



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 23, 2021 – 05:18 PM EST

PDB ID : 2IJR  
Title : Crystal structure of a protein api92 from Yersinia pseudotuberculosis, Pfam DUF1281  
Authors : Jin, X.; Min, T.; Bonanno, J.B.; Sauder, J.M.; Wasserman, S.; Smith, D.; Bursley, S.K.; Shapiro, L.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2006-09-30  
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](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.

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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 : 2.16  
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) : 2.16

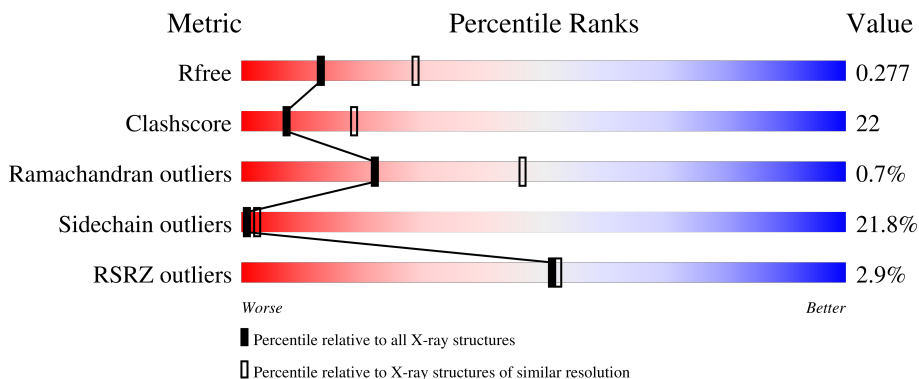
# 1 Overall quality at a glance

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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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 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	300	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2285 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 Hypothetical protein api92.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	282	2241	1425	388	411	9	8	0	2	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	cloning artifact	UNP Q6EVP2
A	2	LEU	-	cloning artifact	UNP Q6EVP2
A	21	MSE	MET	modified residue	UNP Q6EVP2
A	58	MSE	MET	modified residue	UNP Q6EVP2
A	131	MSE	MET	modified residue	UNP Q6EVP2
A	160	MSE	MET	modified residue	UNP Q6EVP2
A	169	MSE	MET	modified residue	UNP Q6EVP2
A	171	MSE	MET	modified residue	UNP Q6EVP2
A	204	MSE	MET	modified residue	UNP Q6EVP2
A	238	MSE	MET	modified residue	UNP Q6EVP2

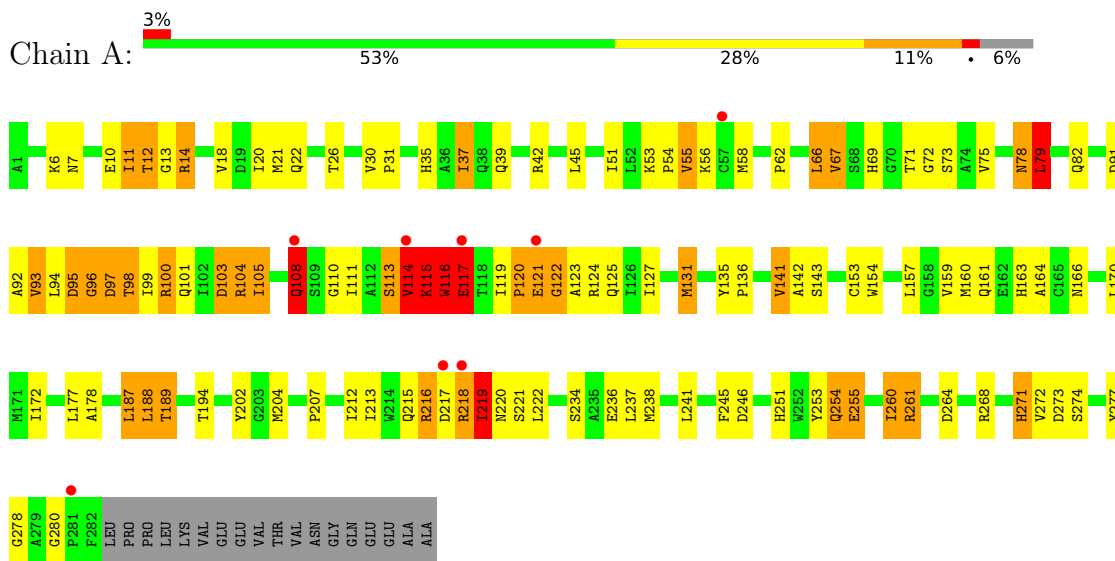
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total	O	0	0
			44	44		

### 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: Hypothetical protein api92



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.66Å 88.66Å 218.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 41.15 – 2.69	Depositor EDS
% Data completeness (in resolution range)	93.3 (20.00-2.70) 93.1 (41.15-2.69)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.90 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.225 , 0.279 0.220 , 0.277	Depositor DCC
$R_{free}$ test set	584 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.2	Xtrriage
Anisotropy	0.328	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 28.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	2285	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

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	0.83	0/2299	1.34	23/3115 (0.7%)

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
1	A	2	10

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	VAL	CB-CA-C	21.62	152.49	111.40
1	A	115	LYS	N-CA-C	17.99	159.58	111.00
1	A	115	LYS	N-CA-CB	-17.60	78.92	110.60
1	A	218	ARG	CB-CA-C	13.39	137.17	110.40
1	A	219	ILE	N-CA-CB	-12.20	82.74	110.80
1	A	116	TRP	N-CA-C	11.81	142.90	111.00
1	A	277	TYR	CB-CA-C	-11.75	86.91	110.40
1	A	218	ARG	N-CA-C	-11.68	79.48	111.00
1	A	278	GLY	N-CA-C	11.45	141.73	113.10
1	A	116	TRP	CB-CA-C	-11.32	87.75	110.40
1	A	14	ARG	N-CA-C	-10.43	82.85	111.00
1	A	114	VAL	N-CA-C	-8.81	87.20	111.00
1	A	73	SER	CB-CA-C	7.91	125.14	110.10
1	A	93	VAL	N-CA-C	-7.71	90.18	111.00
1	A	122	GLY	N-CA-C	-7.39	94.61	113.10
1	A	219	ILE	N-CA-C	7.34	130.81	111.00
1	A	103	ASP	CB-CG-OD2	-7.07	111.94	118.30
1	A	94	LEU	N-CA-C	6.89	129.60	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	VAL	C-N-CA	6.25	137.34	121.70
1	A	79	LEU	CA-CB-CG	6.04	129.19	115.30
1	A	105	ILE	CG1-CB-CG2	-5.67	98.93	111.40
1	A	94	LEU	CB-CA-C	5.46	120.57	110.20
1	A	157	LEU	CA-CB-CG	5.43	127.79	115.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	94	LEU	CA
1	A	115	LYS	CA

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	GLN	Peptide
1	A	113	SER	Peptide
1	A	117	GLU	Peptide
1	A	12	THR	Peptide
1	A	121	GLU	Peptide
1	A	13	GLY	Peptide
1	A	142	ALA	Peptide
1	A	280	GLY	Peptide
1	A	95	ASP	Peptide
1	A	96	GLY	Peptide

## 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	2241	0	2175	98	0
2	A	44	0	0	5	0
All	All	2285	0	2175	98	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 22.

All (98) 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:LYS:N	1:A:115:LYS:CD	2.21	0.93
1:A:115:LYS:N	1:A:115:LYS:HD3	1.85	0.89
1:A:96:GLY:HA2	1:A:97:ASP:OD2	1.73	0.87
1:A:115:LYS:H	1:A:115:LYS:CD	1.48	0.86
1:A:172:ILE:HD13	1:A:241:LEU:HD23	1.62	0.81
1:A:100:ARG:NH1	1:A:104:ARG:HD3	1.98	0.79
1:A:119:ILE:O	1:A:120:PRO:O	2.03	0.77
1:A:95:ASP:O	1:A:99:ILE:HG12	1.85	0.76
1:A:264:ASP:OD2	1:A:274:SER:HB3	1.86	0.76
1:A:261:ARG:HD2	2:A:314:HOH:O	1.90	0.72
1:A:114:VAL:HG12	1:A:115:LYS:O	1.91	0.71
1:A:119:ILE:O	1:A:124:ARG:NH1	2.24	0.71
1:A:11:ILE:HD13	1:A:21:MSE:SE	2.42	0.70
1:A:114:VAL:HG12	1:A:115:LYS:HA	1.75	0.68
1:A:117:GLU:CD	1:A:117:GLU:H	1.98	0.67
1:A:95:ASP:OD1	1:A:98:THR:HG23	1.95	0.67
1:A:116:TRP:O	1:A:116:TRP:CG	2.45	0.65
1:A:119:ILE:CG2	1:A:123:ALA:HB3	2.28	0.64
1:A:100:ARG:NH1	1:A:104:ARG:CD	2.61	0.63
1:A:37[A]:ILE:HD11	2:A:335:HOH:O	1.97	0.63
1:A:67:VAL:CG1	1:A:67:VAL:O	2.47	0.63
1:A:53:LYS:O	1:A:78:ASN:HB2	1.97	0.62
1:A:100:ARG:HH12	1:A:104:ARG:HE	1.47	0.62
1:A:96:GLY:CA	1:A:97:ASP:OD2	2.48	0.62
1:A:217:ASP:HB3	1:A:221:SER:HB3	1.82	0.61
1:A:108:GLN:HA	1:A:110:GLY:N	2.15	0.61
1:A:131:MSE:HE3	1:A:153:CYS:HB2	1.83	0.60
1:A:136:PRO:HA	1:A:141:VAL:HG12	1.82	0.60
1:A:54:PRO:O	1:A:72:GLY:HA3	2.04	0.58
1:A:100:ARG:HH12	1:A:104:ARG:NE	2.02	0.58
1:A:202:TYR:HD2	1:A:237:LEU:HD13	1.68	0.58
1:A:100:ARG:CZ	1:A:104:ARG:HD3	2.34	0.58
1:A:35:HIS:NE2	1:A:160:MSE:HB3	2.18	0.57
1:A:117:GLU:N	1:A:117:GLU:OE2	2.35	0.56
1:A:95:ASP:OD1	1:A:96:GLY:HA3	2.06	0.55
1:A:216:ARG:HH11	1:A:216:ARG:CG	2.19	0.55
1:A:117:GLU:CD	1:A:117:GLU:N	2.59	0.54
1:A:58:MSE:SE	1:A:82:GLN:OE1	2.77	0.53
1:A:100:ARG:HH12	1:A:104:ARG:CD	2.22	0.52
1:A:114:VAL:HG12	1:A:115:LYS:C	2.29	0.52
1:A:21:MSE:HE3	1:A:241:LEU:HD22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:GLU:H	1:A:122:GLY:HA3	1.74	0.51
1:A:55:VAL:HG11	1:A:79:LEU:HD13	1.93	0.51
1:A:7:ASN:OD1	1:A:251:HIS:HE1	1.93	0.50
1:A:100:ARG:O	1:A:100:ARG:HG3	2.10	0.49
1:A:114:VAL:CG1	1:A:115:LYS:HA	2.40	0.49
1:A:166:ASN:CB	1:A:212:ILE:HD13	2.44	0.48
1:A:66:LEU:O	1:A:66:LEU:HD22	2.14	0.48
1:A:272:VAL:O	1:A:273:ASP:HB3	2.14	0.47
1:A:67:VAL:HG12	1:A:67:VAL:O	2.13	0.47
1:A:75:VAL:N	1:A:78:ASN:HD21	2.13	0.47
1:A:114:VAL:HA	1:A:115:LYS:HA	1.36	0.47
1:A:26:THR:HG22	1:A:26:THR:O	2.13	0.47
1:A:187:LEU:HD13	1:A:188:LEU:HD13	1.97	0.47
1:A:42:ARG:NH1	1:A:154:TRP:O	2.48	0.47
1:A:12:THR:HA	1:A:220:ASN:O	2.15	0.47
1:A:21:MSE:HG3	1:A:245:PHE:CD1	2.50	0.47
1:A:22:GLN:OE1	1:A:216:ARG:HG2	2.15	0.46
1:A:39:GLN:HE22	1:A:103:ASP:HB3	1.80	0.46
1:A:62:PRO:O	1:A:189:THR:HG23	2.15	0.46
1:A:35:HIS:CE1	1:A:160:MSE:HB3	2.51	0.45
1:A:170:LEU:CD1	1:A:207:PRO:HG2	2.46	0.45
1:A:14:ARG:NH1	2:A:304:HOH:O	2.48	0.45
1:A:35:HIS:CD2	1:A:160:MSE:HB3	2.51	0.45
1:A:101:GLN:O	1:A:101:GLN:HG2	2.16	0.45
1:A:11:ILE:HG13	1:A:12:THR:N	2.32	0.45
1:A:172:ILE:CD1	1:A:241:LEU:HD23	2.42	0.45
1:A:42:ARG:HB3	1:A:111:ILE:CD1	2.46	0.45
1:A:121:GLU:N	1:A:122:GLY:HA3	2.30	0.45
1:A:255:GLU:HB3	1:A:260:ILE:HG12	1.99	0.45
1:A:92:ALA:C	1:A:93:VAL:O	2.42	0.45
1:A:131:MSE:HE3	1:A:153:CYS:CB	2.46	0.44
1:A:114:VAL:C	1:A:115:LYS:HD3	2.34	0.44
1:A:216:ARG:NH1	1:A:216:ARG:CG	2.82	0.43
1:A:69:HIS:HD2	2:A:321:HOH:O	2.00	0.43
1:A:104:ARG:HD2	1:A:104:ARG:HA	1.42	0.43
1:A:170:LEU:HD11	1:A:207:PRO:HG2	2.00	0.43
1:A:92:ALA:HB1	1:A:93:VAL:O	2.20	0.42
1:A:131:MSE:O	1:A:135:TYR:HB2	2.19	0.42
1:A:56:LYS:H	1:A:82:GLN:NE2	2.18	0.42
1:A:216:ARG:HH11	1:A:216:ARG:HG3	1.84	0.42
1:A:39:GLN:NE2	1:A:103:ASP:HB3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:THR:HG23	1:A:72:GLY:HA3	2.02	0.41
1:A:21:MSE:HG3	1:A:245:PHE:CE1	2.55	0.41
1:A:42:ARG:HB3	1:A:111:ILE:HD11	2.03	0.41
1:A:264:ASP:OD2	1:A:271:HIS:HE1	2.03	0.41
1:A:216:ARG:NH1	1:A:216:ARG:HG3	2.35	0.41
1:A:219:ILE:HG22	1:A:219:ILE:H	1.29	0.41
1:A:31:PRO:HG3	1:A:164:ALA:HB2	2.03	0.41
1:A:69:HIS:CD2	2:A:321:HOH:O	2.74	0.41
1:A:172:ILE:HD13	1:A:241:LEU:CD2	2.40	0.40
1:A:253:TYR:O	1:A:261:ARG:HA	2.22	0.40
1:A:264:ASP:OD2	1:A:271:HIS:CE1	2.73	0.40
1:A:216:ARG:HE	1:A:219:ILE:HA	1.87	0.40
1:A:254:GLN:NE2	1:A:261:ARG:HH21	2.19	0.40
1:A:91:ASP:OD1	1:A:178:ALA:HB3	2.22	0.40
1:A:166:ASN:HB3	1:A:212:ILE:HD13	2.03	0.40
1:A:45:LEU:HB3	1:A:127:ILE:HG12	2.04	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	282/300 (94%)	253 (90%)	27 (10%)	2 (1%)	22   46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	PRO
1	A	116	TRP

### 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	241/247 (98%)	188 (78%)	53 (22%)	<b>1</b> <b>2</b>

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	10	GLU
1	A	11	ILE
1	A	18	VAL
1	A	20	ILE
1	A	30	VAL
1	A	37[A]	ILE
1	A	37[B]	ILE
1	A	51	ILE
1	A	55	VAL
1	A	66	LEU
1	A	67	VAL
1	A	78	ASN
1	A	79	LEU
1	A	97	ASP
1	A	98	THR
1	A	100	ARG
1	A	104	ARG
1	A	105	ILE
1	A	108	GLN
1	A	113	SER
1	A	114	VAL
1	A	115	LYS
1	A	117	GLU
1	A	125	GLN
1	A	131	MSE
1	A	141	VAL
1	A	143	SER
1	A	159	VAL
1	A	161	GLN

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Mol	Chain	Res	Type
1	A	163	HIS
1	A	177	LEU
1	A	187	LEU
1	A	188	LEU
1	A	189	THR
1	A	194	THR
1	A	204	MSE
1	A	213	ILE
1	A	215	GLN
1	A	216	ARG
1	A	218	ARG
1	A	219	ILE
1	A	222	LEU
1	A	234	SER
1	A	236	GLU
1	A	238	MSE
1	A	246	ASP
1	A	254	GLN
1	A	255	GLU
1	A	260	ILE
1	A	261	ARG
1	A	268	ARG
1	A	271	HIS

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	7	ASN
1	A	69	HIS
1	A	78	ASN
1	A	82	GLN
1	A	101	GLN
1	A	186	GLN
1	A	251	HIS
1	A	271	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](#)

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 [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	274/300 (91%)	-0.18	8 (2%) 51 52	3, 13, 34, 53	1 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	114	VAL	4.3
1	A	108	GLN	3.5
1	A	218	ARG	3.4
1	A	57	CYS	3.2
1	A	121	GLU	2.8
1	A	117	GLU	2.6
1	A	281	PRO	2.5
1	A	217	ASP	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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.