



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 03:49 PM GMT

PDB ID : 3PMK  
Title : Crystal structure of the Vesicular Stomatitis Virus RNA free nucleoprotein/p  
hosphoproteincomplex  
Authors : Leyrat, C.; Yabukarski, F.; Tarbouriech, N.; Ruigrok, R.W.H.; Jamin, M.  
Deposited on : 2010-11-17  
Resolution : 3.03 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

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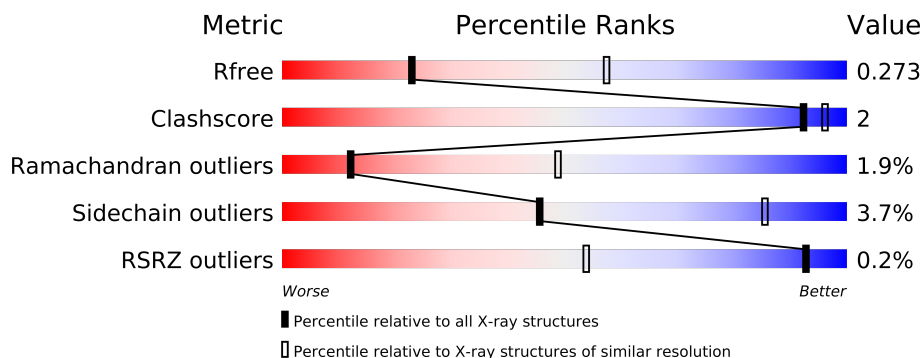
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.03 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))
$R_{free}$	66092	1460 (3.08-3.00)
Clashscore	79885	1881 (3.08-3.00)
Ramachandran outliers	78287	1814 (3.08-3.00)
Sidechain outliers	78261	1817 (3.08-3.00)
RSRZ outliers	66119	1462 (3.08-3.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	404	
1	B	404	
1	C	404	
1	D	404	
1	E	404	
2	N	68	
2	O	68	
2	P	68	
2	Q	68	
2	R	68	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17478 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Nucleocapsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	0	0	0
			3191	2030	534	608	19			
1	B	404	Total	C	N	O	S	0	0	0
			3191	2030	534	608	19			
1	C	404	Total	C	N	O	S	0	0	0
			3191	2030	534	608	19			
1	D	404	Total	C	N	O	S	0	0	0
			3192	2030	534	609	19			
1	E	404	Total	C	N	O	S	0	0	0
			3191	2030	534	608	19			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	GLY	-	EXPRESSION TAG	UNP B7UCZ2
A	20	ALA	-	EXPRESSION TAG	UNP B7UCZ2
A	21	MET	-	EXPRESSION TAG	UNP B7UCZ2
B	19	GLY	-	EXPRESSION TAG	UNP B7UCZ2
B	20	ALA	-	EXPRESSION TAG	UNP B7UCZ2
B	21	MET	-	EXPRESSION TAG	UNP B7UCZ2
C	19	GLY	-	EXPRESSION TAG	UNP B7UCZ2
C	20	ALA	-	EXPRESSION TAG	UNP B7UCZ2
C	21	MET	-	EXPRESSION TAG	UNP B7UCZ2
D	19	GLY	-	EXPRESSION TAG	UNP B7UCZ2
D	20	ALA	-	EXPRESSION TAG	UNP B7UCZ2
D	21	MET	-	EXPRESSION TAG	UNP B7UCZ2
E	19	GLY	-	EXPRESSION TAG	UNP B7UCZ2
E	20	ALA	-	EXPRESSION TAG	UNP B7UCZ2
E	21	MET	-	EXPRESSION TAG	UNP B7UCZ2

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	N	30	Total	C	N	O	0	0	0
			246	151	44	51			
2	O	29	Total	C	N	O	0	0	0
			238	146	42	50			
2	P	29	Total	C	N	O	0	0	0
			240	148	43	49			
2	Q	30	Total	C	N	O	0	0	0
			247	152	44	51			
2	R	29	Total	C	N	O	0	0	0
			240	148	43	49			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	61	LEU	-	EXPRESSION TAG	UNP B7UCZ3
N	62	GLU	-	EXPRESSION TAG	UNP B7UCZ3
N	63	HIS	-	EXPRESSION TAG	UNP B7UCZ3
N	64	HIS	-	EXPRESSION TAG	UNP B7UCZ3
N	65	HIS	-	EXPRESSION TAG	UNP B7UCZ3
N	66	HIS	-	EXPRESSION TAG	UNP B7UCZ3
N	67	HIS	-	EXPRESSION TAG	UNP B7UCZ3
N	68	HIS	-	EXPRESSION TAG	UNP B7UCZ3
O	61	LEU	-	EXPRESSION TAG	UNP B7UCZ3
O	62	GLU	-	EXPRESSION TAG	UNP B7UCZ3
O	63	HIS	-	EXPRESSION TAG	UNP B7UCZ3
O	64	HIS	-	EXPRESSION TAG	UNP B7UCZ3
O	65	HIS	-	EXPRESSION TAG	UNP B7UCZ3
O	66	HIS	-	EXPRESSION TAG	UNP B7UCZ3
O	67	HIS	-	EXPRESSION TAG	UNP B7UCZ3
O	68	HIS	-	EXPRESSION TAG	UNP B7UCZ3
P	61	LEU	-	EXPRESSION TAG	UNP B7UCZ3
P	62	GLU	-	EXPRESSION TAG	UNP B7UCZ3
P	63	HIS	-	EXPRESSION TAG	UNP B7UCZ3
P	64	HIS	-	EXPRESSION TAG	UNP B7UCZ3
P	65	HIS	-	EXPRESSION TAG	UNP B7UCZ3
P	66	HIS	-	EXPRESSION TAG	UNP B7UCZ3
P	67	HIS	-	EXPRESSION TAG	UNP B7UCZ3
P	68	HIS	-	EXPRESSION TAG	UNP B7UCZ3
Q	61	LEU	-	EXPRESSION TAG	UNP B7UCZ3
Q	62	GLU	-	EXPRESSION TAG	UNP B7UCZ3
Q	63	HIS	-	EXPRESSION TAG	UNP B7UCZ3
Q	64	HIS	-	EXPRESSION TAG	UNP B7UCZ3
Q	65	HIS	-	EXPRESSION TAG	UNP B7UCZ3
Q	66	HIS	-	EXPRESSION TAG	UNP B7UCZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	67	HIS	-	EXPRESSION TAG	UNP B7UCZ3
Q	68	HIS	-	EXPRESSION TAG	UNP B7UCZ3
R	61	LEU	-	EXPRESSION TAG	UNP B7UCZ3
R	62	GLU	-	EXPRESSION TAG	UNP B7UCZ3
R	63	HIS	-	EXPRESSION TAG	UNP B7UCZ3
R	64	HIS	-	EXPRESSION TAG	UNP B7UCZ3
R	65	HIS	-	EXPRESSION TAG	UNP B7UCZ3
R	66	HIS	-	EXPRESSION TAG	UNP B7UCZ3
R	67	HIS	-	EXPRESSION TAG	UNP B7UCZ3
R	68	HIS	-	EXPRESSION TAG	UNP B7UCZ3

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	51	Total O 51 51	0	0
3	B	71	Total O 71 71	0	0
3	C	62	Total O 62 62	0	0
3	D	51	Total O 51 51	0	0
3	E	47	Total O 47 47	0	0
3	N	7	Total O 7 7	0	0
3	O	7	Total O 7 7	0	0
3	P	7	Total O 7 7	0	0
3	Q	4	Total O 4 4	0	0
3	R	4	Total O 4 4	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

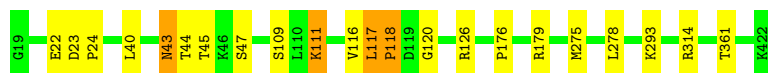
- Molecule 1: Nucleocapsid protein

Chain A: 



- Molecule 1: Nucleocapsid protein

Chain B: 



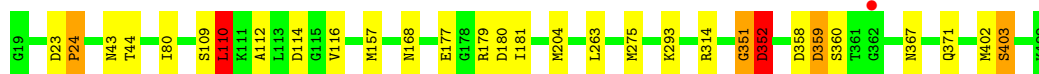
- Molecule 1: Nucleocapsid protein

Chain C: 



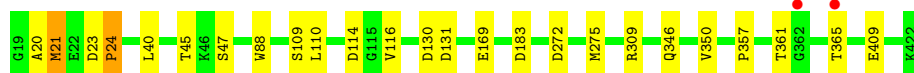
- Molecule 1: Nucleocapsid protein

Chain D: 



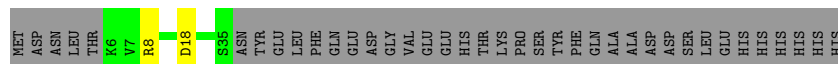
- Molecule 1: Nucleocapsid protein

Chain E: 



- Molecule 2: Phosphoprotein

Chain N: 



## ● Molecule 2: Phosphoprotein

Chain O: 

MET	ASP	ASN	ASN	LEU	THR	T5	L11	K12	S13	Y14	E33	LYS	SER	ASN	TYR	GLU	PHE	GLN	GLU	GLY	VAL	GLU	GLU	HIS	HIS	THR	LYS	PRO	SER	TYR	PHE	GLN	ALA	ALA	ASP	ASP	SER	SER	LEU	GLU	HIS	HIS	HIS	HIS	HIS
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## ● Molecule 2: Phosphoprotein

Chain P: 

MET	ASP	ASN	ASN	THR	K6	V7	R8	D18	K34	SER	ASN	TYR	GLU	LEU	PHE	GLN	GLU	ASP	GLY	VAL	GLU	GLU	HIS	THR	LYS	PRO	SER	SER	TYR	PHE	GLN	ALA	ALA	ASP	ASP	ASP	SER	SER	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
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## ● Molecule 2: Phosphoprotein

Chain Q: 

MET	ASP	ASN	ASN	THR	T5	R16	K34	SER	ASN	TYR	GLU	LEU	PHE	GLN	GLU	ASP	GLY	VAL	GLU	GLU	HIS	THR	LYS	PRO	SER	TYR	PHE	GLN	ALA	ALA	ASP	ASP	SER	SER	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS
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## ● Molecule 2: Phosphoprotein

Chain R: 

MET	ASP	ASN	ASN	LEU	LEU	THR	K6	V7	R8	K34	SER	ASN	ASN	TYR	GLU	LEU	PHE	GLN	GLN	GLU	ASP	GLY	VAL	GLU	GLU	GLU	HIS	THR	LYS	PRO	SER	SER	TYR	PHE	GLN	ALA	ALA	ASP	ASP	SER	SER	LEU	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.56Å 171.97Å 239.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.97 – 3.03 59.97 – 3.03	Depositor EDS
% Data completeness (in resolution range)	89.0 (59.97-3.03) 89.1 (59.97-3.03)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.31 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.244 , 0.278 0.241 , 0.273	Depositor DCC
$R_{free}$ test set	2742 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.4	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 2.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	2 of 54043 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	17478	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 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	0.32	0/3265	0.48	0/4417
1	B	0.32	0/3265	0.48	0/4417
1	C	0.32	0/3265	0.50	0/4417
1	D	0.32	0/3266	0.47	0/4417
1	E	0.32	0/3265	0.48	0/4417
2	N	0.33	0/247	0.46	0/328
2	O	0.33	0/239	0.47	0/319
2	P	0.33	0/241	0.48	0/320
2	Q	0.34	0/248	0.54	0/330
2	R	0.31	0/241	0.46	0/320
All	All	0.32	0/17542	0.48	0/23702

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3191	0	0	3	0
1	B	3191	0	0	5	0
1	C	3191	0	0	8	0
1	D	3192	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3191	0	0	4	0
2	N	246	0	0	0	0
2	O	238	0	0	2	0
2	P	240	0	0	0	0
2	Q	247	0	0	1	0
2	R	240	0	0	0	0
3	A	51	0	0	0	0
3	B	71	0	0	0	0
3	C	62	0	0	0	0
3	D	51	0	0	0	0
3	E	47	0	0	0	0
3	N	7	0	0	0	0
3	O	7	0	0	0	0
3	P	7	0	0	0	0
3	Q	4	0	0	0	0
3	R	4	0	0	0	0
All	All	17478	0	0	31	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (31) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:O:12:LYS:O	2:O:14:TYR:N	2.12	0.83
1:D:43:ASN:ND2	1:D:112:ALA:O	2.28	0.67
1:C:23:ASP:N	1:C:24:PRO:CD	2.61	0.63
1:C:408:ARG:NH1	1:C:408:ARG:CG	2.64	0.60
1:C:52:ARG:NH2	1:C:126:ARG:O	2.34	0.60
1:D:358:ASP:O	1:D:360:SER:N	2.36	0.58
1:A:153:ARG:NH2	1:A:183:ASP:OD2	2.37	0.57
1:B:117:LEU:N	1:B:118:PRO:CD	2.68	0.57
1:D:179:ARG:O	1:D:181:ILE:N	2.39	0.56
1:E:21:MET:O	1:E:23:ASP:N	2.38	0.55
1:D:351:GLY:O	1:D:352:ASP:CB	2.56	0.53
1:E:23:ASP:N	1:E:24:PRO:CD	2.72	0.52
1:D:109:SER:O	1:D:110:LEU:CB	2.58	0.51
1:B:43:ASN:O	1:B:45:THR:N	2.45	0.49
1:D:402:MET:O	1:D:403:SER:CB	2.60	0.49
1:A:23:ASP:N	1:A:24:PRO:CD	2.76	0.49
1:B:23:ASP:N	1:B:24:PRO:CD	2.76	0.49
1:D:23:ASP:N	1:D:24:PRO:CD	2.77	0.47
1:D:263:LEU:O	2:O:14:TYR:OH	2.32	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:367:ASN:ND2	1:A:367:ASN:N	2.63	0.46
1:D:359:ASP:O	1:D:360:SER:CB	2.64	0.46
1:B:40:LEU:N	1:B:109:SER:O	2.50	0.44
1:C:252:ARG:NH1	1:C:252:ARG:CG	2.81	0.43
1:C:146:ARG:CG	1:C:146:ARG:NH1	2.81	0.43
1:C:402:MET:O	1:C:403:SER:CB	2.67	0.42
1:E:40:LEU:N	1:E:109:SER:O	2.53	0.42
2:Q:16:ARG:NH1	2:Q:16:ARG:CG	2.83	0.41
1:C:114:ASP:N	1:C:114:ASP:OD2	2.54	0.41
1:C:21:MET:O	1:C:23:ASP:N	2.54	0.41
1:B:23:ASP:O	1:B:24:PRO:C	2.58	0.40
1:E:130:ASP:O	1:E:131:ASP:CB	2.69	0.40

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	402/404 (100%)	378 (94%)	15 (4%)	9 (2%)	10	43
1	B	402/404 (100%)	364 (90%)	29 (7%)	9 (2%)	10	43
1	C	402/404 (100%)	373 (93%)	25 (6%)	4 (1%)	22	68
1	D	402/404 (100%)	369 (92%)	23 (6%)	10 (2%)	9	38
1	E	402/404 (100%)	363 (90%)	32 (8%)	7 (2%)	14	52
2	N	28/68 (41%)	27 (96%)	1 (4%)	0	100	100
2	O	27/68 (40%)	24 (89%)	1 (4%)	2 (7%)	2	8
2	P	27/68 (40%)	26 (96%)	1 (4%)	0	100	100
2	Q	28/68 (41%)	26 (93%)	2 (7%)	0	100	100
2	R	27/68 (40%)	24 (89%)	3 (11%)	0	100	100
All	All	2147/2360 (91%)	1974 (92%)	132 (6%)	41 (2%)	12	49

All (41) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	LEU
1	B	47	SER
1	B	117	LEU
1	B	176	PRO
1	D	110	LEU
1	D	352	ASP
1	D	359	ASP
2	O	13	SER
1	A	129	ALA
1	C	47	SER
1	D	168	ASN
1	E	20	ALA
1	E	350	VAL
1	E	361	THR
2	O	11	LEU
1	A	21	MET
1	A	360	SER
1	B	22	GLU
1	B	111	LYS
1	B	179	ARG
1	C	98	ALA
1	D	351	GLY
1	E	47	SER
1	E	110	LEU
1	E	357	PRO
1	A	128	SER
1	C	360	SER
1	A	98	ALA
1	A	175	VAL
1	B	44	THR
1	B	118	PRO
1	D	44	THR
1	D	403	SER
1	E	24	PRO
1	A	47	SER
1	D	180	ASP
1	D	80	ILE
1	C	351	GLY
1	A	80	ILE
1	B	120	GLY
1	D	24	PRO

### 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	344/344 (100%)	330 (96%)	14 (4%)	41	82
1	B	344/344 (100%)	335 (97%)	9 (3%)	59	91
1	C	344/344 (100%)	330 (96%)	14 (4%)	41	82
1	D	344/344 (100%)	332 (96%)	12 (4%)	48	87
1	E	344/344 (100%)	331 (96%)	13 (4%)	44	85
2	N	26/61 (43%)	24 (92%)	2 (8%)	18	55
2	O	25/61 (41%)	25 (100%)	0	100	100
2	P	25/61 (41%)	23 (92%)	2 (8%)	17	52
2	Q	26/61 (43%)	25 (96%)	1 (4%)	44	85
2	R	25/61 (41%)	24 (96%)	1 (4%)	42	83
All	All	1847/2025 (91%)	1779 (96%)	68 (4%)	45	85

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	MET
1	A	22	GLU
1	A	42	ILE
1	A	104	ILE
1	A	110	LEU
1	A	114	ASP
1	A	117	LEU
1	A	148	GLN
1	A	170	GLN
1	A	175	VAL
1	A	204	MET
1	A	275	MET
1	A	310	SER
1	A	367	ASN
1	B	43	ASN
1	B	111	LYS
1	B	116	VAL
1	B	126	ARG

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Mol	Chain	Res	Type
1	B	275	MET
1	B	278	LEU
1	B	293	LYS
1	B	314	ARG
1	B	361	THR
1	C	52	ARG
1	C	85	ASP
1	C	88	TRP
1	C	100	ASP
1	C	110	LEU
1	C	116	VAL
1	C	117	LEU
1	C	169	GLU
1	C	252	ARG
1	C	275	MET
1	C	309	ARG
1	C	314	ARG
1	C	366	THR
1	C	408	ARG
1	D	110	LEU
1	D	114	ASP
1	D	116	VAL
1	D	157	MET
1	D	177	GLU
1	D	204	MET
1	D	275	MET
1	D	293	LYS
1	D	314	ARG
1	D	352	ASP
1	D	367	ASN
1	D	371	GLN
1	E	21	MET
1	E	45	THR
1	E	88	TRP
1	E	114	ASP
1	E	116	VAL
1	E	169	GLU
1	E	183	ASP
1	E	272	ASP
1	E	275	MET
1	E	309	ARG
1	E	346	GLN

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Mol	Chain	Res	Type
1	E	365	THR
1	E	409	GLU
2	N	8	ARG
2	N	18	ASP
2	P	8	ARG
2	P	18	ASP
2	Q	16	ARG
2	R	8	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

### 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, 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	404/404 (100%)	-0.23	1 (0%) 93 54	13, 23, 44, 51	0
1	B	404/404 (100%)	-0.20	0 100 100	15, 25, 47, 57	0
1	C	404/404 (100%)	-0.26	1 (0%) 93 54	12, 21, 44, 49	0
1	D	404/404 (100%)	-0.20	1 (0%) 93 54	13, 26, 50, 58	0
1	E	404/404 (100%)	-0.17	2 (0%) 88 35	14, 29, 53, 59	0
2	N	30/68 (44%)	-0.18	0 100 100	23, 35, 57, 72	0
2	O	29/68 (42%)	0.05	0 100 100	22, 38, 72, 87	0
2	P	29/68 (42%)	-0.12	0 100 100	22, 34, 57, 61	0
2	Q	30/68 (44%)	0.06	0 100 100	22, 37, 86, 98	0
2	R	29/68 (42%)	-0.13	0 100 100	21, 35, 65, 78	0
All	All	2167/2360 (91%)	-0.20	5 (0%) 93 54	12, 25, 50, 98	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	365	THR	2.3
1	A	363	GLY	2.3
1	D	362	GLY	2.2
1	C	365	THR	2.1
1	E	362	GLY	2.0

### 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 ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.