



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2022 – 03:26 AM EST

PDB ID : 6X8J  
Title : Caspase-7 in complex with ketomethylene inhibitor reveals tetrahedral adduct  
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Deposited on : 2020-06-01  
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure 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

<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

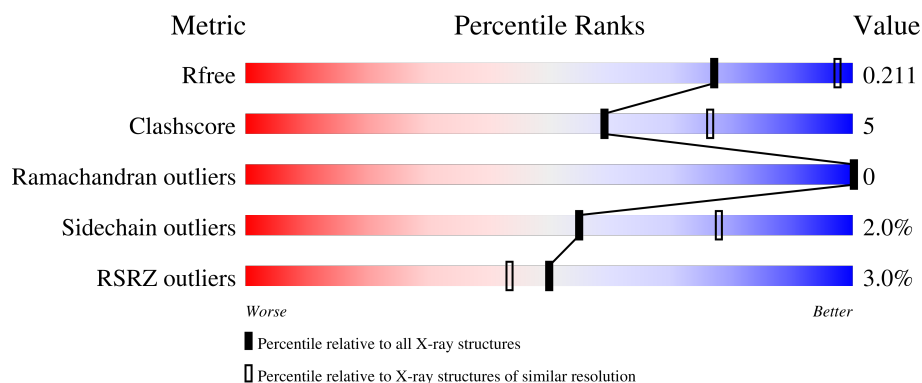
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	198	<div> <div>0%</div> <div>62% 8% . 29%</div> </div>
1	B	198	<div> <div>0%</div> <div>60% 11% 29%</div> </div>
2	C	113	<div> <div>4%</div> <div>70% 9% . 19%</div> </div>
2	D	113	<div> <div>6%</div> <div>70% 11% 19%</div> </div>
3	E	5	<div> <div>80% 20%</div> </div>

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

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3737 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-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	140	Total	C	N	O	S	0	0	0
			1077	676	183	207	11			
1	B	140	Total	C	N	O	S	0	0	0
			1069	671	182	205	11			

- Molecule 2 is a protein called Caspase-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	91	Total	C	N	O	S	0	0	0
			741	479	125	133	4			
2	D	91	Total	C	N	O	S	0	0	0
			727	471	121	131	4			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	304	LEU	-	expression tag	UNP P55210
C	305	GLU	-	expression tag	UNP P55210
C	306	HIS	-	expression tag	UNP P55210
C	307	HIS	-	expression tag	UNP P55210
C	308	HIS	-	expression tag	UNP P55210
C	309	HIS	-	expression tag	UNP P55210
C	310	HIS	-	expression tag	UNP P55210
C	311	HIS	-	expression tag	UNP P55210
D	304	LEU	-	expression tag	UNP P55210
D	305	GLU	-	expression tag	UNP P55210
D	306	HIS	-	expression tag	UNP P55210
D	307	HIS	-	expression tag	UNP P55210
D	308	HIS	-	expression tag	UNP P55210
D	309	HIS	-	expression tag	UNP P55210
D	310	HIS	-	expression tag	UNP P55210
D	311	HIS	-	expression tag	UNP P55210

- 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			

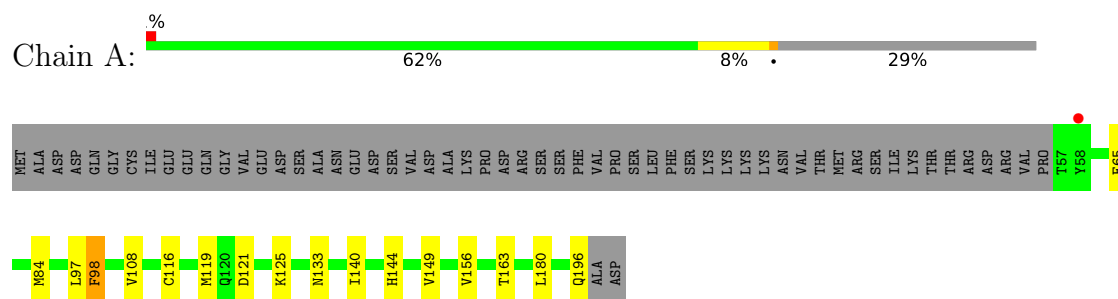
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	19	Total	O	0	0
			19	19		
4	C	10	Total	O	0	0
			10	10		
4	B	9	Total	O	0	0
			9	9		
4	D	5	Total	O	0	0
			5	5		

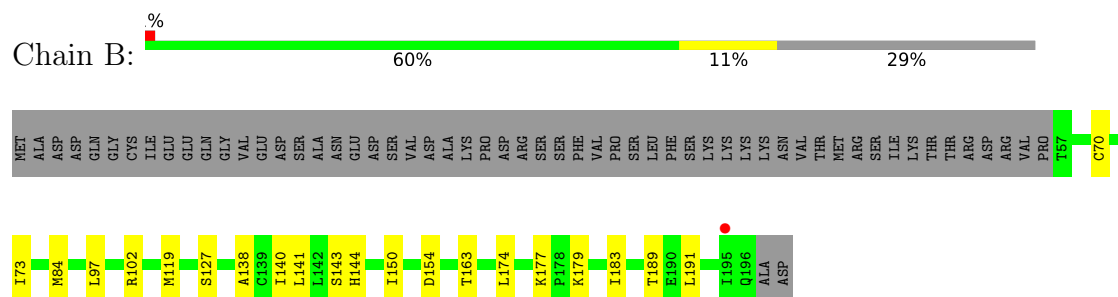
### 3 Residue-property plots [i](#)

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.

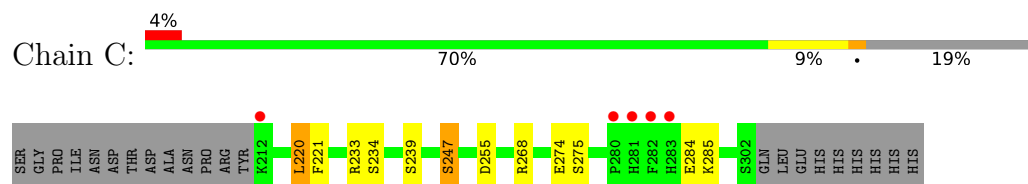
#### • Molecule 1: Caspase-7



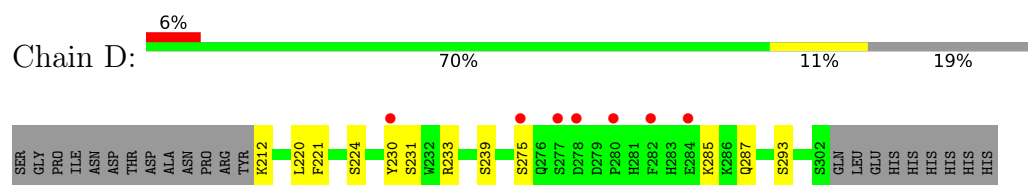
#### • Molecule 1: Caspase-7




#### • Molecule 2: Caspase-7



#### • Molecule 2: Caspase-7




#### • Molecule 3: ketomethylene inhibitor

Chain E:  80% 20%



- Molecule 3: ketomethylene inhibitor

Chain F:  80% 20%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.63Å 88.63Å 186.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.84 – 2.60 48.30 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.84-2.60) 99.8 (48.30-2.60)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.183 , 0.211 0.183 , 0.211	Depositor DCC
$R_{free}$ test set	1335 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.1	Xtriage
Anisotropy	0.602	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3737	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% of the height of the origin peak. No significant pseudotranslation is detected.*

<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	0.36	0/1094	0.50	0/1472
1	B	0.34	0/1086	0.47	0/1463
2	C	0.28	0/763	0.46	0/1033
2	D	0.27	0/749	0.43	0/1017
3	E	0.24	0/24	0.39	0/32
3	F	0.17	0/24	0.36	0/32
All	All	0.32	0/3740	0.47	0/5049

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.

There are no bond angle outliers.

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	1077	0	1030	13	0
1	B	1069	0	1015	12	0
2	C	741	0	715	7	0
2	D	727	0	689	7	0
3	E	40	0	22	0	0
3	F	40	0	22	0	0
4	A	19	0	0	0	0
4	B	9	0	0	1	0
4	C	10	0	0	0	0
4	D	5	0	0	0	0
All	All	3737	0	3493	34	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.

All (34) 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)
2:D:275:SER:HB3	2:D:285:LYS:H	1.43	0.82
2:C:275:SER:HB3	2:C:285:LYS:H	1.47	0.79
2:C:233:ARG:HA	2:C:239:SER:HA	1.79	0.64
2:C:247:SER:OG	2:C:268:ARG:NH1	2.33	0.62
2:D:233:ARG:HA	2:D:239:SER:HA	1.81	0.62
1:A:149:VAL:CG1	1:A:156:VAL:HB	2.30	0.61
1:A:163:THR:HG21	2:C:221:PHE:HE1	1.65	0.61
1:A:196:GLN:HA	2:D:212:LYS:HA	1.84	0.60
1:A:97:LEU:HD13	1:A:140:ILE:HG21	1.86	0.58
1:A:149:VAL:HG13	1:A:156:VAL:HB	1.86	0.55
1:B:143:SER:HB3	1:B:150:ILE:HD11	1.89	0.55
1:B:97:LEU:HD13	1:B:140:ILE:HG21	1.89	0.53
1:A:84:MET:HB3	1:A:144:HIS:CD2	2.44	0.53
1:A:98:PHE:HB2	1:A:108:VAL:HG11	1.91	0.52
1:B:163:THR:HG21	2:D:221:PHE:HE1	1.78	0.49
1:A:65:GLU:HB2	1:A:133:ASN:HB3	1.94	0.48
1:B:174:LEU:HA	1:B:177:LYS:HD2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:LYS:O	1:B:179:LYS:HE3	2.12	0.48
1:B:70:CYS:HA	1:B:138:ALA:O	2.14	0.47
1:B:73:ILE:HD13	1:B:119:MET:HG2	1.97	0.47
1:B:84:MET:HB3	1:B:144:HIS:CD2	2.50	0.47
1:B:141:LEU:HD12	1:B:183:ILE:HG12	1.97	0.47
1:A:98:PHE:CD1	1:A:98:PHE:C	2.88	0.47
1:B:189:THR:HG22	2:D:230:TYR:CE1	2.50	0.46
1:A:121:ASP:OD2	1:A:125:LYS:HE2	2.16	0.45
2:D:224:SER:O	2:D:287:GLN:NE2	2.44	0.44
1:A:180:LEU:HD23	2:C:220:LEU:HB3	2.00	0.44
1:A:97:LEU:HD22	1:A:140:ILE:HD13	2.00	0.43
2:C:274:GLU:HG2	2:C:284:GLU:HA	2.02	0.42
1:B:154:ASP:OD1	1:B:154:ASP:N	2.46	0.42
1:B:102:ARG:NH2	4:B:201:HOH:O	2.36	0.41
1:A:116:CYS:HA	1:A:119:MET:HE2	2.02	0.40
2:C:285:LYS:HA	2:C:285:LYS:HD3	1.98	0.40
2:D:220:LEU:HD12	2:D:293:SER:HB2	2.02	0.40

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	138/198 (70%)	136 (99%)	2 (1%)	0	100	100
1	B	138/198 (70%)	136 (99%)	2 (1%)	0	100	100
2	C	89/113 (79%)	89 (100%)	0	0	100	100
2	D	89/113 (79%)	88 (99%)	1 (1%)	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	460/632 (73%)	455 (99%)	5 (1%)	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	114/172 (66%)	113 (99%)	1 (1%)	78	91
1	B	112/172 (65%)	110 (98%)	2 (2%)	59	80
2	C	81/103 (79%)	77 (95%)	4 (5%)	25	48
2	D	78/103 (76%)	77 (99%)	1 (1%)	69	86
3	E	3/3 (100%)	3 (100%)	0	100	100
3	F	3/3 (100%)	3 (100%)	0	100	100
All	All	391/556 (70%)	383 (98%)	8 (2%)	55	78

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	98	PHE
2	C	220	LEU
2	C	234	SER
2	C	247	SER
2	C	255	ASP
1	B	127	SER
1	B	191	LEU
2	D	231	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	140/198 (70%)	-0.26	1 (0%) 87 86	37, 48, 68, 82	0
1	B	140/198 (70%)	-0.26	1 (0%) 87 86	43, 58, 76, 84	0
2	C	91/113 (80%)	-0.01	5 (5%) 25 19	37, 52, 81, 90	0
2	D	91/113 (80%)	0.08	7 (7%) 13 10	36, 54, 86, 102	0
3	E	3/5 (60%)	0.56	0 100 100	59, 59, 60, 70	0
3	F	3/5 (60%)	1.25	0 100 100	65, 65, 81, 84	0
All	All	468/632 (74%)	-0.13	14 (2%) 50 43	36, 53, 79, 102	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	280	PRO	3.8
2	C	282	PHE	3.4
2	D	277	SER	2.9
2	D	278	ASP	2.8
2	D	280	PRO	2.8
1	A	58	TYR	2.5
2	D	230	TYR	2.4
2	C	281	HIS	2.3
1	B	195	ILE	2.3
2	D	275	SER	2.3
2	D	284	GLU	2.3
2	C	283	HIS	2.1
2	D	282	PHE	2.1
2	C	212	LYS	2.0

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

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.