



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 30, 2017 – 09:41 PM EDT

PDB ID : 5E2Q  
Title : Structure of human DPP3 in complex with angiotensin-II  
Authors : Kumar, P.; Reisinger, M.; Reithofer, V.; Gruber, K.  
Deposited on : unknown  
Resolution : 2.40 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

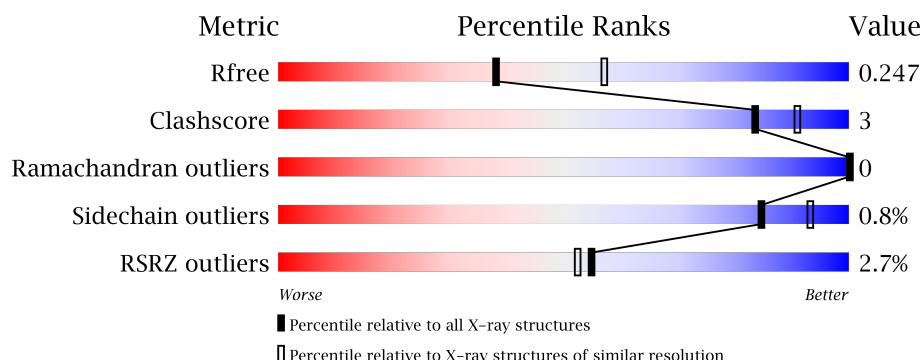
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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.

Mol	Chain	Length	Quality of chain
1	A	726	<div> <div>3%</div> <div>91%</div> <div>8%</div> </div>
2	B	8	<div> <div>88%</div> <div>13%</div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6000 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 Dipeptidyl peptidase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	725	Total	C	N	O	S	0	1	0
			5758	3670	975	1101	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	SER	CYS	engineered mutation	UNP Q9NY33
A	207	CYS	GLU	engineered mutation	UNP Q9NY33
A	451	ALA	GLU	engineered mutation	UNP Q9NY33
A	491	CYS	SER	engineered mutation	UNP Q9NY33
A	519	SER	CYS	engineered mutation	UNP Q9NY33
A	654	SER	CYS	engineered mutation	UNP Q9NY33

- Molecule 2 is a protein called angiotensin-II.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	8	Total	C	N	O	0	0	0
			75	50	13	12			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	K	0	0
			1	1		

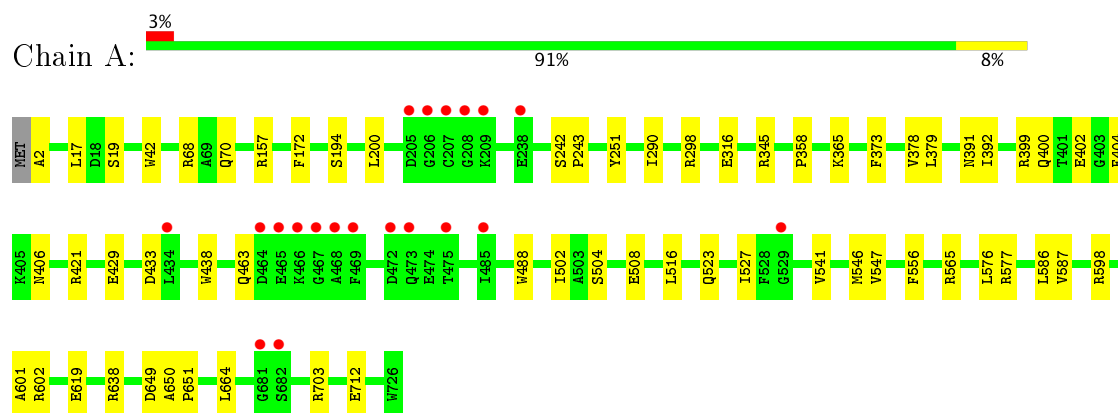
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	162	Total 162	O 162	0	0
5	B	3	Total 3	O 3	0	0

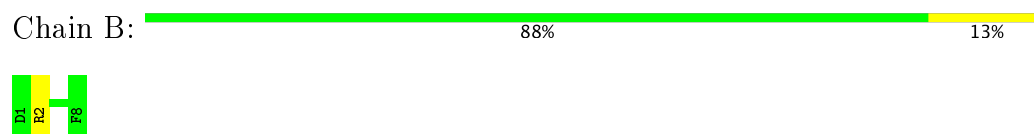
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Dipeptidyl peptidase 3



- Molecule 2: angiotensin-II



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.13Å 105.92Å 64.85Å 90.00° 93.91° 90.00°	Depositor
Resolution (Å)	45.33 – 2.40 45.33 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.3 (45.33-2.40) 97.4 (45.33-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.23 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.206 , 0.247 0.207 , 0.247	Depositor DCC
$R_{free}$ test set	1525 reflections (5.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.5	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 31.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6000	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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: K, MG

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	0.21	0/5893	0.36	0/7983
2	B	0.22	0/78	0.38	0/104
All	All	0.21	0/5971	0.36	0/8087

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	5758	0	5635	32	0
2	B	75	0	71	1	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	162	0	0	3	0
5	B	3	0	0	0	0
All	All	6000	0	5706	32	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 3.

All (32) 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:516:LEU:HD11	1:A:546:MET:HG2	1.70	0.71
1:A:68[A]:ARG:NH1	1:A:712:GLU:OE2	2.27	0.67
1:A:365:LYS:HE2	1:A:400:GLN:HG2	1.76	0.66
1:A:298:ARG:NH2	1:A:402:GLU:OE1	2.30	0.65
1:A:358:PRO:HB3	1:A:619:GLU:HG3	1.78	0.64
1:A:438:TRP:HB2	1:A:541:VAL:HG21	1.85	0.58
1:A:2:ALA:N	5:A:906:HOH:O	2.37	0.56
1:A:316:GLU:HG3	2:B:2:ARG:HD2	1.86	0.56
1:A:399:ARG:HG2	1:A:404:PHE:HB3	1.87	0.55
1:A:194:SER:HB3	1:A:290:ILE:HG13	1.89	0.53
1:A:68[B]:ARG:NH1	1:A:712:GLU:OE2	2.42	0.52
1:A:421:ARG:NH2	1:A:429:GLU:OE1	2.43	0.52
1:A:17:LEU:HD21	1:A:378:VAL:HB	1.92	0.50
1:A:586:LEU:HG	1:A:587:VAL:HG23	1.97	0.47
1:A:391:ASN:ND2	1:A:406:ASN:OD1	2.48	0.46
1:A:19:SER:HB3	1:A:379:LEU:HD23	1.98	0.46
1:A:601:ALA:O	1:A:602:ARG:NH1	2.47	0.46
1:A:42:TRP:CD2	1:A:703:ARG:HD3	2.50	0.45
1:A:421:ARG:NH1	1:A:433:ASP:OD1	2.50	0.45
1:A:650:ALA:HA	1:A:651:PRO:HD3	1.90	0.43
1:A:157:ARG:NH2	5:A:909:HOH:O	2.43	0.43
1:A:504:SER:O	1:A:508:GLU:HG2	2.18	0.43
1:A:463:GLN:OE1	1:A:488:TRP:NE1	2.52	0.43
1:A:577:ARG:HB3	1:A:577:ARG:HH21	1.83	0.42
1:A:172:PHE:HA	1:A:200:LEU:O	2.19	0.42
1:A:242:SER:HA	1:A:243:PRO:HD3	1.81	0.41
1:A:345:ARG:HD2	1:A:527:ILE:HG23	2.02	0.41
1:A:556:PHE:HA	1:A:565:ARG:NH2	2.36	0.41
1:A:502:ILE:HD13	1:A:638:ARG:HG2	2.02	0.41
1:A:598:ARG:HD2	1:A:664:LEU:HD21	2.03	0.41
1:A:70:GLN:NE2	5:A:919:HOH:O	2.48	0.41
1:A:547:VAL:HG13	1:A:576:LEU:HD13	2.03	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	724/726 (100%)	702 (97%)	22 (3%)	0	100	100
2	B	6/8 (75%)	6 (100%)	0	0	100	100
All	All	730/734 (100%)	708 (97%)	22 (3%)	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	609/609 (100%)	604 (99%)	5 (1%)	85	93
2	B	8/8 (100%)	8 (100%)	0	100	100
All	All	617/617 (100%)	612 (99%)	5 (1%)	85	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	251	TYR
1	A	373	PHE
1	A	392	ILE
1	A	523	GLN
1	A	649	ASP

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

Mol	Chain	Res	Type
1	A	450	HIS

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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	725/726 (99%)	-0.03	20 (2%) 53 51	20, 36, 60, 96	0
2	B	8/8 (100%)	0.15	0 100 100	29, 33, 37, 40	0
All	All	733/734 (99%)	-0.03	20 (2%) 55 52	20, 36, 60, 96	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	207	CYS	5.1
1	A	206	GLY	5.1
1	A	467	GLY	4.6
1	A	465	GLU	4.3
1	A	466	LYS	4.1
1	A	682	SER	3.3
1	A	475	THR	3.3
1	A	681	GLY	2.9
1	A	468	ALA	2.8
1	A	238	GLU	2.6
1	A	473	GLN	2.6
1	A	469	PHE	2.5
1	A	205	ASP	2.5
1	A	434	LEU	2.5
1	A	472	ASP	2.5
1	A	464	ASP	2.3
1	A	208	GLY	2.3
1	A	485	ILE	2.3
1	A	209	LYS	2.0
1	A	529	GLY	2.0

## 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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MG	A	801	1/1	0.97	0.14	0.11	22,22,22,22	0
4	K	A	802	1/1	0.99	0.11	-2.52	39,39,39,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.