



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:47 AM UTC

PDB ID : 5JHP / pdb_00005jhp
Title : Crystal structure of the rice Topless related protein 2 (TPR2) N-terminal topless domain (1-209) L179A and I195A mutant in complex with rice D53 repressor EAR peptide motif
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Deposited on : 2016-04-21
Resolution : 3.15 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

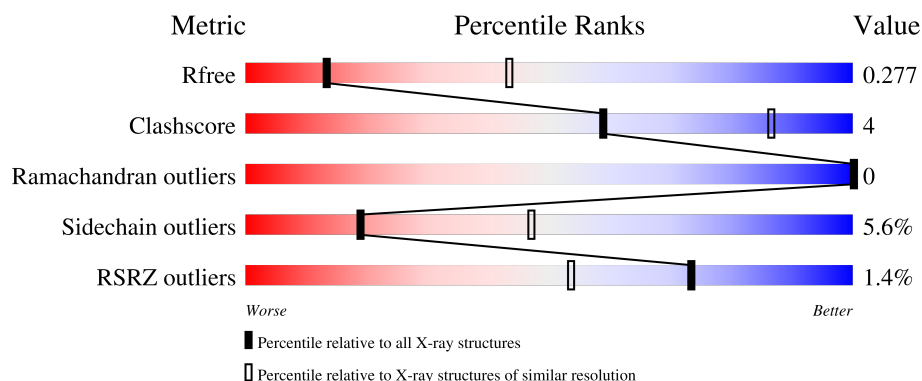
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	209	
1	B	209	
1	C	209	
1	D	209	
2	E	15	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6181 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 Protein TPR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	0	0
			1531	990	251	287	3			
1	B	179	Total	C	N	O	S	0	0	0
			1502	971	247	281	3			
1	C	186	Total	C	N	O	S	0	0	0
			1560	1011	253	293	3			
1	D	183	Total	C	N	O	S	0	0	0
			1515	976	251	285	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	ALA	LEU	engineered mutation	UNP Q5NBT9
A	195	ALA	ILE	engineered mutation	UNP Q5NBT9
B	179	ALA	LEU	engineered mutation	UNP Q5NBT9
B	195	ALA	ILE	engineered mutation	UNP Q5NBT9
C	179	ALA	LEU	engineered mutation	UNP Q5NBT9
C	195	ALA	ILE	engineered mutation	UNP Q5NBT9
D	179	ALA	LEU	engineered mutation	UNP Q5NBT9
D	195	ALA	ILE	engineered mutation	UNP Q5NBT9

- Molecule 2 is a protein called The rice D53 EAR peptide (794-808).

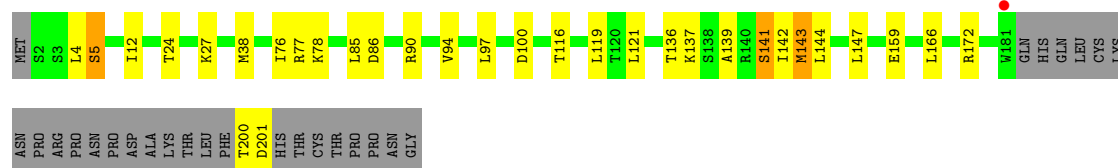
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	9	Total	C	N	O	0	0	0
			73	48	10	15			

3 Residue-property plots

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.

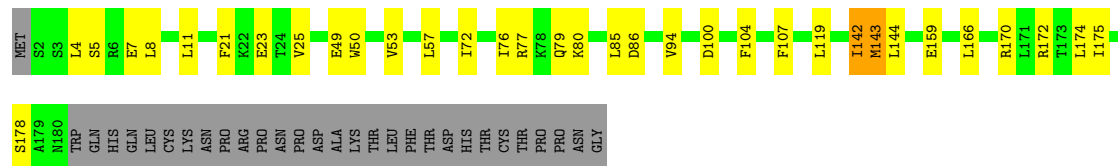
• Molecule 1: Protein TPR1

Chain A: 



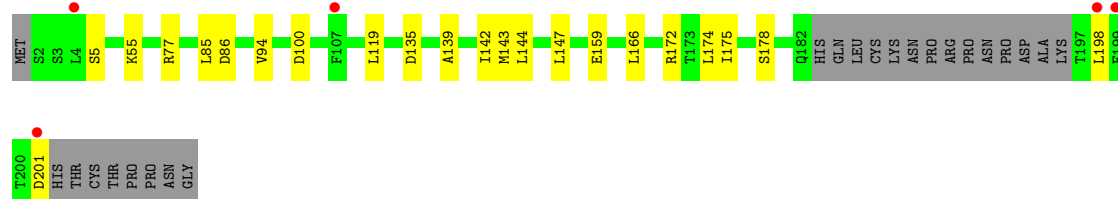
• Molecule 1: Protein TPR1

Chain B: 



• Molecule 1: Protein TPR1

Chain C: 



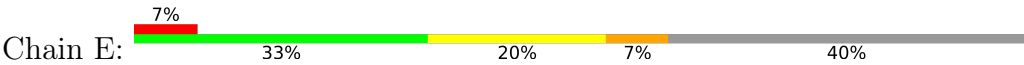
• Molecule 1: Protein TPR1

Chain D: 



CYS
LYS
ASN
PRO
ARG
PRO
ASN
PRO
ASP
ALA
LYS
THR
LEU
PHE
THR
ASP
HIS
THR
CYS
THR
PRO
PRO
ASN
GLY

● Molecule 2: The rice D53 EAR peptide (794-808)



D794
R795
L796
I797
Y798
L801
N802
LEU
GLN
ASP
TRP
ASP
ASP

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.00Å 64.07Å 106.97Å 90.00° 97.03° 90.00°	Depositor
Resolution (Å)	25.81 – 3.15 25.81 – 3.15	Depositor EDS
% Data completeness (in resolution range)	97.4 (25.81-3.15) 97.9 (25.81-3.15)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.232 , 0.284 0.236 , 0.277	Depositor DCC
R_{free} test set	909 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	82.0	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6181	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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](#)

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	0.40	0/1559	0.79	0/2089
1	B	0.40	0/1529	0.77	0/2048
1	C	0.35	0/1589	0.76	2/2131 (0.1%)
1	D	0.35	0/1541	0.81	4/2066 (0.2%)
2	E	0.72	0/73	0.81	0/99
All	All	0.38	0/6291	0.78	6/8433 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	180	ASN	CA-C-N	-7.94	111.42	122.93
1	D	180	ASN	C-N-CA	-7.94	111.42	122.93
1	D	183	HIS	N-CA-C	-6.27	105.53	113.43
1	C	135	ASP	N-CA-C	-5.94	100.97	108.45
1	D	181	TRP	N-CA-C	5.31	118.14	109.59
1	C	135	ASP	N-CA-CB	5.25	120.09	110.76

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	1531	0	1535	17	0
1	B	1502	0	1515	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1560	0	1559	13	0
1	D	1515	0	1511	17	0
2	E	73	0	68	2	0
All	All	6181	0	6188	54	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 4.

All (54) 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:172:ARG:NH2	1:D:5:SER:OG	2.22	0.73
1:B:4:LEU:HD22	1:C:198:LEU:HD11	1.71	0.70
1:B:5:SER:OG	1:C:172:ARG:NH2	2.28	0.67
1:A:85:LEU:HD21	1:A:119:LEU:HD23	1.78	0.65
1:A:77:ARG:HD3	1:A:100:ASP:HB3	1.80	0.64
1:B:85:LEU:HD21	1:B:119:LEU:HD23	1.80	0.62
1:C:77:ARG:HD3	1:C:100:ASP:HB3	1.81	0.62
1:A:27:LYS:HG3	1:D:27:LYS:HG3	1.82	0.62
1:B:172:ARG:NH2	1:C:5:SER:OG	2.33	0.61
1:A:5:SER:OG	1:D:172:ARG:NH2	2.34	0.60
1:B:174:LEU:HD22	1:C:178:SER:HB3	1.85	0.58
1:D:77:ARG:HD3	1:D:100:ASP:HB3	1.84	0.57
1:A:90:ARG:O	1:A:94:VAL:HG23	2.05	0.57
1:B:77:ARG:HD3	1:B:100:ASP:HB3	1.86	0.56
1:C:94:VAL:HG21	1:D:94:VAL:HG21	1.88	0.55
1:C:85:LEU:HD21	1:C:119:LEU:HD23	1.91	0.53
1:C:139:ALA:HA	1:C:142:ILE:HG22	1.91	0.53
1:A:24:THR:HG21	1:D:28:LEU:HB2	1.91	0.53
1:D:95:ASP:O	1:D:99:LYS:HB2	2.09	0.53
1:B:170:ARG:NH2	1:C:201:ASP:OD1	2.42	0.51
1:D:85:LEU:HD21	1:D:119:LEU:HD23	1.92	0.51
2:E:798:TYR:H	2:E:798:TYR:HD1	1.57	0.51
1:A:76:ILE:HA	1:A:143:MET:HE1	1.91	0.51
1:B:79:GLN:HB2	1:B:143:MET:HE3	1.92	0.51
1:D:76:ILE:HA	1:D:143:MET:HE1	1.94	0.49
1:B:21:PHE:O	1:B:25:VAL:HG23	2.14	0.48
1:A:97:LEU:HD21	1:A:116:THR:HG23	1.96	0.48
1:B:50:TRP:CD1	1:B:80:LYS:HG3	2.49	0.47
1:A:78:LYS:NZ	2:E:801:LEU:O	2.45	0.46
1:B:7:GLU:O	1:B:11:LEU:HD13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:90:ARG:O	1:D:94:VAL:HG23	2.16	0.46
1:A:94:VAL:HG21	1:B:94:VAL:HG21	1.98	0.46
1:B:72:ILE:O	1:B:76:ILE:HG13	2.16	0.45
1:A:12:ILE:HG23	1:D:12:ILE:HD13	1.98	0.45
1:A:27:LYS:HA	1:A:27:LYS:HD3	1.81	0.45
1:B:23:GLU:OE2	1:C:55:LYS:NZ	2.50	0.45
1:A:139:ALA:HA	1:A:142:ILE:HG22	2.00	0.44
1:A:137:LYS:O	1:A:141:SER:OG	2.35	0.44
1:B:49:GLU:O	1:B:53:VAL:HG23	2.18	0.43
1:D:68:TYR:O	1:D:72:ILE:HG13	2.18	0.43
1:B:104:PHE:HA	1:B:107:PHE:HD2	1.83	0.43
1:B:143:MET:O	1:B:143:MET:HG2	2.18	0.43
1:C:94:VAL:HG21	1:D:94:VAL:CG2	2.49	0.43
1:D:180:ASN:O	1:D:184:GLN:NE2	2.52	0.43
1:D:67:ARG:HA	1:D:67:ARG:HD3	1.91	0.42
1:B:175:ILE:HD13	1:B:175:ILE:HA	1.89	0.41
1:B:8:LEU:HD13	1:C:175:ILE:HG13	2.02	0.41
1:A:85:LEU:HD23	1:A:85:LEU:HA	1.78	0.41
1:B:57:LEU:HD23	1:B:57:LEU:HA	1.84	0.41
1:B:178:SER:HB3	1:C:174:LEU:HD22	2.02	0.41
1:A:90:ARG:HD2	1:B:94:VAL:HG11	2.03	0.40
1:D:139:ALA:HA	1:D:142:ILE:HG22	2.03	0.40
1:D:177:GLN:O	1:D:181:TRP:N	2.54	0.40
1:B:142:ILE:O	1:B:142:ILE:HG12	2.20	0.40

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	178/209 (85%)	174 (98%)	4 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	177/209 (85%)	173 (98%)	4 (2%)	0	100	100
1	C	182/209 (87%)	177 (97%)	5 (3%)	0	100	100
1	D	181/209 (87%)	178 (98%)	3 (2%)	0	100	100
2	E	7/15 (47%)	5 (71%)	2 (29%)	0	100	100
All	All	725/851 (85%)	707 (98%)	18 (2%)	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	169/195 (87%)	155 (92%)	14 (8%)	10	34
1	B	166/195 (85%)	160 (96%)	6 (4%)	31	59
1	C	172/195 (88%)	166 (96%)	6 (4%)	32	59
1	D	165/195 (85%)	156 (94%)	9 (6%)	19	47
2	E	8/15 (53%)	5 (62%)	3 (38%)	0	0
All	All	680/795 (86%)	642 (94%)	38 (6%)	19	47

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	5	SER
1	A	38	MET
1	A	86	ASP
1	A	121	LEU
1	A	136	THR
1	A	141	SER
1	A	143	MET
1	A	144	LEU
1	A	147	LEU

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Mol	Chain	Res	Type
1	A	159	GLU
1	A	166	LEU
1	A	200	THR
1	A	201	ASP
1	B	86	ASP
1	B	142	ILE
1	B	143	MET
1	B	144	LEU
1	B	159	GLU
1	B	166	LEU
1	C	86	ASP
1	C	143	MET
1	C	144	LEU
1	C	147	LEU
1	C	159	GLU
1	C	166	LEU
1	D	5	SER
1	D	86	ASP
1	D	136	THR
1	D	143	MET
1	D	144	LEU
1	D	147	LEU
1	D	159	GLU
1	D	166	LEU
1	D	184	GLN
2	E	794	ASP
2	E	796	LEU
2	E	798	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	79	GLN
1	A	117	GLN
1	A	127	ASN
1	B	117	GLN
1	D	30	GLN
1	D	184	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 oligosaccharides 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(Å ²)	Q<0.9
1	A	182/209 (87%)	0.13	1 (0%) 87 75	44, 73, 134, 192	0
1	B	179/209 (85%)	0.02	0 100 100	45, 67, 136, 166	0
1	C	186/209 (88%)	0.36	5 (2%) 56 35	65, 95, 170, 234	0
1	D	183/209 (87%)	0.61	3 (1%) 70 50	82, 114, 155, 196	0
2	E	9/15 (60%)	0.98	1 (11%) 10 6	83, 89, 108, 109	0
All	All	739/851 (86%)	0.29	10 (1%) 73 53	44, 90, 153, 234	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	107	PHE	3.5
1	C	201	ASP	3.3
1	D	124	PHE	3.1
1	C	199	PHE	2.9
1	C	198	LEU	2.7
1	C	4	LEU	2.6
1	D	179	ALA	2.3
1	A	181	TRP	2.2
2	E	802	ASN	2.0
1	D	157	PHE	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.