



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 03:15 PM GMT

PDB ID : 4BXT  
Title : Crystal structure of the human metapneumovirus phosphoprotein tetramerization domain  
Authors : Leyrat, C.; Renner, M.; Harlos, K.; Grimes, J.M.  
Deposited on : 2013-07-15  
Resolution : 3.13 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  
<http://wwpdb.org/validation/2016/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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

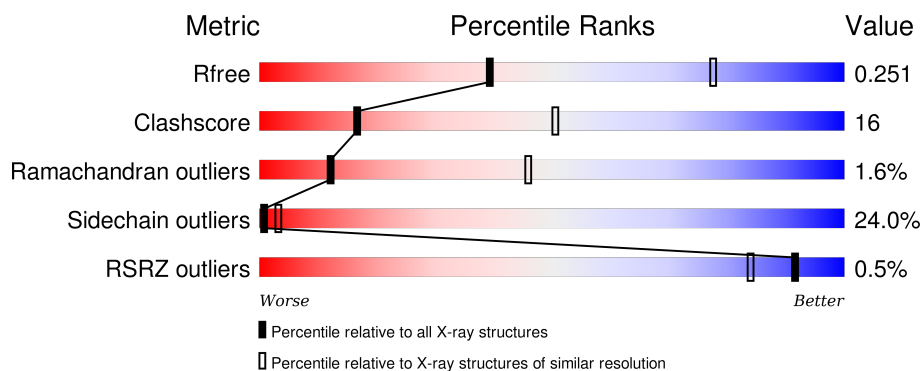
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.13 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1095 (3.18-3.10)
Clashscore	102246	1202 (3.18-3.10)
Ramachandran outliers	100387	1162 (3.18-3.10)
Sidechain outliers	100360	1162 (3.18-3.10)
RSRZ outliers	91569	1097 (3.18-3.10)

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	80	<div> <div>20%</div> <div>10%</div> <div>70%</div> </div>
1	B	80	<div> <div>15%</div> <div>13%</div> <div>•</div> <div>69%</div> </div>
1	C	80	<div> <div>13%</div> <div>13%</div> <div>6%</div> <div>69%</div> </div>
1	D	80	<div> <div>%</div> <div>18%</div> <div>14%</div> <div>•</div> <div>68%</div> </div>
1	E	80	<div> <div>19%</div> <div>8%</div> <div>5%</div> <div>69%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	80	
1	G	80	
1	H	80	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1560 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 PHOSPHOPROTEIN P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	24	Total	C	N	O	S	0	0	0
			189	121	31	36	1			
1	B	25	Total	C	N	O	S	0	0	0
			197	125	33	38	1			
1	C	25	Total	C	N	O	S	0	0	0
			195	124	32	38	1			
1	D	26	Total	C	N	O	S	0	0	0
			203	128	34	40	1			
1	E	25	Total	C	N	O	S	0	0	0
			197	125	33	38	1			
1	F	25	Total	C	N	O	S	0	0	0
			197	125	33	38	1			
1	G	26	Total	C	N	O	S	0	0	0
			201	127	33	40	1			
1	H	23	Total	C	N	O	S	0	0	0
			181	115	30	35	1			



● Molecule 1: PHOSPHOPROTEIN P



Chain E: 

SER	ILE	LEU	THR	PHE	GLU	ARG	ASP	THR	SER	SER	L170	S171	I172	R175	S178	I179	K182	L183	L187	L190	N194	ILE	ALA	THR	ALA	GLY	PRO	THR	THR	ALA	ALA	ARG	ASP	GLY	ILE	ILE	ARG	ASP	ALA	MET	ILE	GLY	VAL	ARG	GLU	LEU	ILE	ILE	ASP	ILE	LYS	GLU
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ALA	LYS	GLY	LYS	ALA	GLU	MET	GLU	GLU	GLU
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• Molecule 1: PHOSPHOPROTEIN P

Chain F: 

SER	ILE	LEU	THR	PHE	GLU	GLU	ARG	ASP	THR	SER	SER	L170	R175	L176	E177	S178	E181	K182	L183	L187	G188	L189	L190	R191	T192	L193	N194	ILE	ALA	THR	ALA	GLY	PRO	THR	THR	ALA	ALA	ARG	ASP	GLY	ILE	ILE	ARG	ASP	ALA	ILE	GLY	MET	ILE	GLY	VAL	ARG	GLU	GLU	LEU	ILE	ILE	ALA	ASP	ILE	ILE	ILE
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LYS	GLU	ALA	LYS	LYS	GLY	LYS	ALA	ALA	GLU	MET	MET	GLU	GLU	GLU
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• Molecule 1: PHOSPHOPROTEIN P

Chain G: 

SER	ILE	LEU	THR	PHE	GLU	GLU	ARG	ASP	THR	SER	S168	S169	L170	S171	I172	E173	A174	R175	L176	E177	S178	I179	E180	E181	K182	L189	L190	R191	T192	L193	ASN	ILE	ALA	THR	ALA	GLY	PRO	THR	THR	ALA	ALA	ARG	ASP	GLY	ILE	ILE	ARG	ASP	ALA	ILE	GLY	VAL	ARG	GLU	GLU	LEU	ILE	ILE	ALA	ASP	ILE	ILE
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ILE	LYS	GLU	ALA	LYS	GLY	LYS	ALA	ALA	GLU	MET	MET	GLU	GLU	GLU
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• Molecule 1: PHOSPHOPROTEIN P

Chain H: 

SER	ILE	LEU	THR	PHE	GLU	GLU	ARG	ASP	THR	SER	SER	LEU	S171	I172	E173	A174	R175	L176	E177	S178	I179	E180	E181	K182	L183	S184	M185	I186	L190	R191	T192	L193	ASN	ILE	ALA	THR	ALA	GLY	PRO	THR	THR	ALA	ALA	ARG	ASP	GLY	ILE	ILE	ARG	ASP	ALA	MET	ILE	GLY	VAL	ARG	GLU	GLU	LEU	ILE	ILE
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ALA	ASP	ILE	ILE	LYS	LYS	GLY	LYS	ALA	ALA	GLU	GLU	MET	MET	GLU	GLU	GLU
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.91Å 48.52Å 64.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.42 – 3.13 46.42 – 3.13	Depositor EDS
% Data completeness (in resolution range)	89.6 (46.42-3.13) 89.6 (46.42-3.13)	Depositor EDS
$R_{merge}$	0.35	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 3.12Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, $R_{free}$	0.235 , 0.252 0.239 , 0.251	Depositor DCC
$R_{free}$ test set	153 reflections (4.47%)	DCC
Wilson B-factor (Å <sup>2</sup> )	57.8	Xtriage
Anisotropy	0.768	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 44.3	EDS
Estimated twinning fraction	0.062 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 3577 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	1560	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.17% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	A	0.42	0/188	0.63	0/250
1	B	0.50	0/196	0.72	0/261
1	C	0.51	0/194	0.71	0/258
1	D	0.47	0/202	0.77	0/269
1	E	0.45	0/196	0.64	0/261
1	F	0.44	0/196	0.68	0/261
1	G	0.77	0/200	0.80	0/266
1	H	0.47	0/180	0.74	0/239
All	All	0.52	0/1552	0.71	0/2065

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	A	189	0	211	3	0
1	B	197	0	217	9	0
1	C	195	0	216	9	2
1	D	203	0	222	5	0
1	E	197	0	217	10	0
1	F	197	0	217	7	0
1	G	201	0	221	13	0
1	H	181	0	200	16	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	1560	0	1721	54	2

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 16.

The worst 5 of 54 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:F:178:SER:OG	1:G:180:GLU:OE2	1.88	0.89
1:H:176:LEU:O	1:H:180:GLU:HG3	1.72	0.88
1:B:191:ARG:NH1	1:F:181:GLU:OE2	2.12	0.83
1:C:176:LEU:O	1:C:180:GLU:HG2	1.84	0.77
1:B:185:MET:O	1:B:189:LEU:HD12	1.86	0.76

All (2) 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)
1:C:191:ARG:NH2	1:H:181:GLU:OE1[4_455]	1.84	0.36
1:C:173:GLU:OE2	1:H:173:GLU:OE1[3_554]	2.19	0.01

## 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	22/80 (28%)	21 (96%)	1 (4%)	0	100	100
1	B	23/80 (29%)	23 (100%)	0	0	100	100
1	C	23/80 (29%)	22 (96%)	0	1 (4%)	3	19
1	D	24/80 (30%)	23 (96%)	1 (4%)	0	100	100
1	E	23/80 (29%)	22 (96%)	0	1 (4%)	3	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	23/80 (29%)	23 (100%)	0	0	100	100
1	G	24/80 (30%)	23 (96%)	1 (4%)	0	100	100
1	H	21/80 (26%)	20 (95%)	0	1 (5%)	3	17
All	All	183/640 (29%)	177 (97%)	3 (2%)	3 (2%)	12	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	170	LEU
1	H	172	ILE
1	E	171	SER

### 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	22/65 (34%)	18 (82%)	4 (18%)	2	9
1	B	23/65 (35%)	17 (74%)	6 (26%)	0	2
1	C	23/65 (35%)	16 (70%)	7 (30%)	0	1
1	D	24/65 (37%)	18 (75%)	6 (25%)	1	2
1	E	23/65 (35%)	17 (74%)	6 (26%)	0	2
1	F	23/65 (35%)	18 (78%)	5 (22%)	1	6
1	G	24/65 (37%)	18 (75%)	6 (25%)	1	2
1	H	21/65 (32%)	17 (81%)	4 (19%)	2	8
All	All	183/520 (35%)	139 (76%)	44 (24%)	1	3

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	178	SER
1	E	172	ILE
1	H	171	SER

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Mol	Chain	Res	Type
1	D	179	ILE
1	D	194	ASN

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

Mol	Chain	Res	Type
1	E	194	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 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 [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(Å²)	Q<0.9
1	A	24/80 (30%)	-0.45	0	100	100	39, 43, 57, 70	0
1	B	25/80 (31%)	-0.27	0	100	100	45, 49, 59, 88	0
1	C	25/80 (31%)	-0.26	0	100	100	47, 55, 66, 72	0
1	D	26/80 (32%)	-0.27	1 (3%)	44	22	45, 51, 59, 67	0
1	E	25/80 (31%)	-0.08	0	100	100	46, 51, 59, 90	0
1	F	25/80 (31%)	-0.37	0	100	100	42, 47, 61, 78	0
1	G	26/80 (32%)	-0.24	0	100	100	40, 52, 66, 67	0
1	H	23/80 (28%)	-0.03	0	100	100	46, 55, 64, 92	0
All	All	199/640 (31%)	-0.25	1 (0%)	91	84	39, 51, 67, 92	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	194	ASN	2.1

### 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.