



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:49 AM UTC

PDB ID : 1NDL / pdb_00001ndl
Title : THE AWD NUCLEOTIDE DIPHOSPHATE KINASE FROM DROSOPHILA
Authors : Janin, J.; Chiadmi, M.; Dumas, C.; Lascu, I.; Lebras, G.; Morera, S.; Veron, M.
Deposited on : 1993-11-27
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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

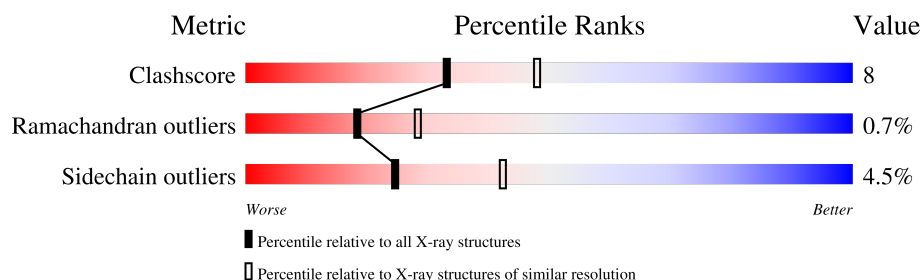
1 Overall quality at a glance

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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	153	 71% 24% 5% •
1	B	153	 66% 28% 5% •
1	C	153	 66% 23% 10% ••

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3924 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	152	Total	C	N	O	S	0	0	0
			1203	777	205	216	5			
1	B	152	Total	C	N	O	S	0	0	0
			1203	777	205	216	5			
1	C	152	Total	C	N	O	S	0	0	0
			1203	777	205	216	5			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	116	Total	O	0	0
			116	116		
2	B	94	Total	O	0	0
			94	94		
2	C	105	Total	O	0	0
			105	105		

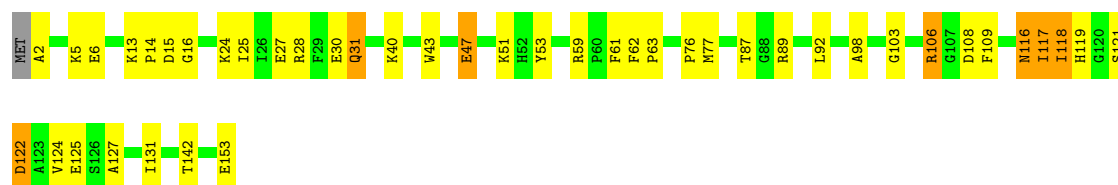
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

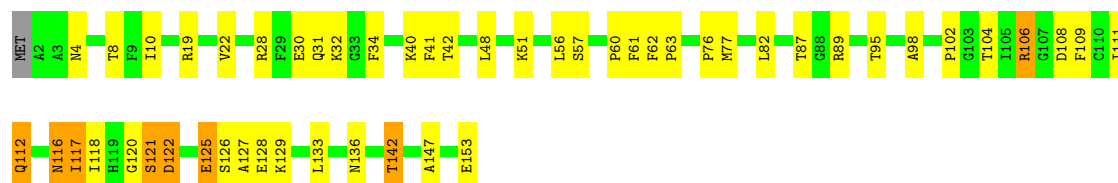
• Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain A: 



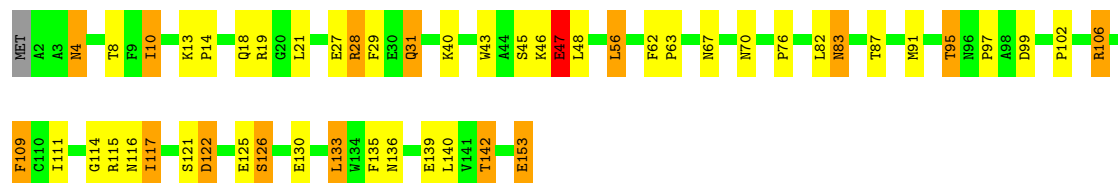
• Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain B: 



• Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain C: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	115.65Å 115.65Å 98.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.167 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3924	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

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	0.97	0/1233	2.06	36/1668 (2.2%)
1	B	0.94	1/1233 (0.1%)	2.20	49/1668 (2.9%)
1	C	0.98	0/1233	2.27	50/1668 (3.0%)
All	All	0.96	1/3699 (0.0%)	2.18	135/5004 (2.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	121	SER	C-N	-5.05	1.27	1.33

All (135) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	28	ARG	CD-NE-CZ	36.36	175.31	124.40
1	A	106	ARG	CD-NE-CZ	22.38	155.73	124.40
1	B	121	SER	CA-C-N	15.97	142.16	120.44
1	B	121	SER	C-N-CA	15.97	142.16	120.44
1	C	121	SER	CA-C-N	13.39	138.22	120.28
1	C	121	SER	C-N-CA	13.39	138.22	120.28
1	B	111	ILE	N-CA-C	12.30	121.34	111.62
1	A	121	SER	CA-C-N	11.64	135.88	120.28
1	A	121	SER	C-N-CA	11.64	135.88	120.28
1	B	121	SER	CA-C-O	11.10	133.42	121.44
1	C	122	ASP	N-CA-CB	-11.05	93.87	110.12
1	B	122	ASP	N-CA-CB	-10.74	94.50	110.07
1	A	43	TRP	CA-C-O	-10.46	108.82	120.32
1	C	111	ILE	N-CA-C	9.89	120.43	112.12
1	C	4	ASN	OD1-CG-ND2	-9.37	113.23	122.60
1	B	106	ARG	CD-NE-CZ	8.99	136.98	124.40
1	B	30	GLU	CA-C-N	8.91	133.39	120.38
1	B	30	GLU	C-N-CA	8.91	133.39	120.38
1	C	121	SER	CA-C-O	8.90	130.98	121.19
1	C	46	LYS	CA-C-O	8.87	130.16	119.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	109	PHE	N-CA-C	8.65	124.89	113.30
1	A	116	ASN	CA-C-N	8.49	137.26	121.97
1	A	116	ASN	C-N-CA	8.49	137.26	121.97
1	C	47	GLU	CB-CG-CD	8.37	126.83	112.60
1	A	122	ASP	CB-CA-C	-8.21	97.17	110.79
1	B	41	PHE	CA-CB-CG	7.70	121.50	113.80
1	C	31	GLN	CB-CA-C	-7.66	97.83	110.85
1	C	136	ASN	N-CA-C	-7.55	100.36	110.55
1	B	104	THR	CA-CB-OG1	-7.49	98.36	109.60
1	A	108	ASP	CA-CB-CG	7.29	119.89	112.60
1	C	29	PHE	CA-CB-CG	-7.06	106.74	113.80
1	A	109	PHE	N-CA-C	7.04	124.17	113.61
1	B	117	ILE	N-CA-C	6.95	123.80	109.34
1	C	117	ILE	N-CA-C	6.93	123.75	109.34
1	C	111	ILE	CA-C-O	-6.83	114.12	120.34
1	C	116	ASN	CA-C-N	6.79	134.18	121.97
1	C	116	ASN	C-N-CA	6.79	134.18	121.97
1	B	111	ILE	N-CA-CB	-6.77	106.09	111.64
1	B	116	ASN	CA-C-N	6.73	134.09	121.97
1	B	116	ASN	C-N-CA	6.73	134.09	121.97
1	B	95	THR	CA-CB-OG1	-6.70	99.55	109.60
1	C	106	ARG	CA-C-N	6.66	127.52	119.99
1	C	106	ARG	C-N-CA	6.66	127.52	119.99
1	B	153	GLU	CA-CB-CG	6.65	127.39	114.10
1	C	111	ILE	CB-CA-C	-6.62	104.42	110.91
1	C	18	GLN	CA-C-O	-6.49	112.77	120.10
1	B	31	GLN	CB-CA-C	-6.46	97.92	110.46
1	A	106	ARG	NE-CZ-NH1	6.44	127.94	121.50
1	C	46	LYS	CA-C-N	6.43	128.81	120.44
1	C	46	LYS	C-N-CA	6.43	128.81	120.44
1	C	87	THR	CA-C-N	6.41	127.24	119.99
1	C	87	THR	C-N-CA	6.41	127.24	119.99
1	A	15	ASP	CA-C-N	6.39	127.03	120.00
1	A	15	ASP	C-N-CA	6.39	127.03	120.00
1	B	108	ASP	CA-C-O	-6.33	112.19	119.60
1	B	108	ASP	CA-CB-CG	6.27	118.87	112.60
1	B	56	LEU	CA-C-N	6.26	128.99	120.54
1	B	56	LEU	C-N-CA	6.26	128.99	120.54
1	A	117	ILE	N-CA-C	6.17	122.18	109.34
1	B	136	ASN	N-CA-C	-6.17	101.65	110.59
1	B	87	THR	CA-C-N	6.14	126.76	119.94
1	B	87	THR	C-N-CA	6.14	126.76	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	116	ASN	OD1-CG-ND2	-6.11	116.49	122.60
1	B	147	ALA	CA-C-N	6.09	129.95	120.82
1	B	147	ALA	C-N-CA	6.09	129.95	120.82
1	A	118	ILE	N-CA-CB	-6.07	103.31	112.35
1	B	112	GLN	OE1-CD-NE2	6.04	128.64	122.60
1	C	99	ASP	CA-CB-CG	6.04	118.64	112.60
1	A	16	GLY	CA-C-N	5.99	128.22	120.56
1	A	16	GLY	C-N-CA	5.99	128.22	120.56
1	B	60	PRO	CA-C-N	5.90	130.75	122.08
1	B	60	PRO	C-N-CA	5.90	130.75	122.08
1	A	47	GLU	CB-CG-CD	5.87	122.57	112.60
1	A	119	HIS	CA-C-O	-5.84	113.94	120.66
1	B	22	VAL	CA-C-O	-5.77	114.64	121.05
1	B	136	ASN	CA-CB-CG	5.72	118.32	112.60
1	C	95	THR	CA-CB-OG1	-5.71	101.03	109.60
1	C	109	PHE	CA-C-O	-5.71	112.53	119.32
1	B	109	PHE	CA-C-O	-5.70	112.54	119.32
1	B	19	ARG	NE-CZ-NH2	5.68	124.31	119.20
1	C	109	PHE	N-CA-C	5.63	120.85	113.30
1	C	102	PRO	N-CA-C	-5.62	102.38	111.14
1	A	125	GLU	CB-CG-CD	5.60	122.12	112.60
1	B	102	PRO	CB-CA-C	5.56	118.64	111.64
1	A	122	ASP	N-CA-C	5.53	117.30	111.28
1	C	121	SER	N-CA-CB	5.52	118.17	109.83
1	A	30	GLU	CA-C-N	5.51	127.93	120.38
1	A	30	GLU	C-N-CA	5.51	127.93	120.38
1	C	43	TRP	CA-C-O	-5.50	114.83	120.54
1	A	59	ARG	CB-CA-C	-5.49	100.85	109.52
1	A	43	TRP	N-CA-C	-5.46	99.61	108.52
1	C	83	ASN	CA-CB-CG	-5.44	107.16	112.60
1	B	122	ASP	N-CA-C	5.44	117.02	111.14
1	A	24	LYS	O-C-N	5.44	127.89	122.12
1	A	31	GLN	CA-C-N	5.41	128.07	120.28
1	A	31	GLN	C-N-CA	5.41	128.07	120.28
1	A	31	GLN	CA-CB-CG	5.38	124.87	114.10
1	A	25	ILE	O-C-N	-5.35	116.33	121.90
1	C	106	ARG	CA-C-O	5.35	126.43	120.82
1	A	59	ARG	N-CA-C	5.34	116.42	109.64
1	B	19	ARG	NE-CZ-NH1	-5.32	116.18	121.50
1	C	21	LEU	CA-C-O	-5.32	113.12	119.35
1	A	87	THR	CA-C-N	5.32	125.88	119.98
1	A	87	THR	C-N-CA	5.32	125.88	119.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	56	LEU	N-CA-CB	-5.30	102.82	110.56
1	C	67	ASN	CA-CB-CG	5.29	117.89	112.60
1	C	122	ASP	N-CA-C	5.29	117.04	111.28
1	C	139	GLU	CA-C-O	-5.29	113.17	119.35
1	A	103	GLY	N-CA-C	-5.26	108.08	114.92
1	C	115	ARG	NE-CZ-NH1	5.25	126.75	121.50
1	B	125	GLU	CA-C-O	-5.24	114.97	120.63
1	C	125	GLU	CB-CG-CD	5.21	121.47	112.60
1	C	142	THR	CA-CB-OG1	-5.21	101.78	109.60
1	B	42	THR	N-CA-CB	-5.20	103.46	111.46
1	C	31	GLN	CA-CB-CG	5.20	124.49	114.10
1	C	130	GLU	CA-C-O	-5.20	115.37	120.82
1	B	30	GLU	N-CA-CB	5.16	117.44	109.91
1	C	97	PRO	CA-C-N	5.13	127.67	120.28
1	C	97	PRO	C-N-CA	5.13	127.67	120.28
1	B	28	ARG	NH1-CZ-NH2	5.12	125.95	119.30
1	C	70	ASN	CA-CB-CG	5.09	117.69	112.60
1	A	53	TYR	CA-C-N	5.08	128.44	120.82
1	A	53	TYR	C-N-CA	5.08	128.44	120.82
1	B	61	PHE	CA-C-N	5.07	127.05	120.26
1	B	61	PHE	C-N-CA	5.07	127.05	120.26
1	C	56	LEU	CA-C-N	5.06	127.31	120.38
1	C	56	LEU	C-N-CA	5.06	127.31	120.38
1	B	42	THR	N-CA-C	5.04	115.96	108.60
1	A	124	VAL	O-C-N	5.04	126.76	121.87
1	B	57	SER	CB-CA-C	-5.03	102.76	110.81
1	C	31	GLN	CG-CD-NE2	-5.02	108.87	116.40
1	C	115	ARG	CD-NE-CZ	5.02	131.43	124.40
1	B	122	ASP	O-C-N	5.01	127.50	122.09
1	B	98	ALA	CA-C-O	-5.01	114.44	120.10
1	C	19	ARG	CA-C-O	5.00	125.49	119.43

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1203	0	1207	18	0
1	B	1203	0	1207	20	0
1	C	1203	0	1207	21	0
2	A	116	0	0	3	0
2	B	94	0	0	4	0
2	C	105	0	0	3	0
All	All	3924	0	3621	56	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 8.

All (56) 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:B:122:ASP:HB2	2:B:167:HOH:O	1.69	0.91
1:C:4:ASN:HD22	1:C:82:LEU:HB2	1.43	0.82
1:B:4:ASN:HD22	1:B:82:LEU:HB2	1.53	0.72
1:B:8:THR:HG23	1:B:10:ILE:HD13	1.75	0.69
1:C:4:ASN:ND2	1:C:82:LEU:HB2	2.06	0.68
1:A:98:ALA:HB2	2:A:254:HOH:O	1.93	0.67
1:B:62:PHE:N	1:B:63:PRO:HD2	2.12	0.63
1:A:40:LYS:O	1:A:76:PRO:HD2	1.99	0.62
1:C:40:LYS:O	1:C:76:PRO:HD2	1.98	0.62
1:B:112:GLN:HE22	1:C:153:GLU:HB3	1.67	0.59
1:A:62:PHE:HB3	1:A:63:PRO:HD3	1.84	0.58
1:B:122:ASP:HB3	1:B:126:SER:OG	2.04	0.58
1:A:153:GLU:HG2	1:C:114:GLY:HA3	1.87	0.56
1:A:6:GLU:HA	2:A:234:HOH:O	2.03	0.56
1:C:8:THR:HG23	1:C:10:ILE:HD12	1.87	0.56
1:C:122:ASP:HB2	2:C:169:HOH:O	2.05	0.56
1:A:127:ALA:O	1:A:131:ILE:HG13	2.04	0.56
1:B:10:ILE:HG22	1:B:77:MET:HE3	1.89	0.54
1:C:62:PHE:HB3	1:C:63:PRO:HD3	1.88	0.54
1:C:122:ASP:HB3	1:C:126:SER:OG	2.08	0.54
1:A:92:LEU:HD22	1:A:118:ILE:HD13	1.90	0.52
1:C:27:GLU:O	1:C:31:GLN:HG3	2.09	0.52
1:B:48:LEU:HD11	1:B:133:LEU:HG	1.92	0.50
1:A:13:LYS:HB3	1:A:14:PRO:HD2	1.92	0.50
1:B:106:ARG:NH2	2:B:188:HOH:O	2.45	0.49
1:A:106:ARG:HD3	1:A:116:ASN:HB2	1.95	0.49
1:A:62:PHE:HB3	1:A:63:PRO:CD	2.44	0.48
1:C:4:ASN:ND2	1:C:82:LEU:HD13	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:GLU:O	1:B:129:LYS:HD3	2.15	0.47
1:C:40:LYS:HE2	1:C:135:PHE:CE1	2.50	0.47
1:C:106:ARG:NH2	2:C:190:HOH:O	2.47	0.47
1:A:13:LYS:HB3	1:A:14:PRO:CD	2.44	0.46
1:C:45:SER:HB2	1:C:47:GLU:OE1	2.16	0.46
1:A:47:GLU:HG2	1:A:51:LYS:HE3	1.99	0.45
1:B:4:ASN:ND2	1:B:82:LEU:HB2	2.26	0.45
1:A:2:ALA:HB3	1:A:5:LYS:HG3	1.99	0.44
1:A:27:GLU:O	1:A:31:GLN:HB2	2.18	0.44
1:B:120:GLY:O	1:B:121:SER:C	2.59	0.43
1:C:140:LEU:C	2:C:255:HOH:O	2.61	0.43
1:B:40:LYS:O	1:B:76:PRO:HD2	2.19	0.43
1:A:14:PRO:HA	2:A:257:HOH:O	2.18	0.43
1:C:13:LYS:HB3	1:C:14:PRO:CD	2.48	0.42
1:B:32:LYS:HG2	1:B:34:PHE:CE2	2.54	0.42
1:C:48:LEU:CD1	1:C:133:LEU:HD22	2.49	0.42
1:B:106:ARG:HD3	1:B:116:ASN:HB2	2.00	0.42
1:B:106:ARG:NH1	1:B:118:ILE:O	2.53	0.42
1:A:28:ARG:HH11	1:A:28:ARG:HD2	1.64	0.41
1:C:47:GLU:H	1:C:47:GLU:CD	2.27	0.41
1:B:142:THR:HA	2:B:224:HOH:O	2.20	0.41
1:B:62:PHE:N	1:B:63:PRO:CD	2.79	0.41
1:B:8:THR:HG23	1:B:10:ILE:CD1	2.46	0.41
2:B:244:HOH:O	1:C:91:MET:HG2	2.20	0.41
1:C:56:LEU:O	1:C:62:PHE:HB2	2.22	0.40
1:B:121:SER:OG	1:B:127:ALA:HA	2.21	0.40
1:A:61:PHE:O	1:A:62:PHE:C	2.63	0.40
1:A:31:GLN:HG2	1:C:109:PHE:CE1	2.57	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	150/153 (98%)	146 (97%)	3 (2%)	1 (1%)	18	28
1	B	150/153 (98%)	143 (95%)	6 (4%)	1 (1%)	18	28
1	C	150/153 (98%)	145 (97%)	4 (3%)	1 (1%)	18	28
All	All	450/459 (98%)	434 (96%)	13 (3%)	3 (1%)	18	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	ILE
1	B	117	ILE
1	C	117	ILE

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	126/127 (99%)	122 (97%)	4 (3%)	34	56
1	B	126/127 (99%)	122 (97%)	4 (3%)	34	56
1	C	126/127 (99%)	117 (93%)	9 (7%)	13	23
All	All	378/381 (99%)	361 (96%)	17 (4%)	24	42

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	MET
1	A	89	ARG
1	A	122	ASP
1	A	142	THR
1	B	51	LYS
1	B	89	ARG
1	B	128	GLU
1	B	142	THR
1	C	10	ILE
1	C	28	ARG

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Mol	Chain	Res	Type
1	C	47	GLU
1	C	83	ASN
1	C	95	THR
1	C	126	SER
1	C	133	LEU
1	C	142	THR
1	C	153	GLU

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	4	ASN
1	A	90	GLN
1	A	136	ASN
1	B	4	ASN
1	B	18	GLN
1	B	112	GLN
1	C	4	ASN
1	C	83	ASN
1	C	136	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.