



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2024 – 10:10 AM EDT

PDB ID : 6QZV
Title : DPP9 bound to a dipeptide (MP) from the N-terminus of BRCA2
Authors : Ross, B.; Geiss-Friedlander, R.; Huber, R.
Deposited on : 2019-03-12
Resolution : 3.00 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

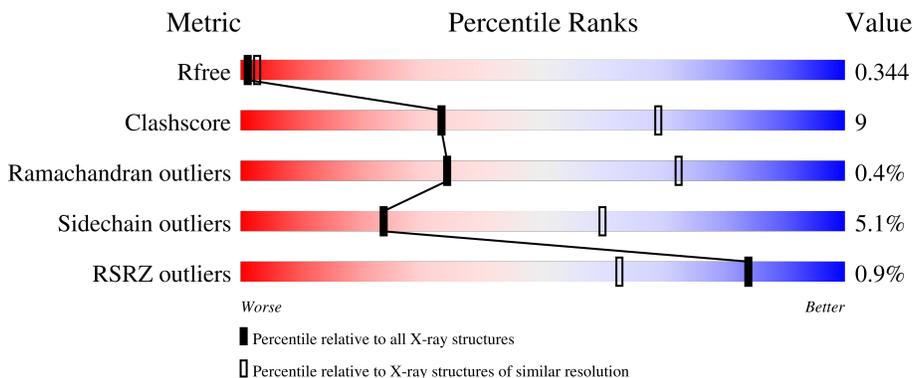
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 $\leq 5\%$. 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	898	 71% 18% • 10%
1	B	898	 69% 20% • 10%
1	C	898	 69% 20% • 10%
1	D	898	 69% 20% • 10%
2	E	2	 50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	 50% 50%
2	G	2	 50% 50%
2	H	2	 50% 50%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 26316 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 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	808	6563	4226	1123	1186	28	0	0	0
1	B	805	6540	4213	1115	1184	28	0	0	0
1	C	808	6560	4222	1118	1192	28	0	0	0
1	D	812	6585	4236	1122	1199	28	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	864	HIS	-	expression tag	UNP Q86TI2
A	865	HIS	-	expression tag	UNP Q86TI2
A	866	HIS	-	expression tag	UNP Q86TI2
A	867	HIS	-	expression tag	UNP Q86TI2
A	868	HIS	-	expression tag	UNP Q86TI2
A	869	HIS	-	expression tag	UNP Q86TI2
B	864	HIS	-	expression tag	UNP Q86TI2
B	865	HIS	-	expression tag	UNP Q86TI2
B	866	HIS	-	expression tag	UNP Q86TI2
B	867	HIS	-	expression tag	UNP Q86TI2
B	868	HIS	-	expression tag	UNP Q86TI2
B	869	HIS	-	expression tag	UNP Q86TI2
C	864	HIS	-	expression tag	UNP Q86TI2
C	865	HIS	-	expression tag	UNP Q86TI2
C	866	HIS	-	expression tag	UNP Q86TI2
C	867	HIS	-	expression tag	UNP Q86TI2
C	868	HIS	-	expression tag	UNP Q86TI2
C	869	HIS	-	expression tag	UNP Q86TI2
D	864	HIS	-	expression tag	UNP Q86TI2
D	865	HIS	-	expression tag	UNP Q86TI2
D	866	HIS	-	expression tag	UNP Q86TI2

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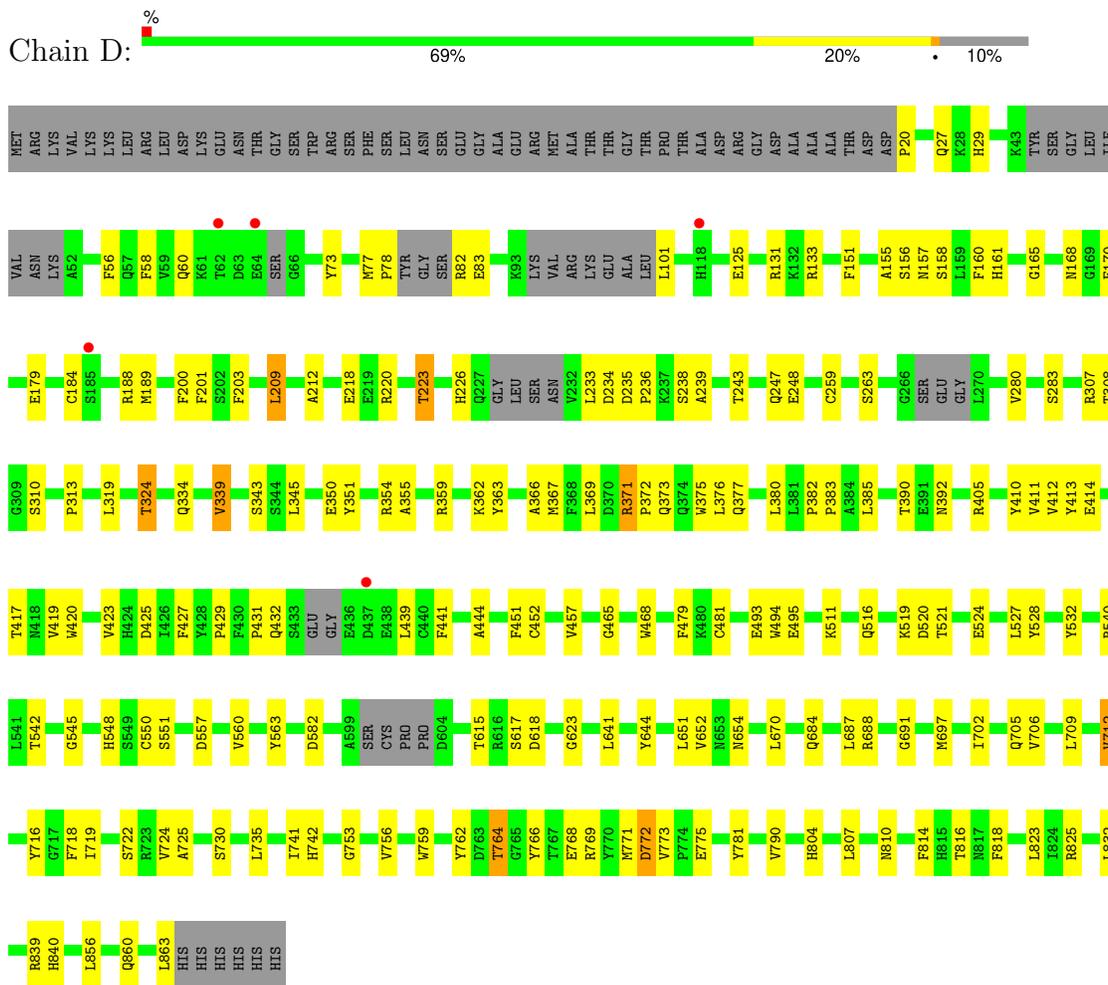
Chain	Residue	Modelled	Actual	Comment	Reference
D	867	HIS	-	expression tag	UNP Q86TI2
D	868	HIS	-	expression tag	UNP Q86TI2
D	869	HIS	-	expression tag	UNP Q86TI2

- Molecule 2 is a protein called MET-PRO.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	S	0	0	0
			16	10	2	3	1			
2	F	2	Total	C	N	O	S	0	0	0
			16	10	2	3	1			
2	G	2	Total	C	N	O	S	0	0	0
			16	10	2	3	1			
2	H	2	Total	C	N	O	S	0	0	0
			16	10	2	3	1			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	2	Total	O	0	0
			2	2		
3	D	2	Total	O	0	0
			2	2		



• Molecule 2: MET-PRO



• Molecule 2: MET-PRO



• Molecule 2: MET-PRO



• Molecule 2: MET-PRO



6232
F233

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	119.52Å 117.22Å 163.40Å 90.00° 105.72° 90.00°	Depositor
Resolution (Å)	43.47 – 3.00 43.47 – 3.00	Depositor EDS
% Data completeness (in resolution range)	88.1 (43.47-3.00) 88.1 (43.47-3.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.8.0232	Depositor
R, R_{free}	0.286 , 0.345 0.287 , 0.344	Depositor DCC
R_{free} test set	3827 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.9	Xtrriage
Anisotropy	0.892	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	26316	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.79 % 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 1.6741e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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	0.66	0/6759	0.70	0/9165
1	B	0.66	0/6733	0.70	0/9128
1	C	0.66	0/6754	0.70	0/9159
1	D	0.66	0/6779	0.70	0/9192
2	E	0.87	0/16	1.31	0/19
2	F	0.66	0/16	0.61	0/19
2	G	0.68	0/16	0.68	0/19
2	H	0.65	0/16	0.68	0/19
All	All	0.66	0/27089	0.70	0/36720

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 [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	6563	0	6348	107	0
1	B	6540	0	6340	124	0
1	C	6560	0	6347	113	0
1	D	6585	0	6365	110	0
2	E	16	0	15	4	0
2	F	16	0	15	3	0
2	G	16	0	15	1	0
2	H	16	0	15	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	2	0	0	1	0
3	D	2	0	0	0	0
All	All	26316	0	25460	446	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 9.

The worst 5 of 446 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:B:420:TRP:HZ3	1:B:694:LYS:HB2	1.26	0.97
1:A:307:ARG:O	1:A:310:SER:HB3	1.68	0.92
1:D:223:THR:HG21	1:D:239:ALA:HB3	1.54	0.87
1:B:420:TRP:CZ3	1:B:694:LYS:HB2	2.13	0.84
1:B:307:ARG:O	1:B:310:SER:HB3	1.78	0.81

There are no symmetry-related clashes.

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	790/898 (88%)	735 (93%)	52 (7%)	3 (0%)	34 72
1	B	785/898 (87%)	729 (93%)	55 (7%)	1 (0%)	51 85
1	C	790/898 (88%)	735 (93%)	50 (6%)	5 (1%)	25 64
1	D	794/898 (88%)	730 (92%)	61 (8%)	3 (0%)	34 72
All	All	3159/3592 (88%)	2929 (93%)	218 (7%)	12 (0%)	34 72

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	232	VAL
1	A	465	GLY
1	D	772	ASP
1	C	207	SER
1	C	348	LYS

5.3.2 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	Percentiles	
1	A	712/785 (91%)	675 (95%)	37 (5%)	23	59
1	B	712/785 (91%)	673 (94%)	39 (6%)	21	57
1	C	714/785 (91%)	677 (95%)	37 (5%)	23	59
1	D	715/785 (91%)	682 (95%)	33 (5%)	27	64
2	E	2/2 (100%)	2 (100%)	0	100	100
2	F	2/2 (100%)	2 (100%)	0	100	100
2	G	2/2 (100%)	2 (100%)	0	100	100
2	H	2/2 (100%)	2 (100%)	0	100	100
All	All	2861/3148 (91%)	2715 (95%)	146 (5%)	24	60

5 of 146 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	101	LEU
1	D	722	SER
1	D	184	CYS
1	D	324	THR
1	B	232	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	684	GLN

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Mol	Chain	Res	Type
1	D	432	GLN
1	C	710	GLN
1	D	334	GLN
1	D	684	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, 95th 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 ²)	Q<0.9
1	A	808/898 (89%)	-0.21	8 (0%) 82 59	10, 26, 60, 83	0
1	B	805/898 (89%)	-0.20	10 (1%) 79 54	8, 24, 53, 81	0
1	C	808/898 (89%)	-0.23	5 (0%) 89 72	9, 23, 54, 80	0
1	D	812/898 (90%)	-0.23	5 (0%) 89 72	9, 23, 55, 77	0
2	E	2/2 (100%)	0.62	0 100 100	43, 43, 43, 44	0
2	F	2/2 (100%)	0.56	0 100 100	30, 30, 30, 31	0
2	G	2/2 (100%)	1.23	0 100 100	38, 38, 38, 38	0
2	H	2/2 (100%)	1.49	0 100 100	42, 42, 42, 45	0
All	All	3241/3600 (90%)	-0.21	28 (0%) 84 63	8, 24, 56, 83	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	111	HIS	4.6
1	B	118	HIS	4.2
1	A	118	HIS	3.7
1	C	118	HIS	3.5
1	B	327	GLN	3.3

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.