

Full wwPDB X-ray Structure Validation Report (i)

Nov 10, 2022 - 03:07 pm GMT

PDB ID	:	7YZD
Title	:	Crystal structure of the zebrafish FoxH1 bound to the TGTTTACT site (fkh
		motif GTAAACA)
Authors	:	Pluta, R.; Macias, M.J.
Deposited on	:	2022-02-19
Resolution	:	2.13 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 (i) 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 (1)) were used in the production of this report:

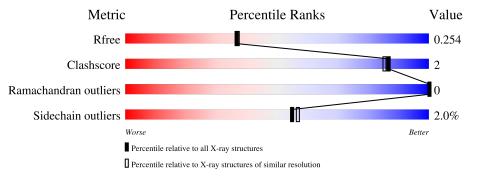
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as 541 be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\hbox{-}RAY\,DIFFRACTION$

The reported resolution of this entry is 2.13 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)

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 <=5%

Mol	Chain	Length	Quality of chain		
1	А	125	79%	10%	10%
2	В	16	100%		
3	С	16	100%		



7YZD

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 1618 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 Forkhead box protein H1.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace			
1	А	112	Total 925	C 606	N 156	O 160	${ m S} { m 3}$	0	0	0

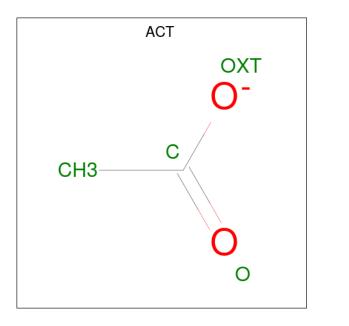
• Molecule 2 is a DNA chain called DNA (5'-D(P*AP*GP*AP*TP*TP*GP*TP*TP*TP*AP *CP*TP*GP*AP*GP*A)-3').

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace			
2	В	16	Total 329	C 159	N 60	O 95	Р 15	0	0	0

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace			
3	С	16	Total 321	C 156	N 57	0 93	Р 15	0	0	0

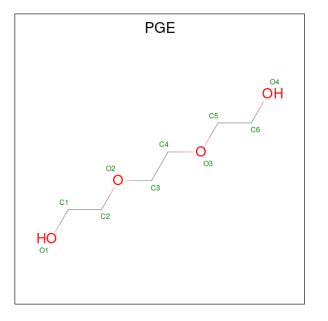
• Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
4	А	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	O 2	0	0

• Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
5	А	1	Total 10	С 6	0 4	0	0

• Molecule 6 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	23	TotalO2323	0	0
6	В	1	Total O 1 1	0	0
6	С	5	$\begin{array}{cc} \text{Total} & \text{O} \\ 5 & 5 \end{array}$	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.

• Molecule 1: Forkhead box protein H1

Chain A:	79%	10%	10%	
GLY GLY LYS LYS LYS LYS AS A100 A100 A100 A100 A100 A100 A100	1179 1179 1184 1184 1184 1184 1184 1184 1186 1186	F 208 GLY		
• Molecule 2: DNA (5'-D(1)-3')	P*AP*GP*AP*TP*TP	*GP*TP*TP*TP	*AP*CP*TP*GP*AP*	GP*A
Chain B:	100%			
There are no outlier residu	es recorded for this chai	in.		
• Molecule 3: DNA (5'-D(' 3')	*TP*CP*TP*CP*AP*(GP*TP*AP*AP*A	AP*CP*AP*AP*TP*C	P*T)-
Chain C:	100%			
There are no outlier residu	es recorded for this chai	in.		



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	36.24Å 96.75 Å 150.81 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.06 - 2.13	Depositor
Resolution (A)	46.06 - 2.13	EDS
% Data completeness	62.6 (46.06 - 2.13)	Depositor
(in resolution range)	58.6(46.06-2.13)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.09 (at 2.14 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
D D.	0.211 , 0.253	Depositor
R, R_{free}	0.212 , 0.254	DCC
R_{free} test set	479 reflections (5.01%)	wwPDB-VP
Wilson B-factor $(Å^2)$	39.7	Xtriage
Anisotropy	0.179	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	1618	wwPDB-VP
Average B, all atoms $(Å^2)$	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.06% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: ACT, PGE

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.32	0/951	0.51	0/1285	
2	В	0.67	0/369	1.03	0/569	
3	С	0.65	0/359	0.95	0/551	
All	All	0.50	0/1679	0.78	0/2405	

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 (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	А	925	0	938	6	0
2	В	329	0	184	0	0
3	С	321	0	183	0	0
4	А	4	0	3	0	0
5	А	10	0	14	0	0
6	А	23	0	0	1	0
6	В	1	0	0	0	0
6	С	5	0	0	0	0
All	All	1618	0	1322	6	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 2.

All (6) 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:A:104:ALA:HB1	1:A:203:LEU:HD12	1.71	0.72
1:A:103:LEU:HD13	1:A:183:LEU:HD12	1.89	0.54
1:A:100:TYR:OH	1:A:200:ALA:O	2.21	0.52
1:A:164:LYS:N	1:A:165:PRO:HD3	2.33	0.43
1:A:126:GLU:HG2	6:A:410:HOH:O	2.18	0.43
1:A:179:ILE:HG21	1:A:184:LEU:HD21	2.02	0.41

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	А	108/125~(86%)	105~(97%)	3~(3%)	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	А	102/112~(91%)	100 (98%)	2(2%)	55 57	



All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	153	ASP
1	А	201	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	112	ASN
1	А	201	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands 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	В	ond leng	gths	В	ond ang	gles
	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
5	PGE	А	302	-	$9,\!9,\!9$	0.30	0	8,8,8	0.30	0
4	ACT	А	301	-	3,3,3	1.30	0	$3,\!3,\!3$	1.50	0

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
5	PGE	А	302	-	-	3/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	А	302	PGE	O3-C5-C6-O4
5	А	302	PGE	O2-C3-C4-O3
5	А	302	PGE	C3-C4-O3-C5

There are no ring outliers.

No monomer is involved in short contacts.

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

