



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:30 am GMT

PDB ID : 4MSK
Title : Co-crystal structure of tankyrase 1 with compound 34
Authors : Huang, X.
Deposited on : 2013-09-18
Resolution : 2.30 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

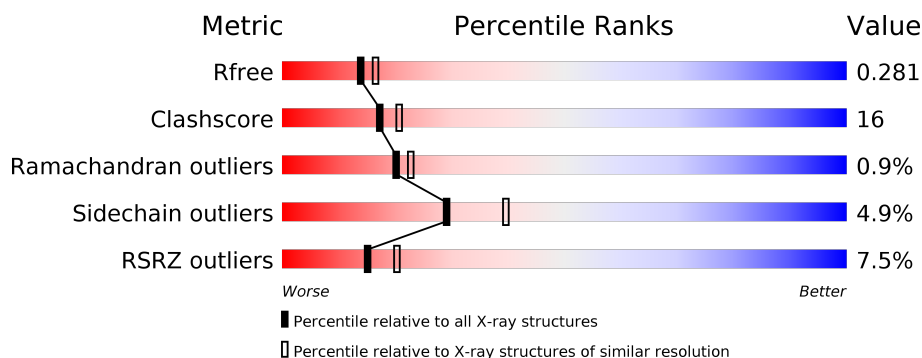
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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 ≥ 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	217	<div> <div>5%</div> <div> <div></div> <div>70%</div> <div>25%</div> <div>• •</div> </div> </div>
1	B	217	<div> <div>5%</div> <div> <div></div> <div>62%</div> <div>32%</div> <div>• •</div> </div> </div>
1	C	217	<div> <div>10%</div> <div> <div></div> <div>65%</div> <div>25%</div> <div>• 8%</div> </div> </div>
1	D	217	<div> <div>9%</div> <div> <div></div> <div>61%</div> <div>28%</div> <div>• 7%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ZN	D	1401	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7031 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	211	Total	C	N	O	S	0	0	0
			1695	1066	310	307	12			
1	B	211	Total	C	N	O	S	0	0	0
			1692	1065	308	307	12			
1	C	200	Total	C	N	O	S	0	0	0
			1634	1032	298	293	11			
1	D	201	Total	C	N	O	S	0	0	0
			1641	1037	300	292	12			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1315	HIS	-	EXPRESSION TAG	UNP O95271
A	1316	HIS	-	EXPRESSION TAG	UNP O95271
A	1317	HIS	-	EXPRESSION TAG	UNP O95271
A	1318	HIS	-	EXPRESSION TAG	UNP O95271
A	1319	HIS	-	EXPRESSION TAG	UNP O95271
A	1320	HIS	-	EXPRESSION TAG	UNP O95271
B	1315	HIS	-	EXPRESSION TAG	UNP O95271
B	1316	HIS	-	EXPRESSION TAG	UNP O95271
B	1317	HIS	-	EXPRESSION TAG	UNP O95271
B	1318	HIS	-	EXPRESSION TAG	UNP O95271
B	1319	HIS	-	EXPRESSION TAG	UNP O95271
B	1320	HIS	-	EXPRESSION TAG	UNP O95271
C	1315	HIS	-	EXPRESSION TAG	UNP O95271
C	1316	HIS	-	EXPRESSION TAG	UNP O95271
C	1317	HIS	-	EXPRESSION TAG	UNP O95271
C	1318	HIS	-	EXPRESSION TAG	UNP O95271
C	1319	HIS	-	EXPRESSION TAG	UNP O95271
C	1320	HIS	-	EXPRESSION TAG	UNP O95271
D	1315	HIS	-	EXPRESSION TAG	UNP O95271
D	1316	HIS	-	EXPRESSION TAG	UNP O95271
D	1317	HIS	-	EXPRESSION TAG	UNP O95271

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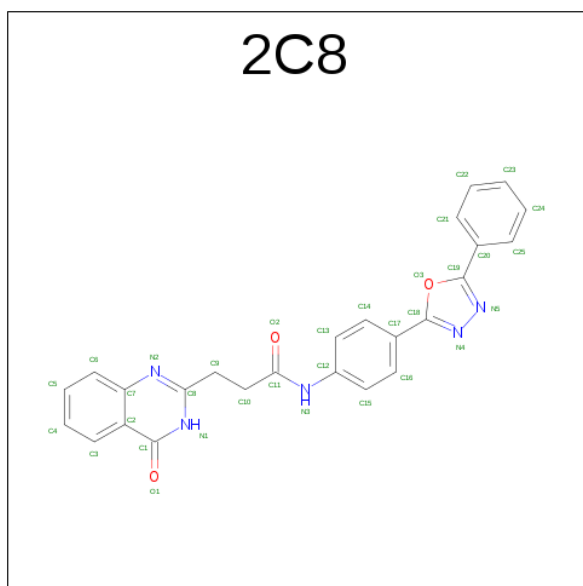
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Chain	Residue	Modelled	Actual	Comment	Reference
D	1318	HIS	-	EXPRESSION TAG	UNP O95271
D	1319	HIS	-	EXPRESSION TAG	UNP O95271
D	1320	HIS	-	EXPRESSION TAG	UNP O95271

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

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

- Molecule 3 is 3-(4-OXO-3,4-DIHYDROQUINAZOLIN-2-YL)-N-[4-(5-PHENYL-1,3,4-OXADIAZOL-2-YL)PHENYL]PROPANAMIDE (three-letter code: 2C8) (formula: C₂₅H₁₉N₅O₃).



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			33	25	5	3		

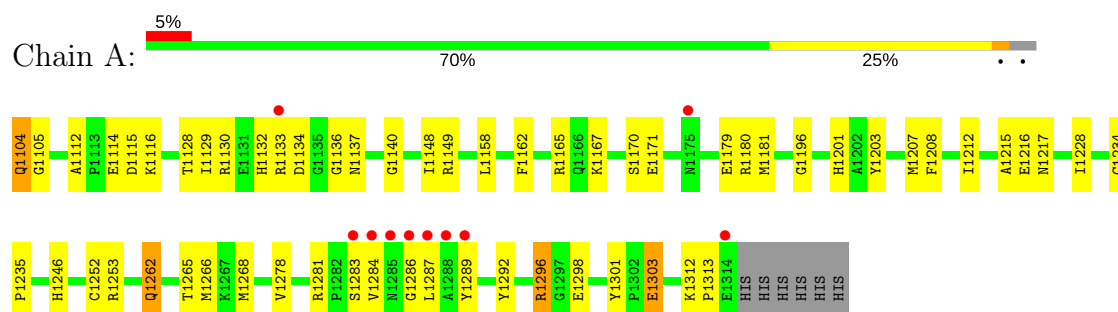
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	63	Total	O	0	0
			63	63		
4	B	62	Total	O	0	0
			62	62		
4	C	62	Total	O	0	0
			62	62		
4	D	46	Total	O	0	0
			46	46		

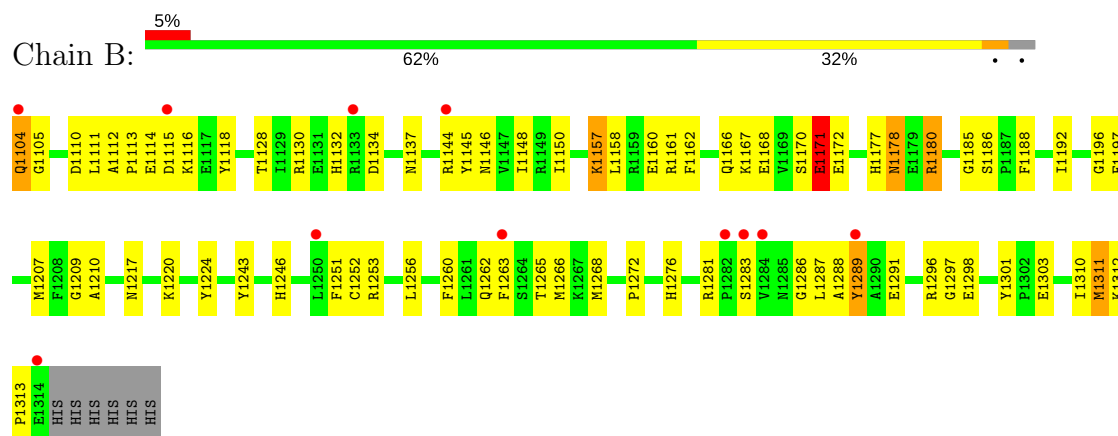
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

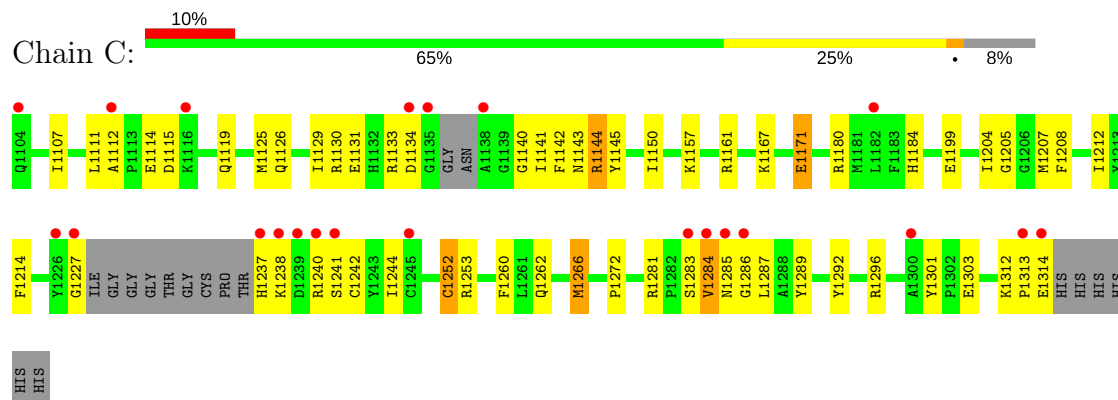
• Molecule 1: Tankyrase-1



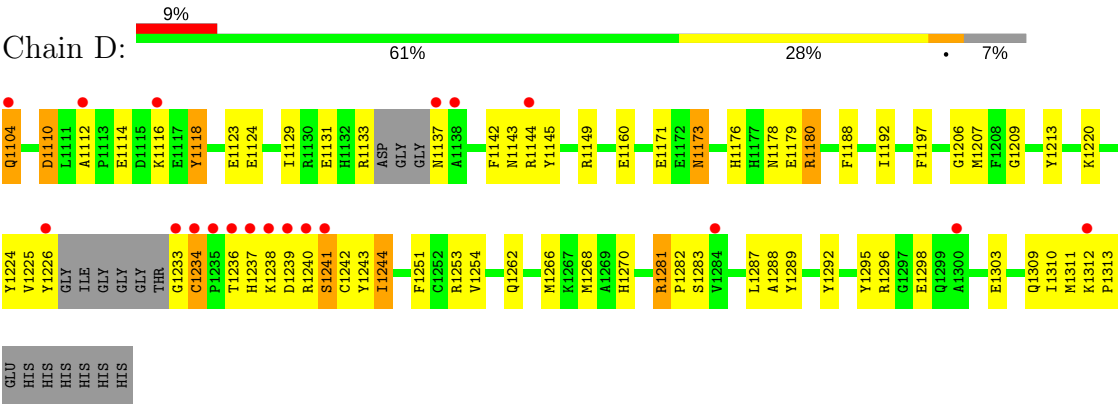
• Molecule 1: Tankyrase-1



• Molecule 1: Tankyrase-1



● Molecule 1: Tankyrase-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	158.23Å 79.78Å 85.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 25.53 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.30) 95.3 (25.53-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 1.99Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.239 , 0.285 0.250 , 0.281	Depositor DCC
R_{free} test set	2459 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.4	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	0.94	EDS
Total number of atoms	7031	wwPDB-VP
Average B, all atoms (Å ²)	33.0	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 49.17 % 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 7.7523e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 2C8

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	0.50	1/1738 (0.1%)	0.68	0/2336
1	B	0.50	1/1734 (0.1%)	0.71	3/2331 (0.1%)
1	C	0.49	1/1674 (0.1%)	0.67	0/2246
1	D	0.48	1/1682 (0.1%)	0.65	0/2259
All	All	0.49	4/6828 (0.1%)	0.68	3/9172 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1171	GLU	CG-CD	8.20	1.64	1.51
1	D	1160	GLU	CG-CD	7.42	1.63	1.51
1	B	1171	GLU	CG-CD	6.32	1.61	1.51
1	A	1216	GLU	CG-CD	5.22	1.59	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1281	ARG	NE-CZ-NH1	6.47	123.54	120.30
1	B	1281	ARG	NE-CZ-NH2	-5.73	117.44	120.30
1	B	1251	PHE	N-CA-C	-5.11	97.21	111.00

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	1695	0	1623	43	1
1	B	1692	0	1625	64	0
1	C	1634	0	1571	46	1
1	D	1641	0	1582	56	1
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	33	0	19	2	0
3	B	33	0	19	1	0
3	C	33	0	19	1	0
3	D	33	0	19	1	0
4	A	63	0	0	3	0
4	B	62	0	0	3	0
4	C	62	0	0	4	0
4	D	46	0	0	1	0
All	All	7031	0	6477	206	2

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 16.

The worst 5 of 206 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:1178:ASN:HD21	1:B:1180:ARG:HH12	1.10	0.99
1:B:1134:ASP:OD1	1:B:1137:ASN:HB3	1.66	0.93
1:C:1167:LYS:O	1:C:1171:GLU:HG3	1.74	0.88
1:B:1112:ALA:HB1	1:B:1114:GLU:OE2	1.74	0.88
1:A:1167:LYS:O	1:A:1171:GLU:HG3	1.78	0.84

All (2) 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)
1:A:1104:GLN:OE1	1:D:1104:GLN:N[3_546]	2.10	0.10
1:C:1107:ILE:CD1	1:C:1107:ILE:CD1[2_665]	2.16	0.04

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	209/217 (96%)	195 (93%)	11 (5%)	3 (1%)	13	13
1	B	209/217 (96%)	201 (96%)	7 (3%)	1 (0%)	32	39
1	C	194/217 (89%)	182 (94%)	11 (6%)	1 (0%)	32	39
1	D	195/217 (90%)	183 (94%)	10 (5%)	2 (1%)	18	20
All	All	807/868 (93%)	761 (94%)	39 (5%)	7 (1%)	20	23

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1313	PRO
1	D	1241	SER
1	A	1133	ARG
1	B	1210	ALA
1	C	1284	VAL

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	177/185 (96%)	171 (97%)	6 (3%)	42	57
1	B	177/185 (96%)	167 (94%)	10 (6%)	25	33
1	C	172/185 (93%)	167 (97%)	5 (3%)	48	64
1	D	174/185 (94%)	161 (92%)	13 (8%)	16	19
All	All	700/740 (95%)	666 (95%)	34 (5%)	29	39

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1311	MET
1	C	1281	ARG
1	D	1281	ARG
1	C	1252	CYS
1	B	1104	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1104	GLN
1	C	1166	GLN
1	D	1223	GLN
1	C	1119	GLN
1	C	1151	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 8 ligands modelled in this entry, 4 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	2C8	A	1402	-	30,37,37	3.02	22 (73%)	41,51,51	2.57	9 (21%)
3	2C8	B	1402	-	30,37,37	3.19	21 (70%)	41,51,51	2.70	9 (21%)
3	2C8	C	1402	-	30,37,37	3.15	21 (70%)	41,51,51	2.68	10 (24%)
3	2C8	D	1402	-	30,37,37	3.30	21 (70%)	41,51,51	2.52	10 (24%)

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	2C8	A	1402	-	-	0/13/17/17	0/4/5/5
3	2C8	B	1402	-	-	0/13/17/17	0/4/5/5
3	2C8	C	1402	-	-	0/13/17/17	0/4/5/5
3	2C8	D	1402	-	-	0/13/17/17	0/4/5/5

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1402	2C8	C10-C11	-3.17	1.45	1.51
3	C	1402	2C8	C12-N3	-2.86	1.36	1.41
3	A	1402	2C8	C12-N3	-2.48	1.36	1.41
3	D	1402	2C8	C12-N3	-2.45	1.36	1.41
3	B	1402	2C8	C12-N3	-2.40	1.37	1.41

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1402	2C8	C2-C7-N2	-10.00	117.97	123.67
3	A	1402	2C8	C2-C7-N2	-8.73	118.69	123.67
3	D	1402	2C8	C2-C7-N2	-8.43	118.86	123.67
3	B	1402	2C8	C2-C1-N1	-8.02	118.80	124.45
3	B	1402	2C8	N2-C8-N1	-7.58	117.32	126.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1402	2C8	2	0
3	B	1402	2C8	1	0
3	C	1402	2C8	1	0
3	D	1402	2C8	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 [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	211/217 (97%)	0.30	10 (4%) 32 39	19, 31, 52, 69	0
1	B	211/217 (97%)	0.22	11 (5%) 28 35	17, 30, 54, 71	0
1	C	200/217 (92%)	0.46	22 (11%) 6 9	19, 32, 57, 85	0
1	D	201/217 (92%)	0.63	19 (9%) 9 12	18, 31, 62, 88	0
All	All	823/868 (94%)	0.40	62 (7%) 15 20	17, 31, 56, 88	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1234	CYS	18.7
1	D	1236	THR	14.7
1	D	1237	HIS	11.2
1	C	1238	LYS	9.1
1	D	1238	LYS	8.9

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(\AA^2)	Q<0.9
3	2C8	A	1402	33/33	0.92	0.15	-0.01	21,23,25,26	0
3	2C8	B	1402	33/33	0.95	0.13	-0.14	21,23,27,28	0
2	ZN	D	1401	1/1	0.47	0.44	-0.51	175,175,175,175	0
3	2C8	D	1402	33/33	0.94	0.12	-0.72	22,24,26,26	0
3	2C8	C	1402	33/33	0.93	0.12	-0.84	19,22,25,26	0
2	ZN	B	1401	1/1	0.96	0.06	-1.85	40,40,40,40	0
2	ZN	A	1401	1/1	0.95	0.08	-2.56	42,42,42,42	0
2	ZN	C	1401	1/1	0.88	0.14	-	80,80,80,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.