



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 3, 2020 – 03:28 am BST

PDB ID : 4CPA
Title : REFINED CRYSTAL STRUCTURE OF THE POTATO INHIBITOR COM-
PLEX OF CARBOXYPEPTIDASE A AT 2.5 ANGSTROMS RESOLUTION
Authors : Lipscomb, W.N.; Rees, D.C.
Deposited on : 1982-03-24
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

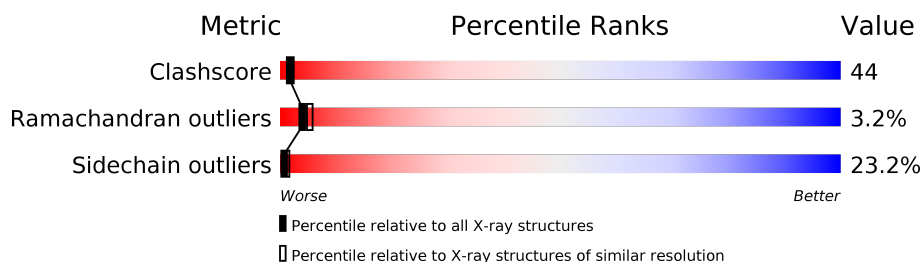
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	307	
1	B	307	
2	I	38	
2	J	38	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5456 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2437	1561	406	465	5			
1	B	307	Total	C	N	O	S	0	0	0
			2437	1561	406	465	5			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLN	GLU	CONFLICT	UNP P00730
A	31	GLU	GLN	CONFLICT	UNP P00730
A	89	ASN	ASP	CONFLICT	UNP P00730
A	93	ASN	ASP	CONFLICT	UNP P00730
A	114	ASN	ASP	CONFLICT	UNP P00730
A	122	GLU	GLN	CONFLICT	UNP P00730
A	185	ASN	ASP	CONFLICT	UNP P00730
A	228	ALA	GLU	CONFLICT	UNP P00730
A	305	VAL	LEU	CONFLICT	UNP P00730
B	28	GLN	GLU	CONFLICT	UNP P00730
B	31	GLU	GLN	CONFLICT	UNP P00730
B	89	ASN	ASP	CONFLICT	UNP P00730
B	93	ASN	ASP	CONFLICT	UNP P00730
B	114	ASN	ASP	CONFLICT	UNP P00730
B	122	GLU	GLN	CONFLICT	UNP P00730
B	185	ASN	ASP	CONFLICT	UNP P00730
B	228	ALA	GLU	CONFLICT	UNP P00730
B	305	VAL	LEU	CONFLICT	UNP P00730

- Molecule 2 is a protein called METALLOCARBOXYPEPTIDASE INHIBITOR.

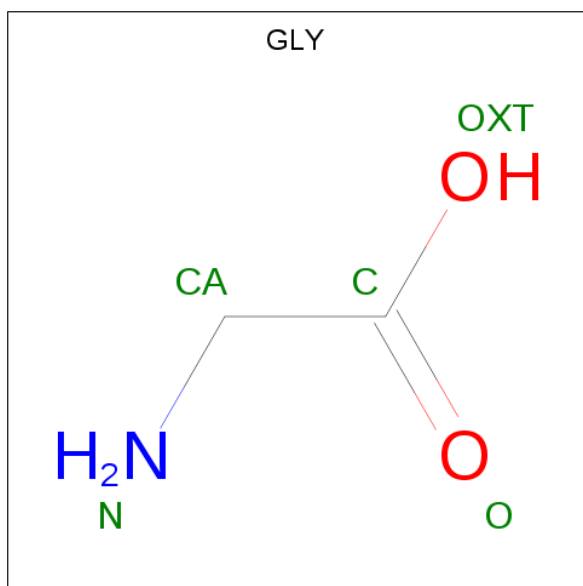
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	I	37	Total	C	N	O	S	X	0	0	0
			285	174	51	52	6	2			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	J	37	Total	C	N	O	S	X	0	0	0
			285	174	51	52	6	2			

- Molecule 3 is GLYCINE (three-letter code: GLY) (formula: $C_2H_5NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			5	2	1	2		
3	B	1	Total	C	N	O	0	0
			5	2	1	2		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

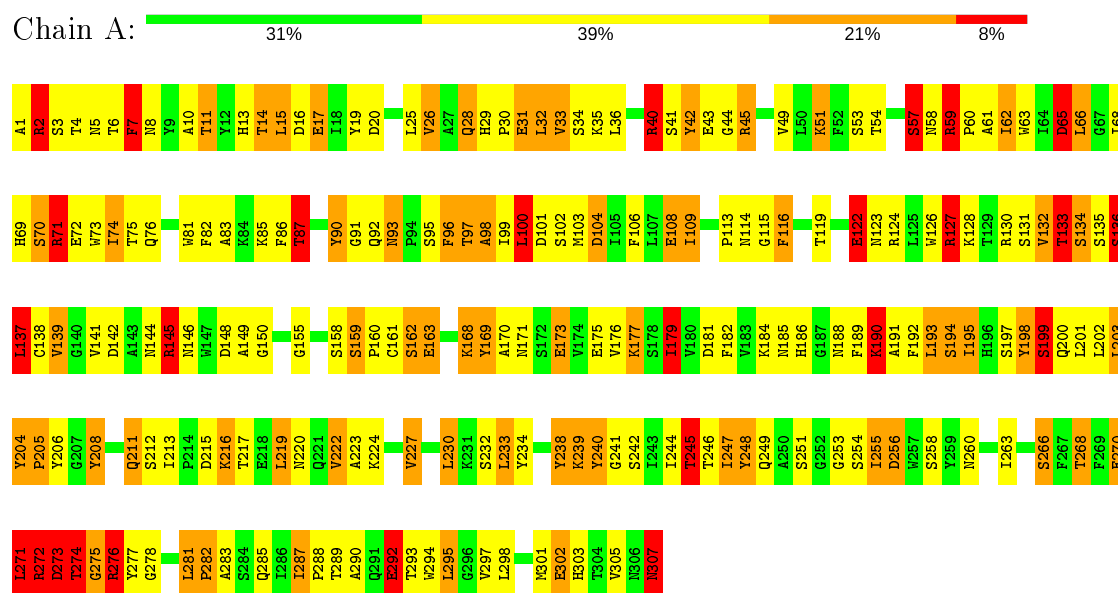
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	J	1	Total	Zn	0	0
			1	1		
4	I	1	Total	Zn	0	0
			1	1		

3 Residue-property plots

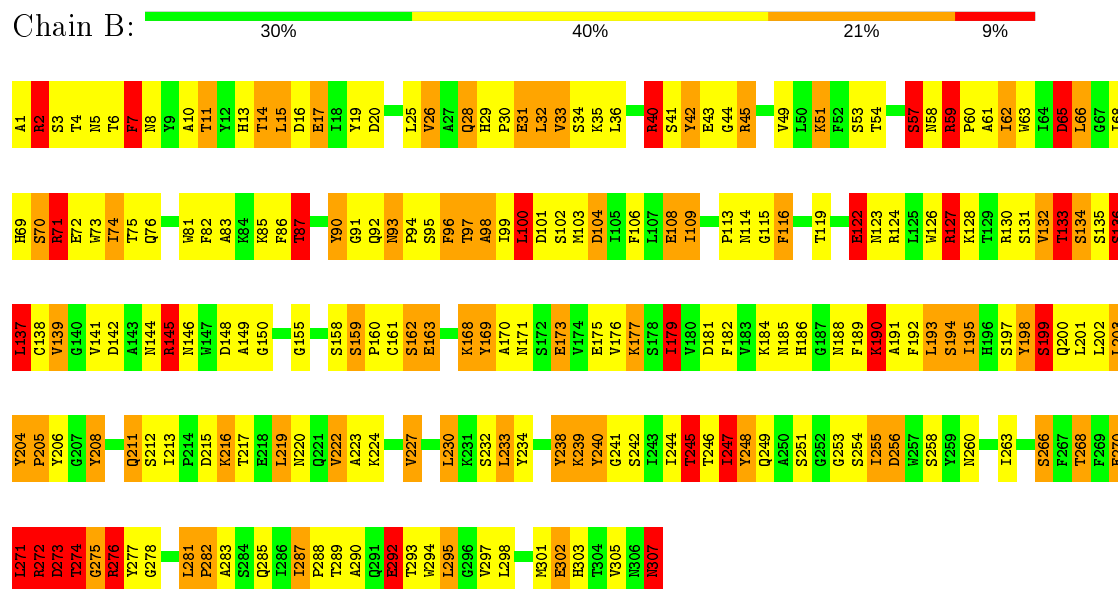
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

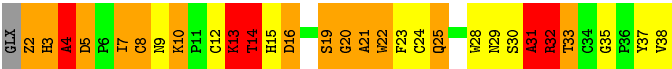
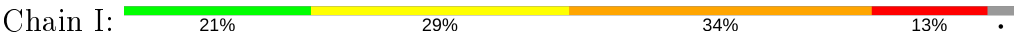
• Molecule 1: CARBOXYPEPTIDASE A



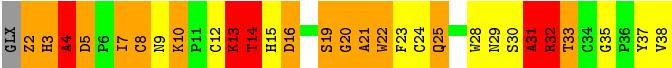
• Molecule 1: CARBOXYPEPTIDASE A



● Molecule 2: METALLOCARBOXYPEPTIDASE INHIBITOR



● Molecule 2: METALLOCARBOXYPEPTIDASE INHIBITOR



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	53.45Å 53.45Å 218.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5456	wwPDB-VP
Average B, all atoms (Å ²)	9.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1.31	3/2503 (0.1%)	2.61	165/3402 (4.9%)
1	B	1.31	3/2503 (0.1%)	2.61	165/3402 (4.9%)
2	I	1.36	0/287	2.87	26/392 (6.6%)
2	J	1.35	0/287	2.87	26/392 (6.6%)
All	All	1.31	6/5580 (0.1%)	2.64	382/7588 (5.0%)

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	12
1	B	0	12
2	I	0	3
2	J	0	3
All	All	0	30

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	302	GLU	CD-OE2	8.98	1.35	1.25
1	A	302	GLU	CD-OE2	8.95	1.35	1.25
1	B	292	GLU	CD-OE1	-5.92	1.19	1.25
1	A	292	GLU	CD-OE1	-5.92	1.19	1.25
1	A	57	SER	CB-OG	5.22	1.49	1.42

The worst 5 of 382 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	127	ARG	NE-CZ-NH2	25.09	132.85	120.30
1	A	127	ARG	NE-CZ-NH2	25.07	132.84	120.30
1	B	2	ARG	CA-CB-CG	23.71	165.56	113.40
1	A	2	ARG	CA-CB-CG	23.70	165.53	113.40
1	B	40	ARG	NE-CZ-NH1	22.30	131.45	120.30

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	ARG	Sidechain
1	A	2	ARG	Sidechain
1	A	40	ARG	Sidechain
1	A	59	ARG	Sidechain
1	A	71	ARG	Sidechain

5.2 Too-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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2437	0	2350	198	0
1	B	2437	0	2350	199	0
2	I	285	0	243	45	0
2	J	285	0	243	45	0
3	A	5	0	2	1	0
3	B	5	0	2	1	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
All	All	5456	0	5190	469	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 44.

The worst 5 of 469 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:SER:HB3	1:B:136:SER:HB2	1.25	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:SER:HB3	1:A:136:SER:HB2	1.25	1.16
1:B:136:SER:HA	1:B:137:LEU:HD22	1.32	1.10
1:B:208:TYR:HB3	1:B:251:SER:HA	1.31	1.08
1:B:60:PRO:HB3	1:B:190:LYS:HD2	1.33	1.08

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	305/307 (99%)	274 (90%)	27 (9%)	4 (1%)	12	21
1	B	305/307 (99%)	274 (90%)	27 (9%)	4 (1%)	12	21
2	I	35/38 (92%)	22 (63%)	6 (17%)	7 (20%)	0	0
2	J	35/38 (92%)	22 (63%)	6 (17%)	7 (20%)	0	0
All	All	680/690 (99%)	592 (87%)	66 (10%)	22 (3%)	4	5

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	SER
1	A	134	SER
1	A	199	SER
1	A	273	ASP
2	I	4	ALA

5.3.2 Protein sidechains [i](#)

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	263/263 (100%)	202 (77%)	61 (23%)	1	1
1	B	263/263 (100%)	202 (77%)	61 (23%)	1	1
2	I	30/30 (100%)	23 (77%)	7 (23%)	1	1
2	J	30/30 (100%)	23 (77%)	7 (23%)	1	1
All	All	586/586 (100%)	450 (77%)	136 (23%)	1	1

5 of 136 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	7	ILE
1	B	35	LYS
1	B	292	GLU
2	I	13	LYS
1	B	6	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	25	GLN
1	B	58	ASN
2	J	25	GLN
2	I	29	ASN
1	B	29	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.