



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 13, 2021 – 06:11 pm GMT

PDB ID : 7NYK
Title : SH3 domain of JNK-interacting Protein 1 (JIP1)
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Deposited on : 2021-03-22
Resolution : 1.45 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.24

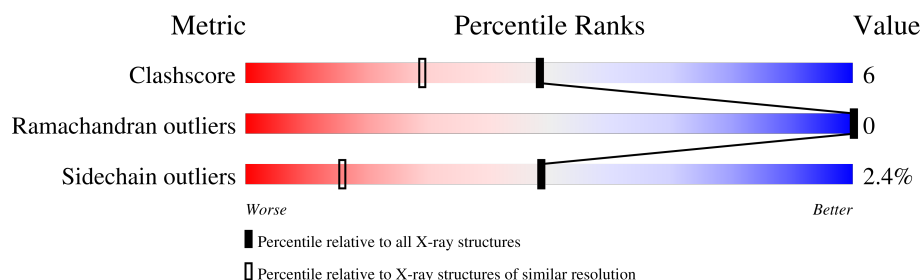
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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))
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)

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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	AAA	63	83% 13% . .
1	BBB	63	89% 10% .
1	CCC	63	75% 21% . .
1	DDD	63	86% 8% . 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2457 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 SH3 domain of JNK-interacting Protein 1 (JIP1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	62	Total	C	N	O	S	0	2	0
			535	344	87	102	2			
1	BBB	62	Total	C	N	O	S	0	0	0
			522	334	87	99	2			
1	CCC	61	Total	C	N	O	S	0	1	0
			523	337	86	98	2			
1	DDD	60	Total	C	N	O	S	0	1	0
			514	329	84	100	1			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	487	GLY	-	expression tag	UNP Q9UQF2
AAA	488	HIS	-	expression tag	UNP Q9UQF2
AAA	489	MET	-	expression tag	UNP Q9UQF2
BBB	487	GLY	-	expression tag	UNP Q9UQF2
BBB	488	HIS	-	expression tag	UNP Q9UQF2
BBB	489	MET	-	expression tag	UNP Q9UQF2
CCC	487	GLY	-	expression tag	UNP Q9UQF2
CCC	488	HIS	-	expression tag	UNP Q9UQF2
CCC	489	MET	-	expression tag	UNP Q9UQF2
DDD	487	GLY	-	expression tag	UNP Q9UQF2
DDD	488	HIS	-	expression tag	UNP Q9UQF2
DDD	489	MET	-	expression tag	UNP Q9UQF2

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	87	Total	O	0	0
			87	87		
2	BBB	106	Total	O	0	0
			106	106		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	CCC	85	Total	O	0	0
			85	85		
2	DDD	85	Total	O	0	0
			85	85		

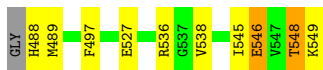
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS failed to run properly.

- Molecule 1: SH3 domain of JNK-interacting Protein 1 (JIP1)

Chain AAA:  83% 13% . .




- Molecule 1: SH3 domain of JNK-interacting Protein 1 (JIP1)

Chain BBB:  89% 10% .



- Molecule 1: SH3 domain of JNK-interacting Protein 1 (JIP1)

Chain CCC:  75% 21% . .



- Molecule 1: SH3 domain of JNK-interacting Protein 1 (JIP1)

Chain DDD:  86% 8% . 5%



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.40Å 82.13Å 46.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.88 – 1.45	Depositor
% Data completeness (in resolution range)	81.1 (53.88-1.45)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 1.45Å)	Xtriage
Refinement program	REFMAC 7.1.007	Depositor
R, R_{free}	0.157 , 0.215	Depositor
Wilson B-factor (Å ²)	16.7	Xtriage
Anisotropy	0.639	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2457	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.58% 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	AAA	0.88	2/556 (0.4%)	0.99	0/755
1	BBB	0.76	0/537	0.96	1/730 (0.1%)
1	CCC	0.77	1/541 (0.2%)	0.96	0/736
1	DDD	0.79	1/528 (0.2%)	0.98	3/719 (0.4%)
All	All	0.80	4/2162 (0.2%)	0.97	4/2940 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	546	GLU	CD-OE1	9.35	1.35	1.25
1	DDD	518	GLU	CD-OE2	-5.42	1.19	1.25
1	AAA	546	GLU	CD-OE2	5.09	1.31	1.25
1	CCC	546	GLU	CD-OE1	5.05	1.31	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DDD	498	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	DDD	494	ARG	NE-CZ-NH2	-6.09	117.25	120.30
1	DDD	498	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	BBB	494	ARG	NE-CZ-NH2	-5.38	117.61	120.30

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	535	0	496	7	1
1	BBB	522	0	480	5	1
1	CCC	523	0	488	11	1
1	DDD	514	0	468	3	0
2	AAA	87	0	0	3	1
2	BBB	106	0	0	4	0
2	CCC	85	0	0	5	1
2	DDD	85	0	0	2	1
All	All	2457	0	1932	24	3

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 6.

The worst 5 of 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:CCC:527:GLU:HG3	2:CCC:619:HOH:O	1.38	1.22
1:AAA:548:THR:HA	2:AAA:608:HOH:O	1.64	0.96
1:BBB:518:GLU:HG2	2:BBB:605:HOH:O	1.76	0.85
1:AAA:548:THR:HG22	2:DDD:678:HOH:O	1.79	0.81
1:CCC:527:GLU:CG	2:CCC:619:HOH:O	2.11	0.78

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CCC:489:MET:O	2:CCC:613:HOH:O[2_455]	1.99	0.21
1:AAA:489:MET:O	2:AAA:632:HOH:O[2_455]	2.00	0.20
1:BBB:518:GLU:O	2:DDD:640:HOH:O[3_444]	2.19	0.01

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	62/63 (98%)	61 (98%)	1 (2%)	0	100	100
1	BBB	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
1	CCC	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
1	DDD	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
All	All	241/252 (96%)	237 (98%)	4 (2%)	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	55/54 (102%)	52 (94%)	3 (6%)	21	2
1	BBB	53/54 (98%)	53 (100%)	0	100	100
1	CCC	54/54 (100%)	53 (98%)	1 (2%)	57	23
1	DDD	52/54 (96%)	51 (98%)	1 (2%)	57	23
All	All	214/216 (99%)	209 (98%)	5 (2%)	49	17

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	488	HIS
1	AAA	536	ARG
1	AAA	548	THR
1	CCC	536	ARG
1	DDD	522	GLU

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 [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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](#)

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.