



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:07 PM UTC

PDB ID : 4ZJ7 / pdb_00004zj7
Title : Crystal structure of the karyopherin Kap121p bound to the extreme C-terminus of the protein phosphatase Cdc14p
Authors : Kobayashi, J.; Hirano, H.; Matsuura, Y.
Deposited on : 2015-04-29
Resolution : 2.40 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

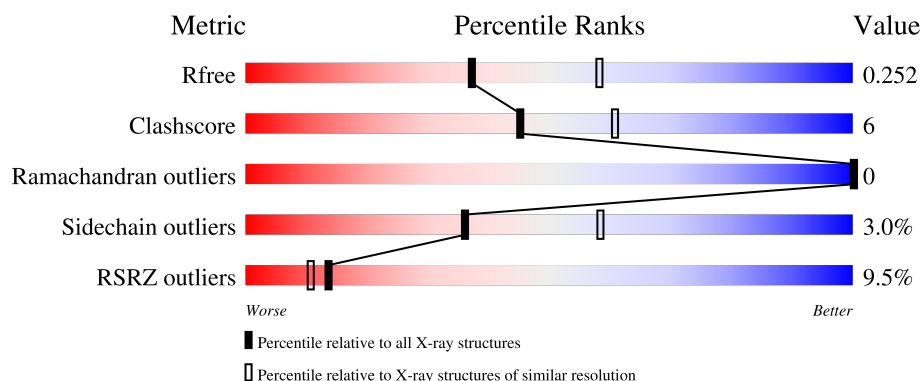
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	9% 80% 14% 6%
2	B	35	11% 86%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7947 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	1017	7775	4997	1248	1495	35	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 Tyrosine-protein phosphatase CDC14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	5	33	20	6	7	0	0	0

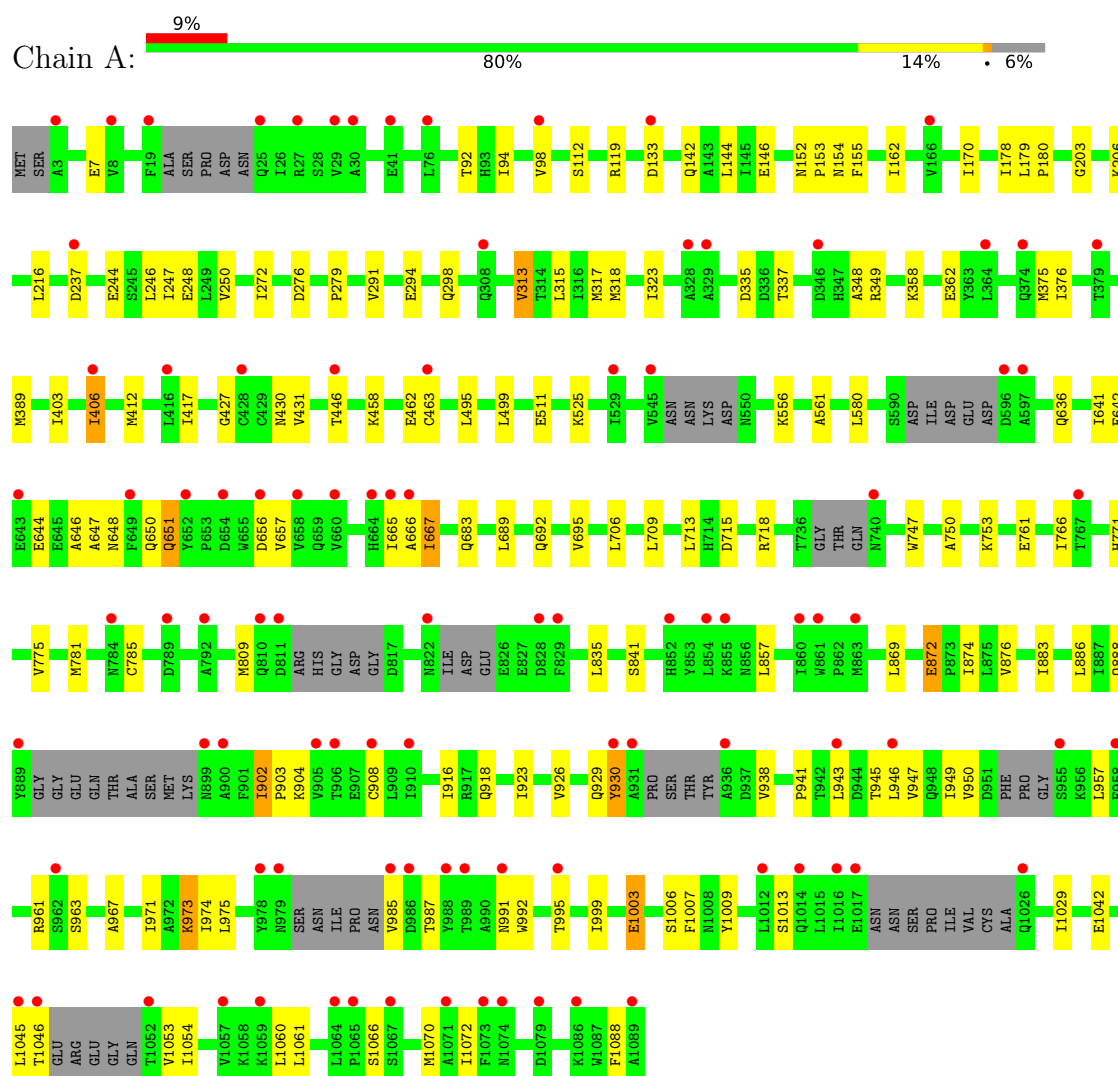
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	138	Total	O	0	0
			138	138		
3	B	1	Total	O	0	0
			1	1		

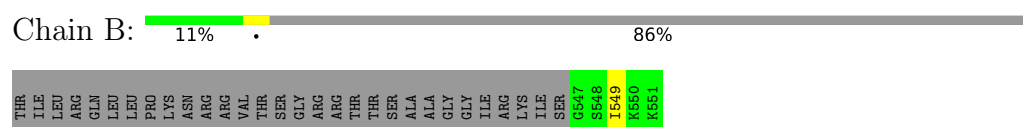
3 Residue-property plots

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: Tyrosine-protein phosphatase CDC14



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	77.26Å 127.76Å 131.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.81 – 2.40 25.81 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (25.81-2.40) 99.3 (25.81-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.219 , 0.252 0.224 , 0.252	Depositor DCC
R_{free} test set	2597 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7947	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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	0.32	0/7909	0.77	8/10774 (0.1%)
2	B	0.17	0/32	0.60	0/39
All	All	0.32	0/7941	0.77	8/10813 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	872	GLU	CA-C-N	7.58	127.12	119.24
1	A	872	GLU	C-N-CA	7.58	127.12	119.24
1	A	406	ILE	CA-C-N	-6.14	112.16	119.84
1	A	406	ILE	C-N-CA	-6.14	112.16	119.84
1	A	525	LYS	CB-CA-C	-5.49	110.26	116.63
1	A	279	PRO	N-CA-C	5.47	117.37	110.70
1	A	902	ILE	CB-CA-C	-5.35	108.68	114.35
1	A	276	ASP	N-CA-C	-5.12	107.09	113.38

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	7775	0	7668	91	0
2	B	33	0	33	1	0
3	A	138	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
All	All	7947	0	7701	91	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 6.

All (91) 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:929:GLN:HG3	1:A:973:LYS:HD2	1.38	1.03
1:A:1009:TYR:HB3	1:A:1053:VAL:HG21	1.60	0.81
1:A:417:ILE:O	1:A:458:LYS:NZ	2.12	0.80
1:A:636:GLN:HE22	1:A:713:LEU:HB2	1.57	0.69
1:A:406:ILE:O	3:A:1101:HOH:O	2.12	0.67
1:A:206:LYS:NZ	1:A:248:GLU:OE2	2.28	0.66
1:A:946:LEU:HD23	1:A:949:ILE:HD12	1.79	0.64
1:A:430:ASN:HA	2:B:549:ILE:HD13	1.79	0.64
1:A:648:ASN:O	1:A:651:GLN:NE2	2.28	0.61
1:A:973:LYS:HE2	1:A:1007:PHE:CD2	2.36	0.59
1:A:683:GLN:NE2	3:A:1110:HOH:O	2.34	0.59
1:A:389:MET:HE1	1:A:430:ASN:HB3	1.86	0.57
1:A:992:TRP:O	1:A:995:THR:HG22	2.04	0.57
1:A:1066:SER:O	1:A:1070:MET:HG2	2.04	0.57
1:A:973:LYS:HE2	1:A:1007:PHE:CE2	2.40	0.56
1:A:706:LEU:HD21	1:A:750:ALA:HA	1.87	0.56
1:A:929:GLN:HG3	1:A:973:LYS:CD	2.25	0.56
1:A:689:LEU:HB3	1:A:692:GLN:HB2	1.87	0.56
1:A:315:LEU:HB3	1:A:375:MET:HE1	1.88	0.55
1:A:335:ASP:HB3	1:A:337:THR:H	1.72	0.54
1:A:1061:LEU:HD21	1:A:1072:ILE:HD12	1.89	0.54
1:A:142:GLN:O	1:A:146:GLU:HG3	2.09	0.53
1:A:947:VAL:HG13	1:A:991:ASN:HD21	1.73	0.53
1:A:872:GLU:O	1:A:876:VAL:HG23	2.09	0.53
1:A:943:LEU:HD22	1:A:974:ILE:HG21	1.90	0.53
1:A:857:LEU:HD23	1:A:886:LEU:HD21	1.90	0.53
1:A:747:TRP:HE1	1:A:785:CYS:HB2	1.74	0.53
1:A:883:ILE:HA	1:A:886:LEU:HD12	1.91	0.53
1:A:112:SER:O	1:A:119:ARG:NH2	2.42	0.52
1:A:709:LEU:HD12	1:A:753:LYS:HG2	1.92	0.52
1:A:92:THR:OG1	1:A:133:ASP:OD2	2.28	0.51
1:A:294:GLU:HG2	1:A:358:LYS:HE3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:561:ALA:HB1	1:A:580:LEU:HD21	1.92	0.51
1:A:1013:SER:HB2	1:A:1053:VAL:HG13	1.92	0.50
1:A:318:MET:HE2	1:A:349:ARG:HA	1.94	0.50
1:A:244:GLU:HA	1:A:247:ILE:HD12	1.94	0.50
1:A:646:ALA:C	1:A:648:ASN:H	2.18	0.50
1:A:417:ILE:HG13	1:A:458:LYS:NZ	2.27	0.49
1:A:144:LEU:HD21	1:A:162:ILE:HD12	1.93	0.49
1:A:170:ILE:HG21	1:A:216:LEU:HD11	1.95	0.49
1:A:376:ILE:HD13	1:A:412:MET:HB3	1.93	0.48
1:A:641:ILE:HD12	1:A:666:ALA:HB2	1.95	0.48
1:A:908:CYS:HB3	1:A:916:ILE:HG22	1.95	0.48
1:A:1006:SER:HA	1:A:1045:LEU:HD12	1.94	0.48
1:A:747:TRP:CG	1:A:781:MET:HG3	2.49	0.48
1:A:417:ILE:HG13	1:A:458:LYS:HZ2	1.79	0.48
1:A:835:LEU:HD12	1:A:874:ILE:HG22	1.96	0.47
1:A:902:ILE:N	1:A:903:PRO:HD2	2.29	0.47
1:A:646:ALA:C	1:A:648:ASN:N	2.73	0.47
1:A:888:GLN:HA	1:A:930:TYR:CE1	2.50	0.47
1:A:170:ILE:HG23	1:A:178:ILE:HG12	1.97	0.46
1:A:999:ILE:HB	1:A:1042:GLU:HG2	1.97	0.46
1:A:657:VAL:HG12	1:A:666:ALA:HA	1.98	0.46
1:A:1003:GLU:H	1:A:1003:GLU:CD	2.23	0.45
1:A:650:GLN:OE1	1:A:656:ASP:HA	2.16	0.45
1:A:641:ILE:HG12	1:A:642:GLU:H	1.82	0.45
1:A:718:ARG:NH1	1:A:761:GLU:OE2	2.50	0.45
1:A:647:ALA:HA	1:A:650:GLN:HB2	1.97	0.44
1:A:715:ASP:HB2	1:A:766:ILE:HD11	1.98	0.44
1:A:152:ASN:HD22	1:A:155:PHE:HD2	1.66	0.44
1:A:945:THR:O	1:A:949:ILE:HG13	2.18	0.44
1:A:246:LEU:O	1:A:250:VAL:HG23	2.18	0.44
1:A:775:VAL:HG22	1:A:841:SER:HA	2.00	0.43
1:A:918:GLN:HB2	1:A:963:SER:HA	2.00	0.43
1:A:152:ASN:HA	1:A:153:PRO:HD2	1.86	0.43
1:A:389:MET:HE3	1:A:427:GLY:HA2	2.00	0.43
1:A:179:LEU:HB2	1:A:180:PRO:HD3	2.01	0.42
1:A:272:ILE:HG21	1:A:313:VAL:HG13	2.01	0.42
1:A:938:VAL:C	1:A:941:PRO:HD2	2.44	0.42
1:A:119:ARG:HD2	1:A:154:ASN:OD1	2.20	0.42
1:A:771:HIS:O	1:A:775:VAL:HG23	2.20	0.42
1:A:946:LEU:HB2	1:A:971:ILE:HD11	2.01	0.42
1:A:1060:LEU:HD12	1:A:1060:LEU:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:GLU:HB3	1:A:556:LYS:HD2	2.02	0.42
1:A:967:ALA:O	1:A:971:ILE:HG12	2.20	0.42
1:A:869:LEU:HD23	1:A:904:LYS:HG2	2.01	0.42
1:A:1054:ILE:HG23	1:A:1088:PHE:CD2	2.55	0.42
1:A:203:GLY:HA2	1:A:206:LYS:HG2	2.02	0.42
1:A:923:ILE:O	1:A:926:VAL:HG12	2.21	0.41
1:A:237:ASP:OD1	1:A:237:ASP:N	2.53	0.41
1:A:349:ARG:NH1	3:A:1115:HOH:O	2.37	0.41
1:A:1070:MET:HE2	1:A:1070:MET:HB3	1.81	0.41
1:A:298:GLN:H	1:A:298:GLN:HG3	1.73	0.41
1:A:458:LYS:HD2	1:A:463:CYS:SG	2.61	0.41
1:A:667:ILE:HG21	1:A:713:LEU:HD13	2.02	0.41
1:A:317:MET:HB2	1:A:348:ALA:HB2	2.03	0.41
1:A:874:ILE:HD12	1:A:874:ILE:H	1.86	0.41
1:A:957:LEU:O	1:A:961:ARG:N	2.54	0.41
1:A:133:ASP:OD1	1:A:133:ASP:N	2.54	0.40
1:A:971:ILE:HG22	1:A:975:LEU:HD12	2.04	0.40
1:A:495:LEU:O	1:A:499:LEU:HG	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	991/1078 (92%)	952 (96%)	39 (4%)	0	100	100
2	B	3/35 (9%)	3 (100%)	0	0	100	100
All	All	994/1113 (89%)	955 (96%)	39 (4%)	0	100	100

There are no Ramachandran outliers to report.

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%)	809 (97%)	25 (3%)	36	58
2	B	3/29 (10%)	3 (100%)	0	100	100
All	All	837/966 (87%)	812 (97%)	25 (3%)	36	58

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	94	ILE
1	A	98	VAL
1	A	291	VAL
1	A	313	VAL
1	A	323	ILE
1	A	362	GLU
1	A	403	ILE
1	A	431	VAL
1	A	446	THR
1	A	462	GLU
1	A	644	GLU
1	A	651	GLN
1	A	665	ILE
1	A	667	ILE
1	A	695	VAL
1	A	809	MET
1	A	930	TYR
1	A	950	VAL
1	A	973	LYS
1	A	985	VAL
1	A	987	THR
1	A	1003	GLU
1	A	1029	ILE
1	A	1046	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	503	GLN
1	A	636	GLN
1	A	668	HIS
1	A	772	ASN
1	A	801	ASN
1	A	918	GLN
1	A	966	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 oligosaccharides 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	1017/1078 (94%)	0.52	97 (9%) 14 11	26, 62, 118, 139	0
2	B	5/35 (14%)	0.35	0 100 100	34, 42, 54, 58	0
All	All	1022/1113 (91%)	0.51	97 (9%) 14 11	26, 61, 117, 139	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	931	ALA	5.5
1	A	930	TYR	5.2
1	A	596	ASP	5.0
1	A	1046	THR	4.8
1	A	1089	ALA	4.7
1	A	1073	PHE	4.7
1	A	784	ASN	4.6
1	A	810	GLN	4.6
1	A	979	ASN	4.4
1	A	899	ASN	4.3
1	A	1016	ILE	4.2
1	A	98	VAL	4.1
1	A	861	TRP	4.0
1	A	985	VAL	3.9
1	A	946	LEU	3.9
1	A	545	VAL	3.9
1	A	789	ASP	3.7
1	A	1052	THR	3.6
1	A	989	THR	3.6
1	A	29	VAL	3.5
1	A	597	ALA	3.5
1	A	664	HIS	3.5
1	A	1017	GLU	3.4
1	A	955	SER	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	1026	GLN	3.4
1	A	811	ASP	3.3
1	A	652	TYR	3.2
1	A	1057	VAL	3.2
1	A	936	ALA	3.2
1	A	978	TYR	3.1
1	A	27	ARG	3.1
1	A	25	GLN	3.1
1	A	910	ILE	3.1
1	A	906	THR	3.0
1	A	988	TYR	3.0
1	A	1079	ASP	3.0
1	A	665	ILE	2.9
1	A	364	LEU	2.9
1	A	995	THR	2.9
1	A	649	PHE	2.9
1	A	822	ASN	2.9
1	A	1071	ALA	2.9
1	A	133	ASP	2.8
1	A	860	ILE	2.8
1	A	463	CYS	2.8
1	A	1014	GLN	2.8
1	A	379	THR	2.7
1	A	406	ILE	2.7
1	A	900	ALA	2.7
1	A	76	LEU	2.6
1	A	166	VAL	2.6
1	A	346	ASP	2.6
1	A	986	ASP	2.6
1	A	19	PHE	2.6
1	A	991	ASN	2.5
1	A	328	ALA	2.5
1	A	855	LYS	2.5
1	A	3	ALA	2.5
1	A	852	HIS	2.5
1	A	1074	ASN	2.5
1	A	1059	LYS	2.4
1	A	658	VAL	2.4
1	A	829	PHE	2.4
1	A	666	ALA	2.4
1	A	237	ASP	2.3
1	A	854	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	41	GLU	2.3
1	A	792	ALA	2.3
1	A	643	GLU	2.3
1	A	1064	LEU	2.3
1	A	958	GLU	2.3
1	A	308	GLN	2.2
1	A	654	ASP	2.2
1	A	656	ASP	2.2
1	A	828	ASP	2.2
1	A	1045	LEU	2.2
1	A	905	VAL	2.2
1	A	740	ASN	2.2
1	A	374	GLN	2.2
1	A	908	CYS	2.2
1	A	962	SER	2.2
1	A	30	ALA	2.1
1	A	428	CYS	2.1
1	A	329	ALA	2.1
1	A	943	LEU	2.1
1	A	767	THR	2.1
1	A	1086	LYS	2.1
1	A	1065	PRO	2.1
1	A	660	VAL	2.1
1	A	416	LEU	2.0
1	A	1012	LEU	2.0
1	A	446	THR	2.0
1	A	529	ILE	2.0
1	A	889	TYR	2.0
1	A	863	MET	2.0
1	A	1067	SER	2.0
1	A	8	VAL	2.0

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 oligosaccharides 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.