



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:13 AM UTC

PDB ID : 1RIL / pdb_00001ril
Title : CRYSTAL STRUCTURE OF RIBONUCLEASE H FROM THERMUS
THERMOPHILUS HB8 REFINED AT 2.8 ANGSTROMS RESOLUTION
Authors : Ishikawa, K.; Okumura, M.; Katayanagi, K.; Kimura, S.; Kanaya, S.; Naka-
mura, H.; Morikawa, K.
Deposited on : 1993-01-14
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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

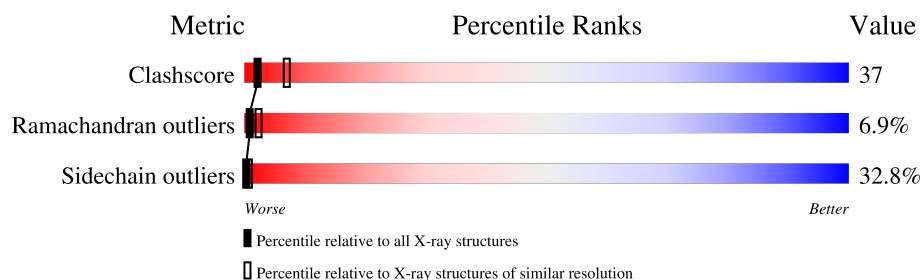
1 Overall quality at a glance

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))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	166	16% 36% 28% 9% 11%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1174 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 RIBONUCLEASE H.

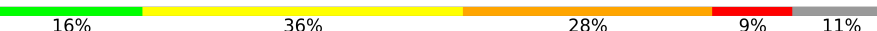
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	147	Total	C	N	O	S	0	0	0
			1174	737	228	204	5			

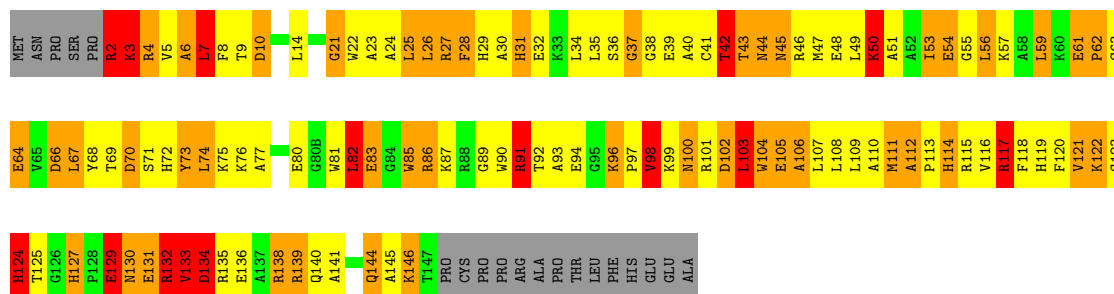
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

• Molecule 1: RIBONUCLEASE H

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	44.70 Å 44.70 Å 314.70 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.205 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1174	wwPDB-VP
Average B, all atoms (Å ²)	6.0	wwPDB-VP

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	1.43	5/1203 (0.4%)	2.85	119/1619 (7.4%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	139	ARG	NE-CZ	-6.23	1.26	1.33
1	A	67	LEU	N-CA	5.65	1.52	1.45
1	A	139	ARG	CD-NE	-5.35	1.38	1.46
1	A	37	GLY	CA-C	5.31	1.56	1.52
1	A	115	ARG	NE-CZ	5.22	1.38	1.33

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	ARG	CD-NE-CZ	21.02	153.83	124.40
1	A	134	ASP	CA-CB-CG	18.75	131.35	112.60
1	A	135	ARG	CD-NE-CZ	13.30	143.02	124.40
1	A	133	VAL	N-CA-CB	-13.20	96.23	110.62
1	A	127	HIS	CA-CB-CG	-12.55	101.25	113.80
1	A	70	ASP	CA-CB-CG	11.44	124.04	112.60
1	A	117	ARG	CA-CB-CG	10.91	135.93	114.10
1	A	117	ARG	CA-C-O	-10.46	109.02	120.43
1	A	106	ALA	O-C-N	9.87	134.15	122.20
1	A	132	ARG	CD-NE-CZ	9.67	137.93	124.40
1	A	2	ARG	CD-NE-CZ	9.61	137.85	124.40
1	A	61	GLU	CA-C-O	9.44	129.34	120.09
1	A	129	GLU	CB-CG-CD	9.11	128.08	112.60
1	A	39	GLU	CA-C-O	-8.92	110.77	121.56
1	A	28	PHE	O-C-N	8.79	133.46	122.65
1	A	40	ALA	CA-C-N	8.56	134.84	122.77
1	A	40	ALA	C-N-CA	8.56	134.84	122.77
1	A	130	ASN	CA-CB-CG	8.49	121.09	112.60
1	A	92	THR	CA-CB-OG1	-8.29	97.17	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	GLU	CB-CG-CD	8.27	126.66	112.60
1	A	59	LEU	CA-CB-CG	8.16	144.86	116.30
1	A	139	ARG	NE-CZ-NH2	8.07	126.46	119.20
1	A	117	ARG	N-CA-CB	7.86	123.24	110.43
1	A	86	ARG	CA-CB-CG	7.79	129.68	114.10
1	A	92	THR	N-CA-CB	-7.75	98.65	110.04
1	A	2	ARG	CG-CD-NE	7.72	128.99	112.00
1	A	7	LEU	CA-C-O	-7.62	112.43	120.58
1	A	133	VAL	CA-C-N	7.58	133.24	121.19
1	A	133	VAL	C-N-CA	7.58	133.24	121.19
1	A	129	GLU	CA-C-N	7.56	130.72	120.44
1	A	129	GLU	C-N-CA	7.56	130.72	120.44
1	A	67	LEU	CB-CA-C	7.53	123.26	109.71
1	A	103	LEU	CA-C-O	-7.52	111.32	119.97
1	A	115	ARG	CG-CD-NE	7.43	128.35	112.00
1	A	40	ALA	N-CA-C	7.40	120.43	111.40
1	A	54	GLU	CB-CG-CD	7.40	125.17	112.60
1	A	119	HIS	CA-CB-CG	7.37	121.17	113.80
1	A	105	GLU	CA-C-O	7.32	128.18	120.42
1	A	119	HIS	N-CA-CB	7.32	121.91	110.71
1	A	85	TRP	N-CA-C	-7.17	103.39	111.14
1	A	124	HIS	CA-CB-CG	-7.12	106.68	113.80
1	A	114	HIS	N-CA-C	6.91	120.30	110.14
1	A	61	GLU	CA-CB-CG	6.89	127.88	114.10
1	A	91	ARG	CD-NE-CZ	6.87	134.01	124.40
1	A	36	SER	CA-C-N	6.75	128.64	121.48
1	A	36	SER	C-N-CA	6.75	128.64	121.48
1	A	91	ARG	NE-CZ-NH2	6.74	125.27	119.20
1	A	48	GLU	CA-CB-CG	6.73	127.56	114.10
1	A	66	ASP	N-CA-C	-6.69	97.61	108.52
1	A	21	GLY	CA-C-O	-6.69	114.19	121.48
1	A	25	LEU	O-C-N	6.66	130.99	123.27
1	A	72	HIS	N-CA-C	-6.52	103.86	110.97
1	A	35	LEU	CA-C-O	-6.47	113.38	120.43
1	A	91	ARG	NE-CZ-NH1	-6.45	115.05	121.50
1	A	105	GLU	CA-CB-CG	6.42	126.94	114.10
1	A	130	ASN	O-C-N	6.39	128.99	122.09
1	A	117	ARG	CB-CA-C	-6.39	99.21	109.75
1	A	69	THR	N-CA-CB	-6.38	99.69	110.99
1	A	125	THR	N-CA-C	-6.33	104.81	112.54
1	A	92	THR	CA-C-O	-6.30	114.87	121.55
1	A	80	GLU	N-CA-C	6.19	119.53	112.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	43	THR	N-CA-C	6.18	119.57	109.24
1	A	3	LYS	N-CA-CB	6.16	120.91	110.49
1	A	93	ALA	CA-C-O	-6.16	112.89	119.97
1	A	100	ASN	OD1-CG-ND2	-6.10	116.50	122.60
1	A	21	GLY	O-C-N	6.03	129.09	123.54
1	A	74	LEU	O-C-N	5.99	128.98	122.15
1	A	24	ALA	CA-C-O	-5.88	113.04	120.28
1	A	28	PHE	CA-CB-CG	-5.87	107.93	113.80
1	A	139	ARG	NE-CZ-NH1	-5.86	115.64	121.50
1	A	28	PHE	N-CA-CB	5.86	118.82	110.44
1	A	118	PHE	CA-CB-CG	5.83	119.63	113.80
1	A	131	GLU	CA-CB-CG	5.80	125.71	114.10
1	A	64	GLU	N-CA-C	-5.80	100.54	109.76
1	A	73	TYR	N-CA-C	5.74	117.21	111.07
1	A	39	GLU	N-CA-C	-5.71	101.30	110.14
1	A	104	TRP	N-CA-C	5.70	117.49	111.28
1	A	82	LEU	CB-CA-C	5.68	120.34	110.68
1	A	37	GLY	N-CA-C	-5.66	102.84	111.10
1	A	118	PHE	N-CA-CB	5.63	118.98	110.42
1	A	25	LEU	CA-C-O	-5.63	114.28	120.30
1	A	50	LYS	N-CA-C	-5.63	105.24	111.71
1	A	89	GLY	O-C-N	5.60	128.25	122.54
1	A	39	GLU	CA-CB-CG	5.57	125.25	114.10
1	A	2	ARG	CA-C-N	5.46	131.97	121.54
1	A	2	ARG	C-N-CA	5.46	131.97	121.54
1	A	9	THR	CA-CB-OG1	-5.45	101.42	109.60
1	A	117	ARG	NE-CZ-NH1	-5.45	116.05	121.50
1	A	72	HIS	CA-C-N	5.43	127.50	120.44
1	A	72	HIS	C-N-CA	5.43	127.50	120.44
1	A	144	GLN	CA-C-O	5.43	128.28	120.51
1	A	131	GLU	CB-CG-CD	5.41	121.79	112.60
1	A	85	TRP	O-C-N	5.38	127.90	122.09
1	A	37	GLY	O-C-N	5.37	128.59	123.65
1	A	7	LEU	O-C-N	5.36	129.36	122.93
1	A	86	ARG	CA-C-N	5.34	127.44	120.28
1	A	86	ARG	C-N-CA	5.34	127.44	120.28
1	A	117	ARG	N-CA-C	-5.33	100.55	109.24
1	A	115	ARG	CD-NE-CZ	-5.29	117.00	124.40
1	A	121	VAL	O-C-N	5.24	128.26	122.66
1	A	8	PHE	CA-C-O	-5.23	114.99	120.80
1	A	138	ARG	CA-C-N	5.22	128.65	120.82
1	A	138	ARG	C-N-CA	5.22	128.65	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	ALA	O-C-N	5.21	128.68	122.27
1	A	139	ARG	O-C-N	5.21	128.10	122.11
1	A	130	ASN	CB-CG-ND2	5.12	124.09	116.40
1	A	61	GLU	CB-CG-CD	5.12	121.31	112.60
1	A	2	ARG	CA-CB-CG	5.08	124.25	114.10
1	A	9	THR	CA-CB-CG2	5.07	119.12	110.50
1	A	91	ARG	CA-C-N	5.05	128.37	120.75
1	A	91	ARG	C-N-CA	5.05	128.37	120.75
1	A	45	ASN	O-C-N	5.04	127.27	122.07
1	A	6	ALA	O-C-N	5.03	129.12	123.28
1	A	127	HIS	CA-C-N	5.03	126.12	119.84
1	A	127	HIS	C-N-CA	5.03	126.12	119.84
1	A	42	THR	CB-CA-C	-5.02	101.93	112.82
1	A	96	LYS	CB-CA-C	5.01	116.65	109.09
1	A	69	THR	CA-C-N	5.00	131.43	122.38
1	A	69	THR	C-N-CA	5.00	131.43	122.38

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	1174	0	1165	87	0
All	All	1174	0	1165	87	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 37.

All (87) 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:112:ALA:HB3	1:A:113:PRO:HD3	1.51	0.89
1:A:3:LYS:HD3	1:A:29:HIS:ND1	1.92	0.84
1:A:2:ARG:NH1	1:A:4:ARG:H	1.80	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ASN:HD22	1:A:73:TYR:HB2	1.55	0.71
1:A:10:ASP:HB2	1:A:133:VAL:HG13	1.71	0.71
1:A:43:THR:OG1	1:A:46:ARG:HG3	1.90	0.71
1:A:46:ARG:HB3	1:A:103:LEU:HD11	1.72	0.70
1:A:53:ILE:HD12	1:A:57:LYS:HG3	1.74	0.70
1:A:70:ASP:HB3	1:A:123:GLY:HA2	1.75	0.67
1:A:71:SER:HB3	1:A:74:LEU:HB2	1.77	0.66
1:A:45:ASN:HB3	1:A:73:TYR:CD2	2.31	0.66
1:A:25:LEU:HD21	1:A:32:GLU:HG2	1.78	0.66
1:A:132:ARG:HH21	1:A:132:ARG:HG2	1.61	0.65
1:A:2:ARG:NH2	1:A:64:GLU:HB3	2.11	0.65
1:A:53:ILE:CD1	1:A:57:LYS:HG3	2.28	0.64
1:A:45:ASN:HD22	1:A:73:TYR:CB	2.12	0.62
1:A:6:ALA:HB3	1:A:27:ARG:HB3	1.81	0.62
1:A:10:ASP:HB2	1:A:133:VAL:CG1	2.30	0.61
1:A:43:THR:O	1:A:44:ASN:C	2.45	0.59
1:A:140:GLN:O	1:A:144:GLN:NE2	2.24	0.58
1:A:105:GLU:O	1:A:106:ALA:C	2.48	0.57
1:A:2:ARG:HA	1:A:63:CYS:HA	1.86	0.57
1:A:21:GLY:HA2	1:A:38:GLY:HA2	1.86	0.57
1:A:2:ARG:HH12	1:A:4:ARG:HB2	1.70	0.56
1:A:37:GLY:O	1:A:140:GLN:HG2	2.06	0.56
1:A:83:GLU:O	1:A:87:LYS:HD3	2.06	0.55
1:A:21:GLY:HA3	1:A:140:GLN:HB3	1.87	0.55
1:A:47:MET:HA	1:A:47:MET:HE2	1.88	0.54
1:A:22:TRP:HB2	1:A:51:ALA:HB2	1.89	0.54
1:A:75:LYS:HA	1:A:120:PHE:CE2	2.43	0.54
1:A:4:ARG:HD3	1:A:66:ASP:OD2	2.09	0.53
1:A:7:LEU:HD21	1:A:55:GLY:HA3	1.91	0.53
1:A:90:TRP:O	1:A:98:VAL:HG13	2.08	0.52
1:A:45:ASN:ND2	1:A:73:TYR:HB2	2.24	0.52
1:A:133:VAL:HG12	1:A:134:ASP:N	2.25	0.52
1:A:124:HIS:CE1	1:A:130:ASN:HB2	2.45	0.51
1:A:3:LYS:HD3	1:A:29:HIS:CE1	2.45	0.51
1:A:3:LYS:HE2	1:A:4:ARG:N	2.26	0.51
1:A:5:VAL:HG21	1:A:63:CYS:SG	2.50	0.51
1:A:2:ARG:O	1:A:3:LYS:HB2	2.11	0.50
1:A:2:ARG:CZ	1:A:4:ARG:H	2.23	0.50
1:A:22:TRP:CH2	1:A:54:GLU:HG3	2.48	0.49
1:A:91:ARG:HG3	1:A:96:LYS:O	2.12	0.49
1:A:112:ALA:CB	1:A:113:PRO:HD3	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ARG:HH12	1:A:4:ARG:H	1.55	0.49
1:A:7:LEU:HD12	1:A:56:LEU:HD13	1.95	0.49
1:A:46:ARG:HG2	1:A:100:ASN:ND2	2.27	0.48
1:A:127:HIS:HB2	1:A:129:GLU:HG2	1.95	0.48
1:A:136:GLU:OE2	1:A:139:ARG:NH2	2.46	0.48
1:A:138:ARG:O	1:A:141:ALA:HB3	2.14	0.48
1:A:117:ARG:HD2	1:A:117:ARG:H	1.79	0.47
1:A:46:ARG:HG2	1:A:100:ASN:HD21	1.78	0.47
1:A:3:LYS:HB3	1:A:29:HIS:HE1	1.80	0.47
1:A:145:ALA:HA	1:A:146:LYS:HZ2	1.79	0.47
1:A:22:TRP:O	1:A:23:ALA:HB2	2.15	0.47
1:A:90:TRP:C	1:A:98:VAL:HG13	2.40	0.46
1:A:107:LEU:O	1:A:110:ALA:HB3	2.15	0.46
1:A:91:ARG:NH2	1:A:97:PRO:HB3	2.30	0.46
1:A:46:ARG:O	1:A:50:LYS:HB2	2.15	0.46
1:A:46:ARG:HA	1:A:103:LEU:CD1	2.46	0.46
1:A:83:GLU:OE2	1:A:86:ARG:NE	2.49	0.46
1:A:85:TRP:CD1	1:A:98:VAL:HG11	2.51	0.45
1:A:127:HIS:C	1:A:129:GLU:N	2.74	0.45
1:A:82:LEU:HA	1:A:85:TRP:CE3	2.51	0.45
1:A:130:ASN:O	1:A:134:ASP:HB2	2.17	0.45
1:A:42:THR:HB	1:A:43:THR:H	1.56	0.45
1:A:117:ARG:HD2	1:A:117:ARG:N	2.32	0.44
1:A:70:ASP:CB	1:A:123:GLY:HA2	2.46	0.44
1:A:2:ARG:HH12	1:A:4:ARG:CB	2.31	0.44
1:A:7:LEU:HD13	1:A:67:LEU:HG	2.00	0.44
1:A:46:ARG:CB	1:A:103:LEU:HD11	2.45	0.44
1:A:22:TRP:HD1	1:A:47:MET:SD	2.42	0.43
1:A:28:PHE:HB2	1:A:31:HIS:O	2.18	0.43
1:A:112:ALA:CB	1:A:113:PRO:CD	2.97	0.42
1:A:103:LEU:O	1:A:106:ALA:HB3	2.19	0.42
1:A:53:ILE:HD12	1:A:53:ILE:O	2.20	0.42
1:A:67:LEU:HD23	1:A:68:TYR:N	2.34	0.42
1:A:46:ARG:NH1	1:A:102:ASP:OD2	2.53	0.42
1:A:85:TRP:HB3	1:A:90:TRP:CE3	2.55	0.42
1:A:90:TRP:CZ3	1:A:104:TRP:HB3	2.55	0.41
1:A:26:LEU:CD2	1:A:59:LEU:HD21	2.50	0.41
1:A:3:LYS:HB3	1:A:29:HIS:CE1	2.55	0.41
1:A:30:ALA:O	1:A:31:HIS:HB3	2.21	0.41
1:A:49:LEU:HD23	1:A:103:LEU:HD12	2.04	0.40
1:A:2:ARG:NH2	1:A:4:ARG:N	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ARG:HH22	1:A:64:GLU:HB3	1.86	0.40
1:A:111:MET:HE3	1:A:116:VAL:CG1	2.51	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	145/166 (87%)	104 (72%)	31 (21%)	10 (7%)	1 2

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	31	HIS
1	A	27	ARG
1	A	76	LYS
1	A	112	ALA
1	A	122	LYS
1	A	62	PRO
1	A	77	ALA
1	A	44	ASN
1	A	98	VAL

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	116/133 (87%)	78 (67%)	38 (33%)	0 1

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	3	LYS
1	A	4	ARG
1	A	7	LEU
1	A	10	ASP
1	A	14	LEU
1	A	26	LEU
1	A	34	LEU
1	A	41	CYS
1	A	42	THR
1	A	50	LYS
1	A	53	ILE
1	A	56	LEU
1	A	61	GLU
1	A	62	PRO
1	A	81	TRP
1	A	82	LEU
1	A	83	GLU
1	A	91	ARG
1	A	98	VAL
1	A	99	LYS
1	A	101	ARG
1	A	102	ASP
1	A	103	LEU
1	A	108	LEU
1	A	109	LEU
1	A	111	MET
1	A	114	HIS
1	A	117	ARG
1	A	121	VAL
1	A	122	LYS
1	A	124	HIS
1	A	129	GLU
1	A	131	GLU
1	A	132	ARG
1	A	133	VAL
1	A	134	ASP
1	A	146	LYS

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	45	ASN
1	A	100	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.