



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2024 – 04:50 PM EST

PDB ID : 3SR3
Title : Crystal structure of the w180a mutant of microcin immunity protein mccf from Bacillus anthracis shows the active site loop in the open conformation.
Authors : Nocek, B.; Zhou, M.; Gu, M.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2011-07-06
Resolution : 1.50 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

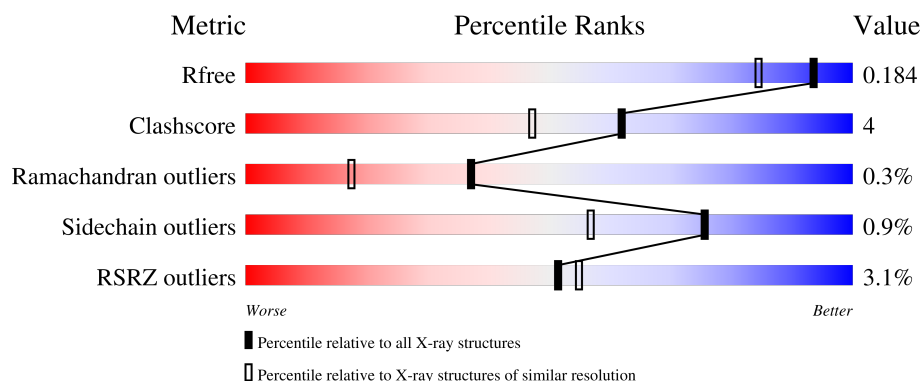
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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}	164625	3717 (1.50-1.50)
Clashscore	180529	4048 (1.50-1.50)
Ramachandran outliers	177936	3970 (1.50-1.50)
Sidechain outliers	177891	3967 (1.50-1.50)
RSRZ outliers	164620	3718 (1.50-1.50)

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	336	
1	B	336	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5719 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 Microcin immunity protein MccF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	8	0
			2650	1710	428	498	14			
1	B	304	Total	C	N	O	S	0	12	0
			2425	1569	393	448	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q81RT8
A	-1	ASN	-	expression tag	UNP Q81RT8
A	0	ALA	-	expression tag	UNP Q81RT8
A	180	ALA	TRP	engineered mutation	UNP Q81RT8
B	-2	SER	-	expression tag	UNP Q81RT8
B	-1	ASN	-	expression tag	UNP Q81RT8
B	0	ALA	-	expression tag	UNP Q81RT8
B	180	ALA	TRP	engineered mutation	UNP Q81RT8

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	352	Total	O	0	0
			352	352		
2	B	292	Total	O	0	0
			292	292		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.31Å 97.14Å 125.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.87 – 1.50 29.87 – 1.50	Depositor EDS
% Data completeness (in resolution range)	91.4 (29.87-1.50) 91.2 (29.87-1.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.69 (at 1.50Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.149 , 0.178 0.158 , 0.184	Depositor DCC
R_{free} test set	4649 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	13.8	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5719	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% 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](#)

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	0.70	0/2737	0.80	1/3718 (0.0%)
1	B	0.61	0/2517	0.73	1/3412 (0.0%)
All	All	0.66	0/5254	0.77	2/7130 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	87	MET	CG-SD-CE	-13.52	78.57	100.20
1	B	87	MET	CG-SD-CE	-9.11	85.63	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	2650	0	2616	24	0
1	B	2425	0	2433	16	0
2	A	352	0	0	7	0
2	B	292	0	0	6	0
All	All	5719	0	5049	40	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 4.

All (40) 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:169:GLN:HA	2:B:541:HOH:O	1.80	0.80
1:A:141:GLU:CB	2:A:569:HOH:O	2.32	0.76
1:B:207[A]:ILE:HD13	1:B:208:GLY:N	2.05	0.71
1:A:144:PRO:HG3	2:A:458:HOH:O	1.95	0.65
1:A:8:LYS:HE2	2:A:573:HOH:O	1.97	0.64
1:A:292:ARG:NH2	2:A:390:HOH:O	2.35	0.60
1:B:140:GLY:C	2:B:530:HOH:O	2.41	0.59
1:A:34:LYS:HG3	1:A:44[A]:ILE:CD1	2.32	0.59
1:A:104:ASN:HB3	2:A:660:HOH:O	2.05	0.56
1:A:179:ASN:HD21	1:A:181:GLU:CG	2.18	0.56
1:B:165:TYR:CD2	1:B:331:TRP:CH2	2.95	0.55
1:B:101:PHE:HE1	1:B:108[B]:MET:SD	2.29	0.55
1:B:8:LYS:HE3	2:B:368:HOH:O	2.08	0.54
1:B:152:TYR:CE1	1:B:308:ILE:HG23	2.44	0.53
1:A:26:SER:HB3	1:A:29:ARG:HD3	1.92	0.52
1:A:179:ASN:C	1:A:179:ASN:OD1	2.48	0.52
1:A:34:LYS:HG3	1:A:44[A]:ILE:HD13	1.91	0.51
1:B:169:GLN:CA	2:B:541:HOH:O	2.47	0.51
1:B:169:GLN:CB	1:B:300:ASP:OD2	2.59	0.51
1:A:227:GLN:NE2	2:A:475:HOH:O	2.43	0.51
1:A:34:LYS:HG3	1:A:44[A]:ILE:HD12	1.95	0.48
1:B:301:CYS:HA	1:B:302:CYS:HA	1.66	0.48
1:A:179:ASN:HD21	1:A:181:GLU:HG3	1.78	0.47
1:B:40:LYS:HE2	2:B:369:HOH:O	2.13	0.47
1:A:208:GLY:HA3	1:A:233:PHE:O	2.15	0.47
1:B:207[A]:ILE:HD12	1:B:226[A]:ILE:CD1	2.46	0.46
1:A:299:PHE:CE1	1:A:325:ILE:HD12	2.51	0.46
1:A:311:PRO:HG2	1:A:327[B]:ILE:HD13	1.98	0.45
1:B:299:PHE:CE1	1:B:325:ILE:HD12	2.51	0.45
1:A:86:GLY:C	1:A:87:MET:HG2	2.38	0.44
1:B:304:THR:HG23	2:B:612:HOH:O	2.17	0.43
1:A:143:GLU:CG	2:A:603:HOH:O	2.66	0.43
1:A:173:TRP:CE2	1:A:267:LYS:HE2	2.53	0.42
1:A:34:LYS:CG	1:A:44[A]:ILE:HD12	2.51	0.41
1:B:105:PRO:HB3	1:B:127:ILE:HD13	2.02	0.41
1:A:106:LYS:HE2	1:A:106:LYS:HB3	1.94	0.41
1:A:174[A]:SER:HA	1:A:188:GLU:O	2.21	0.40
1:A:179:ASN:OD1	1:A:181:GLU:N	2.54	0.40
1:A:144:PRO:HG2	1:A:174[B]:SER:OG	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	339/336 (101%)	329 (97%)	9 (3%)	1 (0%)	37	17
1	B	310/336 (92%)	302 (97%)	7 (2%)	1 (0%)	37	17
All	All	649/672 (97%)	631 (97%)	16 (2%)	2 (0%)	37	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	TYR
1	B	55	TYR

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	291/295 (99%)	289 (99%)	2 (1%)	81	66
1	B	269/295 (91%)	265 (98%)	4 (2%)	60	35
All	All	560/590 (95%)	554 (99%)	6 (1%)	75	48

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	190	ARG
1	A	310	MET
1	B	39	GLN
1	B	152	TYR

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Mol	Chain	Res	Type
1	B	207[A]	ILE
1	B	207[B]	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	227	GLN

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

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	333/336 (99%)	-0.18	13 (3%) 44 47	6, 13, 33, 55	12 (3%)
1	B	304/336 (90%)	-0.15	7 (2%) 61 64	7, 15, 31, 49	12 (3%)
All	All	637/672 (94%)	-0.17	20 (3%) 51 55	6, 14, 32, 55	24 (3%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	144	PRO	5.0
1	A	178	ILE	4.9
1	B	145	PHE	4.0
1	A	141	GLU	3.9
1	A	182	GLU	3.9
1	B	169	GLN	3.6
1	A	177	PHE	3.5
1	B	304	THR	3.5
1	A	142	PHE	3.4
1	A	179	ASN	3.3
1	A	184	THR	3.1
1	A	180	ALA	3.0
1	B	305	HIS	2.9
1	A	292	ARG	2.8
1	A	143	GLU	2.7
1	B	308	ILE	2.6
1	B	302	CYS	2.5
1	A	175	ASP	2.5
1	A	181	GLU	2.2
1	B	306	PRO	2.1

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.