



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 29, 2026 – 12:08 PM EDT

PDB ID : 38ZS / pdb_000038zs
Title : Crystal structure of a Nucleoside diphosphate kinase from *Treponema pallidum*
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2026-09-25
Resolution : 2.54 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 Phenix2.2
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

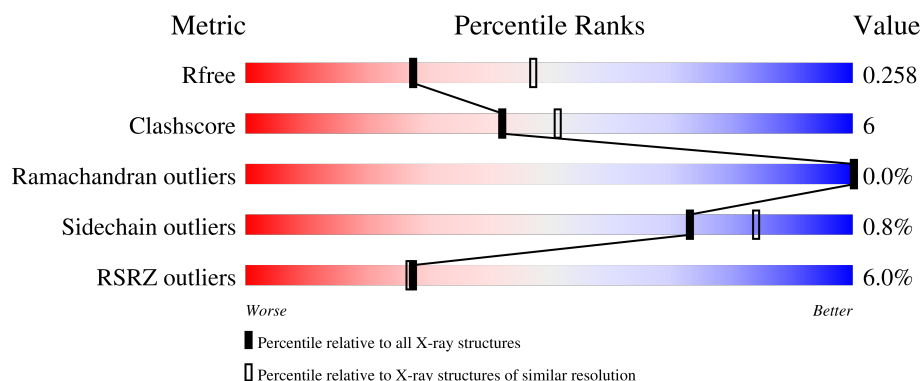
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.54 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	3% 87% 8% .
1	B	157	5% 82% 11% 6%
1	C	157	3% 82% 11% 6%
1	D	157	8% 80% 14% 6%
1	E	157	2% 82% 10% 8%

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Mol	Chain	Length	Quality of chain
1	F	157	
1	G	157	
1	H	157	
1	I	157	
1	J	157	
1	K	157	
1	L	157	
1	M	157	
1	N	157	
1	O	157	
1	P	157	
1	Q	157	
1	R	157	
1	S	157	
1	T	157	
1	U	157	
1	V	157	
1	W	157	
1	X	157	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 27863 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	150	Total	C	N	O	S	0	0	0
			1176	753	204	215	4			
1	B	147	Total	C	N	O	S	0	0	0
			1143	730	198	212	3			
1	C	147	Total	C	N	O	S	0	0	0
			1157	741	199	214	3			
1	D	147	Total	C	N	O	S	0	0	0
			1151	733	203	211	4			
1	E	144	Total	C	N	O	S	0	0	0
			1119	713	196	207	3			
1	F	129	Total	C	N	O	S	0	0	0
			1007	642	175	187	3			
1	G	146	Total	C	N	O	S	0	0	0
			1138	729	197	209	3			
1	H	152	Total	C	N	O	S	0	0	0
			1200	767	210	219	4			
1	I	149	Total	C	N	O	S	0	0	0
			1170	749	201	216	4			
1	J	147	Total	C	N	O	S	0	0	0
			1147	734	199	211	3			
1	K	153	Total	C	N	O	S	0	0	0
			1196	765	209	218	4			
1	L	144	Total	C	N	O	S	0	0	0
			1097	706	190	198	3			
1	M	149	Total	C	N	O	S	0	0	0
			1163	743	201	215	4			
1	N	148	Total	C	N	O	S	0	0	0
			1154	739	199	213	3			
1	O	154	Total	C	N	O	S	0	0	0
			1220	779	216	221	4			
1	P	148	Total	C	N	O	S	0	0	0
			1158	742	200	213	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	145	Total	C	N	O	S	0	0	0
			1137	728	197	209	3			
1	R	152	Total	C	N	O	S	0	0	0
			1187	758	210	215	4			
1	S	147	Total	C	N	O	S	0	0	0
			1141	733	193	212	3			
1	T	152	Total	C	N	O	S	0	0	0
			1186	760	204	218	4			
1	U	147	Total	C	N	O	S	0	0	0
			1144	733	196	211	4			
1	V	148	Total	C	N	O	S	0	0	0
			1143	732	194	214	3			
1	W	152	Total	C	N	O	S	0	0	0
			1193	764	210	215	4			
1	X	148	Total	C	N	O	S	0	0	0
			1154	740	199	212	3			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP O83974
A	-6	ALA	-	expression tag	UNP O83974
A	-5	HIS	-	expression tag	UNP O83974
A	-4	HIS	-	expression tag	UNP O83974
A	-3	HIS	-	expression tag	UNP O83974
A	-2	HIS	-	expression tag	UNP O83974
A	-1	HIS	-	expression tag	UNP O83974
A	0	HIS	-	expression tag	UNP O83974
B	-7	MET	-	initiating methionine	UNP O83974
B	-6	ALA	-	expression tag	UNP O83974
B	-5	HIS	-	expression tag	UNP O83974
B	-4	HIS	-	expression tag	UNP O83974
B	-3	HIS	-	expression tag	UNP O83974
B	-2	HIS	-	expression tag	UNP O83974
B	-1	HIS	-	expression tag	UNP O83974
B	0	HIS	-	expression tag	UNP O83974
C	-7	MET	-	initiating methionine	UNP O83974
C	-6	ALA	-	expression tag	UNP O83974
C	-5	HIS	-	expression tag	UNP O83974
C	-4	HIS	-	expression tag	UNP O83974
C	-3	HIS	-	expression tag	UNP O83974
C	-2	HIS	-	expression tag	UNP O83974
C	-1	HIS	-	expression tag	UNP O83974

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP O83974
D	-7	MET	-	initiating methionine	UNP O83974
D	-6	ALA	-	expression tag	UNP O83974
D	-5	HIS	-	expression tag	UNP O83974
D	-4	HIS	-	expression tag	UNP O83974
D	-3	HIS	-	expression tag	UNP O83974
D	-2	HIS	-	expression tag	UNP O83974
D	-1	HIS	-	expression tag	UNP O83974
D	0	HIS	-	expression tag	UNP O83974
E	-7	MET	-	initiating methionine	UNP O83974
E	-6	ALA	-	expression tag	UNP O83974
E	-5	HIS	-	expression tag	UNP O83974
E	-4	HIS	-	expression tag	UNP O83974
E	-3	HIS	-	expression tag	UNP O83974
E	-2	HIS	-	expression tag	UNP O83974
E	-1	HIS	-	expression tag	UNP O83974
E	0	HIS	-	expression tag	UNP O83974
F	-7	MET	-	initiating methionine	UNP O83974
F	-6	ALA	-	expression tag	UNP O83974
F	-5	HIS	-	expression tag	UNP O83974
F	-4	HIS	-	expression tag	UNP O83974
F	-3	HIS	-	expression tag	UNP O83974
F	-2	HIS	-	expression tag	UNP O83974
F	-1	HIS	-	expression tag	UNP O83974
F	0	HIS	-	expression tag	UNP O83974
G	-7	MET	-	initiating methionine	UNP O83974
G	-6	ALA	-	expression tag	UNP O83974
G	-5	HIS	-	expression tag	UNP O83974
G	-4	HIS	-	expression tag	UNP O83974
G	-3	HIS	-	expression tag	UNP O83974
G	-2	HIS	-	expression tag	UNP O83974
G	-1	HIS	-	expression tag	UNP O83974
G	0	HIS	-	expression tag	UNP O83974
H	-7	MET	-	initiating methionine	UNP O83974
H	-6	ALA	-	expression tag	UNP O83974
H	-5	HIS	-	expression tag	UNP O83974
H	-4	HIS	-	expression tag	UNP O83974
H	-3	HIS	-	expression tag	UNP O83974
H	-2	HIS	-	expression tag	UNP O83974
H	-1	HIS	-	expression tag	UNP O83974
H	0	HIS	-	expression tag	UNP O83974
I	-7	MET	-	initiating methionine	UNP O83974

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-6	ALA	-	expression tag	UNP O83974
I	-5	HIS	-	expression tag	UNP O83974
I	-4	HIS	-	expression tag	UNP O83974
I	-3	HIS	-	expression tag	UNP O83974
I	-2	HIS	-	expression tag	UNP O83974
I	-1	HIS	-	expression tag	UNP O83974
I	0	HIS	-	expression tag	UNP O83974
J	-7	MET	-	initiating methionine	UNP O83974
J	-6	ALA	-	expression tag	UNP O83974
J	-5	HIS	-	expression tag	UNP O83974
J	-4	HIS	-	expression tag	UNP O83974
J	-3	HIS	-	expression tag	UNP O83974
J	-2	HIS	-	expression tag	UNP O83974
J	-1	HIS	-	expression tag	UNP O83974
J	0	HIS	-	expression tag	UNP O83974
K	-7	MET	-	initiating methionine	UNP O83974
K	-6	ALA	-	expression tag	UNP O83974
K	-5	HIS	-	expression tag	UNP O83974
K	-4	HIS	-	expression tag	UNP O83974
K	-3	HIS	-	expression tag	UNP O83974
K	-2	HIS	-	expression tag	UNP O83974
K	-1	HIS	-	expression tag	UNP O83974
K	0	HIS	-	expression tag	UNP O83974
L	-7	MET	-	initiating methionine	UNP O83974
L	-6	ALA	-	expression tag	UNP O83974
L	-5	HIS	-	expression tag	UNP O83974
L	-4	HIS	-	expression tag	UNP O83974
L	-3	HIS	-	expression tag	UNP O83974
L	-2	HIS	-	expression tag	UNP O83974
L	-1	HIS	-	expression tag	UNP O83974
L	0	HIS	-	expression tag	UNP O83974
M	-7	MET	-	initiating methionine	UNP O83974
M	-6	ALA	-	expression tag	UNP O83974
M	-5	HIS	-	expression tag	UNP O83974
M	-4	HIS	-	expression tag	UNP O83974
M	-3	HIS	-	expression tag	UNP O83974
M	-2	HIS	-	expression tag	UNP O83974
M	-1	HIS	-	expression tag	UNP O83974
M	0	HIS	-	expression tag	UNP O83974
N	-7	MET	-	initiating methionine	UNP O83974
N	-6	ALA	-	expression tag	UNP O83974
N	-5	HIS	-	expression tag	UNP O83974

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Chain	Residue	Modelled	Actual	Comment	Reference
N	-4	HIS	-	expression tag	UNP O83974
N	-3	HIS	-	expression tag	UNP O83974
N	-2	HIS	-	expression tag	UNP O83974
N	-1	HIS	-	expression tag	UNP O83974
N	0	HIS	-	expression tag	UNP O83974
O	-7	MET	-	initiating methionine	UNP O83974
O	-6	ALA	-	expression tag	UNP O83974
O	-5	HIS	-	expression tag	UNP O83974
O	-4	HIS	-	expression tag	UNP O83974
O	-3	HIS	-	expression tag	UNP O83974
O	-2	HIS	-	expression tag	UNP O83974
O	-1	HIS	-	expression tag	UNP O83974
O	0	HIS	-	expression tag	UNP O83974
P	-7	MET	-	initiating methionine	UNP O83974
P	-6	ALA	-	expression tag	UNP O83974
P	-5	HIS	-	expression tag	UNP O83974
P	-4	HIS	-	expression tag	UNP O83974
P	-3	HIS	-	expression tag	UNP O83974
P	-2	HIS	-	expression tag	UNP O83974
P	-1	HIS	-	expression tag	UNP O83974
P	0	HIS	-	expression tag	UNP O83974
Q	-7	MET	-	initiating methionine	UNP O83974
Q	-6	ALA	-	expression tag	UNP O83974
Q	-5	HIS	-	expression tag	UNP O83974
Q	-4	HIS	-	expression tag	UNP O83974
Q	-3	HIS	-	expression tag	UNP O83974
Q	-2	HIS	-	expression tag	UNP O83974
Q	-1	HIS	-	expression tag	UNP O83974
Q	0	HIS	-	expression tag	UNP O83974
R	-7	MET	-	initiating methionine	UNP O83974
R	-6	ALA	-	expression tag	UNP O83974
R	-5	HIS	-	expression tag	UNP O83974
R	-4	HIS	-	expression tag	UNP O83974
R	-3	HIS	-	expression tag	UNP O83974
R	-2	HIS	-	expression tag	UNP O83974
R	-1	HIS	-	expression tag	UNP O83974
R	0	HIS	-	expression tag	UNP O83974
S	-7	MET	-	initiating methionine	UNP O83974
S	-6	ALA	-	expression tag	UNP O83974
S	-5	HIS	-	expression tag	UNP O83974
S	-4	HIS	-	expression tag	UNP O83974
S	-3	HIS	-	expression tag	UNP O83974

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Chain	Residue	Modelled	Actual	Comment	Reference
S	-2	HIS	-	expression tag	UNP O83974
S	-1	HIS	-	expression tag	UNP O83974
S	0	HIS	-	expression tag	UNP O83974
T	-7	MET	-	initiating methionine	UNP O83974
T	-6	ALA	-	expression tag	UNP O83974
T	-5	HIS	-	expression tag	UNP O83974
T	-4	HIS	-	expression tag	UNP O83974
T	-3	HIS	-	expression tag	UNP O83974
T	-2	HIS	-	expression tag	UNP O83974
T	-1	HIS	-	expression tag	UNP O83974
T	0	HIS	-	expression tag	UNP O83974
U	-7	MET	-	initiating methionine	UNP O83974
U	-6	ALA	-	expression tag	UNP O83974
U	-5	HIS	-	expression tag	UNP O83974
U	-4	HIS	-	expression tag	UNP O83974
U	-3	HIS	-	expression tag	UNP O83974
U	-2	HIS	-	expression tag	UNP O83974
U	-1	HIS	-	expression tag	UNP O83974
U	0	HIS	-	expression tag	UNP O83974
V	-7	MET	-	initiating methionine	UNP O83974
V	-6	ALA	-	expression tag	UNP O83974
V	-5	HIS	-	expression tag	UNP O83974
V	-4	HIS	-	expression tag	UNP O83974
V	-3	HIS	-	expression tag	UNP O83974
V	-2	HIS	-	expression tag	UNP O83974
V	-1	HIS	-	expression tag	UNP O83974
V	0	HIS	-	expression tag	UNP O83974
W	-7	MET	-	initiating methionine	UNP O83974
W	-6	ALA	-	expression tag	UNP O83974
W	-5	HIS	-	expression tag	UNP O83974
W	-4	HIS	-	expression tag	UNP O83974
W	-3	HIS	-	expression tag	UNP O83974
W	-2	HIS	-	expression tag	UNP O83974
W	-1	HIS	-	expression tag	UNP O83974
W	0	HIS	-	expression tag	UNP O83974
X	-7	MET	-	initiating methionine	UNP O83974
X	-6	ALA	-	expression tag	UNP O83974
X	-5	HIS	-	expression tag	UNP O83974
X	-4	HIS	-	expression tag	UNP O83974
X	-3	HIS	-	expression tag	UNP O83974
X	-2	HIS	-	expression tag	UNP O83974
X	-1	HIS	-	expression tag	UNP O83974

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Chain	Residue	Modelled	Actual	Comment	Reference
X	0	HIS	-	expression tag	UNP O83974

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	12	Total O 12 12	0	0
2	B	15	Total O 15 15	0	0
2	C	5	Total O 5 5	0	0
2	D	4	Total O 4 4	0	0
2	E	9	Total O 9 9	0	0
2	F	9	Total O 9 9	0	0
2	G	7	Total O 7 7	0	0
2	H	14	Total O 14 14	0	0
2	I	4	Total O 4 4	0	0
2	J	8	Total O 8 8	0	0
2	K	11	Total O 11 11	0	0
2	L	3	Total O 3 3	0	0
2	M	5	Total O 5 5	0	0
2	N	14	Total O 14 14	0	0
2	O	10	Total O 10 10	0	0
2	P	7	Total O 7 7	0	0
2	Q	6	Total O 6 6	0	0
2	R	8	Total O 8 8	0	0
2	S	5	Total O 5 5	0	0

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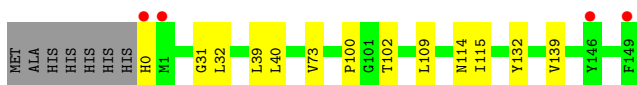
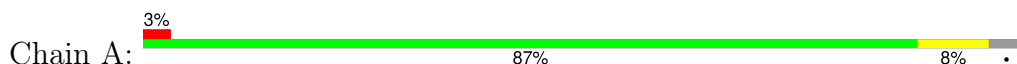
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	T	3	Total 3	O 3	0	0
2	U	5	Total 5	O 5	0	0
2	V	3	Total 3	O 3	0	0
2	W	3	Total 3	O 3	0	0
2	X	12	Total 12	O 12	0	0

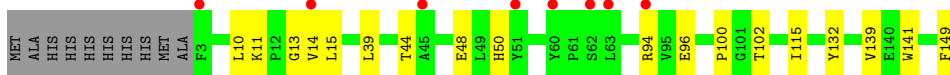
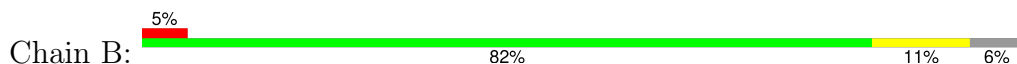
3 Residue-property plots [i](#)

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.

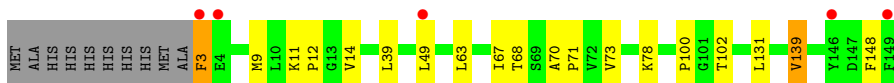
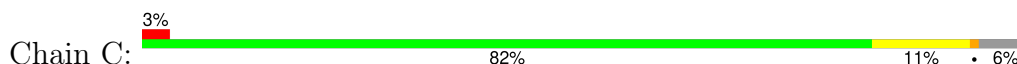
- Molecule 1: Nucleoside diphosphate kinase



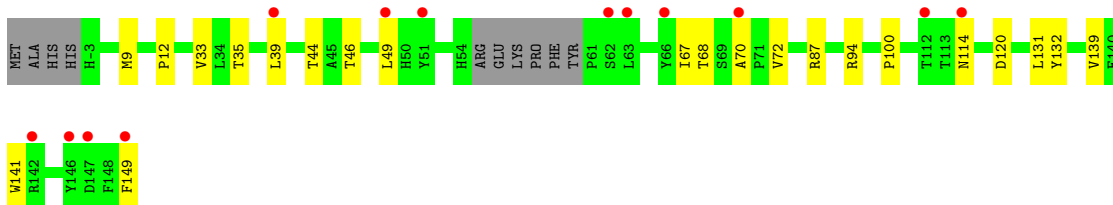
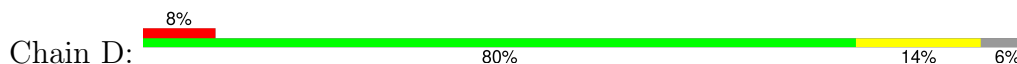
- Molecule 1: Nucleoside diphosphate kinase



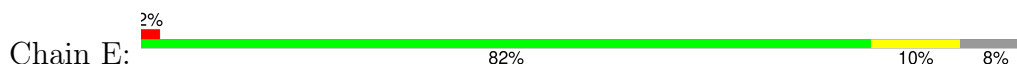
- Molecule 1: Nucleoside diphosphate kinase



- Molecule 1: Nucleoside diphosphate kinase

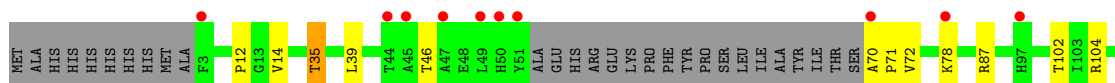


- Molecule 1: Nucleoside diphosphate kinase

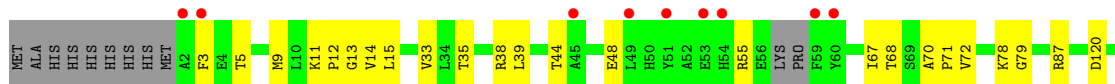
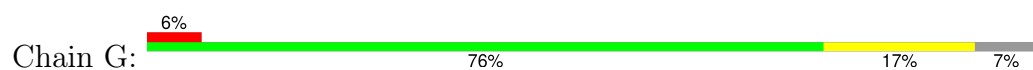




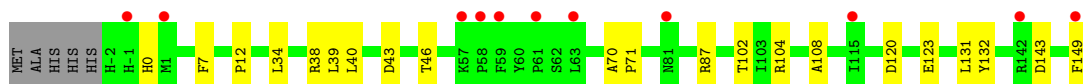
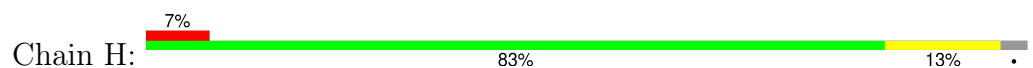
- Molecule 1: Nucleoside diphosphate kinase



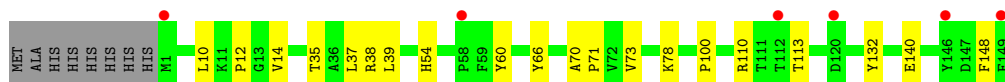
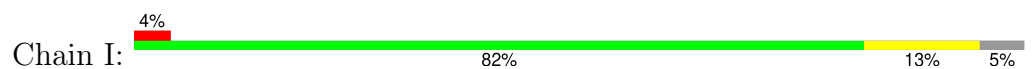
- Molecule 1: Nucleoside diphosphate kinase



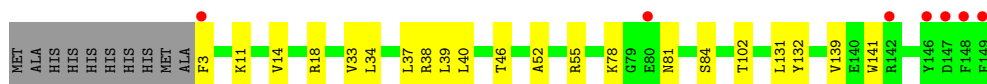
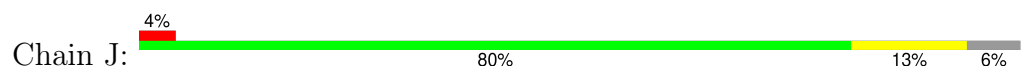
- Molecule 1: Nucleoside diphosphate kinase



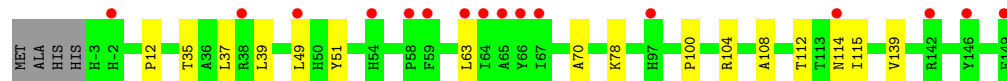
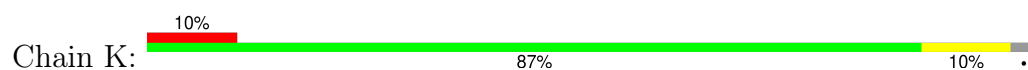
- Molecule 1: Nucleoside diphosphate kinase



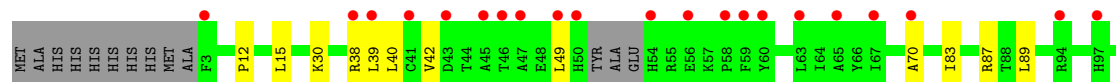
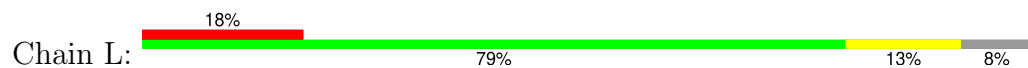
- Molecule 1: Nucleoside diphosphate kinase



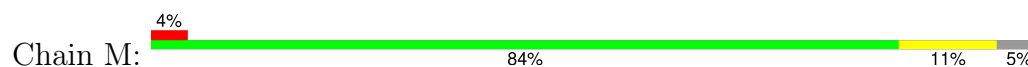
- Molecule 1: Nucleoside diphosphate kinase



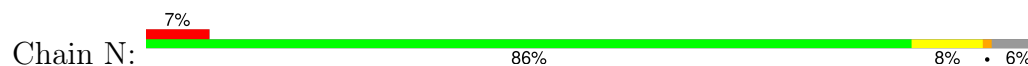
- Molecule 1: Nucleoside diphosphate kinase



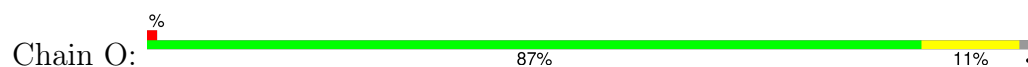
- Molecule 1: Nucleoside diphosphate kinase



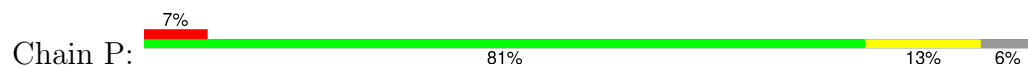
- Molecule 1: Nucleoside diphosphate kinase



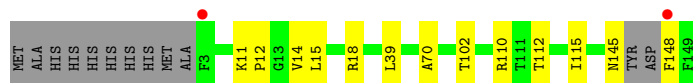
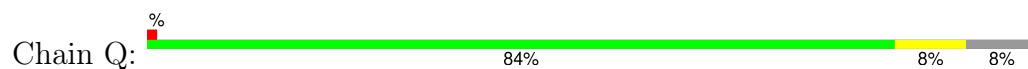
- Molecule 1: Nucleoside diphosphate kinase



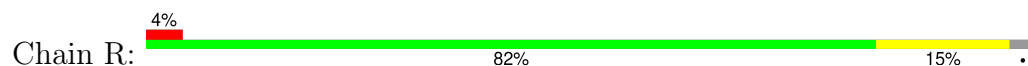
- Molecule 1: Nucleoside diphosphate kinase



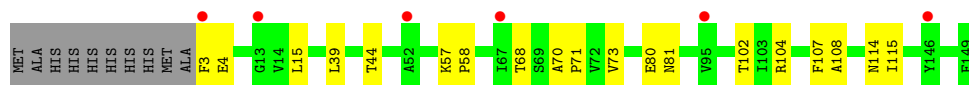
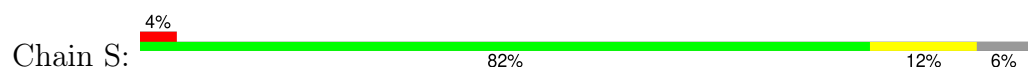
- Molecule 1: Nucleoside diphosphate kinase



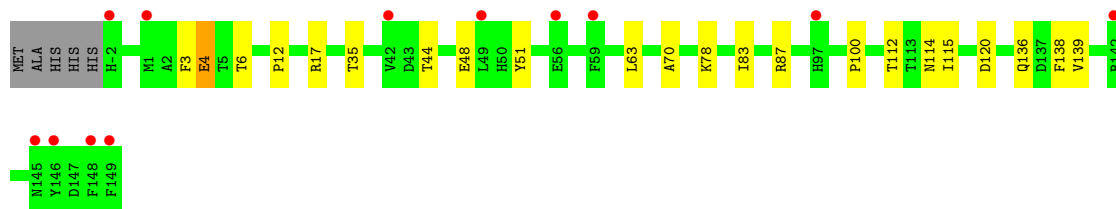
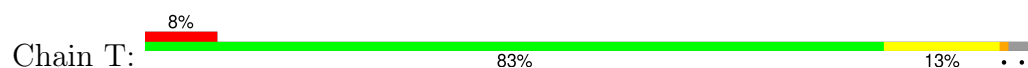
- Molecule 1: Nucleoside diphosphate kinase



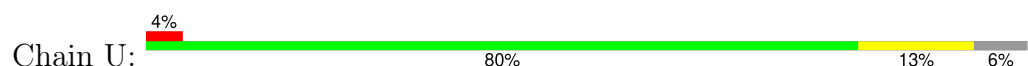
- Molecule 1: Nucleoside diphosphate kinase



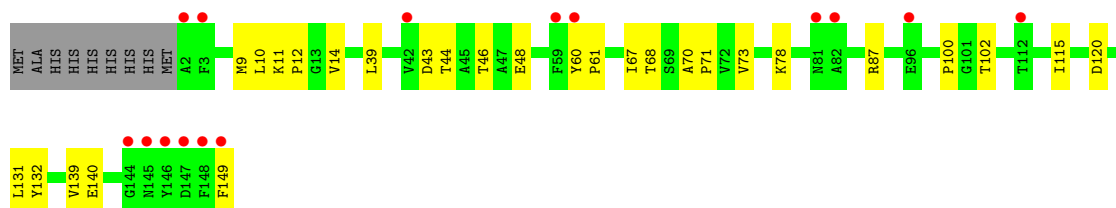
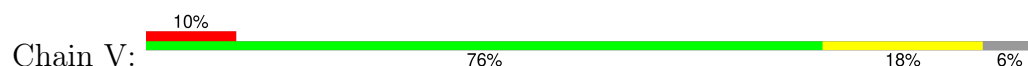
- Molecule 1: Nucleoside diphosphate kinase



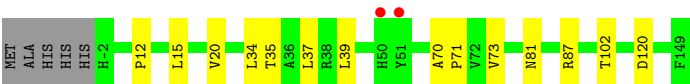
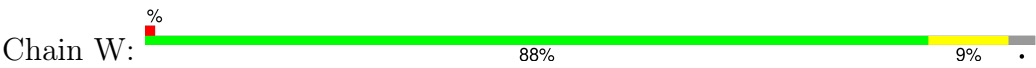
- Molecule 1: Nucleoside diphosphate kinase



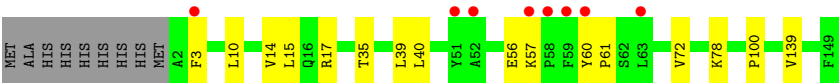
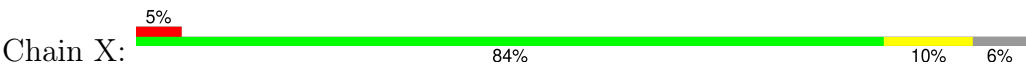
- Molecule 1: Nucleoside diphosphate kinase



● Molecule 1: Nucleoside diphosphate kinase



● Molecule 1: Nucleoside diphosphate kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	67.88Å 107.93Å 128.76Å 88.04° 86.76° 77.50°	Depositor
Resolution (Å)	49.12 – 2.54 49.12 – 2.54	Depositor EDS
% Data completeness (in resolution range)	97.6 (49.12-2.54) 97.6 (49.12-2.54)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 2.54Å)	Xtriage
Refinement program	PHENIX (2.0_5936: ???)	Depositor
R, R_{free}	0.213 , 0.259 0.215 , 0.258	Depositor DCC
R_{free} test set	5880 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.508	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	27863	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.68% 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	0.21	0/1203	0.41	0/1633
1	B	0.22	0/1168	0.39	0/1588
1	C	0.21	0/1183	0.41	0/1606
1	D	0.21	0/1177	0.39	0/1596
1	E	0.23	0/1142	0.44	0/1552
1	F	0.20	0/1026	0.41	0/1390
1	G	0.24	0/1162	0.40	0/1577
1	H	0.22	0/1229	0.43	0/1668
1	I	0.21	0/1196	0.39	0/1623
1	J	0.22	0/1172	0.42	0/1591
1	K	0.19	0/1226	0.37	0/1667
1	L	0.17	0/1120	0.36	0/1522
1	M	0.19	0/1188	0.39	0/1612
1	N	0.20	0/1180	0.41	0/1604
1	O	0.20	0/1251	0.38	0/1698
1	P	0.20	0/1184	0.41	0/1608
1	Q	0.21	0/1161	0.41	0/1574
1	R	0.21	0/1215	0.40	0/1650
1	S	0.24	0/1167	0.42	0/1587
1	T	0.20	0/1214	0.39	0/1649
1	U	0.25	0/1168	0.43	0/1584
1	V	0.27	0/1168	0.46	0/1588
1	W	0.21	0/1222	0.41	0/1659
1	X	0.22	0/1180	0.40	0/1603
All	All	0.22	0/28302	0.41	0/38429

There are no bond length outliers.

There are no bond angle outliers.

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	1176	0	1165	9	0
1	B	1143	0	1123	18	0
1	C	1157	0	1145	16	0
1	D	1151	0	1133	23	0
1	E	1119	0	1116	12	0
1	F	1007	0	998	13	0
1	G	1138	0	1121	27	0
1	H	1200	0	1183	28	0
1	I	1170	0	1162	14	0
1	J	1147	0	1136	22	0
1	K	1196	0	1164	10	0
1	L	1097	0	1073	20	0
1	M	1163	0	1155	16	0
1	N	1154	0	1135	14	0
1	O	1220	0	1197	15	0
1	P	1158	0	1146	16	0
1	Q	1137	0	1131	10	0
1	R	1187	0	1170	27	0
1	S	1141	0	1119	15	0
1	T	1186	0	1163	19	0
1	U	1144	0	1137	17	0
1	V	1143	0	1121	21	0
1	W	1193	0	1177	11	0
1	X	1154	0	1140	12	0
2	A	12	0	0	0	0
2	B	15	0	0	0	0
2	C	5	0	0	0	0
2	D	4	0	0	0	0
2	E	9	0	0	0	0
2	F	9	0	0	0	0
2	G	7	0	0	0	0
2	H	14	0	0	0	0
2	I	4	0	0	0	0
2	J	8	0	0	0	0
2	K	11	0	0	0	0
2	L	3	0	0	0	0
2	M	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	14	0	0	0	0
2	O	10	0	0	0	0
2	P	7	0	0	0	0
2	Q	6	0	0	0	0
2	R	8	0	0	0	0
2	S	5	0	0	0	0
2	T	3	0	0	0	0
2	U	5	0	0	0	0
2	V	3	0	0	0	0
2	W	3	0	0	0	0
2	X	12	0	0	0	0
All	All	27863	0	27310	348	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.

The worst 5 of 348 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:J:46:THR:HG23	1:J:131:LEU:HD21	1.37	1.07
1:V:46:THR:HG23	1:V:131:LEU:HD21	1.39	1.04
1:D:46:THR:HG23	1:D:131:LEU:HD21	1.39	1.01
1:L:49:LEU:HD12	1:L:131:LEU:HD11	1.45	0.97
1:G:15:LEU:HD11	1:G:39:LEU:HD11	1.53	0.90

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	148/157 (94%)	146 (99%)	2 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	145/157 (92%)	143 (99%)	2 (1%)	0	100	100
1	C	145/157 (92%)	142 (98%)	3 (2%)	0	100	100
1	D	143/157 (91%)	140 (98%)	3 (2%)	0	100	100
1	E	142/157 (90%)	140 (99%)	2 (1%)	0	100	100
1	F	125/157 (80%)	123 (98%)	2 (2%)	0	100	100
1	G	142/157 (90%)	140 (99%)	2 (1%)	0	100	100
1	H	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	I	147/157 (94%)	143 (97%)	4 (3%)	0	100	100
1	J	145/157 (92%)	142 (98%)	3 (2%)	0	100	100
1	K	151/157 (96%)	147 (97%)	4 (3%)	0	100	100
1	L	140/157 (89%)	138 (99%)	2 (1%)	0	100	100
1	M	147/157 (94%)	144 (98%)	3 (2%)	0	100	100
1	N	146/157 (93%)	144 (99%)	1 (1%)	1 (1%)	18	25
1	O	152/157 (97%)	150 (99%)	2 (1%)	0	100	100
1	P	146/157 (93%)	142 (97%)	4 (3%)	0	100	100
1	Q	141/157 (90%)	139 (99%)	2 (1%)	0	100	100
1	R	150/157 (96%)	148 (99%)	2 (1%)	0	100	100
1	S	145/157 (92%)	141 (97%)	4 (3%)	0	100	100
1	T	150/157 (96%)	146 (97%)	4 (3%)	0	100	100
1	U	143/157 (91%)	139 (97%)	4 (3%)	0	100	100
1	V	146/157 (93%)	143 (98%)	3 (2%)	0	100	100
1	W	150/157 (96%)	147 (98%)	3 (2%)	0	100	100
1	X	146/157 (93%)	142 (97%)	4 (3%)	0	100	100
All	All	3485/3768 (92%)	3418 (98%)	66 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	115	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	123/131 (94%)	121 (98%)	2 (2%)	55	73
1	B	119/131 (91%)	119 (100%)	0	100	100
1	C	122/131 (93%)	120 (98%)	2 (2%)	55	73
1	D	121/131 (92%)	120 (99%)	1 (1%)	73	84
1	E	118/131 (90%)	116 (98%)	2 (2%)	53	72
1	F	106/131 (81%)	105 (99%)	1 (1%)	70	82
1	G	118/131 (90%)	117 (99%)	1 (1%)	73	84
1	H	126/131 (96%)	125 (99%)	1 (1%)	73	84
1	I	123/131 (94%)	122 (99%)	1 (1%)	73	84
1	J	120/131 (92%)	120 (100%)	0	100	100
1	K	124/131 (95%)	122 (98%)	2 (2%)	55	73
1	L	111/131 (85%)	111 (100%)	0	100	100
1	M	122/131 (93%)	121 (99%)	1 (1%)	73	84
1	N	120/131 (92%)	120 (100%)	0	100	100
1	O	128/131 (98%)	128 (100%)	0	100	100
1	P	121/131 (92%)	120 (99%)	1 (1%)	73	84
1	Q	120/131 (92%)	120 (100%)	0	100	100
1	R	123/131 (94%)	123 (100%)	0	100	100
1	S	119/131 (91%)	119 (100%)	0	100	100
1	T	123/131 (94%)	120 (98%)	3 (2%)	43	61
1	U	120/131 (92%)	120 (100%)	0	100	100
1	V	119/131 (91%)	117 (98%)	2 (2%)	53	72
1	W	124/131 (95%)	122 (98%)	2 (2%)	55	73
1	X	120/131 (92%)	119 (99%)	1 (1%)	73	84
All	All	2890/3144 (92%)	2867 (99%)	23 (1%)	73	84

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	35	THR
1	T	136	GLN

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Mol	Chain	Res	Type
1	T	112	THR
1	V	115	ILE
1	E	139	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	U	50	HIS
1	W	16	GLN
1	W	97	HIS
1	W	81	ASN
1	O	50	HIS

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	150/157 (95%)	0.17	4 (2%) 56 57	26, 39, 68, 92	0
1	B	147/157 (93%)	0.52	8 (5%) 31 31	28, 45, 94, 141	0
1	C	147/157 (93%)	0.33	5 (3%) 48 49	25, 46, 81, 101	0
1	D	147/157 (93%)	0.57	13 (8%) 15 15	27, 50, 102, 114	0
1	E	144/157 (91%)	0.22	3 (2%) 63 64	25, 42, 69, 100	0
1	F	129/157 (82%)	0.71	14 (10%) 10 10	31, 47, 105, 158	0
1	G	146/157 (92%)	0.67	10 (6%) 23 22	33, 55, 101, 118	0
1	H	152/157 (96%)	0.63	11 (7%) 21 20	28, 51, 98, 124	0
1	I	149/157 (94%)	0.49	6 (4%) 42 43	25, 50, 87, 121	0
1	J	147/157 (93%)	0.43	7 (4%) 35 35	29, 48, 89, 166	0
1	K	153/157 (97%)	0.67	16 (10%) 11 11	32, 55, 114, 129	0
1	L	144/157 (91%)	1.12	29 (20%) 3 2	41, 66, 128, 193	0
1	M	149/157 (94%)	0.48	6 (4%) 42 43	29, 48, 89, 127	0
1	N	148/157 (94%)	0.55	11 (7%) 20 19	29, 47, 97, 149	0
1	O	154/157 (98%)	0.31	2 (1%) 75 75	28, 44, 82, 108	0
1	P	148/157 (94%)	0.67	11 (7%) 20 19	30, 48, 94, 119	0
1	Q	145/157 (92%)	0.29	2 (1%) 73 74	27, 42, 68, 88	0
1	R	152/157 (96%)	0.44	6 (3%) 43 44	28, 50, 76, 103	0
1	S	147/157 (93%)	0.51	6 (4%) 41 42	31, 46, 76, 86	0
1	T	152/157 (96%)	0.84	12 (7%) 18 18	34, 61, 92, 102	0
1	U	147/157 (93%)	0.71	7 (4%) 35 35	34, 54, 78, 98	0
1	V	148/157 (94%)	0.92	15 (10%) 12 11	29, 61, 89, 98	0
1	W	152/157 (96%)	0.50	2 (1%) 75 75	33, 49, 82, 101	0
1	X	148/157 (94%)	0.50	8 (5%) 31 31	29, 45, 81, 104	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3545/3768 (94%)	0.55	214 (6%) 27 27	25, 49, 93, 193	0

The worst 5 of 214 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	149	PHE	5.8
1	M	148	PHE	5.5
1	P	59	PHE	5.2
1	M	149	PHE	5.2
1	G	3	PHE	5.1

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 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.