



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:12 AM UTC

PDB ID : 9G7L / pdb_00009g7l
Title : Structure of the proline-rich binding domain of Tesup-1 in complex with dZfc3h1 peptide
Authors : Manolova, T.; Falk, S.
Deposited on : 2024-07-22
Resolution : 1.90 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
Mogul : 2022.3.0, CSD as543be (2022)
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

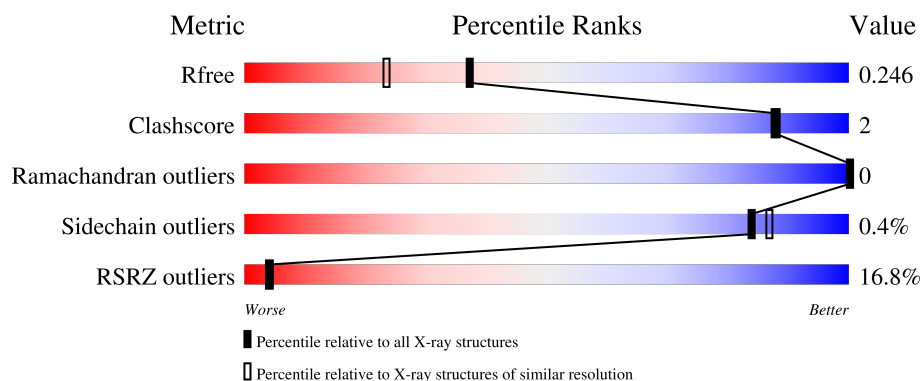
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	152	<div> <div>16%</div> <div>78%</div> <div>7%</div> <div>15%</div> </div>
1	B	152	<div> <div>12%</div> <div>83%</div> <div>5%</div> <div>12%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4503 atoms, of which 2151 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 LD36051p,LD02331p.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	129	Total	C	H	N	O	S	0	0	0
			2174	712	1061	195	201	5			
1	B	133	Total	C	H	N	O	S	0	1	0
			2224	729	1079	199	212	5			

There are 34 discrepancies between the modelled and reference sequences:

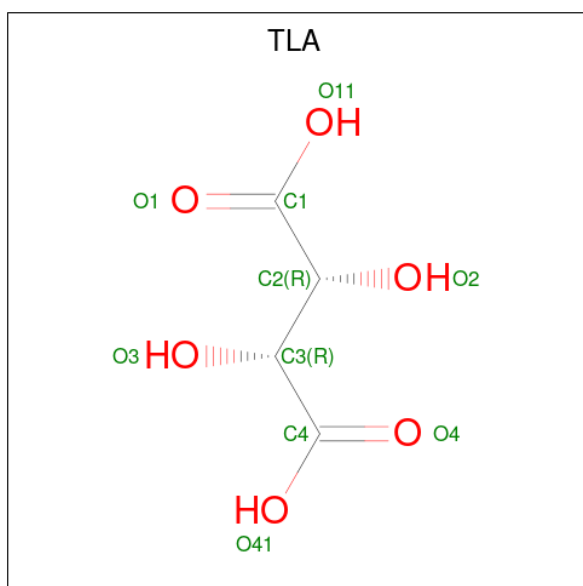
Chain	Residue	Modelled	Actual	Comment	Reference
A	697	GLY	-	expression tag	UNP Q9VBX4
A	698	PRO	-	expression tag	UNP Q9VBX4
A	699	ASP	-	expression tag	UNP Q9VBX4
A	700	SER	-	expression tag	UNP Q9VBX4
A	701	MET	-	expression tag	UNP Q9VBX4
A	821	GLY	-	linker	UNP Q9VBX4
A	822	SER	-	linker	UNP Q9VBX4
A	823	GLY	-	linker	UNP Q9VBX4
A	824	SER	-	linker	UNP Q9VBX4
A	825	GLY	-	linker	UNP Q9VBX4
A	826	SER	-	linker	UNP Q9VBX4
A	827	GLY	-	linker	UNP Q9VBX4
A	828	SER	-	linker	UNP Q9VBX4
A	829	GLY	-	linker	UNP Q9VBX4
A	830	SER	-	linker	UNP Q9VBX4
A	831	GLY	-	linker	UNP Q9VBX4
A	832	SER	-	linker	UNP Q9VBX4
B	697	GLY	-	expression tag	UNP Q9VBX4
B	698	PRO	-	expression tag	UNP Q9VBX4
B	699	ASP	-	expression tag	UNP Q9VBX4
B	700	SER	-	expression tag	UNP Q9VBX4
B	701	MET	-	expression tag	UNP Q9VBX4
B	821	GLY	-	linker	UNP Q9VBX4
B	822	SER	-	linker	UNP Q9VBX4
B	823	GLY	-	linker	UNP Q9VBX4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	824	SER	-	linker	UNP Q9VBX4
B	825	GLY	-	linker	UNP Q9VBX4
B	826	SER	-	linker	UNP Q9VBX4
B	827	GLY	-	linker	UNP Q9VBX4
B	828	SER	-	linker	UNP Q9VBX4
B	829	GLY	-	linker	UNP Q9VBX4
B	830	SER	-	linker	UNP Q9VBX4
B	831	GLY	-	linker	UNP Q9VBX4
B	832	SER	-	linker	UNP Q9VBX4

- Molecule 2 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	H	O	0	0
			14	4	4	6		
2	B	1	Total	C	H	O	0	0
			14	4	4	6		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



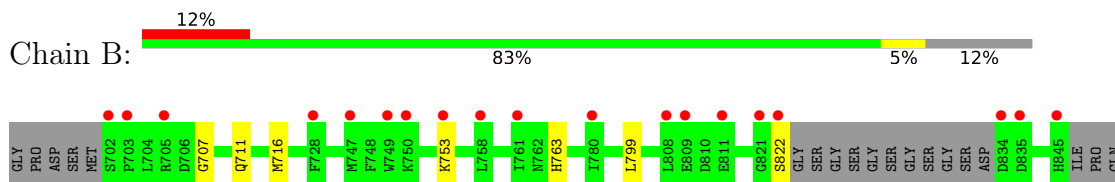
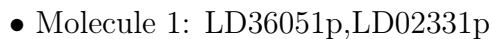
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	35	Total	O	0	0
			35	35		
4	B	35	Total	O	0	0
			35	35		

i

- Molecule 1: LD36051p,LD02331p



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	121.57Å 48.62Å 66.58Å 90.00° 113.04° 90.00°	Depositor
Resolution (Å)	61.27 – 1.90 61.27 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.5 (61.27-1.90) 98.5 (61.27-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.216 , 0.248 0.217 , 0.246	Depositor DCC
R_{free} test set	1401 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.496	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4503	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.70% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.16	0/1148	0.27	0/1556
1	B	0.16	0/1183	0.26	0/1603
All	All	0.16	0/2331	0.27	0/3159

There are no bond length outliers.

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	1113	1061	1061	6	0
1	B	1145	1079	1079	3	0
2	B	20	8	8	0	0
3	B	4	3	3	0	0
4	A	35	0	0	0	0
4	B	35	0	0	0	0
All	All	2352	2151	2151	9	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 2.

All (9) 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:806:ASN:ND2	1:A:807:GLU:OE1	2.20	0.73
1:A:724:LEU:HD23	1:A:784:TYR:CE1	2.45	0.52
1:B:716:MET:HE1	1:B:799:LEU:HD21	1.91	0.52
1:A:796:ARG:NH2	1:A:808:LEU:CD1	2.74	0.50
1:A:716:MET:HE3	1:A:795:CYS:SG	2.52	0.50
1:A:796:ARG:NH2	1:A:813:TYR:O	2.49	0.45
1:A:796:ARG:HG2	1:A:801:LEU:HB2	2.00	0.42
1:B:753:LYS:HG3	1:B:763:HIS:CD2	2.55	0.41
1:B:707:GLY:O	1:B:711:GLN:HG3	2.20	0.40

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	125/152 (82%)	125 (100%)	0	0	100	100
1	B	130/152 (86%)	130 (100%)	0	0	100	100
All	All	255/304 (84%)	255 (100%)	0	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	123/139 (88%)	123 (100%)	0	100	100
1	B	127/139 (91%)	126 (99%)	1 (1%)	73	75
All	All	250/278 (90%)	249 (100%)	1 (0%)	84	87

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	822	SER

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

Mol	Chain	Res	Type
1	A	814	HIS
1	A	816	HIS
1	B	715	HIS
1	B	790	ASN

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 ⓘ

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	TLA	B	901	-	9,9,9	1.32	0	12,12,12	1.38	2 (16%)
3	ACT	B	902	-	3,3,3	1.46	1 (33%)	3,3,3	1.07	0
2	TLA	B	903	-	9,9,9	1.37	0	12,12,12	1.28	2 (16%)

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	Res	Link	Chirals	Torsions	Rings
2	TLA	B	901	-	-	8/12/12/12	-
2	TLA	B	903	-	-	10/12/12/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	902	ACT	CH3-C	2.02	1.57	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	TLA	O4-C4-C3	-2.50	114.96	121.62
2	B	903	TLA	O1-C1-C2	-2.48	115.01	121.62
2	B	901	TLA	O1-C1-C2	-2.44	115.11	121.62
2	B	903	TLA	O4-C4-C3	-2.24	115.64	121.62

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	901	TLA	C1-C2-C3-O3
2	B	901	TLA	C1-C2-C3-C4
2	B	901	TLA	O2-C2-C3-O3
2	B	901	TLA	O2-C2-C3-C4
2	B	903	TLA	O11-C1-C2-O2
2	B	903	TLA	C1-C2-C3-C4
2	B	903	TLA	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
2	B	903	TLA	O1-C1-C2-O2
2	B	903	TLA	C1-C2-C3-O3
2	B	903	TLA	O2-C2-C3-C4
2	B	901	TLA	C2-C3-C4-O4
2	B	901	TLA	C2-C3-C4-O41
2	B	901	TLA	O1-C1-C2-C3
2	B	901	TLA	O11-C1-C2-C3
2	B	903	TLA	O3-C3-C4-O41
2	B	903	TLA	C2-C3-C4-O41
2	B	903	TLA	C2-C3-C4-O4
2	B	903	TLA	O3-C3-C4-O4

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 ⓘ

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	129/152 (84%)	1.10	25 (19%)	3 3	34, 51, 107, 119	0
1	B	133/152 (87%)	1.07	19 (14%)	6 6	25, 52, 93, 110	1 (0%)
All	All	262/304 (86%)	1.08	44 (16%)	4 4	25, 52, 98, 119	1 (0%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	703	PRO	6.7
1	B	822	SER	6.6
1	A	704	LEU	5.1
1	B	845	HIS	5.0
1	A	847	PRO	4.5
1	A	837	VAL	4.3
1	A	819	LYS	4.1
1	A	817	LEU	4.1
1	B	728[A]	PHE	3.8
1	A	708	ASP	3.7
1	B	703	PRO	3.5
1	B	821	GLY	3.4
1	A	808	LEU	3.4
1	B	702	SER	3.2
1	A	709	ILE	3.2
1	B	808	LEU	3.1
1	A	818	ASP	3.0
1	B	834	ASP	3.0
1	A	758	LEU	2.9
1	A	705	ARG	2.8
1	B	750	LYS	2.8
1	A	712	ALA	2.7
1	B	835	ASP	2.6
1	A	803	MET	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	758	LEU	2.6
1	B	753	LYS	2.6
1	A	806	ASN	2.5
1	A	804	THR	2.5
1	B	809	GLU	2.5
1	A	733	SER	2.4
1	A	788	ILE	2.3
1	A	846	ILE	2.3
1	A	800	CYS	2.3
1	A	809	GLU	2.3
1	B	749	TRP	2.2
1	A	807	GLU	2.2
1	A	811	GLU	2.2
1	B	780	ILE	2.1
1	A	801	LEU	2.1
1	B	811	GLU	2.1
1	B	747	MET	2.1
1	A	799	LEU	2.1
1	B	705	ARG	2.1
1	B	761	ILE	2.0

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	TLA	B	901	10/10	0.77	0.13	66,76,91,91	0
2	TLA	B	903	10/10	0.81	0.15	51,69,78,83	0
3	ACT	B	902	4/4	0.92	0.14	45,51,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.