



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:15 AM UTC

PDB ID : 5YHU / pdb_00005yhu
Title : Crystal structure of the DNA-binding domain of human myelin-gene regulatory factor
Authors : Chen, B.; Zhu, Y.; Ye, S.; Zhang, R.
Deposited on : 2017-09-30
Resolution : 1.85 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
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

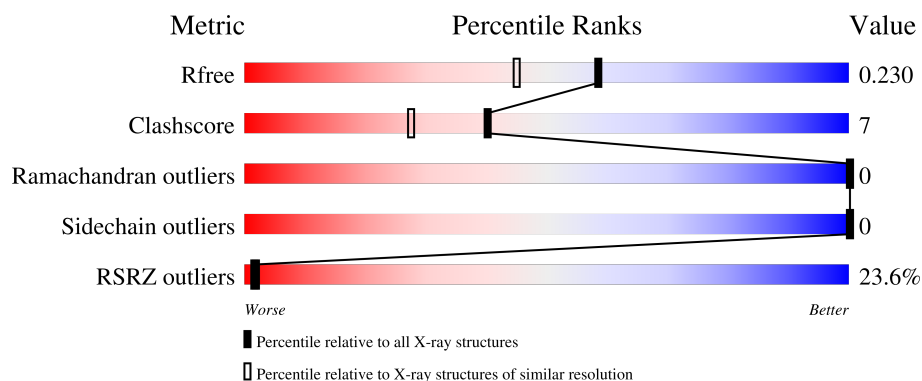
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	A	255	
1	B	255	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3304 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 Myelin regulatory factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	191	Total	C	N	O	S	0	0	0
			1548	986	272	284	6			
1	B	182	Total	C	N	O	S	0	0	0
			1476	947	255	268	6			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	315	GLY	-	expression tag	UNP Q9Y2G1
A	316	PRO	-	expression tag	UNP Q9Y2G1
A	317	MET	-	expression tag	UNP Q9Y2G1
A	318	ALA	-	expression tag	UNP Q9Y2G1
A	319	ASP	-	expression tag	UNP Q9Y2G1
A	320	ILE	-	expression tag	UNP Q9Y2G1
A	321	GLY	-	expression tag	UNP Q9Y2G1
A	322	SER	-	expression tag	UNP Q9Y2G1
B	315	GLY	-	expression tag	UNP Q9Y2G1
B	316	PRO	-	expression tag	UNP Q9Y2G1
B	317	MET	-	expression tag	UNP Q9Y2G1
B	318	ALA	-	expression tag	UNP Q9Y2G1
B	319	ASP	-	expression tag	UNP Q9Y2G1
B	320	ILE	-	expression tag	UNP Q9Y2G1
B	321	GLY	-	expression tag	UNP Q9Y2G1
B	322	SER	-	expression tag	UNP Q9Y2G1

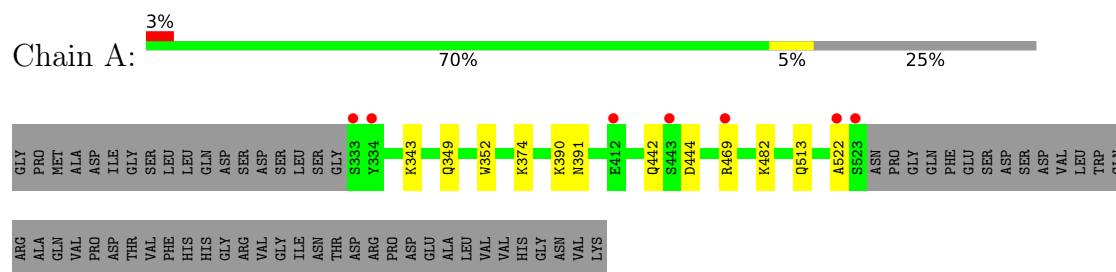
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	244	Total	O	0	0
			244	244		
2	B	36	Total	O	0	0
			36	36		

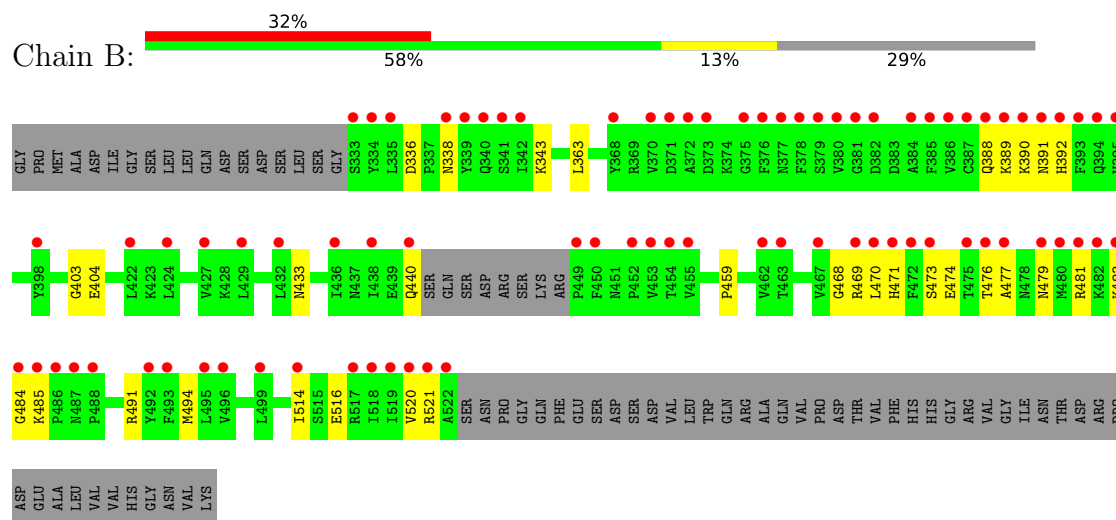
3 Residue-property plots

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: Myelin regulatory factor



• Molecule 1: Myelin regulatory factor



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	105.12Å 105.12Å 297.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.18 – 1.85 34.18 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.3 (34.18-1.85) 92.2 (34.18-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 1.86Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.204 , 0.228 0.206 , 0.230	Depositor DCC
R_{free} test set	2746 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3304	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.16% 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

5.1 Standard geometry

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	0.49	0/1586	0.61	0/2150
1	B	0.22	0/1513	0.46	0/2052
All	All	0.38	0/3099	0.54	0/4202

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

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	1548	0	1538	10	0
1	B	1476	0	1467	30	0
2	A	244	0	0	7	1
2	B	36	0	0	1	0
All	All	3304	0	3005	40	1

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 (40) 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:B:521:ARG:NH1	2:B:601:HOH:O	1.97	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:484:GLY:H	1:B:485:LYS:HZ3	1.31	0.76
1:B:476:THR:HG23	1:B:520:VAL:HG12	1.70	0.73
1:B:476:THR:OG1	1:B:479:ASN:OD1	2.09	0.70
1:B:404:GLU:HG3	1:B:459:PRO:HG3	1.75	0.69
1:B:388:GLN:HB2	1:B:390:LYS:HE3	1.75	0.68
1:A:444:ASP:OD2	2:A:603:HOH:O	2.13	0.67
1:B:392:HIS:HB3	1:B:471:HIS:NE2	2.11	0.66
1:B:484:GLY:H	1:B:485:LYS:NZ	1.95	0.64
1:A:442:GLN:HG2	2:A:602:HOH:O	1.97	0.64
1:A:469:ARG:NH1	2:A:601:HOH:O	2.01	0.61
1:B:388:GLN:HG2	1:B:390:LYS:HG2	1.84	0.60
1:B:390:LYS:HG3	1:B:391:ASN:OD1	2.03	0.59
1:B:477:ALA:HB3	1:B:491:ARG:HG3	1.85	0.56
1:A:390:LYS:HD2	1:A:391:ASN:OD1	2.07	0.55
1:B:390:LYS:HG2	1:B:391:ASN:H	1.71	0.54
1:A:522:ALA:O	2:A:605:HOH:O	2.19	0.52
1:B:440:GLN:HG3	1:B:470:LEU:HD13	1.92	0.52
1:B:363:LEU:HD22	1:B:403:GLY:HA3	1.92	0.51
1:B:473:SER:OG	1:B:474:GLU:HG3	2.11	0.50
1:A:513:GLN:OE1	2:A:606:HOH:O	2.20	0.49
1:B:433:ASN:OD1	1:B:433:ASN:N	2.45	0.48
1:A:374:LYS:NZ	2:A:611:HOH:O	2.38	0.46
1:B:494:MET:HB3	1:B:514:ILE:HD11	1.97	0.46
1:B:481:ARG:N	1:B:481:ARG:HD2	2.31	0.46
1:B:468:GLY:C	1:B:470:LEU:HD22	2.40	0.45
1:B:440:GLN:O	1:B:469:ARG:NE	2.48	0.44
1:A:343:LYS:NZ	2:A:604:HOH:O	2.18	0.44
1:B:483:LYS:HE2	1:B:483:LYS:N	2.33	0.43
1:B:390:LYS:CG	1:B:391:ASN:N	2.82	0.43
1:B:388:GLN:HG3	1:B:390:LYS:HD2	2.00	0.43
1:B:485:LYS:N	1:B:485:LYS:HD3	2.33	0.43
1:B:389:LYS:NZ	1:B:473:SER:O	2.46	0.42
1:B:336:ASP:OD1	1:B:338:ASN:ND2	2.49	0.42
1:B:343:LYS:HE3	1:B:516:GLU:OE2	2.20	0.42
1:B:392:HIS:HB3	1:B:471:HIS:CE1	2.54	0.41
1:B:388:GLN:CG	1:B:390:LYS:HG2	2.50	0.41
1:B:388:GLN:N	1:B:388:GLN:OE1	2.53	0.41
1:A:482:LYS:HA	1:A:482:LYS:HD3	1.94	0.41
1:A:349:GLN:HA	1:A:352:TRP:CE2	2.56	0.40

All (1) 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)
2:A:763:HOH:O	2:A:830:HOH:O[2_555]	2.17	0.03

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	189/255 (74%)	185 (98%)	4 (2%)	0	100	100
1	B	178/255 (70%)	172 (97%)	6 (3%)	0	100	100
All	All	367/510 (72%)	357 (97%)	10 (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	A	171/225 (76%)	171 (100%)	0	100	100
1	B	162/225 (72%)	162 (100%)	0	100	100
All	All	333/450 (74%)	333 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	394	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	440	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 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	A	191/255 (74%)	0.13	7 (3%) 45 49	21, 34, 60, 80	0
1	B	182/255 (71%)	2.06	81 (44%) 0 0	49, 70, 111, 136	0
All	All	373/510 (73%)	1.07	88 (23%) 2 1	21, 54, 102, 136	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	522	ALA	7.5
1	B	486	PRO	6.5
1	B	393	PHE	6.0
1	B	449	PRO	5.9
1	B	334	TYR	5.5
1	B	333	SER	5.2
1	B	487	ASN	4.9
1	B	450	PHE	4.6
1	B	475	THR	4.3
1	B	339	TYR	4.3
1	B	521	ARG	4.2
1	B	424	LEU	4.2
1	B	395	VAL	4.1
1	B	483	LYS	4.0
1	B	470	LEU	4.0
1	B	376	PHE	4.0
1	B	378	PHE	3.9
1	B	372	ALA	3.9
1	B	520	VAL	3.7
1	B	472	PHE	3.6
1	B	481	ARG	3.5
1	B	388	GLN	3.5
1	B	392	HIS	3.4
1	B	488	PRO	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	342	ILE	3.4
1	A	523	SER	3.3
1	B	377	ASN	3.3
1	B	467	VAL	3.3
1	A	522	ALA	3.2
1	B	371	ASP	3.2
1	B	386	VAL	3.2
1	B	480	MET	3.2
1	B	341	SER	3.2
1	B	379	SER	3.1
1	B	473	SER	3.1
1	B	519	ILE	3.1
1	B	335	LEU	3.1
1	B	375	GLY	3.0
1	B	384	ALA	3.0
1	B	440	GLN	3.0
1	A	443	SER	2.9
1	B	427	VAL	2.9
1	B	385	PHE	2.9
1	B	422	LEU	2.8
1	B	471	HIS	2.8
1	B	499	LEU	2.8
1	B	373	ASP	2.8
1	B	492	TYR	2.8
1	B	389	LYS	2.8
1	B	484	GLY	2.8
1	A	333	SER	2.7
1	A	334	TYR	2.7
1	B	387	CYS	2.6
1	B	477	ALA	2.6
1	B	429	LEU	2.6
1	B	482	LYS	2.6
1	B	338	ASN	2.6
1	B	436	ILE	2.5
1	B	438	ILE	2.5
1	B	493	PHE	2.5
1	B	370	VAL	2.5
1	B	453	VAL	2.5
1	B	391	ASN	2.4
1	B	368	TYR	2.4
1	B	381	GLY	2.4
1	B	495	LEU	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	340	GLN	2.3
1	B	390	LYS	2.3
1	B	469	ARG	2.3
1	B	485	LYS	2.3
1	B	432	LEU	2.3
1	B	514	ILE	2.2
1	B	476	THR	2.2
1	B	518	ILE	2.2
1	A	469	ARG	2.2
1	B	463	THR	2.2
1	B	398	TYR	2.2
1	B	380	VAL	2.2
1	B	496	VAL	2.2
1	B	479	ASN	2.1
1	B	394	GLN	2.1
1	B	382	ASP	2.1
1	A	412	GLU	2.1
1	B	462	VAL	2.1
1	B	517	ARG	2.1
1	B	454	THR	2.0
1	B	452	PRO	2.0
1	B	455	VAL	2.0

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

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

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.