



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 09:27 am BST

PDB ID : 6BN8
Title : Crystal structure of DDB1-CRBN-BRD4(BD1) complex bound to dBET55 PROTAC.
Authors : Nowak, R.P.; DeAngelo, S.L.; Buckley, D.; Bradner, J.E.; Fischer, E.S.
Deposited on : 2017-11-16
Resolution : 3.99 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
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

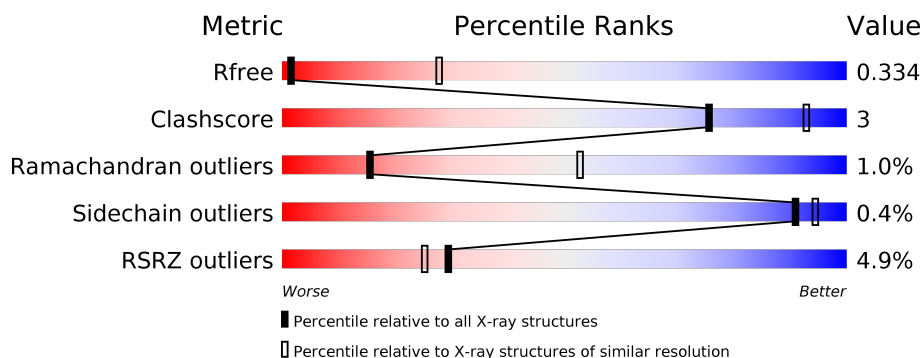
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.99 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	1087 (4.30-3.70)
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)
RSRZ outliers	127900	1028 (4.34-3.66)

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 $\leq 5\%$. 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	864	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>7%</div> </div> </div>
2	B	463	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>8%</div> <div>19%</div> </div> </div>
3	C	127	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>9%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10291 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 DNA damage-binding protein 1, DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	806	Total	C	N	O	S	0	0	0
			6235	3953	1041	1206	35			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP Q16531
A	-26	GLY	-	expression tag	UNP Q16531
A	-25	SER	-	expression tag	UNP Q16531
A	-24	SER	-	expression tag	UNP Q16531
A	-23	HIS	-	expression tag	UNP Q16531
A	-22	HIS	-	expression tag	UNP Q16531
A	-21	HIS	-	expression tag	UNP Q16531
A	-20	HIS	-	expression tag	UNP Q16531
A	-19	HIS	-	expression tag	UNP Q16531
A	-18	HIS	-	expression tag	UNP Q16531
A	-17	SER	-	expression tag	UNP Q16531
A	-16	ALA	-	expression tag	UNP Q16531
A	-15	ALA	-	expression tag	UNP Q16531
A	-14	HIS	-	expression tag	UNP Q16531
A	-13	ILE	-	expression tag	UNP Q16531
A	-12	VAL	-	expression tag	UNP Q16531
A	-11	MET	-	expression tag	UNP Q16531
A	-10	VAL	-	expression tag	UNP Q16531
A	-9	ASP	-	expression tag	UNP Q16531
A	-8	ALA	-	expression tag	UNP Q16531
A	-7	TYR	-	expression tag	UNP Q16531
A	-6	LYS	-	expression tag	UNP Q16531
A	-5	PRO	-	expression tag	UNP Q16531
A	-4	THR	-	expression tag	UNP Q16531
A	-3	LYS	-	expression tag	UNP Q16531
A	-2	GLY	-	expression tag	UNP Q16531

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q16531
A	0	ARG	-	expression tag	UNP Q16531
A	700	GLY	-	linker	UNP Q16531
A	701	ASN	-	linker	UNP Q16531
A	702	GLY	-	linker	UNP Q16531
A	703	ASN	-	linker	UNP Q16531
A	704	SER	-	linker	UNP Q16531
A	705	GLY	-	linker	UNP Q16531

- Molecule 2 is a protein called Protein cereblon.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	375	Total	C	N	O	S	0	0	0
			3005	1919	512	550	24			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	MET	-	initiating methionine	UNP Q96SW2
B	-19	GLY	-	expression tag	UNP Q96SW2
B	-18	SER	-	expression tag	UNP Q96SW2
B	-17	SER	-	expression tag	UNP Q96SW2
B	-16	HIS	-	expression tag	UNP Q96SW2
B	-15	HIS	-	expression tag	UNP Q96SW2
B	-14	HIS	-	expression tag	UNP Q96SW2
B	-13	HIS	-	expression tag	UNP Q96SW2
B	-12	HIS	-	expression tag	UNP Q96SW2
B	-11	HIS	-	expression tag	UNP Q96SW2
B	-10	SER	-	expression tag	UNP Q96SW2
B	-9	ALA	-	expression tag	UNP Q96SW2
B	-8	VAL	-	expression tag	UNP Q96SW2
B	-7	ASP	-	expression tag	UNP Q96SW2
B	-6	GLU	-	expression tag	UNP Q96SW2
B	-5	ASN	-	expression tag	UNP Q96SW2
B	-4	LEU	-	expression tag	UNP Q96SW2
B	-3	TYR	-	expression tag	UNP Q96SW2
B	-2	PHE	-	expression tag	UNP Q96SW2
B	-1	GLN	-	expression tag	UNP Q96SW2
B	0	GLY	-	expression tag	UNP Q96SW2
B	1	GLY	-	expression tag	UNP Q96SW2

- Molecule 3 is a protein called Bromodomain-containing protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	127	Total	C	N	O	S	0	0	0
			1050	681	170	192	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	43	MET	THR	engineered mutation	UNP O60885
C	145	ALA	ASP	engineered mutation	UNP O60885

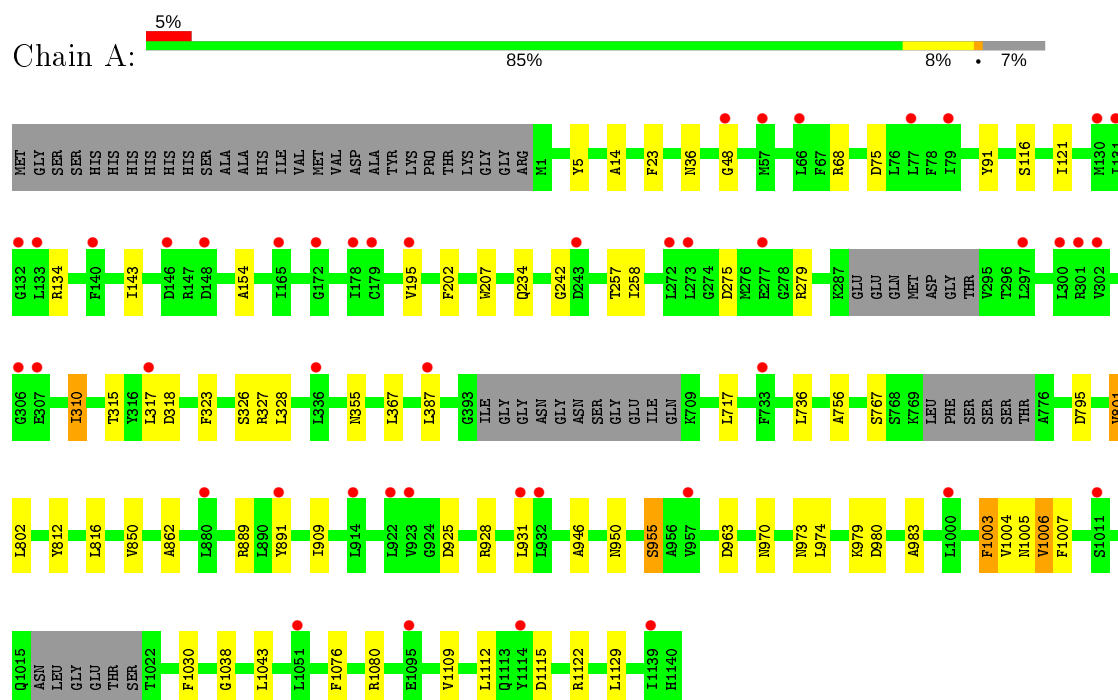
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		

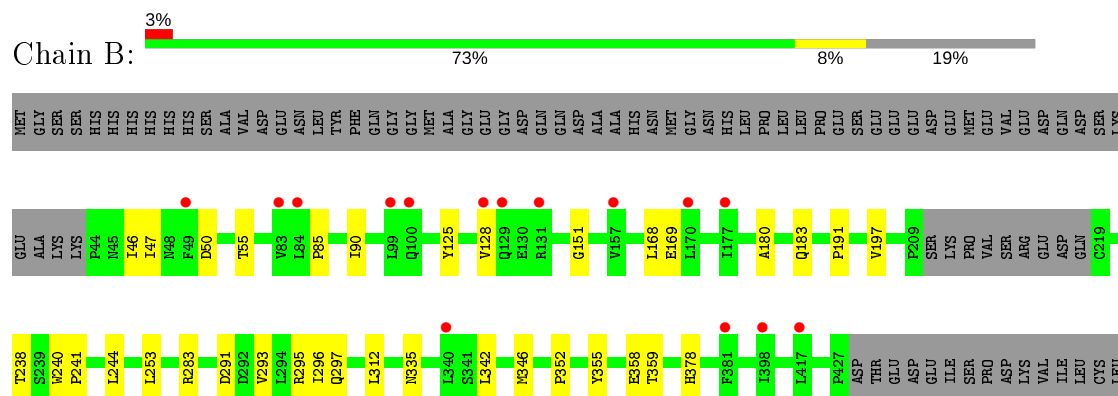
3 Residue-property plots [i](#)

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: DNA damage-binding protein 1, DNA damage-binding protein 1



- Molecule 2: Protein cereblon



- Molecule 3: Bromodomain-containing protein 4





4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	115.20 Å 115.20 Å 597.13 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	99.77 – 3.99 99.77 – 3.99	Depositor EDS
% Data completeness (in resolution range)	100.0 (99.77-3.99) 100.0 (99.77-3.99)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 4.01 Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.289 , 0.333 0.289 , 0.334	Depositor DCC
R_{free} test set	1079 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	171.9	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 116.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.32$, $\langle L^2 \rangle = 0.15$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10291	wwPDB-VP
Average B, all atoms (Å ²)	189.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.24	0/6348	0.44	0/8605
2	B	0.24	0/3077	0.41	0/4177
3	C	0.24	0/1080	0.37	0/1470
All	All	0.24	0/10505	0.42	0/14252

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	6235	0	6089	41	0
2	B	3005	0	2985	20	0
3	C	1050	0	1037	8	0
4	B	1	0	0	0	0
All	All	10291	0	10111	63	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 3.

All (63) 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:1109:VAL:HG12	1:A:1129:LEU:HD22	1.69	0.74
1:A:1115:ASP:HB3	1:A:1122:ARG:HB2	1.71	0.72
3:C:44:ASN:O	3:C:44:ASN:ND2	2.28	0.66
1:A:143:ILE:HG12	1:A:154:ALA:HB2	1.83	0.61
1:A:387:LEU:HG	1:A:717:LEU:HD11	1.85	0.59
1:A:121:ILE:HB	1:A:134:ARG:HB3	1.85	0.58
1:A:234:GLN:OE1	1:A:257:THR:OG1	2.21	0.57
1:A:5:TYR:HB2	1:A:1043:LEU:HD11	1.86	0.57
2:B:168:LEU:HD11	2:B:183:GLN:HB2	1.87	0.57
1:A:736:LEU:HG	1:A:816:LEU:HD22	1.87	0.55
1:A:1005:ASN:O	1:A:1006:VAL:HG12	2.07	0.54
1:A:812:TYR:CZ	2:B:241:PRO:HB3	2.43	0.54
1:A:974:LEU:HD21	1:A:1004:VAL:HG21	1.90	0.53
2:B:55:THR:HG21	2:B:342:LEU:HB2	1.91	0.53
1:A:963:ASP:OD1	1:A:979:LYS:NZ	2.37	0.52
1:A:275:ASP:OD1	1:A:279:ARG:N	2.40	0.52
1:A:980:ASP:HB3	1:A:983:ALA:HB2	1.92	0.52
2:B:283:ARG:NH2	2:B:342:LEU:O	2.43	0.51
2:B:240:TRP:HB3	2:B:244:LEU:HD23	1.93	0.50
3:C:61:ASN:HB2	3:C:168:GLU:HG3	1.94	0.50
2:B:151:GLY:HA3	3:C:152:ALA:HB1	1.92	0.50
1:A:326:SER:O	1:A:355:ASN:ND2	2.46	0.49
1:A:909:ILE:HD12	1:A:925:ASP:HB2	1.94	0.49
1:A:195:VAL:HG22	1:A:202:PHE:HE1	1.78	0.48
1:A:258:ILE:HA	1:A:275:ASP:HA	1.94	0.48
1:A:928:ARG:HB3	1:A:950:ASN:O	2.14	0.47
1:A:1007:PHE:CD1	1:A:1030:PHE:HB3	2.49	0.47
1:A:1005:ASN:HD21	2:B:238:THR:HA	1.79	0.47
1:A:1030:PHE:CZ	1:A:1038:GLY:HA3	2.50	0.46
1:A:1003:PHE:CE2	2:B:197:VAL:HG22	2.50	0.46
1:A:756:ALA:HB1	1:A:801:VAL:HG21	1.98	0.46
1:A:310:ILE:HG21	1:A:328:LEU:HD12	1.97	0.46
1:A:795:ASP:HB2	1:A:802:LEU:HD11	1.98	0.45
2:B:295:ARG:NH1	2:B:358:GLU:OE2	2.47	0.45
3:C:81:TRP:CG	3:C:82:PRO:HD3	2.52	0.44
2:B:293:VAL:O	2:B:297:GLN:HG2	2.17	0.44
1:A:68:ARG:NE	1:A:75:ASP:OD1	2.45	0.44
3:C:96:ASP:OD1	3:C:96:ASP:N	2.51	0.44
1:A:116:SER:OG	1:A:134:ARG:NH1	2.52	0.43
1:A:970:ASN:O	1:A:973:ASN:ND2	2.51	0.43
2:B:253:LEU:HD22	2:B:312:LEU:HD21	1.99	0.43
1:A:207:TRP:HB3	1:A:242:GLY:HA2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:46:ILE:HG22	2:B:47:ILE:H	1.84	0.43
3:C:121:ASN:N	3:C:121:ASN:OD1	2.51	0.43
1:A:1005:ASN:ND2	2:B:238:THR:HA	2.34	0.43
2:B:291:ASP:N	2:B:291:ASP:OD1	2.52	0.43
1:A:889:ARG:HD2	1:A:891:TYR:CZ	2.53	0.43
1:A:955:SER:HB3	1:A:1003:PHE:CE1	2.54	0.43
3:C:52:ASN:HB3	3:C:55:LYS:HB2	2.01	0.43
2:B:352:PRO:HG3	2:B:378:HIS:CG	2.54	0.42
1:A:1080:ARG:NH1	2:B:191:PRO:HD3	2.35	0.42
2:B:346:MET:HA	2:B:359:THR:O	2.20	0.42
2:B:169:GLU:O	2:B:180:ALA:HA	2.20	0.42
2:B:125:TYR:CG	2:B:128:VAL:HG23	2.54	0.42
1:A:195:VAL:HG22	1:A:202:PHE:CE1	2.55	0.41
1:A:14:ALA:HB1	1:A:327:ARG:HG3	2.02	0.41
2:B:90:ILE:HD13	2:B:296:ILE:HG13	2.03	0.41
1:A:23:PHE:CE2	1:A:91:TYR:HB2	2.56	0.41
3:C:46:PRO:HA	3:C:47:PRO:HD3	1.96	0.41
1:A:931:LEU:HD12	1:A:946:ALA:O	2.21	0.41
1:A:315:THR:CG2	1:A:323:PHE:HB3	2.51	0.41
1:A:850:VAL:HB	1:A:862:ALA:HB3	2.03	0.41
1:A:955:SER:HB3	1:A:1003:PHE:HE1	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	796/864 (92%)	733 (92%)	52 (6%)	11 (1%)	11	46
2	B	371/463 (80%)	347 (94%)	22 (6%)	2 (0%)	29	67
3	C	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
All	All	1292/1454 (89%)	1201 (93%)	78 (6%)	13 (1%)	15	53

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	767	SER
1	A	1006	VAL
1	A	36	ASN
1	A	317	LEU
1	A	367	LEU
1	A	1112	LEU
1	A	955	SER
1	A	1076	PHE
2	B	50	ASP
1	A	310	ILE
1	A	48	GLY
2	B	85	PRO
1	A	801	VAL

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	678/749 (90%)	676 (100%)	2 (0%)	92	95
2	B	335/416 (80%)	333 (99%)	2 (1%)	86	92
3	C	117/119 (98%)	117 (100%)	0	100	100
All	All	1130/1284 (88%)	1126 (100%)	4 (0%)	91	94

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

Mol	Chain	Res	Type
1	A	318	ASP
1	A	1003	PHE
2	B	335	ASN
2	B	355	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	123	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	806/864 (93%)	0.23	45 (5%) 24 21	124, 198, 247, 266	0
2	B	375/463 (80%)	0.17	15 (4%) 38 30	131, 166, 208, 229	0
3	C	127/127 (100%)	-0.02	4 (3%) 49 38	153, 188, 228, 240	0
All	All	1308/1454 (89%)	0.19	64 (4%) 29 25	124, 184, 244, 266	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	133	LEU	5.5
3	C	42	SER	5.3
1	A	307	GLU	4.6
2	B	84	LEU	4.4
2	B	83	VAL	4.0
2	B	129	GLN	3.8
1	A	923	VAL	3.8
2	B	100	GLN	3.6
1	A	273	LEU	3.3
1	A	130	MET	3.2
1	A	1000	LEU	3.2
1	A	243	ASP	3.1
1	A	1114	TYR	3.1
1	A	165	ILE	3.1
1	A	1139	ILE	3.0
1	A	317	LEU	3.0
1	A	336	LEU	3.0
1	A	272	LEU	2.9
2	B	49	PHE	2.9
1	A	297	LEU	2.9
2	B	131	ARG	2.9
1	A	178	ILE	2.8
1	A	922	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	132	GLY	2.7
1	A	140	PHE	2.7
1	A	66	LEU	2.6
2	B	157	VAL	2.6
1	A	1051	LEU	2.6
1	A	932	LEU	2.5
1	A	733	PHE	2.5
1	A	79	ILE	2.4
1	A	148	ASP	2.4
1	A	914	LEU	2.4
1	A	57	MET	2.4
1	A	77	LEU	2.4
1	A	172	GLY	2.4
1	A	1011	SER	2.3
2	B	99	LEU	2.3
1	A	277	GLU	2.3
1	A	387	LEU	2.3
1	A	131	ILE	2.3
1	A	931	LEU	2.3
2	B	398	ILE	2.3
1	A	891	TYR	2.3
2	B	340	LEU	2.3
2	B	177	ILE	2.2
1	A	179	CYS	2.2
1	A	1095	GLU	2.2
3	C	58	ARG	2.2
1	A	48	GLY	2.1
1	A	300	LEU	2.1
1	A	301	ARG	2.1
1	A	880	LEU	2.1
2	B	381	PHE	2.1
3	C	97	TYR	2.1
2	B	170	LEU	2.1
1	A	302	VAL	2.1
1	A	306	GLY	2.1
1	A	957	VAL	2.1
1	A	146	ASP	2.0
2	B	417	LEU	2.0
3	C	157	PHE	2.0
2	B	128	VAL	2.0
1	A	195	VAL	2.0

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. 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	B-factors(\AA^2)	Q<0.9
4	ZN	B	501	1/1	0.97	0.31	133,133,133,133	0

6.5 Other polymers [i](#)

There are no such residues in this entry.