

Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2020 - 11:24 AM BST

PDB ID	:	4KZJ
Title	:	Crystal Structure of TR3 LBD L449W Mutant
Authors	:	Li, F.; Zhang, Q.; Li, A.; Tian, X.; Cai, Q.; Wang, W.; Wang, Y.; Chen, H.;
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Deposited on	:	2013-05-30
Resolution	:	2.12 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 following versions of software and data (see references (1)) were used in the production of this report:

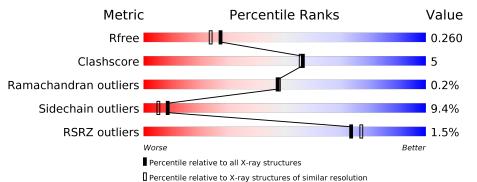
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\operatorname{CCP4}$:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.12 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705(2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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 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	А	257	^{2%} 7 5%	11%	•	• 10%		
1	В	257	% • 74%	13%	•	11%		



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3874 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	1 B	229	Total	С	Ν	Ο	S	0	0	0
			1797	1162	305	323	7	0		
1	Λ	231	Total	С	Ν	Ο	S	0	0	0
			1822	1180	310	325	7	0	0	0

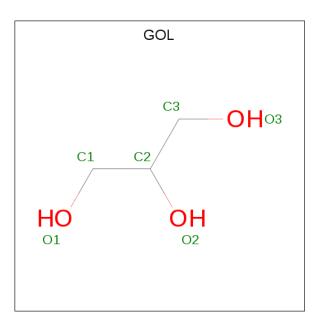
• Molecule 1 is a protein called Nuclear receptor subfamily 4 group A member 1.

Chain	Residue	Modelled	Actual	Comment	Reference
В	19	MET	-	expression tag	UNP P22736
В	118	TRP	LEU	engineered mutation	UNP P22736
В	268	LEU	-	expression tag	UNP P22736
В	269	GLU	-	expression tag	UNP P22736
В	270	HIS	-	expression tag	UNP P22736
В	271	HIS	-	expression tag	UNP P22736
В	272	HIS	-	expression tag	UNP P22736
В	273	HIS	-	expression tag	UNP P22736
В	274	HIS	-	expression tag	UNP P22736
В	275	HIS	-	expression tag	UNP P22736
A	19	MET	-	expression tag	UNP P22736
A	118	TRP	LEU	engineered mutation	UNP P22736
A	268	LEU	-	expression tag	UNP P22736
A	269	GLU	-	expression tag	UNP P22736
A	270	HIS	-	expression tag	UNP P22736
A	271	HIS	-	expression tag	UNP P22736
A	272	HIS	-	expression tag	UNP P22736
А	273	HIS	-	expression tag	UNP P22736
A	274	HIS	-	expression tag	UNP P22736
А	275	HIS	-	expression tag	UNP P22736

There are 20 discrepancies between the modelled and reference sequences:

• Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	$\begin{array}{ccc} {\rm Total} & {\rm C} & {\rm O} \\ 6 & 3 & 3 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} {\rm Total} & {\rm C} & {\rm O} \\ 6 & 3 & 3 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0

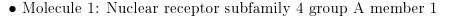
• Molecule 3 is water.

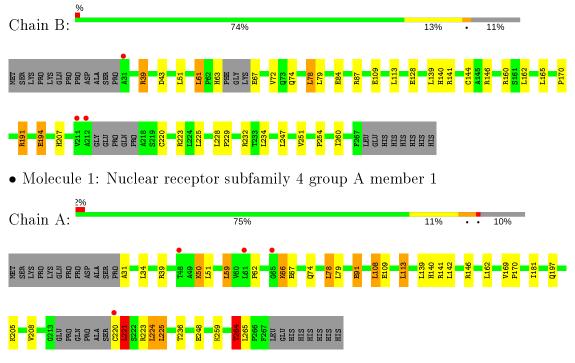
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	124	Total O 124 124	0	0
3	А	113	Total O 113 113	0	0



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 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.







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	74.40Å 76.60Å 127.37Å	Deperitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.16 - 2.12	Depositor
Resolution (A)	37.13 - 2.12	EDS
% Data completeness	$98.5\ (37.16-2.12)$	Depositor
(in resolution range)	$98.5\ (37.13-2.12)$	EDS
R _{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$4.16 (at 2.12 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.212 , 0.250	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.216 , 0.260	DCC
R_{free} test set	2072 reflections $(5.03%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	31.2	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33 , 28.7	EDS
L-test for twinning ²	$< L > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.085 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3874	wwPDB-VP
Average B, all atoms $(Å^2)$	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.90% 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: GOL

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	Bo	nd lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.92	0/1862	0.94	6/2522~(0.2%)	
1	В	0.92	1/1835~(0.1%)	1.02	6/2487~(0.2%)	
All	All	0.92	1/3697~(0.0%)	0.98	12/5009~(0.2%)	

All (1) bond length outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms		$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	В	144	CYS	CB-SG	-9.15	1.66	1.82

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	144	CYS	CB-CA-C	-10.65	89.09	110.40
1	В	232	ARG	CG-CD-NE	-9.32	92.22	111.80
1	В	141	ARG	NE-CZ-NH2	-9.05	115.77	120.30
1	А	141	ARG	NE-CZ-NH1	-8.84	115.88	120.30
1	А	264	THR	CB-CA-C	-7.13	92.34	111.60
1	В	141	ARG	NE-CZ-NH1	6.93	123.76	120.30
1	А	59	LEU	CB-CG-CD2	5.77	120.81	111.00
1	А	113	LEU	CB-CG-CD1	5.34	120.08	111.00
1	А	108	LEU	CB-CG-CD2	5.27	119.95	111.00
1	А	141	ARG	NE-CZ-NH2	5.27	122.93	120.30
1	В	87	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	В	87	ARG	NE-CZ-NH2	-5.05	117.77	120.30

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	1822	0	1863	22	0
1	В	1797	0	1825	16	0
2	А	12	0	16	0	0
2	В	6	0	8	0	0
3	А	113	0	0	3	2
3	В	124	0	0	2	0
All	All	3874	0	3712	37	2

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 5.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
		distance (Å)	overlap (Å)
1:A:66:LYS:HD2	1:A:146:ARG:HH12	1.07	1.17
1:A:66:LYS:HD2	1:A:146:ARG:NH1	1.79	0.98
1:A:66:LYS:CD	1:A:146:ARG:HH12	1.77	0.96
1:B:191:ARG:CZ	1:B:194:GLU:OE1	2.29	0.81
1:A:220:CYS:SG	3:A:441:HOH:O	2.41	0.78
1:A:220:CYS:O	1:A:223:ARG:N	2.26	0.68
1:A:220:CYS:O	1:A:224:LEU:N	2.28	0.67
1:B:109:GLU:HG3	1:B:260:ILE:HG12	1.76	0.66
1:B:61:LEU:HD12	1:B:61:LEU:H	1.64	0.62
1:B:39:ARG:HD3	1:B:43:ASP:OD2	1.99	0.61
1:B:191:ARG:NH2	1:B:194:GLU:OE1	2.33	0.61
1:A:66:LYS:CD	1:A:146:ARG:NH1	2.53	0.59
1:A:225:LEU:HD13	3:A:419:HOH:O	2.03	0.58
1:B:63:HIS:CE1	1:B:146:ARG:NH1	2.73	0.57
1:A:109:GLU:OE1	1:A:259:LYS:HE3	2.05	0.56
1:B:228:LEU:HB2	1:B:229:PRO:HD3	1.89	0.55
1:B:220:CYS:HA	3:B:447:HOH:O	2.08	0.53
1:A:140:HIS:HD2	1:A:142:LEU:H	1.55	0.52
1:B:74:GLN:HG2	1:B:78:LEU:HD22	1.93	0.51
1:B:39:ARG:CD	1:B:43:ASP:OD2	2.61	0.49
1:A:264:THR:O	1:A:264:THR:HG22	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:HIS:CD2	1:A:142:LEU:H	2.31	0.48
1:A:221:LEU:HD12	1:A:221:LEU:N	2.31	0.46
1:A:50:LYS:O	1:A:50:LYS:HD3	2.15	0.46
1:B:61:LEU:N	1:B:61:LEU:HD12	2.28	0.45
1:B:72:VAL:HG12	1:B:251:VAL:HG22	1.98	0.45
1:A:31:ALA:HB3	1:A:34:LEU:H	1.83	0.44
1:A:74:GLN:HG2	1:A:78:LEU:HD22	2.01	0.43
1:A:169:VAL:HB	1:A:170:PRO:HD3	2.00	0.43
1:A:181:ILE:O	1:A:197:GLN:HG3	2.20	0.42
1:A:67:GLU:OE1	1:A:248:GLU:OE2	2.37	0.42
1:B:223:ARG:HB2	3:B:447:HOH:O	2.19	0.41
1:B:61:LEU:H	1:B:61:LEU:CD1	2.33	0.41
1:A:205:LYS:O	1:A:208:VAL:HG22	2.21	0.41
1:B:247:LEU:HD13	1:A:236:THR:HG23	2.03	0.41
1:B:170:PRO:HB2	1:B:207:HIS:CE1	2.56	0.40
1:A:91:GLU:HG3	3:A:436:HOH:O	2.20	0.40

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All (2) 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)
3:A:402:HOH:O	3:A:456:HOH:O[4_445]	1.96	0.24
3:A:402:HOH:O	3:A:461:HOH:O[4_445]	2.06	0.14

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	227/257~(88%)	225~(99%)	1 (0%)	1 (0%)	34	32
1	В	223/257~(87%)	221~(99%)	2(1%)	0	100	100
All	All	450/514~(88%)	446 (99%)	3 (1%)	1 (0%)	47	48



All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	221	LEU

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	А	199/223~(89%)	$181 \ (91\%)$	18 (9%)	9 6
1	В	196/223~(88%)	177~(90%)	19 (10%)	8 5
All	All	395/446~(89%)	358~(91%)	37~(9%)	8 5

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	39	ARG
1	В	51	LEU
1	В	61	LEU
1	В	67	GLU
1	В	78	LEU
1	В	79	LEU
1	В	84	GLU
1	В	113	LEU
1	В	128	GLU
1	В	139	LEU
1	В	140	HIS
1	В	160	ARG
1	В	162	LEU
1	В	165	LEU
1	В	191	ARG
1	В	194	GLU
1	В	225	LEU
1	В	234	LEU
1	В	254	PRO
1	А	39	ARG
1	А	50	LYS
1	А	51	LEU

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Mol	Chain	Res	Type
1	А	59	LEU
1	А	62	PRO
1	А	66	LYS
1	А	78	LEU
1	А	79	LEU
1	А	91	GLU
1	А	108	LEU
1	А	113	LEU
1	А	139	LEU
1	А	162	LEU
1	А	221	LEU
1	А	224	LEU
1	А	225	LEU
1	А	264	THR
1	А	265	LEU

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Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	\mathbf{Res}	Type
1	В	63	HIS
1	В	188	GLN
1	А	140	HIS
1	А	188	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)

3 ligands are modelled in this entry.



In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Γ	Mol	Turne	Chain	Res	Link	Bond lengths			B	ond ang	gles
	IVIOI	Type	Cham	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
	2	GOL	В	301	-	5, 5, 5	0.64	0	$5,\!5,\!5$	0.46	0
	2	GOL	А	302	-	5, 5, 5	0.44	0	$5,\!5,\!5$	0.58	0
	2	GOL	А	301	-	5, 5, 5	0.65	0	$5,\!5,\!5$	0.72	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	\mathbf{Res}	Link	Chirals	Torsions	Rings
2	GOL	В	301	-	-	2/4/4/4	-
2	GOL	А	302	-	-	0/4/4/4	-
2	GOL	А	301	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	301	GOL	O1-C1-C2-C3
2	А	301	GOL	O1-C1-C2-C3
2	А	301	GOL	C1-C2-C3-O3
2	А	301	GOL	O2-C2-C3-O3
2	А	301	GOL	O1-C1-C2-O2
2	В	301	GOL	O1-C1-C2-O2

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)

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, 95^{th} 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	А	231/257~(89%)	0.12	4 (1%) 70 74	23, 34, 62, 82	1 (0%)
1	В	229/257~(89%)	0.12	3 (1%) 77 80	23, 34, 59, 93	0
All	All	460/514~(89%)	0.12	7 (1%) 73 77	23, 35, 60, 93	1 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	31	ALA	5.8
1	В	212	ALA	3.1
1	А	48	THR	3.1
1	В	211	VAL	2.5
1	А	65	GLY	2.2
1	А	220	CYS	2.2
1	A	61	LEU	2.1

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 monosaccharides 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, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathbf{\AA}^2)$	$Q{<}0.9$
2	GOL	А	301	6/6	0.70	0.27	$53,\!56,\!64,\!66$	0
2	GOL	А	302	6/6	0.95	0.14	$39,\!40,\!45,\!47$	0
2	GOL	В	301	6/6	0.95	0.17	$29,\!30,\!35,\!36$	0

6.5 Other polymers (i)

There are no such residues in this entry.

