



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:53 PM UTC

PDB ID : 3OZI / pdb_00003ozi
Title : Crystal structure of the TIR domain from the flax disease resistance protein L6
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Deposited on : 2010-09-25
Resolution : 2.30 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

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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

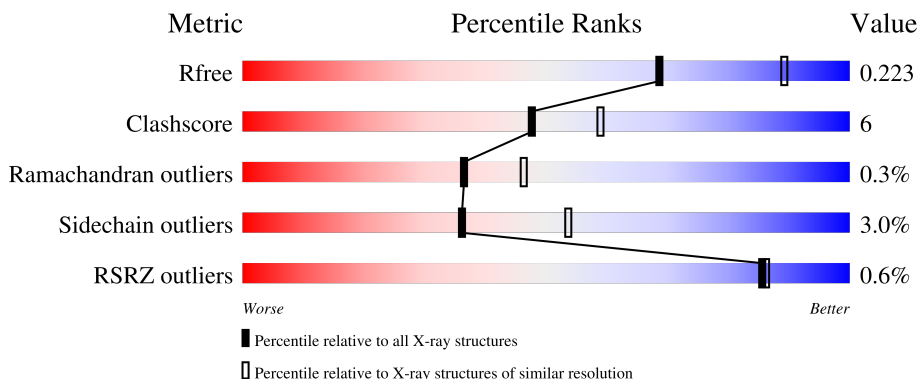
1 Overall quality at a glance

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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	204	
1	B	204	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5755 atoms, of which 2775 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 L6tr.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	170	Total	C	H	N	O	S	0	0	0
			2804	898	1397	249	256	4			
1	B	168	Total	C	H	N	O	S	0	0	0
			2767	887	1378	246	252	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q40254
A	2	ASN	-	expression tag	UNP Q40254
A	3	ALA	-	expression tag	UNP Q40254
B	1	SER	-	expression tag	UNP Q40254
B	2	ASN	-	expression tag	UNP Q40254
B	3	ALA	-	expression tag	UNP Q40254

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Co	0	0
			1	1		

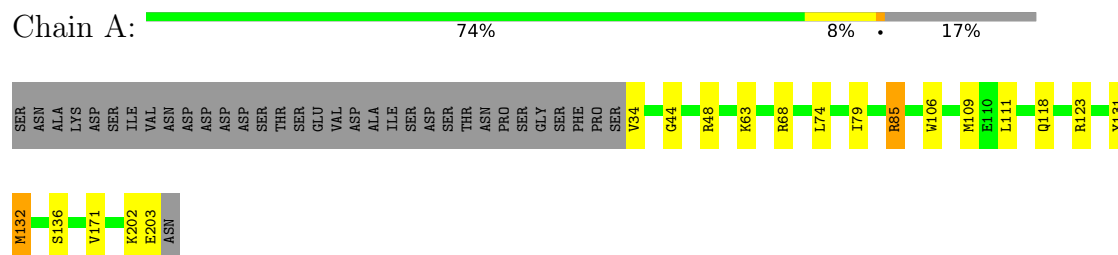
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	98	Total	O	0	0
			98	98		
3	B	85	Total	O	0	0
			85	85		

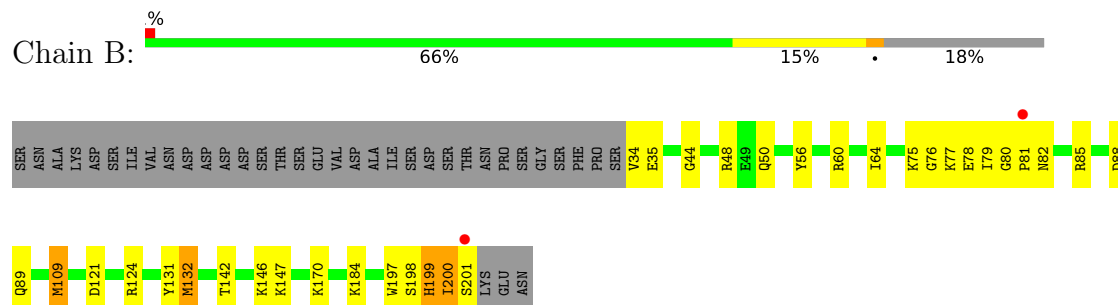
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: L6tr



- Molecule 1: L6tr



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	65.94Å 102.24Å 58.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.30 – 2.30 19.30 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.30-2.30) 99.5 (19.30-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.17 (at 2.30Å)	Xtriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.174 , 0.230 0.175 , 0.223	Depositor DCC
R_{free} test set	918 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 49.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5755	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.55 % 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 3.1210e-04. 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CO

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	0/1440	0.78	1/1937 (0.1%)
1	B	0.59	3/1422 (0.2%)	0.83	6/1914 (0.3%)
All	All	0.53	3/2862 (0.1%)	0.80	7/3851 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	199	HIS	ND1-CE1	5.36	1.38	1.32
1	B	50	GLN	CD-OE1	5.24	1.33	1.23
1	B	82	ASN	CG-OD1	5.07	1.33	1.23

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	199	HIS	CB-CG-CD2	-6.55	122.69	131.20
1	B	121	ASP	CA-C-N	5.68	126.94	119.84
1	B	121	ASP	C-N-CA	5.68	126.94	119.84
1	B	199	HIS	CB-CG-ND1	5.60	131.10	122.70
1	B	80	GLY	CA-C-N	5.20	124.86	119.56
1	B	80	GLY	C-N-CA	5.20	124.86	119.56
1	A	123	ARG	N-CA-C	-5.07	106.61	112.89

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	1407	1397	1397	11	0
1	B	1389	1378	1378	20	0
2	A	1	0	0	0	0
3	A	98	0	0	1	0
3	B	85	0	0	0	0
All	All	2980	2775	2775	31	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 6.

All (31) 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:34:VAL:O	1:A:34:VAL:HG12	1.92	0.69
1:A:111:LEU:HD11	1:A:171:VAL:HG21	1.78	0.63
1:B:56:TYR:CE2	1:B:60:ARG:HD2	2.33	0.62
1:A:106:TRP:HA	1:A:109:MET:HE3	1.83	0.59
1:A:202:LYS:O	1:A:203:GLU:HB2	2.05	0.57
1:B:34:VAL:O	1:B:85:ARG:NH2	2.38	0.56
1:A:34:VAL:O	1:A:34:VAL:CG1	2.54	0.55
1:B:34:VAL:HG13	1:B:35:GLU:H	1.71	0.55
1:A:74:LEU:HD21	1:A:79:ILE:HG12	1.89	0.55
1:A:68:ARG:HB2	3:A:300:HOH:O	2.09	0.53
1:B:34:VAL:HG13	1:B:35:GLU:N	2.23	0.53
1:B:200:ILE:CG2	1:B:200:ILE:O	2.59	0.50
1:B:77:LYS:O	1:B:81:PRO:HG2	2.12	0.49
1:B:109:MET:HE2	1:B:109:MET:HB3	1.74	0.48
1:B:64:ILE:HD11	1:B:197:TRP:HD1	1.78	0.48
1:B:35:GLU:HG3	1:B:89:GLN:CD	2.40	0.46
1:B:44:GLY:O	1:B:48:ARG:HB3	2.17	0.45
1:A:34:VAL:O	1:A:85:ARG:NH2	2.50	0.45
1:B:184:LYS:N	1:B:184:LYS:HD2	2.32	0.44
1:B:88:ASP:O	1:B:124:ARG:NH2	2.51	0.44
1:A:63:LYS:HA	1:A:63:LYS:HD3	1.88	0.44
1:B:199:HIS:C	1:B:201:SER:H	2.25	0.44
1:B:142:THR:HA	1:B:146:LYS:HG2	2.00	0.44
1:A:44:GLY:O	1:A:48:ARG:HB2	2.18	0.43
1:A:131:TYR:CE2	1:A:132:MET:HG3	2.54	0.43
1:B:56:TYR:CZ	1:B:60:ARG:HD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:TYR:CE2	1:B:132:MET:HG3	2.54	0.43
1:B:75:LYS:HB2	1:B:78:GLU:HG3	2.01	0.43
1:B:200:ILE:O	1:B:200:ILE:HG22	2.18	0.42
1:B:76:GLY:O	1:B:79:ILE:HG12	2.19	0.42
1:B:56:TYR:O	1:B:60:ARG:HG3	2.19	0.42

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	168/204 (82%)	160 (95%)	8 (5%)	0	100	100
1	B	166/204 (81%)	159 (96%)	6 (4%)	1 (1%)	21	27
All	All	334/408 (82%)	319 (96%)	14 (4%)	1 (0%)	36	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	200	ILE

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	151/182 (83%)	147 (97%)	4 (3%)	40	59
1	B	149/182 (82%)	144 (97%)	5 (3%)	32	49
All	All	300/364 (82%)	291 (97%)	9 (3%)	36	53

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	ARG
1	A	118	GLN
1	A	132	MET
1	A	136	SER
1	B	109	MET
1	B	132	MET
1	B	147	LYS
1	B	170	LYS
1	B	198	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	B	199	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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

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 [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	170/204 (83%)	-0.51	0 100 100	10, 21, 40, 47	0
1	B	168/204 (82%)	-0.42	2 (1%) 76 77	11, 21, 42, 52	0
All	All	338/408 (82%)	-0.47	2 (0%) 85 86	10, 21, 41, 52	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	81	PRO	2.3
1	B	201	SER	2.2

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 oligosaccharides 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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
2	CO	A	205	1/1	0.99	0.03	29,29,29,29	1

6.5 Other polymers [i](#)

There are no such residues in this entry.