



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2022 – 02:24 AM EST

PDB ID : 6X8I  
Title : Caspase-3 in complex with ketomethylene inhibitor reveals tetrahedral adduct  
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Deposited on : 2020-06-01  
Resolution : 1.50 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](mailto: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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.27  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.27

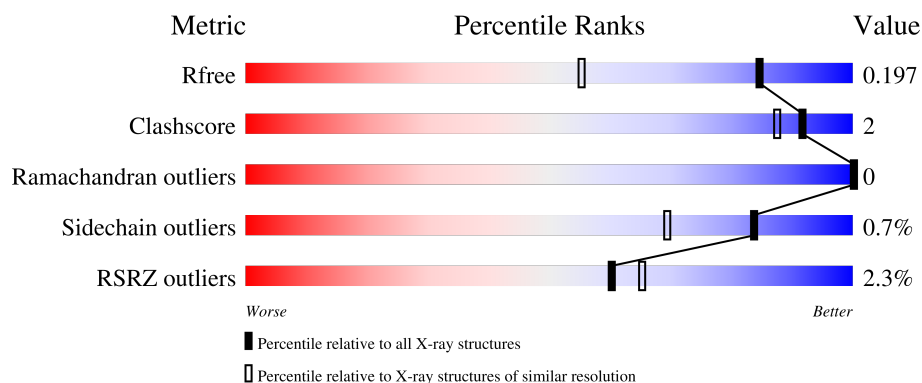
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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))
$R_{free}$	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	175	<div> <div>2%</div> <div>77%</div> <div>19%</div> </div>
1	B	175	<div> <div>2%</div> <div>78%</div> <div>19%</div> </div>
2	C	110	<div> <div>2%</div> <div>78%</div> <div>6%</div> <div>15%</div> </div>
2	D	110	<div> <div>2%</div> <div>77%</div> <div>6%</div> <div>16%</div> </div>
3	E	5	<div> <div>80%</div> <div>20%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	5	 <div>80%20%</div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4178 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 Caspase-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	1	4	0
			1120	693	201	216	10			
1	B	141	Total	C	N	O	S	0	4	0
			1113	689	200	214	10			

- Molecule 2 is a protein called Caspase-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	93	Total	C	N	O	S	0	0	0
			751	494	117	135	5			
2	D	92	Total	C	N	O	S	0	1	0
			759	501	118	135	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	278	LEU	-	expression tag	UNP P42574
C	279	GLU	-	expression tag	UNP P42574
C	280	HIS	-	expression tag	UNP P42574
C	281	HIS	-	expression tag	UNP P42574
C	282	HIS	-	expression tag	UNP P42574
C	283	HIS	-	expression tag	UNP P42574
C	284	HIS	-	expression tag	UNP P42574
C	285	HIS	-	expression tag	UNP P42574
D	278	LEU	-	expression tag	UNP P42574
D	279	GLU	-	expression tag	UNP P42574
D	280	HIS	-	expression tag	UNP P42574
D	281	HIS	-	expression tag	UNP P42574
D	282	HIS	-	expression tag	UNP P42574
D	283	HIS	-	expression tag	UNP P42574
D	284	HIS	-	expression tag	UNP P42574
D	285	HIS	-	expression tag	UNP P42574

- Molecule 3 is a protein called ketomethylene inhibitor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	5	Total	C	N	O	0	0	0
			40	23	4	13			
3	F	5	Total	C	N	O	0	0	0
			40	23	4	13			

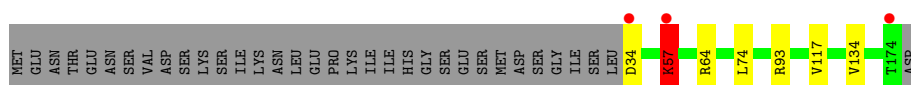
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	115	Total	O	0	0
			115	115		
4	C	62	Total	O	0	0
			62	62		
4	B	101	Total	O	0	0
			101	101		
4	D	60	Total	O	0	0
			60	60		
4	E	7	Total	O	0	0
			7	7		
4	F	10	Total	O	0	0
			10	10		

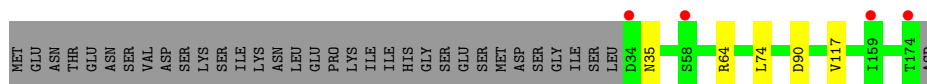
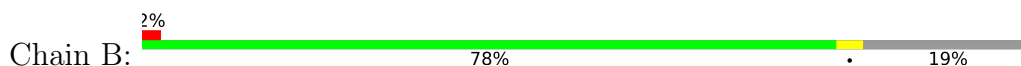
### 3 Residue-property plots [i](#)

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 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.

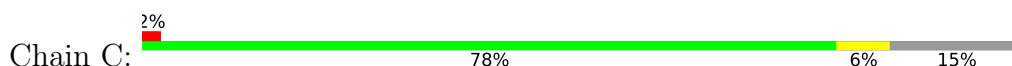
- Molecule 1: Caspase-3



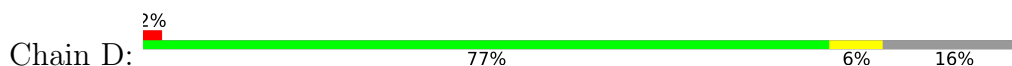
- Molecule 1: Caspase-3



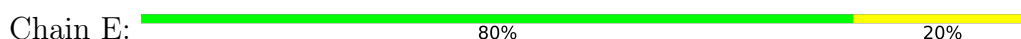
- Molecule 2: Caspase-3



- Molecule 2: Caspase-3



- Molecule 3: ketomethylene inhibitor



- Molecule 3: ketomethylene inhibitor

Chain F:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.65Å 85.01Å 97.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.83 – 1.50 31.83 – 1.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (31.83-1.50) 98.3 (31.83-1.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 1.50Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.172 , 0.197 0.172 , 0.197	Depositor DCC
$R_{free}$ test set	4579 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.0	Xtriage
Anisotropy	0.403	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 48.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4178	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.19 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1866e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACE, Y2Y

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	0.73	0/1147	0.91	2/1538 (0.1%)
1	B	0.68	0/1140	0.86	2/1530 (0.1%)
2	C	0.80	0/774	0.90	0/1050
2	D	0.82	0/785	0.94	2/1063 (0.2%)
3	E	1.11	0/24	1.19	0/32
3	F	1.10	0/24	1.05	0/32
All	All	0.75	0/3894	0.90	6/5245 (0.1%)

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
3	E	0	1
3	F	0	1
All	All	0	2

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	241	ARG	NE-CZ-NH1	10.52	125.56	120.30
2	D	241	ARG	NE-CZ-NH2	-7.58	116.51	120.30
1	A	64	ARG	NE-CZ-NH2	-6.73	116.94	120.30
1	B	64	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	57	LYS	CB-CA-C	5.29	120.99	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	306	VAL	Peptide
3	F	406	VAL	Peptide

## 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	1120	0	1114	4	0
1	B	1113	0	1101	2	0
2	C	751	0	705	5	0
2	D	759	0	731	3	0
3	E	40	0	22	0	0
3	F	40	0	22	0	0
4	A	115	0	0	1	0
4	B	101	0	0	0	0
4	C	62	0	0	2	0
4	D	60	0	0	0	0
4	E	7	0	0	0	0
4	F	10	0	0	0	0
All	All	4178	0	3695	12	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 2.

The worst 5 of 12 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:A:93:ARG:HB2	1:A:134:VAL:HG22	1.62	0.81
2:C:241:ARG:NH2	1:B:35:ASN:OD1	2.32	0.63
2:D:207:ARG:HA	2:D:213:SER:HA	1.83	0.61
2:C:207:ARG:HA	2:C:213:SER:HA	1.86	0.57
2:C:271:LYS:HE3	4:C:318:HOH:O	2.09	0.53

There are no symmetry-related clashes.

## 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	143/175 (82%)	140 (98%)	3 (2%)	0	100	100
1	B	143/175 (82%)	140 (98%)	3 (2%)	0	100	100
2	C	91/110 (83%)	89 (98%)	2 (2%)	0	100	100
2	D	91/110 (83%)	89 (98%)	2 (2%)	0	100	100
3	E	3/5 (60%)	3 (100%)	0	0	100	100
3	F	3/5 (60%)	3 (100%)	0	0	100	100
All	All	474/580 (82%)	464 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	128/159 (80%)	127 (99%)	1 (1%)	81	66
1	B	126/159 (79%)	126 (100%)	0	100	100
2	C	77/98 (79%)	76 (99%)	1 (1%)	69	44
2	D	80/98 (82%)	79 (99%)	1 (1%)	69	44
3	E	3/3 (100%)	3 (100%)	0	100	100
3	F	3/3 (100%)	3 (100%)	0	100	100
All	All	417/520 (80%)	414 (99%)	3 (1%)	84	69

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LYS
2	C	268	MET
2	D	268	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	225	GLN

### 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](#)

There are no ligands in this entry.

## 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](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	141/175 (80%)	-0.11	3 (2%) 63 68	10, 16, 28, 58	1 (0%)
1	B	141/175 (80%)	-0.02	4 (2%) 53 57	11, 18, 32, 41	0
2	C	93/110 (84%)	-0.14	2 (2%) 62 67	8, 13, 24, 56	0
2	D	92/110 (83%)	-0.02	2 (2%) 62 67	8, 13, 23, 39	0
3	E	3/5 (60%)	-0.62	0 100 100	12, 12, 15, 16	0
3	F	3/5 (60%)	-0.71	0 100 100	13, 13, 15, 17	0
All	All	473/580 (81%)	-0.08	11 (2%) 60 65	8, 15, 30, 58	1 (0%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	34	ASP	5.8
2	C	276	TYR	3.7
2	D	276	TYR	3.6
2	C	277	HIS	3.4
1	B	174	THR	3.2

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.