



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 12, 2019 – 04:44 PM EST

PDB ID : 6J4R  
Title : Structural basis for the target DNA recognition and binding by the MYB domain of phosphate starvation response regulator 1  
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Deposited on : 2019-01-10  
Resolution : 2.80 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](mailto: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.

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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	:	2.4
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.4

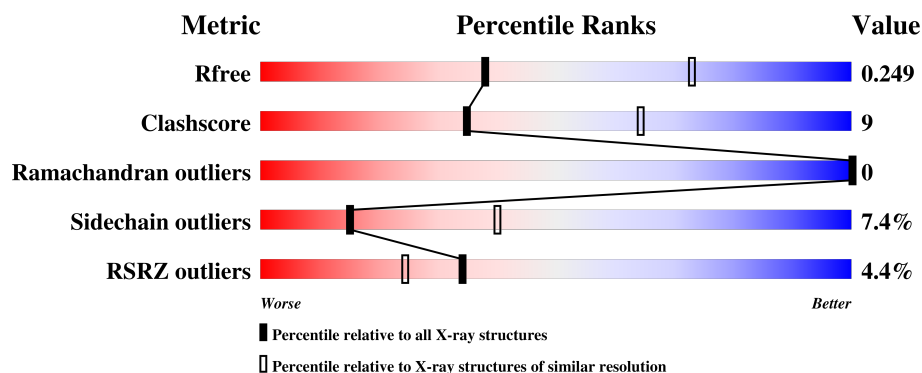
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (2.80-2.80)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	58	<div> <div>2%</div> <div>79% 19% .</div> </div>
1	B	58	<div> <div>7%</div> <div>76% 21% ..</div> </div>
1	C	58	<div> <div>7%</div> <div>83% 9% . 5%</div> </div>
1	D	58	<div> <div>5%</div> <div>84% 12% ..</div> </div>
2	F	11	<div> <div>27% 55% 18%</div> </div>

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Mol	Chain	Length	Quality of chain
3	E	11	 45% 36% 18%
4	X	11	 18% 45% 36%
5	Y	11	 18% 55% 27%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2708 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 Protein PHOSPHATE STARVATION RESPONSE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	58	Total	C	N	O	S	0	0	0
			464	297	85	80	2			
1	B	57	Total	C	N	O	S	0	0	0
			461	294	86	79	2			
1	C	55	Total	C	N	O	S	0	0	0
			438	279	81	76	2			
1	D	57	Total	C	N	O	S	0	0	0
			458	291	87	78	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	11	Total	C	N	O	P	0	0	0
			219	107	40	62	10			

- Molecule 3 is a DNA chain called DNA (5'-D(\*GP\*TP\*CP\*AP\*TP\*AP\*TP\*AP\*TP\*GP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	11	Total	C	N	O	P	0	0	0
			224	109	41	64	10			

- Molecule 4 is a DNA chain called DNA (5'-D(\*GP\*GP\*TP\*AP\*TP\*AP\*TP\*AP\*CP\*TP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	X	11	Total	C	N	O	P	0	0	0
			224	109	41	64	10			

- Molecule 5 is a DNA chain called DNA (5'-D(\*CP\*AP\*GP\*TP\*AP\*TP\*AP\*TP\*AP\*CP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	Y	11	Total 219	C 107	N 40	O 62	P 10	0	0	0

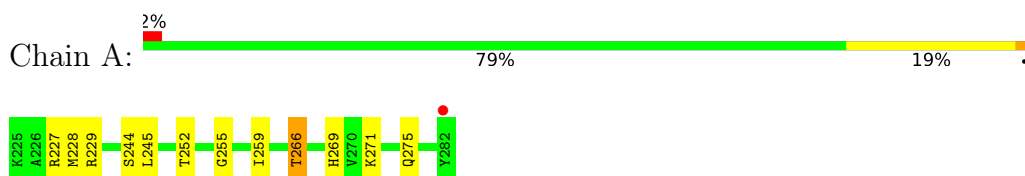
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total 1	O 1	0	0

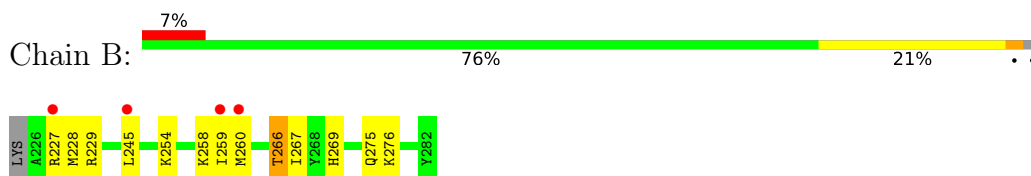
### 3 Residue-property plots [i](#)

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.

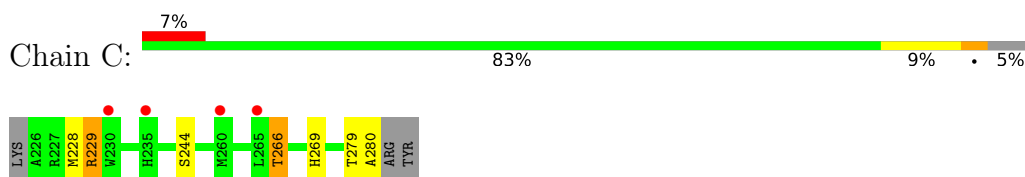
- Molecule 1: Protein PHOSPHATE STARVATION RESPONSE 1



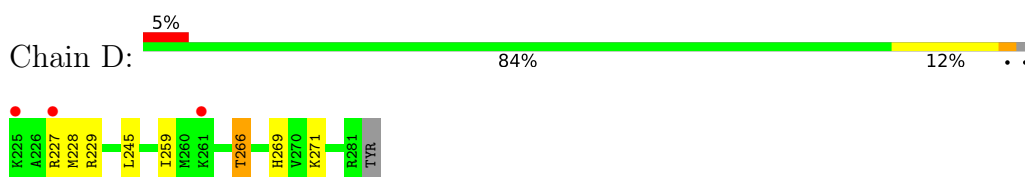
- Molecule 1: Protein PHOSPHATE STARVATION RESPONSE 1



- Molecule 1: Protein PHOSPHATE STARVATION RESPONSE 1



- Molecule 1: Protein PHOSPHATE STARVATION RESPONSE 1



- Molecule 2: DNA (5'-D(\*CP\*CP\*AP\*TP\*AP\*TP\*AP\*TP\*GP\*AP\*C)-3')

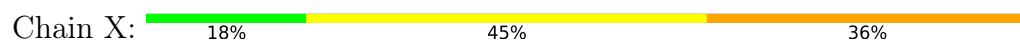


- Molecule 3: DNA (5'-D(\*GP\*TP\*CP\*AP\*TP\*AP\*TP\*AP\*TP\*GP\*G)-3')

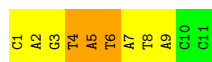




- Molecule 4: DNA (5'-D(\*GP\*GP\*TP\*AP\*TP\*AP\*TP\*AP\*CP\*TP\*G)-3')



- Molecule 5: DNA (5'-D(\*CP\*AP\*GP\*TP\*AP\*TP\*AP\*TP\*AP\*CP\*C)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.97Å 88.97Å 143.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.72 – 2.80 75.61 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (71.72-2.80) 99.1 (75.61-2.80)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.42 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.215 , 0.249 0.217 , 0.249	Depositor DCC
$R_{free}$ test set	720 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	85.3	Xtriage
Anisotropy	0.773	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 80.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2708	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	1.03	3/474 (0.6%)	0.86	1/637 (0.2%)
1	B	0.76	1/471 (0.2%)	0.78	2/633 (0.3%)
1	C	0.54	1/447 (0.2%)	0.71	0/601
1	D	0.65	1/467 (0.2%)	0.71	0/626
2	F	1.03	2/245 (0.8%)	1.22	2/376 (0.5%)
3	E	1.12	2/251 (0.8%)	1.20	3/387 (0.8%)
4	X	0.97	3/251 (1.2%)	1.24	4/387 (1.0%)
5	Y	1.03	2/245 (0.8%)	1.23	3/376 (0.8%)
All	All	0.87	15/2851 (0.5%)	0.97	15/4023 (0.4%)

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	229	ARG	CD-NE	-13.98	1.22	1.46
1	B	229	ARG	CZ-NH2	13.23	1.50	1.33
1	A	229	ARG	NE-CZ	11.79	1.48	1.33
1	D	229	ARG	CZ-NH2	9.15	1.45	1.33
3	E	8	DA	O3'-P	-9.12	1.50	1.61

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	X	5	DT	O5'-P-OP2	7.96	120.25	110.70
1	A	229	ARG	NE-CZ-NH2	-7.50	116.55	120.30
5	Y	6	DT	C1'-O4'-C4'	-6.74	103.36	110.10
5	Y	4	DT	C1'-O4'-C4'	-6.66	103.44	110.10
4	X	2	DG	O5'-P-OP1	-6.32	100.01	105.70

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	464	0	476	7	0
1	B	461	0	474	5	0
1	C	438	0	452	2	0
1	D	458	0	478	10	0
2	F	219	0	123	9	0
3	E	224	0	124	13	0
4	X	224	0	124	7	0
5	Y	219	0	123	9	0
6	F	1	0	0	0	0
All	All	2708	0	2374	44	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 9.

The worst 5 of 44 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:227:ARG:HD2	5:Y:7:DA:H5'	1.67	0.77
5:Y:6:DT:H2''	5:Y:7:DA:O5'	1.87	0.74
4:X:4:DA:C2	5:Y:9:DA:C2	2.77	0.72
1:D:271:LYS:HE3	3:E:2:DT:C7	2.23	0.68
5:Y:1:DC:H2'	5:Y:2:DA:C8	2.32	0.64

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	
1	A	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
1	B	55/58 (95%)	53 (96%)	2 (4%)	0	100	100
1	C	53/58 (91%)	52 (98%)	1 (2%)	0	100	100
1	D	55/58 (95%)	53 (96%)	2 (4%)	0	100	100
All	All	219/232 (94%)	211 (96%)	8 (4%)	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	A	48/49 (98%)	45 (94%)	3 (6%)	20	49
1	B	48/49 (98%)	43 (90%)	5 (10%)	8	23
1	C	46/49 (94%)	42 (91%)	4 (9%)	11	32
1	D	48/49 (98%)	46 (96%)	2 (4%)	32	66
All	All	190/196 (97%)	176 (93%)	14 (7%)	15	40

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	267	ILE
1	B	276	LYS
1	C	266	THR
1	B	266	THR
1	C	244	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	275	GLN
1	B	275	GLN
1	D	275	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

### 5.7 Other polymers ⓘ

There are no such residues in this entry.

### 5.8 Polymer linkage issues ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	58/58 (100%)	0.41	1 (1%) 70 63	76, 100, 150, 156	0
1	B	57/58 (98%)	0.59	4 (7%) 16 9	79, 97, 136, 155	0
1	C	55/58 (94%)	0.57	4 (7%) 15 8	91, 128, 171, 197	0
1	D	57/58 (98%)	0.62	3 (5%) 26 17	65, 89, 145, 173	0
2	F	11/11 (100%)	-0.22	0 100 100	73, 83, 88, 95	0
3	E	11/11 (100%)	-0.29	0 100 100	73, 80, 95, 100	0
4	X	11/11 (100%)	-0.56	0 100 100	92, 95, 99, 100	0
5	Y	11/11 (100%)	-0.49	0 100 100	80, 93, 116, 121	0
All	All	271/276 (98%)	0.40	12 (4%) 34 24	65, 98, 155, 197	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	225	LYS	4.6
1	B	245	LEU	3.5
1	D	227	ARG	3.0
1	A	282	TYR	2.9
1	C	235	HIS	2.6

### 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 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.