



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 08:27 PM GMT

PDB ID : 1DTD  
Title : CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE LEECH CARBOXYPEPTIDASE INHIBITOR AND THE HUMAN CARBOXYPEPTIDASE A2 (LCI-CPA2)  
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Deposited on : 2000-01-12  
Resolution : 1.65 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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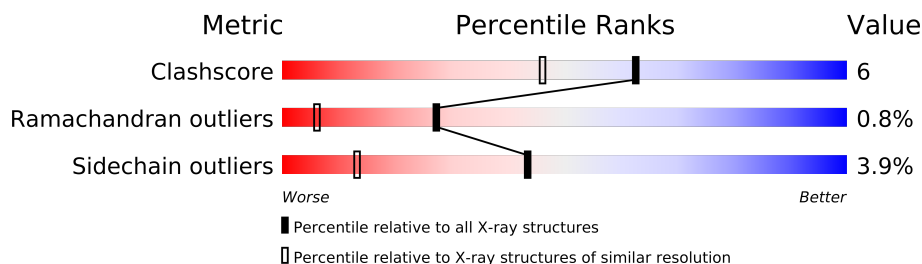
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1001 (1.66-1.66)
Ramachandran outliers	78287	1581 (1.68-1.64)
Sidechain outliers	78261	1580 (1.68-1.64)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	303	
2	B	61	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3085 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CARBOXYPEPTIDASE A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	28	0	0
			2371	1515	399	448	9			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	490	ALA	-	INSERTION	UNP P48052
A	587	SER	ARG	CONFLICT	UNP P48052
A	588	ARG	SER	CONFLICT	UNP P48052

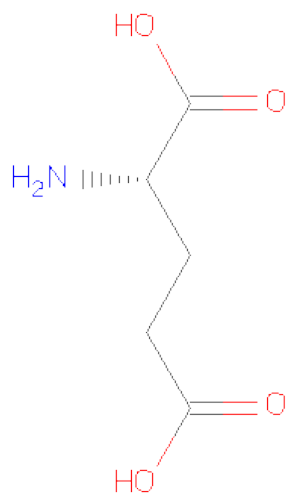
- Molecule 2 is a protein called METALLOCARBOXYPEPTIDASEINHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	61	Total	C	N	O	S	0	0	0
			472	296	78	90	8			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is GLUTAMIC ACID (three-letter code: GLU) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 5 is water.

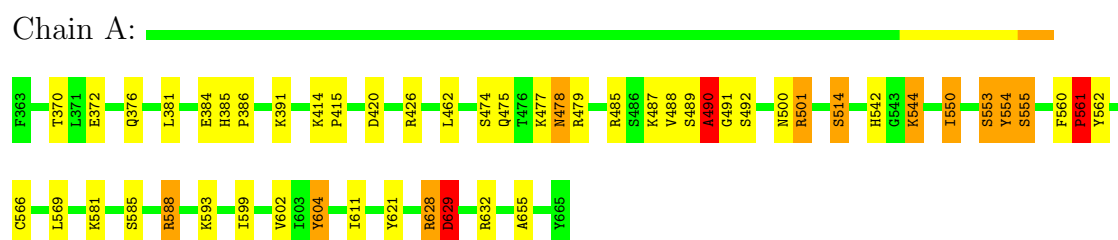
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	176	Total	O	0	0
			176	176		
5	B	55	Total	O	0	0
			55	55		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

#### • Molecule 1: CARBOXYPEPTIDASE A2



#### • Molecule 2: METALLOCARBOXYPEPTIDASEINHIBITOR



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.44Å 80.44Å 114.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	12.00 – 1.65	Depositor
% Data completeness (in resolution range)	98.0 (12.00-1.65)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.187 , 0.234	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3085	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	1.33	10/2436 (0.4%)	1.36	27/3306 (0.8%)
2	B	0.44	0/489	1.08	1/671 (0.1%)
All	All	1.23	10/2925 (0.3%)	1.32	28/3977 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	514	SER	CB-OG	44.11	1.99	1.42
1	A	588	ARG	CD-NE	32.82	2.02	1.46
1	A	491	GLY	C-N	14.98	1.68	1.34
1	A	477	LYS	CG-CD	-10.55	1.16	1.52
1	A	490	ALA	C-N	10.45	1.51	1.33
1	A	487	LYS	CG-CD	9.82	1.85	1.52
1	A	372	GLU	CB-CG	-9.18	1.34	1.52
1	A	632	ARG	CD-NE	8.06	1.60	1.46
1	A	488	VAL	CA-CB	7.98	1.71	1.54
1	A	544	LYS	CD-CE	5.01	1.63	1.51

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	490	ALA	CA-C-N	-24.85	66.49	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	632	ARG	CD-NE-CZ	-19.02	96.97	123.60
1	A	491	GLY	C-N-CA	-18.98	74.26	121.70
1	A	628	ARG	O-C-N	-11.77	103.87	122.70
1	A	553	SER	O-C-N	-11.73	103.92	122.70
1	A	490	ALA	C-N-CA	-11.14	98.90	122.30
1	A	491	GLY	CA-C-N	-11.02	92.96	117.20
1	A	487	LYS	CB-CG-CD	-10.72	83.74	111.60
1	A	550	ILE	CB-CG1-CD1	10.56	143.48	113.90
1	A	372	GLU	CA-CB-CG	-10.49	90.31	113.40
1	A	490	ALA	O-C-N	-10.05	106.11	123.20
1	A	561	PRO	C-N-CA	9.14	144.54	121.70
1	A	488	VAL	CA-CB-CG1	8.85	124.17	110.90
1	A	488	VAL	N-CA-CB	7.89	128.86	111.50
1	A	487	LYS	CG-CD-CE	7.56	134.59	111.90
1	A	561	PRO	O-C-N	-6.98	111.53	122.70
1	A	629	ASP	CB-CA-C	6.84	124.09	110.40
1	A	628	ARG	CB-CA-C	-6.79	96.81	110.40
1	A	479	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	A	553	SER	N-CA-CB	6.19	119.78	110.50
2	B	15	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	485	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	A	426	ARG	NE-CZ-NH2	5.44	123.02	120.30
1	A	553	SER	CA-C-N	5.43	129.14	117.20
1	A	501	ARG	NE-CZ-NH1	-5.40	117.60	120.30
1	A	562	TYR	N-CA-C	5.23	125.13	111.00
1	A	621	TYR	CB-CG-CD1	-5.13	117.92	121.00
1	A	554	TYR	N-CA-C	5.01	124.54	111.00

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	490	ALA	Mainchain
1	A	553	SER	Mainchain,Peptide
1	A	561	PRO	Mainchain,Peptide
1	A	628	ARG	Mainchain,Peptide

## 5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens



added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2371	0	2289	26	1
2	B	472	0	421	5	0
3	A	1	0	0	0	0
4	A	10	0	5	5	0
5	A	176	0	0	2	0
5	B	55	0	0	0	1
All	All	3085	0	2715	31	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (31) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:550:ILE:HD13	5:A:8:HOH:O	1.62	0.96
4:A:300:GLU:HA	4:A:300:GLU:OE1	1.60	0.96
1:A:604:TYR:HH	4:A:300:GLU:N	1.65	0.93
1:A:414:LYS:HB2	1:A:415:PRO:HD2	1.63	0.80
1:A:585:SER:O	1:A:588:ARG:HG2	1.91	0.71
1:A:370:THR:HA	1:A:475:GLN:HE22	1.59	0.68
1:A:420:ASP:OD2	1:A:550:ILE:HD12	1.92	0.67
1:A:542:HIS:HD2	1:A:544:LYS:H	1.45	0.63
2:B:47:ALA:O	2:B:59:ARG:HD2	2.02	0.59
1:A:414:LYS:HB2	1:A:415:PRO:CD	2.34	0.57
1:A:370:THR:HA	1:A:475:GLN:NE2	2.20	0.56
2:B:48:VAL:HG23	2:B:49:GLU:HG2	1.90	0.53
1:A:542:HIS:CD2	1:A:544:LYS:H	2.26	0.52
1:A:490:ALA:HB3	1:A:492:SER:N	2.24	0.52
1:A:550:ILE:HD11	5:A:7:HOH:O	2.08	0.51
1:A:385:HIS:N	1:A:386:PRO:HD3	2.26	0.51
1:A:500:ASN:HD22	4:A:300:GLU:C	2.15	0.50
2:B:7:GLU:HG3	2:B:9:PHE:CE2	2.48	0.49
1:A:602:VAL:HG23	2:B:41:PRO:HG2	1.95	0.48
2:B:7:GLU:HG3	2:B:9:PHE:CZ	2.49	0.47
1:A:561:PRO:HB2	1:A:569:LEU:HD13	1.97	0.47
1:A:474:SER:HA	1:A:478:ASN:O	2.15	0.47
1:A:554:TYR:HB2	1:A:629:ASP:H	1.78	0.47
1:A:384:GLU:HG3	1:A:385:HIS:CE1	2.50	0.46
1:A:560:PHE:HB2	1:A:561:PRO:CD	2.45	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:501:ARG:NH1	4:A:300:GLU:O	2.40	0.45
1:A:501:ARG:HH22	4:A:300:GLU:N	2.14	0.45
1:A:554:TYR:O	1:A:555:SER:CB	2.65	0.44
1:A:420:ASP:OD2	1:A:550:ILE:CD1	2.63	0.43
1:A:599:ILE:HD11	1:A:611:ILE:HD11	2.01	0.42
1:A:581:LYS:HD3	1:A:655:ALA:HB1	2.02	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:514:SER:OG	5:B:119:HOH:O[4_555]	1.95	0.25

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	301/303 (99%)	283 (94%)	15 (5%)	3 (1%)	22	3
2	B	59/61 (97%)	58 (98%)	1 (2%)	0	100	100
All	All	360/364 (99%)	341 (95%)	16 (4%)	3 (1%)	27	6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	555	SER
1	A	561	PRO
1	A	490	ALA

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	255/256 (100%)	245 (96%)	10 (4%)	43	13
2	B	53/53 (100%)	52 (98%)	1 (2%)	69	43
All	All	308/309 (100%)	297 (96%)	11 (4%)	43	15

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	376	GLN
1	A	381	LEU
1	A	391	LYS
1	A	462	LEU
1	A	478	ASN
1	A	489	SER
1	A	566	CYS
1	A	593	LYS
1	A	604	TYR
1	A	629	ASP
2	B	28	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	404	ASN
1	A	475	GLN
1	A	478	ASN
1	A	542	HIS
1	A	605	GLN
1	A	663	HIS
2	B	13	GLN
2	B	16	GLN
2	B	57	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	GLU	A	300	-	9,9,9	1.56	1 (11%)	11,11,11	2.22	4 (36%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GLU	A	300	-	1/1/3/3	0/9/9/9	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	300	GLU	CB-CA	-3.63	1.44	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	300	GLU	CB-CA-N	4.60	121.38	110.14
4	A	300	GLU	CG-CB-CA	-3.09	108.66	114.43
4	A	300	GLU	OE1-CD-CG	-2.96	112.85	123.03
4	A	300	GLU	C-CA-N	-2.37	105.44	109.36

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	300	GLU	CA

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.