

Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	4LG9
Title	:	Crystal structure of TBL1XR1 WD40 repeats
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Deposited on	:	2013-06-27
Resolution	:	2.28 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 (i) 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 (1)) were used in the production of this report:

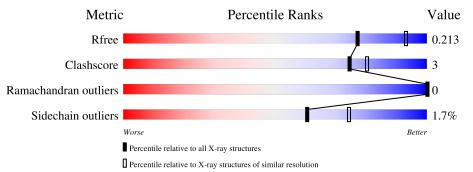
Refmac	: : : :	 1.13 2.35.1 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (proteins) Ideal geometry (DNA, RNA)		0
Validation Pipeline (wwPDB-VP)		

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.28 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)

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 <=5%

Mol	Chain	Length	Quality of chain					
		100						
1	A	400	78%	8%	•	12%		



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2917 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 F-box-like/WD repeat-containing protein TBL1XR1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	351	Total 2734	C 1730	N 471	0 515	S 18	0	13	1

Chain	Residue	Modelled	Actual	Comment	Reference
А	115	MET	-	expression tag	UNP Q9BZK7
А	116	GLY	-	expression tag	UNP Q9BZK7
А	117	SER	-	expression tag	UNP Q9BZK7
А	118	SER	-	expression tag	UNP Q9BZK7
A	119	HIS	-	expression tag	UNP Q9BZK7
А	120	HIS	-	expression tag	UNP Q9BZK7
A	121	HIS	-	expression tag	UNP Q9BZK7
А	122	HIS	-	expression tag	UNP Q9BZK7
А	123	HIS	-	expression tag	UNP Q9BZK7
А	124	HIS	-	expression tag	UNP Q9BZK7
А	125	SER	-	expression tag	UNP Q9BZK7
A	126	SER	-	expression tag	UNP Q9BZK7
А	127	GLY	-	expression tag	UNP Q9BZK7
А	128	LEU	-	expression tag	UNP Q9BZK7
А	129	VAL	-	expression tag	UNP Q9BZK7
А	130	PRO	-	expression tag	UNP Q9BZK7
А	131	ARG	-	expression tag	UNP Q9BZK7
А	132	GLY	-	expression tag	UNP Q9BZK7
А	133	SER	-	expression tag	UNP Q9BZK7
А	438	MET	LEU	engineered mutation	UNP Q9BZK7

There are 20 discrepancies between the modelled and reference sequences:

• Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	23	Total X 23 23	0	0



• Molecule 3 is water.

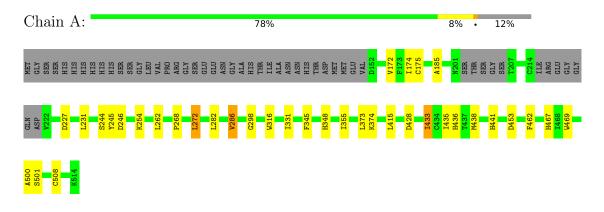
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	160	Total O 160 160	0	0



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. 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. 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: F-box-like/WD repeat-containing protein TBL1XR1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	90.78Å 90.78Å 104.85Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.39 - 2.28	Depositor
Resolution (A)	45.39 - 1.93	EDS
% Data completeness	99.4 (45.39-2.28)	Depositor
(in resolution range)	$98.8 \ (45.39 - 1.93)$	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) > 1$	$3.07 (at 1.94 \text{\AA})$	Xtriage
Refinement program	PHENIX dev_ 1439	Depositor
R, R_{free}	0.163 , 0.208	Depositor
II, IIfree	0.172 , 0.213	DCC
R_{free} test set	1910 reflections (5.08%)	wwPDB-VP
Wilson B-factor $(Å^2)$	7.8	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35 , 49.4	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
F_o, F_c correlation	0.69	EDS
Total number of atoms	2917	wwPDB-VP
Average B, all atoms $(Å^2)$	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.37% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

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

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		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.39	0/2845	0.58	1/3873~(0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	272	LEU	CA-CB-CG	5.04	126.90	115.30

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	А	2734	0	2626	17	1
2	А	23	0	0	0	0
3	А	160	0	0	0	0
All	All	2917	0	2626	17	1

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.

All (17) 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:174:ILE:HD12	1:A:231:LEU:HG	1.89	0.54
1:A:244:SER:OG	1:A:246:ASP:OD1	2.19	0.51
1:A:435[B]:ILE:HG22	1:A:436:HIS:CD2	2.47	0.50
1:A:373[B]:LEU:HD11	1:A:415:LEU:HD21	1.93	0.49
1:A:272:LEU:HA	1:A:282:LEU:O	2.13	0.48
1:A:438:MET:HG2	1:A:469:TRP:CD2	2.50	0.47
1:A:441:HIS:CE1	1:A:467:HIS:CD2	3.04	0.46
1:A:282:LEU:HB2	1:A:316:TRP:CZ2	2.53	0.43
1:A:428:ASP:HB3	1:A:433[A]:ILE:HD13	2.00	0.43
1:A:500:ALA:HB3	1:A:508[C]:CYS:SG	2.59	0.43
1:A:268:PRO:HD2	1:A:286:VAL:HG11	2.02	0.42
1:A:348:HIS:CE1	1:A:374:LYS:HD2	2.54	0.42
1:A:175:CYS:HA	1:A:185:ALA:O	2.20	0.41
1:A:331:ILE:HB	1:A:345:PHE:HB2	2.02	0.41
1:A:262:LEU:HD22	1:A:298:GLY:HA2	2.03	0.41
1:A:172:VAL:HB	1:A:501:SER:HB2	2.03	0.40
1:A:254:LYS:HE3	1:A:254:LYS:HB2	1.84	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:TYR:OH	$1:A:453:ASP:OD2[3_564]$	2.10	0.10

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	А	358/400~(90%)	353~(99%)	5 (1%)	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	297/336~(88%)	291~(98%)	6(2%)	55 70

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	227	ASP
1	А	286	VAL
1	А	355	ILE
1	А	433[A]	ILE
1	А	433[B]	ILE
1	А	462	PHE

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

Mol	Chain	Res	Type
1	А	303	GLN
1	А	362	ASN
1	А	388	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)

Of 23 ligands modelled in this entry, 23 are unknown - 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 (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)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

