W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Oct 23, 2021 – 02:28 PM EDT

PDB ID	:	1CUD
Title	:	CUTINASE, N172K, R196D MUTANT, MONOCLINIC CRYSTAL FORM WITH THREE MOLECULES PER ASYMMETRIC UNIT
Authors	:	Longhi, S.; Cambillau, C.
Deposited on	:	1995-11-16
Resolution	:	2.70 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 following versions of software and data (see references (i)) were used in the production of this report:

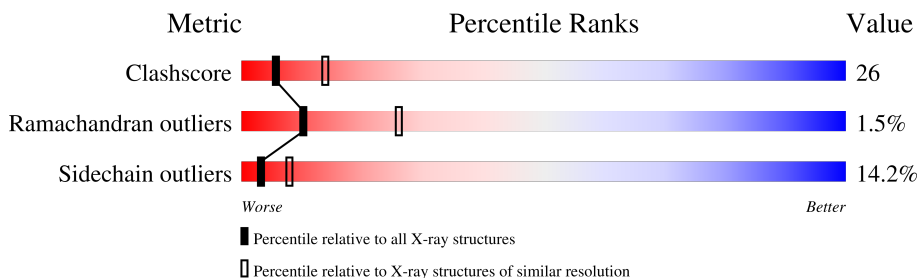|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.70 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	Percentile Ranks	Value
Clashscore		26
Ramachandran outliers		1.5%
Sidechain outliers		14.2%

Worse ... *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)

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	214	43% 45% • 8%
1	B	214	47% 36% 8% 8%
1	C	214	46% 40% 5% 8%

WORLDWIDE PDB PROTEIN DATA BANK

2   Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 6762 atoms, of which 1964 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 CUTINASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	197	Total	C	H	N	O	S	0	0	0
			1770	894	332	257	282	5			
1	B	197	Total	C	H	N	O	S	0	0	0
			1770	894	332	257	282	5			
1	C	197	Total	C	H	N	O	S	0	0	0
			1770	894	332	257	282	5			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	ALA	ARG	conflict	UNP P00590
A	172	LYS	ASN	engineered mutation	UNP P00590
A	196	GLU	ARG	engineered mutation	UNP P00590
B	32	ALA	ARG	conflict	UNP P00590
B	172	LYS	ASN	engineered mutation	UNP P00590
B	196	GLU	ARG	engineered mutation	UNP P00590
C	32	ALA	ARG	conflict	UNP P00590
C	172	LYS	ASN	engineered mutation	UNP P00590
C	196	GLU	ARG	engineered mutation	UNP P00590

- Molecule 2 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	132	Total	H	O	0	0
			396	264	132		
2	B	193	Total	H	O	0	0
			579	386	193		
2	C	159	Total	H	O	0	0
			477	318	159		

3 Residue-property plots ⓘ

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.
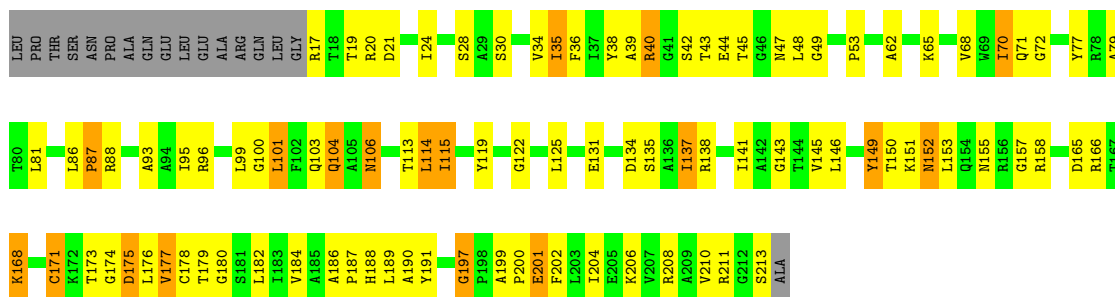
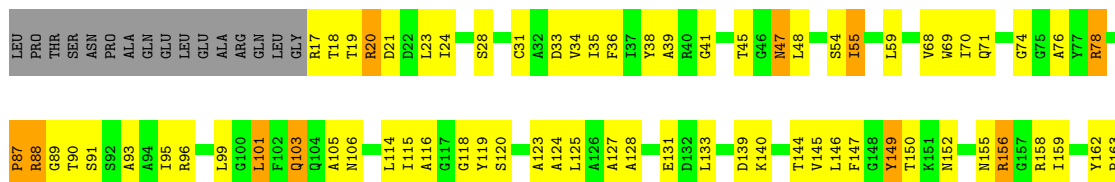Note EDS was not executed.

- Molecule 1: CUTINASE

Chain A:

- Molecule 1: CUTINASE

Chain B:

- Molecule 1: CUTINASE

Chain C:

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	65.90Å 73.30Å 71.20Å 90.00° 112.70° 90.00°	Depositor
Resolution (Å)	6.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.70)	Depositor
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.141 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6762	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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	0.65	0/1461	0.94	2/1982 (0.1%)
1	B	0.59	0/1461	0.88	2/1982 (0.1%)
1	C	0.53	0/1461	0.88	0/1982
All	All	0.59	0/4383	0.90	4/5946 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	176	LEU	CA-CB-CG	5.70	128.40	115.30
1	A	159	ILE	N-CA-C	-5.68	95.66	111.00
1	B	175	ASP	N-CA-C	-5.65	95.74	111.00
1	B	180	GLY	N-CA-C	5.07	125.78	113.10

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	1438	332	1424	79	0
1	B	1438	332	1424	74	0
1	C	1438	332	1424	69	0
2	A	132	264	0	7	0
2	B	193	386	0	10	0
2	C	159	318	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4798	1964	4272	219	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 26.

The worst 5 of 219 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:62:ALA:HA	1:C:179:THR:HG21	1.47	0.95
1:C:96:ARG:HG3	1:C:96:ARG:HH11	1.39	0.87
1:B:35:ILE:HG22	1:B:114:LEU:HB3	1.61	0.83
1:A:158:ARG:HG3	2:A:221:HOH:O	1.77	0.83
1:A:19:THR:HA	1:A:47:ASN:ND2	1.94	0.81

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	195/214 (91%)	170 (87%)	23 (12%)	2 (1%)	15	37
1	B	195/214 (91%)	169 (87%)	22 (11%)	4 (2%)	7	18
1	C	195/214 (91%)	173 (89%)	19 (10%)	3 (2%)	10	26
All	All	585/642 (91%)	512 (88%)	64 (11%)	9 (2%)	10	26

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	197	GLY
1	C	87	PRO
1	A	197	GLY

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Mol	Chain	Res	Type
1	B	149	TYR
1	C	149	TYR

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	146/159 (92%)	125 (86%)	21 (14%)	3	8
1	B	146/159 (92%)	125 (86%)	21 (14%)	3	8
1	C	146/159 (92%)	126 (86%)	20 (14%)	3	8
All	All	438/477 (92%)	376 (86%)	62 (14%)	3	8

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	114	LEU
1	C	156	ARG
1	B	153	LEU
1	C	139	ASP
1	C	184	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	B	152	ASN
1	C	47	ASN
1	C	106	ASN

5.3.3 RNA (i)

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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.