



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2024 – 08:48 AM EST

PDB ID : 3HYZ  
Title : Crystal structure of Hsp90 with fragment 42-C03  
Authors : Barker, J.; Mather, O.; Cheng, R.K.Y.; Palan, S.; Felicetti, B.; Whittaker, M.  
Deposited on : 2009-06-23  
Resolution : 2.30 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.36  
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) : 2.36

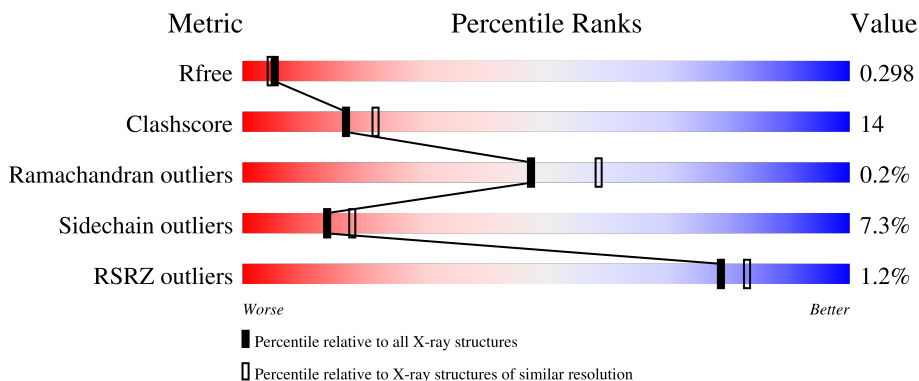
# 1 Overall quality at a glance

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))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	249	
1	B	249	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 3514 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 Heat shock protein HSP 90-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	204	1622	1030	268	319	5	0	2	0
1	B	209	1650	1048	271	326	5	0	1	0

There are 42 discrepancies between the modelled and reference sequences:

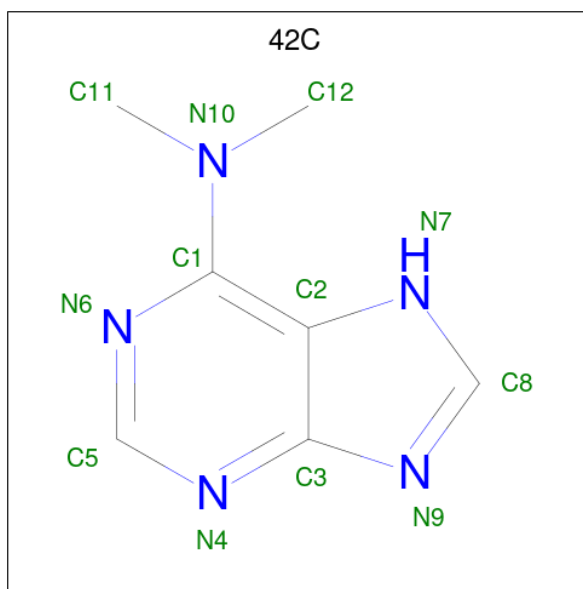
Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	expression tag	UNP P07900
A	-11	GLY	-	expression tag	UNP P07900
A	-10	SER	-	expression tag	UNP P07900
A	-9	SER	-	expression tag	UNP P07900
A	-8	HIS	-	expression tag	UNP P07900
A	-7	HIS	-	expression tag	UNP P07900
A	-6	HIS	-	expression tag	UNP P07900
A	-5	HIS	-	expression tag	UNP P07900
A	-4	HIS	-	expression tag	UNP P07900
A	-3	HIS	-	expression tag	UNP P07900
A	-2	SER	-	expression tag	UNP P07900
A	-1	SER	-	expression tag	UNP P07900
A	0	GLY	-	expression tag	UNP P07900
A	1	LEU	-	expression tag	UNP P07900
A	2	VAL	-	expression tag	UNP P07900
A	3	PRO	-	expression tag	UNP P07900
A	4	ARG	-	expression tag	UNP P07900
A	5	GLY	-	expression tag	UNP P07900
A	6	SER	-	expression tag	UNP P07900
A	7	HIS	-	expression tag	UNP P07900
A	8	MET	-	expression tag	UNP P07900
B	-12	MET	-	expression tag	UNP P07900
B	-11	GLY	-	expression tag	UNP P07900
B	-10	SER	-	expression tag	UNP P07900
B	-9	SER	-	expression tag	UNP P07900

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	HIS	-	expression tag	UNP P07900
B	-7	HIS	-	expression tag	UNP P07900
B	-6	HIS	-	expression tag	UNP P07900
B	-5	HIS	-	expression tag	UNP P07900
B	-4	HIS	-	expression tag	UNP P07900
B	-3	HIS	-	expression tag	UNP P07900
B	-2	SER	-	expression tag	UNP P07900
B	-1	SER	-	expression tag	UNP P07900
B	0	GLY	-	expression tag	UNP P07900
B	1	LEU	-	expression tag	UNP P07900
B	2	VAL	-	expression tag	UNP P07900
B	3	PRO	-	expression tag	UNP P07900
B	4	ARG	-	expression tag	UNP P07900
B	5	GLY	-	expression tag	UNP P07900
B	6	SER	-	expression tag	UNP P07900
B	7	HIS	-	expression tag	UNP P07900
B	8	MET	-	expression tag	UNP P07900

- Molecule 2 is N,N-dimethyl-7H-purin-6-amine (three-letter code: 42C) (formula: C<sub>7</sub>H<sub>9</sub>N<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			12	7	5		
2	B	1	Total	C	N	0	0
			12	7	5		

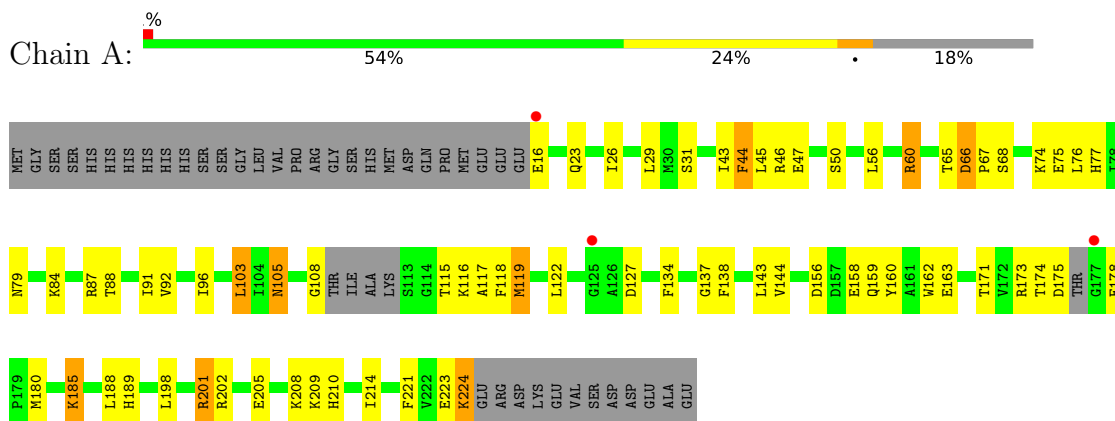
- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	A	91	Total 91	O 91	0	0
3	B	127	Total 127	O 127	0	0

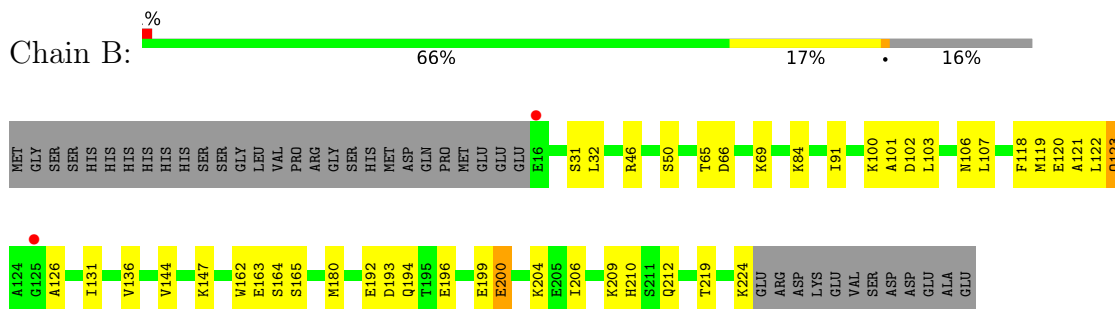
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Heat shock protein HSP 90-alpha



- Molecule 1: Heat shock protein HSP 90-alpha



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.49Å 89.25Å 98.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.10 – 2.30 23.10 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (23.10-2.30) 99.5 (23.10-2.30)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.5.0066	Depositor
R, $R_{free}$	0.236 , 0.305 0.234 , 0.298	Depositor DCC
$R_{free}$ test set	1322 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.9	Xtrriage
Anisotropy	0.134	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3514	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.01 % 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 2.9139e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 42C

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	0.73	0/1652	0.78	1/2222 (0.0%)
1	B	0.77	0/1679	0.80	0/2263
All	All	0.75	0/3331	0.79	1/4485 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	LEU	CA-CB-CG	-5.08	103.62	115.30

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	1622	0	1621	60	0
1	B	1650	0	1653	31	0
2	A	12	0	9	1	0
2	B	12	0	9	0	0
3	A	91	0	0	8	0
3	B	127	0	0	11	0
All	All	3514	0	3292	92	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 (92) 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:224:LYS:HA	1:A:224:LYS:HE3	1.42	1.00
1:A:92:VAL:HG22	1:A:185:LYS:HG3	1.49	0.95
1:A:173[A]:ARG:NH1	1:A:175:ASP:HA	1.95	0.80
1:A:223:GLU:HA	1:A:224:LYS:C	2.04	0.78
1:A:201:ARG:HD3	3:A:317:HOH:O	1.84	0.78
1:B:123:GLN:HE21	1:B:123:GLN:HA	1.54	0.73
1:B:196:GLU:O	1:B:199[A]:GLU:HG3	1.88	0.72
1:A:173[A]:ARG:HH12	1:A:175:ASP:HA	1.55	0.71
1:B:131:ILE:HG13	1:B:136:VAL:HG23	1.72	0.71
1:A:137:GLY:HA3	3:A:284:HOH:O	1.94	0.68
1:A:75:GLU:HG2	1:A:77:HIS:CD2	2.29	0.68
1:B:102:ASP:O	1:B:106:ASN:HB2	1.95	0.67
1:A:224:LYS:HE3	1:A:224:LYS:CA	2.23	0.67
1:A:65:THR:O	1:A:66:ASP:CB	2.44	0.66
1:A:103:LEU:HD13	1:A:162:TRP:HB2	1.79	0.64
1:B:65:THR:HG23	3:B:270:HOH:O	1.97	0.63
1:A:88:THR:HA	1:A:188:LEU:O	1.99	0.62
1:A:60:ARG:HG2	1:A:76:LEU:HD11	1.82	0.61
1:A:44:PHE:C	1:A:44:PHE:CD1	2.74	0.61
1:A:127:ASP:HB2	3:A:325:HOH:O	2.01	0.60
1:A:66:ASP:OD1	1:A:68:SER:OG	2.19	0.59
1:A:209:LYS:HE2	1:A:210:HIS:NE2	2.16	0.59
1:B:84:LYS:HE2	1:B:199[B]:GLU:OE2	2.02	0.59
1:B:200:GLU:HG2	1:B:204:LYS:HE2	1.84	0.57
1:A:105:ASN:HD22	1:A:105:ASN:N	2.02	0.56
1:A:65:THR:O	1:A:66:ASP:HB2	2.05	0.56
1:A:75:GLU:HG3	3:A:242:HOH:O	2.05	0.55
1:A:44:PHE:CD1	1:A:45:LEU:N	2.75	0.55
1:A:91:ILE:N	1:A:91:ILE:HD12	2.23	0.54
1:B:209:LYS:HE2	1:B:210:HIS:NE2	2.24	0.53
1:B:212:GLN:HG2	3:B:330:HOH:O	2.08	0.52
1:A:224:LYS:HD2	1:A:224:LYS:H	1.75	0.52
1:B:101:ALA:N	3:B:287:HOH:O	2.30	0.51
1:B:32:LEU:HD21	1:B:122:LEU:HD13	1.92	0.51
1:A:115:THR:O	1:A:119:MET:HG2	2.11	0.51
1:A:60:ARG:HG2	1:A:76:LEU:CD1	2.41	0.51
1:B:120:GLU:O	1:B:123:GLN:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:GLU:HB3	3:B:316:HOH:O	2.10	0.51
1:B:206:ILE:HG22	3:B:290:HOH:O	2.11	0.51
1:A:23:GLN:HB3	1:A:26:ILE:HD13	1.92	0.50
1:B:46:ARG:HD3	1:B:210:HIS:HB3	1.94	0.50
1:A:118:PHE:HD1	1:A:134:PHE:CD1	2.30	0.49
1:A:46:ARG:O	1:A:50:SER:HB2	2.12	0.49
1:B:219:THR:HA	3:B:282:HOH:O	2.11	0.49
1:B:118:PHE:CZ	1:B:122:LEU:HD11	2.47	0.49
1:A:160:TYR:CE2	1:A:174:THR:HG22	2.48	0.49
1:B:200:GLU:O	1:B:204:LYS:HG3	2.12	0.48
1:A:118:PHE:CD1	1:A:134:PHE:CD1	3.02	0.48
1:A:16:GLU:HB3	3:A:312:HOH:O	2.14	0.48
1:A:223:GLU:CA	1:A:224:LYS:C	2.78	0.47
1:B:103:LEU:HD22	1:B:162:TRP:HB2	1.96	0.47
1:A:159:GLN:HG2	1:A:175:ASP:CB	2.44	0.47
1:B:165:SER:N	3:B:313:HOH:O	2.46	0.47
1:A:84:LYS:HA	1:A:198:LEU:HD13	1.96	0.46
1:A:56:LEU:O	1:A:60:ARG:HB2	2.15	0.46
1:A:221:PHE:HD1	1:A:221:PHE:N	2.14	0.46
1:B:103:LEU:HD23	1:B:107:LEU:HD12	1.98	0.46
1:A:202:ARG:NH1	1:A:205:GLU:OE1	2.49	0.46
1:A:116:LYS:O	1:A:117:ALA:C	2.55	0.45
1:B:131:ILE:CG1	1:B:136:VAL:HG23	2.45	0.45
1:A:105:ASN:O	1:A:108:GLY:N	2.38	0.45
1:B:200:GLU:CG	1:B:204:LYS:HE2	2.47	0.45
1:A:43:ILE:O	1:A:47:GLU:HG2	2.17	0.44
1:A:137:GLY:O	1:A:138:PHE:C	2.56	0.44
1:B:100:LYS:HB3	3:B:287:HOH:O	2.18	0.44
1:A:221:PHE:N	1:A:221:PHE:CD1	2.86	0.44
1:A:159:GLN:HG2	1:A:175:ASP:HB3	2.00	0.43
1:A:87:ARG:HA	1:A:198:LEU:HD11	2.00	0.43
1:B:164:SER:HA	3:B:238:HOH:O	2.18	0.43
1:B:147:LYS:CE	3:B:337:HOH:O	2.66	0.43
1:A:29:LEU:HB2	1:A:115:THR:HG23	2.00	0.43
1:A:44:PHE:CE2	1:A:144:VAL:HG21	2.54	0.43
1:A:224:LYS:HD2	1:A:224:LYS:N	2.34	0.43
1:A:122:LEU:HD23	1:A:122:LEU:HA	1.84	0.42
1:A:224:LYS:CA	1:A:224:LYS:CE	2.93	0.42
1:B:144:VAL:HA	1:B:194:GLN:HG3	2.01	0.42
1:B:193:ASP:HA	3:B:297:HOH:O	2.20	0.42
1:A:44:PHE:CG	1:A:45:LEU:N	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:TRP:HA	1:A:171:THR:O	2.18	0.41
1:A:77:HIS:HE1	1:A:79:ASN:HD21	1.66	0.41
1:A:75:GLU:HG2	1:A:77:HIS:HD2	1.79	0.41
1:B:66:ASP:OD1	1:B:66:ASP:C	2.59	0.41
1:B:91:ILE:HD12	1:B:91:ILE:N	2.36	0.41
1:A:26:ILE:HD12	1:A:26:ILE:N	2.35	0.41
1:A:163:GLU:HB3	3:A:286:HOH:O	2.20	0.41
1:A:189:HIS:HB3	3:A:265:HOH:O	2.20	0.41
1:A:66:ASP:HA	1:A:67:PRO:HD2	1.93	0.41
1:A:103:LEU:HD23	1:A:103:LEU:HA	1.64	0.41
2:A:237:42C:H8	3:A:300:HOH:O	2.21	0.41
1:B:121:ALA:HB1	1:B:126:ALA:HB2	2.02	0.41
1:A:224:LYS:HA	1:A:224:LYS:CE	2.29	0.40
1:A:56:LEU:HD22	1:A:76:LEU:HB3	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	200/249 (80%)	180 (90%)	19 (10%)	1 (0%)	29	35
1	B	208/249 (84%)	199 (96%)	9 (4%)	0	100	100
All	All	408/498 (82%)	379 (93%)	28 (7%)	1 (0%)	47	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	ASP

### 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	178/216 (82%)	161 (90%)	17 (10%)	8	10
1	B	181/216 (84%)	172 (95%)	9 (5%)	24	34
All	All	359/432 (83%)	333 (93%)	26 (7%)	14	18

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	SER
1	A	44	PHE
1	A	60	ARG
1	A	74	LYS
1	A	96	ILE
1	A	103	LEU
1	A	105	ASN
1	A	119	MET
1	A	156	ASP
1	A	158	GLU
1	A	178	GLU
1	A	180	MET
1	A	185	LYS
1	A	201	ARG
1	A	208	LYS
1	A	214	ILE
1	A	224	LYS
1	B	31	SER
1	B	50	SER
1	B	69	LYS
1	B	119	MET
1	B	123	GLN
1	B	180	MET
1	B	192	GLU
1	B	200	GLU
1	B	224	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	77	HIS
1	A	105	ASN
1	A	189	HIS
1	B	106	ASN
1	B	123	GLN
1	B	133	GLN
1	B	189	HIS

### 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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

2 ligands 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	42C	B	237	-	9,13,13	1.20	1 (11%)	8,18,18	2.14	3 (37%)
2	42C	A	237	-	9,13,13	1.50	3 (33%)	8,18,18	2.41	3 (37%)

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	42C	B	237	-	-	0/4/4/4	0/2/2/2
2	42C	A	237	-	-	0/4/4/4	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	237	42C	C5-N4	2.43	1.36	1.32
2	A	237	42C	C2-C3	2.21	1.46	1.40
2	B	237	42C	C3-N4	-2.12	1.34	1.37
2	A	237	42C	C1-N6	2.03	1.36	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	237	42C	N6-C1-N10	4.56	121.85	117.06
2	B	237	42C	C3-C2-N7	-3.52	105.73	109.40
2	A	237	42C	C3-C2-N7	-3.41	105.84	109.40
2	B	237	42C	N4-C5-N6	-3.34	123.46	128.68
2	A	237	42C	N4-C5-N6	-2.65	124.54	128.68
2	B	237	42C	C5-N4-C3	2.34	118.94	113.45

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	237	42C	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	204/249 (81%)	-0.17	3 (1%) 73 79	20, 31, 54, 62	1 (0%)
1	B	209/249 (83%)	-0.42	2 (0%) 82 86	15, 25, 39, 46	1 (0%)
All	All	413/498 (82%)	-0.29	5 (1%) 79 83	15, 29, 49, 62	2 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	16	GLU	2.7
1	A	16	GLU	2.7
1	A	177	GLY	2.7
1	A	125	GLY	2.1
1	B	125	GLY	2.1

### 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 monosaccharides 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	42C	A	237	12/12	0.94	0.11	33,34,35,35	0
2	42C	B	237	12/12	0.98	0.08	10,15,18,20	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.