



wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 08:34 am BST

PDB ID : 5ZZ9
Title : Crystal structure of Homer2 EVH1/Drebrin PPXXF complex
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Deposited on : 2018-05-31
Resolution : 2.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

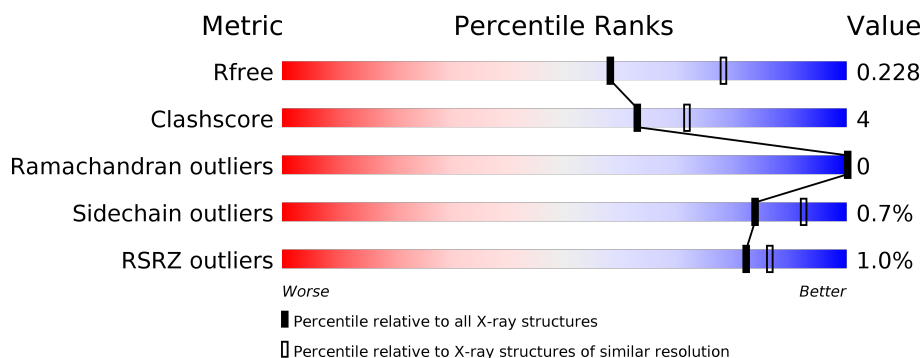
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 ≥ 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	123	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 84%, green 9%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 84% 9% 7% </div> </div>
1	B	123	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 84%, green 9%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 84% 9% 7% </div> </div>
1	C	123	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 77%, green 15%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 77% 15% 8% </div> </div>
2	D	28	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 11%, orange 1%, yellow 50%, green 46%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 11% 50% 46% </div> </div>
2	E	28	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 61%, green 7%, grey 32%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 61% 7% 32% </div> </div>
2	F	28	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 32%, green 11%, grey 57%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 32% 11% 57% </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2969 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 Homer protein homolog 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	114	Total	C	N	O	S	0	0	0
			868	552	146	169	1			
1	B	114	Total	C	N	O	S	0	0	0
			865	553	143	168	1			
1	C	113	Total	C	N	O	S	0	0	0
			869	554	148	166	1			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9QWW1
A	0	GLY	-	expression tag	UNP Q9QWW1
A	1	SER	-	expression tag	UNP Q9QWW1
A	2	GLY	-	expression tag	UNP Q9QWW1
A	3	GLY	-	expression tag	UNP Q9QWW1
A	4	SER	-	expression tag	UNP Q9QWW1
A	5	GLY	-	expression tag	UNP Q9QWW1
A	6	GLY	-	expression tag	UNP Q9QWW1
B	-1	GLY	-	expression tag	UNP Q9QWW1
B	0	GLY	-	expression tag	UNP Q9QWW1
B	1	SER	-	expression tag	UNP Q9QWW1
B	2	GLY	-	expression tag	UNP Q9QWW1
B	3	GLY	-	expression tag	UNP Q9QWW1
B	4	SER	-	expression tag	UNP Q9QWW1
B	5	GLY	-	expression tag	UNP Q9QWW1
B	6	GLY	-	expression tag	UNP Q9QWW1
C	-1	GLY	-	expression tag	UNP Q9QWW1
C	0	GLY	-	expression tag	UNP Q9QWW1
C	1	SER	-	expression tag	UNP Q9QWW1
C	2	GLY	-	expression tag	UNP Q9QWW1
C	3	GLY	-	expression tag	UNP Q9QWW1
C	4	SER	-	expression tag	UNP Q9QWW1
C	5	GLY	-	expression tag	UNP Q9QWW1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	6	GLY	-	expression tag	UNP Q9QWW1

- Molecule 2 is a protein called Peptide from Drebrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	15	Total	C	N	O	S	0	0	0
			98	64	15	18	1			
2	E	19	Total	C	N	O	S	0	1	0
			155	100	20	33	2			
2	F	12	Total	C	N	O	S	0	1	0
			83	54	12	15	2			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1015	SER	-	expression tag	UNP Q16643
D	1016	GLY	-	expression tag	UNP Q16643
D	1017	GLU	-	expression tag	UNP Q16643
D	1018	ASN	-	expression tag	UNP Q16643
D	1019	LEU	-	expression tag	UNP Q16643
D	1020	GLN	-	expression tag	UNP Q16643
E	1015	SER	-	expression tag	UNP Q16643
E	1016	GLY	-	expression tag	UNP Q16643
E	1017	GLU	-	expression tag	UNP Q16643
E	1018	ASN	-	expression tag	UNP Q16643
E	1019	LEU	-	expression tag	UNP Q16643
E	1020	GLN	-	expression tag	UNP Q16643
F	1015	SER	-	expression tag	UNP Q16643
F	1016	GLY	-	expression tag	UNP Q16643
F	1017	GLU	-	expression tag	UNP Q16643
F	1018	ASN	-	expression tag	UNP Q16643
F	1019	LEU	-	expression tag	UNP Q16643
F	1020	GLN	-	expression tag	UNP Q16643

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		
3	B	10	Total	O	0	0
			10	10		

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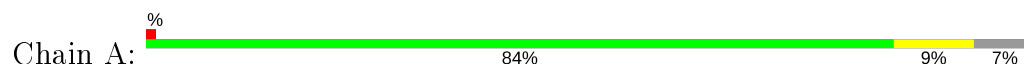
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	9	Total 9	O 9	0	0
3	D	1	Total 1	O 1	0	0
3	E	2	Total 2	O 2	0	0

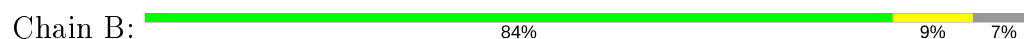
3 Residue-property plots [i](#)

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: Homer protein homolog 2



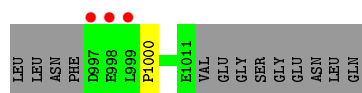
- Molecule 1: Homer protein homolog 2



- Molecule 1: Homer protein homolog 2



- Molecule 2: Peptide from Drebrin



- Molecule 2: Peptide from Drebrin



- Molecule 2: Peptide from Drebrin

Chain F: 32% 11% 57%

LEU	LEU	ASN	PHE	ASP	GLU	L999	P1000	E1001	P1002	E1010	GLU	VAL	GLU	GLY	SER	GLY	GLU	ASN	LEU	GLN
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	45.34Å 47.81Å 50.41Å 70.44° 83.56° 90.39°	Depositor
Resolution (Å)	47.15 – 2.30 47.15 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.2 (47.15-2.30) 96.3 (47.15-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.192 , 0.228 0.192 , 0.228	Depositor DCC
R_{free} test set	821 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	42.5	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2969	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.14% of the height of the origin peak. No significant pseudotranslation is detected.*

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	0.28	0/888	0.50	0/1212
1	B	0.28	0/885	0.48	0/1208
1	C	0.33	0/889	0.55	0/1213
2	D	0.27	0/102	0.49	0/143
2	E	0.30	0/163	0.51	0/224
2	F	0.40	0/90	0.72	0/126
All	All	0.30	0/3017	0.52	0/4126

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	868	0	805	6	0
1	B	865	0	808	7	0
1	C	869	0	818	11	0
2	D	98	0	78	1	0
2	E	155	0	138	1	0
2	F	83	0	68	2	0
3	A	9	0	0	1	0
3	B	10	0	0	0	0
3	C	9	0	0	0	0
3	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	2	0	0	0	0
All	All	2969	0	2715	24	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 4.

The worst 5 of 24 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:12:ILE:HD12	1:B:58:GLY:HA2	1.68	0.73
1:C:62:ILE:HG22	1:C:63:ILE:HG13	1.71	0.72
1:A:70:ASN:ND2	3:A:202:HOH:O	2.35	0.58
1:A:45:ASP:OD2	1:A:52:ARG:NH2	2.37	0.57
1:B:9:GLU:OE1	1:B:52:ARG:NH1	2.38	0.56

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	112/123 (91%)	109 (97%)	3 (3%)	0	100	100
1	B	112/123 (91%)	110 (98%)	2 (2%)	0	100	100
1	C	111/123 (90%)	110 (99%)	1 (1%)	0	100	100
2	D	13/28 (46%)	13 (100%)	0	0	100	100
2	E	18/28 (64%)	18 (100%)	0	0	100	100
2	F	11/28 (39%)	11 (100%)	0	0	100	100
All	All	377/453 (83%)	371 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	89/102 (87%)	87 (98%)	2 (2%)	52	69
1	B	89/102 (87%)	89 (100%)	0	100	100
1	C	90/102 (88%)	90 (100%)	0	100	100
2	D	9/25 (36%)	9 (100%)	0	100	100
2	E	19/25 (76%)	19 (100%)	0	100	100
2	F	9/25 (36%)	9 (100%)	0	100	100
All	All	305/381 (80%)	303 (99%)	2 (1%)	84	92

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

Mol	Chain	Res	Type
1	A	9	GLU
1	A	16	ARG

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

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](#)

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	114/123 (92%)	-0.15	1 (0%) 84 88	31, 42, 80, 102	0
1	B	114/123 (92%)	-0.09	0 100 100	30, 45, 75, 93	0
1	C	113/123 (91%)	-0.07	0 100 100	33, 48, 83, 103	0
2	D	15/28 (53%)	0.65	3 (20%) 1 1	37, 47, 108, 117	0
2	E	19/28 (67%)	0.15	0 100 100	43, 59, 92, 143	0
2	F	12/28 (42%)	0.01	0 100 100	48, 61, 88, 100	0
All	All	387/453 (85%)	-0.06	4 (1%) 82 86	30, 47, 86, 143	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	997	ASP	5.1
2	D	998	GLU	5.1
2	D	999	LEU	3.1
1	A	8	GLY	2.7

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](#)

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.