	1 st	Substrate analog
3DUL	1SUS	SAH	1 st	Reaction product
3E1S	2EWV	ADP	11 th	Substrate analog
3E5B	3POX	PYR	1 st	Reaction product analog
3EIZ	3E1Y	POP	1 st	Substrate
3EK6	2BND	UDP	1 st	Reaction product
3ETF	4ITA	NDP	1 st	Cofactor
3EX9	3FF0	GOL	1 st	Substrate mimic
3EXR	1KW1	LG6	1 st	Substrate analog
3FIL	3GY0	NAP	1 st	Cofactor
3F6F	1PN9	GTX	1 st	Specific inhibitor
3FTD	2ZBR	SFG	1 st	Cofactor analog
3FV6	2QR1	ADP	1 st	Natural ligand
3G1S	3G1F	2OM	1 st	Substrate analog
3GBT	2W41	ADP	2 nd	Reaction product
3GD0				No significant results
3GLK	3JRX	S1A	1 st	Specific ligand
3GPG	3GQO	APR	1 st	Specific ligand
3GQH				No significant results
3GSZ	3BR9	DEY	1 st	Specific inhibitor

3H2G	1GKK	SEP	2 nd	Specific ligand
3H38	4WC0	ATP	1 st	Substrate
3H49	2FV7	ADP	1 st	Reaction product
3H71	2YA6	DAN	1 st	Specific inhibitor
3HBH	2DKV	MES	1 st	Substrate mimic
3HIS	2GA4	ADE	1 st	Reaction product
3HJ4	4FHY	3AT	1 st	Substrate analog
3HNX	2YHH	MAN	1 st	Natural ligand
3I0C	3V0N	3GW	1 st	Specific inhibitor
3I3I	1QLL	TDA	1 st	Specific inhibitor
3I8S	3WIC	GNP	1 st	Substrate analog
3IK8	4TYO	39X	1 st	Specific inhibitor
3ILY				No significant results
3ITY	3ITV	PSJ	1 st	Substrate
3IUJ	4BCC	JKT	2 nd	Covalent inhibitor
3JYL	1QOR	NDP	1 st	Cofactor
3K0M	4J5A	67Z	1 st	Specific inhibitor
3KAJ	2WYO	GSH	1 st	Product analog
3KDH	3NJ0	PYV	1 st	Natural ligand mimic
3KJE	1YR7	GSP	1 st	Substrate analog
3KJT	4IKM	TYI	1 st	Modified amino acid
3KP7	4EJW	SRY	1 st	Specific inhibitor
3KR9	3DXY	SAM	84 th	Substrate
3KX7	3KVU	ACO	1 st	Cofactor
3LIG	3LFI	BGC	1 st	Substrate
3LOI	1XE8	GUN	3 rd	Specific ligand analog
3LXZ	3UBL	GSH	1 st	Substrate
3M4D	3M3R	BCD	1 st	Natural ligand
3N6J	1ECQ	DXG	1 st	Substrate analog
3NK6	3GYQ	SAM	1 st	Substrate
3PTE	1YQS	BSA	1 st	Specific inhibitor
3SSW	1ZT9	TRP	1 st	Specific ligand
3VZT	3VZU	ANP	1 st	Specific ligand
4AKE	3LR3	ADP	1 st	Reaction product
4PGM	1E59	VO3	1 st	Specific inhibitor
4PTI	1YLC	ABA	1 st	Modified amino acid

REFERENCES

- Atzeni, P., Polticelli, F., Toti, D. (2011) A framework for semi-automatic identification, disambiguation and storage of protein-related abbreviations in scientific literature, *Proceedings - International Conference on Data Engineering*, **5767646**, 59-61
- Atzeni, P., Polticelli, F., Toti, D. (2011) An automatic identification and resolution system for protein-related abbreviations in scientific papers, *Lecture Notes in Computer Science*, **6623**, 171-176
- Brylinski, M., Skolnick, J. (2008) A threading-based method (FINDSITE) for ligand-binding site prediction and functional annotation. *Proc Natl Acad Sci U S A*, **105(1)**, 129-134
- Capra, J.A., Laskowski, R.A., Thornton, J.M., Singh, M., Funkhouser, T.A. (2009) Predicting Protein Ligand Binding Sites by Combining Evolutionary Sequence Conservation and 3D Structure. *PLoS Comput Biol*, **5(12)**
- Furnham, N., Holliday, G.L., de Beer, T.A., Jacobsen, J.O., Pearson, W.R., Thornton, J.M. (2014) The Catalytic Site Atlas 2, *Nucleic Acids Res.*, **42**, D485-D489
- Haas, J., Roth, S., Arnold, K., Kiefer, F., Schmidt, T., Bordoli, L., Schwede, T. (2013) The Protein Model Portal—a comprehensive resource for protein structure and model information, *Database (Oxford)*, 2013:bat031.
- Levy, et al., (2015) retrieved from the web, <http://home.wlu.edu/levys/software/kd/>
- Dessailly, B.H., et al. (2008) LigASite: a database of biologically relevant binding sites in proteins with known apo-structures, *Nucleic Acids Res*, **36**, 667-673
- Laskowski, R.A., et al. (2005a) ProFunc: a server for predicting protein function from 3D structure, *Nucleic Acids Res.*, **3**, W89-W93
- Laskowski, R.A., et al. (2005b) Protein function prediction using local 3D templates. *J Mol Biol*, **351**, 614-626
- Roy, A., Yang, J., Zhang, Y. (2012) COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. *Nucleic Acids Research*, **40**, W471-W477
- Toti, D., Atzeni, P., Polticelli, F. (2012) Automatic Protein Abbreviations Discovery and Resolution from Full-Text Scientific Papers: The PRAISED Framework, *Bio-Algorithms and Med-Systems*, **8**, 13-
- Viet Hung, L., Caprari, S., Bizai, M., Toti, D., Polticelli, F. (2015) LIBRA: LIgand Binding site Recognition Application, *Bioinformatics*, **31(24)**, 4020-4022
- Yang, J., Roy, A., Zhang, Y. (2013) Protein-ligand binding site recognition using complementary binding-specific substructure comparison and sequence profile alignment, *Bioinformatics*, **29(20)**, 2588-95