

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 6, 2023 - 09:09 am GMT

PDB ID : 2C2O

Title : Crystal structures of caspase-3 in complex with aza-peptide Michael acceptor

inhibitors.

Authors: Ganesan, R.; Jelakovic, S.; Ekici, O.D.; Li, Z.Z.; James, K.E.; Asgian, J.L.;

Campbell, A.; Mikolajczyk, J.; Salvesen, G.S.; Gruetter, M.G.; Powers, J.C.

Deposited on : 2005-09-29

Resolution : 2.45 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
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 (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{-}467$ 

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

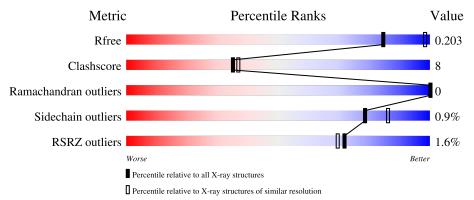
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.45 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
$R_{free}$	130704	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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% 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	147	85%	15%					
2	В	103	80%	18% •					



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2200 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 SUBUNIT P17.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	147	Total 1153	C 712	N 208	O 224	S 9	0	0	1

• Molecule 2 is a protein called CASPASE-3 SUBUNIT P12.

Mo	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	103	Total 843	C 547	N 135	O 154	S 7	0	0	0

• Molecule 3 is a protein called AZA-PEPTIDE INHIBITOR (5S, 8R, 11S)-14-{4-[BENZYL(METHYL) AMINO]-4-OXOBUTANOYL}-8-(2-CARBOXYETHYL)-5-(CARBOXYMETH YL)-11-(1-METHYLETHYL)-3,6,9,12-TETRAOXO-1-PHENYL-2-OXA-4,7,10,13,14-PEN TAAZAHEXADECAN-16-OIC ACID.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	С	5	Total 55	C 36	N 6	O 13	0	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	86	Total O 86 86	0	0
4	В	62	Total O 62 62	0	0
4	С	1	Total O 1 1	0	0

SEQUENCE-PLOTS INFOmissingINFO



# 3 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	66.40Å 83.49Å 96.36Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.55 - 2.45	Depositor
Resolution (A)	19.55 - 2.45	EDS
% Data completeness	99.4 (19.55-2.45)	Depositor
(in resolution range)	99.5 (19.55-2.45)	EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.73 (at 2.46Å)	Xtriage
Refinement program	CNS 1.1	Depositor
D D.	0.168 , 0.215	Depositor
$R, R_{free}$	0.160 , 0.203	DCC
$R_{free}$ test set	1040 reflections (10.30%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.3	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 42.0	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2200	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.36% of the height of the origin peak. No significant pseudotranslation is detected.

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



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 4 Model quality (i)

#### 4.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PHQ, MX3

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		
10101		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.34	0/1168	0.57	1/1565 (0.1%)	
2	В	0.37	0/868	0.59	0/1171	
3	С	0.24	0/23	0.55	0/30	
All	All	0.35	0/2059	0.58	$1/2766 \ (0.0\%)$	

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
3	С	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	129	GLY	N-CA-C	-5.30	99.85	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group	
3	С	4	VAL	Mainchain	

#### 4.2 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	1153	0	1148	17	1
2	В	843	0	807	17	0
3	С	55	0	39	4	0
4	A	86	0	0	3	0
4	В	62	0	0	0	0
4	С	1	0	0	0	0
All	All	2200	0	1994	33	1

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 8.

All (33) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash
	A 100 MET HOO I I 100 W T TO		overlap (Å)
1:A:100:MET:HG3	1:A:139:ILE:HG23	1.68	0.73
2:B:207:ARG:HA	2:B:213:SER:HA	1.81	0.63
2:B:230:LEU:HB2	2:B:235:ILE:CD1	2.28	0.63
2:B:230:LEU:HB2	2:B:235:ILE:HD13	1.81	0.60
1:A:75:ARG:HG3	1:A:85:VAL:HG11	1.84	0.60
1:A:74:LEU:HD13	1:A:117:VAL:HG11	1.83	0.60
2:B:240:ASN:OD1	2:B:263:PRO:HB2	2.01	0.60
2:B:228:ASP:OD1	2:B:229:LYS:HG3	2.01	0.59
1:A:87:ASN:HB2	4:A:2032:HOH:O	2.04	0.57
2:B:206:TRP:HH2	2:B:256:PHE:HB3	1.69	0.57
2:B:187:ILE:HD13	2:B:187:ILE:H	1.70	0.55
2:B:194:LEU:C	2:B:194:LEU:HD13	2.29	0.54
1:A:168:LEU:HD22	2:B:259:LYS:HG3	1.89	0.53
2:B:255:THR:O	2:B:259:LYS:HE3	2.09	0.53
1:A:41:TYR:HB2	1:A:112:SER:OG	2.10	0.52
1:A:121:HIS:HB3	3:C:5:MX3:H142	1.94	0.50
1:A:121:HIS:ND1	3:C:5:MX3:H9C1	2.28	0.49
1:A:113:SER:HB3	1:A:155:PRO:HG2	1.96	0.48
2:B:230:LEU:HB2	2:B:235:ILE:HD11	1.98	0.46
1:A:74:LEU:CD1	1:A:117:VAL:HG11	2.45	0.45
1:A:41:TYR:HB2	1:A:112:SER:HG	1.80	0.45
1:A:121:HIS:HB3	3:C:5:MX3:C14	2.48	0.44
4:A:2025:HOH:O	2:B:224:LYS:HG2	2.18	0.44
2:B:197:TYR:HB2	2:B:264:CYS:HB3	2.00	0.43
1:A:91:LEU:O	1:A:130:THR:HG23	2.19	0.42

Continued on next page...



, ,	omtomorod	trom	previous	maaa
	011.1.111111.111		THETHINS	THEFT

Atom-1	Atom-2	$egin{aligned} & & & & & & & & & & & & & & & & & & &$	Clash overlap (Å)
2:B:194:LEU:HD13	2:B:195:TYR:N	2.34	0.42
1:A:53:LYS:O	1:A:63:SER:HA	2.20	0.42
1:A:120:SER:OG	1:A:121:HIS:N	2.53	0.42
1:A:34:ASP:HA	4:A:2003:HOH:O	2.20	0.42
2:B:262:ILE:O	2:B:262:ILE:HG23	2.19	0.42
2:B:195:TYR:HB2	2:B:266:VAL:HB	2.02	0.41
2:B:213:SER:OG	2:B:216:ILE:HG12	2.20	0.41
1:A:122:GLY:H	3:C:5:MX3:H141	1.87	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:123:GLU:OE2	1:A:123:GLU:OE2[2_665]	2.18	0.02

#### 4.3 Torsion angles (i)

#### 4.3.1 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	Perce	ntiles
1	A	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
2	В	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
3	С	2/5 (40%)	2 (100%)	0	0	100	100
All	All	248/255 (97%)	239 (96%)	9 (4%)	0	100	100

There are no Ramachandran outliers to report.

#### 4.3.2 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	Perce	ntiles
1	A	131/132~(99%)	131 (100%)	0	100	100
2	В	90/90 (100%)	88 (98%)	2 (2%)	52	64
3	С	3/3 (100%)	3 (100%)	0	100	100
All	All	224/225 (100%)	222 (99%)	2 (1%)	78	86

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	187	ILE
2	В	262	ILE

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

Mol	Chain	Res	Type
1	A	80	ASN

#### 4.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

### 4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 4.6 Ligand geometry (i)

There are no ligands in this entry.

#### 4.7 Other polymers (i)

There are no such residues in this entry.



# 4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 5 Fit of model and data (i)

#### 5.1 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,  $95^{th}$  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>	# RSRZ > 2	$OWAB(A^2)$	Q<0.9
1	A	147/147 (100%)	-0.61	2 (1%) 75 74	11, 20, 34, 46	0
2	В	103/103 (100%)	-0.65	2 (1%) 66 64	9, 15, 46, 52	0
3	С	3/5 (60%)	-0.39	0 100 100	35, 35, 36, 38	0
All	All	253/255 (99%)	-0.62	4 (1%) 72 69	9, 18, 42, 52	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	173	GLU	3.4
2	В	185	HIS	2.3
2	В	175	ALA	2.3
1	A	33	LEU	2.0

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

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

### 5.3 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.4 Ligands (i)

There are no ligands in this entry.

## 5.5 Other polymers (i)

There are no such residues in this entry.

