Full wwPDB X-ray Structure Validation Report (i)

Feb 6, 2024 – 08:15 PM EST

PDB ID	:	2ETA
Title	:	Crystal structure of the ankyrin repeat domain of the TRPV2
Authors	:	Jin, X.; Gaudet, R.
Deposited on	:	2005-10-27
Resolution	:	2.20 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:

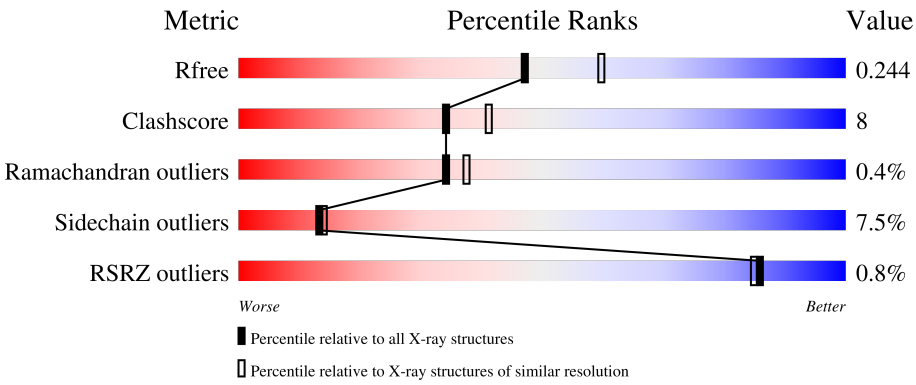
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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% 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	256	76% 14% • 7%
1	B	256	% 76% 16% • 6%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4025 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 Transient receptor potential cation channel subfamily V member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	239	1871	1187	321	351	12	0	0	0
1	B	240	1877	1190	322	353	12	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	151	PRO	LEU	SEE REMARK 999	UNP Q9WUD2
A	322	ALA	-	cloning artifact	UNP Q9WUD2
A	323	ALA	-	cloning artifact	UNP Q9WUD2
A	324	ALA	-	cloning artifact	UNP Q9WUD2
A	325	HIS	-	expression tag	UNP Q9WUD2
A	326	HIS	-	expression tag	UNP Q9WUD2
A	327	HIS	-	expression tag	UNP Q9WUD2
A	328	HIS	-	expression tag	UNP Q9WUD2
A	329	HIS	-	expression tag	UNP Q9WUD2
A	330	HIS	-	expression tag	UNP Q9WUD2
B	151	PRO	LEU	SEE REMARK 999	UNP Q9WUD2
B	322	ALA	-	cloning artifact	UNP Q9WUD2
B	323	ALA	-	cloning artifact	UNP Q9WUD2
B	324	ALA	-	cloning artifact	UNP Q9WUD2
B	325	HIS	-	expression tag	UNP Q9WUD2
B	326	HIS	-	expression tag	UNP Q9WUD2
B	327	HIS	-	expression tag	UNP Q9WUD2
B	328	HIS	-	expression tag	UNP Q9WUD2
B	329	HIS	-	expression tag	UNP Q9WUD2
B	330	HIS	-	expression tag	UNP Q9WUD2

- Molecule 2 is water.

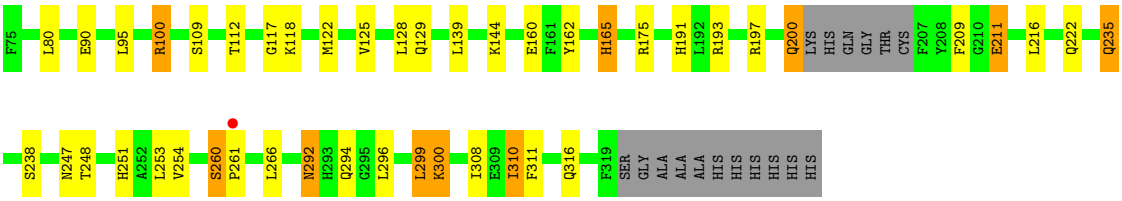
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	143	143	143	0	0
			Total	O		
2	B	134	134	134	0	0

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.

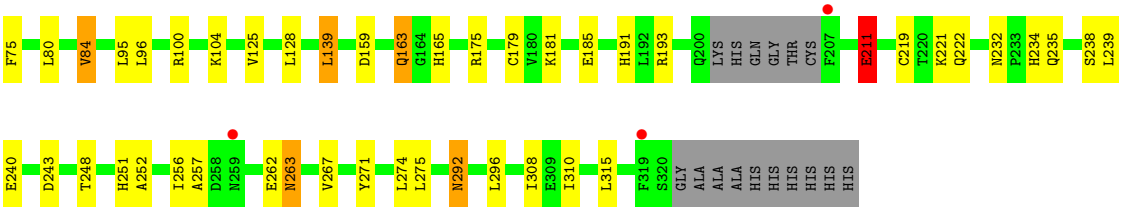
• Molecule 1: Transient receptor potential cation channel subfamily V member 2

Chain A:



• Molecule 1: Transient receptor potential cation channel subfamily V member 2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	60.77Å 60.77Å 339.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 37.93 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.8 (20.00-2.20) 98.7 (37.93-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.29 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.189 , 0.242 0.192 , 0.244	Depositor DCC
R_{free} test set	3361 reflections (10.06%)	wwPDB-VP
Wilson B-factor (Å^2)	37.4	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 44.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4025	wwPDB-VP
Average B, all atoms (Å^2)	35.0	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 22.23 % 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 5.9442e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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	0.74	2/1907 (0.1%)	0.76	2/2584 (0.1%)
1	B	0.69	1/1913 (0.1%)	0.72	1/2592 (0.0%)
All	All	0.71	3/3820 (0.1%)	0.74	3/5176 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	300	LYS	CD-CE	14.00	1.86	1.51
1	A	300	LYS	CE-NZ	7.74	1.68	1.49
1	B	179	CYS	CB-SG	-6.39	1.71	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	211	GLU	CB-CA-C	-8.59	93.22	110.40
1	A	300	LYS	CD-CE-NZ	-8.30	92.60	111.70
1	A	211	GLU	CB-CA-C	-6.02	98.37	110.40

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	1871	0	1866	33	0
1	B	1877	0	1871	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	143	0	0	1	0
2	B	134	0	0	3	0
All	All	4025	0	3737	63	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 8.

All (63) 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:300:LYS:CE	1:A:300:LYS:NZ	1.68	1.51
1:A:300:LYS:CE	1:A:300:LYS:CD	1.86	1.49
1:A:100:ARG:HG2	1:A:100:ARG:HH11	1.21	1.01
1:B:104:LYS:HD2	2:B:391:HOH:O	1.60	0.99
1:A:118:LYS:HA	1:A:122:MET:HE1	1.46	0.98
1:B:191:HIS:HE1	1:B:238:SER:H	1.14	0.93
1:A:118:LYS:HA	1:A:122:MET:CE	2.01	0.90
1:A:191:HIS:HE1	1:A:238:SER:H	1.14	0.88
1:B:232:ASN:HD21	1:B:235:GLN:H	1.25	0.84
1:A:247:ASN:ND2	1:A:292:ASN:OD1	2.12	0.82
1:B:191:HIS:CE1	1:B:238:SER:H	2.02	0.76
1:A:248:THR:H	1:A:251:HIS:HD2	1.36	0.74
1:A:300:LYS:CE	1:A:300:LYS:CG	2.65	0.74
1:A:191:HIS:CE1	1:A:238:SER:H	2.03	0.73
1:A:118:LYS:CG	1:A:122:MET:HE2	2.22	0.69
1:A:248:THR:H	1:A:251:HIS:CD2	2.10	0.69
1:B:193:ARG:HA	1:B:211:GLU:O	1.92	0.69
1:A:300:LYS:NZ	1:A:300:LYS:CD	2.56	0.68
1:B:232:ASN:HD22	1:B:234:HIS:H	1.40	0.67
1:A:112:THR:HG23	1:A:117:GLY:HA2	1.76	0.66
1:A:193:ARG:HA	1:A:211:GLU:O	1.99	0.62
1:A:100:ARG:HG2	1:A:100:ARG:NH1	2.01	0.61
1:B:75:PHE:N	2:B:456:HOH:O	2.33	0.61
1:B:84:VAL:HG21	1:B:139:LEU:HD21	1.83	0.60
1:B:248:THR:H	1:B:251:HIS:HD2	1.49	0.60
1:A:118:LYS:HG3	1:A:122:MET:HE2	1.83	0.59
1:B:251:HIS:HE1	1:B:296:LEU:O	1.88	0.56
1:A:112:THR:CG2	1:A:117:GLY:HA2	2.36	0.56
1:B:257:ALA:HA	1:B:263:ASN:HD21	1.71	0.54
1:A:235:GLN:HB2	2:A:399:HOH:O	2.07	0.53
1:B:232:ASN:ND2	1:B:234:HIS:H	2.05	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:ASN:C	1:B:292:ASN:HD22	2.11	0.52
1:B:232:ASN:ND2	1:B:235:GLN:H	2.02	0.52
1:A:292:ASN:HB2	1:A:296:LEU:H	1.77	0.50
1:A:200:GLN:HE21	1:A:200:GLN:HA	1.76	0.49
1:B:219:CYS:SG	1:B:252:ALA:HB1	2.52	0.49
1:A:118:LYS:HG3	1:A:122:MET:CE	2.42	0.49
1:A:125:VAL:O	1:A:128:LEU:HG	2.12	0.49
1:B:248:THR:H	1:B:251:HIS:CD2	2.28	0.48
1:B:181:LYS:O	1:B:185:GLU:HG3	2.14	0.48
1:A:292:ASN:HB3	1:A:294:GLN:H	1.79	0.47
1:B:239:LEU:HD21	1:B:274:LEU:HD22	1.95	0.47
1:A:162:TYR:O	1:A:165:HIS:HB2	2.13	0.47
1:A:299:LEU:HD22	1:A:311:PHE:CE1	2.50	0.47
1:A:118:LYS:HG2	1:A:122:MET:HE2	1.97	0.46
1:B:159:ASP:O	1:B:163:GLN:HG2	2.16	0.45
1:A:175:ARG:HA	1:A:222:GLN:OE1	2.17	0.45
1:A:118:LYS:HA	1:A:122:MET:HE2	1.95	0.45
1:A:260:SER:HA	1:A:261:PRO:HD2	1.78	0.44
1:A:209:PHE:CD1	1:A:216:LEU:HB2	2.53	0.44
1:B:175:ARG:HA	1:B:222:GLN:OE1	2.19	0.43
1:B:219:CYS:HA	1:B:256:ILE:HG12	1.99	0.43
1:B:271:TYR:CE2	1:B:275:LEU:HD11	2.53	0.43
1:B:191:HIS:HD2	2:B:462:HOH:O	2.02	0.42
1:B:221:LYS:HZ3	1:B:221:LYS:HG3	1.74	0.42
1:B:267:VAL:HG12	1:B:310:ILE:HD12	2.01	0.42
1:B:125:VAL:O	1:B:128:LEU:HG	2.19	0.42
1:B:308:ILE:H	1:B:308:ILE:HG13	1.70	0.41
1:B:292:ASN:ND2	1:B:296:LEU:H	2.19	0.41
1:A:118:LYS:CG	1:A:122:MET:CE	2.97	0.41
1:A:254:VAL:HG22	1:A:310:ILE:HD12	2.03	0.40
1:B:96:LEU:HD21	1:B:100:ARG:HH21	1.86	0.40
1:B:243:ASP:C	1:B:243:ASP:OD1	2.59	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	235/256 (92%)	230 (98%)	4 (2%)	1 (0%)	34	37
1	B	236/256 (92%)	231 (98%)	4 (2%)	1 (0%)	34	37
All	All	471/512 (92%)	461 (98%)	8 (2%)	2 (0%)	34	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	292	ASN
1	B	211	GLU

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	A	206/218 (94%)	186 (90%)	20 (10%)	8	7
1	B	207/218 (95%)	196 (95%)	11 (5%)	22	27
All	All	413/436 (95%)	382 (92%)	31 (8%)	13	14

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LEU
1	A	90	GLU
1	A	95	LEU
1	A	100	ARG
1	A	109	SER
1	A	129	GLN
1	A	139	LEU
1	A	144	LYS
1	A	160	GLU
1	A	165	HIS

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Mol	Chain	Res	Type
1	A	197	ARG
1	A	200	GLN
1	A	235	GLN
1	A	253	LEU
1	A	260	SER
1	A	266	LEU
1	A	299	LEU
1	A	308	ILE
1	A	310	ILE
1	A	316	GLN
1	B	80	LEU
1	B	84	VAL
1	B	95	LEU
1	B	139	LEU
1	B	163	GLN
1	B	165	HIS
1	B	240	GLU
1	B	262	GLU
1	B	263	ASN
1	B	292	ASN
1	B	315	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	ASN
1	A	178	GLN
1	A	191	HIS
1	A	200	GLN
1	A	247	ASN
1	A	251	HIS
1	A	286	GLN
1	A	292	ASN
1	B	191	HIS
1	B	232	ASN
1	B	251	HIS
1	B	263	ASN
1	B	292	ASN

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)

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	239/256 (93%)	-0.21	1 (0%)	92	91	23, 33, 53, 60	0
1	B	240/256 (93%)	-0.30	3 (1%)	77	75	24, 32, 45, 53	0
All	All	479/512 (93%)	-0.25	4 (0%)	86	85	23, 32, 49, 60	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	259	ASN	2.9
1	B	207	PHE	2.5
1	B	319	PHE	2.4
1	A	261	PRO	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 monosaccharides 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.