



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:55 PM UTC

PDB ID : 4I8M / pdb_00004i8m
Title : Crystal structure of rabbit Ryanodine receptor 1 (residues 1-536) disease mutant V219I
Authors : Kimlicka, L.; Van Petegem, F.
Deposited on : 2012-12-03
Resolution : 2.80 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

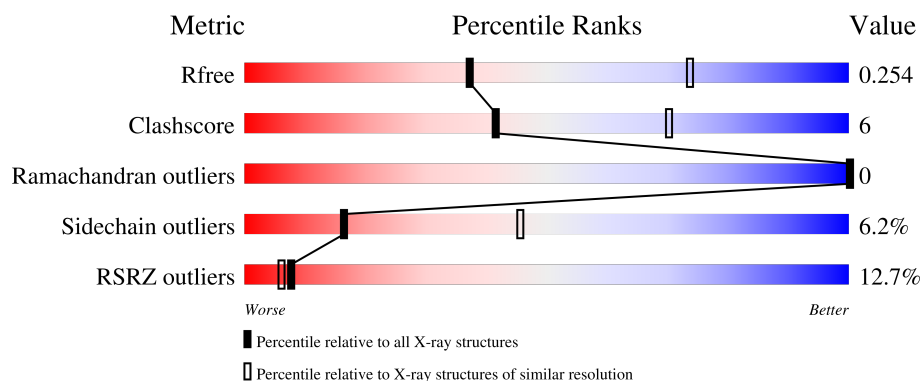
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	536	11% 76% 11% 10%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3620 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	480	3578	2257	627	668	26	0	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	219	ILE	VAL	engineered mutation	UNP P11716

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	6	3	3	0	0

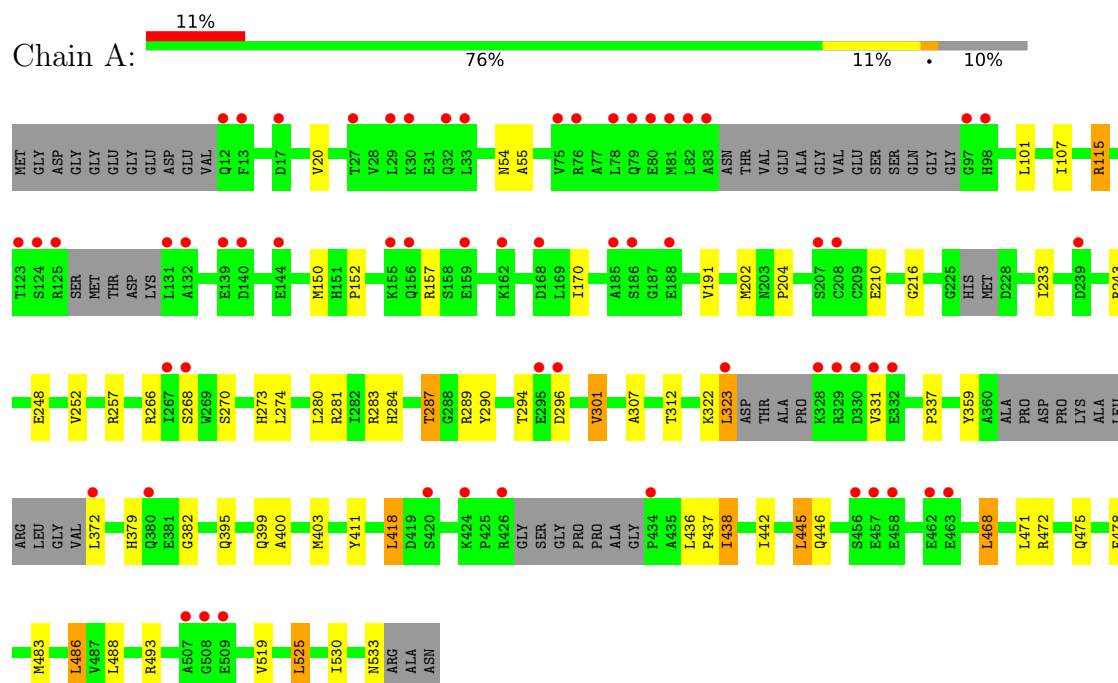
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total 36	O 36	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: Ryanodine receptor 1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	169.27Å 169.27Å 305.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.94 – 2.80 46.94 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.94-2.80) 100.0 (46.94-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.235 , 0.253 0.234 , 0.254	Depositor DCC
R_{free} test set	2084 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	69.9	Xtriage
Anisotropy	0.562	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 64.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3620	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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: 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	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/3651	0.76	0/4964

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	3578	0	3339	44	0
2	A	6	0	8	1	0
3	A	36	0	0	1	0
All	All	3620	0	3347	44	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 6.

All (44) 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:399:GLN:HG2	1:A:403:MET:HE2	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:HIS:HD2	1:A:382:GLY:H	1.29	0.77
1:A:274:LEU:HD11	1:A:280:LEU:HD23	1.68	0.74
1:A:468:LEU:HD12	1:A:533:ASN:HB3	1.69	0.74
1:A:233:ILE:HG12	1:A:284:HIS:CE1	2.34	0.63
1:A:257:ARG:O	1:A:284:HIS:HE1	1.82	0.62
1:A:379:HIS:CD2	1:A:382:GLY:H	2.15	0.61
1:A:107:ILE:CD1	1:A:202:MET:HE1	2.33	0.58
1:A:266:ARG:O	1:A:270:SER:HB3	2.05	0.56
1:A:472:ARG:HA	1:A:475:GLN:HE21	1.71	0.55
1:A:284:HIS:HD2	1:A:287:THR:H	1.53	0.55
1:A:107:ILE:HD13	1:A:202:MET:HE1	1.88	0.55
1:A:216:GLY:HA3	1:A:270:SER:O	2.08	0.54
1:A:289:ARG:CB	1:A:301:VAL:HG13	2.37	0.54
1:A:411:TYR:HB2	1:A:486:LEU:HD11	1.92	0.52
1:A:418:LEU:HD23	1:A:493:ARG:HB3	1.91	0.51
1:A:436:LEU:HB2	1:A:438:ILE:HD12	1.91	0.50
1:A:400:ALA:HA	1:A:403:MET:HE3	1.94	0.50
1:A:289:ARG:HB3	1:A:301:VAL:HG13	1.94	0.49
1:A:210:GLU:HG3	1:A:337:PRO:HG3	1.95	0.49
1:A:284:HIS:HB3	1:A:287:THR:HG22	1.95	0.48
1:A:322:LYS:O	1:A:323:LEU:HD23	2.12	0.48
1:A:248:GLU:OE2	1:A:257:ARG:NH2	2.47	0.47
1:A:274:LEU:CD1	1:A:280:LEU:HD23	2.43	0.46
1:A:266:ARG:NH2	1:A:331:VAL:O	2.48	0.46
1:A:294:THR:HG22	1:A:296:ASP:H	1.81	0.46
1:A:115:ARG:HG2	1:A:115:ARG:HH11	1.82	0.45
1:A:289:ARG:HB2	1:A:301:VAL:HG13	1.98	0.44
1:A:210:GLU:H	1:A:273:HIS:CE1	2.36	0.43
1:A:152:PRO:HB3	1:A:157:ARG:HB2	2.01	0.42
1:A:445:LEU:HD12	1:A:525:LEU:HD12	2.01	0.42
1:A:101:LEU:HB3	1:A:150:MET:HE1	2.00	0.42
1:A:20:VAL:HG12	1:A:204:PRO:HA	2.01	0.42
1:A:472:ARG:HD2	1:A:533:ASN:O	2.19	0.42
1:A:257:ARG:O	1:A:284:HIS:CE1	2.68	0.42
1:A:478:PHE:CD1	1:A:483:MET:HG3	2.54	0.42
1:A:436:LEU:HA	1:A:437:PRO:HD3	1.90	0.42
1:A:55:ALA:O	1:A:281:ARG:NH2	2.54	0.41
1:A:268:SER:H	2:A:601:GOL:H2	1.85	0.41
1:A:283:ARG:HB2	1:A:290:TYR:CE2	2.56	0.41
1:A:359:TYR:C	1:A:359:TYR:CD1	2.99	0.41
1:A:257:ARG:HD3	3:A:712:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:ARG:NH1	1:A:307:ALA:O	2.55	0.40
1:A:442:ILE:HG22	1:A:446:GLN:OE1	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	467/536 (87%)	457 (98%)	10 (2%)	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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	356/449 (79%)	334 (94%)	22 (6%)	16	45

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	115	ARG
1	A	170	ILE
1	A	191	VAL

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Mol	Chain	Res	Type
1	A	243	ARG
1	A	252	VAL
1	A	287	THR
1	A	301	VAL
1	A	312	THR
1	A	323	LEU
1	A	372	LEU
1	A	395	GLN
1	A	418	LEU
1	A	438	ILE
1	A	445	LEU
1	A	468	LEU
1	A	471	LEU
1	A	486	LEU
1	A	488	LEU
1	A	519	VAL
1	A	525	LEU
1	A	530	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	54	ASN
1	A	56	GLN
1	A	57	ASN
1	A	197	GLN
1	A	203	ASN
1	A	278	GLN
1	A	284	HIS
1	A	379	HIS
1	A	394	GLN
1	A	399	GLN
1	A	405	HIS
1	A	412	ASN
1	A	475	GLN
1	A	495	ASN
1	A	520	ASN
1	A	533	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 ⓘ

1 ligand is 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	GOL	A	601	-	5,5,5	0.38	0	5,5,5	0.31	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	Res	Link	Chirals	Torsions	Rings
2	GOL	A	601	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GOL	O1-C1-C2-C3
2	A	601	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	GOL	1	0

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	480/536 (89%)	0.72	61 (12%) 8 6	36, 75, 120, 157	1 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	131	LEU	6.4
1	A	434	PRO	6.1
1	A	186	SER	5.9
1	A	330	ASP	5.6
1	A	83	ALA	5.5
1	A	328	LYS	5.0
1	A	98	HIS	5.0
1	A	329	ARG	4.9
1	A	155	LYS	4.8
1	A	509	GLU	4.7
1	A	140	ASP	4.6
1	A	185	ALA	4.0
1	A	97	GLY	3.8
1	A	331	VAL	3.7
1	A	296	ASP	3.6
1	A	30	LYS	3.6
1	A	208	CYS	3.6
1	A	144	GLU	3.5
1	A	29	LEU	3.5
1	A	458	GLU	3.4
1	A	12	GLN	3.3
1	A	76	ARG	3.2
1	A	457	GLU	3.2
1	A	207	SER	3.1
1	A	81	MET	3.0
1	A	125	ARG	3.0
1	A	75	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	323	LEU	2.9
1	A	79	GLN	2.9
1	A	239	ASP	2.8
1	A	33	LEU	2.7
1	A	332	GLU	2.7
1	A	132	ALA	2.6
1	A	267	ILE	2.6
1	A	424	LYS	2.6
1	A	456	SER	2.5
1	A	78	LEU	2.5
1	A	82	LEU	2.5
1	A	156	GLN	2.5
1	A	462	GLU	2.5
1	A	420	SER	2.4
1	A	295	GLU	2.4
1	A	372	LEU	2.4
1	A	27	THR	2.4
1	A	426	ARG	2.4
1	A	168	ASP	2.3
1	A	188	GLU	2.3
1	A	162	LYS	2.3
1	A	508	GLY	2.3
1	A	507	ALA	2.2
1	A	463	GLU	2.2
1	A	17	ASP	2.2
1	A	13	PHE	2.2
1	A	380	GLN	2.2
1	A	139	GLU	2.1
1	A	123	THR	2.1
1	A	80	GLU	2.1
1	A	32	GLN	2.0
1	A	159	GLU	2.0
1	A	124	SER	2.0
1	A	268	SER	2.0

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

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($\text{\AA}^2$)	Q<0.9
2	GOL	A	601	6/6	0.85	0.26	107,107,107,107	0

6.5 Other polymers [i](#)

There are no such residues in this entry.