



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:03 AM UTC

PDB ID : 2IT2 / pdb\_00002it2  
Title : Structure of PH1069 protein from *Pyrococcus horikoshii*  
Authors : Lokanath, N.K.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2006-10-18  
Resolution : 1.50 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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

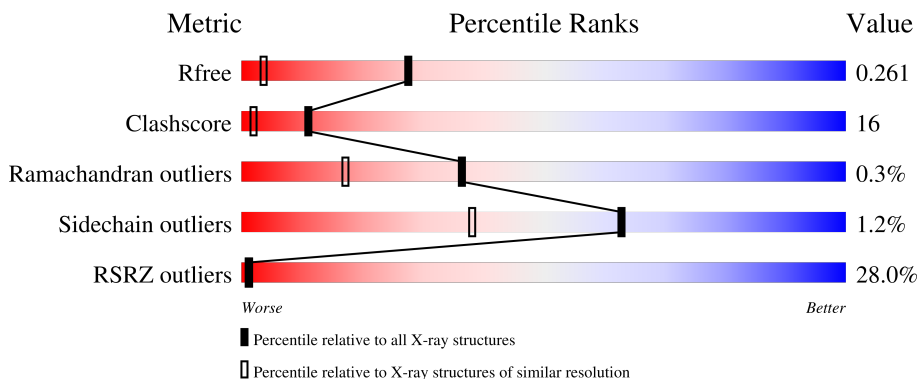
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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))
$R_{free}$	180053	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	200	
1	B	200	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3446 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 UPF0130 protein PH1069.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	189	1539	985	267	278	2	7	0	0	0
1	B	196	1593	1020	277	288	2	6	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP O58796
A	2	LEU	-	expression tag	UNP O58796
A	3	LEU	-	expression tag	UNP O58796
A	4	TYR	-	expression tag	UNP O58796
B	1	MSE	-	expression tag	UNP O58796
B	2	LEU	-	expression tag	UNP O58796
B	3	LEU	-	expression tag	UNP O58796
B	4	TYR	-	expression tag	UNP O58796

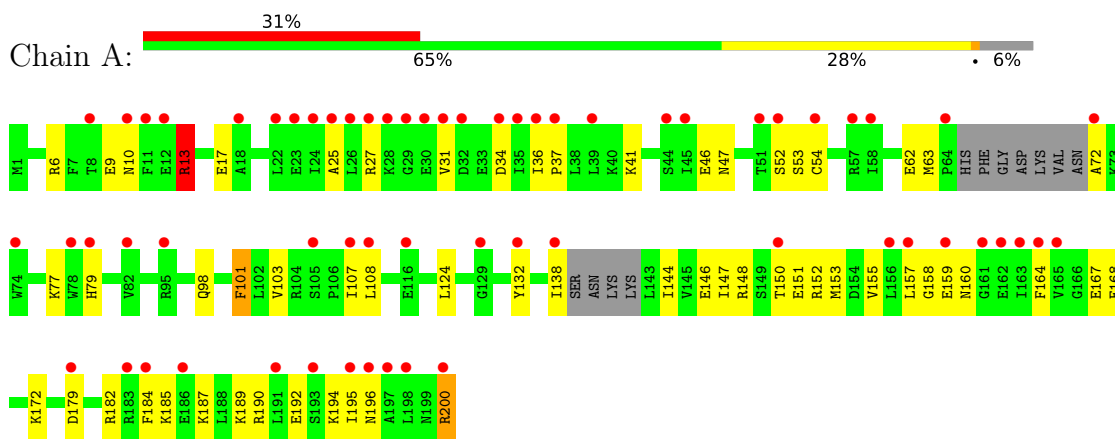
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	151	Total	O	0	0
			151	151		
2	B	163	Total	O	0	0
			163	163		

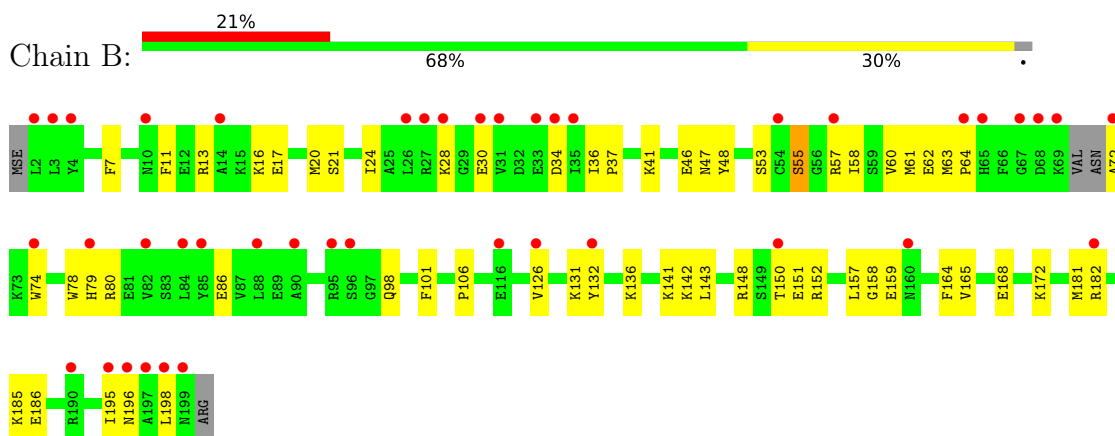
### 3 Residue-property plots [i](#)

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: UPF0130 protein PH1069



- Molecule 1: UPF0130 protein PH1069



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	37.43Å 53.90Å 53.21Å 104.60° 102.90° 109.30°	Depositor
Resolution (Å)	17.55 – 1.50 17.55 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (17.55-1.50) 93.2 (17.55-1.50)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	10.58 (at 1.50Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.250 , 0.265 0.249 , 0.261	Depositor DCC
$R_{free}$ test set	2703 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.0	Xtrriage
Anisotropy	0.314	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.46 , 69.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3446	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.09% 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	0.53	0/1554	0.96	5/2068 (0.2%)
1	B	0.61	2/1611 (0.1%)	0.95	7/2146 (0.3%)
All	All	0.57	2/3165 (0.1%)	0.95	12/4214 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	78	TRP	NE1-CE2	10.37	1.48	1.37
1	B	74	TRP	NE1-CE2	10.35	1.48	1.37

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	55	SER	N-CA-C	6.30	119.90	112.72
1	B	47	ASN	N-CA-C	6.09	119.75	112.93
1	B	46	GLU	N-CA-C	6.00	118.31	111.11
1	B	165	VAL	N-CA-C	5.87	118.30	109.20
1	A	46	GLU	N-CA-C	5.53	118.02	111.33
1	B	11	PHE	N-CA-C	5.46	117.66	111.11
1	A	155	VAL	N-CA-C	5.38	115.85	107.99
1	B	60	VAL	N-CA-C	-5.18	99.05	107.28
1	A	101	PHE	N-CA-C	-5.15	100.12	108.52
1	A	13	ARG	CD-NE-CZ	-5.10	117.26	124.40
1	A	200	ARG	CD-NE-CZ	-5.07	117.30	124.40
1	B	80	ARG	CD-NE-CZ	-5.03	117.36	124.40

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	1539	0	1606	61	0
1	B	1593	0	1655	45	0
2	A	151	0	0	11	0
2	B	163	0	0	12	0
All	All	3446	0	3261	105	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 16.

All (105) 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:54:CYS:SG	1:A:107:ILE:HG22	1.93	1.08
1:A:9:GLU:HG2	1:A:10:ASN:HD22	1.36	0.91
1:B:13:ARG:HG2	2:B:307:HOH:O	1.81	0.81
1:A:107:ILE:HD11	1:A:146:GLU:CG	2.11	0.80
1:B:195:ILE:HD12	1:B:196:ASN:N	1.97	0.80
1:A:54:CYS:SG	1:A:107:ILE:CG2	2.72	0.76
1:A:54:CYS:HG	1:A:107:ILE:HG22	1.47	0.75
1:A:9:GLU:HG2	1:A:10:ASN:ND2	2.02	0.75
1:A:41:LYS:HG3	1:A:195:ILE:HG21	1.72	0.72
1:A:196:ASN:ND2	2:A:332:HOH:O	2.24	0.71
1:B:63:MSE:HA	2:B:252:HOH:O	1.92	0.69
1:A:41:LYS:HG3	1:A:195:ILE:CG2	2.23	0.68
1:B:136:LYS:NZ	2:B:321:HOH:O	2.25	0.68
1:B:126:VAL:HG13	1:B:131:LYS:HD3	1.75	0.67
1:A:107:ILE:HD13	1:A:148:ARG:HB2	1.77	0.67
1:A:41:LYS:CG	1:A:195:ILE:HG21	2.25	0.67
1:A:107:ILE:HD12	1:A:147:ILE:O	1.95	0.67
1:A:13:ARG:NH1	2:A:335:HOH:O	2.28	0.66
1:A:167:GLU:N	2:A:339:HOH:O	2.27	0.66
1:A:41:LYS:HZ1	1:A:196:ASN:HB2	1.60	0.66
1:A:41:LYS:CG	1:A:195:ILE:CG2	2.75	0.64
1:A:101:PHE:HB2	1:A:157:LEU:HD11	1.81	0.63
1:A:77:LYS:NZ	2:A:268:HOH:O	2.31	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:SER:HB3	1:A:108:LEU:HD23	1.83	0.61
1:A:107:ILE:HD11	1:A:146:GLU:HG2	1.82	0.61
1:B:41:LYS:HG2	1:B:195:ILE:HD11	1.82	0.61
1:A:107:ILE:HD11	1:A:146:GLU:HG3	1.81	0.60
1:B:61:MSE:HE2	1:B:72:ALA:HB1	1.83	0.60
1:B:148:ARG:NH1	2:B:359:HOH:O	2.26	0.60
1:B:17:GLU:HA	1:B:20:MSE:HE2	1.82	0.60
1:B:181:MSE:SE	1:B:185:LYS:HE2	2.53	0.59
1:B:16:LYS:O	1:B:20:MSE:HG3	2.03	0.58
1:A:124:LEU:C	1:A:124:LEU:HD23	2.29	0.58
1:A:36:ILE:HB	1:A:37:PRO:HD3	1.86	0.57
1:A:185:LYS:O	1:A:189:LYS:HG3	2.04	0.57
1:B:159:GLU:HG3	1:B:164:PHE:CE2	2.40	0.57
1:B:61:MSE:SE	1:B:63:MSE:HE2	2.55	0.56
1:B:41:LYS:CG	1:B:195:ILE:HD11	2.35	0.56
1:A:124:LEU:HD23	1:A:124:LEU:O	2.05	0.56
1:A:159:GLU:HG2	1:A:160:ASN:ND2	2.21	0.55
1:A:190:ARG:O	1:A:194:LYS:HG3	2.07	0.55
1:B:24:ILE:HG13	1:B:28:LYS:HE2	1.90	0.54
1:A:132:TYR:CD2	1:A:150:THR:HG22	2.43	0.54
1:A:168:GLU:HG2	1:A:172:LYS:HE3	1.89	0.54
1:B:21:SER:O	1:B:24:ILE:HG22	2.08	0.54
1:A:158:GLY:HA2	1:A:164:PHE:CD2	2.44	0.53
1:B:196:ASN:HD22	1:B:196:ASN:H	1.56	0.53
1:B:86:GLU:HG2	2:B:354:HOH:O	2.08	0.53
1:A:77:LYS:NZ	1:A:77:LYS:HB3	2.24	0.53
1:A:151:GLU:HB2	1:A:184:PHE:CE1	2.44	0.53
1:A:63:MSE:HB3	1:A:72:ALA:HB2	1.91	0.52
1:A:47:ASN:HD21	1:A:200:ARG:CZ	2.21	0.52
1:A:41:LYS:NZ	1:A:196:ASN:HB2	2.23	0.52
1:A:150:THR:HG23	2:A:229:HOH:O	2.11	0.51
1:A:13:ARG:O	1:A:17:GLU:HG3	2.11	0.50
1:B:79:HIS:HD2	2:B:316:HOH:O	1.93	0.50
1:A:41:LYS:HG2	1:A:195:ILE:CG2	2.40	0.50
1:B:34:ASP:OD2	1:B:185:LYS:HD2	2.11	0.50
1:B:57:ARG:HG3	2:B:223:HOH:O	2.11	0.50
1:B:195:ILE:HD12	1:B:195:ILE:C	2.36	0.49
1:A:103:VAL:HG21	1:A:153:MSE:HE3	1.93	0.49
1:A:179:ASP:OD1	1:A:182:ARG:NH2	2.44	0.49
1:B:61:MSE:HE1	1:B:63:MSE:SE	2.62	0.49
1:B:168:GLU:OE2	1:B:172:LYS:HE2	2.13	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:LYS:NZ	2:A:301:HOH:O	2.46	0.48
1:B:131:LYS:HG2	2:B:274:HOH:O	2.13	0.48
1:B:141:LYS:NZ	2:B:288:HOH:O	2.46	0.48
1:A:34:ASP:OD2	1:A:185:LYS:HG3	2.13	0.48
1:B:58:ILE:HG13	1:B:181:MSE:HE3	1.96	0.48
1:B:79:HIS:CD2	2:B:316:HOH:O	2.67	0.47
1:B:143:LEU:C	1:B:143:LEU:HD23	2.40	0.47
1:B:53:SER:HA	2:B:276:HOH:O	2.16	0.46
1:A:47:ASN:HD21	1:A:200:ARG:NH1	2.14	0.46
1:A:41:LYS:NZ	2:A:303:HOH:O	2.49	0.45
1:A:185:LYS:HG2	2:A:300:HOH:O	2.15	0.45
1:B:182:ARG:NH1	2:B:352:HOH:O	2.49	0.45
1:A:25:ALA:HB1	1:A:31:VAL:HG23	1.99	0.45
1:B:132:TYR:CE2	1:B:150:THR:HG22	2.52	0.45
1:A:13:ARG:HA	1:A:13:ARG:HD3	1.74	0.43
1:B:182:ARG:HG2	1:B:186:GLU:OE2	2.18	0.43
1:A:47:ASN:ND2	1:A:200:ARG:CZ	2.82	0.43
1:B:101:PHE:HB2	1:B:157:LEU:HD11	2.00	0.43
1:A:41:LYS:HG2	1:A:195:ILE:HG22	2.00	0.43
1:A:124:LEU:C	1:A:124:LEU:CD2	2.92	0.43
1:B:62:GLU:HA	1:B:98:GLN:O	2.19	0.42
1:B:28:LYS:HE3	1:B:30:GLU:CD	2.44	0.42
1:A:189:LYS:HG3	2:A:300:HOH:O	2.18	0.42
1:B:55:SER:HA	1:B:106:PRO:HB3	2.02	0.42
1:A:79:HIS:CD2	2:A:336:HOH:O	2.73	0.41
1:B:48:TYR:CE2	1:B:198:LEU:HD13	2.55	0.41
1:A:79:HIS:CE1	2:A:337:HOH:O	2.72	0.41
1:B:7:PHE:HB2	1:B:142:LYS:HA	2.02	0.41
1:B:36:ILE:HB	1:B:37:PRO:HD3	2.03	0.41
1:A:132:TYR:HB3	1:A:148:ARG:HE	1.86	0.41
1:A:187:LYS:HG2	1:A:190:ARG:HH22	1.86	0.41
1:A:132:TYR:HB3	1:A:148:ARG:HH21	1.86	0.41
1:A:158:GLY:HA2	1:A:164:PHE:CE2	2.56	0.41
1:B:151:GLU:N	1:B:151:GLU:CD	2.79	0.41
1:B:63:MSE:HB2	1:B:64:PRO:HD2	2.01	0.41
1:A:138:ILE:HD13	1:A:144:ILE:HG23	2.02	0.40
1:B:158:GLY:HA2	1:B:164:PHE:CD2	2.56	0.40
1:A:62:GLU:HA	1:A:98:GLN:O	2.21	0.40
1:A:152:ARG:NE	1:B:152:ARG:HD3	2.35	0.40
1:B:181:MSE:O	1:B:185:LYS:HG2	2.22	0.40
1:A:190:ARG:O	1:A:194:LYS:CG	2.68	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	183/200 (92%)	176 (96%)	6 (3%)	1 (0%)	24	8
1	B	192/200 (96%)	186 (97%)	6 (3%)	0	100	100
All	All	375/400 (94%)	362 (96%)	12 (3%)	1 (0%)	36	17

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	SER

### 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	170/173 (98%)	166 (98%)	4 (2%)	43	15
1	B	176/173 (102%)	176 (100%)	0	100	100
All	All	346/346 (100%)	342 (99%)	4 (1%)	63	38

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

Mol	Chain	Res	Type
1	A	6	ARG
1	A	13	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	27	ARG
1	A	192	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	47	ASN
1	A	134	ASN
1	A	160	ASN
1	B	123	ASN
1	B	196	ASN

### 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 oligosaccharides 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

### 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, 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	182/200 (91%)	1.72	62 (34%) <b>1</b> <b>1</b>	14, 25, 36, 43	0
1	B	190/200 (95%)	1.36	42 (22%) <b>2</b> <b>2</b>	13, 21, 33, 42	0
All	All	372/400 (93%)	1.53	104 (27%) <b>1</b> <b>1</b>	13, 23, 35, 43	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	ILE	5.9
1	B	85	TYR	5.5
1	B	74	TRP	5.3
1	A	29	GLY	5.2
1	A	74	TRP	5.0
1	A	39	LEU	4.9
1	A	35	ILE	4.3
1	B	132	TYR	4.0
1	A	34	ASP	4.0
1	B	2	LEU	4.0
1	B	196	ASN	3.9
1	B	198	LEU	3.9
1	A	200	ARG	3.8
1	A	36	ILE	3.8
1	B	67	GLY	3.7
1	A	163	ILE	3.6
1	A	78	TRP	3.5
1	B	3	LEU	3.5
1	A	132	TYR	3.5
1	A	64	PRO	3.5
1	B	72	ALA	3.4
1	B	150	THR	3.4
1	A	95	ARG	3.4
1	B	195	ILE	3.3

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	52	SER	3.3
1	B	27	ARG	3.2
1	B	34	ASP	3.1
1	A	27	ARG	3.1
1	B	79	HIS	3.1
1	B	68	ASP	3.1
1	A	197	ALA	3.0
1	A	107	ILE	3.0
1	A	162	GLU	3.0
1	A	79	HIS	3.0
1	A	164	PHE	3.0
1	B	57	ARG	2.9
1	B	64	PRO	2.9
1	B	28	LYS	2.9
1	A	12	GLU	2.9
1	A	24	ILE	2.8
1	A	196	ASN	2.8
1	A	186	GLU	2.8
1	B	126	VAL	2.8
1	A	28	LYS	2.8
1	A	183	ARG	2.8
1	A	72	ALA	2.7
1	B	65	HIS	2.8
1	B	160	ASN	2.7
1	B	199	ASN	2.7
1	B	82	VAL	2.7
1	B	95	ARG	2.7
1	B	54	CYS	2.7
1	A	26	LEU	2.6
1	A	31	VAL	2.6
1	A	45	ILE	2.6
1	A	18	ALA	2.5
1	B	33	GLU	2.5
1	B	84	LEU	2.5
1	A	54	CYS	2.5
1	A	184	PHE	2.5
1	B	116	GLU	2.4
1	A	193	SER	2.4
1	A	108	LEU	2.4
1	A	32	ASP	2.4
1	A	159	GLU	2.4
1	A	30	GLU	2.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	82	VAL	2.3
1	A	161	GLY	2.3
1	A	179	ASP	2.3
1	B	90	ALA	2.3
1	B	31	VAL	2.3
1	B	30	GLU	2.3
1	B	88	LEU	2.3
1	A	165	VAL	2.3
1	A	150	THR	2.3
1	A	57	ARG	2.3
1	B	69	LYS	2.3
1	A	195	ILE	2.3
1	B	35	ILE	2.3
1	A	105	SER	2.3
1	B	4	TYR	2.3
1	A	11	PHE	2.2
1	B	26	LEU	2.2
1	B	14	ALA	2.2
1	A	23	GLU	2.2
1	B	197	ALA	2.2
1	A	8	THR	2.2
1	A	44	SER	2.2
1	B	10	ASN	2.2
1	A	116	GLU	2.2
1	A	156	LEU	2.1
1	A	22	LEU	2.1
1	A	25	ALA	2.1
1	A	157	LEU	2.1
1	A	198	LEU	2.1
1	A	10	ASN	2.1
1	B	190	ARG	2.1
1	B	96	SER	2.1
1	A	37	PRO	2.1
1	A	51	THR	2.1
1	A	58	ILE	2.1
1	A	129	GLY	2.1
1	B	182	ARG	2.0
1	A	191	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.