W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:32 PM GMT

PDB ID	:	4TOR
Title	:	Crystal structure of Tankyrase 1 with IWR-8
Authors	:	Chen, H.; Zhang, X.; Lum, L.; Chen, C.
Deposited on	:	2014-06-06
Resolution	:	1.50 Å(reported)

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

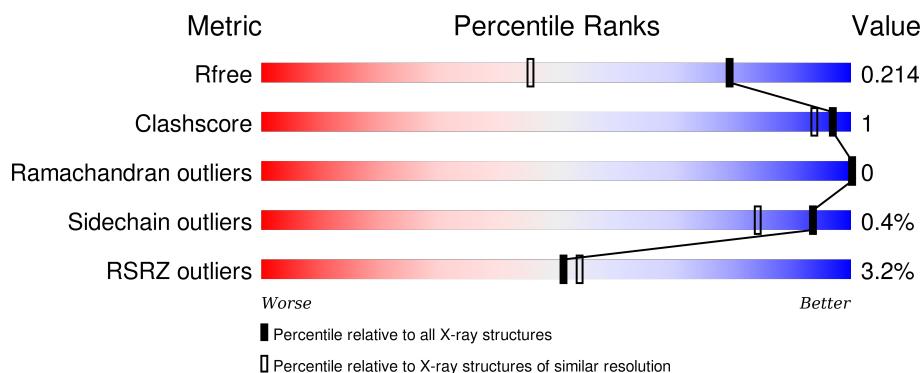|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 1.50 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	Percentile Ranks	Value
Rfree		0.214
Clashscore		1
Ramachandran outliers		0
Sidechain outliers		0.4%
RSRZ outliers		3.2%

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (1.50-1.50)

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 >=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 <=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	236	4% / 86% • 11%
1	B	236	2% / 87% • 11%
1	C	236	3% / 86% • 11%
1	D	236	3% / 86% • 11%

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
4	CL	A	1406	-	-	-	X
4	CL	A	1407	-	-	-	X
4	CL	B	1404	-	-	-	X
4	CL	B	1406	-	-	-	X
4	CL	C	1403	-	-	-	X
4	CL	C	1405	-	-	-	X
4	CL	C	1407	-	-	-	X
4	CL	D	1405	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 14272 atoms, of which 6495 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 3313	C 1066	H 1619	N 312	O 305	S 11	0	2	0
1	B	209	Total 3326	C 1071	H 1625	N 314	O 305	S 11	0	3	0
1	C	209	Total 3333	C 1072	H 1632	N 312	O 306	S 11	0	3	0
1	D	209	Total 3313	C 1066	H 1619	N 312	O 305	S 11	0	2	0

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1080	MET	-	initiating methionine	UNP O95271
A	1081	GLY	-	expression tag	UNP O95271
A	1082	SER	-	expression tag	UNP O95271
A	1083	SER	-	expression tag	UNP O95271
A	1084	HIS	-	expression tag	UNP O95271
A	1085	HIS	-	expression tag	UNP O95271
A	1086	HIS	-	expression tag	UNP O95271
A	1087	HIS	-	expression tag	UNP O95271
A	1088	HIS	-	expression tag	UNP O95271
A	1089	HIS	-	expression tag	UNP O95271
A	1090	SER	-	expression tag	UNP O95271
A	1091	SER	-	expression tag	UNP O95271
A	1092	GLY	-	expression tag	UNP O95271
A	1093	LEU	-	expression tag	UNP O95271
A	1094	GLU	-	expression tag	UNP O95271
A	1095	VAL	-	expression tag	UNP O95271
A	1096	LEU	-	expression tag	UNP O95271
A	1097	PHE	-	expression tag	UNP O95271
A	1098	GLN	-	expression tag	UNP O95271
A	1099	GLY	-	expression tag	UNP O95271
A	1100	PRO	-	expression tag	UNP O95271

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1101	HIS	-	expression tag	UNP O95271
A	1102	MET	-	expression tag	UNP O95271
A	1103	ALA	-	expression tag	UNP O95271
A	1104	SER	-	expression tag	UNP O95271
A	1266	ILE	MET	engineered mutation	UNP O95271
B	1080	MET	-	initiating methionine	UNP O95271
B	1081	GLY	-	expression tag	UNP O95271
B	1082	SER	-	expression tag	UNP O95271
B	1083	SER	-	expression tag	UNP O95271
B	1084	HIS	-	expression tag	UNP O95271
B	1085	HIS	-	expression tag	UNP O95271
B	1086	HIS	-	expression tag	UNP O95271
B	1087	HIS	-	expression tag	UNP O95271
B	1088	HIS	-	expression tag	UNP O95271
B	1089	HIS	-	expression tag	UNP O95271
B	1090	SER	-	expression tag	UNP O95271
B	1091	SER	-	expression tag	UNP O95271
B	1092	GLY	-	expression tag	UNP O95271
B	1093	LEU	-	expression tag	UNP O95271
B	1094	GLU	-	expression tag	UNP O95271
B	1095	VAL	-	expression tag	UNP O95271
B	1096	LEU	-	expression tag	UNP O95271
B	1097	PHE	-	expression tag	UNP O95271
B	1098	GLN	-	expression tag	UNP O95271
B	1099	GLY	-	expression tag	UNP O95271
B	1100	PRO	-	expression tag	UNP O95271
B	1101	HIS	-	expression tag	UNP O95271
B	1102	MET	-	expression tag	UNP O95271
B	1103	ALA	-	expression tag	UNP O95271
B	1104	SER	-	expression tag	UNP O95271
B	1266	ILE	MET	engineered mutation	UNP O95271
C	1080	MET	-	initiating methionine	UNP O95271
C	1081	GLY	-	expression tag	UNP O95271
C	1082	SER	-	expression tag	UNP O95271
C	1083	SER	-	expression tag	UNP O95271
C	1084	HIS	-	expression tag	UNP O95271
C	1085	HIS	-	expression tag	UNP O95271
C	1086	HIS	-	expression tag	UNP O95271
C	1087	HIS	-	expression tag	UNP O95271
C	1088	HIS	-	expression tag	UNP O95271
C	1089	HIS	-	expression tag	UNP O95271
C	1090	SER	-	expression tag	UNP O95271

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1091	SER	-	expression tag	UNP O95271
C	1092	GLY	-	expression tag	UNP O95271
C	1093	LEU	-	expression tag	UNP O95271
C	1094	GLU	-	expression tag	UNP O95271
C	1095	VAL	-	expression tag	UNP O95271
C	1096	LEU	-	expression tag	UNP O95271
C	1097	PHE	-	expression tag	UNP O95271
C	1098	GLN	-	expression tag	UNP O95271
C	1099	GLY	-	expression tag	UNP O95271
C	1100	PRO	-	expression tag	UNP O95271
C	1101	HIS	-	expression tag	UNP O95271
C	1102	MET	-	expression tag	UNP O95271
C	1103	ALA	-	expression tag	UNP O95271
C	1104	SER	-	expression tag	UNP O95271
C	1266	ILE	MET	engineered mutation	UNP O95271
D	1080	MET	-	initiating methionine	UNP O95271
D	1081	GLY	-	expression tag	UNP O95271
D	1082	SER	-	expression tag	UNP O95271
D	1083	SER	-	expression tag	UNP O95271
D	1084	HIS	-	expression tag	UNP O95271
D	1085	HIS	-	expression tag	UNP O95271
D	1086	HIS	-	expression tag	UNP O95271
D	1087	HIS	-	expression tag	UNP O95271
D	1088	HIS	-	expression tag	UNP O95271
D	1089	HIS	-	expression tag	UNP O95271
D	1090	SER	-	expression tag	UNP O95271
D	1091	SER	-	expression tag	UNP O95271
D	1092	GLY	-	expression tag	UNP O95271
D	1093	LEU	-	expression tag	UNP O95271
D	1094	GLU	-	expression tag	UNP O95271
D	1095	VAL	-	expression tag	UNP O95271
D	1096	LEU	-	expression tag	UNP O95271
D	1097	PHE	-	expression tag	UNP O95271
D	1098	GLN	-	expression tag	UNP O95271
D	1099	GLY	-	expression tag	UNP O95271
D	1100	PRO	-	expression tag	UNP O95271
D	1101	HIS	-	expression tag	UNP O95271
D	1102	MET	-	expression tag	UNP O95271
D	1103	ALA	-	expression tag	UNP O95271
D	1104	SER	-	expression tag	UNP O95271
D	1266	ILE	MET	engineered mutation	UNP O95271

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total 1	Zn 1	0	0
2	A	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0

- Molecule 3 is 1-[(1-acetyl-5-bromo-1H-indol-6-yl)sulfonyl]-N-ethyl-N-(3-methylphenyl)piperidine-4-carboxamide (three-letter code: IW8) (formula: $C_{25}H_{28}BrN_3O_4S$).
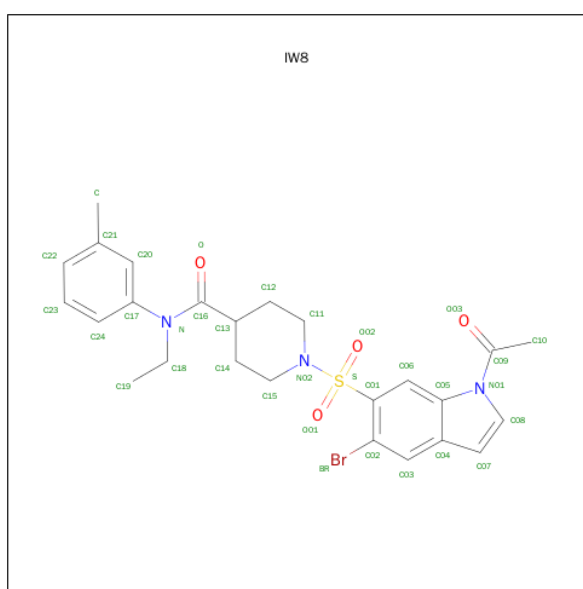
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 34	Br 1	C 25	N 3	O 4	S 1	0	0
3	B	1	Total 34	Br 1	C 25	N 3	O 4	S 1	0	0
3	C	1	Total 34	Br 1	C 25	N 3	O 4	S 1	0	0
3	D	1	Total 34	Br 1	C 25	N 3	O 4	S 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	6	Total 6	Cl 6	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total 5	Cl 5	0	0
4	D	6	Total 6	Cl 6	0	0
4	C	6	Total 6	Cl 6	0	0

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	212	Total 212	O 212	0	0
5	B	214	Total 214	O 214	0	0
5	C	200	Total 200	O 200	0	0
5	D	198	Total 198	O 198	0	0

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.
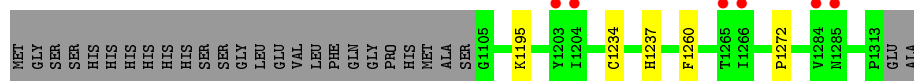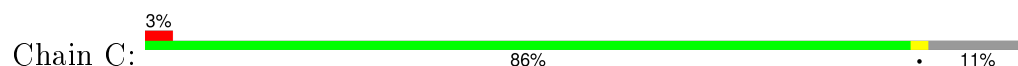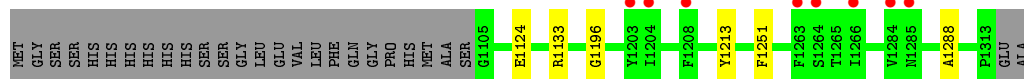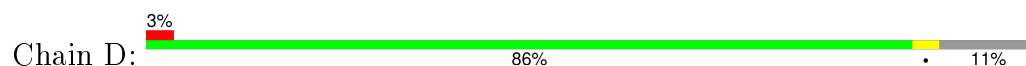
- Molecule 1: Tankyrase-1
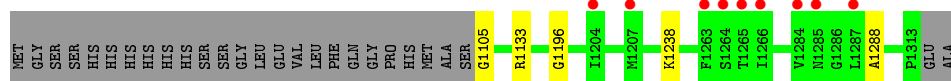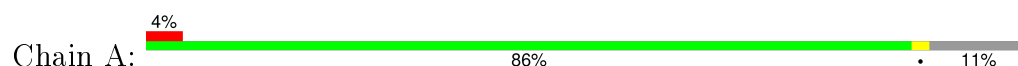
- Molecule 1: Tankyrase-1
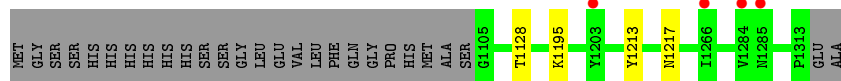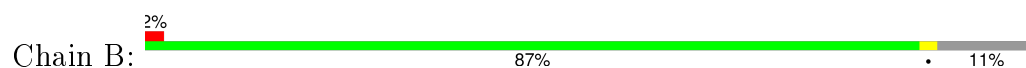
- Molecule 1: Tankyrase-1

- Molecule 1: Tankyrase-1

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α, β, γ	108.38Å　　108.38Å　　122.22Å 90.00°　　90.00°　　120.00°	Depositor
Resolution (Å)	37.37　–　1.50 37.37　–　1.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (37.37-1.50) 99.1 (37.37-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	1.63 (at 1.50Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.177　,　0.207 0.190　,　0.214	Depositor DCC
R_{free} test set	6415 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	15.4	Xtriage
Anisotropy	0.672	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 48.7	EDS
Estimated twinning fraction	0.479 for h,-h-k,-l	Xtriage
L-test for twinning [2]	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Outliers	2 of 128406 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	14272	wwPDB-VP
Average B, all atoms (Å^2)	25.0	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 30.18 % 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 1.3656e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CL, IW8

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	0.38	0/1740	0.55	0/2341
1	B	0.38	0/1751	0.53	0/2356
1	C	0.37	0/1747	0.53	0/2349
1	D	0.38	0/1740	0.54	0/2341
All	All	0.38	0/6978	0.54	0/9387

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	1694	1619	1629	5	0
1	B	1701	1625	1636	2	0
1	C	1701	1632	1641	2	0
1	D	1694	1619	1629	5	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
3	A	34	0	28	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	34	0	28	1	0
3	C	34	0	28	1	0
3	D	34	0	28	3	0
4	A	5	0	0	0	0
4	B	6	0	0	0	0
4	C	6	0	0	0	0
4	D	6	0	0	0	0
5	A	212	0	0	1	2
5	B	214	0	0	0	1
5	C	200	0	0	0	2
5	D	198	0	0	0	2
All	All	7777	6495	6647	17	5

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 1.

The worst 5 of 17 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)
3:A:1402:IW8:H25	3:A:1402:IW8:H21	1.77	0.66
3:C:1402:IW8:H25	3:C:1402:IW8:H21	1.87	0.56
1:A:1133:ARG:CD	1:A:1288:ALA:HB2	2.41	0.51
3:A:1402:IW8:H12	3:A:1402:IW8:C20	2.41	0.49
1:D:1213:TYR:HB2	3:D:1402:IW8:H17	1.96	0.47

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1518:HOH:O	5:D:1529:HOH:O[5_454]	2.12	0.08
5:A:1523:HOH:O	5:A:1528:HOH:O[4_585]	2.16	0.04
5:C:1684:HOH:O	5:D:1587:HOH:O[3_364]	2.16	0.04
5:A:1511:HOH:O	5:A:1513:HOH:O[4_585]	2.19	0.01
5:C:1550:HOH:O	5:C:1559:HOH:O[4_475]	2.19	0.01

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	209/236 (89%)	206 (99%)	3 (1%)	0	100	100
1	B	210/236 (89%)	208 (99%)	2 (1%)	0	100	100
1	C	210/236 (89%)	209 (100%)	1 (0%)	0	100	100
1	D	209/236 (89%)	206 (99%)	3 (1%)	0	100	100
All	All	838/944 (89%)	829 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	178/199 (89%)	177 (99%)	1 (1%)	90	78
1	B	179/199 (90%)	178 (99%)	1 (1%)	90	78
1	C	179/199 (90%)	177 (99%)	2 (1%)	80	58
1	D	178/199 (89%)	178 (100%)	0	100	100
All	All	714/796 (90%)	710 (99%)	4 (1%)	93	78

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

Mol	Chain	Res	Type
1	A	1238	LYS
1	B	1195	LYS

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Mol	Chain	Res	Type
1	C	1195[A]	LYS
1	C	1195[B]	LYS

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

Mol	Chain	Res	Type
1	B	1246	HIS
1	C	1223	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 31 ligands modelled in this entry, 27 are monoatomic - leaving 4 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	IW8	A	1402	-	34,37,37	4.06	20 (58%)	43,55,55	4.53	27 (62%)
3	IW8	B	1402	-	34,37,37	4.05	21 (61%)	43,55,55	4.27	25 (58%)
3	IW8	C	1402	-	34,37,37	4.06	21 (61%)	43,55,55	4.40	28 (65%)
3	IW8	D	1402	-	34,37,37	4.03	20 (58%)	43,55,55	4.53	27 (62%)

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	IW8	A	1402	-	-	0/26/40/40	0/4/4/4
3	IW8	B	1402	-	-	0/26/40/40	0/4/4/4
3	IW8	C	1402	-	-	0/26/40/40	0/4/4/4
3	IW8	D	1402	-	-	0/26/40/40	0/4/4/4

The worst 5 of 82 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1402	IW8	C05-N01	-11.05	1.24	1.39
3	B	1402	IW8	C05-N01	-10.76	1.24	1.39
3	C	1402	IW8	C05-N01	-10.72	1.24	1.39
3	D	1402	IW8	C05-N01	-10.33	1.25	1.39
3	B	1402	IW8	O02-S	-6.56	1.35	1.43

The worst 5 of 107 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1402	IW8	BR-C02-C03	-8.60	104.41	119.04
3	D	1402	IW8	BR-C02-C03	-8.36	104.82	119.04
3	C	1402	IW8	BR-C02-C03	-7.66	106.01	119.04
3	B	1402	IW8	BR-C02-C03	-7.55	106.21	119.04
3	B	1402	IW8	C14-C13-C12	-5.31	97.96	109.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1402	IW8	3	0
3	B	1402	IW8	1	0
3	C	1402	IW8	1	0
3	D	1402	IW8	3	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 (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	209/236 (88%)	0.02	9 (4%)	39	41	13, 19, 38, 56	0
1	B	209/236 (88%)	-0.11	4 (1%)	70	73	12, 19, 34, 44	0
1	C	209/236 (88%)	-0.05	6 (2%)	55	58	13, 20, 36, 45	0
1	D	209/236 (88%)	-0.09	8 (3%)	44	46	13, 19, 38, 53	0
All	All	836/944 (88%)	-0.06	27 (3%)	51	54	12, 19, 37, 56	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1284	VAL	6.4
1	D	1266	ILE	5.5
1	A	1285	ASN	5.4
1	A	1284	VAL	5.1
1	A	1266	ILE	4.1

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 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, 95th 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(Å²)	Q<0.9
4	CL	A	1407	1/1	0.99	0.18	6.61	15,15,15,15	0
4	CL	A	1406	1/1	0.99	0.13	4.84	20,20,20,20	0
4	CL	D	1405	1/1	0.99	0.16	4.56	14,14,14,14	0
4	CL	C	1407	1/1	0.99	0.13	4.27	19,19,19,19	0
4	CL	B	1404	1/1	0.98	0.11	3.42	18,18,18,18	0
4	CL	B	1406	1/1	0.99	0.17	3.33	15,15,15,15	0
4	CL	C	1405	1/1	0.99	0.17	3.32	16,16,16,16	0
4	CL	C	1403	1/1	0.98	0.10	2.63	19,19,19,19	0
3	IW8	A	1402	34/34	0.91	0.11	1.19	16,22,32,89	0
3	IW8	D	1402	34/34	0.89	0.11	0.92	17,21,30,127	0
3	IW8	C	1402	34/34	0.89	0.11	0.82	17,23,33,110	0
3	IW8	B	1402	34/34	0.90	0.11	0.77	17,23,33,135	0
4	CL	A	1405	1/1	0.95	0.09	0.34	26,26,26,26	0
4	CL	D	1406	1/1	0.95	0.10	0.31	25,25,25,25	0
4	CL	A	1403	1/1	0.75	0.14	-0.29	60,60,60,60	0
2	ZN	D	1401	1/1	1.00	0.06	-0.31	14,14,14,14	0
4	CL	B	1403	1/1	0.95	0.09	-0.62	23,23,23,23	0
4	CL	C	1406	1/1	0.94	0.08	-0.62	27,27,27,27	0
4	CL	B	1405	1/1	0.99	0.06	-0.82	24,24,24,24	0
2	ZN	B	1401	1/1	1.00	0.04	-0.98	14,14,14,14	0
4	CL	D	1403	1/1	0.98	0.05	-1.01	23,23,23,23	0
4	CL	C	1404	1/1	0.99	0.06	-1.02	25,25,25,25	0
4	CL	B	1407	1/1	0.97	0.06	-1.07	30,30,30,30	0
4	CL	D	1404	1/1	0.96	0.06	-1.22	31,31,31,31	0
2	ZN	A	1401	1/1	1.00	0.06	-1.30	15,15,15,15	0
4	CL	A	1404	1/1	0.97	0.05	-1.31	28,28,28,28	0
4	CL	B	1408	1/1	0.94	0.05	-2.19	27,27,27,27	0
4	CL	D	1408	1/1	0.94	0.05	-2.25	29,29,29,29	0
2	ZN	C	1401	1/1	1.00	0.05	-2.35	16,16,16,16	0
4	CL	C	1408	1/1	0.96	0.04	-3.45	27,27,27,27	0
4	CL	D	1407	1/1	0.97	0.05	-4.49	31,31,31,31	0

6.5 Other polymers ⓘ

There are no such residues in this entry.