



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:08 AM GMT

PDB ID : 2PJT  
Title : Crystal structure of the catalytic domain of MMP-13 complexed with WAY-344  
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Deposited on : 2007-04-16  
Resolution : 2.80 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

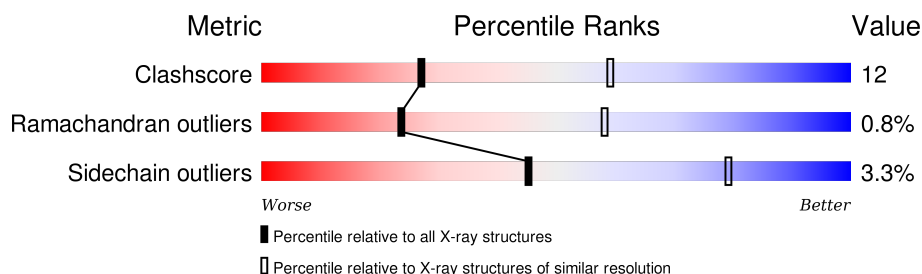
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	165	
1	B	165	
1	C	165	
1	D	165	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5412 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 Collagenase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	0	0	0
			1292	840	207	241	4			
1	B	164	Total	C	N	O	S	0	0	0
			1307	849	209	244	5			
1	C	159	Total	C	N	O	S	0	0	0
			1271	827	201	238	5			
1	D	161	Total	C	N	O	S	0	0	0
			1284	835	205	240	4			

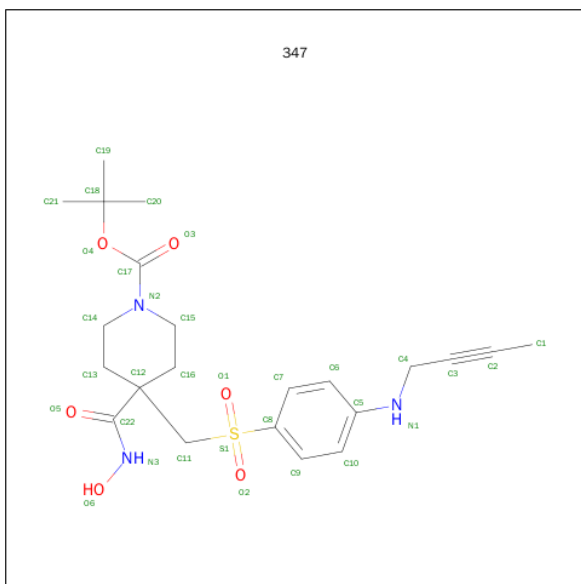
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		
3	A	3	Total	Ca	0	0
			3	3		
3	D	2	Total	Ca	0	0
			2	2		
3	C	3	Total	Ca	0	0
			3	3		

- Molecule 4 is TERT-BUTYL 4-([4-(BUT-2-YN-1-YLAMINO)PHENYL]SULFONYL)METHYL-4-[(HYDROXYAMINO)CARBONYL]PIPERIDINE-1-CARBOXYLATE (three-letter code: 347) (formula: C<sub>22</sub>H<sub>31</sub>N<sub>3</sub>O<sub>6</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			32	22	3	6	1		
4	B	1	Total	C	N	O	S	0	0
			32	22	3	6	1		
4	C	1	Total	C	N	O	S	0	0
			32	22	3	6	1		
4	D	1	Total	C	N	O	S	0	0
			32	22	3	6	1		

- Molecule 5 is water.

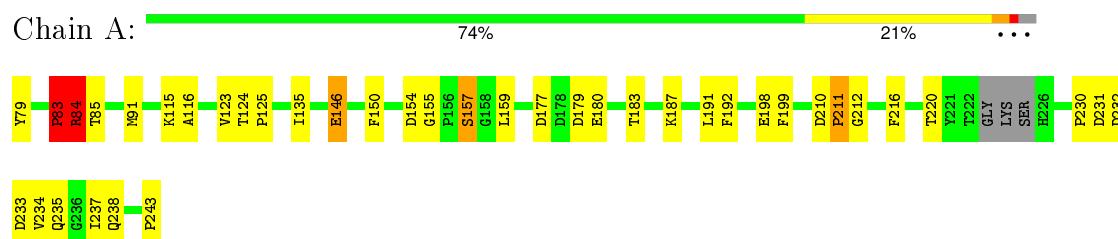
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	25	Total	O	0	0
			25	25		
5	B	33	Total	O	0	0
			33	33		
5	C	25	Total	O	0	0
			25	25		
5	D	29	Total	O	0	0
			29	29		

### 3 Residue-property plots

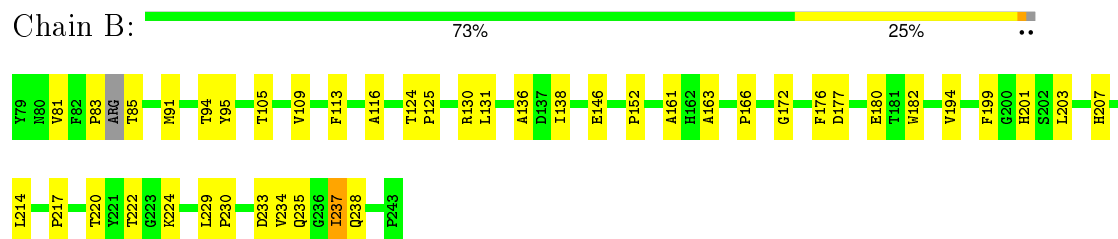
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

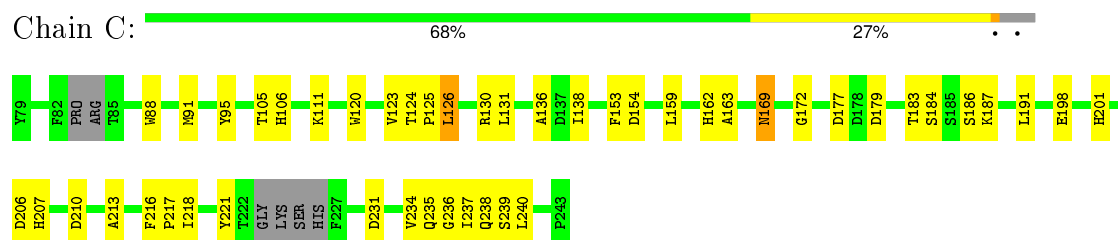
#### • Molecule 1: Collagenase 3



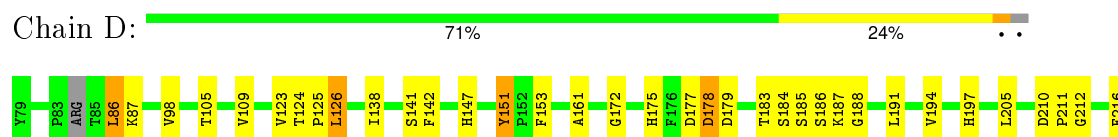
#### • Molecule 1: Collagenase 3



#### • Molecule 1: Collagenase 3



#### • Molecule 1: Collagenase 3



P217	
T220	
Y221	
T222	
GLY	
LYS	
SER	
H226	
L229	
P230	
D233	
I237	
Q238	
Y241	
G242	
P243	

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.35Å 35.79Å 139.41Å 90.00° 108.94° 90.00°	Depositor
Resolution (Å)	19.95 – 2.80	Depositor
% Data completeness (in resolution range)	92.5 (19.95-2.80)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.212 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5412	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 347, 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	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.55	1/1339 (0.1%)	0.73	3/1820 (0.2%)
1	B	0.44	0/1354	0.63	0/1839
1	C	0.45	0/1315	0.63	0/1785
1	D	0.42	0/1330	0.60	0/1807
All	All	0.47	1/5338 (0.0%)	0.65	3/7251 (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
1	A	1	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	84	ARG	CD-NE	-9.60	1.30	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	ARG	N-CA-C	9.33	136.20	111.00
1	A	83	PRO	N-CA-C	8.20	133.43	112.10
1	A	83	PRO	C-N-CA	5.82	136.25	121.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	85	THR	CA



All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	83	PRO	Peptide
1	A	84	ARG	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	1292	0	1198	24	8
1	B	1307	0	1219	27	4
1	C	1271	0	1183	34	0
1	D	1284	0	1189	34	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	3	0	0	0	0
3	B	2	0	0	0	0
3	C	3	0	0	0	0
3	D	2	0	0	0	0
4	A	32	0	30	2	0
4	B	32	0	31	2	0
4	C	32	0	30	2	0
4	D	32	0	30	2	0
5	A	25	0	0	1	1
5	B	33	0	0	1	4
5	C	25	0	0	0	1
5	D	29	0	0	0	0
All	All	5412	0	4910	122	9

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 12.

The worst 5 of 122 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:C:183:THR:HG21	1:C:187:LYS:O	1.72	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:THR:N	5:B:408:HOH:O	2.09	0.86
1:A:243:PRO:OXT	5:A:405:HOH:O	2.02	0.78
1:A:237:ILE:HD12	1:A:238:GLN:H	1.52	0.74
1:D:153:PHE:HB3	1:D:177:ASP:OD2	1.88	0.74

The worst 5 of 9 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:PRO:C	5:B:408:HOH:O[2_667]	0.57	1.63
5:A:421:HOH:O	5:C:417:HOH:O[3_546]	0.78	1.42
1:A:83:PRO:O	5:B:408:HOH:O[2_667]	1.14	1.06
1:A:83:PRO:O	1:B:85:THR:N[2_667]	1.15	1.05
1:A:84:ARG:O	1:B:83:PRO:C[2_667]	1.42	0.78

## 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	158/165 (96%)	142 (90%)	14 (9%)	2 (1%)	15	44
1	B	160/165 (97%)	141 (88%)	17 (11%)	2 (1%)	15	44
1	C	153/165 (93%)	141 (92%)	12 (8%)	0	100	100
1	D	155/165 (94%)	143 (92%)	11 (7%)	1 (1%)	30	65
All	All	626/660 (95%)	567 (91%)	54 (9%)	5 (1%)	24	58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	THR
1	B	224	LYS

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Mol	Chain	Res	Type
1	B	166	PRO
1	D	211	PRO
1	A	211	PRO

### 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	137/141 (97%)	132 (96%)	5 (4%)	42	76
1	B	140/141 (99%)	137 (98%)	3 (2%)	61	90
1	C	136/141 (96%)	132 (97%)	4 (3%)	50	83
1	D	137/141 (97%)	131 (96%)	6 (4%)	35	69
All	All	550/564 (98%)	532 (97%)	18 (3%)	45	79

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

Mol	Chain	Res	Type
1	C	126	LEU
1	C	169	ASN
1	D	151	TYR
1	B	235	GLN
1	B	237	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	80	ASN
1	D	207	HIS
1	C	169	ASN
1	B	127	ASN
1	C	92	ASN

### 5.3.3 RNA ⓘ

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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 22 ligands modelled in this entry, 18 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	347	A	401	2	33,33,33	2.14	12 (36%)	41,48,48	1.97	3 (7%)
4	347	B	401	2	33,33,33	2.57	16 (48%)	41,48,48	1.86	10 (24%)
4	347	C	401	2	33,33,33	2.44	15 (45%)	41,48,48	1.68	5 (12%)
4	347	D	401	2	33,33,33	2.11	13 (39%)	41,48,48	2.05	5 (12%)

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	347	A	401	2	-	0/31/46/46	0/2/2/2
4	347	B	401	2	-	0/31/46/46	0/2/2/2
4	347	C	401	2	-	0/31/46/46	0/2/2/2
4	347	D	401	2	-	0/31/46/46	0/2/2/2

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	401	347	C14-N2	-2.40	1.42	1.47
4	D	401	347	C7-C6	2.02	1.42	1.38
4	C	401	347	C16-C15	2.04	1.57	1.52
4	C	401	347	C7-C6	2.08	1.42	1.38
4	A	401	347	C7-C6	2.20	1.42	1.38

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	401	347	O1-S1-C8	-5.13	102.75	108.38
4	C	401	347	O1-S1-C8	-4.05	103.94	108.38
4	B	401	347	O1-S1-C8	-3.75	104.27	108.38
4	A	401	347	O1-S1-C8	-3.19	104.88	108.38
4	B	401	347	O6-N3-C22	-2.57	116.34	119.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	347	2	0
4	B	401	347	2	0
4	C	401	347	2	0
4	D	401	347	2	0

## 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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.