



# Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 04:26 AM GMT

PDB ID : 3W3Y  
Title : Crystal structure of Kap121p bound to Nup53p  
Authors : Kobayashi, J.; Matsuura, Y.  
Deposited on : 2012-12-28  
Resolution : 2.80 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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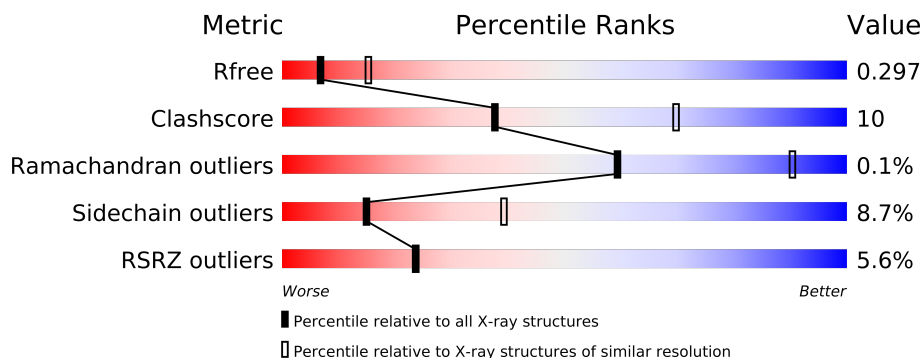
The following versions of software and data (see [references](#)) were used in the production of this report:

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 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))
$R_{free}$	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (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. 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	1078	
2	B	48	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7862 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 Importin subunit beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1026	7799	5011	1250	1501	37	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PRO	DELETION	UNP P32337
A	?	-	SER	DELETION	UNP P32337
A	?	-	SER	DELETION	UNP P32337
A	?	-	LYS	DELETION	UNP P32337
A	?	-	LEU	DELETION	UNP P32337
A	?	-	MET	DELETION	UNP P32337
A	?	-	ILE	DELETION	UNP P32337
A	?	-	MET	DELETION	UNP P32337
A	?	-	SER	DELETION	UNP P32337
A	?	-	LYS	DELETION	UNP P32337
A	?	-	ASN	DELETION	UNP P32337

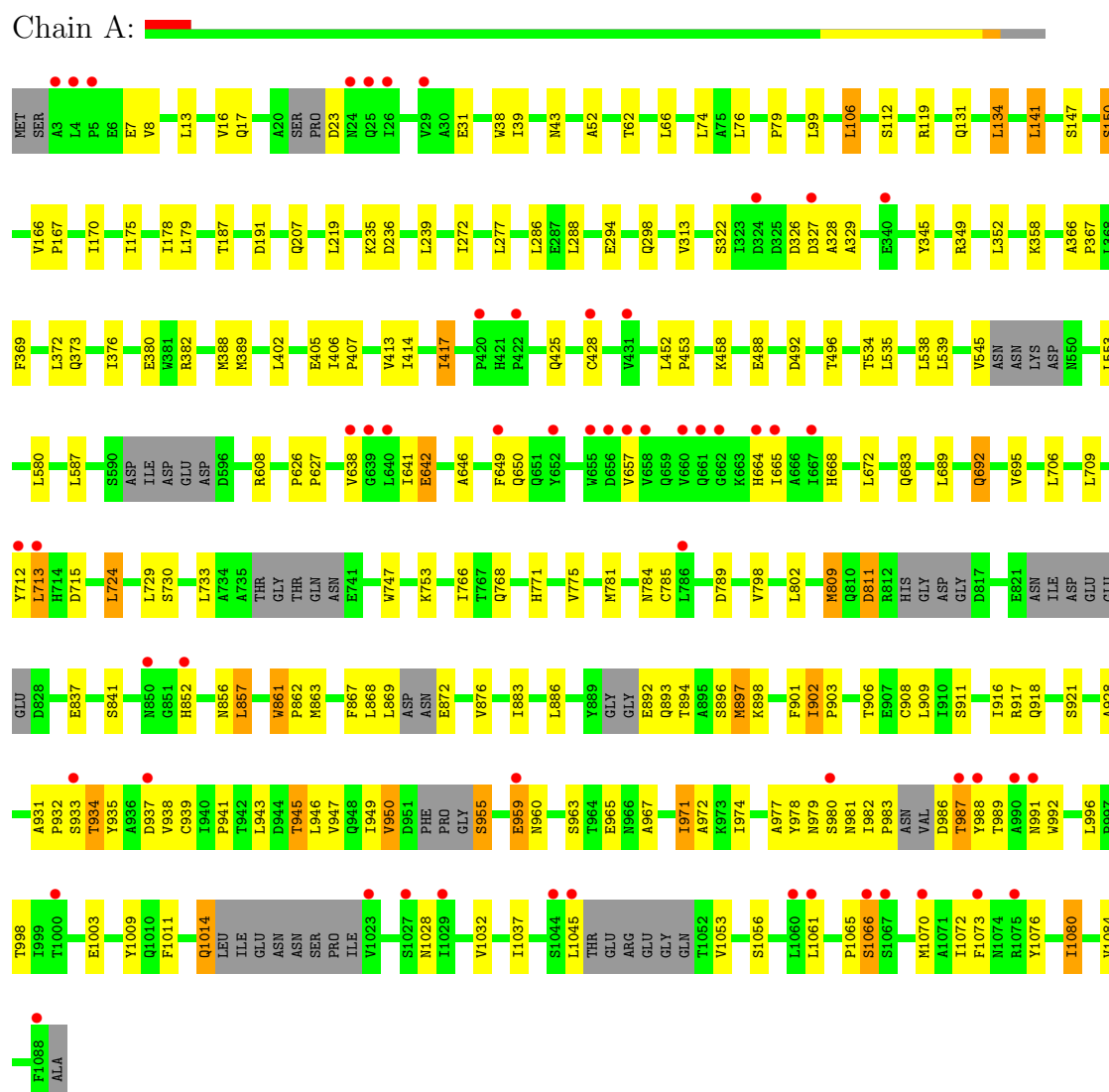
- Molecule 2 is a protein called Nucleoporin NUP53.

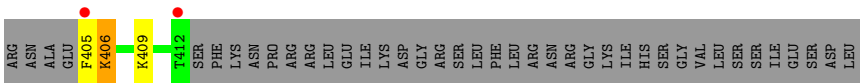
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	8	63	40	11	12	0	0	0

### 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: Importin subunit beta-3





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.33Å 131.44Å 131.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.33 – 2.80 30.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.5 (30.33-2.80) 94.7 (30.31-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.89 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.251 , 0.297 0.251 , 0.297	Depositor DCC
$R_{free}$ test set	1633 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	62.6	Xtriage
Anisotropy	0.628	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 34.5	EDS
Estimated twinning fraction	0.039 for -h,l,k	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	1 of 32279 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7862	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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	0.55	0/7935	0.76	4/10822 (0.0%)
2	B	0.68	0/63	1.20	0/82
All	All	0.55	0/7998	0.77	4/10904 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	646	ALA	CB-CA-C	-7.90	98.25	110.10
1	A	646	ALA	N-CA-C	7.75	131.93	111.00
1	A	724	LEU	CA-CB-CG	6.53	130.31	115.30
1	A	608	ARG	NE-CZ-NH1	-5.64	117.48	120.30

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	7799	0	7659	151	0
2	B	63	0	66	5	0
All	All	7862	0	7725	156	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 10.

All (156) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:405:PHE:HD1	2:B:406:LYS:HB2	1.09	1.13
1:A:406:ILE:HG23	1:A:407:PRO:HD3	1.13	1.11
1:A:892:GLU:HB3	1:A:934:THR:HG21	1.44	0.99
1:A:965:GLU:HG2	1:A:998:THR:HG23	1.44	0.99
1:A:902:ILE:N	1:A:903:PRO:HD2	1.78	0.97
2:B:405:PHE:CD1	2:B:406:LYS:HB2	2.00	0.96
1:A:638:VAL:HG23	1:A:665:ILE:CG2	1.97	0.93
1:A:406:ILE:CG2	1:A:407:PRO:HD3	2.00	0.90
1:A:892:GLU:CD	1:A:934:THR:HG22	1.96	0.86
1:A:534:THR:O	1:A:538:LEU:HD13	1.79	0.82
1:A:987:THR:HG23	1:A:991:ASN:HD21	1.44	0.82
1:A:894:THR:O	1:A:897:MET:HG3	1.80	0.81
1:A:414:ILE:O	1:A:417:ILE:HG22	1.82	0.79
1:A:892:GLU:CG	1:A:934:THR:CG2	2.61	0.79
1:A:988:TYR:HA	1:A:991:ASN:HD22	1.46	0.79
1:A:932:PRO:O	1:A:978:TYR:OH	2.00	0.78
1:A:406:ILE:HG23	1:A:407:PRO:CD	2.05	0.76
1:A:965:GLU:CG	1:A:998:THR:HG23	2.15	0.76
1:A:932:PRO:O	1:A:978:TYR:CE1	2.40	0.75
1:A:638:VAL:CG2	1:A:665:ILE:CG2	2.65	0.74
1:A:892:GLU:CG	1:A:934:THR:HG22	2.17	0.74
1:A:892:GLU:CB	1:A:934:THR:HG21	2.16	0.73
1:A:892:GLU:HG2	1:A:934:THR:CG2	2.18	0.73
1:A:892:GLU:HB3	1:A:934:THR:CG2	2.16	0.73
1:A:369:PHE:O	1:A:373:GLN:HG2	1.89	0.72
1:A:980:SER:C	1:A:981:ASN:HD22	1.93	0.72
1:A:650:GLN:HG2	1:A:657:VAL:HG22	1.71	0.71
1:A:641:ILE:HG23	1:A:664:HIS:HB3	1.71	0.71
1:A:902:ILE:N	1:A:903:PRO:CD	2.52	0.71
1:A:987:THR:HG23	1:A:991:ASN:ND2	2.04	0.71
1:A:946:LEU:HD13	1:A:971:ILE:HG22	1.72	0.71
2:B:405:PHE:HE1	2:B:406:LYS:HE2	1.56	0.69
1:A:946:LEU:CD1	1:A:971:ILE:HG22	2.22	0.69
1:A:638:VAL:HG23	1:A:665:ILE:HG22	1.74	0.69
1:A:987:THR:HG22	1:A:988:TYR:N	2.09	0.68
1:A:902:ILE:HG21	1:A:938:VAL:HG11	1.77	0.67
1:A:641:ILE:HG22	1:A:664:HIS:O	1.96	0.65
1:A:861:TRP:HE1	1:A:897:MET:HE1	1.61	0.65
1:A:16:VAL:HG23	1:A:66:LEU:HD12	1.79	0.65
1:A:1066:SER:O	1:A:1070:MET:HG2	1.96	0.65
1:A:937:ASP:O	1:A:941:PRO:HG2	1.97	0.64
1:A:131:GLN:HB3	1:A:134:LEU:HB2	1.80	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:893:GLN:HG2	1:A:893:GLN:O	1.98	0.63
1:A:892:GLU:CB	1:A:934:THR:CG2	2.76	0.61
1:A:861:TRP:HE1	1:A:897:MET:CE	2.12	0.61
1:A:492:ASP:O	1:A:496:THR:HG23	2.00	0.61
1:A:1080:ILE:HD12	1:A:1080:ILE:O	2.01	0.60
1:A:932:PRO:O	1:A:978:TYR:CZ	2.54	0.60
1:A:294:GLU:HG2	1:A:358:LYS:HE3	1.82	0.60
1:A:898:LYS:O	1:A:902:ILE:CG1	2.50	0.60
1:A:366:ALA:HB3	1:A:367:PRO:CD	2.32	0.59
1:A:987:THR:CG2	1:A:988:TYR:N	2.64	0.59
1:A:898:LYS:O	1:A:902:ILE:HG12	2.01	0.59
1:A:932:PRO:O	1:A:978:TYR:HE1	1.81	0.59
1:A:901:PHE:C	1:A:903:PRO:HD2	2.22	0.59
1:A:712:TYR:CD1	1:A:713:LEU:HD13	2.38	0.58
1:A:987:THR:CG2	1:A:991:ASN:HD21	2.15	0.58
1:A:971:ILE:HD11	1:A:992:TRP:HB2	1.86	0.58
1:A:638:VAL:CG2	1:A:665:ILE:HG23	2.34	0.58
1:A:715:ASP:HB2	1:A:766:ILE:HD11	1.86	0.58
1:A:191:ASP:OD2	1:A:235:LYS:HG2	2.05	0.57
1:A:945:THR:O	1:A:949:ILE:HG13	2.04	0.57
1:A:1028:ASN:O	1:A:1032:VAL:HG23	2.05	0.57
1:A:345:TYR:O	1:A:349:ARG:HG3	2.05	0.56
1:A:650:GLN:CG	1:A:657:VAL:HG22	2.35	0.56
1:A:7:GLU:HG2	1:A:8:VAL:H	1.70	0.56
1:A:170:ILE:HG23	1:A:178:ILE:HG12	1.87	0.56
1:A:980:SER:C	1:A:981:ASN:ND2	2.59	0.55
1:A:99:LEU:HD21	1:A:134:LEU:HG	1.89	0.54
1:A:695:VAL:O	1:A:695:VAL:HG22	2.08	0.53
1:A:932:PRO:HB3	1:A:977:ALA:HB1	1.90	0.53
1:A:861:TRP:NE1	1:A:897:MET:CE	2.73	0.52
1:A:893:GLN:CG	1:A:893:GLN:O	2.56	0.52
1:A:388:MET:SD	1:A:413:VAL:HG22	2.50	0.52
1:A:167:PRO:HG3	1:A:207:GLN:HG2	1.92	0.52
1:A:76:LEU:O	1:A:79:PRO:HB3	2.10	0.51
1:A:1061:LEU:HD21	1:A:1072:ILE:HD12	1.92	0.51
1:A:1009:TYR:HB3	1:A:1053:VAL:HG21	1.93	0.51
1:A:626:PRO:HB2	1:A:627:PRO:HD3	1.91	0.51
1:A:1003:GLU:H	1:A:1003:GLU:CD	2.14	0.51
1:A:892:GLU:OE1	1:A:933:SER:OG	2.26	0.50
1:A:902:ILE:CG2	1:A:938:VAL:HG11	2.41	0.50
1:A:417:ILE:HG13	1:A:458:LYS:HD3	1.94	0.50
1:A:1037:ILE:HD12	1:A:1084:VAL:HG22	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:911:SER:O	1:A:917:ARG:HD3	2.11	0.50
1:A:372:LEU:O	1:A:376:ILE:HG12	2.12	0.50
1:A:861:TRP:N	1:A:862:PRO:HD2	2.26	0.49
1:A:747:TRP:HE1	1:A:785:CYS:HB2	1.77	0.49
1:A:417:ILE:O	1:A:425:GLN:HG2	2.12	0.49
1:A:996:LEU:N	1:A:996:LEU:HD23	2.28	0.49
1:A:328:ALA:O	1:A:329:ALA:C	2.50	0.49
1:A:112:SER:O	1:A:119:ARG:NH2	2.45	0.48
1:A:906:THR:HA	1:A:909:LEU:HD12	1.96	0.48
1:A:747:TRP:CG	1:A:781:MET:HG3	2.49	0.47
1:A:939:CYS:HB3	1:A:974:ILE:HG12	1.95	0.47
1:A:327:ASP:O	1:A:328:ALA:HB3	2.15	0.47
1:A:934:THR:OG1	1:A:934:THR:O	2.31	0.47
1:A:775:VAL:HG22	1:A:841:SER:HA	1.95	0.46
1:A:322:SER:O	1:A:382:ARG:NH2	2.49	0.46
1:A:366:ALA:HB3	1:A:367:PRO:HD3	1.97	0.46
1:A:683:GLN:HB2	1:A:724:LEU:HD13	1.97	0.46
1:A:857:LEU:O	1:A:857:LEU:HD12	2.15	0.46
1:A:928:ALA:O	1:A:977:ALA:HB2	2.17	0.45
1:A:946:LEU:HD12	1:A:971:ILE:HG22	1.99	0.45
1:A:413:VAL:HG13	1:A:428:CYS:SG	2.57	0.45
1:A:898:LYS:O	1:A:902:ILE:HG13	2.17	0.45
1:A:798:VAL:O	1:A:802:LEU:HG	2.16	0.45
1:A:771:HIS:O	1:A:775:VAL:HG23	2.17	0.45
1:A:809:MET:C	1:A:811:ASP:H	2.19	0.45
1:A:13:LEU:O	1:A:17:GLN:HG3	2.17	0.44
1:A:933:SER:C	1:A:935:TYR:H	2.21	0.44
1:A:950:VAL:O	1:A:955:SER:OG	2.35	0.44
1:A:66:LEU:C	1:A:66:LEU:HD13	2.38	0.44
1:A:987:THR:HG22	1:A:988:TYR:H	1.81	0.44
1:A:965:GLU:CD	1:A:998:THR:HG23	2.39	0.43
1:A:417:ILE:CG1	1:A:458:LYS:HD3	2.48	0.43
1:A:972:ALA:HB1	1:A:1011:PHE:CD2	2.53	0.43
1:A:52:ALA:HB1	1:A:106:LEU:HD13	2.00	0.43
1:A:918:GLN:HB2	1:A:963:SER:OG	2.18	0.43
1:A:641:ILE:HG12	1:A:642:GLU:N	2.32	0.43
1:A:1011:PHE:HA	1:A:1014:GLN:HG3	2.00	0.43
1:A:272:ILE:HG21	1:A:313:VAL:HB	2.01	0.43
2:B:405:PHE:HD1	2:B:406:LYS:CB	2.02	0.43
1:A:638:VAL:HG23	1:A:665:ILE:HG23	1.89	0.43
1:A:13:LEU:HG	1:A:17:GLN:OE1	2.19	0.43
2:B:405:PHE:CD1	2:B:406:LYS:N	2.86	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:7:GLU:HG2	1:A:8:VAL:N	2.33	0.43
1:A:872:GLU:O	1:A:876:VAL:HG23	2.18	0.42
1:A:39:ILE:HG22	1:A:39:ILE:O	2.19	0.42
1:A:641:ILE:HG22	1:A:664:HIS:C	2.39	0.42
1:A:1073:PHE:HA	1:A:1076:TYR:CD2	2.54	0.42
1:A:141:LEU:HD12	1:A:141:LEU:HA	1.84	0.42
1:A:406:ILE:CG2	1:A:407:PRO:CD	2.82	0.42
1:A:892:GLU:HG2	1:A:934:THR:HG23	1.98	0.42
1:A:883:ILE:HA	1:A:886:LEU:HD12	2.02	0.42
1:A:959:GLU:OE1	1:A:959:GLU:N	2.53	0.42
1:A:959:GLU:CD	1:A:959:GLU:H	2.23	0.42
1:A:982:ILE:HA	1:A:983:PRO:HD2	1.92	0.42
1:A:863:MET:HE3	1:A:867:PHE:CE2	2.55	0.41
1:A:967:ALA:O	1:A:971:ILE:HG23	2.20	0.41
1:A:908:CYS:HB3	1:A:916:ILE:HG22	2.01	0.41
1:A:1076:TYR:CG	1:A:1080:ILE:HD11	2.55	0.41
1:A:768:GLN:HG3	1:A:837:GLU:HG3	2.02	0.41
1:A:931:ALA:HB1	1:A:934:THR:HG23	2.02	0.41
1:A:943:LEU:O	1:A:947:VAL:HG23	2.21	0.41
1:A:863:MET:CE	1:A:867:PHE:CE2	3.04	0.41
1:A:452:LEU:HB2	1:A:453:PRO:HD3	2.03	0.40
1:A:747:TRP:CD1	1:A:781:MET:HG3	2.56	0.40
1:A:147:SER:O	1:A:150:SER:HB3	2.21	0.40
1:A:709:LEU:HD12	1:A:753:LYS:HG2	2.04	0.40
1:A:38:TRP:CE3	1:A:43:ASN:HB3	2.56	0.40
1:A:692:GLN:HG2	1:A:692:GLN:H	1.63	0.40
1:A:175:ILE:HA	1:A:178:ILE:HG22	2.02	0.40
1:A:856:ASN:ND2	1:A:856:ASN:H	2.20	0.40
1:A:369:PHE:HE2	1:A:402:LEU:HD21	1.86	0.40
1:A:191:ASP:OD2	1:A:235:LYS:HE2	2.21	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	1000/1078 (93%)	955 (96%)	44 (4%)	1 (0%)	59	90
2	B	6/48 (12%)	5 (83%)	1 (17%)	0	100	100
All	All	1006/1126 (89%)	960 (95%)	45 (4%)	1 (0%)	59	90

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	852	HIS

### 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	834/937 (89%)	763 (92%)	71 (8%)	15	41
2	B	8/44 (18%)	6 (75%)	2 (25%)	1	2
All	All	842/981 (86%)	769 (91%)	73 (9%)	15	39

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASP
1	A	31	GLU
1	A	62	THR
1	A	74	LEU
1	A	106	LEU
1	A	134	LEU
1	A	141	LEU
1	A	150	SER
1	A	166	VAL
1	A	179	LEU
1	A	187	THR
1	A	219	LEU
1	A	236	ASP
1	A	239	LEU
1	A	277	LEU
1	A	286	LEU

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Mol	Chain	Res	Type
1	A	288	LEU
1	A	298	GLN
1	A	326	ASP
1	A	352	LEU
1	A	380	GLU
1	A	389	MET
1	A	405	GLU
1	A	417	ILE
1	A	488	GLU
1	A	535	LEU
1	A	539	LEU
1	A	545	VAL
1	A	553	LEU
1	A	580	LEU
1	A	587	LEU
1	A	642	GLU
1	A	649	PHE
1	A	668	HIS
1	A	672	LEU
1	A	689	LEU
1	A	692	GLN
1	A	706	LEU
1	A	713	LEU
1	A	729	LEU
1	A	730	SER
1	A	733	LEU
1	A	784	ASN
1	A	789	ASP
1	A	809	MET
1	A	811	ASP
1	A	857	LEU
1	A	861	TRP
1	A	868	LEU
1	A	869	LEU
1	A	896	SER
1	A	897	MET
1	A	902	ILE
1	A	921	SER
1	A	934	THR
1	A	945	THR
1	A	950	VAL
1	A	955	SER

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Mol	Chain	Res	Type
1	A	959	GLU
1	A	960	ASN
1	A	971	ILE
1	A	979	ASN
1	A	986	ASP
1	A	987	THR
1	A	989	THR
1	A	1014	GLN
1	A	1045	LEU
1	A	1056	SER
1	A	1065	PRO
1	A	1066	SER
1	A	1080	ILE
2	B	406	LYS
2	B	409	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	303	ASN
1	A	430	ASN
1	A	541	ASN
1	A	856	ASN
1	A	888	GLN
1	A	893	GLN
1	A	979	ASN
1	A	981	ASN
1	A	991	ASN

### 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	1026/1078 (95%)	0.12	56 (5%) 24 24	34, 81, 148, 204	0
2	B	8/48 (16%)	0.54	2 (25%) 1 1	47, 62, 89, 94	0
All	All	1034/1126 (91%)	0.13	58 (5%) 24 23	34, 81, 148, 204	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	639	GLY	5.9
1	A	638	VAL	5.7
1	A	786	LEU	5.5
1	A	652	TYR	5.0
1	A	4	LEU	4.5
1	A	1070	MET	4.5
1	A	649	PHE	4.4
1	A	987	THR	4.1
1	A	667	ILE	3.9
1	A	1000	THR	3.7
1	A	665	ILE	3.6
1	A	937	ASP	3.5
1	A	662	GLY	3.5
1	A	1023	VAL	3.3
1	A	660	VAL	3.2
1	A	1027	SER	3.2
1	A	661	GLN	3.1
1	A	26	ILE	3.1
1	A	1061	LEU	3.1
1	A	422	PRO	3.1
1	A	25	GLN	3.0
1	A	1066	SER	3.0
1	A	1088	PHE	3.0
1	A	656	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	655	TRP	3.0
1	A	1073	PHE	2.9
1	A	1060	LEU	2.9
1	A	988	TYR	2.8
1	A	1075	ARG	2.7
1	A	664	HIS	2.7
1	A	658	VAL	2.6
1	A	850	ASN	2.6
2	B	405	PHE	2.5
1	A	428	CYS	2.4
1	A	431	VAL	2.4
1	A	324	ASP	2.4
1	A	24	ASN	2.4
1	A	420	PRO	2.4
1	A	713	LEU	2.4
1	A	5	PRO	2.4
1	A	990	ALA	2.4
1	A	657	VAL	2.4
1	A	933	SER	2.4
1	A	959	GLU	2.4
1	A	3	ALA	2.4
1	A	1045	LEU	2.3
1	A	29	VAL	2.3
1	A	991	ASN	2.3
1	A	327	ASP	2.2
1	A	1067	SER	2.2
1	A	980	SER	2.2
1	A	340	GLU	2.2
1	A	640	LEU	2.1
1	A	712	TYR	2.1
1	A	1044	SER	2.1
2	B	412	THR	2.1
1	A	852	HIS	2.1
1	A	1029	ILE	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.