



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 7R24 / pdb_00007r24
Title : Crystal structure of rat Arc CTD in complex with two anti-Arc nanobodies
Authors : Markusson, S.; Kursula, P.
Deposited on : 2022-02-04
Resolution : 2.70 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
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

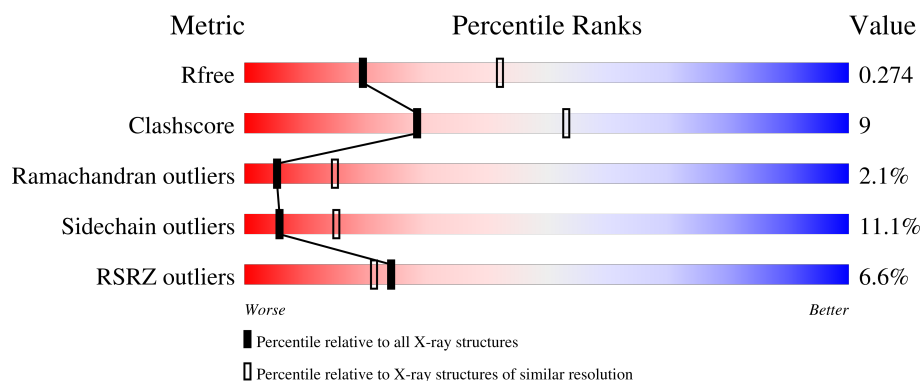
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	A	397	 3% 28% 7% 62%
2	C	120	 2% 78% 18% ..
3	E	128	 9% 70% 23% ...

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6236 atoms, of which 3068 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 Activity-regulated cytoskeleton-associated protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	150	Total	C	H	N	O	S	0	0	0
			2526	823	1245	218	238	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q63053
A	114	ALA	MET	engineered mutation	UNP Q63053
A	115	ALA	HIS	engineered mutation	UNP Q63053
A	116	ALA	VAL	engineered mutation	UNP Q63053
A	117	ALA	TRP	engineered mutation	UNP Q63053
A	118	ALA	ARG	engineered mutation	UNP Q63053
A	119	ALA	GLU	engineered mutation	UNP Q63053
A	120	ALA	VAL	engineered mutation	UNP Q63053

- Molecule 2 is a protein called anti-Arc nanobody.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	118	Total	C	H	N	O	S	0	2	0
			1803	570	889	162	179	3			

- Molecule 3 is a protein called anti-Arc nanobody.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	E	125	Total	C	H	N	O	S	0	0	0
			1907	610	934	170	188	5			

- Molecule 1: Activity-regulated cytoskeleton-associated protein.



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	40.88Å 92.81Å 114.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.51 – 2.70 38.51 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (38.51-2.70) 83.6 (38.51-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.62 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.257 , 0.274 0.257 , 0.274	Depositor DCC
R_{free} test set	1248 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.822	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 26.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6236	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% 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	0.12	0/1314	0.29	0/1772
2	C	0.10	0/949	0.29	0/1286
3	E	0.11	0/994	0.29	0/1343
All	All	0.11	0/3257	0.29	0/4401

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

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	1281	1245	1245	21	0
2	C	914	889	870	15	0
3	E	973	934	934	23	0
All	All	3168	3068	3049	55	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 9.

The worst 5 of 55 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)
3:E:14:VAL:HG11	3:E:20:LEU:HD11	1.42	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:14:VAL:HG23	3:E:126:VAL:HG13	1.68	0.75
2:C:36:VAL:HG11	2:C:81:VAL:HG21	1.69	0.73
2:C:85:MET:HE2	2:C:88:LEU:HD21	1.75	0.69
3:E:93:THR:HG23	3:E:125:THR:HA	1.77	0.67

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	148/397 (37%)	138 (93%)	5 (3%)	5 (3%)	3	7
2	C	118/120 (98%)	110 (93%)	7 (6%)	1 (1%)	16	37
3	E	123/128 (96%)	110 (89%)	11 (9%)	2 (2%)	7	20
All	All	389/645 (60%)	358 (92%)	23 (6%)	8 (2%)	5	15

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	GLN
1	A	294	LYS
3	E	113	GLN
2	C	115	GLN
1	A	340	HIS

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	138/338 (41%)	126 (91%)	12 (9%)	9	24
2	C	98/97 (101%)	89 (91%)	9 (9%)	8	22
3	E	100/102 (98%)	83 (83%)	17 (17%)	2	6
All	All	336/537 (63%)	298 (89%)	38 (11%)	6	14

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	59	SER
3	E	125	THR
3	E	104	MET
3	E	114	ASN
3	E	127	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	244	GLN
1	A	274	GLN
1	A	351	GLN
2	C	35	ASN
3	E	84	GLN

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 [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	150/397 (37%)	0.82	11 (7%) 21 18	44, 65, 87, 112	0
2	C	118/120 (98%)	0.50	3 (2%) 58 55	42, 53, 71, 81	0
3	E	125/128 (97%)	0.99	12 (9%) 13 11	60, 72, 82, 85	0
All	All	393/645 (60%)	0.78	26 (6%) 24 21	42, 65, 82, 112	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	343	PRO	4.1
1	A	360	LEU	4.1
1	A	350	ILE	3.7
1	A	337	PHE	3.2
3	E	109	ILE	3.0

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.