Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:18 am BST

PDB ID	:	4DJS
Title	:	Structure of beta-catenin in complex with a stapled peptide inhibitor
Authors	:	Bowman, B.R.; Grossmann, T.N.; Yeh, J.T.-H.; Verdine, G.L.
Deposited on	:	2012-02-02
Resolution	:	3.03 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

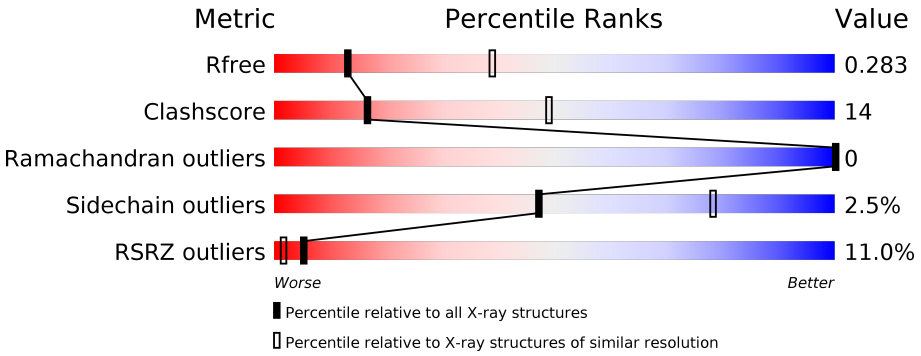
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.03 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}	130704	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)
RSRZ outliers	127900	2287 (3.04-3.00)

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 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 <=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	518	11%, 68%, 28%, ••
2	B	17	24%, 59%, 6%, 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4007 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 Catenin beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	507	3864	2426	702	710	26	0	0	0

- Molecule 2 is a protein called stapled peptide RRWPQ(MK8)ILD(MK8)HVRRVWR.

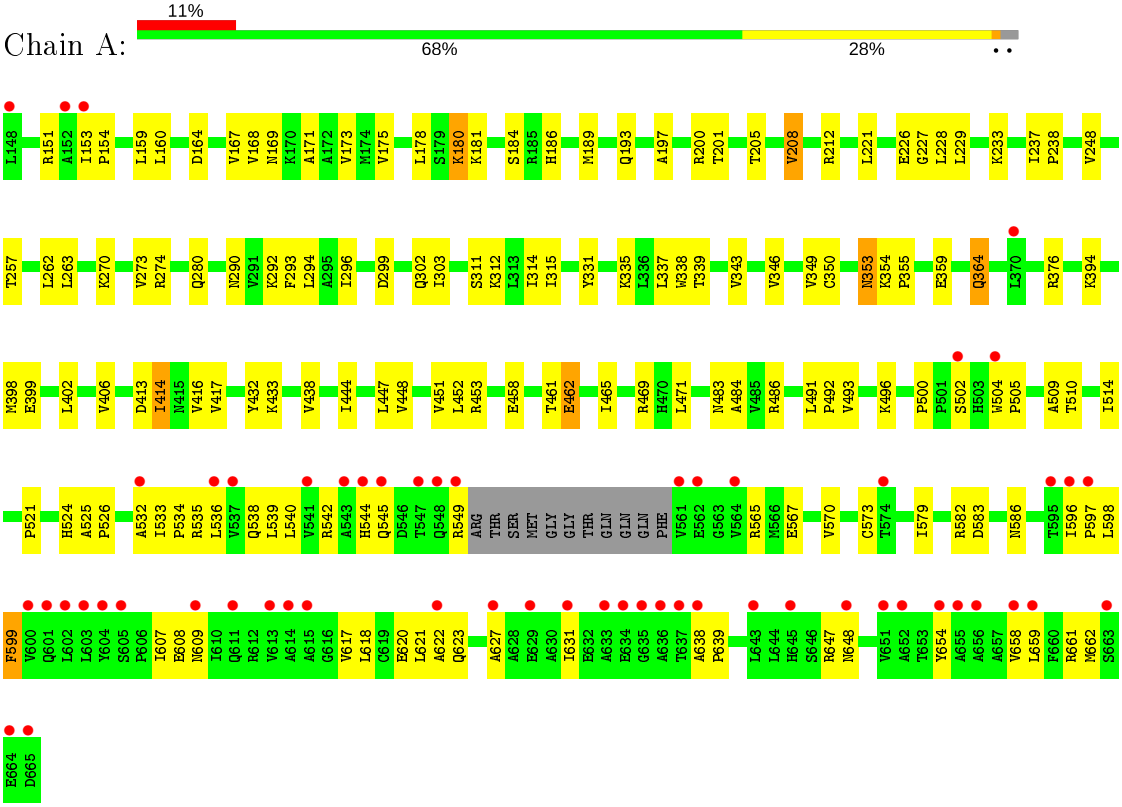
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	15	143	96	29	18	0	0	0

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: Catenin beta-1

Chain A:



- Molecule 2: stapled peptide RRWPQ(MK8)ILD(MK8)HVRRVWR

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	63.06Å 74.81Å 135.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.26 – 3.03 50.26 – 3.03	Depositor EDS
% Data completeness (in resolution range)	93.3 (50.26-3.03) 93.4 (50.26-3.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.41 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357), CNS	Depositor
R, R_{free}	0.263 , 0.291 0.260 , 0.283	Depositor DCC
R_{free} test set	1289 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å^2)	62.7	Xtriage
Anisotropy	0.753	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 75.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	4007	wwPDB-VP
Average B, all atoms (Å^2)	110.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.02% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MK8

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	0/3917	0.36	0/5314
2	B	0.20	0/128	0.36	0/171
All	All	0.20	0/4045	0.36	0/5485

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	10	MK8	Mainchain

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	3864	0	4012	109	0
2	B	143	0	144	8	0
All	All	4007	0	4156	116	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 14.

All (116) 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:A:500:PRO:HA	1:A:502:SER:H	1.47	0.80
1:A:364:GLN:H	1:A:364:GLN:NE2	1.86	0.74
1:A:538:GLN:HE21	1:A:542:ARG:HH21	1.40	0.69
1:A:608:GLU:HB3	1:A:648:ASN:HD22	1.55	0.69
1:A:237:ILE:HB	1:A:238:PRO:HD3	1.77	0.66
1:A:399:GLU:H	1:A:399:GLU:CD	1.99	0.65
1:A:579:ILE:HD12	1:A:582:ARG:HH21	1.63	0.64
1:A:151:ARG:HA	1:A:151:ARG:HE	1.65	0.62
1:A:638:ALA:HB3	1:A:639:PRO:HD3	1.80	0.61
1:A:491:LEU:HB2	1:A:492:PRO:HD3	1.82	0.61
1:A:201:THR:O	1:A:205:THR:HG22	1.99	0.61
1:A:355:PRO:O	1:A:359:GLU:HG2	2.00	0.60
1:A:169:ASN:O	1:A:173:VAL:HG23	2.01	0.60
2:B:9:ASP:O	2:B:10:MK8:HB1A	2.03	0.59
1:A:533:ILE:HB	1:A:534:PRO:HD3	1.84	0.59
1:A:417:VAL:HG21	1:A:453:ARG:HH12	1.66	0.59
1:A:538:GLN:NE2	1:A:542:ARG:HH21	2.01	0.58
1:A:540:LEU:HD13	1:A:573:CYS:HB2	1.85	0.58
1:A:504:TRP:N	1:A:505:PRO:HD2	2.18	0.58
1:A:151:ARG:NE	1:A:151:ARG:HA	2.19	0.58
1:A:350:CYS:HB3	1:A:353:ASN:HB2	1.87	0.57
1:A:525:ALA:HB3	1:A:526:PRO:HD3	1.86	0.57
1:A:469:ARG:HH11	1:A:509:ALA:HA	1.69	0.56
1:A:618:LEU:HD23	1:A:621:LEU:HD12	1.86	0.56
1:A:186:HIS:HA	1:A:189:MET:HE2	1.87	0.56
2:B:10:MK8:O	2:B:14:ARG:HD3	2.06	0.55
1:A:596:ILE:H	1:A:596:ILE:HD12	1.70	0.55
1:A:354:LYS:HB2	1:A:354:LYS:NZ	2.22	0.54
1:A:414:ILE:H	1:A:414:ILE:HD12	1.72	0.54
1:A:394:LYS:NZ	1:A:394:LYS:HB2	2.21	0.54
1:A:280:GLN:NE2	1:A:314:ILE:HG23	2.23	0.54
1:A:444:ILE:HG21	1:A:484:ALA:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:532:ALA:O	1:A:536:LEU:HB2	2.08	0.54
1:A:620:GLU:O	1:A:623:GLN:HG2	2.08	0.53
2:B:10:MK8:HB1A	2:B:13:ARG:CG	2.39	0.53
1:A:171:ALA:O	1:A:175:VAL:HG23	2.09	0.53
1:A:237:ILE:H	1:A:237:ILE:HD12	1.73	0.52
1:A:189:MET:SD	1:A:226:GLU:HB2	2.50	0.51
1:A:535:ARG:NH2	1:A:539:LEU:HD21	2.25	0.51
1:A:228:LEU:HD22	1:A:262:LEU:HD23	1.93	0.51
1:A:208:VAL:HG11	1:A:248:VAL:HG21	1.92	0.51
1:A:540:LEU:HD11	1:A:570:VAL:HG13	1.92	0.51
1:A:197:ALA:HA	1:A:200:ARG:NH2	2.26	0.51
1:A:205:THR:O	1:A:205:THR:HG23	2.11	0.50
1:A:500:PRO:HA	1:A:502:SER:N	2.22	0.50
1:A:302:GLN:HB2	1:A:343:VAL:HG22	1.93	0.50
1:A:257:THR:HG23	2:B:11:HIS:CG	2.46	0.50
1:A:221:LEU:O	1:A:227:GLY:HA3	2.11	0.50
1:A:583:ASP:HB3	1:A:586:ASN:ND2	2.27	0.49
1:A:469:ARG:NH1	1:A:509:ALA:HA	2.27	0.49
1:A:538:GLN:HE21	1:A:542:ARG:NH2	2.08	0.49
2:B:8:LEU:O	2:B:12:VAL:HG23	2.12	0.49
1:A:160:LEU:HD22	1:A:171:ALA:HB1	1.95	0.49
1:A:159:LEU:HD23	1:A:171:ALA:HB2	1.94	0.49
1:A:229:LEU:HG	1:A:233:LYS:HE2	1.94	0.49
1:A:299:ASP:O	1:A:303:ILE:HG13	2.12	0.48
1:A:452:LEU:HD11	1:A:493:VAL:HG11	1.95	0.48
1:A:579:ILE:HD12	1:A:582:ARG:NH2	2.26	0.48
1:A:290:ASN:O	1:A:294:LEU:HG	2.13	0.48
1:A:312:LYS:HE2	1:A:346:VAL:HG12	1.96	0.48
1:A:521:PRO:HA	1:A:524:HIS:CE1	2.48	0.48
1:A:414:ILE:CD1	1:A:414:ILE:H	2.27	0.48
1:A:486:ARG:HA	1:A:491:LEU:HG	1.96	0.48
1:A:496:LYS:NZ	1:A:496:LYS:HB3	2.29	0.48
1:A:280:GLN:NE2	1:A:314:ILE:CG2	2.77	0.48
1:A:607:ILE:HG22	1:A:609:ASN:H	1.79	0.48
1:A:458:GLU:HA	1:A:461:THR:OG1	2.15	0.47
1:A:483:ASN:HD22	1:A:486:ARG:HH21	1.63	0.47
1:A:270:LYS:O	1:A:274:ARG:HG3	2.14	0.47
1:A:654:TYR:O	1:A:658:VAL:HG23	2.14	0.47
1:A:599:PHE:CZ	1:A:617:VAL:HG21	2.49	0.47
1:A:483:ASN:HD22	1:A:486:ARG:NH2	2.12	0.47
1:A:180:LYS:HD2	1:A:180:LYS:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:ILE:N	1:A:596:ILE:HD12	2.28	0.47
1:A:153:ILE:N	1:A:154:PRO:HD2	2.30	0.46
1:A:181:LYS:HB2	1:A:184:SER:OG	2.15	0.46
1:A:461:THR:O	1:A:465:ILE:HG12	2.15	0.46
1:A:263:LEU:HD21	1:A:273:VAL:HG21	1.98	0.45
1:A:338:TRP:CE2	1:A:376:ARG:HD2	2.52	0.45
2:B:3:TRP:CD2	2:B:4:PRO:HA	2.51	0.45
1:A:354:LYS:N	1:A:355:PRO:HD2	2.32	0.45
1:A:544:HIS:CD2	1:A:598:LEU:HD11	2.51	0.45
1:A:510:THR:O	1:A:514:ILE:HG13	2.16	0.45
1:A:545:GLN:O	1:A:549:ARG:HG3	2.17	0.45
1:A:458:GLU:O	1:A:462:GLU:HB2	2.17	0.44
1:A:438:VAL:HG11	1:A:471:LEU:HD11	1.97	0.44
1:A:538:GLN:O	1:A:542:ARG:HG3	2.17	0.44
1:A:447:LEU:O	1:A:451:VAL:HG23	2.17	0.44
1:A:627:ALA:O	1:A:631:ILE:HG13	2.18	0.44
1:A:346:VAL:O	1:A:349:VAL:HG22	2.18	0.44
1:A:399:GLU:N	1:A:399:GLU:CD	2.70	0.44
1:A:181:LYS:HB2	1:A:184:SER:HG	1.81	0.44
1:A:622:ALA:C	1:A:661:ARG:HG2	2.38	0.44
1:A:432:TYR:CZ	1:A:433:LYS:HG3	2.54	0.43
1:A:565:ARG:HB3	1:A:567:GLU:OE2	2.18	0.43
2:B:6:MK8:HB1A	2:B:9:ASP:HB2	2.00	0.43
1:A:159:LEU:HD11	1:A:167:VAL:HG11	2.01	0.43
2:B:6:MK8:C	2:B:6:MK8:HDA	2.49	0.43
1:A:331:TYR:O	1:A:337:LEU:HD21	2.18	0.42
1:A:335:LYS:O	1:A:339:THR:HG22	2.19	0.42
1:A:290:ASN:HB3	1:A:293:PHE:HB3	2.01	0.42
1:A:398:MET:O	1:A:402:LEU:HG	2.20	0.42
1:A:237:ILE:N	1:A:237:ILE:HD12	2.34	0.42
1:A:659:LEU:HD23	1:A:662:MET:CE	2.49	0.42
1:A:311:SER:O	1:A:315:ILE:HG13	2.19	0.42
1:A:596:ILE:N	1:A:597:PRO:CD	2.82	0.42
1:A:444:ILE:O	1:A:448:VAL:HG23	2.20	0.41
1:A:659:LEU:HA	1:A:662:MET:HE2	2.02	0.41
1:A:178:LEU:HB3	1:A:184:SER:HB2	2.02	0.41
1:A:413:ASP:OD2	1:A:416:VAL:HG23	2.21	0.41
1:A:164:ASP:O	1:A:168:VAL:HG23	2.20	0.41
1:A:159:LEU:HD11	1:A:167:VAL:CG1	2.50	0.41
1:A:599:PHE:CE1	1:A:617:VAL:HG11	2.56	0.41
1:A:292:LYS:O	1:A:296:ILE:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:LEU:O	1:A:406:VAL:HG23	2.21	0.41
1:A:189:MET:HG3	1:A:227:GLY:HA2	2.03	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	503/518 (97%)	480 (95%)	23 (5%)	0	100	100
2	B	11/17 (65%)	10 (91%)	1 (9%)	0	100	100
All	All	514/535 (96%)	490 (95%)	24 (5%)	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	420/429 (98%)	410 (98%)	10 (2%)	49	79
2	B	13/15 (87%)	12 (92%)	1 (8%)	13	41
All	All	433/444 (98%)	422 (98%)	11 (2%)	47	78

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	180	LYS
1	A	193	GLN
1	A	208	VAL
1	A	212	ARG
1	A	353	ASN
1	A	364	GLN
1	A	414	ILE
1	A	462	GLU
1	A	599	PHE
1	A	647	ARG
2	B	2	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	A	193	GLN
1	A	302	GLN
1	A	364	GLN
1	A	395	GLN
1	A	440	GLN
1	A	483	ASN
1	A	488	HIS
1	A	538	GLN
1	A	601	GLN
1	A	623	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)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\|>2$
2	MK8	B	6	2	5,8,9	2.94	2 (40%)	4,10,12	1.22	1 (25%)
2	MK8	B	10	2	5,8,9	3.20	2 (40%)	4,10,12	0.42	0

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
2	MK8	B	6	2	-	1/6/8/11	-
2	MK8	B	10	2	-	5/6/8/11	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	6	MK8	O-C	5.36	1.37	1.19
2	B	10	MK8	O-C	5.23	1.37	1.19
2	B	10	MK8	CB-CA	-4.81	1.49	1.55
2	B	6	MK8	CB-CA	-3.77	1.50	1.55

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	6	MK8	CB-CG-CD	2.29	120.21	113.14

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	10	MK8	N-CA-CB-CG
2	B	6	MK8	CA-CB-CG-CD
2	B	10	MK8	CB1-CA-CB-CG
2	B	10	MK8	C-CA-CB-CG
2	B	10	MK8	CE-CD-CG-CB
2	B	10	MK8	O-C-CA-CB1

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	6	MK8	2	0
2	B	10	MK8	3	0

5.5 Carbohydrates (i)

There are no carbohydrates 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, 95^{th} 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	507/518 (97%)	0.38	57 (11%) 5 1	35, 89, 233, 466	0
2	B	13/17 (76%)	-0.17	0 100 100	64, 89, 111, 124	0
All	All	520/535 (97%)	0.37	57 (10%) 5 2	35, 89, 233, 466	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	603	LEU	6.9
1	A	604	TYR	6.7
1	A	635	GLY	6.4
1	A	658	VAL	5.8
1	A	595	THR	5.6
1	A	654	TYR	5.4
1	A	602	LEU	5.2
1	A	596	ILE	5.0
1	A	629	GLU	5.0
1	A	655	ALA	4.8
1	A	665	ASP	4.6
1	A	636	ALA	4.5
1	A	597	PRO	4.3
1	A	613	VAL	4.2
1	A	631	ILE	4.0
1	A	633	ALA	4.0
1	A	532	ALA	3.9
1	A	548	GLN	3.8
1	A	634	GLU	3.6
1	A	541	VAL	3.6
1	A	562	GLU	3.5
1	A	622	ALA	3.5
1	A	643	LEU	3.4
1	A	537	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	504	TRP	3.3
1	A	545	GLN	3.1
1	A	664	GLU	3.1
1	A	561	VAL	3.1
1	A	544	HIS	3.1
1	A	153	ILE	3.0
1	A	605	SER	2.9
1	A	659	LEU	2.9
1	A	648	ASN	2.8
1	A	543	ALA	2.8
1	A	547	THR	2.8
1	A	536	LEU	2.7
1	A	574	THR	2.7
1	A	611	GLN	2.7
1	A	148	LEU	2.6
1	A	627	ALA	2.6
1	A	645	HIS	2.6
1	A	609	ASN	2.5
1	A	637	THR	2.5
1	A	152	ALA	2.4
1	A	651	VAL	2.4
1	A	601	GLN	2.4
1	A	614	ALA	2.4
1	A	615	ALA	2.3
1	A	652	ALA	2.2
1	A	656	ALA	2.2
1	A	564	VAL	2.2
1	A	638	ALA	2.2
1	A	600	VAL	2.2
1	A	370	LEU	2.2
1	A	549	ARG	2.1
1	A	663	SER	2.1
1	A	502	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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. The B-factors column lists the minimum, median, 95^{th} 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	B-factors(Å^2)	Q<0.9
2	MK8	B	6	9/10	0.94	0.23	69,84,99,107	0
2	MK8	B	10	9/10	0.94	0.27	89,97,111,118	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.