



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 06:16 PM GMT

PDB ID : 1VF6
Title : 2.1 Angstrom crystal structure of the PALS-1-L27N and PATJ L27 heterodimer complex
Authors : Li, Y.; Lavie, A.; Margolis, B.; Karnak, D.
Deposited on : 2004-04-09
Resolution : 2.10 Å (reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

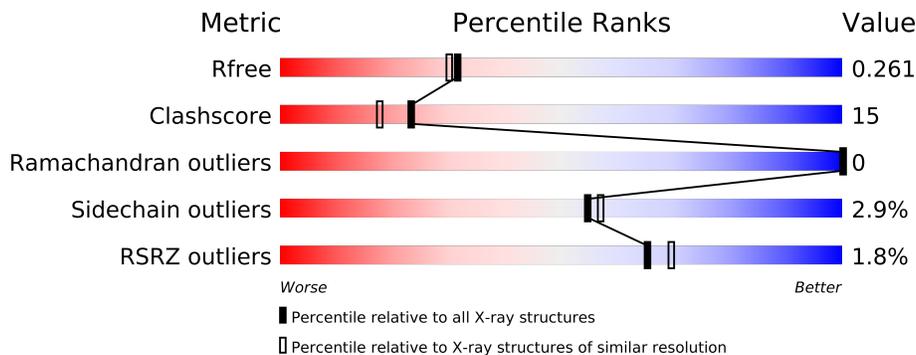
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.10 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}	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	83	
1	B	83	
2	C	72	
2	D	72	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 1867 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PALS1-associated tight junction protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	58	476	304	81	89	2	0	0	0
1	B	60	493	315	84	92	2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	MET	-	INITIATING METHIONINE	UNP Q8NI35
B	8	MET	-	INITIATING METHIONINE	UNP Q8NI35

- Molecule 2 is a protein called MAGUK p55 subfamily member 5.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	51	414	258	72	84	0	0	0
2	D	48	390	244	68	78	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	109	MET	-	EXPRESSION TAG	UNP Q9JLB2
C	110	GLY	-	EXPRESSION TAG	UNP Q9JLB2
C	111	SER	-	EXPRESSION TAG	UNP Q9JLB2
C	112	SER	-	EXPRESSION TAG	UNP Q9JLB2
C	113	HIS	-	EXPRESSION TAG	UNP Q9JLB2
C	114	HIS	-	EXPRESSION TAG	UNP Q9JLB2
C	115	HIS	-	EXPRESSION TAG	UNP Q9JLB2
C	116	HIS	-	EXPRESSION TAG	UNP Q9JLB2
C	117	HIS	-	EXPRESSION TAG	UNP Q9JLB2
C	118	HIS	-	EXPRESSION TAG	UNP Q9JLB2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	119	SER	-	EXPRESSION TAG	UNP Q9JLB2
C	120	GLN	-	EXPRESSION TAG	UNP Q9JLB2
C	121	ASP	-	EXPRESSION TAG	UNP Q9JLB2
C	122	PRO	-	EXPRESSION TAG	UNP Q9JLB2
D	109	MET	-	EXPRESSION TAG	UNP Q9JLB2
D	110	GLY	-	EXPRESSION TAG	UNP Q9JLB2
D	111	SER	-	EXPRESSION TAG	UNP Q9JLB2
D	112	SER	-	EXPRESSION TAG	UNP Q9JLB2
D	113	HIS	-	EXPRESSION TAG	UNP Q9JLB2
D	114	HIS	-	EXPRESSION TAG	UNP Q9JLB2
D	115	HIS	-	EXPRESSION TAG	UNP Q9JLB2
D	116	HIS	-	EXPRESSION TAG	UNP Q9JLB2
D	117	HIS	-	EXPRESSION TAG	UNP Q9JLB2
D	118	HIS	-	EXPRESSION TAG	UNP Q9JLB2
D	119	SER	-	EXPRESSION TAG	UNP Q9JLB2
D	120	GLN	-	EXPRESSION TAG	UNP Q9JLB2
D	121	ASP	-	EXPRESSION TAG	UNP Q9JLB2
D	122	PRO	-	EXPRESSION TAG	UNP Q9JLB2

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	31	Total O 31 31	0	0
3	B	21	Total O 21 21	0	0
3	C	30	Total O 30 30	0	0
3	D	12	Total O 12 12	0	0

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.

- Molecule 1: PALS1-associated tight junction protein

Chain A:



- Molecule 1: PALS1-associated tight junction protein

Chain B:



- Molecule 2: MAGUK p55 subfamily member 5

Chain C:



- Molecule 2: MAGUK p55 subfamily member 5

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	111.06Å 111.06Å 193.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.10 43.25 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.10) 94.3 (43.25-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.10Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.242 , 0.262 0.241 , 0.261	Depositor DCC
R_{free} test set	1235 reflections (4.83%)	DCC
Wilson B-factor (Å ²)	42.2	Xtrriage
Anisotropy	0.248	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 67.5	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Outliers	0 of 25593 reflections	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	1867	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.33	0/480	0.51	0/641
1	B	0.34	0/497	0.49	0/664
2	C	0.37	0/420	0.48	0/569
2	D	0.34	0/395	0.45	0/534
All	All	0.35	0/1792	0.49	0/2408

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	476	0	506	23	0
1	B	493	0	525	17	0
2	C	414	0	398	10	0
2	D	390	0	379	15	0
3	A	31	0	0	5	0
3	B	21	0	0	3	0
3	C	30	0	0	1	0
3	D	12	0	0	0	0
All	All	1867	0	1808	52	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

The worst 5 of 52 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:68:LEU:HD22	2:D:169:VAL:HG21	1.61	0.82
1:A:20:LYS:O	1:A:24:GLN:HG2	1.84	0.77
1:A:15:VAL:HG13	2:C:146:ASP:HB3	1.68	0.76
1:A:53:LEU:HD12	1:B:67:ILE:HD12	1.70	0.74
1:B:54:GLN:HE22	2:D:165:ILE:HD12	1.53	0.72

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	56/83 (68%)	54 (96%)	2 (4%)	0	100	100
1	B	58/83 (70%)	58 (100%)	0	0	100	100
2	C	49/72 (68%)	49 (100%)	0	0	100	100
2	D	46/72 (64%)	46 (100%)	0	0	100	100
All	All	209/310 (67%)	207 (99%)	2 (1%)	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	56/76 (74%)	54 (96%)	2 (4%)	47	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	58/76 (76%)	56 (97%)	2 (3%)	49	49
2	C	49/68 (72%)	49 (100%)	0	100	100
2	D	46/68 (68%)	44 (96%)	2 (4%)	40	37
All	All	209/288 (73%)	203 (97%)	6 (3%)	55	57

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	17	ASP
2	D	158	ASP
1	B	55	GLN
1	A	64	LEU
2	D	157	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	65	ASN
1	B	55	GLN
1	A	59	GLN
1	B	54	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	58/83 (69%)	0.29	0 100 100	36, 51, 67, 82	0
1	B	60/83 (72%)	0.31	1 (1%) 67 71	37, 46, 66, 78	0
2	C	51/72 (70%)	0.13	0 100 100	34, 44, 65, 74	0
2	D	48/72 (66%)	0.67	3 (6%) 19 22	42, 57, 74, 79	0
All	All	217/310 (70%)	0.34	4 (1%) 65 69	34, 49, 71, 82	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	164	LYS	2.3
2	D	125	GLU	2.2
1	B	69	GLU	2.1
2	D	157	ARG	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates 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.