



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:09 PM UTC

PDB ID : 1Y3H / pdb_00001y3h
Title : Crystal Structure of Inorganic Polyphosphate/ATP-NAD kinase from Mycobacterium tuberculosis
Authors : Mori, S.; Yamasaki, M.; Maruyama, Y.; Momma, K.; kawai, S.; Hashimoto, W.; Mikami, B.; Murata, K.
Deposited on : 2004-11-24
Resolution : 2.80 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

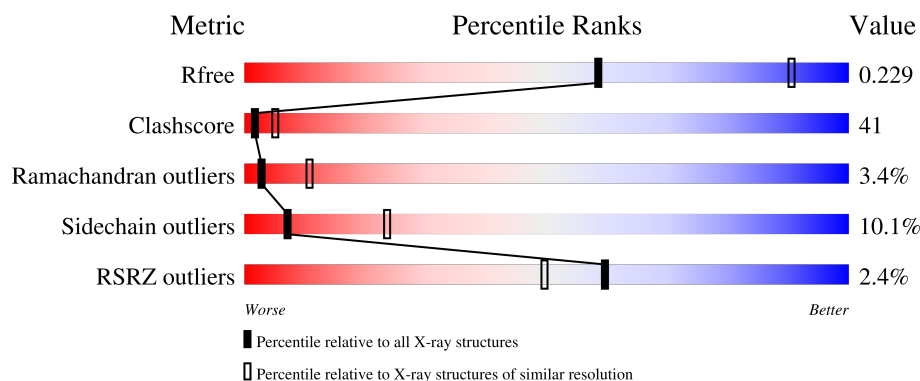
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	307	4% 38% 42% 7% 13%
1	B	307	% 33% 48% 7% 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4070 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 Inorganic polyphosphate/ATP-NAD kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2025	1279	369	371	6			
1	B	267	Total	C	N	O	S	0	0	0
			2018	1275	368	369	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	302	ILE	THR	engineered mutation	UNP P0A5S6
B	302	ILE	THR	engineered mutation	UNP P0A5S6

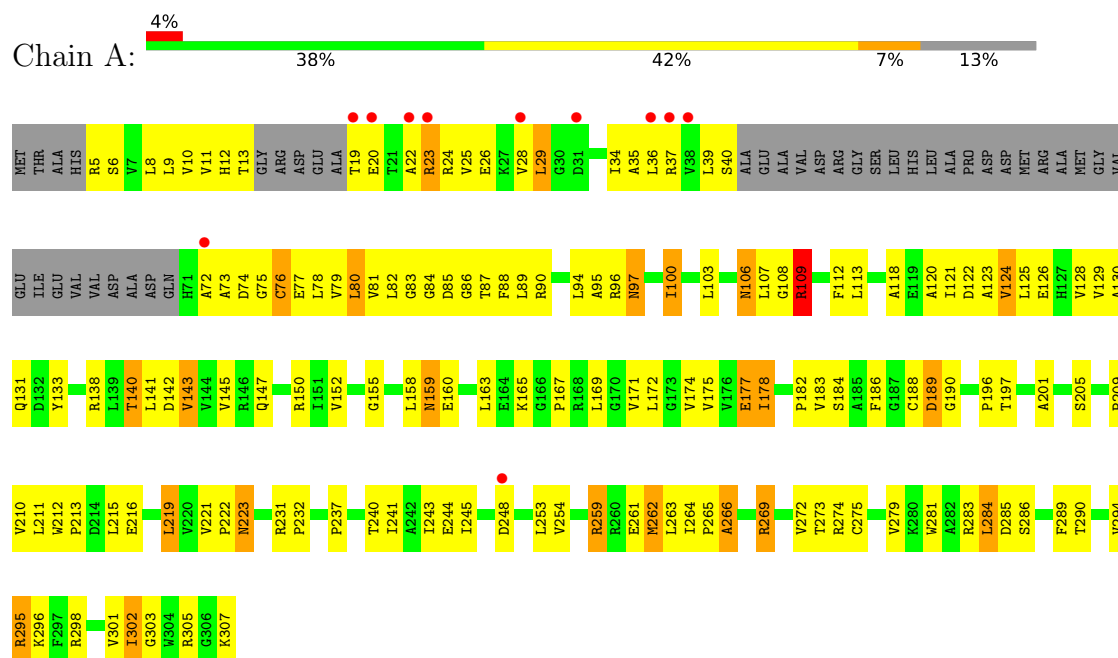
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	13	Total	O	0	0
			13	13		
2	B	14	Total	O	0	0
			14	14		

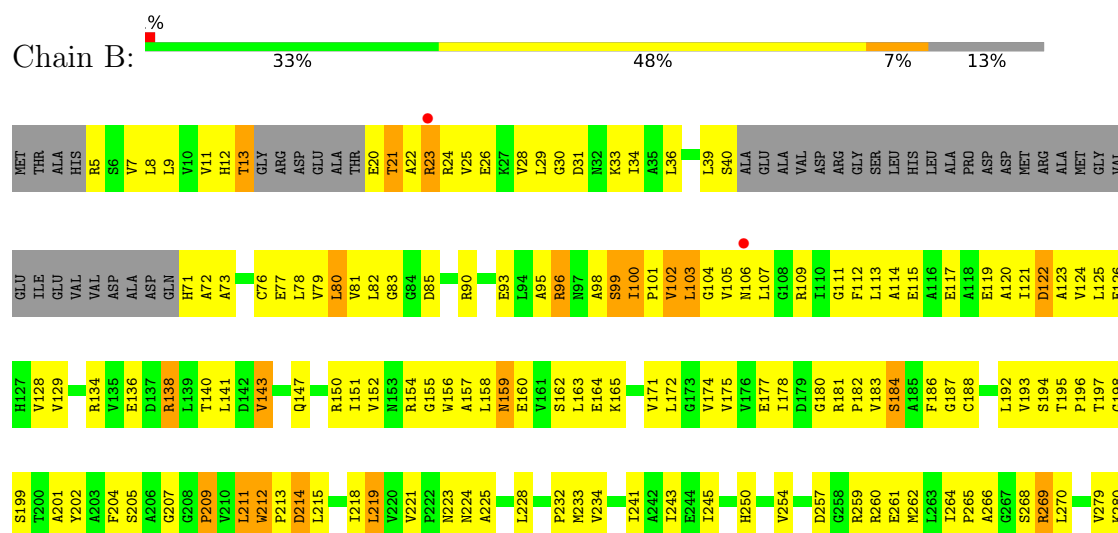
3 Residue-property plots

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: Inorganic polyphosphate/ATP-NAD kinase



• Molecule 1: Inorganic polyphosphate/ATP-NAD kinase



W281	A282	R283	L284	D285
F289	T290	V294	R295	K296
F297	R298	L299	P300	V301
I302	G303	W304	K307	

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	140.18Å 69.44Å 106.43Å 90.00° 130.29° 90.00°	Depositor
Resolution (Å)	9.96 – 2.80 9.96 – 2.80	Depositor EDS
% Data completeness (in resolution range)	79.4 (9.96-2.80) 82.2 (9.96-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.25 (at 2.65Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.221 , 0.235 0.235 , 0.229	Depositor DCC
R_{free} test set	846 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	46.7	Xtriage
Anisotropy	0.430	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 72.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.007 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4070	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.23% 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	0.52	0/2057	1.04	7/2794 (0.3%)
1	B	0.49	0/2050	1.04	7/2784 (0.3%)
All	All	0.51	0/4107	1.04	14/5578 (0.3%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	212	TRP	CA-C-N	7.82	129.61	119.84
1	B	212	TRP	C-N-CA	7.82	129.61	119.84
1	A	302	ILE	N-CA-C	6.46	117.42	108.89
1	A	189	ASP	N-CA-C	-6.37	105.50	113.28
1	A	269	ARG	N-CA-C	6.35	118.80	108.26
1	A	100	ILE	CA-C-N	6.32	126.34	119.89
1	A	100	ILE	C-N-CA	6.32	126.34	119.89
1	B	21	THR	N-CA-C	-5.89	106.18	113.19
1	A	145	VAL	N-CA-C	-5.89	99.84	108.97
1	B	228	LEU	N-CA-C	-5.81	103.68	112.04
1	B	100	ILE	CA-C-N	5.51	125.51	119.89
1	B	100	ILE	C-N-CA	5.51	125.51	119.89
1	B	194	SER	N-CA-C	5.47	118.53	109.94
1	A	86	GLY	N-CA-C	-5.23	107.83	114.16

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	2025	0	2071	178	0
1	B	2018	0	2064	175	0
2	A	13	0	0	0	0
2	B	14	0	0	0	0
All	All	4070	0	4135	334	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 41.

All (334) 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:25:VAL:HG13	1:A:125:LEU:HD21	1.26	1.11
1:A:109:ARG:H	1:A:109:ARG:HD2	1.14	1.05
1:B:25:VAL:HG13	1:B:125:LEU:HD21	1.34	1.02
1:A:259:ARG:HH11	1:A:259:ARG:HB3	1.27	0.99
1:A:109:ARG:HD2	1:A:109:ARG:N	1.82	0.93
1:A:23:ARG:H	1:A:23:ARG:HE	1.23	0.85
1:A:259:ARG:HB3	1:A:259:ARG:NH1	1.93	0.84
1:B:9:LEU:HD11	1:B:82:LEU:HD13	1.61	0.83
1:A:138:ARG:HH22	1:A:283:ARG:HH21	1.27	0.82
1:B:96:ARG:HG2	1:B:96:ARG:HH11	1.44	0.82
1:A:22:ALA:HB3	1:A:23:ARG:HH21	1.44	0.81
1:A:23:ARG:HA	1:A:26:GLU:HG2	1.61	0.80
1:A:290:THR:HG23	1:B:183:VAL:HG12	1.63	0.79
1:B:221:VAL:HG22	1:B:232:PRO:HB3	1.62	0.79
1:B:138:ARG:HG3	1:B:138:ARG:HH11	1.48	0.77
1:B:98:ALA:O	1:B:99:SER:HB3	1.83	0.77
1:A:307:LYS:HB2	1:B:269:ARG:CZ	2.15	0.77
1:B:192:LEU:HD11	1:B:202:TYR:CD2	2.19	0.77
1:B:23:ARG:HA	1:B:26:GLU:HG2	1.65	0.76
1:A:261:GLU:HG2	1:A:262:MET:H	1.52	0.75
1:A:20:GLU:HA	1:A:23:ARG:NH1	2.02	0.75
1:B:24:ARG:HG2	1:B:24:ARG:HH11	1.51	0.75
1:A:6:SER:HA	1:A:35:ALA:HB3	1.68	0.74
1:A:29:LEU:HD23	1:A:36:LEU:HD22	1.67	0.74
1:A:301:VAL:HG12	1:A:301:VAL:O	1.89	0.73
1:A:96:ARG:HG2	1:A:96:ARG:HH11	1.54	0.72
1:B:23:ARG:HA	1:B:26:GLU:OE2	1.88	0.72
1:A:158:LEU:HG	1:A:158:LEU:O	1.90	0.71
1:B:5:ARG:HH21	1:B:34:ILE:HD13	1.53	0.71
1:B:143:VAL:HG12	1:B:270:LEU:HD11	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:GLU:HG2	1:A:262:MET:N	2.05	0.71
1:B:124:VAL:O	1:B:128:VAL:HG23	1.90	0.70
1:A:109:ARG:H	1:A:109:ARG:CD	2.01	0.69
1:A:182:PRO:HG2	1:B:301:VAL:HG11	1.73	0.69
1:A:124:VAL:HG13	1:A:125:LEU:H	1.58	0.68
1:A:223:ASN:C	1:A:223:ASN:HD22	2.02	0.68
1:B:192:LEU:HD11	1:B:202:TYR:HD2	1.57	0.68
1:B:143:VAL:CG1	1:B:270:LEU:HD11	2.23	0.68
1:B:103:LEU:HD12	1:B:104:GLY:N	2.09	0.67
1:A:34:ILE:HD12	1:A:129:VAL:HG12	1.75	0.67
1:A:259:ARG:HH11	1:A:259:ARG:CB	2.04	0.67
1:A:25:VAL:HG22	1:A:125:LEU:HD11	1.78	0.66
1:B:30:GLY:O	1:B:33:LYS:N	2.28	0.66
1:B:157:ALA:HA	1:B:257:ASP:OD1	1.96	0.66
1:A:9:LEU:HD12	1:A:10:VAL:H	1.60	0.66
1:B:20:GLU:HA	1:B:23:ARG:CZ	2.26	0.65
1:A:150:ARG:HB2	1:A:150:ARG:NH1	2.11	0.65
1:B:82:LEU:HB3	1:B:107:LEU:HD11	1.79	0.65
1:B:125:LEU:O	1:B:129:VAL:HG22	1.97	0.65
1:B:136:GLU:HG2	1:B:283:ARG:HG3	1.78	0.65
1:B:20:GLU:C	1:B:22:ALA:H	2.04	0.65
1:B:260:ARG:HG3	1:B:260:ARG:HH11	1.62	0.64
1:A:20:GLU:HA	1:A:23:ARG:CZ	2.28	0.64
1:A:171:VAL:CG1	1:A:188:CYS:N	2.60	0.64
1:A:196:PRO:HG2	1:A:215:LEU:O	1.97	0.64
1:B:112:PHE:CZ	1:B:296:LYS:HG2	2.32	0.64
1:B:265:PRO:HG2	1:B:268:SER:HB3	1.80	0.63
1:A:215:LEU:HD12	1:A:216:GLU:H	1.63	0.63
1:A:298:ARG:HH21	1:A:298:ARG:HG3	1.61	0.63
1:A:150:ARG:HB2	1:A:150:ARG:HH11	1.64	0.63
1:A:9:LEU:HB2	1:A:36:LEU:HD11	1.80	0.63
1:B:184:SER:HB3	1:B:186:PHE:CE1	2.33	0.63
1:A:290:THR:HG23	1:B:183:VAL:CG1	2.28	0.62
1:B:39:LEU:HG	1:B:40:SER:H	1.63	0.62
1:B:138:ARG:HD2	1:B:281:TRP:CE2	2.33	0.62
1:A:178:ILE:N	1:A:178:ILE:HD12	2.14	0.62
1:A:189:ASP:HB2	1:A:223:ASN:ND2	2.14	0.62
1:A:20:GLU:HG2	1:A:23:ARG:NH1	2.14	0.62
1:B:24:ARG:NH1	1:B:28:VAL:HG21	2.15	0.62
1:B:25:VAL:HA	1:B:125:LEU:HD11	1.80	0.62
1:B:140:THR:HG21	1:B:279:VAL:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:LYS:HB2	1:B:269:ARG:NH2	2.14	0.61
1:A:24:ARG:O	1:A:28:VAL:HG23	2.01	0.61
1:B:21:THR:HB	1:B:121:ILE:HD13	1.82	0.61
1:B:138:ARG:HG3	1:B:138:ARG:NH1	2.16	0.61
1:A:8:LEU:HD12	1:A:37:ARG:HB2	1.82	0.60
1:A:219:LEU:HD22	1:A:221:VAL:HG23	1.82	0.60
1:B:159:ASN:HB3	1:B:160:GLU:OE1	2.00	0.60
1:A:23:ARG:H	1:A:23:ARG:NE	1.98	0.60
1:A:253:LEU:HD22	1:A:261:GLU:OE2	2.01	0.60
1:B:8:LEU:HD22	1:B:73:ALA:HB3	1.84	0.60
1:B:81:VAL:HG12	1:B:103:LEU:O	2.00	0.60
1:A:215:LEU:HD12	1:A:216:GLU:N	2.16	0.60
1:A:29:LEU:CD2	1:A:36:LEU:HD22	2.32	0.60
1:A:140:THR:HG21	1:A:279:VAL:HG23	1.84	0.60
1:B:261:GLU:HG2	1:B:262:MET:N	2.17	0.59
1:B:223:ASN:C	1:B:223:ASN:HD22	2.09	0.59
1:A:210:VAL:O	1:A:211:LEU:HD23	2.02	0.59
1:B:121:ILE:O	1:B:124:VAL:HG12	2.02	0.59
1:A:143:VAL:HG13	1:A:272:VAL:HG22	1.85	0.59
1:B:24:ARG:HG2	1:B:24:ARG:NH1	2.14	0.59
1:A:211:LEU:HD22	1:B:234:VAL:HB	1.84	0.58
1:A:172:LEU:C	1:A:172:LEU:HD23	2.28	0.58
1:B:23:ARG:HA	1:B:26:GLU:CG	2.32	0.58
1:A:9:LEU:CB	1:A:36:LEU:HD11	2.34	0.58
1:A:20:GLU:HG2	1:A:23:ARG:HH11	1.67	0.58
1:A:183:VAL:HG23	1:A:184:SER:H	1.67	0.58
1:B:106:ASN:ND2	1:B:114:ALA:HB2	2.18	0.58
1:A:90:ARG:HG2	1:A:259:ARG:HH21	1.65	0.58
1:B:9:LEU:HB2	1:B:36:LEU:HD11	1.85	0.58
1:B:26:GLU:HA	1:B:36:LEU:CD2	2.33	0.58
1:B:78:LEU:HG	1:B:79:VAL:N	2.19	0.57
1:B:199:SER:O	1:B:204:PHE:HB2	2.04	0.57
1:A:301:VAL:O	1:A:301:VAL:CG1	2.52	0.57
1:B:302:ILE:HD12	1:B:303:GLY:N	2.20	0.57
1:A:171:VAL:HG12	1:A:188:CYS:H	1.70	0.57
1:B:163:LEU:HD12	1:B:164:GLU:N	2.19	0.57
1:B:95:ALA:CB	1:B:102:VAL:HG22	2.35	0.56
1:B:184:SER:HB3	1:B:186:PHE:HE1	1.69	0.56
1:A:23:ARG:HA	1:A:26:GLU:OE2	2.05	0.56
1:B:138:ARG:HD2	1:B:281:TRP:NE1	2.20	0.56
1:A:97:ASN:HD22	1:A:97:ASN:N	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:GLU:HG2	1:B:283:ARG:CG	2.36	0.56
1:B:25:VAL:O	1:B:29:LEU:HB2	2.06	0.55
1:B:80:LEU:CD2	1:B:103:LEU:HG	2.35	0.55
1:B:254:VAL:HG23	1:B:264:ILE:HG13	1.88	0.55
1:B:290:THR:O	1:B:294:VAL:HG23	2.06	0.55
1:A:124:VAL:HG13	1:A:125:LEU:N	2.21	0.55
1:A:171:VAL:HG12	1:A:188:CYS:N	2.21	0.55
1:B:5:ARG:HH21	1:B:34:ILE:CD1	2.19	0.55
1:A:9:LEU:HD12	1:A:10:VAL:N	2.22	0.55
1:A:159:ASN:ND2	1:A:197:THR:HG22	2.21	0.55
1:A:26:GLU:HA	1:A:36:LEU:CD2	2.37	0.55
1:A:9:LEU:HD11	1:A:82:LEU:CD1	2.37	0.55
1:A:23:ARG:HA	1:A:26:GLU:CG	2.34	0.55
1:B:12:HIS:O	1:B:13:THR:HG23	2.07	0.55
1:A:82:LEU:N	1:A:82:LEU:HD12	2.22	0.54
1:A:241:ILE:N	1:A:241:ILE:HD12	2.22	0.54
1:B:96:ARG:HG2	1:B:96:ARG:NH1	2.20	0.54
1:A:140:THR:HG21	1:A:279:VAL:H	1.72	0.54
1:B:8:LEU:HD22	1:B:73:ALA:CB	2.37	0.54
1:A:244:GLU:HG2	1:A:269:ARG:HB3	1.89	0.54
1:B:260:ARG:HG3	1:B:260:ARG:NH1	2.19	0.54
1:B:302:ILE:HD12	1:B:303:GLY:H	1.73	0.54
1:A:8:LEU:HD22	1:A:73:ALA:HB3	1.89	0.54
1:A:138:ARG:HH22	1:A:283:ARG:NH2	2.00	0.54
1:A:261:GLU:CG	1:A:262:MET:H	2.21	0.54
1:A:36:LEU:HD12	1:A:37:ARG:N	2.22	0.54
1:A:5:ARG:NH2	1:A:34:ILE:HD11	2.22	0.54
1:A:23:ARG:CA	1:A:26:GLU:HG2	2.34	0.53
1:A:112:PHE:CZ	1:A:296:LYS:HG2	2.43	0.53
1:A:298:ARG:HG3	1:A:298:ARG:NH2	2.23	0.53
1:B:103:LEU:HB2	1:B:282:ALA:HB3	1.90	0.53
1:B:219:LEU:HD22	1:B:221:VAL:HG23	1.90	0.53
1:B:147:GLN:HB3	1:B:152:VAL:HG21	1.89	0.53
1:A:254:VAL:HG23	1:A:264:ILE:CG1	2.38	0.53
1:B:213:PRO:HG3	1:B:289:PHE:HB2	1.89	0.53
1:B:150:ARG:HB2	1:B:150:ARG:HH11	1.73	0.53
1:A:80:LEU:HD13	1:A:81:VAL:N	2.24	0.53
1:B:150:ARG:HB2	1:B:150:ARG:NH1	2.24	0.53
1:A:269:ARG:NH2	1:B:307:LYS:HD2	2.23	0.53
1:B:20:GLU:C	1:B:22:ALA:N	2.64	0.53
1:A:96:ARG:HG2	1:A:96:ARG:NH1	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:ILE:HD12	1:B:241:ILE:N	2.24	0.52
1:B:165:LYS:HA	1:B:172:LEU:HD12	1.91	0.52
1:A:174:VAL:HG12	1:A:186:PHE:O	2.10	0.52
1:A:177:GLU:C	1:A:178:ILE:HD12	2.34	0.52
1:B:162:SER:HB2	1:B:192:LEU:CD1	2.39	0.52
1:B:301:VAL:HG12	1:B:301:VAL:O	2.10	0.52
1:A:245:ILE:N	1:A:245:ILE:HD12	2.24	0.52
1:B:154:ARG:HG3	1:B:155:GLY:N	2.23	0.52
1:B:121:ILE:O	1:B:124:VAL:CG1	2.58	0.52
1:A:261:GLU:O	1:A:262:MET:HB3	2.10	0.52
1:B:23:ARG:CA	1:B:26:GLU:HG2	2.37	0.51
1:B:171:VAL:CG1	1:B:188:CYS:N	2.73	0.51
1:A:290:THR:O	1:A:294:VAL:HG23	2.10	0.51
1:B:205:SER:C	1:B:207:GLY:H	2.18	0.51
1:A:5:ARG:HD2	1:A:77:GLU:OE1	2.10	0.51
1:A:269:ARG:CZ	1:B:307:LYS:HD2	2.40	0.51
1:B:7:VAL:O	1:B:36:LEU:HD12	2.10	0.51
1:A:163:LEU:O	1:A:190:GLY:HA3	2.11	0.51
1:B:105:VAL:HG13	1:B:117:GLU:O	2.10	0.51
1:B:297:PHE:O	1:B:298:ARG:HB2	2.09	0.51
1:A:97:ASN:N	1:A:97:ASN:ND2	2.57	0.51
1:A:88:PHE:HD2	1:A:113:LEU:HD13	1.76	0.51
1:A:95:ALA:HB1	1:A:100:ILE:O	2.11	0.51
1:A:305:ARG:NH1	1:B:245:ILE:O	2.43	0.51
1:B:196:PRO:HG2	1:B:215:LEU:O	2.11	0.51
1:B:140:THR:HG22	1:B:158:LEU:CD1	2.42	0.50
1:B:254:VAL:HG23	1:B:264:ILE:CG1	2.41	0.50
1:A:129:VAL:HG23	1:A:130:ALA:N	2.25	0.50
1:B:25:VAL:CG1	1:B:125:LEU:HD21	2.25	0.50
1:B:106:ASN:OD1	1:B:111:GLY:N	2.45	0.49
1:A:210:VAL:C	1:A:211:LEU:HD23	2.37	0.49
1:A:261:GLU:CG	1:A:262:MET:N	2.74	0.49
1:B:22:ALA:C	1:B:24:ARG:N	2.70	0.49
1:B:98:ALA:HB3	1:B:100:ILE:HG12	1.93	0.49
1:A:240:THR:HG23	1:A:273:THR:CG2	2.42	0.49
1:B:188:CYS:HB3	1:B:225:ALA:HA	1.94	0.49
1:B:98:ALA:O	1:B:99:SER:CB	2.57	0.49
1:B:284:LEU:HD12	1:B:284:LEU:O	2.12	0.49
1:A:34:ILE:CD1	1:A:129:VAL:HG12	2.40	0.49
1:B:90:ARG:HG2	1:B:259:ARG:CZ	2.43	0.49
1:A:183:VAL:HG23	1:A:184:SER:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:GLU:OE1	1:B:180:GLY:HA2	2.13	0.49
1:A:118:ALA:O	1:A:121:ILE:HG13	2.13	0.49
1:B:134:ARG:HB3	1:B:283:ARG:HB2	1.93	0.49
1:A:223:ASN:C	1:A:223:ASN:ND2	2.70	0.49
1:A:9:LEU:HD11	1:A:82:LEU:HD13	1.95	0.48
1:B:122:ASP:O	1:B:126:GLU:N	2.41	0.48
1:B:21:THR:HB	1:B:121:ILE:CD1	2.42	0.48
1:B:82:LEU:HB3	1:B:107:LEU:HD21	1.95	0.48
1:A:123:ALA:O	1:A:126:GLU:HB3	2.14	0.48
1:A:302:ILE:HD12	1:A:303:GLY:H	1.78	0.48
1:B:29:LEU:HG	1:B:34:ILE:HB	1.94	0.48
1:B:122:ASP:HA	1:B:125:LEU:HB2	1.95	0.48
1:B:103:LEU:HD12	1:B:104:GLY:H	1.76	0.48
1:A:81:VAL:HG12	1:A:103:LEU:O	2.14	0.48
1:B:174:VAL:CG2	1:B:175:VAL:N	2.76	0.48
1:A:237:PRO:HB2	1:A:274:ARG:NH1	2.29	0.48
1:B:93:GLU:O	1:B:96:ARG:HB3	2.14	0.47
1:B:265:PRO:O	1:B:266:ALA:C	2.56	0.47
1:B:250:HIS:O	1:B:266:ALA:HB2	2.15	0.47
1:A:88:PHE:CD2	1:A:113:LEU:HD13	2.50	0.47
1:B:20:GLU:C	1:B:20:GLU:OE2	2.57	0.47
1:B:23:ARG:H	1:B:23:ARG:HE	1.62	0.47
1:B:83:GLY:O	1:B:106:ASN:HA	2.14	0.47
1:A:19:THR:O	1:A:23:ARG:NH2	2.47	0.47
1:A:177:GLU:HA	1:A:182:PRO:HA	1.97	0.47
1:A:36:LEU:HD12	1:A:37:ARG:H	1.80	0.47
1:A:302:ILE:HG23	1:A:302:ILE:O	2.14	0.47
1:B:223:ASN:HD22	1:B:224:ASN:N	2.13	0.47
1:B:294:VAL:HG13	1:B:299:LEU:HB2	1.97	0.47
1:A:142:ASP:HB2	1:A:275:CYS:HB2	1.96	0.47
1:B:22:ALA:C	1:B:24:ARG:H	2.22	0.47
1:B:23:ARG:HA	1:B:26:GLU:CD	2.40	0.47
1:B:141:LEU:O	1:B:156:TRP:HA	2.15	0.47
1:A:6:SER:O	1:A:77:GLU:N	2.47	0.46
1:A:182:PRO:CG	1:B:301:VAL:HG11	2.44	0.46
1:B:174:VAL:HG22	1:B:175:VAL:N	2.29	0.46
1:B:212:TRP:HA	1:B:213:PRO:HD2	1.69	0.46
1:A:11:VAL:HG12	1:A:82:LEU:HD13	1.97	0.46
1:B:112:PHE:HZ	1:B:296:LYS:HG2	1.77	0.46
1:B:174:VAL:CG2	1:B:243:ILE:HG23	2.45	0.46
1:B:157:ALA:CA	1:B:257:ASP:OD1	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:PRO:O	1:B:211:LEU:HD23	2.16	0.46
1:A:97:ASN:ND2	1:A:97:ASN:H	2.13	0.46
1:B:119:GLU:N	1:B:119:GLU:CD	2.74	0.46
1:B:214:ASP:OD2	1:B:214:ASP:N	2.42	0.46
1:A:124:VAL:O	1:A:125:LEU:C	2.58	0.46
1:B:96:ARG:NH1	1:B:96:ARG:CG	2.75	0.46
1:A:85:ASP:O	1:A:89:LEU:HG	2.16	0.46
1:A:183:VAL:HG13	1:B:290:THR:HG23	1.98	0.46
1:A:301:VAL:CG1	1:B:182:PRO:HG2	2.46	0.46
1:B:294:VAL:HA	1:B:299:LEU:HG	1.98	0.46
1:A:78:LEU:HG	1:A:79:VAL:N	2.32	0.45
1:A:29:LEU:O	1:A:34:ILE:HB	2.16	0.45
1:B:24:ARG:HH12	1:B:28:VAL:HG21	1.78	0.45
1:B:162:SER:HB2	1:B:192:LEU:HD13	1.97	0.45
1:A:165:LYS:HA	1:A:172:LEU:HD12	1.98	0.45
1:B:195:THR:O	1:B:198:GLY:N	2.49	0.45
1:A:26:GLU:HA	1:A:36:LEU:HD23	1.99	0.45
1:A:84:GLY:O	1:A:87:THR:HB	2.17	0.45
1:A:39:LEU:HG	1:A:40:SER:H	1.81	0.45
1:B:120:ALA:O	1:B:124:VAL:HG12	2.17	0.45
1:A:90:ARG:NH1	1:A:94:LEU:HD21	2.32	0.45
1:A:269:ARG:HD3	1:B:307:LYS:C	2.42	0.45
1:B:172:LEU:O	1:B:187:GLY:HA2	2.17	0.45
1:B:205:SER:C	1:B:207:GLY:N	2.74	0.45
1:B:178:ILE:N	1:B:178:ILE:HD12	2.32	0.44
1:A:138:ARG:HD2	1:A:281:TRP:CE2	2.52	0.44
1:B:31:ASP:C	1:B:33:LYS:H	2.24	0.44
1:B:158:LEU:H	1:B:257:ASP:CG	2.25	0.44
1:B:115:GLU:OE2	1:B:283:ARG:HA	2.17	0.44
1:A:90:ARG:HG2	1:A:259:ARG:HE	1.81	0.44
1:B:39:LEU:HG	1:B:40:SER:N	2.32	0.44
1:B:77:GLU:HG2	1:B:78:LEU:N	2.33	0.44
1:B:212:TRP:O	1:B:215:LEU:HB3	2.17	0.44
1:A:126:GLU:O	1:A:129:VAL:HG22	2.17	0.44
1:A:174:VAL:CG2	1:A:243:ILE:HG22	2.48	0.44
1:A:158:LEU:O	1:A:158:LEU:CG	2.65	0.44
1:A:290:THR:CG2	1:B:183:VAL:HG12	2.41	0.44
1:B:24:ARG:NH2	1:B:122:ASP:OD2	2.51	0.44
1:A:138:ARG:NH2	1:A:283:ARG:HH21	2.05	0.43
1:B:24:ARG:O	1:B:28:VAL:HG23	2.19	0.43
1:A:85:ASP:OD1	1:A:113:LEU:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:LEU:HB3	1:A:107:LEU:HD21	2.00	0.43
1:A:174:VAL:HG22	1:A:175:VAL:N	2.33	0.43
1:A:209:PRO:HB3	1:B:232:PRO:HG2	2.00	0.43
1:A:221:VAL:HG22	1:A:232:PRO:HB3	2.00	0.43
1:B:101:PRO:HA	1:B:280:LYS:HB2	2.00	0.43
1:B:204:PHE:CD1	1:B:204:PHE:C	2.96	0.43
1:A:284:LEU:O	1:A:286:SER:N	2.52	0.43
1:A:78:LEU:HD12	1:A:79:VAL:H	1.83	0.43
1:A:138:ARG:O	1:A:140:THR:CG2	2.66	0.43
1:B:85:ASP:OD1	1:B:113:LEU:HB2	2.19	0.43
1:B:163:LEU:HD21	1:B:245:ILE:HD11	2.01	0.43
1:A:106:ASN:HD22	1:A:106:ASN:HA	1.60	0.43
1:B:172:LEU:C	1:B:172:LEU:HD23	2.43	0.43
1:B:209:PRO:HD2	1:B:219:LEU:HD11	2.01	0.43
1:B:8:LEU:CD2	1:B:73:ALA:HB3	2.49	0.42
1:A:120:ALA:O	1:A:124:VAL:HG12	2.18	0.42
1:A:265:PRO:O	1:A:266:ALA:C	2.61	0.42
1:A:301:VAL:HG11	1:B:182:PRO:HG2	2.00	0.42
1:A:90:ARG:HH12	1:A:94:LEU:HD21	1.83	0.42
1:A:253:LEU:HD23	1:A:263:LEU:HA	2.02	0.42
1:A:37:ARG:NH1	1:A:74:ASP:O	2.53	0.42
1:A:140:THR:CG2	1:A:279:VAL:H	2.31	0.42
1:B:9:LEU:CB	1:B:36:LEU:HD11	2.49	0.42
1:B:180:GLY:O	1:B:181:ARG:HD2	2.20	0.42
1:A:8:LEU:HD13	1:A:73:ALA:HB1	2.02	0.42
1:A:155:GLY:HA3	1:A:262:MET:HE1	2.01	0.42
1:A:172:LEU:CD2	1:A:174:VAL:HB	2.50	0.42
1:B:22:ALA:O	1:B:25:VAL:N	2.52	0.42
1:A:22:ALA:HB3	1:A:23:ARG:NH2	2.22	0.42
1:A:213:PRO:HD3	1:A:289:PHE:CG	2.55	0.42
1:A:20:GLU:CD	1:A:20:GLU:O	2.63	0.42
1:A:301:VAL:HG13	1:B:182:PRO:CG	2.50	0.42
1:A:141:LEU:HD13	1:A:272:VAL:HG11	2.01	0.41
1:A:8:LEU:HB2	1:A:76:CYS:SG	2.59	0.41
1:A:83:GLY:N	1:A:107:LEU:HG	2.35	0.41
1:A:147:GLN:HB3	1:A:152:VAL:HG21	2.03	0.41
1:A:212:TRP:CZ3	1:B:233:MET:HB3	2.55	0.41
1:A:237:PRO:CB	1:A:274:ARG:NH1	2.83	0.41
1:A:24:ARG:HG2	1:A:24:ARG:HH11	1.85	0.41
1:B:140:THR:HG22	1:B:158:LEU:HD12	2.02	0.41
1:B:11:VAL:O	1:B:40:SER:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:THR:HG22	1:B:158:LEU:HD13	2.01	0.41
1:A:125:LEU:O	1:A:128:VAL:HB	2.21	0.41
1:A:150:ARG:NH1	1:A:150:ARG:CB	2.83	0.41
1:B:80:LEU:HD13	1:B:81:VAL:N	2.34	0.41
1:A:182:PRO:HG3	1:B:304:TRP:CE3	2.55	0.41
1:A:221:VAL:O	1:A:222:PRO:C	2.62	0.41
1:A:131:GLN:HA	1:A:133:TYR:CE1	2.55	0.41
1:A:167:PRO:C	1:A:169:LEU:N	2.79	0.41
1:A:178:ILE:N	1:A:178:ILE:CD1	2.80	0.41
1:A:254:VAL:HG23	1:A:264:ILE:HG13	2.02	0.41
1:A:237:PRO:HB2	1:A:274:ARG:HH11	1.85	0.40
1:B:90:ARG:O	1:B:93:GLU:CB	2.69	0.40
1:A:83:GLY:O	1:A:106:ASN:HA	2.21	0.40
1:B:223:ASN:C	1:B:223:ASN:ND2	2.76	0.40
1:A:26:GLU:HB2	1:A:36:LEU:HD23	2.04	0.40
1:B:122:ASP:O	1:B:123:ALA:C	2.65	0.40
1:B:218:ILE:O	1:B:234:VAL:HA	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	262/307 (85%)	216 (82%)	35 (13%)	11 (4%)	2	7
1	B	261/307 (85%)	232 (89%)	22 (8%)	7 (3%)	4	15
All	All	523/614 (85%)	448 (86%)	57 (11%)	18 (3%)	3	11

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	HIS

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Mol	Chain	Res	Type
1	A	72	ALA
1	A	201	ALA
1	B	72	ALA
1	B	76	CYS
1	A	76	CYS
1	A	108	GLY
1	A	262	MET
1	A	295	ARG
1	B	151	ILE
1	A	109	ARG
1	A	266	ALA
1	A	285	ASP
1	B	99	SER
1	B	285	ASP
1	B	201	ALA
1	A	75	GLY
1	B	193	VAL

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	213/242 (88%)	190 (89%)	23 (11%)	6	21
1	B	212/242 (88%)	192 (91%)	20 (9%)	8	27
All	All	425/484 (88%)	382 (90%)	43 (10%)	7	23

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

Mol	Chain	Res	Type
1	A	13	THR
1	A	23	ARG
1	A	29	LEU
1	A	80	LEU
1	A	97	ASN
1	A	106	ASN

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Mol	Chain	Res	Type
1	A	109	ARG
1	A	122	ASP
1	A	124	VAL
1	A	140	THR
1	A	143	VAL
1	A	159	ASN
1	A	160	GLU
1	A	177	GLU
1	A	178	ILE
1	A	205	SER
1	A	219	LEU
1	A	223	ASN
1	A	231	ARG
1	A	248	ASP
1	A	259	ARG
1	A	284	LEU
1	A	295	ARG
1	B	13	THR
1	B	23	ARG
1	B	71	HIS
1	B	80	LEU
1	B	96	ARG
1	B	102	VAL
1	B	103	LEU
1	B	109	ARG
1	B	122	ASP
1	B	138	ARG
1	B	143	VAL
1	B	159	ASN
1	B	184	SER
1	B	197	THR
1	B	209	PRO
1	B	211	LEU
1	B	214	ASP
1	B	219	LEU
1	B	269	ARG
1	B	295	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN

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Mol	Chain	Res	Type
1	A	159	ASN
1	A	223	ASN
1	B	131	GLN
1	B	147	GLN
1	B	159	ASN
1	B	223	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 [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	268/307 (87%)	-0.03	11 (4%) 41 33	11, 59, 106, 126	0
1	B	267/307 (86%)	-0.20	2 (0%) 84 77	16, 57, 83, 111	0
All	All	535/614 (87%)	-0.11	13 (2%) 59 49	11, 58, 101, 126	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	23	ARG	3.5
1	A	38	VAL	3.0
1	A	72	ALA	2.9
1	A	36	LEU	2.6
1	A	28	VAL	2.5
1	A	20	GLU	2.5
1	A	19	THR	2.5
1	A	23	ARG	2.3
1	A	37	ARG	2.3
1	A	22	ALA	2.2
1	B	106	ASN	2.1
1	A	31	ASP	2.1
1	A	248	ASP	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.