



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:16 PM UTC

PDB ID : 1PV9 / pdb_00001pv9
Title : Prolidase from *Pyrococcus furiosus*
Authors : Maher, M.J.; Ghosh, M.; Grunden, A.M.; Menon, A.L.; Adams, M.W.; Freeman, H.C.; Guss, J.M.
Deposited on : 2003-06-27
Resolution : 2.00 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 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
Xtriage (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

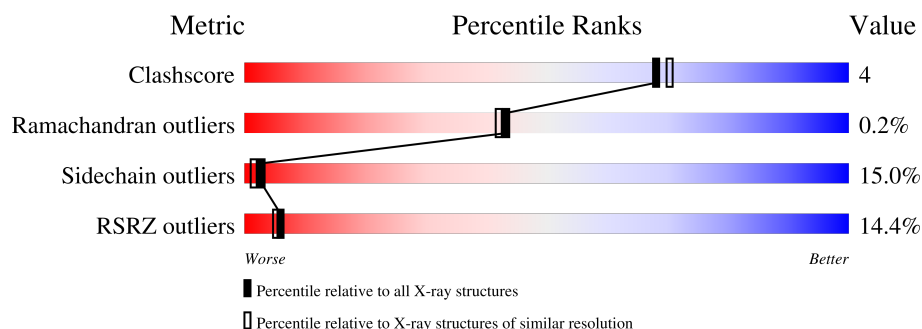
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 ≥ 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	348	
1	B	348	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5376 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 Xaa-Pro dipeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	337	Total	C	N	O	S	0	0	0
			2673	1706	439	519	9			
1	B	318	Total	C	N	O	S	0	0	0
			2523	1610	417	487	9			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

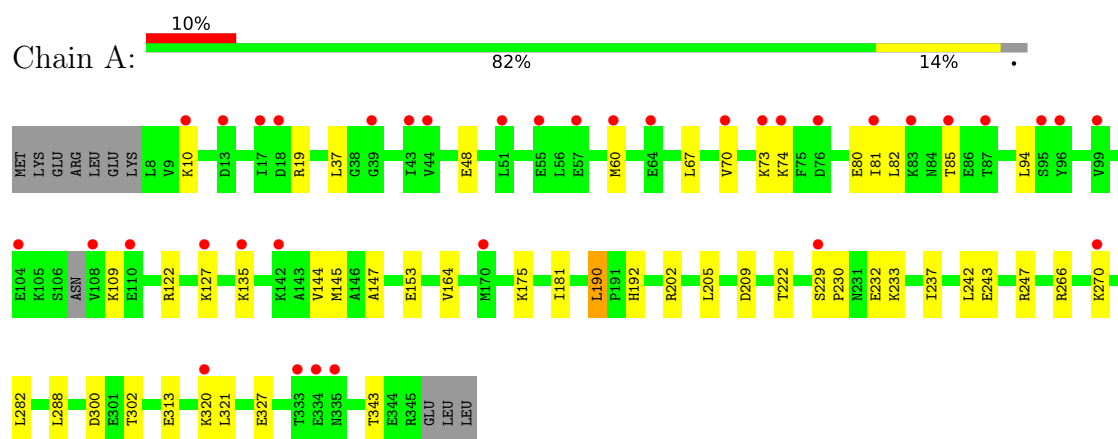
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	100	Total	O	0	0
			100	100		
3	B	76	Total	O	0	0
			76	76		

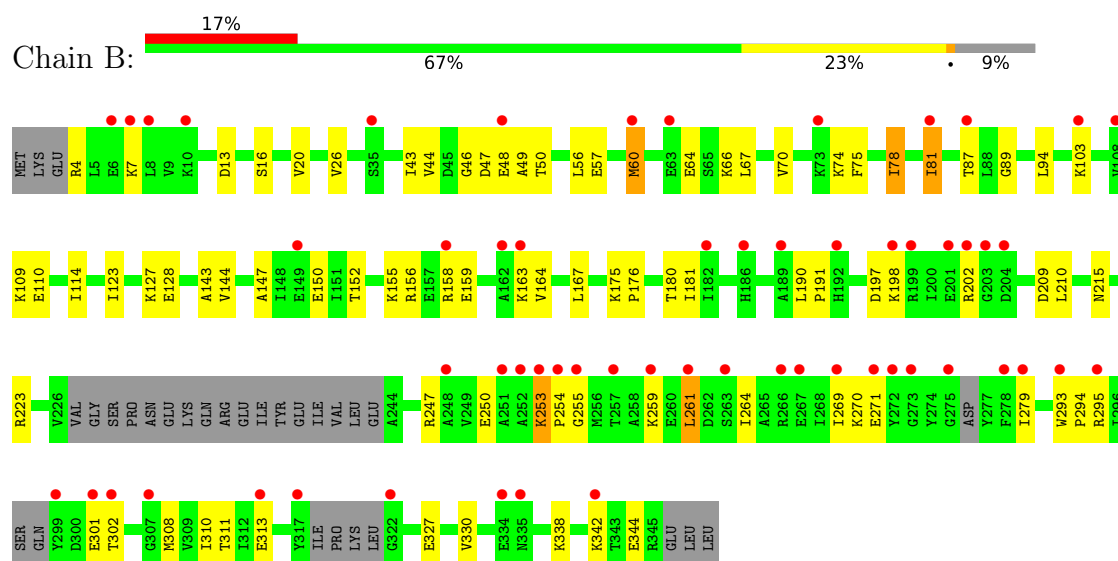
3 Residue-property plots [i](#)

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: Xaa-Pro dipeptidase



• Molecule 1: Xaa-Pro dipeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.48Å 97.23Å 69.88Å 90.00° 97.09° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.8 (20.00-2.00) 95.0 (20.00-2.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.245 , 0.277 0.313 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.429	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 53.4	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	0.91	EDS
Total number of atoms	5376	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% 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](#)

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

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	0.39	0/2715	0.79	0/3655
1	B	0.39	0/2559	0.78	1/3437 (0.0%)
All	All	0.39	0/5274	0.79	1/7092 (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	B	255	GLY	N-CA-C	-5.15	107.77	113.79

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	2673	0	2715	14	0
1	B	2523	0	2563	23	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	100	0	0	1	0
3	B	76	0	0	0	0
All	All	5376	0	5278	35	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 4.

All (35) 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:B:75:PHE:O	1:B:78:ILE:HG22	1.75	0.84
1:B:181:ILE:HB	1:B:209:ASP:HB3	1.64	0.79
1:A:300:ASP:OD1	1:A:302:THR:HG23	1.91	0.70
1:B:313:GLU:HB3	1:B:327:GLU:HB2	1.76	0.66
1:A:313:GLU:HB3	1:A:327:GLU:HB2	1.78	0.65
1:A:181:ILE:HB	1:A:209:ASP:HB3	1.78	0.64
1:B:143:ALA:HB1	1:B:164:VAL:HG13	1.84	0.59
1:A:122:ARG:HD3	1:A:288:LEU:HD12	1.87	0.56
1:B:43:ILE:HG21	1:B:81:ILE:HD11	1.88	0.55
1:B:164:VAL:HG11	1:B:210:LEU:HD22	1.93	0.51
1:A:190:LEU:HD13	1:B:60:MET:HG3	1.93	0.49
1:B:261:LEU:HA	1:B:264:ILE:HD12	1.94	0.48
1:A:313:GLU:CB	1:A:327:GLU:HB2	2.44	0.48
1:A:266:ARG:HG2	1:A:270:LYS:HD2	1.96	0.47
1:B:147:ALA:HB2	1:B:164:VAL:HG21	1.96	0.47
1:A:222:THR:HB	1:A:327:GLU:HB3	1.97	0.47
1:B:313:GLU:CB	1:B:327:GLU:HB2	2.45	0.47
1:A:122:ARG:HD2	3:A:417:HOH:O	2.16	0.45
1:A:147:ALA:HB2	1:A:164:VAL:HG11	1.99	0.45
1:B:20:VAL:HG22	1:B:89:GLY:HA3	1.98	0.44
1:B:175:LYS:HB2	1:B:176:PRO:CD	2.47	0.44
1:B:190:LEU:HA	1:B:191:PRO:HD3	1.84	0.44
1:B:310:ILE:HG13	1:B:330:VAL:HG23	1.99	0.43
1:A:229:SER:HA	1:A:230:PRO:HD3	1.88	0.43
1:A:313:GLU:HB3	1:A:327:GLU:CB	2.45	0.43
1:A:19:ARG:HD2	1:A:82:LEU:HD23	2.00	0.43
1:B:44:VAL:HG22	1:B:49:ALA:HB2	2.00	0.42
1:A:192:HIS:HD2	1:B:57:GLU:OE2	2.03	0.41
1:B:87:THR:HG23	1:B:110:GLU:HG3	2.02	0.41
1:B:123:ILE:O	1:B:308:MET:HG2	2.21	0.41
1:B:175:LYS:HB2	1:B:176:PRO:HD2	2.03	0.41
1:B:180:THR:HG23	1:B:210:LEU:HB3	2.02	0.41
1:B:253:LYS:HA	1:B:254:PRO:HD2	1.83	0.40
1:B:293:TRP:HA	1:B:294:PRO:HA	1.85	0.40
1:B:223:ARG:NH2	1:B:327:GLU:O	2.53	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	333/348 (96%)	320 (96%)	13 (4%)	0	100	100
1	B	308/348 (88%)	298 (97%)	9 (3%)	1 (0%)	36	35
All	All	641/696 (92%)	618 (96%)	22 (3%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	46	GLY

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	289/300 (96%)	257 (89%)	32 (11%)	6	3
1	B	271/300 (90%)	219 (81%)	52 (19%)	1	1
All	All	560/600 (93%)	476 (85%)	84 (15%)	3	1

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LYS
1	A	37	LEU
1	A	48	GLU
1	A	60	MET
1	A	67	LEU

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Mol	Chain	Res	Type
1	A	70	VAL
1	A	73	LYS
1	A	74	LYS
1	A	80	GLU
1	A	81	ILE
1	A	85	THR
1	A	94	LEU
1	A	109	LYS
1	A	127	LYS
1	A	135	LYS
1	A	144	VAL
1	A	145	MET
1	A	153	GLU
1	A	175	LYS
1	A	190	LEU
1	A	202	ARG
1	A	205	LEU
1	A	232	GLU
1	A	233	LYS
1	A	237	ILE
1	A	242	LEU
1	A	243	GLU
1	A	247	ARG
1	A	282	LEU
1	A	320	LYS
1	A	321	LEU
1	A	343	THR
1	B	4	ARG
1	B	7	LYS
1	B	13	ASP
1	B	16	SER
1	B	26	VAL
1	B	47	ASP
1	B	48	GLU
1	B	50	THR
1	B	56	LEU
1	B	60	MET
1	B	64	GLU
1	B	66	LYS
1	B	67	LEU
1	B	70	VAL
1	B	74	LYS

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Mol	Chain	Res	Type
1	B	78	ILE
1	B	81	ILE
1	B	94	LEU
1	B	103	LYS
1	B	109	LYS
1	B	114	ILE
1	B	127	LYS
1	B	128	GLU
1	B	144	VAL
1	B	150	GLU
1	B	152	THR
1	B	155	LYS
1	B	156	ARG
1	B	158	ARG
1	B	159	GLU
1	B	163	LYS
1	B	167	LEU
1	B	197	ASP
1	B	198	LYS
1	B	202	ARG
1	B	215	ASN
1	B	247	ARG
1	B	250	GLU
1	B	253	LYS
1	B	259	LYS
1	B	261	LEU
1	B	269	ILE
1	B	270	LYS
1	B	271	GLU
1	B	279	ILE
1	B	295	ARG
1	B	301	GLU
1	B	302	THR
1	B	311	THR
1	B	338	LYS
1	B	342	LYS
1	B	344	GLU

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

Mol	Chain	Res	Type
1	A	171	ASN

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Mol	Chain	Res	Type
1	B	215	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](#)

Of 4 ligands modelled in this entry, 4 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 [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, 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	337/348 (96%)	0.79	36 (10%)	11 10	8, 20, 25, 29	33 (9%)
1	B	318/348 (91%)	1.33	58 (18%)	3 3	0, 20, 25, 29	38 (11%)
All	All	655/696 (94%)	1.05	94 (14%)	6 5	0, 20, 25, 29	71 (10%)

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	255	GLY	14.2
1	B	202	ARG	8.8
1	B	293	TRP	8.0
1	B	266	ARG	7.3
1	A	83	LYS	7.0
1	B	198	LYS	5.8
1	B	149	GLU	5.5
1	A	18	ASP	5.4
1	B	271	GLU	5.3
1	B	267	GLU	4.9
1	A	55	GLU	4.8
1	B	10	LYS	4.7
1	B	278	PHE	4.5
1	B	259	LYS	4.4
1	B	301	GLU	4.4
1	A	334	GLU	4.3
1	A	74	LYS	4.2
1	B	103	LYS	4.1
1	B	48	GLU	4.0
1	A	320	LYS	3.9
1	B	299	TYR	3.8
1	B	335	ASN	3.8
1	B	192	HIS	3.7
1	B	186	HIS	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	87	THR	3.7
1	B	263	SER	3.7
1	A	10	LYS	3.7
1	A	13	ASP	3.7
1	B	87	THR	3.6
1	A	76	ASP	3.5
1	A	81	ILE	3.4
1	B	251	ALA	3.4
1	B	334	GLU	3.4
1	B	199	ARG	3.3
1	B	6	GLU	3.3
1	B	275	GLY	3.3
1	B	204	ASP	3.3
1	B	307	GLY	3.2
1	A	127	LYS	3.2
1	B	322	GLY	3.2
1	B	257	THR	3.1
1	B	252	ALA	3.1
1	A	104	GLU	3.1
1	B	201	GLU	3.1
1	B	7	LYS	3.1
1	B	279	ILE	3.1
1	B	253	LYS	3.0
1	A	99	VAL	2.9
1	B	254	PRO	2.9
1	A	110	GLU	2.9
1	A	43	ILE	2.8
1	A	142	LYS	2.8
1	B	73	LYS	2.8
1	A	60	MET	2.7
1	A	270	LYS	2.7
1	B	60	MET	2.7
1	B	35	SER	2.6
1	A	39	GLY	2.6
1	B	313	GLU	2.6
1	A	64	GLU	2.6
1	B	162	ALA	2.5
1	A	51	LEU	2.5
1	B	8	LEU	2.5
1	A	170	MET	2.5
1	B	342	LYS	2.5
1	A	57	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	317	TYR	2.5
1	B	203	GLY	2.5
1	A	108	VAL	2.4
1	B	189	ALA	2.4
1	A	96	TYR	2.4
1	A	85	THR	2.4
1	B	302	THR	2.4
1	B	269	ILE	2.4
1	A	229	SER	2.4
1	A	333	THR	2.4
1	A	335	ASN	2.3
1	A	135	LYS	2.3
1	B	158	ARG	2.3
1	B	295	ARG	2.3
1	B	163	LYS	2.3
1	B	272	TYR	2.3
1	B	63	GLU	2.2
1	B	273	GLY	2.2
1	B	261	LEU	2.2
1	A	95	SER	2.1
1	B	182	ILE	2.1
1	B	108	VAL	2.1
1	A	73	LYS	2.1
1	A	17	ILE	2.1
1	A	44	VAL	2.1
1	A	70	VAL	2.1
1	B	248	ALA	2.1
1	B	81	ILE	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 oligosaccharides 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, 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	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	B	402	1/1	0.83	0.14	53,53,53,53	0
2	ZN	B	401	1/1	0.84	0.14	55,55,55,55	0
2	ZN	A	402	1/1	0.98	0.10	38,38,38,38	0
2	ZN	A	401	1/1	0.99	0.09	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.