



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2023 – 06:39 AM EDT

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 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

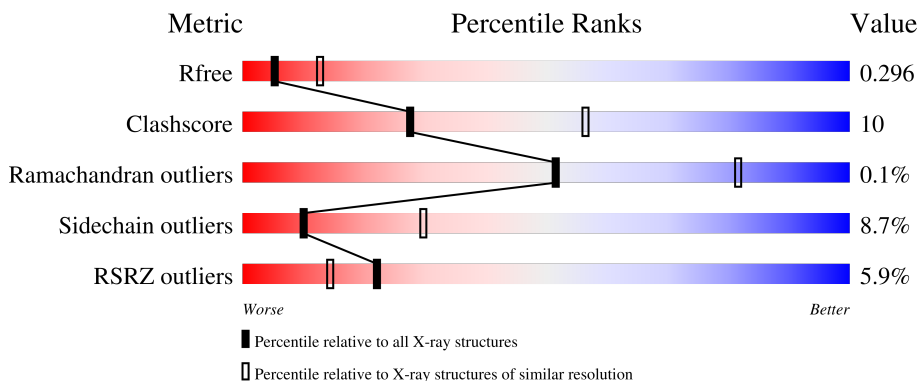
1 Overall quality at a glance i

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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	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 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 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

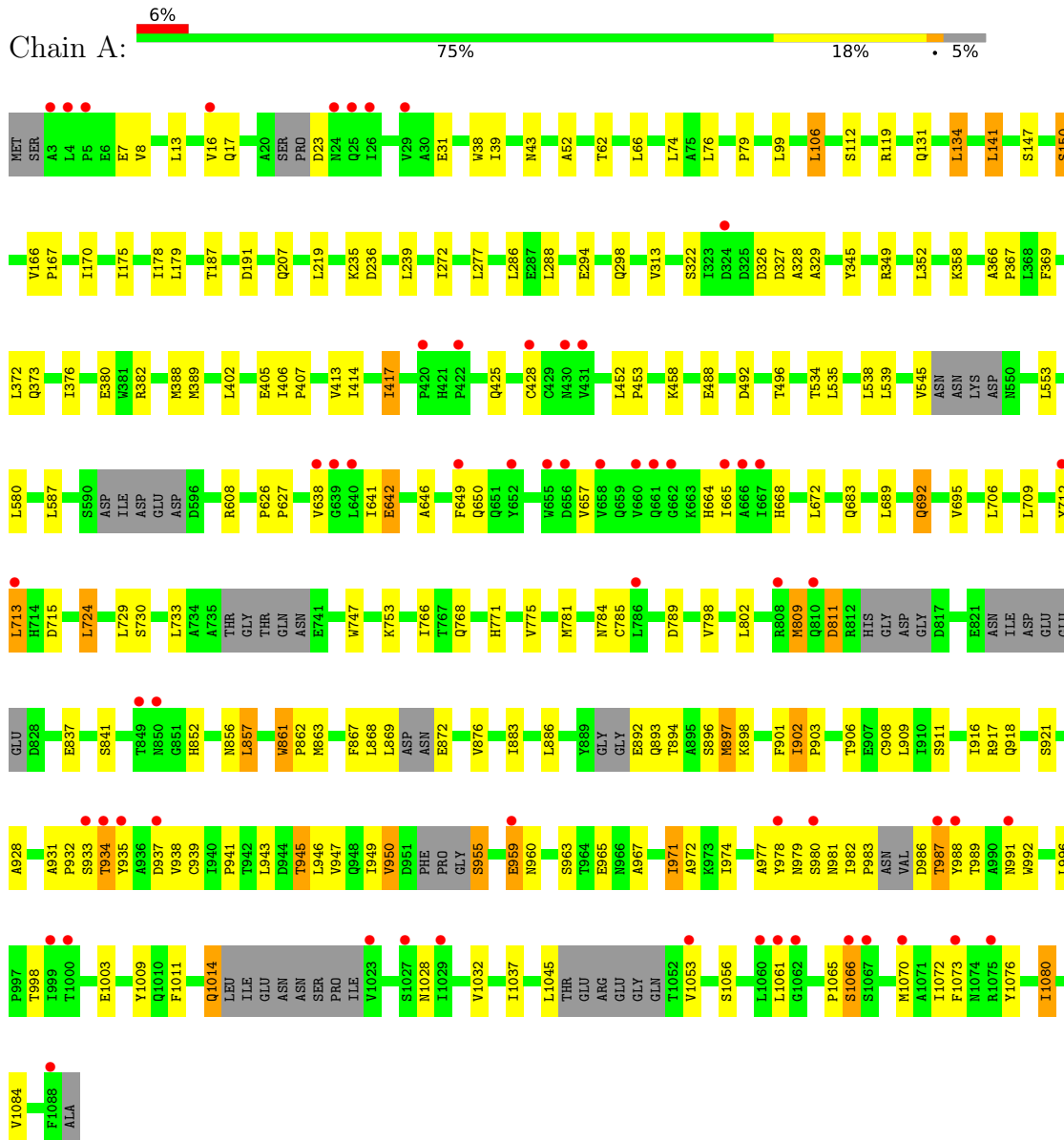
- Molecule 2 is a protein called Nucleoporin NUP53.

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

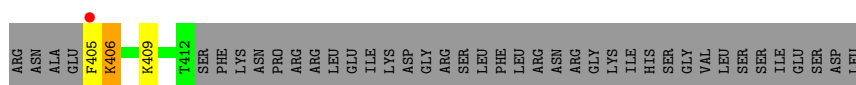
3 Residue-property plots i

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Importin subunit beta-3



- Molecule 2: Nucleoporin NUP53



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.251 , 0.297 0.249 , 0.296	Depositor DCC
R_{free} test set	1633 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	62.6	Xtrriage
Anisotropy	0.628	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 45.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.039 for -h,l,k	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7862	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtrriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [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	0.55	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 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	7799	0	7659	151	0
2	B	63	0	66	5	0
All	All	7862	0	7725	156	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 10.

All (156) 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)
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
1:A:946:LEU:CD1	1:A:971:ILE:HG22	2.22	0.69
2:B:405:PHE:HE1	2:B:406:LYS:HE2	1.56	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:GLN:HB3	1:A:134:LEU:HB2	1.80	0.63
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:492:ASP:O	1:A:496:THR:HG23	2.00	0.61
1:A:861:TRP:HE1	1:A:897:MET:CE	2.12	0.61
1:A:1080:ILE:O	1:A:1080:ILE:HD12	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:971:ILE:HD11	1:A:992:TRP:HB2	1.86	0.58
1:A:987:THR:CG2	1:A:991:ASN:HD21	2.15	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:7:GLU:HG2	1:A:8:VAL:H	1.70	0.56
1:A:650:GLN:CG	1:A:657:VAL:HG22	2.35	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:O	1:A:893:GLN:CG	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:417:ILE:HG13	1:A:458:LYS:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:902:ILE:CG2	1:A:938:VAL:HG11	2.41	0.50
1:A:1037:ILE:HD12	1:A:1084:VAL:HG22	1.93	0.50
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:O	1:A:934:THR:OG1	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:413:VAL:HG13	1:A:428:CYS:SG	2.57	0.45
1:A:946:LEU:HD12	1:A:971:ILE:HG22	1.99	0.45
1:A:798:VAL:O	1:A:802:LEU:HG	2.16	0.45
1:A:898:LYS:O	1:A:902:ILE:HG13	2.17	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:417:ILE:CG1	1:A:458:LYS:HD3	2.48	0.43
1:A:965:GLU:CD	1:A:998:THR:HG23	2.39	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:272:ILE:HG21	1:A:313:VAL:HB	2.01	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
2:B:405:PHE:HD1	2:B:406:LYS:CB	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:LEU:HG	1:A:17:GLN:OE1	2.19	0.43
1:A:638:VAL:HG23	1:A:665:ILE:HG23	1.89	0.43
1:A:7:GLU:HG2	1:A:8:VAL:N	2.33	0.43
2:B:405:PHE:CD1	2:B:406:LYS:N	2.86	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:141:LEU:HD12	1:A:141:LEU:HA	1.84	0.42
1:A:1073:PHE:HA	1:A:1076:TYR:CD2	2.54	0.42
1:A:406:ILE:CG2	1:A:407:PRO:CD	2.82	0.42
1:A:883:ILE:HA	1:A:886:LEU:HD12	2.02	0.42
1:A:892:GLU:HG2	1:A:934:THR:HG23	1.98	0.42
1:A:959:GLU:N	1:A:959:GLU:OE1	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:908:CYS:HB3	1:A:916:ILE:HG22	2.01	0.41
1:A:967:ALA:O	1:A:971:ILE:HG23	2.20	0.41
1:A:768:GLN:HG3	1:A:837:GLU:HG3	2.02	0.41
1:A:1076:TYR:CG	1:A:1080:ILE:HD11	2.55	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:38:TRP:CE3	1:A:43:ASN:HB3	2.56	0.40
1:A:147:SER:O	1:A:150:SER:HB3	2.21	0.40
1:A:692:GLN:H	1:A:692:GLN:HG2	1.63	0.40
1:A:709:LEU:HD12	1:A:753:LYS:HG2	2.04	0.40
1:A:747:TRP:CD1	1:A:781:MET:HG3	2.56	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:191:ASP:OD2	1:A:235:LYS:HE2	2.21	0.40
1:A:369:PHE:HE2	1:A:402:LEU:HD21	1.86	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	1000/1078 (93%)	955 (96%)	44 (4%)	1 (0%)	51	81
2	B	6/48 (12%)	5 (83%)	1 (17%)	0	100	100
All	All	1006/1126 (89%)	960 (95%)	45 (4%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	852	HIS

5.3.2 Protein sidechains [i](#)

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%)	10	31
2	B	8/44 (18%)	6 (75%)	2 (25%)	0	2
All	All	842/981 (86%)	769 (91%)	73 (9%)	10	30

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

Sometimes 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 [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 monosaccharides 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

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, 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	1026/1078 (95%)	0.11	60 (5%) 23 15	34, 81, 148, 204	0
2	B	8/48 (16%)	0.55	1 (12%) 3 2	47, 62, 89, 94	0
All	All	1034/1126 (91%)	0.11	61 (5%) 22 14	34, 81, 148, 204	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	639	GLY	6.2
1	A	638	VAL	5.1
1	A	652	TYR	4.9
1	A	4	LEU	4.7
1	A	786	LEU	4.4
1	A	1070	MET	4.2
1	A	649	PHE	4.1
1	A	987	THR	4.1
1	A	667	ILE	3.6
1	A	937	ASP	3.5
1	A	1066	SER	3.4
1	A	665	ILE	3.4
1	A	1060	LEU	3.3
1	A	1000	THR	3.3
1	A	933	SER	3.2
1	A	661	GLN	3.2
1	A	1023	VAL	3.2
1	A	1061	LEU	3.1
1	A	26	ILE	3.1
1	A	25	GLN	3.0
1	A	324	ASP	2.9
1	A	428	CYS	2.9
1	A	660	VAL	2.9
1	A	656	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	5	PRO	2.8
1	A	1027	SER	2.8
1	A	24	ASN	2.7
1	A	1062	GLY	2.7
1	A	662	GLY	2.6
1	A	713	LEU	2.6
1	A	431	VAL	2.6
1	A	658	VAL	2.5
1	A	934	THR	2.5
1	A	655	TRP	2.5
1	A	1029	ILE	2.5
1	A	988	TYR	2.5
1	A	978	TYR	2.4
1	A	1073	PHE	2.4
1	A	640	LEU	2.4
1	A	422	PRO	2.4
1	A	1088	PHE	2.4
1	A	991	ASN	2.3
1	A	1067	SER	2.3
1	A	1075	ARG	2.3
1	A	1053	VAL	2.3
1	A	959	GLU	2.3
1	A	980	SER	2.2
1	A	430	ASN	2.2
1	A	712	TYR	2.2
1	A	3	ALA	2.1
2	B	405	PHE	2.1
1	A	935	TYR	2.1
1	A	808	ARG	2.1
1	A	666	ALA	2.1
1	A	810	GLN	2.1
1	A	29	VAL	2.1
1	A	16	VAL	2.1
1	A	849	THR	2.1
1	A	999	ILE	2.0
1	A	420	PRO	2.0
1	A	850	ASN	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 [i](#)

There are no monosaccharides 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.