



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2018 – 03:11 pm GMT

PDB ID : 1VHG
Title : Crystal structure of ADP compounds hydrolase
Authors : Structural GenomiX
Deposited on : 2003-12-01
Resolution : 2.70 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 : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

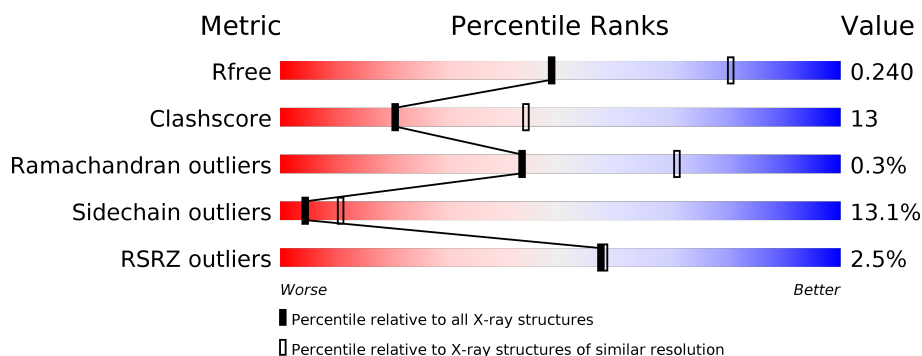
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	111664	2449 (2.70-2.70)
Clashscore	122126	2756 (2.70-2.70)
Ramachandran outliers	120053	2716 (2.70-2.70)
Sidechain outliers	120020	2716 (2.70-2.70)
RSRZ outliers	108989	2376 (2.70-2.70)

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	198	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 64%, yellow 64%, yellow 87%, orange 87%, orange 94%, red 94%, red 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 64% 23% 7% • 7% </div> </div>
1	B	198	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 4%, green 4%, green 64%, yellow 64%, yellow 89%, orange 89%, orange 94%, red 94%, red 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 64% 25% • • 7% </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3149 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 ADP compounds hydrolase nudE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	185	Total	C	N	O	Se	0	1	0
			1480	941	250	282	7			
1	B	185	Total	C	N	O	Se	0	0	0
			1464	932	248	278	6			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	cloning artifact	UNP P45799
A	0	SER	-	cloning artifact	UNP P45799
A	1	LEU	-	cloning artifact	UNP P45799
A	42	MSE	MET	modified residue	UNP P45799
A	51	MSE	MET	modified residue	UNP P45799
A	115	MSE	MET	modified residue	UNP P45799
A	124	MSE	MET	modified residue	UNP P45799
A	155	MSE	MET	modified residue	UNP P45799
A	156	MSE	MET	modified residue	UNP P45799
A	187	GLU	-	cloning artifact	UNP P45799
A	188	GLY	-	cloning artifact	UNP P45799
A	189	GLY	-	cloning artifact	UNP P45799
A	190	SER	-	cloning artifact	UNP P45799
A	191	HIS	-	cloning artifact	UNP P45799
A	192	HIS	-	cloning artifact	UNP P45799
A	193	HIS	-	cloning artifact	UNP P45799
A	194	HIS	-	cloning artifact	UNP P45799
A	195	HIS	-	cloning artifact	UNP P45799
A	196	HIS	-	cloning artifact	UNP P45799
B	-1	MSE	-	cloning artifact	UNP P45799
B	0	SER	-	cloning artifact	UNP P45799
B	1	LEU	-	cloning artifact	UNP P45799
B	42	MSE	MET	modified residue	UNP P45799
B	51	MSE	MET	modified residue	UNP P45799
B	115	MSE	MET	modified residue	UNP P45799

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Chain	Residue	Modelled	Actual	Comment	Reference
B	124	MSE	MET	modified residue	UNP P45799
B	155	MSE	MET	modified residue	UNP P45799
B	156	MSE	MET	modified residue	UNP P45799
B	187	GLU	-	cloning artifact	UNP P45799
B	188	GLY	-	cloning artifact	UNP P45799
B	189	GLY	-	cloning artifact	UNP P45799
B	190	SER	-	cloning artifact	UNP P45799
B	191	HIS	-	cloning artifact	UNP P45799
B	192	HIS	-	cloning artifact	UNP P45799
B	193	HIS	-	cloning artifact	UNP P45799
B	194	HIS	-	cloning artifact	UNP P45799
B	195	HIS	-	cloning artifact	UNP P45799
B	196	HIS	-	cloning artifact	UNP P45799

- Molecule 2 is water.

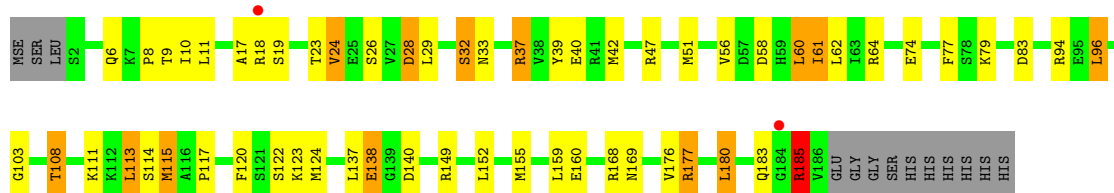
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	97	Total O 97 97	0	0
2	B	108	Total O 108 108	0	0

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 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.

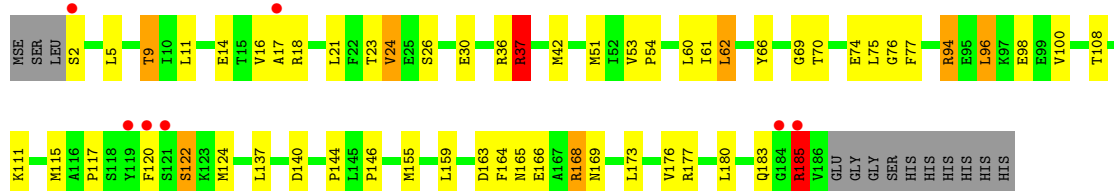
• Molecule 1: ADP compounds hydrolase nudE

Chain A: 



• Molecule 1: ADP compounds hydrolase nudE

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 3 2	Depositor
Cell constants a, b, c, α , β , γ	193.17Å 193.17Å 193.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.17 – 2.70 41.18 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (41.17-2.70) 100.0 (41.18-2.70)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.59 (at 2.69Å)	Xtriage
Refinement program	REFMAC 4.0	Depositor
R, R_{free}	0.211 , 0.272 0.190 , 0.240	Depositor DCC
R_{free} test set	868 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 66.2	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	0.93	EDS
Total number of atoms	3149	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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](#)

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	0.58	0/1504	1.18	8/2028 (0.4%)
1	B	0.57	0/1488	1.26	14/2009 (0.7%)
All	All	0.58	0/2992	1.22	22/4037 (0.5%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	37	ARG	NE-CZ-NH2	-10.69	114.95	120.30
1	B	37	ARG	NE-CZ-NH1	10.12	125.36	120.30
1	A	185	ARG	NE-CZ-NH2	8.82	124.71	120.30
1	B	37	ARG	CD-NE-CZ	7.70	134.38	123.60
1	B	94	ARG	NE-CZ-NH2	-7.63	116.49	120.30
1	A	185	ARG	CD-NE-CZ	7.33	133.86	123.60
1	B	94	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	A	47	ARG	CD-NE-CZ	6.88	133.24	123.60
1	B	185	ARG	NE-CZ-NH2	6.68	123.64	120.30
1	B	185	ARG	CD-NE-CZ	6.68	132.95	123.60
1	A	96	LEU	CA-CB-CG	6.40	130.03	115.30
1	B	163	ASP	CB-CG-OD2	6.03	123.72	118.30
1	B	185	ARG	CA-CB-CG	5.86	126.30	113.40
1	B	36	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	A	113	LEU	CA-CB-CG	5.67	128.35	115.30
1	A	83	ASP	CB-CG-OD1	5.62	123.36	118.30
1	B	177	ARG	CD-NE-CZ	5.53	131.35	123.60
1	B	177	ARG	NE-CZ-NH2	5.53	123.06	120.30
1	B	62	LEU	CA-CB-CG	5.35	127.60	115.30
1	A	103	GLY	N-CA-C	-5.28	99.91	113.10
1	B	14	GLU	CA-CB-CG	5.04	124.49	113.40
1	A	177	ARG	CG-CD-NE	5.04	122.38	111.80

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	1480	0	1465	49	1
1	B	1464	0	1441	38	1
2	A	97	0	0	6	0
2	B	108	0	0	4	0
All	All	3149	0	2906	78	1

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 13.

All (78) 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:115[A]:MSE:HE3	1:A:168:ARG:HD2	1.56	0.87
1:A:51:MSE:HE3	1:A:79:LYS:HE3	1.56	0.86
1:A:17:ALA:HB3	1:A:24:VAL:HG13	1.60	0.81
1:A:11:LEU:HB2	1:A:28:ASP:HB3	1.69	0.75
1:A:185:ARG:HH21	1:A:185:ARG:HB2	1.52	0.74
1:A:115[A]:MSE:HE3	1:A:168:ARG:CD	2.17	0.74
1:A:51:MSE:HE2	1:A:77:PHE:HB2	1.74	0.70
1:B:17:ALA:HB3	1:B:24:VAL:HG13	1.75	0.68
1:A:122:SER:HA	2:A:269:HOH:O	1.93	0.68
1:B:51:MSE:HE1	1:B:169:ASN:HA	1.77	0.67
1:A:51:MSE:HE3	1:A:79:LYS:CE	2.27	0.65
1:A:183:GLN:HE21	1:A:185:ARG:HD3	1.62	0.64
1:A:149:ARG:HD3	2:A:263:HOH:O	2.00	0.62
1:B:166:GLU:OE2	1:B:168:ARG:HD3	2.00	0.61
1:A:51:MSE:HE2	1:A:77:PHE:HD1	1.64	0.61
1:A:51:MSE:HE2	1:A:77:PHE:CD1	2.36	0.61
1:B:96:LEU:HD22	1:B:100:VAL:HB	1.83	0.61
1:B:122:SER:HA	2:B:246:HOH:O	1.99	0.61
1:A:185:ARG:NH2	1:A:185:ARG:HB2	2.16	0.60
1:B:51:MSE:HE2	1:B:77:PHE:HD1	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:MSE:HE1	1:A:169:ASN:HA	1.85	0.58
1:A:6:GLN:HB3	1:A:32:SER:OG	2.04	0.57
1:A:58:ASP:HA	1:A:152:LEU:HD12	1.87	0.57
1:B:155:MSE:HE2	1:B:173:LEU:HD12	1.87	0.57
1:A:152:LEU:O	1:A:155:MSE:HG3	2.04	0.56
1:A:185:ARG:HH21	1:A:185:ARG:CB	2.19	0.55
1:A:17:ALA:HB3	1:A:24:VAL:CG1	2.34	0.54
1:A:124:MSE:HE2	1:A:168:ARG:HD2	1.90	0.53
1:A:56:VAL:HG23	1:A:61:ILE:HD11	1.91	0.53
1:B:51:MSE:HE2	1:B:77:PHE:CD1	2.44	0.52
1:A:60:LEU:HD13	1:A:152:LEU:HD21	1.91	0.51
1:A:60:LEU:HD13	1:A:152:LEU:CD2	2.40	0.51
1:A:140:ASP:O	1:B:37:ARG:NH2	2.44	0.51
1:B:51:MSE:HE2	1:B:77:PHE:HB2	1.93	0.51
1:A:8:PRO:HG2	1:B:66:TYR:CZ	2.46	0.50
1:B:115:MSE:SE	2:B:208:HOH:O	2.79	0.50
1:A:40:GLU:HB2	1:B:21:LEU:HD13	1.94	0.50
1:A:29:LEU:HD12	1:A:39:TYR:HD1	1.78	0.49
1:B:185:ARG:HH21	1:B:185:ARG:CB	2.26	0.49
1:B:9:THR:HG23	2:B:280:HOH:O	2.12	0.48
1:A:51:MSE:HB2	1:A:124:MSE:SE	2.63	0.48
1:A:37:ARG:NH2	1:B:140:ASP:O	2.47	0.48
1:B:94:ARG:O	1:B:98:GLU:HG3	2.14	0.47
1:A:19:SER:HB2	1:B:16:VAL:CG1	2.44	0.47
1:B:185:ARG:HH21	1:B:185:ARG:HB2	1.79	0.47
1:A:117:PRO:HB3	1:B:70:THR:CG2	2.45	0.46
1:B:53:VAL:HG11	1:B:176:VAL:HG21	1.97	0.46
1:A:108:THR:HG22	2:A:197:HOH:O	2.15	0.46
1:B:183:GLN:HG3	1:B:185:ARG:HG2	1.96	0.46
1:B:115:MSE:HE3	1:B:168:ARG:NE	2.31	0.46
1:A:10:ILE:HG13	1:A:29:LEU:CD2	2.45	0.45
1:B:115:MSE:SE	1:B:124:MSE:HB2	2.67	0.45
1:B:185:ARG:NH2	1:B:185:ARG:HB2	2.31	0.45
1:A:56:VAL:HG23	1:A:61:ILE:CD1	2.47	0.45
1:A:115[A]:MSE:CE	1:A:168:ARG:HH21	2.31	0.44
1:B:54:PRO:HG2	1:B:61:ILE:HB	2.00	0.44
1:B:75:LEU:O	1:B:164:PHE:HA	2.17	0.44
1:A:64:ARG:HD3	1:B:5:LEU:HD11	2.00	0.44
1:B:76:GLY:HA3	2:B:222:HOH:O	2.17	0.44
1:B:16:VAL:HG21	1:B:26:SER:HB2	1.99	0.44
1:A:94:ARG:HH11	1:A:94:ARG:HG2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:VAL:CG2	1:A:61:ILE:HD11	2.48	0.44
1:A:117:PRO:HB3	1:B:70:THR:HG21	2.00	0.44
1:A:176:VAL:HG12	1:A:180:LEU:HD22	2.00	0.43
1:A:117:PRO:HA	1:A:120:PHE:O	2.18	0.43
1:A:138:GLU:HB2	2:A:257:HOH:O	2.19	0.43
1:A:74:GLU:HG3	2:A:290:HOH:O	2.19	0.43
1:A:160:GLU:OE2	1:A:160:GLU:HA	2.19	0.42
1:A:117:PRO:O	1:B:69:GLY:HA3	2.19	0.42
1:A:177:ARG:HD3	2:A:198:HOH:O	2.19	0.42
1:B:16:VAL:CG2	1:B:26:SER:HB2	2.50	0.42
1:B:155:MSE:HE2	1:B:173:LEU:CD1	2.49	0.42
1:A:60:LEU:HB3	1:A:62:LEU:HD22	2.02	0.41
1:B:11:LEU:HD11	1:B:30:GLU:HB2	2.01	0.41
1:B:144:PRO:O	1:B:146:PRO:HD3	2.20	0.41
1:B:183:GLN:HE21	1:B:185:ARG:HD3	1.86	0.41
1:A:29:LEU:HD12	1:A:39:TYR:CD1	2.56	0.40
1:B:117:PRO:HA	1:B:120:PHE:O	2.22	0.40

All (1) 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:33:ASN:O	1:B:37:ARG:NH1[15_554]	2.10	0.10

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	184/198 (93%)	173 (94%)	11 (6%)	0	100	100
1	B	183/198 (92%)	176 (96%)	6 (3%)	1 (0%)	31	58
All	All	367/396 (93%)	349 (95%)	17 (5%)	1 (0%)	43	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	165	ASN

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	163/168 (97%)	139 (85%)	24 (15%)	3	8
1	B	159/168 (95%)	140 (88%)	19 (12%)	6	13
All	All	322/336 (96%)	279 (87%)	43 (13%)	4	10

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	THR
1	A	18	ARG
1	A	23	THR
1	A	24	VAL
1	A	26	SER
1	A	28	ASP
1	A	32	SER
1	A	37	ARG
1	A	42	MSE
1	A	60	LEU
1	A	61	ILE
1	A	96	LEU
1	A	108	THR
1	A	111	LYS
1	A	113	LEU
1	A	114	SER
1	A	115[A]	MSE
1	A	115[B]	MSE
1	A	123	LYS
1	A	137	LEU
1	A	138	GLU
1	A	159	LEU

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Mol	Chain	Res	Type
1	A	180	LEU
1	A	185	ARG
1	B	2	SER
1	B	9	THR
1	B	18	ARG
1	B	23	THR
1	B	24	VAL
1	B	37	ARG
1	B	42	MSE
1	B	60	LEU
1	B	62	LEU
1	B	74	GLU
1	B	96	LEU
1	B	108	THR
1	B	111	LYS
1	B	122	SER
1	B	137	LEU
1	B	159	LEU
1	B	168	ARG
1	B	180	LEU
1	B	185	ARG

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

Mol	Chain	Res	Type
1	A	183	GLN
1	B	183	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

There are no ligands in this entry.

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 [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	179/198 (90%)	-0.26	2 (1%) 80 81	22, 35, 67, 85	0
1	B	179/198 (90%)	-0.11	7 (3%) 39 38	20, 36, 75, 95	0
All	All	358/396 (90%)	-0.19	9 (2%) 57 58	20, 35, 72, 95	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	SER	5.6
1	B	185	ARG	2.6
1	B	119	TYR	2.5
1	B	121	SER	2.3
1	B	17	ALA	2.2
1	B	120	PHE	2.2
1	A	18	ARG	2.2
1	B	184	GLY	2.1
1	A	184	GLY	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.