



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:57 PM GMT

PDB ID : 4DYT
Title : Crystal Structure of WSN/A Influenza Nucleoprotein with Three Mutations (E53D, Y289H, Y313V)
Authors : Lewis, H.A.; Baldwin, E.T.; Steinbacher, S.; Maskos, K.; Mortl, M.; Kiefer-sauer, R.; Edavettal, S.; McDonnell, P.A.; Pearce, B.C.; Langley, D.R.
Deposited on : 2012-02-29
Resolution : 3.00 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
<http://wwpdb.org/validation/2016/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
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

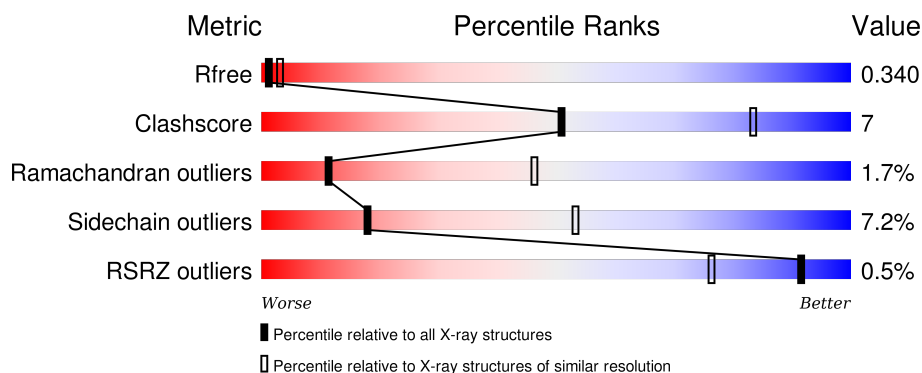
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 ≥ 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	500	
1	B	500	
1	C	500	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8534 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 Nucleocapsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	432	Total	C	N	O	S	0	0	0
			2941	1796	540	582	23			
1	B	429	Total	C	N	O	S	0	0	0
			2844	1720	531	569	24			
1	C	433	Total	C	N	O	S	3	0	0
			2736	1659	504	553	20			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	INITIATING METHIONINE	UNP B4URF1
A	53	ASP	GLU	ENGINEERED MUTATION	UNP B4URF1
A	289	HIS	TYR	ENGINEERED MUTATION	UNP B4URF1
A	313	VAL	TYR	ENGINEERED MUTATION	UNP B4URF1
A	499	LEU	-	EXPRESSION TAG	UNP B4URF1
A	500	GLU	-	EXPRESSION TAG	UNP B4URF1
A	501	HIS	-	EXPRESSION TAG	UNP B4URF1
A	502	HIS	-	EXPRESSION TAG	UNP B4URF1
A	503	HIS	-	EXPRESSION TAG	UNP B4URF1
A	504	HIS	-	EXPRESSION TAG	UNP B4URF1
A	505	HIS	-	EXPRESSION TAG	UNP B4URF1
A	506	HIS	-	EXPRESSION TAG	UNP B4URF1
B	7	MET	-	INITIATING METHIONINE	UNP B4URF1
B	53	ASP	GLU	ENGINEERED MUTATION	UNP B4URF1
B	289	HIS	TYR	ENGINEERED MUTATION	UNP B4URF1
B	313	VAL	TYR	ENGINEERED MUTATION	UNP B4URF1
B	499	LEU	-	EXPRESSION TAG	UNP B4URF1
B	500	GLU	-	EXPRESSION TAG	UNP B4URF1
B	501	HIS	-	EXPRESSION TAG	UNP B4URF1
B	502	HIS	-	EXPRESSION TAG	UNP B4URF1
B	503	HIS	-	EXPRESSION TAG	UNP B4URF1
B	504	HIS	-	EXPRESSION TAG	UNP B4URF1
B	505	HIS	-	EXPRESSION TAG	UNP B4URF1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	506	HIS	-	EXPRESSION TAG	UNP B4URF1
C	7	MET	-	INITIATING METHIONINE	UNP B4URF1
C	53	ASP	GLU	ENGINEERED MUTATION	UNP B4URF1
C	289	HIS	TYR	ENGINEERED MUTATION	UNP B4URF1
C	313	VAL	TYR	ENGINEERED MUTATION	UNP B4URF1
C	499	LEU	-	EXPRESSION TAG	UNP B4URF1
C	500	GLU	-	EXPRESSION TAG	UNP B4URF1
C	501	HIS	-	EXPRESSION TAG	UNP B4URF1
C	502	HIS	-	EXPRESSION TAG	UNP B4URF1
C	503	HIS	-	EXPRESSION TAG	UNP B4URF1
C	504	HIS	-	EXPRESSION TAG	UNP B4URF1
C	505	HIS	-	EXPRESSION TAG	UNP B4URF1
C	506	HIS	-	EXPRESSION TAG	UNP B4URF1

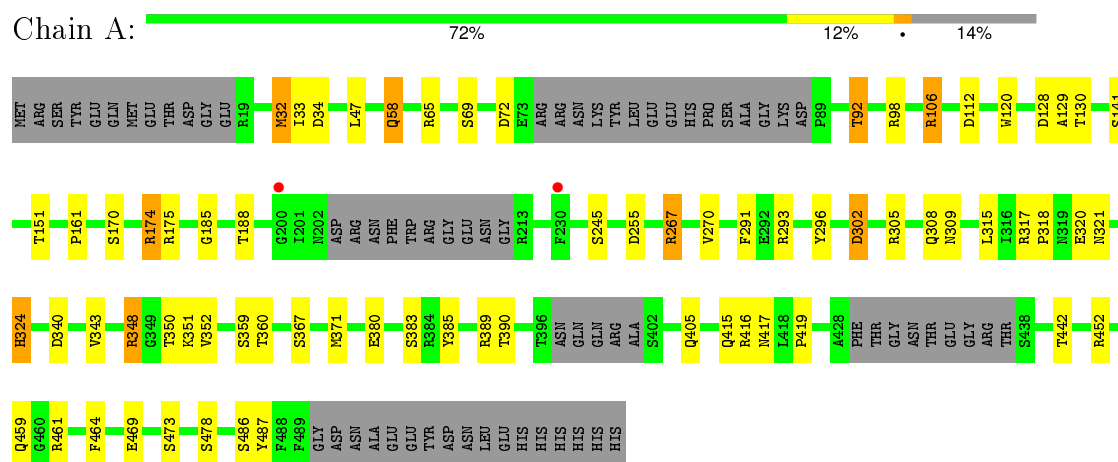
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total O 5 5	0	0
2	B	5	Total O 5 5	0	0
2	C	3	Total O 3 3	0	0

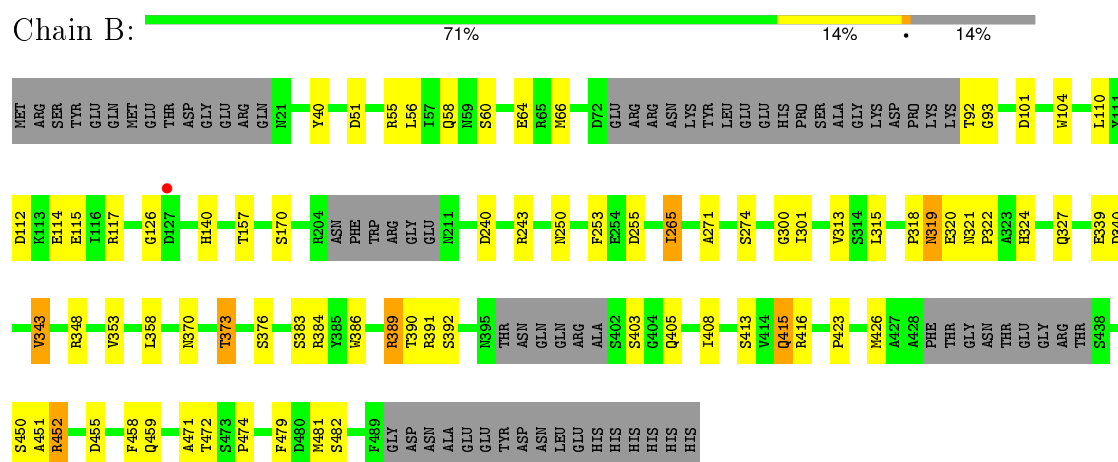
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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.

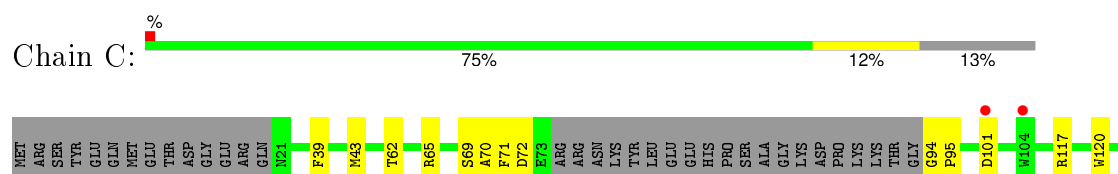
- Molecule 1: Nucleocapsid protein

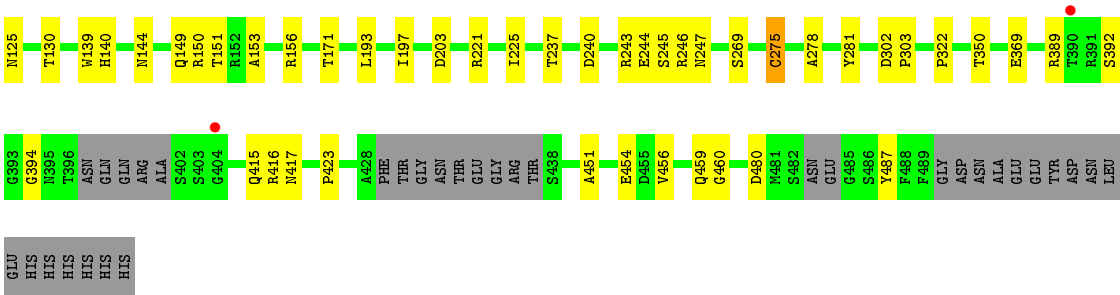


- Molecule 1: Nucleocapsid protein



- Molecule 1: Nucleocapsid protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	120.46Å 135.93Å 191.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.08 – 3.00 46.49 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.2 (45.08-3.00) 90.8 (46.49-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.270 , 0.342 0.266 , 0.340	Depositor DCC
R_{free} test set	945 reflections (3.39%)	DCC
Wilson B-factor (Å ²)	79.6	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 129.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 28853 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	8534	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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, 0.375 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	0.34	0/2991	0.49	0/4062
1	B	0.33	0/2892	0.49	0/3934
1	C	0.38	2/2779 (0.1%)	0.48	1/3794 (0.0%)
All	All	0.35	2/8662 (0.0%)	0.49	1/11790 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	322	PRO	CB-CG	-9.08	1.04	1.50
1	C	322	PRO	N-CD	-5.06	1.40	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	322	PRO	CA-N-CD	-5.58	103.69	111.50

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	2941	0	2384	42	0
1	B	2844	0	2184	48	0
1	C	2736	0	1951	27	0
2	A	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	5	0	0	1	0
2	C	3	0	0	1	0
All	All	8534	0	6519	103	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 7.

All (103) 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:A:459:GLN:HA	1:B:415:GLN:HG3	1.36	1.07
1:B:459:GLN:HA	1:C:415:GLN:HG3	1.60	0.82
1:B:370:ASN:ND2	1:B:373:THR:H	1.81	0.78
1:A:320:GLU:HG2	1:A:360:THR:HA	1.67	0.75
1:A:415:GLN:HE21	1:C:460:GLY:H	1.38	0.69
1:B:370:ASN:HD21	1:B:373:THR:H	1.39	0.68
1:C:139:TRP:HB2	1:C:275:CYS:HB2	1.79	0.64
1:B:426:MET:HA	1:B:426:MET:CE	2.27	0.64
1:C:278:ALA:HA	1:C:281:TYR:HD2	1.63	0.63
1:A:348:ARG:HD2	1:A:350:THR:OG1	1.98	0.63
1:A:308:GLN:HE22	1:A:383:SER:H	1.47	0.63
1:B:321:ASN:HD22	1:B:322:PRO:HD2	1.64	0.63
1:A:324:HIS:HD2	1:A:359:SER:H	1.47	0.62
1:B:300:GLY:O	1:B:389:ARG:NH2	2.32	0.61
1:C:62:THR:HA	1:C:65:ARG:HB2	1.83	0.60
1:B:271:ALA:HA	1:B:391:ARG:HA	1.84	0.60
1:A:34:ASP:OD2	1:A:291:PHE:HB2	2.03	0.59
1:B:450:SER:HA	1:B:452:ARG:HH21	1.69	0.58
1:B:112:ASP:HB2	1:B:115:GLU:HB3	1.85	0.58
1:C:39:PHE:O	1:C:43:MET:HG2	2.04	0.57
1:A:405:GLN:HG3	1:C:487:TYR:HB3	1.86	0.56
1:A:106:ARG:HH21	1:A:371:MET:HG2	1.69	0.56
1:A:478:SER:HA	2:A:605:HOH:O	2.04	0.56
1:B:104:TRP:HE1	1:B:376:SER:HG	1.53	0.56
1:A:32:MET:HG3	1:A:33:ILE:N	2.21	0.55
1:B:250:ASN:HA	1:B:253:PHE:HB3	1.89	0.55
1:A:486:SER:HB3	1:B:408:ILE:HD11	1.89	0.55
1:A:415:GLN:NE2	1:C:460:GLY:H	2.04	0.55
1:A:308:GLN:NE2	1:A:383:SER:H	2.05	0.54
1:A:417:ASN:O	1:A:419:PRO:HD3	2.08	0.54
1:B:114:GLU:HG2	2:B:603:HOH:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:269:SER:HA	1:C:392:SER:HA	1.89	0.54
1:A:317:ARG:HB3	1:A:318:PRO:HD2	1.91	0.53
1:A:47:LEU:O	1:A:98:ARG:NH2	2.41	0.53
1:B:324:HIS:HD2	1:B:358:LEU:HA	1.73	0.52
1:A:69:SER:OG	1:A:92:THR:HG21	2.09	0.52
1:A:106:ARG:HH11	1:A:367:SER:HA	1.74	0.52
1:A:267:ARG:NH1	1:B:408:ILE:O	2.42	0.52
1:B:479:PHE:C	1:B:481:MET:H	2.13	0.51
1:A:170:SER:HA	1:A:188:THR:HG23	1.92	0.51
1:A:120:TRP:HE1	1:A:129:ALA:HB3	1.75	0.51
1:B:265:ILE:HD11	1:B:451:ALA:HB3	1.92	0.50
1:B:114:GLU:HA	1:B:117:ARG:HE	1.75	0.50
1:B:340:ASP:HB3	1:B:343:VAL:HG13	1.94	0.49
1:B:56:LEU:HA	1:B:313:VAL:O	2.12	0.49
1:B:426:MET:HE2	1:B:426:MET:HA	1.94	0.49
1:C:243:ARG:HG3	1:C:244:GLU:N	2.28	0.49
1:C:240:ASP:O	1:C:244:GLU:HG2	2.14	0.48
1:A:296:TYR:HA	1:A:302:ASP:OD2	2.13	0.48
1:B:66:MET:HA	1:B:92:THR:HG21	1.94	0.48
1:C:153:ALA:HA	1:C:156:ARG:HB3	1.96	0.47
1:B:327:GLN:NE2	1:B:353:VAL:O	2.45	0.47
1:A:58:GLN:HG3	1:A:315:LEU:HG	1.95	0.47
1:B:301:ILE:O	1:B:301:ILE:HG12	2.15	0.47
1:C:278:ALA:HA	1:C:281:TYR:CD2	2.49	0.46
1:B:315:LEU:HA	1:B:376:SER:HB3	1.96	0.46
1:C:149:GLN:C	1:C:151:THR:H	2.19	0.45
1:A:120:TRP:HE1	1:A:129:ALA:CB	2.30	0.45
1:B:40:TYR:HE1	1:B:60:SER:HA	1.80	0.45
1:A:174:ARG:HG2	1:A:175:ARG:N	2.31	0.45
1:B:301:ILE:HB	1:B:386:TRP:CH2	2.51	0.45
1:B:93:GLY:HA2	1:B:110:LEU:HA	1.98	0.45
1:A:486:SER:HB3	1:B:408:ILE:CD1	2.46	0.45
1:A:417:ASN:HA	1:C:456:VAL:HA	1.97	0.45
1:B:64:GLU:HB3	1:B:140:HIS:HE1	1.81	0.45
1:B:455:ASP:O	1:C:417:ASN:HA	2.17	0.45
1:C:193:LEU:O	1:C:197:ILE:HG12	2.17	0.44
1:C:144:ASN:ND2	1:C:171:THR:HG21	2.32	0.44
1:A:461:ARG:HD2	1:B:413:SER:OG	2.18	0.44
1:B:348:ARG:HA	1:B:383:SER:HB2	2.00	0.43
1:B:390:THR:HG22	1:B:392:SER:N	2.33	0.43
1:C:245:SER:C	1:C:247:ASN:H	2.22	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:472:THR:O	1:B:474:PRO:HD3	2.18	0.43
1:B:318:PRO:O	1:B:319:ASN:HB2	2.18	0.43
1:B:390:THR:HG22	1:B:392:SER:H	1.84	0.43
1:C:94:GLY:HA2	1:C:95:PRO:HD3	1.86	0.43
1:A:185:GLY:HA2	1:A:270:VAL:HG21	2.01	0.42
1:C:237:THR:O	1:C:240:ASP:HB2	2.19	0.42
1:A:487:TYR:HB3	1:B:405:GLN:HB3	2.01	0.42
1:A:380:GLU:OE1	1:A:380:GLU:HA	2.20	0.42
1:A:350:THR:O	1:A:352:VAL:N	2.51	0.42
1:B:51:ASP:O	1:B:55:ARG:HG3	2.19	0.42
1:B:112:ASP:HB2	1:B:115:GLU:CB	2.48	0.42
1:A:267:ARG:HH12	1:B:408:ILE:H	1.66	0.42
1:B:426:MET:HA	1:B:426:MET:HE3	2.00	0.42
1:C:69:SER:C	1:C:71:PHE:H	2.22	0.42
1:A:452:ARG:HA	1:A:452:ARG:HD3	1.88	0.42
1:A:487:TYR:HB3	1:B:405:GLN:CB	2.50	0.41
1:C:117:ARG:HA	1:C:120:TRP:HB3	2.02	0.41
1:A:151:THR:HG23	1:A:161:PRO:HB3	2.01	0.41
1:B:321:ASN:HD22	1:B:322:PRO:CD	2.31	0.41
1:C:221:ARG:O	1:C:225:ILE:HG12	2.19	0.41
1:C:140:HIS:O	1:C:144:ASN:ND2	2.54	0.41
1:C:302:ASP:HB2	1:C:303:PRO:HD3	2.02	0.41
1:A:305:ARG:NH2	1:A:469:GLU:HB2	2.35	0.41
1:C:451:ALA:HA	2:C:601:HOH:O	2.20	0.41
1:B:390:THR:HG21	1:B:458:PHE:CE1	2.56	0.41
1:A:340:ASP:O	1:A:343:VAL:N	2.54	0.41
1:B:240:ASP:HA	1:B:243:ARG:HG2	2.03	0.41
1:A:385:TYR:HB3	1:A:464:PHE:O	2.21	0.41
1:A:348:ARG:NH2	1:A:380:GLU:O	2.53	0.41
1:B:339:GLU:O	1:B:340:ASP:C	2.59	0.41
1:A:321:ASN:HB3	1:A:324:HIS:HB2	2.03	0.40

There are no symmetry-related clashes.

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	422/500 (84%)	375 (89%)	44 (10%)	3 (1%)	26	70
1	B	419/500 (84%)	368 (88%)	43 (10%)	8 (2%)	10	43
1	C	423/500 (85%)	357 (84%)	55 (13%)	11 (3%)	7	33
All	All	1264/1500 (84%)	1100 (87%)	142 (11%)	22 (2%)	11	46

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	351	LYS
1	B	101	ASP
1	A	72	ASP
1	A	245	SER
1	B	320	GLU
1	C	394	GLY
1	C	480	ASP
1	B	471	ALA
1	B	482	SER
1	C	101	ASP
1	C	125	ASN
1	C	150	ARG
1	B	319	ASN
1	B	403	SER
1	C	70	ALA
1	C	203	ASP
1	C	369	GLU
1	C	246	ARG
1	B	126	GLY
1	C	459	GLN
1	B	423	PRO
1	C	423	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	227/426 (53%)	205 (90%)	22 (10%)	10	37
1	B	199/426 (47%)	186 (94%)	13 (6%)	21	58
1	C	161/426 (38%)	154 (96%)	7 (4%)	35	75
All	All	587/1278 (46%)	545 (93%)	42 (7%)	18	53

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	MET
1	A	58	GLN
1	A	65	ARG
1	A	92	THR
1	A	106	ARG
1	A	112	ASP
1	A	128	ASP
1	A	130	THR
1	A	141	SER
1	A	174	ARG
1	A	255	ASP
1	A	267	ARG
1	A	293	ARG
1	A	302	ASP
1	A	309	ASN
1	A	324	HIS
1	A	348	ARG
1	A	389	ARG
1	A	390	THR
1	A	416	ARG
1	A	442	THR
1	A	473	SER
1	B	58	GLN
1	B	157	THR
1	B	170	SER
1	B	255	ASP
1	B	265	ILE
1	B	274	SER
1	B	343	VAL
1	B	373	THR
1	B	384	ARG
1	B	389	ARG
1	B	415	GLN
1	B	416	ARG

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Mol	Chain	Res	Type
1	B	452	ARG
1	C	72	ASP
1	C	130	THR
1	C	275	CYS
1	C	350	THR
1	C	389	ARG
1	C	416	ARG
1	C	454	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	GLN
1	A	272	HIS
1	A	289	HIS
1	A	308	GLN
1	A	324	HIS
1	A	334	HIS
1	A	415	GLN
1	B	142	ASN
1	B	211	ASN
1	B	235	GLN
1	B	241	GLN
1	B	289	HIS
1	B	308	GLN
1	B	309	ASN
1	B	321	ASN
1	B	370	ASN
1	B	415	GLN
1	C	140	HIS
1	C	168	GLN
1	C	334	HIS

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 [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, 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	432/500 (86%)	-0.37	2 (0%)	91 76	53, 74, 98, 104	0
1	B	429/500 (85%)	-0.37	1 (0%)	95 87	53, 81, 98, 103	0
1	C	433/500 (86%)	-0.27	4 (0%)	85 64	63, 97, 118, 124	2 (0%)
All	All	1294/1500 (86%)	-0.34	7 (0%)	91 76	53, 83, 109, 124	2 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	200	GLY	2.8
1	B	127	ASP	2.6
1	A	230	PHE	2.4
1	C	104	TRP	2.3
1	C	390	THR	2.3
1	C	404	GLY	2.2
1	C	101	ASP	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.