



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 27, 2021 – 05:00 pm BST

PDB ID : 7OCX
Title : Crystal Structure of the PID-3 TOFU-6 RRM domain complex
Authors : Basquin, J.; Ketting, R.F.; Falk, S.
Deposited on : 2021-04-28
Resolution : 1.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
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) : 2.23.2

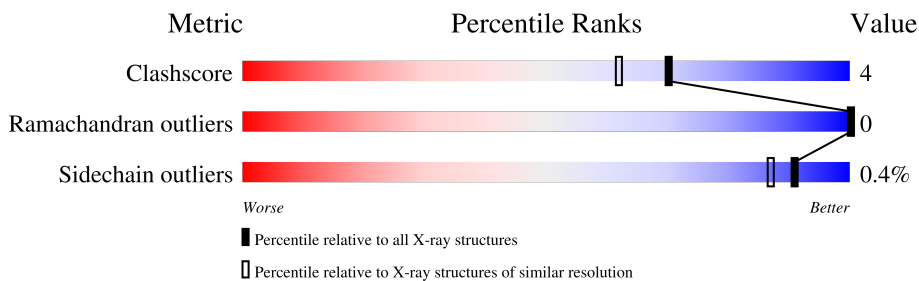
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	84	
1	B	84	
2	C	103	
2	D	103	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 5212 atoms, of which 2494 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 pid-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	77	1184	373	595	103	111	2	0	0	0
1	B	81	1229	389	615	107	115	3	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	191	GLY	-	expression tag	UNP O76616
A	192	PRO	-	expression tag	UNP O76616
A	193	ASP	-	expression tag	UNP O76616
A	194	SER	-	expression tag	UNP O76616
A	195	MET	-	expression tag	UNP O76616
B	191	GLY	-	expression tag	UNP O76616
B	192	PRO	-	expression tag	UNP O76616
B	193	ASP	-	expression tag	UNP O76616
B	194	SER	-	expression tag	UNP O76616
B	195	MET	-	expression tag	UNP O76616

- Molecule 2 is a protein called Embryonic developmental protein tofu-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	C	93	1392	459	670	128	132	3	0	2	0
2	D	84	1268	414	614	117	120	3	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP Q09293
C	-2	PRO	-	expression tag	UNP Q09293

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	ASP	-	expression tag	UNP Q09293
C	0	SER	-	expression tag	UNP Q09293
D	-3	GLY	-	expression tag	UNP Q09293
D	-2	PRO	-	expression tag	UNP Q09293
D	-1	ASP	-	expression tag	UNP Q09293
D	0	SER	-	expression tag	UNP Q09293

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	52	Total O 52 52	0	0
3	B	43	Total O 43 43	0	0
3	C	19	Total O 19 19	0	0
3	D	25	Total O 25 25	0	0

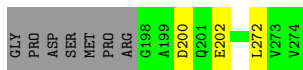
3 Residue-property plots [i](#)

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 was not executed.

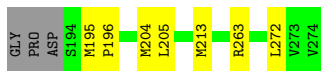
- Molecule 1: Protein pid-3

Chain A: 




- Molecule 1: Protein pid-3

Chain B: 



- Molecule 2: Embryonic developmental protein tofu-6

Chain C: 



- Molecule 2: Embryonic developmental protein tofu-6

Chain D: 



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	43.98Å 68.00Å 130.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.68 – 1.70	Depositor
% Data completeness (in resolution range)	98.0 (41.68-1.70)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.194 , 0.232	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5212	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

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	0.44	0/597	0.72	0/806
1	B	0.44	0/623	0.74	0/842
2	C	0.50	1/745 (0.1%)	0.65	0/1010
2	D	0.51	1/668 (0.1%)	0.67	0/904
All	All	0.47	2/2633 (0.1%)	0.69	0/3562

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	42	CYS	CB-SG	-8.14	1.68	1.82
2	C	42	CYS	CB-SG	-7.25	1.70	1.82

There are no bond angle outliers.

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	589	595	595	2	0
1	B	614	615	615	6	0
2	C	722	670	674	7	0
2	D	654	614	612	5	0
3	A	52	0	0	0	0
3	B	43	0	0	0	0
3	C	19	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	25	0	0	0	0
All	All	2718	2494	2496	18	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 (18) 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)
2:C:59[A]:ASN:ND2	3:C:101:HOH:O	2.32	0.62
2:D:79:ILE:HD13	2:D:84:THR:HG23	1.83	0.61
2:C:57:PHE:CE2	2:C:59[B]:ASN:ND2	2.74	0.55
1:B:195:MET:HG3	1:B:196:PRO:HD2	1.90	0.54
1:A:200:ASP:OD1	1:A:202:GLU:HG2	2.10	0.51
1:B:204:MET:HE3	1:B:272:LEU:HD22	1.96	0.48
2:D:79:ILE:CD1	2:D:84:THR:HG23	2.45	0.47
1:B:205:LEU:C	1:B:205:LEU:HD12	2.36	0.46
1:B:204:MET:CE	1:B:272:LEU:CD2	2.94	0.45
1:B:263:ARG:NH1	2:C:67:ASP:OD2	2.50	0.44
2:C:47:GLN:HA	2:C:54:GLN:HA	2.00	0.43
2:D:77:ASN:OD1	2:D:86:LYS:HD3	2.19	0.42
2:C:57:PHE:CZ	2:C:59[B]:ASN:OD1	2.72	0.42
1:A:272:LEU:HD12	1:A:272:LEU:HA	1.92	0.41
2:D:18:ARG:HB2	2:D:86:LYS:HB2	2.02	0.41
2:C:54:GLN:C	2:C:55:LEU:HD12	2.41	0.41
1:B:263:ARG:HH12	2:C:67:ASP:CG	2.24	0.41
2:D:47:GLN:HB3	2:D:54:GLN:HG2	2.02	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	75/84 (89%)	75 (100%)	0	0	100	100
1	B	79/84 (94%)	79 (100%)	0	0	100	100
2	C	93/103 (90%)	89 (96%)	4 (4%)	0	100	100
2	D	82/103 (80%)	80 (98%)	2 (2%)	0	100	100
All	All	329/374 (88%)	323 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	63/70 (90%)	63 (100%)	0	100	100
1	B	65/70 (93%)	64 (98%)	1 (2%)	65	51
2	C	74/87 (85%)	74 (100%)	0	100	100
2	D	68/87 (78%)	68 (100%)	0	100	100
All	All	270/314 (86%)	269 (100%)	1 (0%)	91	87

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	213	MET

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

Mol	Chain	Res	Type
2	D	59	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 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 was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.