



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 9BUV / pdb_00009buv
Title : Crystal structure of Cry1Fa R226Q
Authors : Poland, B.W.; Kakani, K.; Yamamoto, T.
Deposited on : 2024-05-17
Resolution : 2.02 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

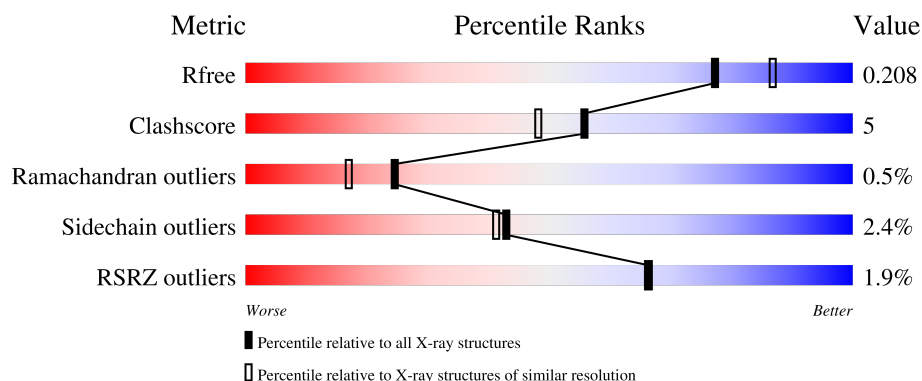
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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	1174	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4800 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 Pesticidal crystal protein Cry1Fa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	573	Total	C	N	O	S	0	0	0
			4567	2904	804	853	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	226	GLN	ARG	engineered mutation	UNP Q03746

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	233	Total	O	0	0
			233	233		

- Molecule 1: Pesticidal crystal protein Cry1Fa



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.23Å 68.35Å 121.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.91 – 2.02 60.91 – 2.02	Depositor EDS
% Data completeness (in resolution range)	100.0 (60.91-2.02) 100.0 (60.91-2.02)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.40 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.8.0405	Depositor
R, R_{free}	0.154 , 0.197 0.166 , 0.208	Depositor DCC
R_{free} test set	1790 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	14.7	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4800	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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

5.1 Standard geometry

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	0.63	0/4687	1.05	9/6398 (0.1%)

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
1	A	0	9

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	220	ASN	CB-CA-C	-10.99	91.43	110.45
1	A	88	THR	CB-CA-C	-8.81	96.71	110.81
1	A	519	ARG	NE-CZ-NH2	-6.53	113.33	119.20
1	A	220	ASN	CA-CB-CG	6.46	119.06	112.60
1	A	595	PHE	CA-CB-CG	6.04	119.84	113.80
1	A	582	ASP	CB-CA-C	-5.64	98.12	111.65
1	A	172	ASP	CA-CB-CG	5.45	118.05	112.60
1	A	183	ASP	CA-CB-CG	5.06	117.66	112.60
1	A	219	THR	CA-CB-OG1	-5.02	102.07	109.60

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	125	ARG	Sidechain
1	A	324	ARG	Sidechain
1	A	42	ARG	Sidechain
1	A	430	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	451	ARG	Sidechain
1	A	494	ARG	Sidechain
1	A	517	ARG	Sidechain
1	A	519	ARG	Sidechain
1	A	521	ARG	Sidechain

5.2 Too-close contacts ⓘ

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	4567	0	4432	42	0
2	A	233	0	0	4	0
All	All	4800	0	4432	42	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 5.

All (42) 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:515:ARG:HH11	1:A:515:ARG:HG3	1.35	0.91
1:A:306:THR:HG21	1:A:340:ASN:H	1.42	0.84
1:A:306:THR:HG23	1:A:339:PHE:CD1	2.26	0.71
1:A:264:GLU:OE1	2:A:1201:HOH:O	2.07	0.70
1:A:368:GLY:O	1:A:369:PHE:C	2.36	0.67
1:A:353:ARG:HG3	1:A:385:GLN:CD	2.21	0.66
1:A:49:VAL:HG13	1:A:50:PRO:HD2	1.80	0.63
1:A:517:ARG:HD3	1:A:565:ASN:O	2.00	0.60
1:A:338:VAL:O	1:A:338:VAL:HG23	2.02	0.60
1:A:217:ARG:HG3	1:A:217:ARG:HH11	1.67	0.59
1:A:521:ARG:HD2	2:A:1255:HOH:O	2.02	0.58
1:A:264:GLU:OE2	1:A:295:HIS:CE1	2.57	0.57
1:A:353:ARG:HD3	2:A:1290:HOH:O	2.04	0.57
1:A:511:GLN:CD	1:A:511:GLN:H	2.12	0.57
1:A:125:ARG:HH12	1:A:181:GLY:CA	2.21	0.54
1:A:515:ARG:HG3	1:A:515:ARG:NH1	2.12	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:519:ARG:HD2	1:A:596:GLU:OE1	2.09	0.51
1:A:512:LEU:N	1:A:513:PRO:CD	2.74	0.51
1:A:353:ARG:CD	2:A:1290:HOH:O	2.60	0.50
1:A:220:ASN:ND2	1:A:223:GLN:OE1	2.45	0.50
1:A:264:GLU:OE2	1:A:295:HIS:HE1	1.94	0.50
1:A:515:ARG:HH11	1:A:515:ARG:CG	2.15	0.49
1:A:519:ARG:HD3	1:A:561:TYR:CD1	2.47	0.49
1:A:338:VAL:O	1:A:338:VAL:CG2	2.62	0.48
1:A:435:ILE:HD13	1:A:435:ILE:N	2.30	0.46
1:A:481:VAL:HG22	1:A:493:LEU:CD2	2.45	0.46
1:A:43:PHE:CZ	1:A:57:GLY:HA3	2.50	0.46
1:A:434:GLU:HG2	1:A:435:ILE:HD13	1.98	0.46
1:A:306:THR:HG21	1:A:340:ASN:N	2.22	0.45
1:A:245:PHE:N	1:A:246:PRO:CD	2.80	0.45
1:A:311:ARG:CZ	1:A:434:GLU:HB2	2.47	0.45
1:A:532:VAL:HA	1:A:578:THR:O	2.16	0.45
1:A:68:PRO:HG3	1:A:99:ARG:HG2	1.99	0.44
1:A:511:GLN:CD	1:A:511:GLN:N	2.76	0.44
1:A:36:ILE:HG21	1:A:66:ILE:HD11	1.99	0.44
1:A:216:LEU:HD22	1:A:226:GLN:HE21	1.83	0.44
1:A:217:ARG:HH11	1:A:217:ARG:CG	2.30	0.44
1:A:366:ARG:HH21	1:A:368:GLY:CA	2.32	0.42
1:A:68:PRO:HG3	1:A:99:ARG:CG	2.51	0.41
1:A:330:ARG:NH1	1:A:350:GLU:OE2	2.54	0.41
1:A:206:LEU:HD13	1:A:206:LEU:HA	1.92	0.40
1:A:371:ASN:N	1:A:372:PRO:CD	2.84	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	571/1174 (49%)	557 (98%)	11 (2%)	3 (0%)	24 17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	PHE
1	A	367	GLY
1	A	371	ASN

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	497/1034 (48%)	485 (98%)	12 (2%)	43 41

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	88	THR
1	A	149	THR
1	A	219	THR
1	A	220	ASN
1	A	346	TRP
1	A	371	ASN
1	A	435	ILE
1	A	511	GLN
1	A	515	ARG
1	A	554	LEU
1	A	600	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	ASN

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Mol	Chain	Res	Type
1	A	226	GLN
1	A	247	ASN
1	A	295	HIS
1	A	371	ASN
1	A	396	ASN
1	A	466	GLN
1	A	507	ASN
1	A	514	GLN
1	A	545	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 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	573/1174 (48%)	-0.28	11 (1%) 66 66	7, 14, 30, 84	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	370	GLY	5.5
1	A	369	PHE	4.4
1	A	371	ASN	3.3
1	A	220	ASN	3.0
1	A	368	GLY	2.9
1	A	346	TRP	2.9
1	A	511	GLN	2.6
1	A	372	PRO	2.2
1	A	47	GLU	2.1
1	A	601	THR	2.1
1	A	412	SER	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.