



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:10 PM GMT

PDB ID : 4UW1  
Title : X-ray crystal structure of human TNKS in complex with a small molecule inhibitor  
Authors : Oliver, A.W.; Rajasekaran, M.B.; Pearl, L.H.  
Deposited on : 2014-08-08  
Resolution : 3.37 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

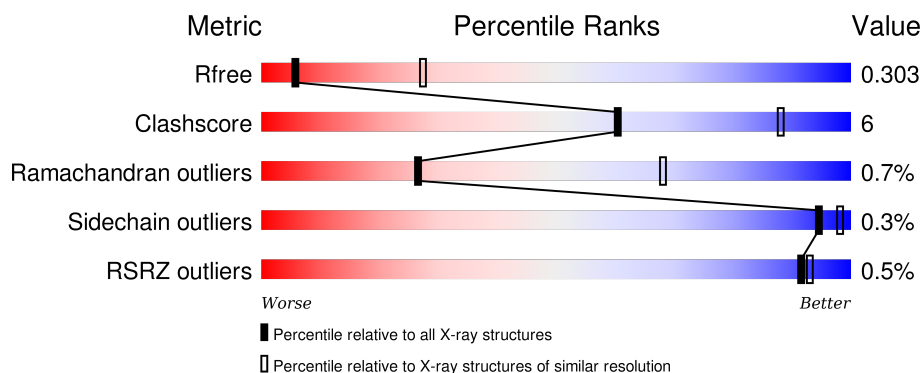
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.37 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))
$R_{free}$	91344	1084 (3.46-3.30)
Clashscore	102246	1158 (3.46-3.30)
Ramachandran outliers	100387	1139 (3.46-3.30)
Sidechain outliers	100360	1138 (3.46-3.30)
RSRZ outliers	91569	1089 (3.46-3.30)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	258	<div> <div></div> <div>71%10%19%</div> </div>
1	B	258	<div> <div></div> <div>70%11%19%</div> </div>
1	C	258	<div> <div></div> <div>64%15%21%</div> </div>
1	D	258	<div> <div>%</div> <div>70%12%18%</div> </div>
1	E	258	<div> <div>%</div> <div>66%14%20%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	258	
1	G	258	
1	H	258	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	2314	-	-	-	X
3	GOL	D	2316	-	-	-	X
4	EDO	G	2314	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12945 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 TANKYRASE-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	0	0
			1571	1000	281	279	11			
1	B	209	Total	C	N	O	S	0	0	0
			1608	1019	287	291	11			
1	C	205	Total	C	N	O	S	0	3	0
			1573	999	283	281	10			
1	D	211	Total	C	N	O	S	0	0	0
			1593	1007	285	290	11			
1	E	207	Total	C	N	O	S	0	0	0
			1584	1001	285	287	11			
1	F	209	Total	C	N	O	S	0	0	0
			1575	1002	277	286	10			
1	G	209	Total	C	N	O	S	0	2	0
			1601	1016	285	290	10			
1	H	210	Total	C	N	O	S	0	0	0
			1624	1025	296	292	11			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1068	MET	-	EXPRESSION TAG	UNP O95271
A	1069	HIS	-	EXPRESSION TAG	UNP O95271
A	1070	HIS	-	EXPRESSION TAG	UNP O95271
A	1071	HIS	-	EXPRESSION TAG	UNP O95271
A	1072	HIS	-	EXPRESSION TAG	UNP O95271
A	1073	HIS	-	EXPRESSION TAG	UNP O95271
A	1074	HIS	-	EXPRESSION TAG	UNP O95271
A	1075	SER	-	EXPRESSION TAG	UNP O95271
A	1076	SER	-	EXPRESSION TAG	UNP O95271
A	1077	GLY	-	EXPRESSION TAG	UNP O95271
A	1078	VAL	-	EXPRESSION TAG	UNP O95271
A	1079	ASP	-	EXPRESSION TAG	UNP O95271
A	1080	LEU	-	EXPRESSION TAG	UNP O95271

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1081	GLY	-	EXPRESSION TAG	UNP O95271
A	1082	THR	-	EXPRESSION TAG	UNP O95271
A	1083	GLU	-	EXPRESSION TAG	UNP O95271
A	1084	ASN	-	EXPRESSION TAG	UNP O95271
A	1085	LEU	-	EXPRESSION TAG	UNP O95271
A	1086	TYR	-	EXPRESSION TAG	UNP O95271
A	1087	PHE	-	EXPRESSION TAG	UNP O95271
A	1088	GLN	-	EXPRESSION TAG	UNP O95271
A	1089	SER	-	EXPRESSION TAG	UNP O95271
A	1090	MET	-	EXPRESSION TAG	UNP O95271
A	1266	ILE	MET	VARIANT	UNP O95271
B	1068	MET	-	EXPRESSION TAG	UNP O95271
B	1069	HIS	-	EXPRESSION TAG	UNP O95271
B	1070	HIS	-	EXPRESSION TAG	UNP O95271
B	1071	HIS	-	EXPRESSION TAG	UNP O95271
B	1072	HIS	-	EXPRESSION TAG	UNP O95271
B	1073	HIS	-	EXPRESSION TAG	UNP O95271
B	1074	HIS	-	EXPRESSION TAG	UNP O95271
B	1075	SER	-	EXPRESSION TAG	UNP O95271
B	1076	SER	-	EXPRESSION TAG	UNP O95271
B	1077	GLY	-	EXPRESSION TAG	UNP O95271
B	1078	VAL	-	EXPRESSION TAG	UNP O95271
B	1079	ASP	-	EXPRESSION TAG	UNP O95271
B	1080	LEU	-	EXPRESSION TAG	UNP O95271
B	1081	GLY	-	EXPRESSION TAG	UNP O95271
B	1082	THR	-	EXPRESSION TAG	UNP O95271
B	1083	GLU	-	EXPRESSION TAG	UNP O95271
B	1084	ASN	-	EXPRESSION TAG	UNP O95271
B	1085	LEU	-	EXPRESSION TAG	UNP O95271
B	1086	TYR	-	EXPRESSION TAG	UNP O95271
B	1087	PHE	-	EXPRESSION TAG	UNP O95271
B	1088	GLN	-	EXPRESSION TAG	UNP O95271
B	1089	SER	-	EXPRESSION TAG	UNP O95271
B	1090	MET	-	EXPRESSION TAG	UNP O95271
B	1266	ILE	MET	VARIANT	UNP O95271
C	1068	MET	-	EXPRESSION TAG	UNP O95271
C	1069	HIS	-	EXPRESSION TAG	UNP O95271
C	1070	HIS	-	EXPRESSION TAG	UNP O95271
C	1071	HIS	-	EXPRESSION TAG	UNP O95271
C	1072	HIS	-	EXPRESSION TAG	UNP O95271
C	1073	HIS	-	EXPRESSION TAG	UNP O95271
C	1074	HIS	-	EXPRESSION TAG	UNP O95271

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1075	SER	-	EXPRESSION TAG	UNP O95271
C	1076	SER	-	EXPRESSION TAG	UNP O95271
C	1077	GLY	-	EXPRESSION TAG	UNP O95271
C	1078	VAL	-	EXPRESSION TAG	UNP O95271
C	1079	ASP	-	EXPRESSION TAG	UNP O95271
C	1080	LEU	-	EXPRESSION TAG	UNP O95271
C	1081	GLY	-	EXPRESSION TAG	UNP O95271
C	1082	THR	-	EXPRESSION TAG	UNP O95271
C	1083	GLU	-	EXPRESSION TAG	UNP O95271
C	1084	ASN	-	EXPRESSION TAG	UNP O95271
C	1085	LEU	-	EXPRESSION TAG	UNP O95271
C	1086	TYR	-	EXPRESSION TAG	UNP O95271
C	1087	PHE	-	EXPRESSION TAG	UNP O95271
C	1088	GLN	-	EXPRESSION TAG	UNP O95271
C	1089	SER	-	EXPRESSION TAG	UNP O95271
C	1090	MET	-	EXPRESSION TAG	UNP O95271
C	1266	ILE	MET	VARIANT	UNP O95271
D	1068	MET	-	EXPRESSION TAG	UNP O95271
D	1069	HIS	-	EXPRESSION TAG	UNP O95271
D	1070	HIS	-	EXPRESSION TAG	UNP O95271
D	1071	HIS	-	EXPRESSION TAG	UNP O95271
D	1072	HIS	-	EXPRESSION TAG	UNP O95271
D	1073	HIS	-	EXPRESSION TAG	UNP O95271
D	1074	HIS	-	EXPRESSION TAG	UNP O95271
D	1075	SER	-	EXPRESSION TAG	UNP O95271
D	1076	SER	-	EXPRESSION TAG	UNP O95271
D	1077	GLY	-	EXPRESSION TAG	UNP O95271
D	1078	VAL	-	EXPRESSION TAG	UNP O95271
D	1079	ASP	-	EXPRESSION TAG	UNP O95271
D	1080	LEU	-	EXPRESSION TAG	UNP O95271
D	1081	GLY	-	EXPRESSION TAG	UNP O95271
D	1082	THR	-	EXPRESSION TAG	UNP O95271
D	1083	GLU	-	EXPRESSION TAG	UNP O95271
D	1084	ASN	-	EXPRESSION TAG	UNP O95271
D	1085	LEU	-	EXPRESSION TAG	UNP O95271
D	1086	TYR	-	EXPRESSION TAG	UNP O95271
D	1087	PHE	-	EXPRESSION TAG	UNP O95271
D	1088	GLN	-	EXPRESSION TAG	UNP O95271
D	1089	SER	-	EXPRESSION TAG	UNP O95271
D	1090	MET	-	EXPRESSION TAG	UNP O95271
D	1266	ILE	MET	VARIANT	UNP O95271
E	1068	MET	-	EXPRESSION TAG	UNP O95271

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1069	HIS	-	EXPRESSION TAG	UNP O95271
E	1070	HIS	-	EXPRESSION TAG	UNP O95271
E	1071	HIS	-	EXPRESSION TAG	UNP O95271
E	1072	HIS	-	EXPRESSION TAG	UNP O95271
E	1073	HIS	-	EXPRESSION TAG	UNP O95271
E	1074	HIS	-	EXPRESSION TAG	UNP O95271
E	1075	SER	-	EXPRESSION TAG	UNP O95271
E	1076	SER	-	EXPRESSION TAG	UNP O95271
E	1077	GLY	-	EXPRESSION TAG	UNP O95271
E	1078	VAL	-	EXPRESSION TAG	UNP O95271
E	1079	ASP	-	EXPRESSION TAG	UNP O95271
E	1080	LEU	-	EXPRESSION TAG	UNP O95271
E	1081	GLY	-	EXPRESSION TAG	UNP O95271
E	1082	THR	-	EXPRESSION TAG	UNP O95271
E	1083	GLU	-	EXPRESSION TAG	UNP O95271
E	1084	ASN	-	EXPRESSION TAG	UNP O95271
E	1085	LEU	-	EXPRESSION TAG	UNP O95271
E	1086	TYR	-	EXPRESSION TAG	UNP O95271
E	1087	PHE	-	EXPRESSION TAG	UNP O95271
E	1088	GLN	-	EXPRESSION TAG	UNP O95271
E	1089	SER	-	EXPRESSION TAG	UNP O95271
E	1090	MET	-	EXPRESSION TAG	UNP O95271
E	1266	ILE	MET	VARIANT	UNP O95271
F	1068	MET	-	EXPRESSION TAG	UNP O95271
F	1069	HIS	-	EXPRESSION TAG	UNP O95271
F	1070	HIS	-	EXPRESSION TAG	UNP O95271
F	1071	HIS	-	EXPRESSION TAG	UNP O95271
F	1072	HIS	-	EXPRESSION TAG	UNP O95271
F	1073	HIS	-	EXPRESSION TAG	UNP O95271
F	1074	HIS	-	EXPRESSION TAG	UNP O95271
F	1075	SER	-	EXPRESSION TAG	UNP O95271
F	1076	SER	-	EXPRESSION TAG	UNP O95271
F	1077	GLY	-	EXPRESSION TAG	UNP O95271
F	1078	VAL	-	EXPRESSION TAG	UNP O95271
F	1079	ASP	-	EXPRESSION TAG	UNP O95271
F	1080	LEU	-	EXPRESSION TAG	UNP O95271
F	1081	GLY	-	EXPRESSION TAG	UNP O95271
F	1082	THR	-	EXPRESSION TAG	UNP O95271
F	1083	GLU	-	EXPRESSION TAG	UNP O95271
F	1084	ASN	-	EXPRESSION TAG	UNP O95271
F	1085	LEU	-	EXPRESSION TAG	UNP O95271
F	1086	TYR	-	EXPRESSION TAG	UNP O95271

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1087	PHE	-	EXPRESSION TAG	UNP 095271
F	1088	GLN	-	EXPRESSION TAG	UNP 095271
F	1089	SER	-	EXPRESSION TAG	UNP 095271
F	1090	MET	-	EXPRESSION TAG	UNP 095271
F	1266	ILE	MET	VARIANT	UNP 095271
G	1068	MET	-	EXPRESSION TAG	UNP 095271
G	1069	HIS	-	EXPRESSION TAG	UNP 095271
G	1070	HIS	-	EXPRESSION TAG	UNP 095271
G	1071	HIS	-	EXPRESSION TAG	UNP 095271
G	1072	HIS	-	EXPRESSION TAG	UNP 095271
G	1073	HIS	-	EXPRESSION TAG	UNP 095271
G	1074	HIS	-	EXPRESSION TAG	UNP 095271
G	1075	SER	-	EXPRESSION TAG	UNP 095271
G	1076	SER	-	EXPRESSION TAG	UNP 095271
G	1077	GLY	-	EXPRESSION TAG	UNP 095271
G	1078	VAL	-	EXPRESSION TAG	UNP 095271
G	1079	ASP	-	EXPRESSION TAG	UNP 095271
G	1080	LEU	-	EXPRESSION TAG	UNP 095271
G	1081	GLY	-	EXPRESSION TAG	UNP 095271
G	1082	THR	-	EXPRESSION TAG	UNP 095271
G	1083	GLU	-	EXPRESSION TAG	UNP 095271
G	1084	ASN	-	EXPRESSION TAG	UNP 095271
G	1085	LEU	-	EXPRESSION TAG	UNP 095271
G	1086	TYR	-	EXPRESSION TAG	UNP 095271
G	1087	PHE	-	EXPRESSION TAG	UNP 095271
G	1088	GLN	-	EXPRESSION TAG	UNP 095271
G	1089	SER	-	EXPRESSION TAG	UNP 095271
G	1090	MET	-	EXPRESSION TAG	UNP 095271
G	1266	ILE	MET	VARIANT	UNP 095271
H	1068	MET	-	EXPRESSION TAG	UNP 095271
H	1069	HIS	-	EXPRESSION TAG	UNP 095271
H	1070	HIS	-	EXPRESSION TAG	UNP 095271
H	1071	HIS	-	EXPRESSION TAG	UNP 095271
H	1072	HIS	-	EXPRESSION TAG	UNP 095271
H	1073	HIS	-	EXPRESSION TAG	UNP 095271
H	1074	HIS	-	EXPRESSION TAG	UNP 095271
H	1075	SER	-	EXPRESSION TAG	UNP 095271
H	1076	SER	-	EXPRESSION TAG	UNP 095271
H	1077	GLY	-	EXPRESSION TAG	UNP 095271
H	1078	VAL	-	EXPRESSION TAG	UNP 095271
H	1079	ASP	-	EXPRESSION TAG	UNP 095271
H	1080	LEU	-	EXPRESSION TAG	UNP 095271

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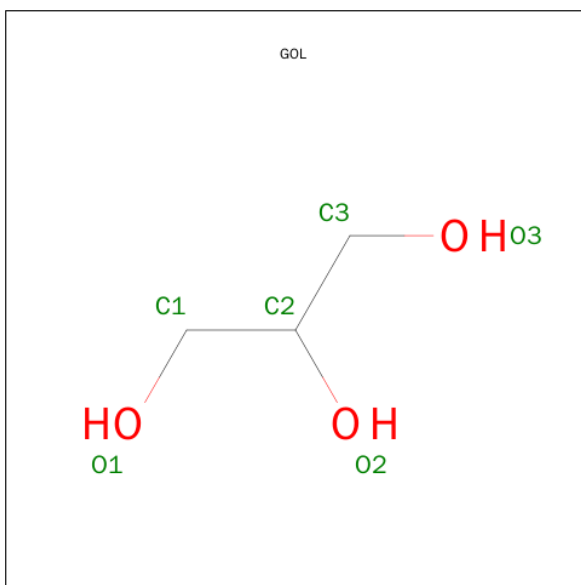
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Chain	Residue	Modelled	Actual	Comment	Reference
H	1081	GLY	-	EXPRESSION TAG	UNP O95271
H	1082	THR	-	EXPRESSION TAG	UNP O95271
H	1083	GLU	-	EXPRESSION TAG	UNP O95271
H	1084	ASN	-	EXPRESSION TAG	UNP O95271
H	1085	LEU	-	EXPRESSION TAG	UNP O95271
H	1086	TYR	-	EXPRESSION TAG	UNP O95271
H	1087	PHE	-	EXPRESSION TAG	UNP O95271
H	1088	GLN	-	EXPRESSION TAG	UNP O95271
H	1089	SER	-	EXPRESSION TAG	UNP O95271
H	1090	MET	-	EXPRESSION TAG	UNP O95271
H	1266	ILE	MET	VARIANT	UNP O95271

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

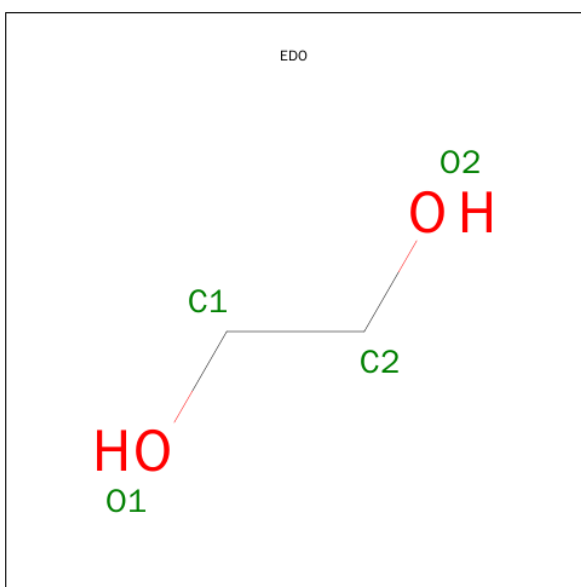
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	H	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



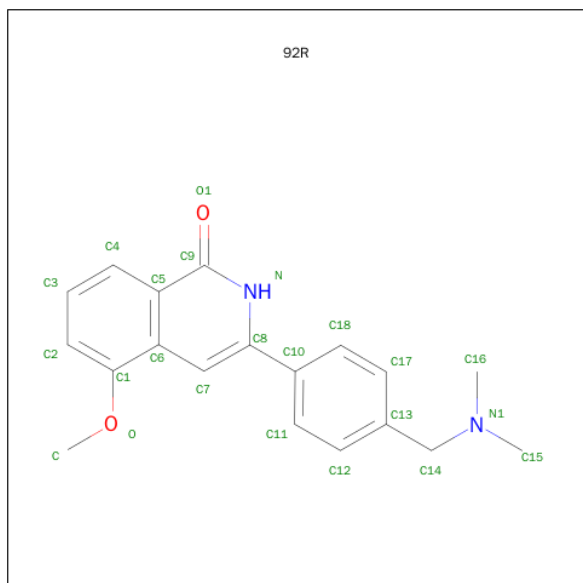
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			4	2	2		
4	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is 3-{4-[(DIMETHYLAMINO)METHYL]PHENYL}-5-METHOXYISOQUINOLIN-1(2H)-ONE (three-letter code: 92R) (formula: C<sub>19</sub>H<sub>20</sub>N<sub>2</sub>O<sub>2</sub>).



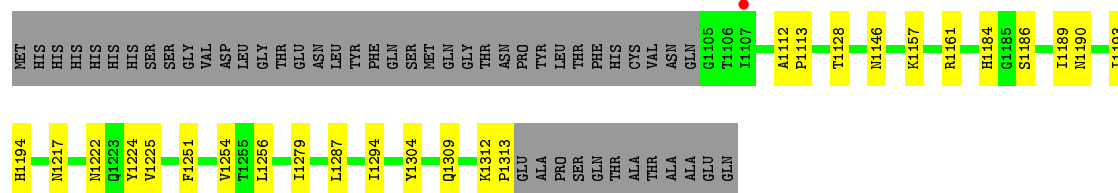
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			20	17	1	2		
5	B	1	Total	C	N	O	0	0
			23	19	2	2		
5	C	1	Total	C	N	O	0	0
			23	19	2	2		
5	D	1	Total	C	N	O	0	0
			20	17	1	2		
5	E	1	Total	C	N	O	0	0
			23	19	2	2		
5	F	1	Total	C	N	O	0	0
			23	19	2	2		
5	G	1	Total	C	N	O	0	0
			23	19	2	2		
5	H	1	Total	C	N	O	0	0
			23	19	2	2		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

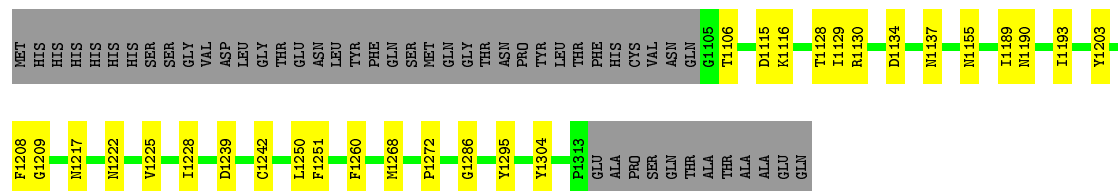
#### • Molecule 1: TANKYRASE-1

Chain A: 



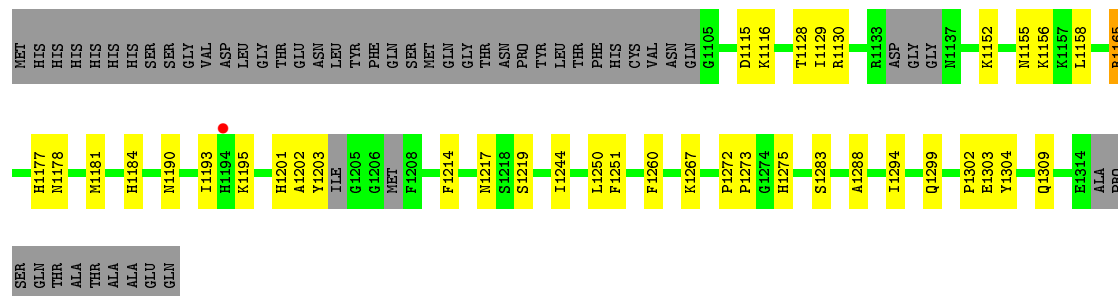
#### • Molecule 1: TANKYRASE-1

Chain B: 



#### • Molecule 1: TANKYRASE-1

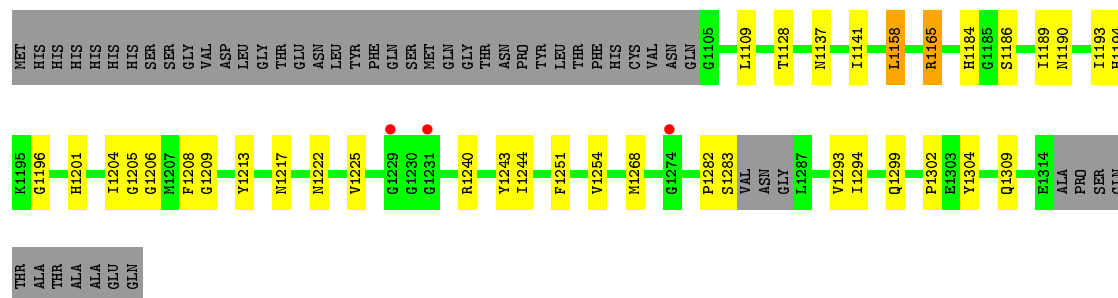
Chain C: 



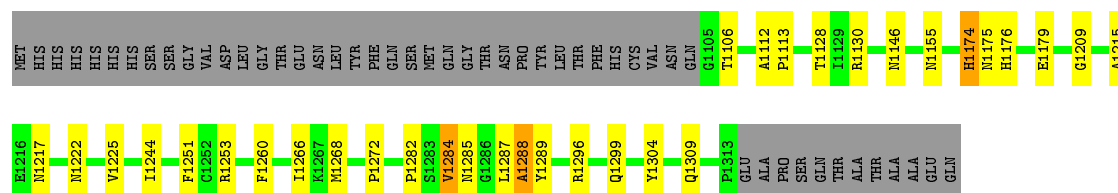
#### • Molecule 1: TANKYRASE-1

Chain D: 

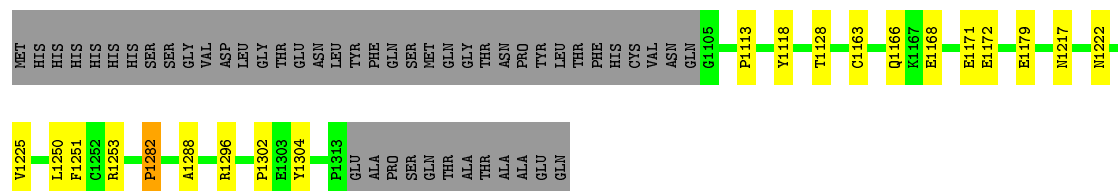
- Molecule 1: TANKYRASE-1



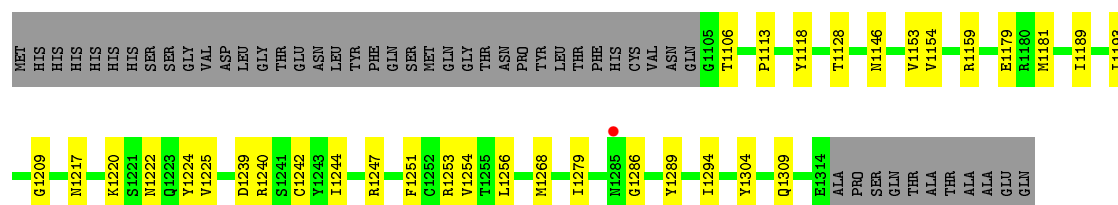
- Molecule 1: TANKYRASE-1



- Molecule 1: TANKYRASE-1



- Molecule 1: TANKYRASE-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.59Å 82.31Å 86.73Å 71.38° 67.31° 89.51°	Depositor
Resolution (Å)	46.92 – 3.37 46.92 – 3.37	Depositor EDS
% Data completeness (in resolution range)	98.9 (46.92-3.37) 88.0 (46.92-3.37)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 3.40Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.266 , 0.322 0.252 , 0.303	Depositor DCC
$R_{free}$ test set	1358 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.1	Xtriage
Anisotropy	0.504	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 47.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 27051 reflections	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	12945	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.07 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.4912e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, 92R, EDO

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	0.20	0/1613	0.36	0/2189
1	B	0.21	0/1650	0.35	0/2229
1	C	0.21	0/1621	0.36	0/2189
1	D	0.21	0/1635	0.35	0/2216
1	E	0.24	0/1625	0.38	0/2199
1	F	0.21	0/1617	0.36	0/2191
1	G	0.22	0/1651	0.35	0/2239
1	H	0.21	0/1667	0.36	0/2255
All	All	0.21	0/13079	0.36	0/17707

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 [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	1571	0	1419	17	0
1	B	1608	0	1465	14	0
1	C	1573	0	1415	24	0
1	D	1593	0	1410	18	0
1	E	1584	0	1427	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1575	0	1409	17	0
1	G	1601	0	1435	11	0
1	H	1624	0	1485	20	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	6	0	8	1	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
4	A	4	0	6	0	0
4	C	4	0	6	1	0
4	G	4	0	6	1	0
5	A	20	0	12	3	0
5	B	23	0	20	0	0
5	C	23	0	20	0	0
5	D	20	0	12	2	0
5	E	23	0	20	1	0
5	F	23	0	20	1	0
5	G	23	0	20	0	0
5	H	23	0	20	1	0
All	All	12945	0	11651	138	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 (138) 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:1251:PHE:HB3	1:B:1304:TYR:HB2	1.65	0.78
1:D:1251:PHE:HB3	1:D:1304:TYR:HB2	1.71	0.73
1:F:1174:HIS:O	1:F:1176:HIS:N	2.22	0.72
1:A:1251:PHE:HB3	1:A:1304:TYR:HB2	1.72	0.72
1:G:1251:PHE:HB3	1:G:1304:TYR:HB2	1.74	0.68
1:F:1282:PRO:HA	1:F:1287:LEU:HB3	1.76	0.68
1:H:1153:VAL:HG21	1:H:1193:ILE:HD12	1.77	0.66
1:C:1251:PHE:HB3	1:C:1304:TYR:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:1251:PHE:HB3	1:H:1304:TYR:HB2	1.81	0.62
1:A:1161:ARG:NH2	1:G:1171:GLU:OE2	2.32	0.62
1:B:1128:THR:HB	1:B:1217:ASN:HA	1.81	0.62
1:E:1128:THR:HB	1:E:1217:ASN:HA	1.81	0.62
1:E:1158:LEU:HD11	1:E:1196:GLY:HA3	1.82	0.61
1:G:1179:GLU:OE2	1:G:1253:ARG:NH1	2.34	0.60
1:G:1128:THR:HB	1:G:1217:ASN:HA	1.84	0.60
1:C:1244:ILE:O	1:C:1309:GLN:NE2	2.35	0.60
1:F:1251:PHE:HB3	1:F:1304:TYR:HB2	1.86	0.58
1:E:1251:PHE:HB3	1:E:1304:TYR:HB2	1.84	0.57
1:E:1165:ARG:NH2	1:E:1299:GLN:OE1	2.37	0.57
1:H:1179:GLU:OE2	1:H:1253:ARG:NE	2.37	0.55
1:D:1128:THR:HB	1:D:1217:ASN:HA	1.89	0.55
1:F:1106:THR:OG1	1:F:1155:ASN:ND2	2.40	0.54
1:E:1244:ILE:O	1:E:1309:GLN:NE2	2.40	0.54
1:D:1215:ALA:HB2	5:D:3000:92R:H3	1.89	0.53
1:H:1239:ASP:HB3	1:H:1242:CYS:HB2	1.90	0.53
1:E:1209:GLY:HA3	1:E:1268:MET:H	1.74	0.53
1:H:1224:TYR:CD1	5:H:3000:92R:H11	2.44	0.53
1:E:1222:ASN:HA	1:E:1225:VAL:HG23	1.91	0.52
1:F:1215:ALA:HB2	5:F:3000:92R:H3	1.90	0.52
1:D:1244:ILE:O	1:D:1309:GLN:NE2	2.41	0.52
1:A:1184:HIS:HE1	5:A:3000:92R:H18	1.74	0.52
1:C:1288:ALA:HB2	1:F:1130:ARG:HH22	1.75	0.52
1:F:1128:THR:HB	1:F:1217:ASN:HA	1.92	0.52
1:B:1115:ASP:OD1	1:B:1116:LYS:N	2.43	0.52
1:C:1283:SER:HA	1:C:1288:ALA:HA	1.92	0.52
1:E:1137:ASN:OD1	1:E:1240:ARG:NH2	2.40	0.52
1:D:1115:ASP:OD1	1:D:1116:LYS:N	2.42	0.51
1:F:1146:ASN:HB3	1:F:1309:GLN:HB2	1.91	0.51
1:C:1260:PHE:HB2	1:C:1275:HIS:CD2	2.47	0.50
1:C:1155:ASN:ND2	1:C:1158:LEU:HG	2.27	0.50
1:C:1177:HIS:ND1	1:C:1177:HIS:O	2.45	0.49
1:C:1201:HIS:ND1	1:C:1201:HIS:O	2.42	0.49
1:H:1240:ARG:O	1:H:1247:ARG:NH2	2.46	0.49
1:C:1294:ILE:HD12	1:C:1299:GLN:HB2	1.94	0.49
1:A:1256:LEU:HD13	1:A:1279:ILE:HD11	1.95	0.49
1:D:1224:TYR:CD1	5:D:3000:92R:H11	2.48	0.48
1:B:1106:THR:OG1	1:B:1155:ASN:ND2	2.45	0.48
1:F:1179:GLU:OE1	1:F:1253:ARG:NH2	2.43	0.48
1:A:1222:ASN:HA	1:A:1225:VAL:HG23	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1287:LEU:HD23	1:A:1287:LEU:H	1.78	0.48
1:B:1260:PHE:CD2	1:B:1272:PRO:HG2	2.49	0.48
1:A:1157:LYS:HD3	1:A:1161:ARG:HH21	1.78	0.48
1:A:1146:ASN:HB3	1:A:1309:GLN:HB2	1.95	0.47
1:C:1165:ARG:HG3	1:C:1165:ARG:O	2.11	0.47
1:H:1128:THR:HB	1:H:1217:ASN:HA	1.96	0.47
1:C:1128:THR:HB	1:C:1217:ASN:HA	1.95	0.47
1:C:1190:ASN:HA	1:C:1193:ILE:HG12	1.96	0.47
1:D:1222:ASN:HA	1:D:1225:VAL:HG23	1.97	0.47
1:B:1190:ASN:HA	1:B:1193:ILE:HG12	1.96	0.47
1:H:1244:ILE:O	1:H:1309:GLN:NE2	2.47	0.47
1:H:1256:LEU:HD13	1:H:1279:ILE:HD11	1.97	0.47
1:D:1159:ARG:O	1:D:1159:ARG:HG3	2.15	0.47
1:H:1222:ASN:HA	1:H:1225:VAL:HG23	1.97	0.47
1:F:1284:VAL:HA	1:F:1285:ASN:HA	1.62	0.47
1:C:1115:ASP:OD1	1:C:1116:LYS:N	2.48	0.47
1:C:1152:LYS:NZ	1:C:1303:GLU:OE2	2.41	0.46
1:H:1189:ILE:O	1:H:1193:ILE:HG12	2.15	0.46
1:D:1125:MET:SD	1:D:1306:ILE:HG21	2.55	0.46
1:F:1222:ASN:HA	1:F:1225:VAL:HG23	1.98	0.46
1:H:1220:LYS:NZ	1:H:1289:TYR:O	2.49	0.46
1:F:1209:GLY:HA3	1:F:1268:MET:H	1.81	0.46
1:B:1189:ILE:HD12	1:B:1250:LEU:HG	1.98	0.46
1:E:1282:PRO:HA	1:E:1283:SER:HA	1.70	0.45
1:E:1141:ILE:O	1:E:1243:TYR:OH	2.28	0.45
1:E:1208:PHE:HB2	1:E:1293:VAL:HG21	1.98	0.45
1:E:1294:ILE:HD12	1:E:1299:GLN:HB2	1.97	0.45
1:C:1129:ILE:O	1:C:1219:SER:OG	2.27	0.45
1:E:1109:LEU:HD22	1:H:1154:VAL:HG11	1.99	0.45
1:D:1243:TYR:HB3	1:F:1244:ILE:HD11	1.98	0.45
1:F:1260:PHE:CG	1:F:1272:PRO:HG2	2.52	0.45
1:C:1195:LYS:HE2	1:C:1195:LYS:HB2	1.69	0.45
1:F:1288:ALA:HA	1:F:1289:TYR:HA	1.49	0.45
1:B:1208:PHE:O	1:B:1295:TYR:OH	2.32	0.44
1:H:1106:THR:HG21	1:H:1193:ILE:HG22	1.98	0.44
1:H:1159:ARG:HH21	1:H:1253:ARG:HH11	1.66	0.44
1:B:1134:ASP:OD2	1:B:1137:ASN:N	2.48	0.44
1:D:1106:THR:OG1	1:D:1155:ASN:ND2	2.50	0.44
1:B:1239:ASP:HB3	1:B:1242:CYS:HB2	1.99	0.44
1:D:1122:GLU:HG3	1:D:1147:VAL:HG21	2.00	0.44
1:C:1152:LYS:HE3	1:C:1152:LYS:HB3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1186:SER:O	1:E:1189:ILE:HG13	2.18	0.44
1:B:1129:ILE:O	1:B:1130:ARG:NE	2.51	0.44
1:B:1203:TYR:HE1	1:B:1228:ILE:HG12	1.82	0.43
1:F:1296:ARG:HB2	1:F:1299:GLN:HG3	2.00	0.43
1:A:1186:SER:O	1:A:1189:ILE:HG13	2.18	0.43
1:G:1163:CYS:HA	1:G:1166:GLN:HB2	2.01	0.43
1:C:1181:MET:HB3	1:C:1251:PHE:CZ	2.54	0.43
1:D:1193:ILE:HG13	1:D:1194:HIS:ND1	2.33	0.43
1:G:1168:GLU:O	1:G:1172:GLU:HG3	2.18	0.43
1:A:1224:TYR:CD1	5:A:3000:92R:H11	2.53	0.43
1:E:1190:ASN:O	1:E:1194:HIS:ND1	2.40	0.43
1:A:1254:VAL:HG13	1:A:1294:ILE:HD13	2.00	0.43
1:E:1190:ASN:HA	1:E:1193:ILE:HG12	2.01	0.43
1:A:1112:ALA:HA	1:A:1113:PRO:HD3	1.89	0.43
1:D:1153:VAL:HB	1:D:1302:PRO:O	2.19	0.43
1:B:1209:GLY:HA3	1:B:1268:MET:H	1.84	0.43
1:E:1254:VAL:HG13	1:E:1294:ILE:HD13	2.00	0.42
1:A:1190:ASN:O	1:A:1194:HIS:ND1	2.38	0.42
1:C:1250:LEU:HD13	1:C:1302:PRO:HB3	2.01	0.42
1:G:1296:ARG:HD2	4:G:2314:EDO:H21	2.00	0.42
1:A:1312:LYS:HA	1:A:1313:PRO:HD3	1.92	0.42
1:G:1250:LEU:HD13	1:G:1302:PRO:HB3	2.00	0.42
1:E:1184:HIS:NE2	5:E:3000:92R:H18	2.34	0.42
1:F:1112:ALA:HA	1:F:1113:PRO:HD3	1.85	0.42
1:H:1181:MET:HB3	1:H:1251:PHE:CZ	2.54	0.42
3:A:2314:GOL:H11	5:A:3000:92R:H17	2.02	0.42
1:A:1190:ASN:N	1:A:1190:ASN:OD1	2.53	0.42
1:C:1272:PRO:HB2	1:C:1275:HIS:CD2	2.55	0.42
1:B:1222:ASN:HA	1:B:1225:VAL:HG23	2.02	0.42
1:G:1282:PRO:HD2	1:G:1288:ALA:HB1	2.02	0.42
1:H:1254:VAL:HG13	1:H:1294:ILE:HD13	2.02	0.41
1:C:1267:LYS:NZ	4:C:2316:EDO:O2	2.53	0.41
1:C:1155:ASN:OD1	1:C:1156:LYS:N	2.54	0.41
1:D:1177:HIS:HD2	1:D:1179:GLU:HB2	1.85	0.41
1:C:1273:PRO:HB3	1:E:1201:HIS:CE1	2.55	0.41
1:C:1184:HIS:HB2	1:C:1214:PHE:CE2	2.55	0.41
1:E:1206:GLY:HA3	1:E:1213:TYR:CZ	2.55	0.41
1:G:1222:ASN:HA	1:G:1225:VAL:HG23	2.03	0.41
1:D:1312:LYS:HA	1:D:1313:PRO:HD3	1.94	0.41
1:D:1251:PHE:HD2	1:D:1304:TYR:CD2	2.39	0.41
1:A:1128:THR:HB	1:A:1217:ASN:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1190:ASN:HA	1:A:1193:ILE:HG12	2.01	0.41
1:H:1209:GLY:HA3	1:H:1268:MET:H	1.85	0.40
1:H:1146:ASN:N	1:H:1309:GLN:O	2.38	0.40
1:D:1260:PHE:CG	1:D:1272:PRO:HG2	2.56	0.40
1:E:1204:ILE:HD12	1:E:1205:GLY:N	2.36	0.40
1:H:1113:PRO:HA	1:H:1118:TYR:CD1	2.57	0.40
1:G:1113:PRO:HA	1:G:1118:TYR:CD1	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	207/258 (80%)	200 (97%)	7 (3%)	0	100	100
1	B	207/258 (80%)	196 (95%)	10 (5%)	1 (0%)	34	74
1	C	200/258 (78%)	184 (92%)	13 (6%)	3 (2%)	13	50
1	D	209/258 (81%)	198 (95%)	11 (5%)	0	100	100
1	E	203/258 (79%)	191 (94%)	11 (5%)	1 (0%)	34	74
1	F	207/258 (80%)	193 (93%)	9 (4%)	5 (2%)	7	41
1	G	209/258 (81%)	203 (97%)	5 (2%)	1 (0%)	34	74
1	H	208/258 (81%)	194 (93%)	13 (6%)	1 (0%)	34	74
All	All	1650/2064 (80%)	1559 (94%)	79 (5%)	12 (1%)	26	68

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	1175	ASN
1	C	1202	ALA
1	G	1282	PRO

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Mol	Chain	Res	Type
1	C	1178	ASN
1	F	1174	HIS
1	F	1288	ALA
1	C	1130	ARG
1	F	1284	VAL
1	H	1286	GLY
1	B	1286	GLY
1	F	1266	ILE
1	E	1302	PRO

### 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	147/219 (67%)	147 (100%)	0	100	100
1	B	154/219 (70%)	154 (100%)	0	100	100
1	C	147/219 (67%)	145 (99%)	2 (1%)	74	89
1	D	149/219 (68%)	149 (100%)	0	100	100
1	E	152/219 (69%)	150 (99%)	2 (1%)	76	90
1	F	146/219 (67%)	146 (100%)	0	100	100
1	G	152/219 (69%)	152 (100%)	0	100	100
1	H	158/219 (72%)	158 (100%)	0	100	100
All	All	1205/1752 (69%)	1201 (100%)	4 (0%)	94	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1165	ARG
1	C	1203	TYR
1	E	1158	LEU
1	E	1165	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1184	HIS
1	B	1262	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 22 ligands modelled in this entry, 8 are monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	GOL	A	2314	-	5,5,5	0.36	0	5,5,5	0.22	0
4	EDO	A	2315	-	3,3,3	0.44	0	2,2,2	0.40	0
5	92R	A	3000	-	22,22,25	1.24	3 (13%)	26,31,35	1.13	2 (7%)
5	92R	B	3000	-	25,25,25	1.18	3 (12%)	30,35,35	1.04	2 (6%)
3	GOL	C	2315	-	5,5,5	0.36	0	5,5,5	0.23	0
4	EDO	C	2316	-	3,3,3	0.44	0	2,2,2	0.42	0
5	92R	C	3000	-	25,25,25	1.18	3 (12%)	30,35,35	1.04	2 (6%)
3	GOL	D	2316	-	5,5,5	0.35	0	5,5,5	0.23	0
5	92R	D	3000	-	22,22,25	1.24	3 (13%)	26,31,35	1.14	2 (7%)
5	92R	E	3000	-	25,25,25	1.19	3 (12%)	30,35,35	1.05	2 (6%)
5	92R	F	3000	-	25,25,25	1.17	3 (12%)	30,35,35	1.04	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	G	2314	-	3,3,3	0.44	0	2,2,2	0.40	0
5	92R	G	3000	-	25,25,25	1.17	3 (12%)	30,35,35	1.05	2 (6%)
5	92R	H	3000	-	25,25,25	1.17	3 (12%)	30,35,35	1.04	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	2314	-	-	0/4/4/4	0/0/0/0
4	EDO	A	2315	-	-	0/1/1/1	0/0/0/0
5	92R	A	3000	-	-	0/6/6/10	0/3/3/3
5	92R	B	3000	-	-	0/10/10/10	0/3/3/3
3	GOL	C	2315	-	-	0/4/4/4	0/0/0/0
4	EDO	C	2316	-	-	0/1/1/1	0/0/0/0
5	92R	C	3000	-	-	0/10/10/10	0/3/3/3
3	GOL	D	2316	-	-	0/4/4/4	0/0/0/0
5	92R	D	3000	-	-	0/6/6/10	0/3/3/3
5	92R	E	3000	-	-	0/10/10/10	0/3/3/3
5	92R	F	3000	-	-	0/10/10/10	0/3/3/3
4	EDO	G	2314	-	-	0/1/1/1	0/0/0/0
5	92R	G	3000	-	-	0/10/10/10	0/3/3/3
5	92R	H	3000	-	-	0/10/10/10	0/3/3/3

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	3000	92R	C8-N	2.59	1.38	1.34
5	D	3000	92R	C8-N	2.59	1.38	1.34
5	H	3000	92R	C8-N	2.60	1.38	1.34
5	A	3000	92R	C8-N	2.62	1.38	1.34
5	B	3000	92R	C8-N	2.62	1.39	1.34
5	C	3000	92R	C8-N	2.66	1.39	1.34
5	A	3000	92R	C9-N	2.67	1.37	1.33
5	G	3000	92R	C8-N	2.68	1.39	1.34
5	E	3000	92R	C8-N	2.68	1.39	1.34
5	D	3000	92R	C9-N	2.70	1.37	1.33
5	B	3000	92R	C9-N	2.70	1.37	1.33
5	G	3000	92R	C9-N	2.72	1.37	1.33
5	C	3000	92R	C9-N	2.72	1.37	1.33
5	E	3000	92R	C9-N	2.74	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	3000	92R	C9-N	2.75	1.38	1.33
5	H	3000	92R	C9-N	2.80	1.38	1.33
5	H	3000	92R	C9-C5	3.69	1.47	1.41
5	G	3000	92R	C9-C5	3.71	1.47	1.41
5	A	3000	92R	C9-C5	3.72	1.47	1.41
5	D	3000	92R	C9-C5	3.75	1.47	1.41
5	C	3000	92R	C9-C5	3.76	1.47	1.41
5	B	3000	92R	C9-C5	3.79	1.47	1.41
5	E	3000	92R	C9-C5	3.79	1.47	1.41
5	F	3000	92R	C9-C5	3.79	1.47	1.41

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	3000	92R	C7-C8-N	-3.43	119.20	121.51
5	E	3000	92R	C7-C8-N	-3.42	119.20	121.51
5	A	3000	92R	C7-C8-N	-3.42	119.20	121.51
5	G	3000	92R	C7-C8-N	-3.40	119.21	121.51
5	F	3000	92R	C7-C8-N	-3.37	119.24	121.51
5	B	3000	92R	C7-C8-N	-3.35	119.25	121.51
5	C	3000	92R	C7-C8-N	-3.34	119.25	121.51
5	H	3000	92R	C7-C8-N	-3.32	119.27	121.51
5	G	3000	92R	C9-N-C8	4.12	125.37	116.49
5	C	3000	92R	C9-N-C8	4.13	125.37	116.49
5	E	3000	92R	C9-N-C8	4.13	125.38	116.49
5	F	3000	92R	C9-N-C8	4.14	125.40	116.49
5	B	3000	92R	C9-N-C8	4.14	125.41	116.49
5	H	3000	92R	C9-N-C8	4.14	125.41	116.49
5	A	3000	92R	C9-N-C8	4.16	125.44	116.49
5	D	3000	92R	C9-N-C8	4.16	125.46	116.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2314	GOL	1	0
5	A	3000	92R	3	0
4	C	2316	EDO	1	0
5	D	3000	92R	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	3000	92R	1	0
5	F	3000	92R	1	0
4	G	2314	EDO	1	0
5	H	3000	92R	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	209/258 (81%)	0.06	1 (0%) 91 93	25, 46, 74, 91	0
1	B	209/258 (81%)	-0.04	0 100 100	15, 44, 65, 76	0
1	C	205/258 (79%)	-0.03	1 (0%) 91 93	18, 45, 71, 86	0
1	D	211/258 (81%)	-0.08	2 (0%) 85 88	20, 48, 68, 95	0
1	E	207/258 (80%)	0.14	3 (1%) 78 80	20, 46, 73, 87	0
1	F	209/258 (81%)	0.01	0 100 100	19, 43, 71, 81	0
1	G	209/258 (81%)	-0.07	0 100 100	21, 47, 71, 80	0
1	H	210/258 (81%)	-0.01	1 (0%) 91 93	20, 43, 66, 85	0
All	All	1669/2064 (80%)	-0.00	8 (0%) 91 93	15, 46, 71, 95	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1107	ILE	2.5
1	E	1274	GLY	2.4
1	E	1229	GLY	2.4
1	D	1105	GLY	2.3
1	H	1285	ASN	2.3
1	E	1231	GLY	2.1
1	C	1194	HIS	2.1
1	D	1136	GLY	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	G	2314	4/4	0.94	0.40	4.85	28,28,29,29	0
3	GOL	D	2316	6/6	0.93	0.37	4.05	19,19,19,20	0
3	GOL	A	2314	6/6	0.83	0.43	2.46	33,33,34,34	0
3	GOL	C	2315	6/6	0.91	0.37	1.09	26,27,27,27	0
5	92R	F	3000	23/23	0.93	0.29	0.74	4,11,23,24	0
5	92R	H	3000	23/23	0.95	0.27	0.73	10,11,18,18	0
5	92R	E	3000	23/23	0.93	0.29	0.66	8,12,18,19	0
4	EDO	A	2315	4/4	0.91	0.23	0.45	23,23,23,24	0
5	92R	B	3000	23/23	0.90	0.29	0.42	35,36,39,39	0
5	92R	A	3000	20/23	0.95	0.27	0.22	25,30,32,32	0
5	92R	C	3000	23/23	0.89	0.23	-0.34	25,28,35,36	0
5	92R	G	3000	23/23	0.97	0.19	-0.57	1,4,12,12	0
5	92R	D	3000	20/23	0.91	0.22	-0.72	24,27,29,29	0
2	ZN	C	2000	1/1	0.99	0.05	-1.58	19,19,19,19	0
2	ZN	D	2000	1/1	0.99	0.05	-1.74	17,17,17,17	0
2	ZN	A	2000	1/1	1.00	0.05	-1.82	30,30,30,30	0
2	ZN	H	2000	1/1	0.98	0.08	-1.98	29,29,29,29	0
2	ZN	G	2000	1/1	0.99	0.05	-1.99	27,27,27,27	0
4	EDO	C	2316	4/4	0.96	0.15	-2.61	22,22,22,23	0
2	ZN	E	2000	1/1	0.99	0.02	-3.53	37,37,37,37	0
2	ZN	F	2000	1/1	0.98	0.05	-	44,44,44,44	0
2	ZN	B	2000	1/1	0.99	0.07	-	40,40,40,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.