



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:14 PM GMT

PDB ID : 1WSI
Title : Crystal structure of E.coli RNase HI active site mutant (E48A/K87A/D134N)
Authors : Tsunaka, Y.; Takano, K.; Matsumura, H.; Yamagata, Y.; Kanaya, S.
Deposited on : 2004-11-07
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

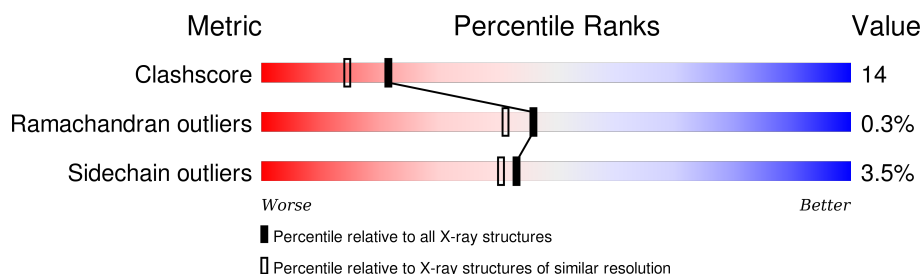
1 Overall quality at a glance

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	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	155	
1	B	155	
1	C	155	
1	D	155	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5124 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 HI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	152	Total	C	N	O	S	0	0	0
			1204	755	222	221	6			
1	B	149	Total	C	N	O	S	0	0	0
			1186	745	219	216	6			
1	C	153	Total	C	N	O	S	0	0	0
			1211	760	223	222	6			
1	D	152	Total	C	N	O	S	0	0	0
			1207	757	222	222	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	ALA	GLU	ENGINEERED	UNP P0A7Y4
A	87	ALA	LYS	ENGINEERED	UNP P0A7Y4
A	134	ASN	ASP	ENGINEERED	UNP P0A7Y4
B	48	ALA	GLU	ENGINEERED	UNP P0A7Y4
B	87	ALA	LYS	ENGINEERED	UNP P0A7Y4
B	134	ASN	ASP	ENGINEERED	UNP P0A7Y4
C	48	ALA	GLU	ENGINEERED	UNP P0A7Y4
C	87	ALA	LYS	ENGINEERED	UNP P0A7Y4
C	134	ASN	ASP	ENGINEERED	UNP P0A7Y4
D	48	ALA	GLU	ENGINEERED	UNP P0A7Y4
D	87	ALA	LYS	ENGINEERED	UNP P0A7Y4
D	134	ASN	ASP	ENGINEERED	UNP P0A7Y4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	56	Total	O	0	0
			56	56		
2	B	78	Total	O	0	0
			78	78		

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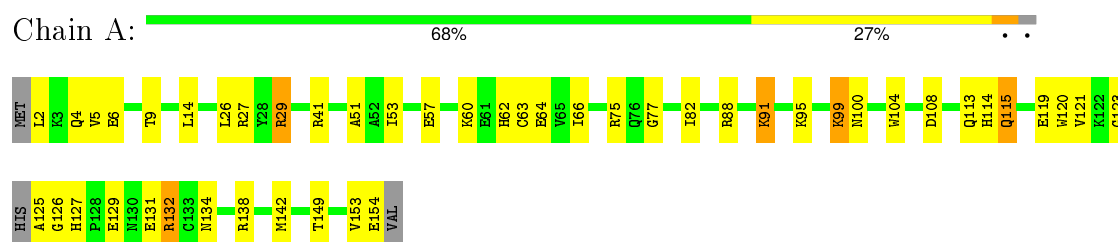
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	89	Total	O	0	0
			89	89		
2	D	93	Total	O	0	0
			93	93		

3 Residue-property plots [i](#)

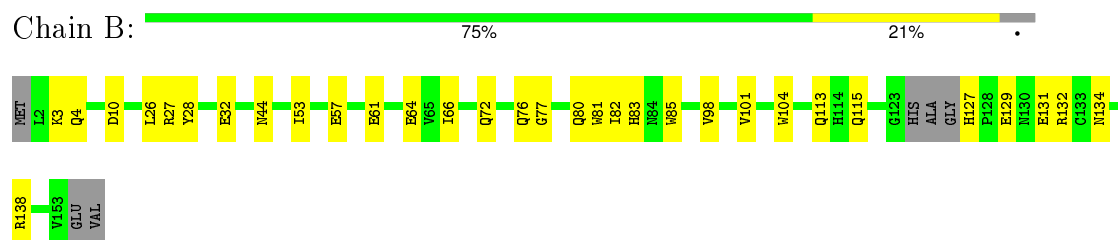
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

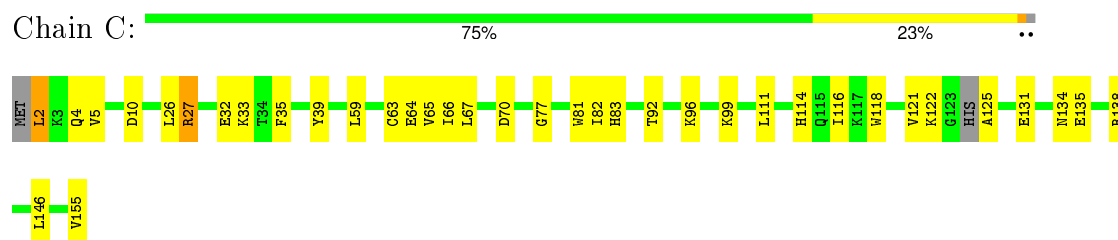
• Molecule 1: Ribonuclease HI



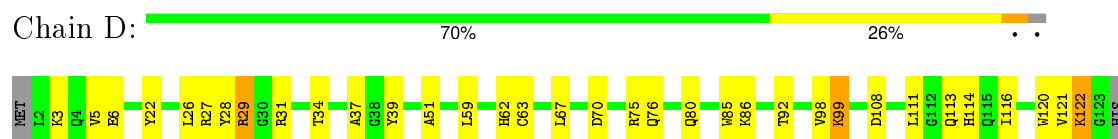
• Molecule 1: Ribonuclease HI



• Molecule 1: Ribonuclease HI



• Molecule 1: Ribonuclease HI



ALA	G126	R127	P128	E129	R132	C133	M134	R138	L146	V153	E154	V155
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	121.12Å 80.12Å 64.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.217 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5124	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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	0.30	0/1230	0.54	0/1663
1	B	0.30	0/1212	0.58	0/1639
1	C	0.33	0/1237	0.57	0/1673
1	D	0.33	0/1233	0.58	0/1666
All	All	0.32	0/4912	0.57	0/6641

There are no bond length outliers.

There are no bond angle outliers.

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	1204	0	1181	47	0
1	B	1186	0	1167	22	0
1	C	1211	0	1190	34	0
1	D	1207	0	1185	41	0
2	A	56	0	0	2	0
2	B	78	0	0	1	0
2	C	89	0	0	1	0
2	D	93	0	0	3	0
All	All	5124	0	4723	134	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 14.

All (134) 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:C:155:VAL:HG12	1:D:92:THR:HG22	1.48	0.92
1:A:121:VAL:HG12	1:A:125:ALA:HB3	1.56	0.86
1:D:29:ARG:HG2	1:D:29:ARG:O	1.75	0.84
1:C:155:VAL:HG22	1:D:85:TRP:HE1	1.46	0.81
1:B:134:ASN:HD21	1:B:138:ARG:HE	1.30	0.80
1:A:64:GLU:HA	1:A:115:GLN:HG3	1.63	0.79
1:C:155:VAL:CG1	1:D:92:THR:HG22	2.14	0.77
1:B:27:ARG:HG2	1:B:32:GLU:HG3	1.66	0.77
1:D:122:LYS:HA	1:D:122:LYS:HE3	1.67	0.77
1:A:132:ARG:O	1:A:132:ARG:HD3	1.85	0.76
1:D:28:TYR:O	1:D:29:ARG:HD3	1.86	0.75
1:A:14:LEU:HD11	1:A:142:MET:HE3	1.68	0.74
1:C:155:VAL:CG1	1:D:98:VAL:HG12	2.20	0.72
1:D:132:ARG:HG3	2:D:208:HOH:O	1.91	0.70
1:A:5:VAL:HG11	1:A:26:LEU:HD11	1.75	0.69
1:C:92:THR:HG22	1:D:155:VAL:HG22	1.73	0.68
1:A:88:ARG:HB3	1:A:91:LYS:HG2	1.76	0.66
1:B:10:ASP:OD2	1:B:134:ASN:HA	1.95	0.66
1:D:5:VAL:HG11	1:D:26:LEU:HD11	1.77	0.65
1:C:2:LEU:CD1	1:C:64:GLU:HB2	2.26	0.65
1:B:127:HIS:O	1:B:131:GLU:HG3	1.96	0.65
1:D:86:LYS:HD2	1:D:108:ASP:OD2	1.97	0.65
1:D:70:ASP:HB3	1:D:121:VAL:HG23	1.79	0.65
1:A:5:VAL:HG11	1:A:26:LEU:CD1	2.29	0.62
1:A:82:ILE:HD11	1:A:108:ASP:HB2	1.80	0.62
1:A:127:HIS:HB3	1:A:129:GLU:OE2	1.99	0.62
1:B:98:VAL:HG23	1:B:101:VAL:HB	1.81	0.61
1:D:29:ARG:NH2	1:D:31:ARG:HD2	2.17	0.60
1:C:92:THR:HG22	1:D:155:VAL:CG2	2.31	0.59
1:A:121:VAL:CG1	1:A:125:ALA:HB3	2.30	0.59
1:A:99:LYS:HD2	1:A:100:ASN:ND2	2.19	0.58
1:A:66:ILE:HG23	1:A:66:ILE:O	2.05	0.56
1:B:3:LYS:HD2	1:B:28:TYR:CZ	2.40	0.56
1:D:5:VAL:HG11	1:D:26:LEU:CD1	2.36	0.56
1:A:4:GLN:HB3	1:A:64:GLU:CD	2.26	0.56
1:A:5:VAL:HG12	1:A:6:GLU:N	2.20	0.55
1:C:27:ARG:HG3	1:C:32:GLU:HG2	1.88	0.55
1:A:62:HIS:HD2	1:A:113:GLN:O	1.89	0.55
1:D:134:ASN:HD21	1:D:138:ARG:NE	2.05	0.55
1:A:91:LYS:HZ2	1:A:95:LYS:HA	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:GLU:CD	1:B:129:GLU:H	2.10	0.55
1:B:82:ILE:HG23	1:B:83:HIS:N	2.23	0.54
1:A:115:GLN:HG3	1:A:115:GLN:O	2.08	0.53
1:A:82:ILE:HD11	1:A:108:ASP:CB	2.37	0.53
1:D:62:HIS:HD2	1:D:113:GLN:O	1.90	0.53
1:D:27:ARG:NH2	1:D:129:GLU:OE1	2.42	0.52
1:C:4:GLN:HE22	1:C:64:GLU:CD	2.13	0.52
1:C:99:LYS:HE2	1:D:154:GLU:OE2	2.09	0.52
1:D:29:ARG:HH22	1:D:31:ARG:HH11	1.56	0.52
1:C:155:VAL:HG13	1:D:98:VAL:HG12	1.92	0.52
1:A:64:GLU:HG3	1:A:64:GLU:O	2.10	0.52
1:B:3:LYS:HE2	1:B:61:GLU:CD	2.31	0.51
1:C:134:ASN:ND2	1:C:138:ARG:HD2	2.26	0.51
1:D:5:VAL:HG12	1:D:6:GLU:N	2.24	0.51
1:A:29:ARG:HA	1:A:29:ARG:CZ	2.40	0.51
1:A:2:LEU:N	2:A:170:HOH:O	2.43	0.51
1:C:2:LEU:HD13	1:C:64:GLU:HB2	1.94	0.50
1:A:77:GLY:HA3	1:A:104:TRP:CH2	2.47	0.50
1:C:65:VAL:HB	1:C:116:ILE:HD13	1.92	0.50
1:A:153:VAL:O	1:A:154:GLU:HB2	2.10	0.50
1:D:111:LEU:HD22	1:D:116:ILE:HG13	1.94	0.50
1:C:70:ASP:HB3	1:C:121:VAL:HG23	1.94	0.49
1:A:123:GLY:HA2	1:A:126:GLY:HA3	1.93	0.49
1:D:70:ASP:CB	1:D:121:VAL:HG23	2.42	0.49
1:A:123:GLY:HA2	1:A:126:GLY:CA	2.43	0.49
1:C:134:ASN:HD21	1:C:138:ARG:HD2	1.78	0.49
1:C:155:VAL:HG21	2:D:184:HOH:O	2.13	0.49
1:A:63:CYS:O	1:A:114:HIS:HB3	2.13	0.48
1:C:4:GLN:NE2	1:C:64:GLU:HB3	2.28	0.48
1:B:32:GLU:CD	1:B:132:ARG:HH22	2.17	0.48
1:A:132:ARG:C	1:A:132:ARG:HD3	2.33	0.48
1:B:85:TRP:CD1	1:B:98:VAL:HG11	2.49	0.47
1:C:67:LEU:HD22	1:C:118:TRP:CZ3	2.49	0.47
1:C:92:THR:HA	1:D:155:VAL:HG11	1.95	0.47
1:D:34:THR:HG22	2:D:244:HOH:O	2.15	0.47
1:A:75:ARG:HA	1:A:120:TRP:CH2	2.49	0.47
1:C:5:VAL:HG11	1:C:26:LEU:HD11	1.97	0.47
1:D:153:VAL:HG12	1:D:155:VAL:HG13	1.97	0.47
1:D:70:ASP:HB3	1:D:121:VAL:CG2	2.43	0.47
1:A:4:GLN:HB3	1:A:64:GLU:CG	2.44	0.47
1:B:53:ILE:O	1:B:57:GLU:HG3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:LEU:HD11	1:A:142:MET:CE	2.39	0.47
1:D:99:LYS:HB3	1:D:99:LYS:NZ	2.31	0.46
1:B:4:GLN:OE1	1:B:66:ILE:HD11	2.15	0.46
1:B:98:VAL:CG2	1:B:101:VAL:HB	2.46	0.46
1:C:155:VAL:HG11	1:D:98:VAL:HG12	1.96	0.46
1:B:134:ASN:ND2	1:B:138:ARG:HE	2.05	0.46
1:A:88:ARG:CB	1:A:91:LYS:HG2	2.43	0.46
1:B:44:ASN:ND2	2:B:203:HOH:O	2.48	0.46
1:C:26:LEU:HD11	1:C:59:LEU:HD21	1.97	0.45
1:C:122:LYS:O	1:C:125:ALA:N	2.49	0.45
1:D:26:LEU:HD11	1:D:59:LEU:HD21	1.98	0.45
1:D:5:VAL:CG1	1:D:6:GLU:N	2.79	0.45
1:C:82:ILE:HG23	1:C:83:HIS:N	2.32	0.45
1:A:53:ILE:O	1:A:57:GLU:HG3	2.17	0.45
1:A:115:GLN:HE21	1:A:115:GLN:HB2	1.58	0.45
1:D:76:GLN:O	1:D:80:GLN:HB2	2.17	0.45
1:B:26:LEU:C	1:B:26:LEU:HD23	2.36	0.45
1:A:9:THR:HB	1:A:51:ALA:HB1	1.99	0.45
1:A:119:GLU:HG2	1:A:121:VAL:HG13	2.00	0.44
1:D:75:ARG:HG3	1:D:120:TRP:CD2	2.52	0.44
1:D:134:ASN:HD21	1:D:138:ARG:HE	1.64	0.44
1:A:134:ASN:ND2	1:A:138:ARG:HE	2.16	0.43
1:C:77:GLY:HA2	1:C:81:TRP:CE3	2.53	0.43
1:A:5:VAL:CG1	1:A:6:GLU:N	2.81	0.43
1:B:76:GLN:O	1:B:80:GLN:HB2	2.19	0.43
1:A:4:GLN:HA	1:A:64:GLU:HG2	2.01	0.43
1:A:5:VAL:HG13	1:A:27:ARG:O	2.19	0.43
1:C:131:GLU:O	1:C:135:GLU:HG3	2.18	0.43
1:D:22:TYR:HB2	1:D:51:ALA:HB2	2.01	0.42
1:C:63:CYS:O	1:C:114:HIS:HB3	2.18	0.42
1:D:153:VAL:HG12	1:D:155:VAL:H	1.84	0.42
1:C:10:ASP:HA	2:C:234:HOH:O	2.17	0.42
1:C:111:LEU:HD22	1:C:116:ILE:HG13	2.01	0.42
1:A:64:GLU:HA	1:A:115:GLN:CG	2.44	0.41
1:D:22:TYR:CE2	1:D:37:ALA:HB3	2.55	0.41
1:C:66:ILE:O	1:C:66:ILE:HG23	2.20	0.41
1:A:29:ARG:HB2	1:A:29:ARG:NH1	2.35	0.41
1:B:77:GLY:HA3	1:B:104:TRP:CH2	2.56	0.41
1:C:92:THR:HG23	1:C:96:LYS:O	2.19	0.41
1:B:134:ASN:HD21	1:B:138:ARG:NE	2.07	0.41
1:C:33:LYS:HD2	1:C:35:PHE:HZ	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ARG:HB3	1:A:91:LYS:CG	2.49	0.41
1:A:29:ARG:HB2	1:A:29:ARG:HH11	1.86	0.41
1:A:9:THR:HB	1:A:51:ALA:CB	2.50	0.41
1:B:64:GLU:HA	1:B:115:GLN:HB3	2.03	0.41
1:D:3:LYS:HD2	1:D:28:TYR:CZ	2.55	0.41
1:D:39:TYR:HA	1:D:146:LEU:O	2.21	0.41
1:B:77:GLY:HA2	1:B:81:TRP:CE3	2.56	0.40
1:D:63:CYS:O	1:D:114:HIS:HB3	2.21	0.40
1:A:29:ARG:HA	1:A:29:ARG:NE	2.36	0.40
1:C:39:TYR:HA	1:C:146:LEU:O	2.21	0.40
1:A:77:GLY:O	1:A:82:ILE:HG22	2.21	0.40
1:A:60:LYS:HE2	2:A:204:HOH:O	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	148/155 (96%)	135 (91%)	13 (9%)	0	100	100
1	B	145/155 (94%)	141 (97%)	4 (3%)	0	100	100
1	C	149/155 (96%)	145 (97%)	4 (3%)	0	100	100
1	D	148/155 (96%)	142 (96%)	4 (3%)	2 (1%)	14	6
All	All	590/620 (95%)	563 (95%)	25 (4%)	2 (0%)	46	41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	127	HIS
1	D	128	PRO

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	122/125 (98%)	114 (93%)	8 (7%)	21	14
1	B	121/125 (97%)	119 (98%)	2 (2%)	68	71
1	C	123/125 (98%)	121 (98%)	2 (2%)	70	73
1	D	123/125 (98%)	118 (96%)	5 (4%)	37	32
All	All	489/500 (98%)	472 (96%)	17 (4%)	43	40

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ARG
1	A	41	ARG
1	A	91	LYS
1	A	99	LYS
1	A	115	GLN
1	A	131	GLU
1	A	132	ARG
1	A	149	THR
1	B	72	GLN
1	B	113	GLN
1	C	2	LEU
1	C	27	ARG
1	D	29	ARG
1	D	67	LEU
1	D	99	LYS
1	D	122	LYS
1	D	127	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	62	HIS

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Mol	Chain	Res	Type
1	A	72	GLN
1	A	105	GLN
1	A	134	ASN
1	A	143	ASN
1	A	152	GLN
1	B	62	HIS
1	B	72	GLN
1	B	76	GLN
1	B	80	GLN
1	B	84	ASN
1	B	105	GLN
1	B	113	GLN
1	B	115	GLN
1	B	134	ASN
1	B	143	ASN
1	B	152	GLN
1	C	4	GLN
1	C	45	ASN
1	C	84	ASN
1	C	105	GLN
1	C	134	ASN
1	C	143	ASN
1	C	152	GLN
1	D	45	ASN
1	D	62	HIS
1	D	76	GLN
1	D	105	GLN
1	D	130	ASN
1	D	134	ASN
1	D	143	ASN
1	D	152	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.