W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

May 14, 2020 – 10:20 am BST

PDB ID	:	6MLX
Title	:	Crystal structure of T. pallidum Leucine Rich Repeat protein (TpLRR)
Authors	:	Ramaswamy, R.; Loveless, B.C.; Houston, S.; Cameron, C.E.; Boulanger, M.J.
Deposited on	:	2018-09-28
Resolution	:	2.00 Å(reported)

The following versions of software and data (see references (1)) 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.
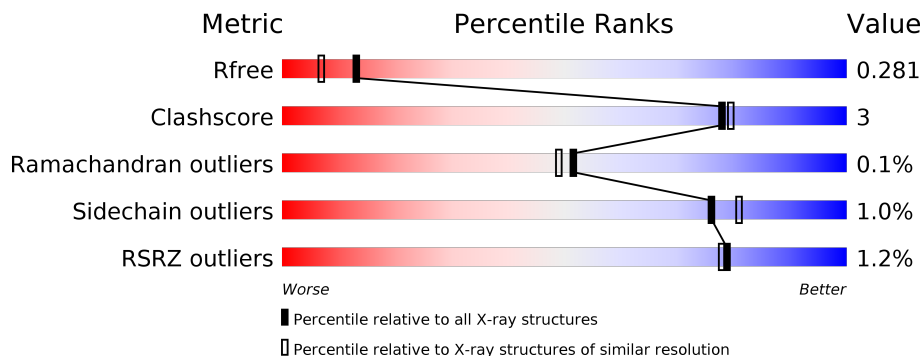
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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 <=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	217	87% 10% •
1	B	217	89% 9% •
1	C	217	92% 7% •
1	D	217	91% 7% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6978 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 Leucine-rich repeat protein TpLRR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total 1611	C 1034	N 283	O 286	S 8	0	0	0
1	B	213	Total 1616	C 1037	N 284	O 287	S 8	0	0	0
1	C	214	Total 1621	C 1040	N 285	O 288	S 8	0	0	0
1	D	213	Total 1616	C 1037	N 284	O 287	S 8	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	SER	-	expression tag	UNP O06686
A	34	MET	-	expression tag	UNP O06686
A	35	GLY	-	expression tag	UNP O06686
A	247	ALA	-	expression tag	UNP O06686
A	248	ALA	-	expression tag	UNP O06686
A	249	ALA	-	expression tag	UNP O06686
B	33	SER	-	expression tag	UNP O06686
B	34	MET	-	expression tag	UNP O06686
B	35	GLY	-	expression tag	UNP O06686
B	247	ALA	-	expression tag	UNP O06686
B	248	ALA	-	expression tag	UNP O06686
B	249	ALA	-	expression tag	UNP O06686
C	33	SER	-	expression tag	UNP O06686
C	34	MET	-	expression tag	UNP O06686
C	35	GLY	-	expression tag	UNP O06686
C	247	ALA	-	expression tag	UNP O06686
C	248	ALA	-	expression tag	UNP O06686
C	249	ALA	-	expression tag	UNP O06686
D	33	SER	-	expression tag	UNP O06686
D	34	MET	-	expression tag	UNP O06686
D	35	GLY	-	expression tag	UNP O06686

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	247	ALA	-	expression tag	UNP O06686
D	248	ALA	-	expression tag	UNP O06686
D	249	ALA	-	expression tag	UNP O06686

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	102	Total 102	O 102	0	0
2	B	139	Total 139	O 139	0	0
2	C	121	Total 121	O 121	0	0
2	D	152	Total 152	O 152	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.
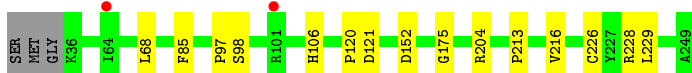
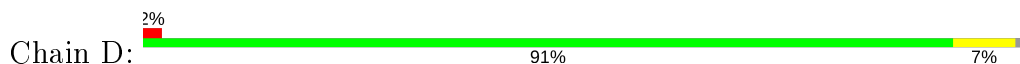- Molecule 1: Leucine-rich repeat protein TpLRR
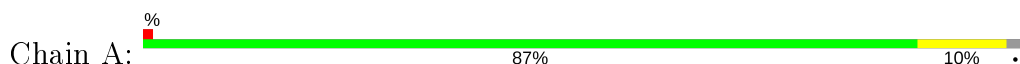
- Molecule 1: Leucine-rich repeat protein TpLRR
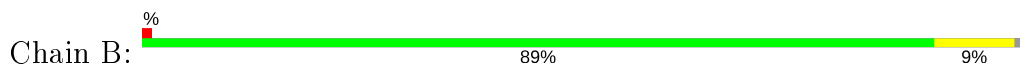
- Molecule 1: Leucine-rich repeat protein TpLRR

- Molecule 1: Leucine-rich repeat protein TpLRR

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	104.08Å 104.08Å 185.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.31 – 2.00 90.80 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.2 (69.31-2.00) 96.2 (90.80-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.19 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.234 , 0.281 0.234 , 0.281	Depositor DCC
R_{free} test set	3242 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å^2)	27.4	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 28.8	EDS
L-test for twinning[2]	$<|L|> = 0.48, <L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6978	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.32% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $<|L|>$, $<L^2>$ 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	0.46	1/1642 (0.1%)	0.63	0/2219
1	B	0.45	0/1647	0.62	0/2226
1	C	0.42	0/1652	0.60	0/2233
1	D	0.46	0/1647	0.62	0/2226
All	All	0.44	1/6588 (0.0%)	0.62	0/8904

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	49	PRO	N-CD	-6.62	1.38	1.47

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	1611	0	1664	13	0
1	B	1616	0	1669	11	0
1	C	1621	0	1674	7	0
1	D	1616	0	1669	8	0
2	A	102	0	0	0	0
2	B	139	0	0	1	0
2	C	121	0	0	1	0
2	D	152	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6978	0	6676	38	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.

The worst 5 of 38 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:235:ARG:O	1:B:239:LYS:HD2	1.81	0.80
1:D:152:ASP:OD1	1:D:178:ARG:NH1	2.14	0.80
1:B:41:LYS:NZ	2:B:301:HOH:O	2.18	0.77
1:A:47:LEU:HD12	1:C:228:ARG:HG3	1.71	0.70
1:B:120:PRO:HG2	1:B:123:LEU:HB2	1.74	0.69

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	210/217 (97%)	206 (98%)	3 (1%)	1 (0%)	29	23
1	B	211/217 (97%)	209 (99%)	2 (1%)	0	100	100
1	C	212/217 (98%)	209 (99%)	3 (1%)	0	100	100
1	D	211/217 (97%)	209 (99%)	2 (1%)	0	100	100
All	All	844/868 (97%)	833 (99%)	10 (1%)	1 (0%)	51	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	GLU

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	176/178 (99%)	174 (99%)	2 (1%)	73	78
1	B	176/178 (99%)	174 (99%)	2 (1%)	73	78
1	C	176/178 (99%)	173 (98%)	3 (2%)	60	65
1	D	176/178 (99%)	176 (100%)	0	100	100
All	All	704/712 (99%)	697 (99%)	7 (1%)	76	81

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	239	LYS
1	C	204	ARG
1	C	98	SER
1	A	238	ARG
1	C	121	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	128	HIS
1	D	105	GLN
1	D	128	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)

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(Å²)	Q<0.9
1	A	212/217 (97%)	0.37	2 (0%)	84	83	27, 30, 33, 34	0
1	B	213/217 (98%)	0.23	2 (0%)	84	83	20, 25, 28, 29	0
1	C	214/217 (98%)	0.32	2 (0%)	84	83	28, 30, 35, 36	0
1	D	213/217 (98%)	0.20	4 (1%)	66	65	20, 25, 28, 31	0
All	All	852/868 (98%)	0.28	10 (1%)	79	78	20, 28, 33, 36	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	TYR	4.3
1	D	248	ALA	3.1
1	D	247	ALA	2.7
1	A	50	ASP	2.5
1	D	227	TYR	2.4

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 (i)

There are no such residues in this entry.