Full wwPDB X-ray Structure Validation Report (i)

Nov 15, 2023 – 10:19 AM JST

PDB ID	:	6J6L
Title	:	Crystal structure of mouse Ryanodine Receptor 2 SPRY1 Domain (650-844) disease mutant I784F
Authors	:	Ma, R.; Lin, L.; Yuchi, Z.
Deposited on	:	2019-01-15
Resolution	:	1.45 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 (i)) were used in the production of this report:

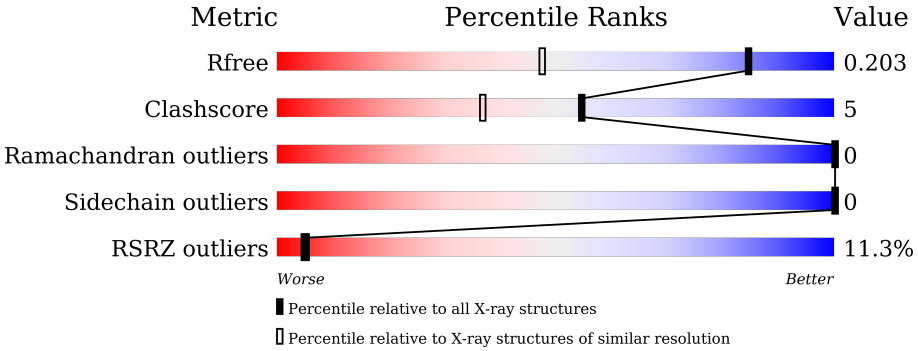
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 1.45 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	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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	198	12% 91% 5% •
1	B	198	10% 84% 11% • 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IPA	B	901	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6323 atoms, of which 2816 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.

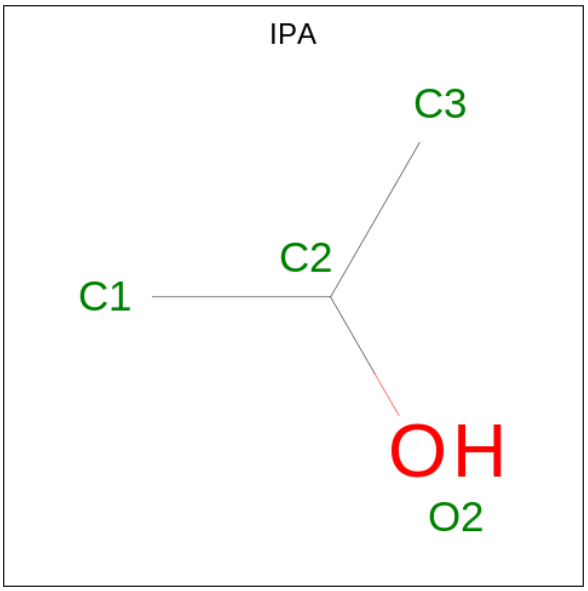
- Molecule 1 is a protein called Ryanodine receptor 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	190	2879	960	1384	249	277	9	0	9	0
1	B	189	2864	954	1384	244	274	8	0	7	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP E9Q401
A	-1	ASN	-	expression tag	UNP E9Q401
A	0	ALA	-	expression tag	UNP E9Q401
A	784	PHE	ILE	engineered mutation	UNP E9Q401
B	-2	SER	-	expression tag	UNP E9Q401
B	-1	ASN	-	expression tag	UNP E9Q401
B	0	ALA	-	expression tag	UNP E9Q401
B	784	PHE	ILE	engineered mutation	UNP E9Q401

- Molecule 2 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	12	3	8	1	0	0
			Total	C	H	O		
2	A	1	12	3	8	1	0	0
			Total	C	H	O		
2	B	1	12	3	8	1	0	0
			Total	C	H	O		
2	B	1	12	3	8	1	0	0
			Total	C	H	O		
2	B	1	12	3	8	1	0	0
			Total	C	H	O		
2	B	1	12	3	8	1	0	0

- Molecule 3 is water.

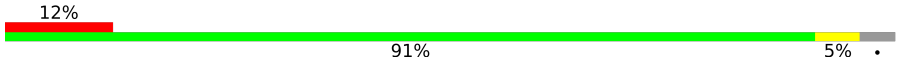
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	253	253	253	0	0
			Total	O		
3	B	255	255	255	0	0

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.

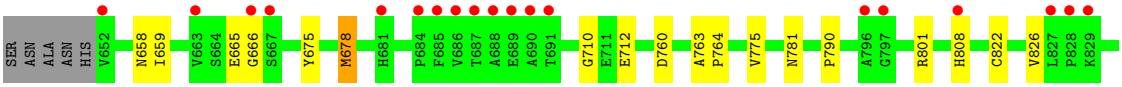
• Molecule 1: Ryanodine receptor 2

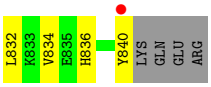
Chain A:



• Molecule 1: Ryanodine receptor 2

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	52.95Å 64.38Å 108.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.86 – 1.45 30.86 – 1.45	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.86-1.45) 97.0 (30.86-1.45)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.19 (at 1.45Å)	Xtriage
Refinement program	PHENIX 1.14_3247	Depositor
R, R_{free}	0.172 , 0.204 0.172 , 0.203	Depositor DCC
R_{free} test set	2000 reflections (3.03%)	wwPDB-VP
Wilson B-factor (Å^2)	13.5	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 44.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6323	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.89% of the height of the origin peak. No significant pseudotranslation is detected.*

[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)

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

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	0.49	0/1580	0.71	0/2147
1	B	0.49	0/1545	0.70	1/2103 (0.0%)
All	All	0.49	0/3125	0.71	1/4250 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	678	MET	CG-SD-CE	-6.85	89.25	100.20

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	1495	1384	1339	9	0
1	B	1480	1384	1364	19	0
2	A	8	16	16	1	0
2	B	16	32	32	11	0
3	A	253	0	0	5	4
3	B	255	0	0	3	0
All	All	3507	2816	2751	30	4

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 (30) 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:B:712:GLU:OE2	2:B:901:IPA:H13	1.81	0.80
1:B:666:GLY:H	2:B:904:IPA:H33	1.57	0.68
1:A:700:THR:HG21	2:B:901:IPA:H2	1.78	0.65
1:B:775:VAL:O	2:B:902:IPA:H11	2.02	0.58
1:B:836:HIS:HB2	2:B:903:IPA:H31	1.86	0.58
2:B:904:IPA:H31	3:B:1152:HOH:O	2.04	0.57
1:B:710:GLY:HA3	2:B:901:IPA:O2	2.08	0.53
2:B:901:IPA:H11	3:B:1229:HOH:O	2.09	0.52
1:A:739[A]:ARG:NH2	3:A:1010:HOH:O	2.43	0.51
1:B:665:GLU:HA	2:B:904:IPA:H33	1.91	0.51
1:B:808:HIS:HB2	3:B:1039:HOH:O	2.11	0.50
1:B:760:ASP:O	1:B:764:PRO:HA	2.13	0.48
1:B:675:TYR:CE1	1:B:790:PRO:HB3	2.51	0.46
1:B:678:MET:HG2	1:B:801:ARG:NH2	2.30	0.46
1:A:763:ALA:HB3	1:A:764:PRO:C	2.37	0.45
1:B:764:PRO:HD2	1:B:781:ASN:HA	1.97	0.45
1:B:834:VAL:O	2:B:903:IPA:H32	2.16	0.45
2:A:902:IPA:H13	3:A:1204:HOH:O	2.18	0.44
1:A:728:ASP:OD2	3:A:1002:HOH:O	2.21	0.43
1:A:832:LEU:HD23	1:B:840:TYR:CD2	2.54	0.43
1:B:659[A]:ILE:HD13	1:B:822:CYS:HB3	2.01	0.42
1:B:775:VAL:O	2:B:902:IPA:C1	2.66	0.42
1:A:739[A]:ARG:CZ	3:A:1015:HOH:O	2.67	0.42
1:A:824:GLU:OE2	3:A:1001:HOH:O	2.21	0.41
1:B:826:VAL:HG22	1:B:832:LEU:HD13	2.01	0.41
1:A:732:LEU:HB3	1:A:779:PHE:CZ	2.56	0.41
1:B:763:ALA:HB3	1:B:764:PRO:C	2.41	0.41
1:B:826:VAL:CG2	1:B:832:LEU:HD13	2.51	0.41
1:A:763:ALA:HB3	1:A:764:PRO:CA	2.52	0.40
1:B:658:ASN:OD1	1:B:832:LEU:HD12	2.21	0.40

All (4) 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:1015:HOH:O	3:A:1144:HOH:O[4_455]	1.84	0.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1015:HOH:O	3:A:1023:HOH:O[4_455]	1.90	0.30
3:A:1023:HOH:O	3:A:1096:HOH:O[4_555]	1.90	0.30
3:A:1153:HOH:O	3:A:1203:HOH:O[4_455]	2.01	0.19

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	197/198 (100%)	191 (97%)	6 (3%)	0	100	100
1	B	194/198 (98%)	187 (96%)	7 (4%)	0	100	100
All	All	391/396 (99%)	378 (97%)	13 (3%)	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	157/165 (95%)	157 (100%)	0	100	100
1	B	156/165 (94%)	156 (100%)	0	100	100
All	All	313/330 (95%)	313 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

6 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	IPA	B	901	-	3,3,3	0.39	0	3,3,3	0.27	0
2	IPA	B	903	-	3,3,3	0.60	0	3,3,3	0.26	0
2	IPA	B	904	-	3,3,3	0.45	0	3,3,3	0.23	0
2	IPA	A	902	-	3,3,3	0.47	0	3,3,3	0.32	0
2	IPA	B	902	-	3,3,3	0.46	0	3,3,3	0.57	0
2	IPA	A	901	-	3,3,3	0.56	0	3,3,3	0.26	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	IPA	4	0
2	B	903	IPA	2	0
2	B	904	IPA	3	0
2	A	902	IPA	1	0
2	B	902	IPA	2	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 (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	190/198 (95%)	0.69	23 (12%)	4	4	8, 16, 45, 65	0
1	B	189/198 (95%)	0.35	20 (10%)	6	6	8, 15, 37, 51	0
All	All	379/396 (95%)	0.52	43 (11%)	5	5	8, 16, 40, 65	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	686	VAL	7.9
1	A	688	ALA	7.3
1	A	684	PRO	6.9
1	A	828	PRO	5.7
1	A	685	PHE	5.7
1	A	651	HIS	5.7
1	B	684	PRO	5.4
1	A	652	VAL	5.0
1	B	688	ALA	5.0
1	B	687	THR	4.9
1	B	686	VAL	4.9
1	A	784	PHE	4.7
1	A	796	ALA	4.4
1	B	808	HIS	4.4
1	A	829	LYS	4.4
1	A	687	THR	4.2
1	B	691	THR	3.7
1	B	652	VAL	3.7
1	B	829	LYS	3.6
1	B	685	PHE	3.6
1	A	827	LEU	3.6
1	B	690	ALA	3.5
1	A	670[A]	TYR	3.5
1	A	689	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	683	GLU	3.3
1	B	797	GLY	3.0
1	A	840	TYR	3.0
1	B	828	PRO	2.9
1	B	666	GLY	2.9
1	B	840	TYR	2.7
1	B	667	SER	2.7
1	A	681	HIS	2.6
1	A	669	GLN	2.6
1	B	681	HIS	2.6
1	B	689	GLU	2.6
1	B	796	ALA	2.4
1	A	667	SER	2.3
1	A	668	ALA	2.3
1	B	827	LEU	2.3
1	B	663	VAL	2.3
1	A	682	THR	2.1
1	A	826	VAL	2.1
1	A	782	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 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, 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	IPA	B	902	4/4	0.70	0.30	36,44,57,68	0
2	IPA	B	903	4/4	0.70	0.33	23,37,51,61	0
2	IPA	A	901	4/4	0.71	0.23	19,38,54,64	0
2	IPA	B	901	4/4	0.90	0.23	18,25,36,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	IPA	A	902	4/4	0.91	0.14	23,43,48,48	0
2	IPA	B	904	4/4	0.93	0.11	13,32,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.