

wwPDB X-ray Structure Validation Summary Report (i)

Jan 30, 2024 – 09:03 PM EST

PDB ID : 1KBC

Title: PROCARBOXYPEPTIDASE TERNARY COMPLEX

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Deposited on : 1997-04-29

Resolution : 1.80 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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

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)

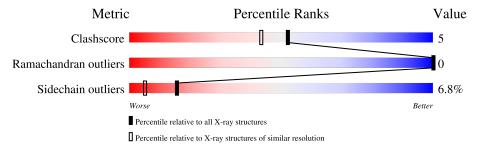
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.80 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$		
Clashscore	141614	6793 (1.80-1.80)		
Ramachandran outliers	138981	6697 (1.80-1.80)		
Sidechain outliers	138945	6696 (1.80-1.80)		

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 of 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain						
1	A	164	82%	16%					
1	В	164	84%	15%	•				



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2955 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 NEUTROPHIL COLLAGENASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	164	10001	С	11	О	S	0	0	0
		101	1294	819	220	253	2		Ŭ	
1	D	164	Total	С	N	Ο	S	0	0	0
1		164	1294	819	220	253	2	0	U	

• Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

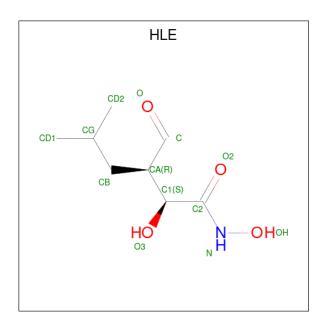
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Ca 2 2	0	0
2	В	2	Total Ca 2 2	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Zn 2 2	0	0
3	В	2	Total Zn 2 2	0	0

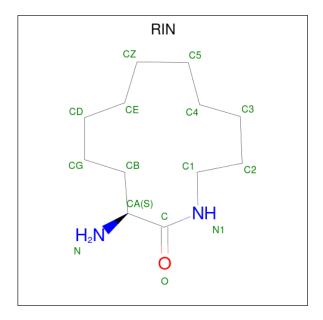
• Molecule 4 is 3-FORMYL-2-HYDROXY-5-METHYL-HEXANOIC ACID HYDROX-YAMIDE (three-letter code: HLE) (formula: $C_8H_{15}NO_4$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 13				0	0
4	В	1	Total 13	C 8		O 4	0	0

 \bullet Molecule 5 is 3-AMINO-AZACYCLOTRIDECAN-2-ONE (three-letter code: RIN) (formula: $C_{12}H_{24}N_2O).$



\mathbf{Mol}	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total 15	C 12	N 2	O 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	В	1	Total 15	C 12	N 2	O 1	0	0

• Molecule 6 is water.

Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
6	A	207	Total O 207 207	0	0
6	В	96	Total O 96 96	0	0

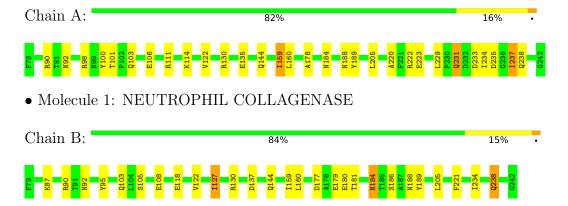


3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: NEUTROPHIL COLLAGENASE





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	44.70Å 80.80Å 108.10Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	6.00 - 1.80	Depositor	
% Data completeness	(Not available) (6.00-1.80)	Depositor	
(in resolution range)	(1101 available) (0.00 1.00)		
R_{merge}	0.07	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	X-PLOR 3.1	Depositor	
R, R_{free}	0.191 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2955	wwPDB-VP	
Average B, all atoms (Å ²)	27.0	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: HLE, RIN, ZN, CA

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		nd lengths	Bond angles		
MIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.74	2/1333~(0.2%)	0.86	6/1816 (0.3%)	
1	В	0.63	1/1333 (0.1%)	0.96	3/1816 (0.2%)	
All	All	0.69	3/2666 (0.1%)	0.91	9/3632~(0.2%)	

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$Ideal(\AA)$
1	A	188	ASN	N-CA	10.23	1.66	1.46
1	В	189	TYR	CB-CG	7.61	1.63	1.51
1	A	189	TYR	N-CA	7.27	1.60	1.46

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\mathrm{Ideal}(^{o})$
1	В	189	TYR	CB-CG-CD1	-15.00	112.00	121.00
1	В	189	TYR	CB-CG-CD2	14.31	129.59	121.00
1	В	188	ASN	C-N-CA	14.01	156.73	121.70
1	A	188	ASN	C-N-CA	9.25	144.82	121.70
1	A	188	ASN	N-CA-CB	-8.37	95.54	110.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	1294	0	1189	17	0
1	В	1294	0	1188	11	0
2	A	2	0	0	0	0
2	В	2	0	0	0	0
3	A	2	0	0	0	0
3	В	2	0	0	0	0
4	A	13	0	13	0	0
4	В	13	0	13	0	0
5	A	15	0	22	0	0
5	В	15	0	22	0	0
6	A	207	0	0	3	0
6	В	96	0	0	1	0
All	All	2955	0	2447	28	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 5.

The worst 5 of 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:234:ILE:O	1:B:238:GLN:HG2	1.93	0.68
1:B:103:GLN:HE22	1:B:181:THR:HA	1.58	0.68
1:B:105:SER:OG	1:B:108:GLU:HG3	2.04	0.58
1:B:144:GLN:HG3	1:B:179:GLU:HG3	1.88	0.56
1:A:237:ILE:HD12	1:A:238:GLN:N	2.22	0.55

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	162/164 (99%)	157 (97%)	5 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	В	162/164 (99%)	157 (97%)	5 (3%)	0	100	100
All	All	324/328 (99%)	314 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	133/133 (100%)	123 (92%)	10 (8%)	13 4		
1	В	133/133 (100%)	125 (94%)	8 (6%)	19 7		
All	All	266/266 (100%)	248 (93%)	18 (7%)	16 5		

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	160	LEU
1	В	238	GLN
1	В	205	LEU
1	A	231	GLN
1	В	159	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	238	GLN
1	В	218	ASN
1	В	103	GLN
1	A	231	GLN
1	В	184	ASN



5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	Tuno	Chain	Res	Link	Bo	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
4	HLE	A	1	5,3	10,12,12	0.84	0	11,15,15	0.92	1 (9%)	
4	HLE	В	1	5,3	10,12,12	0.77	0	11,15,15	1.12	1 (9%)	
5	RIN	A	2	4	15,15,15	0.45	0	17,17,17	0.92	0	
5	RIN	В	2	4	15,15,15	0.43	0	17,17,17	0.76	0	

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	HLE	A	1	5,3	-	2/16/16/16	-
4	HLE	В	1	5,3	-	2/16/16/16	-
5	RIN	A	2	4	-	6/18/18/18	0/0/1/1
5	RIN	В	2	4	-	6/18/18/18	0/0/1/1



There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
4	A	1	HLE	O3-C1-C2	-2.08	106.16	110.63
4	В	1	HLE	O3-C1-C2	-2.06	106.19	110.63

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	2	RIN	C3-C4-C5-CZ
4	В	1	HLE	O3-C1-C2-N
4	В	1	HLE	O3-C1-C2-O2
5	В	2	RIN	CD-CE-CZ-C5
5	A	2	RIN	C2-C3-C4-C5

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

