



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 17, 2017 – 10:58 PM EST

PDB ID : 5U8O
Title : Crystal Structure of Beta-lactamase domain protein, from Burkholderia multivorans
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2016-12-14
Resolution : 2.40 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

<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	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
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-20028442

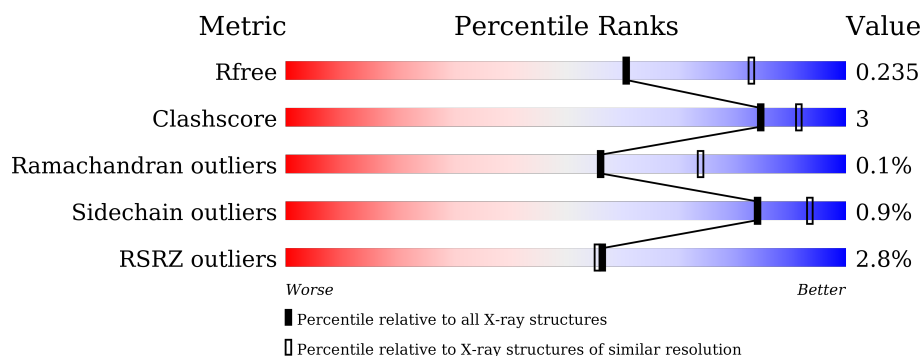
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	367	<div> <div>5%</div> <div> <div></div> <div>88%</div> <div>8%</div> <div>••</div> </div> </div>
1	B	367	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div>•</div> </div> </div>
1	C	367	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>5%</div> </div> </div>
1	D	367	<div> <div>3%</div> <div> <div></div> <div>92%</div> <div>5%</div> <div>•</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
3	UNX	A	403	-	-	-	X
3	UNX	B	403	-	-	-	X
3	UNX	C	403	-	-	-	X
3	UNX	D	403	-	-	-	X
4	CA	A	404	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11297 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 Zn-dependent hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	1	0
			2703	1712	497	478	16			
1	B	360	Total	C	N	O	S	0	0	0
			2821	1783	524	498	16			
1	C	349	Total	C	N	O	S	0	3	0
			2690	1706	495	473	16			
1	D	354	Total	C	N	O	S	0	1	0
			2720	1722	499	484	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP A0A0H3KRR5
A	-6	ALA	-	expression tag	UNP A0A0H3KRR5
A	-5	HIS	-	expression tag	UNP A0A0H3KRR5
A	-4	HIS	-	expression tag	UNP A0A0H3KRR5
A	-3	HIS	-	expression tag	UNP A0A0H3KRR5
A	-2	HIS	-	expression tag	UNP A0A0H3KRR5
A	-1	HIS	-	expression tag	UNP A0A0H3KRR5
A	0	HIS	-	expression tag	UNP A0A0H3KRR5
B	-7	MET	-	expression tag	UNP A0A0H3KRR5
B	-6	ALA	-	expression tag	UNP A0A0H3KRR5
B	-5	HIS	-	expression tag	UNP A0A0H3KRR5
B	-4	HIS	-	expression tag	UNP A0A0H3KRR5
B	-3	HIS	-	expression tag	UNP A0A0H3KRR5
B	-2	HIS	-	expression tag	UNP A0A0H3KRR5
B	-1	HIS	-	expression tag	UNP A0A0H3KRR5
B	0	HIS	-	expression tag	UNP A0A0H3KRR5
C	-7	MET	-	expression tag	UNP A0A0H3KRR5
C	-6	ALA	-	expression tag	UNP A0A0H3KRR5
C	-5	HIS	-	expression tag	UNP A0A0H3KRR5
C	-4	HIS	-	expression tag	UNP A0A0H3KRR5
C	-3	HIS	-	expression tag	UNP A0A0H3KRR5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP A0A0H3KRR5
C	-1	HIS	-	expression tag	UNP A0A0H3KRR5
C	0	HIS	-	expression tag	UNP A0A0H3KRR5
D	-7	MET	-	expression tag	UNP A0A0H3KRR5
D	-6	ALA	-	expression tag	UNP A0A0H3KRR5
D	-5	HIS	-	expression tag	UNP A0A0H3KRR5
D	-4	HIS	-	expression tag	UNP A0A0H3KRR5
D	-3	HIS	-	expression tag	UNP A0A0H3KRR5
D	-2	HIS	-	expression tag	UNP A0A0H3KRR5
D	-1	HIS	-	expression tag	UNP A0A0H3KRR5
D	0	HIS	-	expression tag	UNP A0A0H3KRR5

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

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

- Molecule 3 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total X 1 1	0	0
3	A	1	Total X 1 1	0	0
3	D	1	Total X 1 1	0	0
3	C	1	Total X 1 1	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ca 1 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		

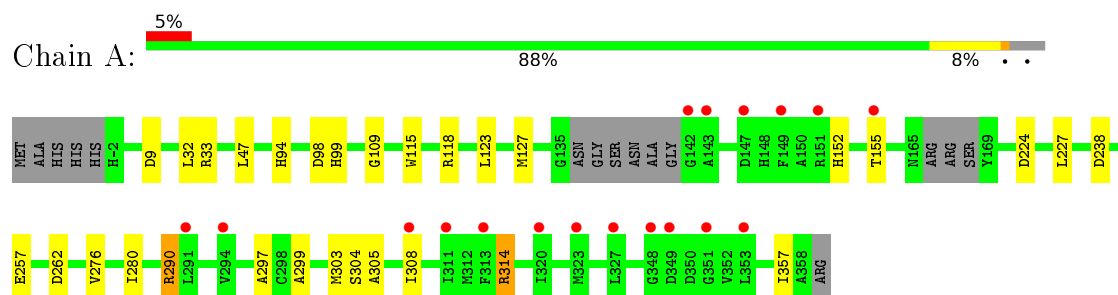
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	104	Total	O	0	0
			104	104		
6	B	111	Total	O	0	2
			113	113		
6	C	75	Total	O	0	0
			75	75		
6	D	57	Total	O	0	0
			57	57		

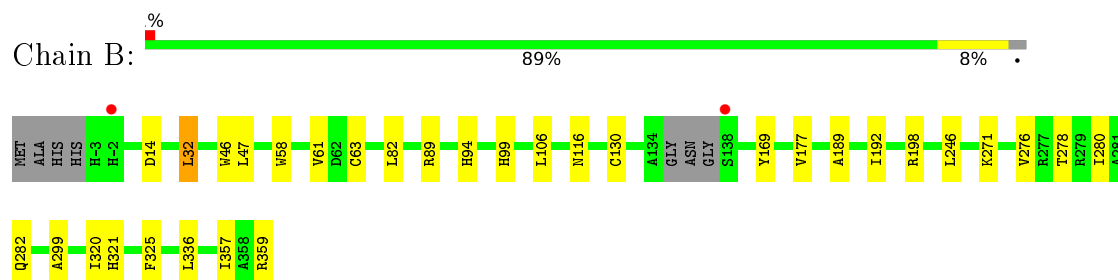
3 Residue-property plots [i](#)

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

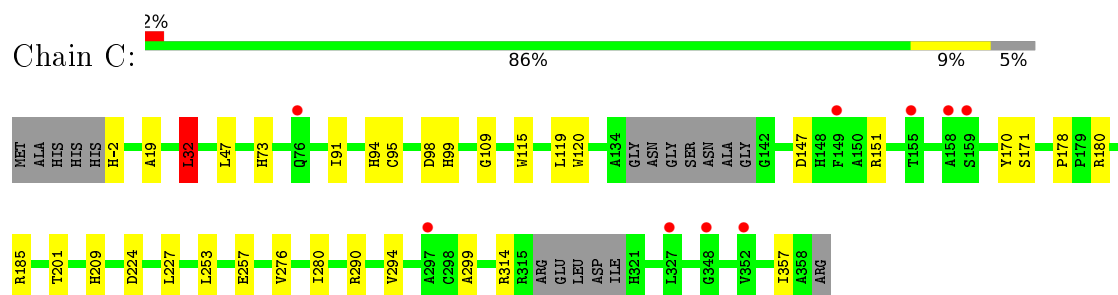
- Molecule 1: Zn-dependent hydrolase



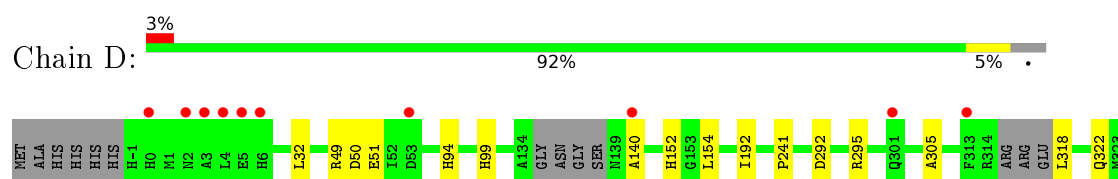
- Molecule 1: Zn-dependent hydrolase



- Molecule 1: Zn-dependent hydrolase



- Molecule 1: Zn-dependent hydrolase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	45.52Å 106.83Å 144.33Å 90.00° 91.30° 90.00°	Depositor
Resolution (Å)	48.10 – 2.40 48.10 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.2 (48.10-2.40) 98.4 (48.10-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.39Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.163 , 0.222 0.175 , 0.235	Depositor DCC
R_{free} test set	1982 reflections (3.87%)	DCC
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.557	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 66.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11297	wwPDB-VP
Average B, all atoms (Å ²)	47.0	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 32.07 % 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 9.9713e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: UNX, ZN, CA, CL

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	0.40	0/2777	0.58	0/3788
1	B	0.41	0/2897	0.59	1/3944 (0.0%)
1	C	0.39	0/2771	0.59	1/3778 (0.0%)
1	D	0.37	0/2794	0.57	1/3809 (0.0%)
All	All	0.39	0/11239	0.58	3/15319 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	32	LEU	CA-CB-CG	7.44	132.42	115.30
1	D	32	LEU	CA-CB-CG	6.25	129.69	115.30
1	B	32	LEU	CA-CB-CG	5.95	128.97	115.30

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	2703	0	2584	17	0
1	B	2821	0	2727	18	0
1	C	2690	0	2559	18	0
1	D	2720	0	2600	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	104	0	0	4	0
6	B	113	0	0	0	0
6	C	75	0	0	0	0
6	D	57	0	0	2	0
All	All	11297	0	10470	62	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 (62) 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:32:LEU:HD11	1:A:47:LEU:HD12	1.79	0.64
1:D:51:GLU:OE2	6:D:501:HOH:O	2.15	0.64
1:B:14:ASP:OD2	1:B:271:LYS:NZ	2.31	0.61
1:C:180:ARG:HD3	1:D:241:PRO:HG3	1.82	0.60
1:B:32:LEU:HD11	1:B:47:LEU:HD12	1.87	0.56
1:B:94:HIS:HE1	1:B:99:HIS:CE1	2.25	0.55
1:D:292:ASP:OD1	1:D:295:ARG:NH1	2.39	0.55
1:A:98:ASP:N	1:A:98:ASP:OD2	2.38	0.54
1:C:253:LEU:HD22	1:C:280:ILE:HD12	1.90	0.54
1:C:257:GLU:HG3	1:C:280:ILE:HG21	1.90	0.52
1:C:185[B]:ARG:CZ	1:C:185[B]:ARG:HB2	2.40	0.52
1:A:262:ASP:HB3	6:A:591:HOH:O	2.08	0.52
1:C:276:VAL:O	1:C:280:ILE:HG12	2.11	0.51
1:D:140:ALA:HB1	1:D:324:THR:HG21	1.94	0.50
1:A:257:GLU:HG3	1:A:280:ILE:HG21	1.93	0.50
1:D:318:LEU:HD22	1:D:322:GLN:HB3	1.95	0.49
1:B:189:ALA:HB2	1:B:198:ARG:HE	1.77	0.49
1:B:357:ILE:HD11	1:B:359:ARG:CZ	2.43	0.49
1:A:297:ALA:HB1	1:A:303:MET:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:TRP:HB2	1:B:61:VAL:HB	1.94	0.48
1:C:109:GLY:HA2	1:C:115:TRP:NE1	2.28	0.48
1:C:98:ASP:N	1:C:98:ASP:OD2	2.43	0.48
1:A:276:VAL:O	1:A:280:ILE:HG12	2.15	0.47
1:A:109:GLY:HA2	1:A:115:TRP:NE1	2.29	0.47
1:C:32:LEU:HD11	1:C:47:LEU:HG	1.97	0.47
1:A:299:ALA:HA	1:A:357:ILE:HG12	1.96	0.47
1:B:130:CYS:SG	1:B:177:VAL:HG11	2.55	0.46
1:B:357:ILE:HD11	1:B:359:ARG:NH2	2.30	0.46
1:D:192:ILE:O	6:D:502:HOH:O	2.21	0.46
1:B:299:ALA:HA	1:B:357:ILE:HG12	1.98	0.46
1:D:94:HIS:HE1	1:D:99:HIS:CE1	2.34	0.46
1:C:299:ALA:HA	1:C:357:ILE:HG12	1.99	0.45
1:C:95:CYS:O	1:C:170:TYR:OH	2.28	0.45
1:A:152:HIS:HB3	1:A:305:ALA:HB3	1.98	0.44
1:B:321:HIS:CE1	1:B:325:PHE:HE2	2.34	0.44
1:B:276:VAL:O	1:B:280:ILE:HG12	2.18	0.44
1:C:91:ILE:HG12	1:C:120:TRP:HB2	1.98	0.44
1:B:359:ARG:HA	1:B:359:ARG:HD3	1.82	0.44
1:C:119:LEU:HD22	1:C:178:PRO:HG2	2.00	0.44
1:C:224:ASP:HA	1:C:227:LEU:HD21	2.00	0.43
1:A:123:LEU:O	1:A:127:MET:HG2	2.18	0.43
1:B:58:TRP:CD1	1:B:82:LEU:HD22	2.53	0.43
1:A:304:SER:O	1:A:308:ILE:HG12	2.18	0.43
1:B:63:CYS:SG	1:B:106:LEU:HD12	2.59	0.43
1:A:224:ASP:HA	1:A:227:LEU:HD21	2.01	0.43
1:D:152:HIS:HB3	1:D:305:ALA:HB3	2.00	0.43
1:C:147:ASP:O	1:C:151:ARG:HG3	2.19	0.43
1:A:290:ARG:HD3	1:A:290:ARG:HA	1.69	0.42
1:C:290:ARG:O	1:C:294:VAL:HG23	2.20	0.42
1:A:94:HIS:HE1	1:A:99:HIS:CE1	2.38	0.42
1:C:94:HIS:HE1	1:C:99:HIS:CE1	2.37	0.42
1:D:154:LEU:HD12	1:D:154:LEU:HA	1.83	0.42
1:B:89:ARG:NH2	1:B:192:ILE:HG12	2.35	0.42
1:A:314:ARG:NH2	6:A:511:HOH:O	2.53	0.41
1:C:19:ALA:HB1	1:C:73:HIS:CE1	2.55	0.41
1:C:201:THR:HA	1:C:209:HIS:O	2.19	0.41
1:A:118:ARG:HD3	6:A:548:HOH:O	2.19	0.41
1:A:33:ARG:HD3	6:A:575:HOH:O	2.21	0.41
1:B:278:THR:O	1:B:282:GLN:HG3	2.20	0.41
1:B:246:LEU:HD23	1:B:336:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:ILE:HA	1:B:320:ILE:HD12	1.90	0.40
1:D:49:ARG:NH1	1:D:50:ASP:O	2.54	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	347/367 (95%)	339 (98%)	8 (2%)	0	100	100
1	B	356/367 (97%)	346 (97%)	10 (3%)	0	100	100
1	C	346/367 (94%)	336 (97%)	9 (3%)	1 (0%)	46	63
1	D	349/367 (95%)	340 (97%)	9 (3%)	0	100	100
All	All	1398/1468 (95%)	1361 (97%)	36 (3%)	1 (0%)	56	74

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	314	ARG

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	268/298 (90%)	263 (98%)	5 (2%)	65	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	286/298 (96%)	284 (99%)	2 (1%)	88	95
1	C	264/298 (89%)	261 (99%)	3 (1%)	80	92
1	D	270/298 (91%)	270 (100%)	0	100	100
All	All	1088/1192 (91%)	1078 (99%)	10 (1%)	84	93

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASP
1	A	155	THR
1	A	238	ASP
1	A	290	ARG
1	A	314	ARG
1	B	116	ASN
1	B	169	TYR
1	C	-2	HIS
1	C	32	LEU
1	C	171	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
1	B	-3	HIS
1	C	94	HIS
1	D	55	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 14 ligands modelled in this entry, 4 are unknown and 10 are 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	352/367 (95%)	-0.05	18 (5%) 32 32	19, 39, 95, 125	0
1	B	360/367 (98%)	-0.40	2 (0%) 90 90	21, 39, 68, 90	0
1	C	349/367 (95%)	-0.18	9 (2%) 59 58	25, 45, 85, 111	0
1	D	354/367 (96%)	-0.13	11 (3%) 52 52	27, 51, 85, 118	0
All	All	1415/1468 (96%)	-0.19	40 (2%) 56 55	19, 44, 84, 125	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	ASN	4.5
1	D	3	ALA	4.4
1	A	155	THR	3.9
1	D	313	PHE	3.9
1	C	158	ALA	3.9
1	A	294	VAL	3.6
1	A	143	ALA	3.5
1	D	4	LEU	3.5
1	A	327	LEU	3.4
1	A	349	ASP	3.2
1	A	142	GLY	3.2
1	D	5	GLU	3.1
1	C	348	GLY	3.1
1	D	301	GLN	3.0
1	A	351	GLY	3.0
1	A	313	PHE	3.0
1	D	325	PHE	2.9
1	A	308	ILE	2.8
1	C	327	LEU	2.8
1	A	320	ILE	2.8
1	D	53	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	76	GLN	2.6
1	A	311	ILE	2.5
1	D	140	ALA	2.4
1	D	6	HIS	2.4
1	C	149	PHE	2.4
1	B	138	SER	2.3
1	D	0	HIS	2.3
1	A	348	GLY	2.2
1	C	159	SER	2.2
1	A	149	PHE	2.2
1	C	297	ALA	2.2
1	C	155	THR	2.2
1	A	151	ARG	2.2
1	C	352	VAL	2.1
1	A	353	LEU	2.1
1	A	147	ASP	2.1
1	A	323	MET	2.0
1	A	291	LEU	2.0
1	B	-2	HIS	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. 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(Å ²)	Q<0.9
4	CA	A	404	1/1	0.85	0.26	11.41	87,87,87,87	0
3	UNX	C	403	1/1	0.72	0.40	10.93	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	UNX	B	403	1/1	0.80	0.42	10.50	30,30,30,30	0
3	UNX	A	403	1/1	0.93	0.45	10.38	30,30,30,30	0
3	UNX	D	403	1/1	0.82	0.28	2.86	30,30,30,30	0
2	ZN	B	402	1/1	0.96	0.05	-2.73	59,59,59,59	0
2	ZN	C	402	1/1	0.98	0.07	-3.27	46,46,46,46	1
2	ZN	D	402	1/1	0.94	0.04	-3.51	62,62,62,62	0
2	ZN	A	402	1/1	1.00	0.06	-4.08	51,51,51,51	0
2	ZN	D	401	1/1	0.96	0.04	-4.28	68,68,68,68	0
2	ZN	C	401	1/1	0.97	0.08	-	63,63,63,63	0
5	CL	B	404	1/1	0.87	0.14	-	68,68,68,68	0
2	ZN	A	401	1/1	0.98	0.07	-	57,57,57,57	0
2	ZN	B	401	1/1	0.98	0.07	-	40,40,40,40	1

6.5 Other polymers [i](#)

There are no such residues in this entry.