



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7OR6 / pdb_00007or6
Title : The crystal structure of the domain-swapped dimer of onconase
Authors : Merlino, A.; Loreto, D.
Deposited on : 2021-06-04
Resolution : 2.12 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

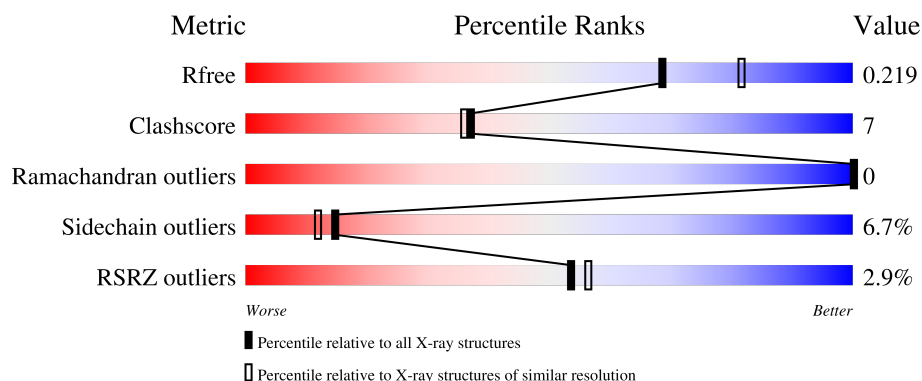
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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	AAA	105	4% 82% 17% .
1	BBB	105	2% 77% 19% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1785 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 Protein P-30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	104	Total	C	N	O	S	0	4	0
			859	539	150	161	9			
1	BBB	104	Total	C	N	O	S	0	1	0
			834	526	143	156	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	1	PCA	-	insertion	UNP P22069
BBB	1	PCA	-	insertion	UNP P22069

- Molecule 2 is water.

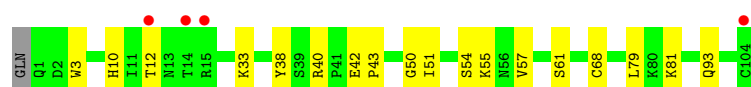
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	53	Total	O	0	0
			53	53		
2	BBB	39	Total	O	0	0
			39	39		

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.

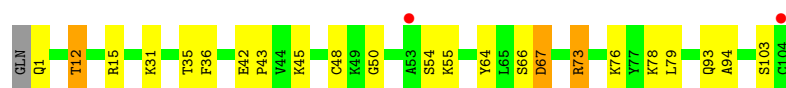
- Molecule 1: Protein P-30

Chain AAA: 



- Molecule 1: Protein P-30

Chain BBB: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	28.29Å 60.05Å 101.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.72 – 2.12 51.72 – 2.12	Depositor EDS
% Data completeness (in resolution range)	92.9 (51.72-2.12) 92.9 (51.72-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.12Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.185 , 0.243 (Not available) , 0.219	Depositor DCC
R_{free} test set	499 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	22.9	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1785	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.09% 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: PCA

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	AAA	0.95	0/870	1.31	0/1174
1	BBB	0.96	0/844	1.34	2/1140 (0.2%)
All	All	0.95	0/1714	1.33	2/2314 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	45	LYS	CA-C-N	5.24	128.03	120.38
1	BBB	45	LYS	C-N-CA	5.24	128.03	120.38

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	AAA	859	0	842	15	0
1	BBB	834	0	825	16	0
2	AAA	53	0	0	0	0
2	BBB	39	0	0	0	0
All	All	1785	0	1667	24	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 7.

All (24) 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:AAA:50:GLY:H	1:AAA:93:GLN:HE21	1.12	0.98
1:BBB:50:GLY:H	1:BBB:93:GLN:HE21	1.10	0.94
1:AAA:38:TYR:HA	1:BBB:12:THR:HG22	1.68	0.74
1:AAA:50:GLY:H	1:AAA:93:GLN:NE2	1.87	0.72
1:BBB:50:GLY:N	1:BBB:93:GLN:HE21	1.90	0.67
1:AAA:42:GLU:HG2	1:AAA:43:PRO:HD3	1.78	0.66
1:BBB:42:GLU:HG2	1:BBB:43:PRO:HD3	1.85	0.58
1:BBB:15:ARG:HB3	1:BBB:64:TYR:CE1	2.40	0.57
1:AAA:12:THR:HG23	1:BBB:36:PHE:HB3	1.87	0.56
1:AAA:10[B]:HIS:HD2	1:BBB:35:THR:O	1.93	0.52
1:BBB:48:CYS:O	1:BBB:93:GLN:HA	2.10	0.51
1:BBB:66:SER:HB3	1:BBB:79:LEU:HD11	1.93	0.51
1:AAA:79:LEU:HD21	1:AAA:81[B]:LYS:HE2	1.93	0.50
1:BBB:50:GLY:H	1:BBB:93:GLN:NE2	1.93	0.49
1:AAA:38:TYR:HD1	1:BBB:12:THR:CG2	2.26	0.49
1:BBB:35:THR:OG1	1:BBB:67:ASP:OD1	2.23	0.45
1:AAA:42:GLU:H	1:AAA:42:GLU:CD	2.24	0.45
1:AAA:33:LYS:HA	1:AAA:68:CYS:O	2.17	0.45
1:AAA:51:ILE:CD1	1:AAA:57:VAL:HG21	2.47	0.44
1:AAA:12:THR:CG2	1:BBB:36:PHE:HB3	2.48	0.43
1:AAA:3:TRP:HB2	1:BBB:94:ALA:HB1	2.02	0.42
1:BBB:73:ARG:HE	1:BBB:76:LYS:HG3	1.83	0.42
1:AAA:40:ARG:NH2	1:AAA:42:GLU:OE2	2.53	0.40
1:AAA:38:TYR:HD1	1:BBB:12:THR:HG23	1.87	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	AAA	4/105 (4%)	4 (100%)	0	0	100	100
1	BBB	73/105 (70%)	72 (99%)	1 (1%)	0	100	100
All	All	77/210 (37%)	76 (99%)	1 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	70/98 (71%)	66 (94%)	4 (6%)	18	16
1	BBB	98/98 (100%)	90 (92%)	8 (8%)	10	8
All	All	168/196 (86%)	156 (93%)	12 (7%)	15	10

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

Mol	Chain	Res	Type
1	AAA	54	SER
1	AAA	55	LYS
1	AAA	61[A]	SER
1	AAA	61[B]	SER
1	BBB	12	THR
1	BBB	31	LYS
1	BBB	54	SER
1	BBB	55	LYS
1	BBB	67	ASP
1	BBB	73	ARG
1	BBB	78	LYS
1	BBB	103	SER

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	PCA	AAA	1	1	7,8,9	0.45	0	9,10,12	0.75	0
1	PCA	BBB	1	1	7,8,9	0.53	0	9,10,12	1.15	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PCA	AAA	1	1	-	0/0/11/13	0/1/1/1
1	PCA	BBB	1	1	-	0/0/11/13	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	1	PCA	CB-CA-C	-2.67	109.00	112.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	AAA	103/105 (98%)	0.19	4 (3%) 43 46	9, 21, 38, 78	4 (3%)
1	BBB	103/105 (98%)	0.33	2 (1%) 66 69	10, 25, 41, 53	1 (0%)
All	All	206/210 (98%)	0.26	6 (2%) 53 56	9, 23, 42, 78	5 (2%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	104	CYS	5.7
1	AAA	104	CYS	3.3
1	AAA	14	THR	3.2
1	AAA	12	THR	2.7
1	BBB	53	ALA	2.3
1	AAA	15	ARG	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	PCA	AAA	1	8/9	0.91	0.07	27,33,34,36	0
1	PCA	BBB	1	8/9	0.92	0.07	24,25,27,31	0

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.