



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:14 AM UTC

PDB ID : 1XIQ / pdb_00001xiq
Title : Plasmodium falciparum Nucleoside diphosphate kinase B
Authors : Robien, M.A.; Bosch, J.; Hol, W.G.J.; Structural Genomics of Pathogenic Protozoa Consortium (SGPP)
Deposited on : 2004-09-21
Resolution : 3.05 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:

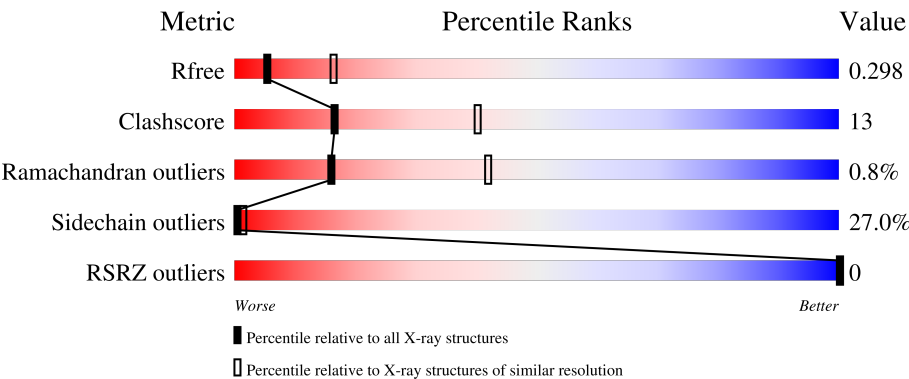
MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	157	57%33% • • 5%
1	B	157	51%35%9%5%
1	C	157	54%32%8%5%
1	D	157	57%31%7%5%
1	E	157	48%36%10%5%

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Mol	Chain	Length	Quality of chain
1	F	157	55% 31% 8% • 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7164 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 Nucleoside diphosphate kinase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	149	Total	C	N	O	S	0	0	0
			1194	769	202	215	8			
1	B	149	Total	C	N	O	S	0	0	0
			1194	769	202	215	8			
1	C	149	Total	C	N	O	S	0	0	0
			1194	769	202	215	8			
1	D	149	Total	C	N	O	S	0	0	0
			1194	769	202	215	8			
1	E	149	Total	C	N	O	S	0	0	0
			1194	769	202	215	8			
1	F	149	Total	C	N	O	S	0	0	0
			1194	769	202	215	8			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP Q8ID43
A	-6	ALA	-	expression tag	UNP Q8ID43
A	-5	HIS	-	expression tag	UNP Q8ID43
A	-4	HIS	-	expression tag	UNP Q8ID43
A	-3	HIS	-	expression tag	UNP Q8ID43
A	-2	HIS	-	expression tag	UNP Q8ID43
A	-1	HIS	-	expression tag	UNP Q8ID43
A	0	HIS	-	expression tag	UNP Q8ID43
B	-7	MET	-	expression tag	UNP Q8ID43
B	-6	ALA	-	expression tag	UNP Q8ID43
B	-5	HIS	-	expression tag	UNP Q8ID43
B	-4	HIS	-	expression tag	UNP Q8ID43
B	-3	HIS	-	expression tag	UNP Q8ID43
B	-2	HIS	-	expression tag	UNP Q8ID43
B	-1	HIS	-	expression tag	UNP Q8ID43
B	0	HIS	-	expression tag	UNP Q8ID43
C	-7	MET	-	expression tag	UNP Q8ID43

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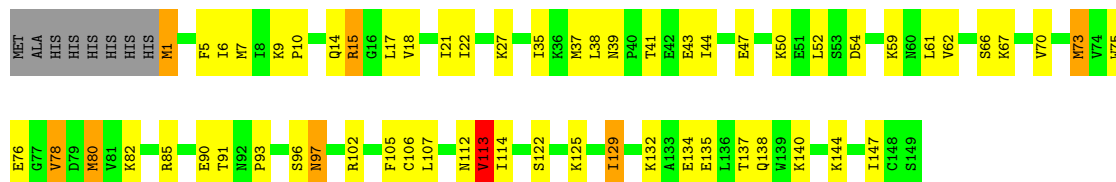
Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	ALA	-	expression tag	UNP Q8ID43
C	-5	HIS	-	expression tag	UNP Q8ID43
C	-4	HIS	-	expression tag	UNP Q8ID43
C	-3	HIS	-	expression tag	UNP Q8ID43
C	-2	HIS	-	expression tag	UNP Q8ID43
C	-1	HIS	-	expression tag	UNP Q8ID43
C	0	HIS	-	expression tag	UNP Q8ID43
D	-7	MET	-	expression tag	UNP Q8ID43
D	-6	ALA	-	expression tag	UNP Q8ID43
D	-5	HIS	-	expression tag	UNP Q8ID43
D	-4	HIS	-	expression tag	UNP Q8ID43
D	-3	HIS	-	expression tag	UNP Q8ID43
D	-2	HIS	-	expression tag	UNP Q8ID43
D	-1	HIS	-	expression tag	UNP Q8ID43
D	0	HIS	-	expression tag	UNP Q8ID43
E	-7	MET	-	expression tag	UNP Q8ID43
E	-6	ALA	-	expression tag	UNP Q8ID43
E	-5	HIS	-	expression tag	UNP Q8ID43
E	-4	HIS	-	expression tag	UNP Q8ID43
E	-3	HIS	-	expression tag	UNP Q8ID43
E	-2	HIS	-	expression tag	UNP Q8ID43
E	-1	HIS	-	expression tag	UNP Q8ID43
E	0	HIS	-	expression tag	UNP Q8ID43
F	-7	MET	-	expression tag	UNP Q8ID43
F	-6	ALA	-	expression tag	UNP Q8ID43
F	-5	HIS	-	expression tag	UNP Q8ID43
F	-4	HIS	-	expression tag	UNP Q8ID43
F	-3	HIS	-	expression tag	UNP Q8ID43
F	-2	HIS	-	expression tag	UNP Q8ID43
F	-1	HIS	-	expression tag	UNP Q8ID43
F	0	HIS	-	expression tag	UNP Q8ID43

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.

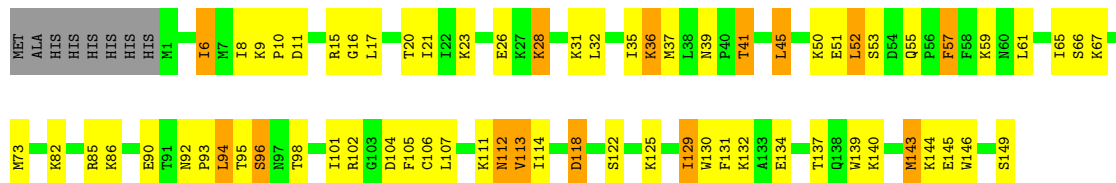
• Molecule 1: Nucleoside diphosphate kinase B

Chain A: 



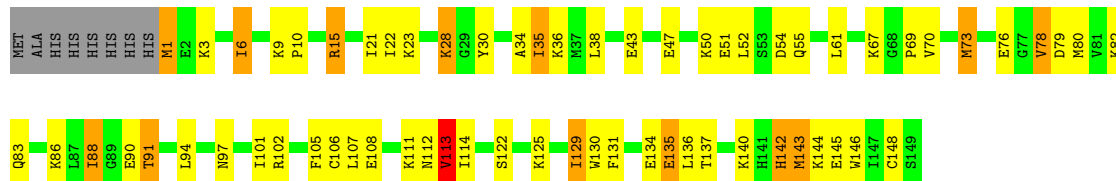
• Molecule 1: Nucleoside diphosphate kinase B

Chain B: 



• Molecule 1: Nucleoside diphosphate kinase B

Chain C: 



• Molecule 1: Nucleoside diphosphate kinase B

Chain D: 





• Molecule 1: Nucleoside diphosphate kinase B



• Molecule 1: Nucleoside diphosphate kinase B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.59Å 112.42Å 68.59Å 90.00° 119.05° 90.00°	Depositor
Resolution (Å)	52.70 – 3.05 52.70 – 3.05	Depositor EDS
% Data completeness (in resolution range)	99.5 (52.70-3.05) 99.4 (52.70-3.05)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.229 , 0.286 0.239 , 0.298	Depositor DCC
R_{free} test set	876 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	69.2	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.011 for -h-l,k,h 0.011 for l,k,-h-l 0.026 for h,-k,-h-l 0.023 for -h-l,-k,l 0.448 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7164	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.46% 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	0.62	2/1219 (0.2%)	0.93	1/1638 (0.1%)
1	B	0.57	0/1219	0.91	0/1638
1	C	0.58	0/1219	0.87	0/1638
1	D	0.57	0/1219	0.90	0/1638
1	E	0.55	0/1219	0.90	1/1638 (0.1%)
1	F	0.62	2/1219 (0.2%)	0.91	0/1638
All	All	0.59	4/7314 (0.1%)	0.90	2/9828 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	73	MET	SD-CE	-5.79	1.65	1.79
1	F	73	MET	SD-CE	-5.76	1.65	1.79
1	A	1	MET	SD-CE	5.09	1.92	1.79
1	F	7	MET	SD-CE	-5.06	1.67	1.79

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	78	VAL	CB-CA-C	-5.20	103.50	111.71
1	E	113	VAL	N-CA-C	5.10	119.95	109.34

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	1194	0	1228	36	0
1	B	1194	0	1228	49	0
1	C	1194	0	1228	39	0
1	D	1194	0	1228	30	0
1	E	1194	0	1228	47	0
1	F	1194	0	1228	32	0
All	All	7164	0	7368	188	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 13.

All (188) 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:75:TRP:HB3	1:A:80:MET:HE3	1.34	1.05
1:A:15:ARG:HH11	1:A:15:ARG:HG2	1.17	1.04
1:A:75:TRP:CB	1:A:80:MET:HE3	1.90	1.01
1:D:15:ARG:HH11	1:D:15:ARG:HG2	1.26	0.99
1:E:75:TRP:HB3	1:E:80:MET:HE3	1.46	0.97
1:E:75:TRP:CB	1:E:80:MET:HE3	1.97	0.95
1:B:102:ARG:HD3	1:B:112:ASN:HB2	1.47	0.93
1:C:15:ARG:HG2	1:C:15:ARG:HH11	1.33	0.93
1:A:75:TRP:HB3	1:A:80:MET:CE	1.98	0.93
1:E:75:TRP:HB3	1:E:80:MET:CE	2.00	0.90
1:D:102:ARG:HD3	1:D:112:ASN:HB2	1.57	0.85
1:C:143:MET:SD	1:E:143:MET:HE2	2.24	0.78
1:E:3:LYS:HD2	1:E:76:GLU:HG3	1.65	0.76
1:E:102:ARG:HD3	1:E:112:ASN:HB2	1.67	0.76
1:C:102:ARG:HD3	1:C:112:ASN:HB2	1.69	0.74
1:A:106:CYS:SG	1:A:113:VAL:HG13	2.28	0.74
1:A:15:ARG:HG2	1:A:15:ARG:NH1	1.95	0.73
1:B:125:LYS:O	1:B:129:ILE:HG23	1.89	0.73
1:C:22:ILE:HG12	1:C:73:MET:CE	2.21	0.70
1:C:15:ARG:HG2	1:C:15:ARG:NH1	2.04	0.69
1:F:44:ILE:HA	1:F:129:ILE:HD11	1.76	0.67
1:C:22:ILE:HG12	1:C:73:MET:HE1	1.74	0.67
1:B:11:ASP:HB2	1:C:146:TRP:O	1.95	0.67
1:C:3:LYS:HG3	1:C:76:GLU:HG3	1.76	0.66
1:F:125:LYS:O	1:F:129:ILE:HG22	1.95	0.66
1:A:44:ILE:HA	1:A:129:ILE:HD11	1.79	0.65
1:B:31:LYS:HG3	1:B:139:TRP:CZ2	2.32	0.65
1:A:75:TRP:HB2	1:A:80:MET:HE3	1.77	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:ILE:HG23	1:B:114:ILE:HD11	1.78	0.64
1:A:73:MET:HE2	1:A:75:TRP:HE1	1.61	0.64
1:D:15:ARG:NH2	1:D:105:PHE:O	2.30	0.64
1:A:125:LYS:O	1:A:129:ILE:HG22	1.97	0.63
1:B:32:LEU:HD23	1:E:37:MET:HE3	1.78	0.63
1:E:88:ILE:HG12	1:E:114:ILE:HG21	1.81	0.63
1:A:15:ARG:NH2	1:A:105:PHE:O	2.31	0.63
1:D:9:LYS:HB3	1:D:10:PRO:HD2	1.80	0.62
1:C:15:ARG:NH2	1:C:105:PHE:O	2.32	0.62
1:E:75:TRP:HB2	1:E:80:MET:HE3	1.81	0.62
1:B:21:ILE:HG12	1:B:101:ILE:HD13	1.82	0.61
1:D:15:ARG:HG2	1:D:15:ARG:NH1	2.01	0.61
1:B:94:LEU:HD13	1:C:79:ASP:OD2	2.00	0.60
1:B:145:GLU:OE2	1:F:142:HIS:CE1	2.54	0.60
1:B:15:ARG:NH2	1:B:105:PHE:O	2.30	0.59
1:A:38:LEU:HA	1:F:137:THR:HG21	1.85	0.59
1:D:11:ASP:HB2	1:E:146:TRP:O	2.03	0.58
1:E:75:TRP:CB	1:E:80:MET:CE	2.71	0.57
1:B:9:LYS:HB3	1:B:10:PRO:HD2	1.85	0.57
1:C:35:ILE:HD12	1:C:73:MET:HG2	1.84	0.57
1:D:40:PRO:HG2	1:D:66:SER:HA	1.85	0.57
1:A:93:PRO:HA	1:A:96:SER:OG	2.05	0.57
1:A:137:THR:HG21	1:F:38:LEU:HA	1.86	0.56
1:C:30:TYR:CD1	1:C:80:MET:SD	2.98	0.56
1:C:36:LYS:HE3	1:C:38:LEU:HD13	1.86	0.56
1:E:31:LYS:HG3	1:E:139:TRP:CZ2	2.40	0.56
1:F:55:GLN:HG2	1:F:56:PRO:HD2	1.86	0.56
1:C:6:ILE:HG23	1:C:114:ILE:HD11	1.87	0.56
1:E:6:ILE:HG23	1:E:114:ILE:HD11	1.88	0.56
1:D:31:LYS:HG3	1:D:139:TRP:CZ2	2.41	0.56
1:F:62:VAL:O	1:F:66:SER:HB2	2.07	0.55
1:E:105:PHE:HE1	1:F:27:LYS:HD3	1.71	0.55
1:F:17:LEU:O	1:F:21:ILE:HD12	2.07	0.55
1:B:145:GLU:OE2	1:F:142:HIS:HE1	1.89	0.54
1:D:102:ARG:CD	1:D:112:ASN:HB2	2.32	0.54
1:B:111:LYS:HD2	1:C:146:TRP:HA	1.89	0.54
1:A:132:LYS:HB2	1:A:135:GLU:HG3	1.89	0.53
1:A:147:ILE:CG2	1:C:107:LEU:HD12	2.39	0.53
1:C:91:THR:HA	1:C:102:ARG:NH1	2.24	0.53
1:A:14:GLN:HG3	1:B:146:TRP:CE2	2.43	0.53
1:D:55:GLN:HG3	1:D:56:PRO:HD2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:6:ILE:HG23	1:F:114:ILE:HD11	1.91	0.53
1:B:17:LEU:O	1:B:21:ILE:HD12	2.08	0.53
1:C:34:ALA:HB1	1:C:131:PHE:CE2	2.44	0.53
1:E:91:THR:HA	1:E:102:ARG:NH1	2.24	0.52
1:F:1:MET:HE3	1:F:1:MET:HA	1.91	0.52
1:E:6:ILE:HG22	1:E:73:MET:HE3	1.92	0.52
1:B:45:LEU:HD11	1:B:65:ILE:HG22	1.92	0.52
1:B:102:ARG:CD	1:B:112:ASN:HB2	2.30	0.52
1:B:36:LYS:HA	1:E:35:ILE:O	2.11	0.51
1:B:32:LEU:O	1:E:37:MET:HE1	2.10	0.51
1:C:106:CYS:SG	1:C:113:VAL:HG13	2.51	0.51
1:E:34:ALA:HB1	1:E:131:PHE:CE1	2.46	0.51
1:B:143:MET:HE1	1:F:143:MET:HG2	1.93	0.50
1:B:37:MET:HB2	1:E:35:ILE:HG22	1.94	0.50
1:D:146:TRP:CE2	1:F:14:GLN:HG3	2.47	0.50
1:B:52:LEU:HD23	1:B:55:GLN:HG3	1.94	0.50
1:F:35:ILE:HD12	1:F:73:MET:HE2	1.93	0.50
1:C:35:ILE:O	1:D:36:LYS:HA	2.10	0.50
1:A:102:ARG:HD3	1:A:112:ASN:HB2	1.94	0.49
1:B:8:ILE:HD13	1:B:73:MET:HE3	1.93	0.49
1:A:18:VAL:O	1:A:22:ILE:HG13	2.12	0.49
1:E:85:ARG:HD2	1:E:118:ASP:HA	1.92	0.49
1:B:16:GLY:HA2	1:E:26:GLU:OE2	2.13	0.49
1:C:143:MET:SD	1:E:143:MET:CE	3.00	0.49
1:C:35:ILE:HG22	1:D:37:MET:HB2	1.95	0.49
1:E:30:TYR:CD1	1:E:80:MET:HE2	2.48	0.49
1:A:73:MET:HE2	1:A:75:TRP:NE1	2.28	0.48
1:B:36:LYS:HD2	1:B:131:PHE:CE1	2.48	0.48
1:A:9:LYS:HB3	1:A:10:PRO:CD	2.43	0.48
1:B:35:ILE:O	1:E:36:LYS:HA	2.14	0.48
1:A:62:VAL:O	1:A:66:SER:HB2	2.12	0.48
1:D:102:ARG:HD3	1:D:112:ASN:CB	2.38	0.48
1:F:32:LEU:HD11	1:F:35:ILE:HB	1.95	0.48
1:A:17:LEU:O	1:A:21:ILE:HD12	2.14	0.47
1:C:88:ILE:HG12	1:C:114:ILE:HG21	1.96	0.47
1:B:137:THR:HG21	1:E:38:LEU:HA	1.95	0.47
1:F:9:LYS:NZ	1:F:112:ASN:HD21	2.13	0.47
1:D:6:ILE:O	1:D:73:MET:HB2	2.15	0.47
1:D:8:ILE:N	1:D:8:ILE:HD12	2.30	0.47
1:B:26:GLU:OE1	1:E:16:GLY:HA2	2.14	0.47
1:B:28:LYS:O	1:B:28:LYS:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:LYS:HB3	1:D:10:PRO:CD	2.45	0.47
1:A:37:MET:HB2	1:F:35:ILE:HG22	1.97	0.47
1:D:33:ILE:HD11	1:D:74:VAL:CG1	2.45	0.46
1:A:44:ILE:HG23	1:A:129:ILE:HD11	1.97	0.46
1:C:30:TYR:CE1	1:C:80:MET:SD	3.09	0.46
1:D:28:LYS:NZ	1:F:106:CYS:O	2.49	0.45
1:B:137:THR:HB	1:E:39:ASN:ND2	2.32	0.45
1:D:106:CYS:SG	1:D:113:VAL:HG13	2.56	0.45
1:A:35:ILE:HG22	1:F:37:MET:HB2	1.98	0.45
1:D:15:ARG:HA	1:E:143:MET:HE3	1.98	0.45
1:F:106:CYS:SG	1:F:113:VAL:HG13	2.56	0.45
1:E:51:GLU:HG2	1:E:52:LEU:N	2.31	0.45
1:F:8:ILE:HG12	1:F:21:ILE:HD13	1.99	0.45
1:B:92:ASN:HA	1:B:93:PRO:HD3	1.86	0.45
1:B:107:LEU:HB3	1:C:78:VAL:HG13	1.99	0.45
1:D:111:LYS:HD2	1:E:146:TRP:HA	1.98	0.45
1:E:8:ILE:HD12	1:E:18:VAL:HA	1.98	0.45
1:B:23:LYS:HD2	1:E:20:THR:OG1	2.16	0.44
1:F:31:LYS:HD2	1:F:141:HIS:HB2	1.98	0.44
1:B:143:MET:CE	1:F:143:MET:HG2	2.47	0.44
1:E:106:CYS:SG	1:E:113:VAL:HG13	2.57	0.44
1:C:1:MET:HE1	1:C:148:CYS:SG	2.58	0.44
1:B:11:ASP:HB3	1:B:111:LYS:HD3	1.99	0.44
1:A:1:MET:HB3	1:A:76:GLU:HG2	2.00	0.44
1:E:88:ILE:HG12	1:E:114:ILE:CG2	2.47	0.44
1:B:118:ASP:OD1	1:B:118:ASP:N	2.49	0.43
1:A:6:ILE:HG23	1:A:114:ILE:HD11	2.01	0.43
1:A:147:ILE:HG22	1:C:107:LEU:HD12	1.99	0.43
1:A:35:ILE:O	1:F:36:LYS:HA	2.18	0.43
1:F:92:ASN:ND2	1:F:95:THR:OG1	2.50	0.43
1:A:41:THR:HG22	1:A:44:ILE:HD12	2.01	0.43
1:B:137:THR:HB	1:E:39:ASN:HD21	1.84	0.43
1:F:5:PHE:CZ	1:F:7:MET:HB2	2.53	0.43
1:C:21:ILE:HG12	1:C:101:ILE:HD13	2.00	0.43
1:F:119:SER:OG	1:F:122:SER:HB2	2.19	0.43
1:A:5:PHE:CZ	1:A:7:MET:HB2	2.53	0.42
1:A:97:ASN:ND2	1:A:97:ASN:H	2.16	0.42
1:B:106:CYS:O	1:C:28:LYS:HE2	2.20	0.42
1:E:102:ARG:CD	1:E:112:ASN:HB2	2.43	0.42
1:B:41:THR:O	1:B:45:LEU:HB2	2.20	0.42
1:B:93:PRO:HA	1:B:96:SER:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:30:TYR:CG	1:E:80:MET:HE2	2.55	0.42
1:D:91:THR:HA	1:D:102:ARG:NH1	2.35	0.42
1:E:5:PHE:CZ	1:E:7:MET:HB2	2.55	0.42
1:A:107:LEU:HD23	1:B:28:LYS:HE2	2.01	0.42
1:D:8:ILE:N	1:D:8:ILE:CD1	2.82	0.42
1:E:108:GLU:OE2	1:E:110:SER:OG	2.35	0.42
1:C:69:PRO:HG3	1:D:139:TRP:CE3	2.54	0.42
1:D:8:ILE:HD13	1:D:73:MET:HE3	2.01	0.42
1:B:139:TRP:CE3	1:E:69:PRO:HG3	2.55	0.42
1:A:39:ASN:ND2	1:A:67:LYS:O	2.53	0.41
1:D:15:ARG:NH1	1:D:15:ARG:CG	2.75	0.41
1:C:36:LYS:HA	1:D:35:ILE:O	2.21	0.41
1:C:142:HIS:CG	1:E:146:TRP:HE1	2.38	0.41
1:C:129:ILE:HG22	1:C:130:TRP:CD1	2.55	0.41
1:F:22:ILE:CG1	1:F:73:MET:HE1	2.50	0.41
1:B:39:ASN:HD22	1:B:39:ASN:N	2.19	0.41
1:E:47:GLU:OE2	1:E:129:ILE:HD11	2.21	0.41
1:F:22:ILE:HG12	1:F:73:MET:HE1	2.03	0.41
1:A:112:ASN:O	1:A:114:ILE:N	2.49	0.41
1:B:129:ILE:CG1	1:B:130:TRP:CD1	3.04	0.41
1:C:10:PRO:HA	1:C:69:PRO:O	2.21	0.41
1:B:57:PHE:HD1	1:B:57:PHE:HA	1.76	0.41
1:D:125:LYS:O	1:D:129:ILE:HG23	2.20	0.41
1:E:145:GLU:H	1:E:145:GLU:HG2	1.68	0.41
1:F:90:GLU:HB2	1:F:96:SER:HB3	2.03	0.41
1:B:11:ASP:HB3	1:B:111:LYS:CD	2.51	0.41
1:E:55:GLN:HE21	1:E:55:GLN:HB3	1.62	0.41
1:E:96:SER:O	1:F:86:LYS:HE2	2.21	0.40
1:B:9:LYS:HB3	1:B:10:PRO:CD	2.51	0.40
1:C:88:ILE:HG12	1:C:114:ILE:CG2	2.50	0.40
1:D:79:ASP:O	1:D:83:GLN:HB2	2.22	0.40
1:E:85:ARG:HD2	1:E:117:SER:O	2.21	0.40
1:B:6:ILE:CG2	1:B:114:ILE:HD11	2.50	0.40
1:B:104:ASP:O	1:C:28:LYS:HD2	2.21	0.40
1:C:3:LYS:CG	1:C:76:GLU:HG3	2.50	0.40
1:C:79:ASP:O	1:C:83:GLN:HB2	2.22	0.40
1:C:131:PHE:HD2	1:C:135:GLU:HB3	1.87	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	147/157 (94%)	141 (96%)	5 (3%)	1 (1%)	18	45
1	B	147/157 (94%)	143 (97%)	3 (2%)	1 (1%)	18	45
1	C	147/157 (94%)	141 (96%)	5 (3%)	1 (1%)	18	45
1	D	147/157 (94%)	140 (95%)	5 (3%)	2 (1%)	9	29
1	E	147/157 (94%)	141 (96%)	5 (3%)	1 (1%)	18	45
1	F	147/157 (94%)	141 (96%)	5 (3%)	1 (1%)	18	45
All	All	882/942 (94%)	847 (96%)	28 (3%)	7 (1%)	16	42

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	VAL
1	B	113	VAL
1	C	113	VAL
1	D	113	VAL
1	E	113	VAL
1	F	113	VAL
1	D	54	ASP

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	132/139 (95%)	108 (82%)	24 (18%)	2 7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	132/139 (95%)	98 (74%)	34 (26%)	0	2
1	C	132/139 (95%)	91 (69%)	41 (31%)	0	0
1	D	132/139 (95%)	94 (71%)	38 (29%)	0	1
1	E	132/139 (95%)	88 (67%)	44 (33%)	0	0
1	F	132/139 (95%)	99 (75%)	33 (25%)	0	2
All	All	792/834 (95%)	578 (73%)	214 (27%)	0	1

All (214) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ARG
1	A	27	LYS
1	A	43	GLU
1	A	47	GLU
1	A	50	LYS
1	A	52	LEU
1	A	54	ASP
1	A	59	LYS
1	A	61	LEU
1	A	70	VAL
1	A	78	VAL
1	A	80	MET
1	A	82	LYS
1	A	85	ARG
1	A	90	GLU
1	A	91	THR
1	A	97	ASN
1	A	113	VAL
1	A	122	SER
1	A	129	ILE
1	A	134	GLU
1	A	138	GLN
1	A	140	LYS
1	A	144	LYS
1	B	6	ILE
1	B	20	THR
1	B	28	LYS
1	B	36	LYS
1	B	41	THR
1	B	45	LEU

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Mol	Chain	Res	Type
1	B	50	LYS
1	B	51	GLU
1	B	52	LEU
1	B	53	SER
1	B	57	PHE
1	B	59	LYS
1	B	61	LEU
1	B	66	SER
1	B	67	LYS
1	B	82	LYS
1	B	85	ARG
1	B	86	LYS
1	B	90	GLU
1	B	94	LEU
1	B	95	THR
1	B	96	SER
1	B	98	THR
1	B	112	ASN
1	B	113	VAL
1	B	118	ASP
1	B	122	SER
1	B	129	ILE
1	B	132	LYS
1	B	134	GLU
1	B	140	LYS
1	B	143	MET
1	B	144	LYS
1	B	149	SER
1	C	1	MET
1	C	6	ILE
1	C	9	LYS
1	C	15	ARG
1	C	23	LYS
1	C	28	LYS
1	C	35	ILE
1	C	43	GLU
1	C	47	GLU
1	C	50	LYS
1	C	51	GLU
1	C	52	LEU
1	C	54	ASP
1	C	55	GLN

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Mol	Chain	Res	Type
1	C	61	LEU
1	C	67	LYS
1	C	70	VAL
1	C	73	MET
1	C	78	VAL
1	C	82	LYS
1	C	86	LYS
1	C	88	ILE
1	C	90	GLU
1	C	91	THR
1	C	94	LEU
1	C	97	ASN
1	C	108	GLU
1	C	111	LYS
1	C	113	VAL
1	C	122	SER
1	C	125	LYS
1	C	129	ILE
1	C	134	GLU
1	C	135	GLU
1	C	136	LEU
1	C	137	THR
1	C	140	LYS
1	C	142	HIS
1	C	143	MET
1	C	144	LYS
1	C	145	GLU
1	D	6	ILE
1	D	8	ILE
1	D	13	VAL
1	D	15	ARG
1	D	20	THR
1	D	28	LYS
1	D	33	ILE
1	D	38	LEU
1	D	41	THR
1	D	42	GLU
1	D	44	ILE
1	D	45	LEU
1	D	50	LYS
1	D	51	GLU
1	D	52	LEU

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Mol	Chain	Res	Type
1	D	54	ASP
1	D	57	PHE
1	D	59	LYS
1	D	61	LEU
1	D	64	TYR
1	D	67	LYS
1	D	70	VAL
1	D	81	VAL
1	D	82	LYS
1	D	83	GLN
1	D	85	ARG
1	D	86	LYS
1	D	90	GLU
1	D	94	LEU
1	D	95	THR
1	D	98	THR
1	D	112	ASN
1	D	125	LYS
1	D	129	ILE
1	D	132	LYS
1	D	134	GLU
1	D	135	GLU
1	D	140	LYS
1	E	1	MET
1	E	3	LYS
1	E	6	ILE
1	E	8	ILE
1	E	9	LYS
1	E	23	LYS
1	E	36	LYS
1	E	45	LEU
1	E	46	LYS
1	E	47	GLU
1	E	50	LYS
1	E	51	GLU
1	E	52	LEU
1	E	55	GLN
1	E	57	PHE
1	E	59	LYS
1	E	60	ASN
1	E	61	LEU
1	E	62	VAL

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Mol	Chain	Res	Type
1	E	66	SER
1	E	67	LYS
1	E	80	MET
1	E	85	ARG
1	E	86	LYS
1	E	91	THR
1	E	96	SER
1	E	97	ASN
1	E	107	LEU
1	E	111	LYS
1	E	113	VAL
1	E	118	ASP
1	E	120	VAL
1	E	122	SER
1	E	125	LYS
1	E	129	ILE
1	E	134	GLU
1	E	135	GLU
1	E	136	LEU
1	E	137	THR
1	E	138	GLN
1	E	140	LYS
1	E	142	HIS
1	E	143	MET
1	E	145	GLU
1	F	1	MET
1	F	3	LYS
1	F	7	MET
1	F	21	ILE
1	F	23	LYS
1	F	27	LYS
1	F	36	LYS
1	F	42	GLU
1	F	43	GLU
1	F	47	GLU
1	F	51	GLU
1	F	52	LEU
1	F	54	ASP
1	F	55	GLN
1	F	67	LYS
1	F	70	VAL
1	F	82	LYS

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Mol	Chain	Res	Type
1	F	85	ARG
1	F	87	LEU
1	F	91	THR
1	F	94	LEU
1	F	95	THR
1	F	97	ASN
1	F	98	THR
1	F	109	VAL
1	F	112	ASN
1	F	118	ASP
1	F	122	SER
1	F	129	ILE
1	F	140	LYS
1	F	143	MET
1	F	144	LYS
1	F	147	ILE

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

Mol	Chain	Res	Type
1	A	39	ASN
1	A	83	GLN
1	A	92	ASN
1	A	97	ASN
1	B	39	ASN
1	B	112	ASN
1	B	128	ASN
1	C	55	GLN
1	C	141	HIS
1	D	83	GLN
1	D	112	ASN
1	D	128	ASN
1	E	39	ASN
1	E	55	GLN
1	E	60	ASN
1	E	92	ASN
1	E	138	GLN
1	F	39	ASN
1	F	112	ASN
1	F	138	GLN

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 [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	149/157 (94%)	-1.43	0 100 100	17, 39, 120, 151	0
1	B	149/157 (94%)	-1.32	0 100 100	16, 40, 139, 151	0
1	C	149/157 (94%)	-1.32	0 100 100	16, 39, 139, 151	0
1	D	149/157 (94%)	-1.35	0 100 100	17, 40, 142, 151	0
1	E	149/157 (94%)	-1.37	0 100 100	16, 39, 140, 151	0
1	F	149/157 (94%)	-1.34	0 100 100	16, 39, 119, 151	0
All	All	894/942 (94%)	-1.36	0 100 100	16, 40, 139, 151	0

There are no RSRZ outliers to report.

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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.