



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 05:36 am BST

PDB ID : 1TQE
Title : Mechanism of recruitment of class II histone deacetylases by myocyte enhancer factor-2
Authors : Chen, L.; Han, A.; He, J.; Wu, Y.; Liu, J.O.
Deposited on : 2004-06-17
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 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	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

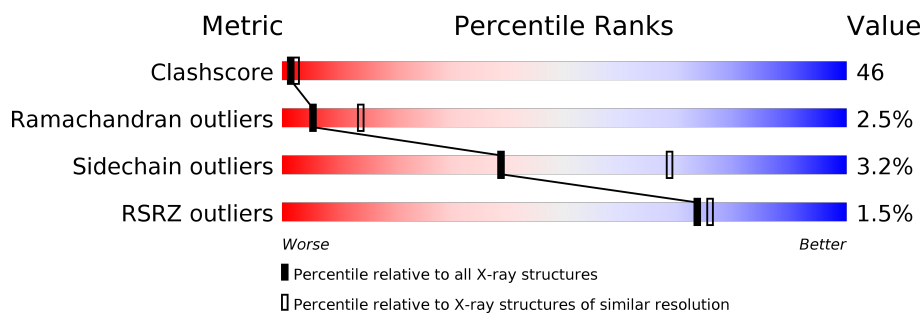
1 Overall quality at a glance

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))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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 on 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	C	17	<div> <div></div> <div>94%</div> <div>6%</div> </div>
1	E	17	<div> <div></div> <div>94%</div> <div>6%</div> </div>
2	D	17	<div> <div>18%</div> <div>82%</div> </div>
2	F	17	<div> <div>18%</div> <div>82%</div> </div>
3	P	93	<div> <div>%</div> <div>35%</div> <div>59%</div> <div>..</div> </div>
3	Q	93	<div> <div>%</div> <div>40%</div> <div>55%</div> <div>..</div> </div>
3	R	93	<div> <div>34%</div> <div>59%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
3	S	93	<div><div></div><div>2%34%57%5%•</div></div>
4	X	26	<div><div></div><div>8%19%65%•12%</div></div>
4	Y	26	<div><div></div><div>4%35%42%12%12%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4730 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 DNA chain called MEF2 binding site of nur77 promoter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	17	Total	C	N	O	P	0	0	0
			347	168	66	97	16			
1	E	17	Total	C	N	O	P	0	0	0
			347	168	66	97	16			

- Molecule 2 is a DNA chain called MEF2 binding site of nur77 promoter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	17	Total	C	N	O	P	0	0	0
			344	168	57	103	16			
2	F	17	Total	C	N	O	P	0	0	0
			344	168	57	103	16			

- Molecule 3 is a protein called Myocyte-specific enhancer factor 2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	90	Total	C	N	O	S	0	0	0
			751	472	138	137	4			
3	Q	90	Total	C	N	O	S	0	0	0
			751	472	138	137	4			
3	R	90	Total	C	N	O	S	0	0	0
			751	472	138	137	4			
3	S	90	Total	C	N	O	S	0	0	0
			751	472	138	137	4			

- Molecule 4 is a protein called Histone deacetylase 9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	X	23	Total	C	N	O	0	0	0
			172	108	29	35			
4	Y	23	Total	C	N	O	0	0	0
			172	108	29	35			

There are 12 discrepancies between the modelled and reference sequences:

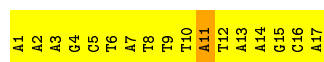
Chain	Residue	Modelled	Actual	Comment	Reference
X	103	SER	-	CLONING ARTIFACT	UNP Q99N13
X	104	PRO	-	CLONING ARTIFACT	UNP Q99N13
X	105	LYS	-	CLONING ARTIFACT	UNP Q99N13
X	106	GLY	-	CLONING ARTIFACT	UNP Q99N13
X	107	THR	-	CLONING ARTIFACT	UNP Q99N13
X	108	GLY	VAL	CONFLICT	UNP Q99N13
Y	103	SER	-	CLONING ARTIFACT	UNP Q99N13
Y	104	PRO	-	CLONING ARTIFACT	UNP Q99N13
Y	105	LYS	-	CLONING ARTIFACT	UNP Q99N13
Y	106	GLY	-	CLONING ARTIFACT	UNP Q99N13
Y	107	THR	-	CLONING ARTIFACT	UNP Q99N13
Y	108	GLY	VAL	CONFLICT	UNP Q99N13

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

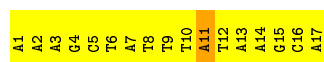
- Molecule 1: MEF2 binding site of nur77 promoter

Chain C: 



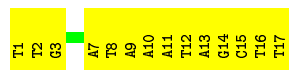
- Molecule 1: MEF2 binding site of nur77 promoter

Chain E: 



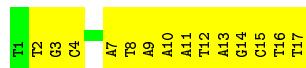
- Molecule 2: MEF2 binding site of nur77 promoter

Chain D: 



- Molecule 2: MEF2 binding site of nur77 promoter

Chain F: 

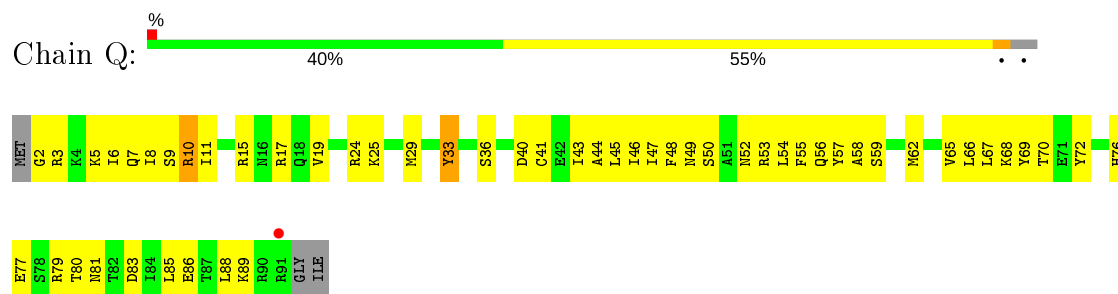


- Molecule 3: Myocyte-specific enhancer factor 2B

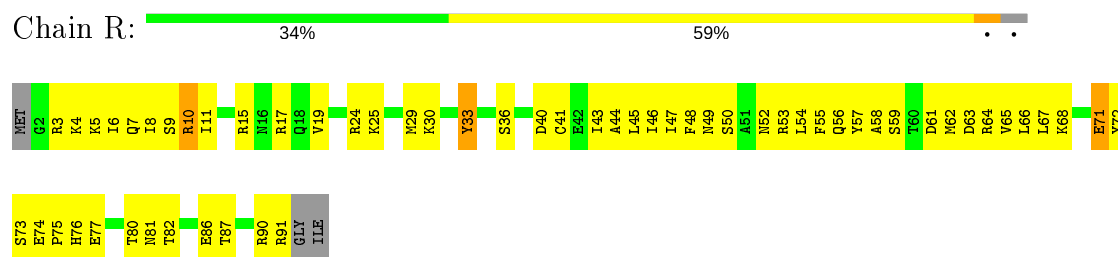
Chain P: 



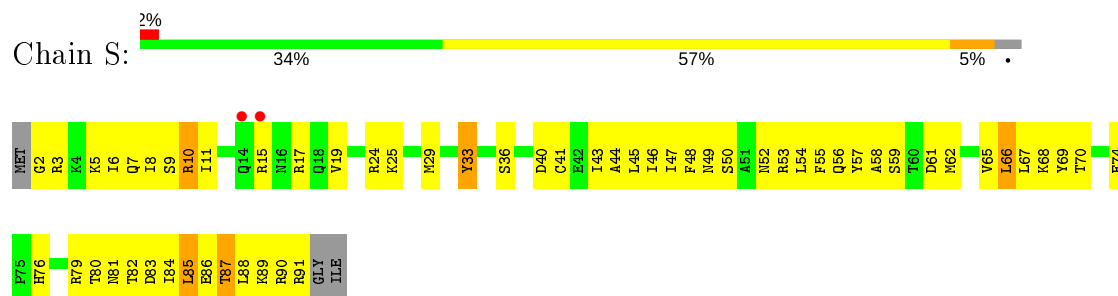
- Molecule 3: Myocyte-specific enhancer factor 2B



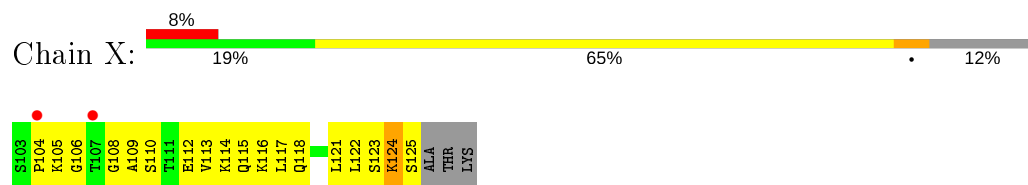
- Molecule 3: Myocyte-specific enhancer factor 2B



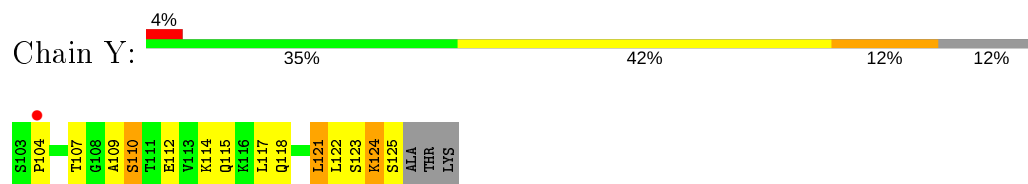
- Molecule 3: Myocyte-specific enhancer factor 2B



- Molecule 4: Histone deacetylase 9



- Molecule 4: Histone deacetylase 9



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	44.80Å 66.93Å 66.97Å 76.67° 71.83° 71.81°	Depositor
Resolution (Å)	30.00 – 2.70 29.22 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.3 (30.00-2.70) 55.2 (29.22-2.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.263 , 0.289 0.275 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.699	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for h,h-k,h-l 0.469 for -h,-l,-k 0.027 for -h,-h+l,-h+k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4730	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.96% 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	C	0.52	0/390	0.81	0/600
1	E	0.54	0/390	0.79	0/600
2	D	0.54	0/384	0.85	0/591
2	F	0.58	0/384	0.87	0/591
3	P	0.45	0/760	0.66	0/1016
3	Q	0.49	0/760	0.64	0/1016
3	R	0.48	0/760	0.66	0/1016
3	S	0.50	0/760	0.68	0/1016
4	X	0.46	0/173	0.70	0/229
4	Y	0.45	0/173	0.70	0/229
All	All	0.50	0/4934	0.73	0/6904

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	E	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	11	DA	Sidechain
1	E	11	DA	Sidechain

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	C	347	0	194	43	0
1	E	347	0	194	49	0
2	D	344	0	197	29	0
2	F	344	0	197	36	0
3	P	751	0	778	72	0
3	Q	751	0	778	66	0
3	R	751	0	778	82	0
3	S	751	0	778	79	0
4	X	172	0	182	24	0
4	Y	172	0	182	18	0
All	All	4730	0	4258	414	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 46.

The worst 5 of 414 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:C:13:DA:H2''	1:C:14:DA:H5''	1.24	1.19
1:E:13:DA:H2''	1:E:14:DA:H5''	1.23	1.16
2:F:2:DT:H1'	2:F:3:DG:H5''	1.33	1.09
3:R:62:MET:SD	3:R:66:LEU:HD21	2.05	0.95
1:C:13:DA:C2'	1:C:14:DA:H5''	1.98	0.93

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	P	88/93 (95%)	72 (82%)	15 (17%)	1 (1%)	14	34
3	Q	88/93 (95%)	70 (80%)	17 (19%)	1 (1%)	14	34
3	R	88/93 (95%)	72 (82%)	13 (15%)	3 (3%)	3	8
3	S	88/93 (95%)	72 (82%)	13 (15%)	3 (3%)	3	8
4	X	21/26 (81%)	17 (81%)	3 (14%)	1 (5%)	2	4
4	Y	21/26 (81%)	14 (67%)	6 (29%)	1 (5%)	2	4
All	All	394/424 (93%)	317 (80%)	67 (17%)	10 (2%)	5	14

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	X	124	LYS
3	R	72	TYR
4	Y	124	LYS
3	S	68	LYS
3	Q	10	ARG

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	
3	P	84/86 (98%)	81 (96%)	3 (4%)	35	64
3	Q	84/86 (98%)	83 (99%)	1 (1%)	71	88
3	R	84/86 (98%)	83 (99%)	1 (1%)	71	88
3	S	84/86 (98%)	81 (96%)	3 (4%)	35	64
4	X	20/22 (91%)	19 (95%)	1 (5%)	24	51
4	Y	20/22 (91%)	17 (85%)	3 (15%)	3	7
All	All	376/388 (97%)	364 (97%)	12 (3%)	39	68

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	R	33	TYR
3	S	33	TYR
4	Y	107	THR
4	X	121	LEU
3	S	85	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	R	7	GLN
3	S	56	GLN
3	R	76	HIS
3	Q	7	GLN
3	R	56	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 carbohydrates 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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	C	17/17 (100%)	-0.52	0	100	100	55, 83, 175, 190	0
1	E	17/17 (100%)	-0.49	0	100	100	56, 83, 187, 193	0
2	D	17/17 (100%)	-0.49	0	100	100	55, 87, 174, 191	0
2	F	17/17 (100%)	-0.53	0	100	100	54, 87, 175, 178	0
3	P	90/93 (96%)	-0.20	1 (1%)	80	82	47, 78, 105, 137	0
3	Q	90/93 (96%)	-0.14	1 (1%)	80	82	44, 76, 116, 158	0
3	R	90/93 (96%)	-0.09	0	100	100	46, 80, 108, 137	0
3	S	90/93 (96%)	-0.10	2 (2%)	62	63	43, 75, 103, 141	0
4	X	23/26 (88%)	0.24	2 (8%)	10	8	59, 103, 119, 158	0
4	Y	23/26 (88%)	0.30	1 (4%)	35	33	59, 102, 130, 153	0
All	All	474/492 (96%)	-0.15	7 (1%)	73	76	43, 81, 140, 193	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	P	91	ARG	4.4
4	X	104	PRO	4.1
4	X	107	THR	3.2
3	S	15	ARG	2.6
3	S	14	GLN	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.