



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6GPG / pdb_00006gpg
Title : Structure of the RIG-I Singleton-Merten syndrome variant C268F
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Deposited on : 2018-06-05
Resolution : 2.89 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Xtrriage (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

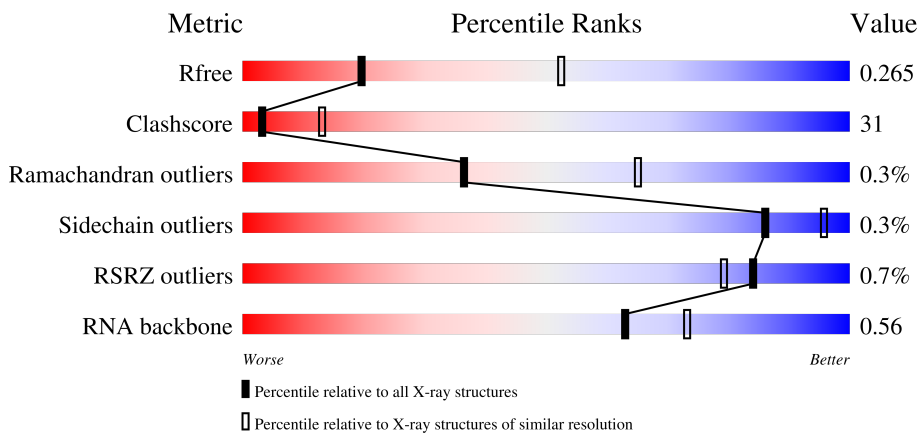
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)
RNA backbone	3983	1120 (3.10-2.70)

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	B	14	 29% 57% 7% 7%
1	C	14	 21% 50% 21% 7%
2	A	714	 51% 39% 9%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5812 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 RNA chain called RNA (5'-R(*CP*GP*AP*CP*GP*CP*UP*AP*GP*CP*GP*UP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	B	13	Total 273	C 123	N 49	O 89	P 12	0	0	0
1	C	13	Total 279	C 124	N 51	O 91	P 13	0	0	0

- Molecule 2 is a protein called Probable ATP-dependent RNA helicase DDX58.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	651	Total 5258	C 3369	N 893	O 966	S 30	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	212	MET	-	initiating methionine	UNP O95786
A	213	HIS	-	expression tag	UNP O95786
A	214	HIS	-	expression tag	UNP O95786
A	215	HIS	-	expression tag	UNP O95786
A	216	HIS	-	expression tag	UNP O95786
A	217	HIS	-	expression tag	UNP O95786
A	218	HIS	-	expression tag	UNP O95786
A	219	SER	-	expression tag	UNP O95786
A	220	SER	-	expression tag	UNP O95786
A	221	GLY	-	expression tag	UNP O95786
A	222	LEU	-	expression tag	UNP O95786
A	223	GLU	-	expression tag	UNP O95786
A	224	VAL	-	expression tag	UNP O95786
A	225	LEU	-	expression tag	UNP O95786
A	226	PHE	-	expression tag	UNP O95786
A	227	GLN	-	expression tag	UNP O95786
A	228	GLY	-	expression tag	UNP O95786

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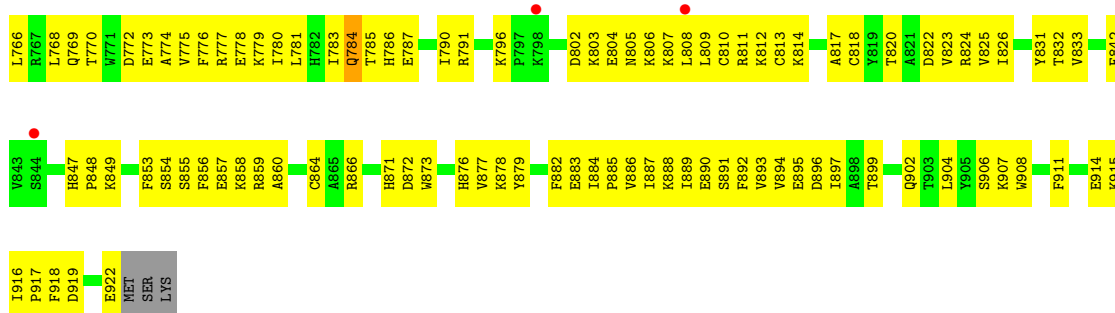
Chain	Residue	Modelled	Actual	Comment	Reference
A	229	PRO	-	expression tag	UNP O95786
A	230	HIS	-	expression tag	UNP O95786
A	231	MET	-	expression tag	UNP O95786
A	268	PHE	CYS	engineered mutation	UNP O95786

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg 1 1	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	175.62Å 175.62Å 109.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.47 – 2.89 46.47 – 2.89	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.47-2.89) 99.7 (46.47-2.89)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 2.91Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.210 , 0.260 0.219 , 0.265	Depositor DCC
R_{free} test set	1110 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	108.1	Xtrriage
Anisotropy	0.122	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 109.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5812	wwPDB-VP
Average B, all atoms (Å ²)	139.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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: MG, ZN

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	B	0.28	0/304	0.48	0/472
1	C	0.28	0/311	0.53	0/483
2	A	0.42	0/5368	0.73	4/7237 (0.1%)
All	All	0.40	0/5983	0.70	4/8192 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	6

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	488	ARG	CA-C-N	-6.53	114.86	122.63
2	A	488	ARG	C-N-CA	-6.53	114.86	122.63
2	A	784	GLN	CA-CB-CG	5.11	124.33	114.10
2	A	536	LYS	CG-CD-CE	5.00	122.80	111.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	346	LEU	Peptide
2	A	378	SER	Peptide
2	A	507	GLN	Peptide

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Mol	Chain	Res	Type	Group
2	A	701	ASP	Peptide
2	A	853	PHE	Peptide

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	B	273	0	143	16	0
1	C	279	0	142	9	0
2	A	5258	0	5304	339	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
All	All	5812	0	5589	351	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 31.

The worst 5 of 351 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)
2:A:847:HIS:CG	2:A:858:LYS:HZ1	1.27	1.48
2:A:847:HIS:CG	2:A:858:LYS:NZ	1.98	1.27
2:A:657:LYS:HZ2	2:A:691:HIS:CA	1.51	1.23
2:A:786:HIS:O	2:A:790:ILE:HD12	1.37	1.22
2:A:847:HIS:CD2	2:A:858:LYS:NZ	2.14	1.15

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
2	A	645/714 (90%)	598 (93%)	45 (7%)	2 (0%)	36 65

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	379	LYS
2	A	705	ASP

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
2	A	585/640 (91%)	583 (100%)	2 (0%)	86 96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	701	ASP
2	A	751	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	847	HIS
2	A	902	GLN
2	A	912	HIS
2	A	619	GLN
2	A	623	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	12/14 (85%)	2 (16%)	0
1	C	13/14 (92%)	2 (15%)	1 (7%)
All	All	25/28 (89%)	4 (16%)	1 (4%)

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	3	A
1	B	13	C
1	C	3	A
1	C	14	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C	2	G

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

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 [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	B	13/14 (92%)	-1.02	0	100 100	104, 123, 186, 196	0
1	C	13/14 (92%)	-0.85	0	100 100	95, 117, 197, 205	0
2	A	651/714 (91%)	-0.31	5 (0%)	82 77	68, 130, 220, 259	0
All	All	677/742 (91%)	-0.33	5 (0%)	84 79	68, 130, 219, 259	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	493	LEU	2.7
2	A	719	GLY	2.6
2	A	844	SER	2.4
2	A	808	LEU	2.1
2	A	798	LYS	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(\AA^2)	Q<0.9
4	MG	A	1002	1/1	0.88	0.18	83,83,83,83	0
3	ZN	A	1001	1/1	0.99	0.02	160,160,160,160	0

6.5 Other polymers [i](#)

There are no such residues in this entry.