

# Full wwPDB X-ray Structure Validation Report (i)

### Feb 4, 2024 – 11:58 AM EST

PDB ID	:	1RLV
Title	:	Crystal structure of a dimeric Archaeal Splicing Endonuclease
Authors	:	Li, H.; Abelson, J.
Deposited on	:	2003-11-26
Resolution	:	3.00 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 (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\;DIFFRACTION$ 

The reported resolution of this entry is 3.00 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 <=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	Qua	lity of chain		
1	А	305	.% ■ 44%	39%	16%	
1	В	305	% 44%	40%	16%	



#### $1 \mathrm{RLV}$

## 2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 5058 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 Putative tRNA-intron endonuclease.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	304	Total	С	Ν	0	$\mathbf{S}$	0	0	0
1	Л	504	2529	1618	433	472	6	0	0	0
1	р	204	Total	С	Ν	0	S	0	0	0
	Ъ	504	2529	1618	433	472	6		U	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	152	VAL	ILE	conflict	UNP O29362
В	152	VAL	ILE	conflict	UNP O29362



# 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: Putative tRNA-intron endonuclease







# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 43 21 2	Depositor	
Cell constants	126.82Å 126.82Å 130.23Å	Deperitor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor	
$\mathbf{P}_{\text{oscolution}}(\hat{\mathbf{A}})$	19.92 - 3.00	Depositor	
Resolution (A)	19.92 - 3.00	EDS	
% Data completeness	97.0 (19.92-3.00)	Depositor	
(in resolution range)	$97.1\ (19.92\text{-}3.00)$	EDS	
R <sub>merge</sub>	(Not available)	Depositor	
R <sub>sym</sub>	(Not available)	Depositor	
$< I/\sigma(I) > 1$	4.07 (at 2.98Å)	Xtriage	
Refinement program	CNS 1.1	Depositor	
D D	0.229 , $0.276$	Depositor	
$\Lambda, \Lambda_{free}$	0.271 , $0.259$	DCC	
$R_{free}$ test set	1027 reflections $(4.86%)$	wwPDB-VP	
Wilson B-factor $(Å^2)$	52.9	Xtriage	
Anisotropy	0.514	Xtriage	
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.38 , $85.5$	EDS	
L-test for twinning <sup>2</sup>	$<  L  > = 0.49, < L^2 > = 0.33$	Xtriage	
Estimated twinning fraction	0.016 for -h,l,k	Vtriago	
Estimated twinning fraction	0.014 for -l,-k,-h	Atriage	
$F_o, F_c$ correlation	0.87	EDS	
Total number of atoms	5058	wwPDB-VP	
Average B, all atoms $(Å^2)$	45.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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).

Mal	Chain	Bond	lengths	Bond angles	
	Ullalli	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.33	0/2573	0.53	0/3451
1	В	0.33	0/2573	0.53	0/3451
All	All	0.33	0/5146	0.53	0/6902

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	А	2529	0	2545	169	0
1	В	2529	0	2545	160	0
All	All	5058	0	5090	304	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 30.

All (304) 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:280:ARG:HA	1:A:302:ARG:HH22	1.17	1.08	
1:B:280:ARG:HA	1:B:302:ARG:HH22	1.16	1.06	



		Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlan (Å)
1.A.284.ASN.HB3	1·B·284·ASN·HD22	1.31	0.94
1:B:273:ILE:HD12	1:B:273:ILE:H	1.32	0.94
1.A.284.ASN.HD22	1.B.284.ASN.HB3	1.32	0.93
1:A:273:ILE:H	1:A:273:ILE:HD12	1.32	0.93
1:B:39:GLN:HE22	1:B:46:PHE:H	1.20	0.90
1:B:266:ASP:HB3	1:B:293:TYB:HA	1.54	0.89
1:A:39:GLN:HE22	1:A:46:PHE:H	1.23	0.86
1:A:266:ASP:HB3	1:A:293:TYR:HA	1.54	0.85
1:B:150:ALA:H	1:B:162:GLN:HE21	1.24	0.85
1:A:150:ALA:H	1:A:162:GLN:HE21	1.23	0.83
1:A:214:ARG:HH22	1:B:271:ARG:HG2	1.46	0.80
1:A:149:ILE:HB	1:A:162:GLN:HG3	1.64	0.80
1:A:153:LEU:H	1:A:199:ASN:HD21	1.30	0.79
1:A:24:ARG:HB2	1:A:24:ARG:HH11	1.48	0.79
1:A:92:PRO:HG2	1:A:117:LEU:HA	1.66	0.78
1:A:271:ARG:HG2	1:B:214:ARG:HH22	1.47	0.78
1:B:24:ARG:HH11	1:B:24:ARG:HB2	1.49	0.78
1:B:153:LEU:H	1:B:199:ASN:HD21	1.30	0.77
1:A:39:GLN:HE21	1:A:52:VAL:HG21	1.48	0.77
1:B:149:ILE:HB	1:B:162:GLN:HG3	1.64	0.77
1:A:214:ARG:NH2	1:B:271:ARG:HG2	2.01	0.76
1:B:92:PRO:HG2	1:B:117:LEU:HA	1.67	0.76
1:B:39:GLN:HE21	1:B:52:VAL:HG21	1.52	0.75
1:A:232:VAL:HB	1:A:246:TYR:HB2	1.68	0.75
1:B:232:VAL:HB	1:B:246:TYR:HB2	1.68	0.74
1:B:39:GLN:NE2	1:B:46:PHE:H	1.84	0.74
1:A:271:ARG:HG2	1:B:214:ARG:NH2	2.03	0.73
1:A:212:VAL:HG23	1:A:213:GLU:HG2	1.71	0.72
1:B:280:ARG:HA	1:B:302:ARG:NH2	2.00	0.72
1:A:280:ARG:HA	1:A:302:ARG:NH2	2.00	0.72
1:A:39:GLN:NE2	1:A:46:PHE:H	1.88	0.71
1:B:212:VAL:HG23	1:B:213:GLU:HG2	1.72	0.71
1:A:284:ASN:ND2	1:B:284:ASN:HB3	2.05	0.71
1:A:107:ILE:HD11	1:A:133:VAL:HG11	1.72	0.71
1:A:150:ALA:H	1:A:162:GLN:NE2	1.89	0.71
1:B:150:ALA:H	1:B:162:GLN:NE2	1.89	0.70
1:B:249:VAL:HG13	1:B:254:ASP:HB2	1.74	0.70
1:A:249:VAL:HG13	1:A:254:ASP:HB2	1.73	0.70
1:A:180:THR:HG21	1:B:126:SER:HB3	1.72	0.70
1:A:284:ASN:HB3	1:B:284:ASN:ND2	2.04	0.70
1:B:84:GLY:O	1:B:85:GLU:HB3	1.91	0.69



	louo pugom	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:146:LEU:O	1:A:194:LYS:HE3	1.92	0.69
1:B:146:LEU:O	1:B:194:LYS:HE3	1.92	0.69
1:A:39:GLN:NE2	1:A:52:VAL:HG21	2.07	0.69
1:B:107:ILE:HD11	1:B:133:VAL:HG11	1.73	0.68
1:B:158:VAL:HG22	1:B:181:LEU:HB2	1.75	0.68
1:A:142:GLN:HE22	1:A:249:VAL:H	1.40	0.68
1:B:24:ARG:O	1:B:24:ARG:HG3	1.93	0.68
1:A:24:ARG:HG3	1:A:24:ARG:O	1.95	0.67
1:A:158:VAL:HG22	1:A:181:LEU:HB2	1.76	0.67
1:B:39:GLN:NE2	1:B:52:VAL:HG21	2.10	0.67
1:A:15:LEU:HD23	1:A:18:ARG:NH2	2.10	0.66
1:A:197:LEU:HD13	1:A:200:ALA:HB3	1.77	0.66
1:B:197:LEU:HD13	1:B:200:ALA:HB3	1.77	0.66
1:B:15:LEU:HD23	1:B:18:ARG:NH2	2.10	0.66
1:B:142:GLN:HE22	1:B:249:VAL:H	1.42	0.65
1:A:126:SER:HB3	1:B:180:THR:HG21	1.77	0.64
1:B:41:LYS:HE2	1:B:75:ASP:OD2	1.98	0.64
1:A:84:GLY:O	1:A:85:GLU:HB3	1.98	0.64
1:A:2:ILE:HG12	1:A:3:GLY:H	1.63	0.63
1:B:2:ILE:HG12	1:B:3:GLY:H	1.63	0.63
1:A:237:PHE:CE1	1:B:98:GLU:HB2	2.34	0.63
1:A:41:LYS:HE2	1:A:75:ASP:OD2	1.99	0.63
1:A:273:ILE:H	1:A:273:ILE:CD1	2.09	0.62
1:A:98:GLU:HB2	1:B:237:PHE:CE1	2.35	0.62
1:B:153:LEU:N	1:B:199:ASN:HD21	1.97	0.62
1:A:153:LEU:HD12	1:A:158:VAL:HG12	1.81	0.61
1:A:107:ILE:HD11	1:A:133:VAL:HG21	1.82	0.61
1:A:226:LEU:HB3	1:A:233:VAL:HG21	1.83	0.61
1:A:281:LEU:HD21	1:B:280:ARG:HG2	1.83	0.61
1:A:280:ARG:HG2	1:B:281:LEU:HD21	1.82	0.61
1:B:226:LEU:HB3	1:B:233:VAL:HG21	1.82	0.61
1:A:160:THR:OG1	1:A:162:GLN:HG2	2.01	0.60
1:B:153:LEU:HD12	1:B:158:VAL:HG12	1.83	0.59
1:A:222:VAL:HG23	1:A:226:LEU:HD22	1.83	0.59
1:A:2:ILE:HG23	1:A:3:GLY:N	2.17	0.59
1:A:265:ALA:HA	1:A:268:ARG:NH1	2.17	0.59
1:A:197:LEU:HB3	1:A:200:ALA:O	2.03	0.59
1:A:208:ARG:O	1:A:211:GLU:HB2	2.03	0.59
1:B:107:ILE:HD11	1:B:133:VAL:HG21	1.83	0.59
1:B:142:GLN:NE2	1:B:249:VAL:H	2.01	0.59
1:A:126:SER:OG	1:B:175:LYS:HE2	2.03	0.59



	lo ao pagom	Interatomic Clash			
Atom-1	Atom-2	distance (Å)	overlap (Å)		
1:A:153:LEU:N	1:A:199:ASN:HD21	1.98	0.58		
1:B:20:PHE:HD2	1:B:34:GLU:HG2	1.67	0.58		
1:B:266:ASP:CB	1:B:293:TYR:HA	2.31	0.58		
1:B:2:ILE:HG23	1:B:3:GLY:N	2.18	0.58		
1:B:160:THR:OG1	1:B:162:GLN:HG2	2.02	0.58		
1:A:142:GLN:NE2	1:A:249:VAL:H	2.00	0.58		
1:B:89:THR:C	1:B:91:LYS:H	2.06	0.58		
1:B:152:VAL:HA	1:B:199:ASN:ND2	2.19	0.58		
1:B:208:ARG:O	1:B:211:GLU:HB2	2.03	0.58		
1:A:89:THR:C	1:A:91:LYS:H	2.07	0.58		
1:A:102:ILE:HD11	1:A:275:LEU:HD13	1.86	0.58		
1:B:102:ILE:HD11	1:B:275:LEU:HD13	1.85	0.58		
1:A:199:ASN:H	1:A:199:ASN:HD22	1.52	0.57		
1:B:197:LEU:HB3	1:B:200:ALA:O	2.04	0.57		
1:A:20:PHE:HD2	1:A:34:GLU:HG2	1.68	0.57		
1:B:102:ILE:HD11	1:B:275:LEU:CD1	2.34	0.57		
1:A:102:ILE:HD11	1:A:275:LEU:CD1	2.35	0.57		
1:B:222:VAL:HG23	1:B:226:LEU:HD22	1.85	0.57		
1:B:117:LEU:HD22	1:B:118:ARG:N	2.20	0.56		
1:A:152:VAL:HA	1:A:199:ASN:ND2	2.19	0.56		
1:A:117:LEU:HD22	1:A:118:ARG:N	2.20	0.56		
1:B:265:ALA:HA	1:B:268:ARG:NH1	2.19	0.56		
1:A:212:VAL:HG23	1:A:213:GLU:N	2.21	0.56		
1:B:92:PRO:HG3	1:B:114:PHE:HB3	1.88	0.56		
1:A:207:LYS:HE3	1:A:207:LYS:O	2.06	0.55		
1:B:199:ASN:HD22	1:B:199:ASN:H	1.53	0.55		
1:B:212:VAL:HG23	1:B:213:GLU:N	2.22	0.55		
1:A:244:ARG:HD2	1:A:246:TYR:OH	2.07	0.55		
1:A:92:PRO:HG3	1:A:114:PHE:HB3	1.87	0.55		
1:B:85:GLU:HG2	1:B:86:PHE:CE1	2.42	0.55		
1:A:266:ASP:CB	1:A:293:TYR:HA	2.32	0.55		
1:A:121:VAL:HG13	1:A:272:LEU:HD13	1.90	0.54		
1:A:120:ALA:HB1	1:A:128:ILE:HD13	1.90	0.54		
1:B:176:GLY:O	1:B:177:ASP:HB2	2.08	0.54		
1:B:121:VAL:HG13	1:B:272:LEU:HD13	1.90	0.54		
1:B:150:ALA:CB	1:B:196:ASN:HB3	2.38	0.54		
1:B:280:ARG:HD2	1:B:302:ARG:NH2	2.22	0.53		
1:A:280:ARG:HD2	1:A:302:ARG:NH2	2.23	0.53		
1:B:207:LYS:HE3	1:B:207:LYS:O	2.07	0.53		
1:A:184:ILE:HG23	1:A:185:GLU:N	2.24	0.53		
1:A:244:ARG:HG3	1:A:258:SER:CB	2.39	0.53		



	Interatomic	Clash			
Atom-1	Atom-2	distance $(Å)$	overlap (Å)		
1·A·176·GLY·O	1.A.177.ASP.HB2	2.07	0.53		
1:A:228:GLU:O	1:A:228:GLU:HG2	2.09	0.53		
1·B·222·VAL·O	1·B·226·LEU·HD22	2.09	0.53		
1:A:226:LEU:O	$1 \cdot A \cdot 231 \cdot PHE \cdot HB2$	2.08	0.53		
1:A:85:GLU:HG2	1:A:86:PHE:CE1	2.44	0.52		
1:B:244:ABG:HG3	1:B:258:SEB:CB	2.39	0.52		
1:A:150:ALA:CB	1:A:196:ASN:HB3	2.40	0.52		
1:B:244:ARG:HD2	1:B:246:TYR:OH	2.10	0.52		
1:B:226:LEU:O	1:B:231:PHE:HB2	2.10	0.51		
1:A:224:ARG:HH11	1:A:224:ABG:HB3	1.75	0.51		
1:B:120:ALA:HB1	1:B:128:ILE:HD13	1.92	0.51		
1:B:224:ARG:HH11	1:B:224:ABG:HB3	1.76	0.51		
1.B.228.GLU.O	1·B·228·GLU·HG2	2.09	0.51		
1:A:24:ABG:HG2	1:A:29:TYB:CE1	2.46	0.51		
1:A:240:GLY:HA3	1·B·277·ARG·HB2	1.92	0.51		
1·A·277·ABG·HB2	1·B·240·GLY·HA3	1.92	0.51		
1.B.273.ILE.H	1.B.273.ILE.CD1	2.08	0.50		
1.B.14.SEB.HB2	1·B·18·ARG·HH12	1.76	0.50		
1.B.104.MET.HE1	1.B.300.PHE.HE1	1.70	0.50		
1.B.184.ILE.HG23	1.B.185.GLU·N	2.25	0.50		
1:A:14:SEB:HB2	1·A·18·ARG·HH12	1.77	0.50		
1:A:225:ASN:OD1	1:A:229:ABG:HD2	2.11	0.50		
1·B·20·PHE·CD2	1·B·34·GLU·HG2	2.45	0.50		
1:B:70:TYB:CE2	1:B:74:ABG:HG3	2.47	0.50		
1:A:20:PHE:CD2	1:A:34:GLU:HG2	2.46	0.50		
1:B:168:ARG:NH2	1:B:169:TYR:OH	2.44	0.50		
1:B:156:GLU:HB3	1:B:157:TYB:CE1	2.47	0.49		
1:A:116:GLU:HB3	1:A:118:ARG:HH21	1.77	0.49		
1:B:266:ASP:HB3	1:B:294:GLY:H	1.76	0.49		
1:A:266:ASP:HB3	1:A:294:GLY:H	1.77	0.49		
1:A:24:ARG:HG2	1:A:29:TYR:HE1	1.77	0.49		
1:B:225:ASN:OD1	1:B:229:ARG:HD2	2.12	0.49		
1:A:222:VAL:O	1:A:226:LEU:HD22	2.13	0.49		
1:A:254:ASP:C	1:A:256:PRO:HD2	2.32	0.49		
1:A:277:ARG:HG2	1:B:277:ARG:HD3	1.95	0.48		
1:B:254:ASP:C	1:B:256:PRO:HD2	2.33	0.48		
1:A:70:TYR:CE2	1:A:74:ARG:HG3	2.47	0.48		
1:A:156:GLU:HB3	1:A:157:TYR:CE1	2.48	0.48		
1:B:116:GLU:HB3	1:B:118:ARG:HH21	1.78	0.48		
1:A:24:ARG:CG	1:A:29:TYR:HE1	2.27	0.48		
1:A:96:ILE:HG21	1:A:119:LEU:HD22	1.96	0.48		



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:168:ARG:NH2	1:A:169:TYR:OH	2.44	0.48
1:B:24:ARG:HG2	1:B:29:TYR:CE1	2.48	0.48
1:A:266:ASP:O	1:A:266:ASP:OD2	2.32	0.47
1:A:128:ILE:HD11	1:A:130:TYR:CD2	2.50	0.47
1:A:219:ARG:HE	1:A:242:GLU:HG3	1.79	0.47
1:B:219:ARG:HE	1:B:242:GLU:HG3	1.78	0.47
1:B:8:VAL:HG12	1:B:29:TYR:CD2	2.50	0.47
1:B:24:ARG:HG2	1:B:29:TYR:HE1	1.79	0.47
1:B:280:ARG:CA	1:B:302:ARG:HH22	2.06	0.47
1:A:171:TYR:CD2	1:A:189:LEU:HD11	2.50	0.46
1:A:118:ARG:HD3	1:A:305:VAL:O	2.15	0.46
1:A:13:LYS:O	1:A:17:ARG:HG3	2.16	0.46
1:A:192:LEU:HD23	1:A:194:LYS:HD2	1.97	0.46
1:A:36:VAL:HG21	1:A:63:PHE:CZ	2.51	0.46
1:A:154:SER:HB2	1:A:159:ILE:HD12	1.96	0.46
1:A:191:ASP:OD1	1:A:202:ARG:NH1	2.49	0.46
1:B:24:ARG:CG	1:B:29:TYR:HE1	2.29	0.46
1:A:33:LEU:HD13	1:A:60:MET:SD	2.56	0.46
1:A:142:GLN:NE2	1:A:248:LYS:HA	2.31	0.46
1:B:171:TYR:CD2	1:B:189:LEU:HD11	2.51	0.46
1:A:152:VAL:HA	1:A:199:ASN:HD21	1.81	0.45
1:A:175:LYS:HE2	1:B:126:SER:OG	2.16	0.45
1:B:14:SER:HB2	1:B:18:ARG:NH1	2.31	0.45
1:B:104:MET:CE	1:B:300:PHE:HE1	2.28	0.45
1:B:266:ASP:O	1:B:266:ASP:OD2	2.33	0.45
1:A:14:SER:HB2	1:A:18:ARG:NH1	2.31	0.45
1:A:280:ARG:CA	1:A:302:ARG:HH22	2.06	0.45
1:B:150:ALA:HB2	1:B:196:ASN:HB3	1.97	0.45
1:A:150:ALA:HB2	1:A:196:ASN:HB3	1.99	0.45
1:A:277:ARG:HD3	1:B:277:ARG:HG2	1.97	0.45
1:B:154:SER:O	1:B:155:ASP:O	2.35	0.45
1:B:85:GLU:HG2	1:B:86:PHE:CD1	2.51	0.45
1:A:155:ASP:HB3	1:B:57:GLU:OE1	2.17	0.45
1:A:213:GLU:HB2	1:A:216:PHE:HB2	1.98	0.45
1:A:104:MET:CE	1:A:298:LEU:HB3	2.47	0.45
1:A:104:MET:CE	1:A:300:PHE:HE1	2.29	0.45
1:A:182:SER:OG	1:A:184:ILE:HG22	2.17	0.45
1:B:96:ILE:HG21	1:B:119:LEU:HD22	1.98	0.45
1:B:152:VAL:HA	1:B:199:ASN:HD21	1.80	0.45
1:A:206:VAL:HG23	1:A:207:LYS:N	2.32	0.45
1:B:199:ASN:ND2	1:B:199:ASN:H	2.15	0.45



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:156:GLU:O	1:A:183:LEU:HD13	2.17	0.45
1:B:213:GLU:HB2	1:B:216:PHE:HB2	1.99	0.45
1:B:258:SER:OG	1:B:287:LYS:HE3	2.17	0.45
1:A:199:ASN:HD22	1:A:199:ASN:N	2.15	0.44
1:B:31:HIS:ND1	1:B:33:LEU:HB2	2.33	0.44
1:B:154:SER:HB2	1:B:159:ILE:HD12	1.98	0.44
1:A:85:GLU:HG2	1:A:86:PHE:CD1	2.52	0.44
1:B:142:GLN:NE2	1:B:248:LYS:HA	2.32	0.44
1:B:266:ASP:HA	1:B:293:TYR:HB2	2.00	0.44
1:B:24:ARG:HH11	1:B:24:ARG:CB	2.26	0.44
1:B:118:ARG:HD3	1:B:305:VAL:O	2.17	0.44
1:B:244:ARG:HG3	1:B:258:SER:HB3	2.00	0.44
1:A:244:ARG:HG3	1:A:258:SER:HB3	2.00	0.44
1:A:285:VAL:HG22	1:A:285:VAL:O	2.18	0.44
1:B:191:ASP:OD1	1:B:202:ARG:NH1	2.51	0.44
1:B:206:VAL:HG23	1:B:207:LYS:N	2.32	0.44
1:B:206:VAL:O	1:B:210:ARG:HG3	2.17	0.44
1:A:226:LEU:HB3	1:A:233:VAL:CG2	2.48	0.44
1:A:184:ILE:CG2	1:A:185:GLU:N	2.80	0.44
1:A:214:ARG:HH22	1:B:271:ARG:CG	2.25	0.44
1:A:266:ASP:HA	1:A:293:TYR:HB2	1.99	0.44
1:B:239:PHE:HE2	1:B:285:VAL:HG21	1.83	0.44
1:B:104:MET:CE	1:B:298:LEU:HB3	2.48	0.43
1:A:59:ARG:HD3	1:A:59:ARG:HA	1.84	0.43
1:A:239:PHE:HE2	1:A:285:VAL:HG21	1.83	0.43
1:B:13:LYS:O	1:B:17:ARG:HG3	2.17	0.43
1:B:26:ASP:OD1	1:B:26:ASP:N	2.51	0.43
1:B:192:LEU:HD23	1:B:194:LYS:HD2	1.99	0.43
1:A:57:GLU:OE1	1:B:155:ASP:HB3	2.18	0.43
1:A:298:LEU:HD23	1:A:298:LEU:HA	1.82	0.43
1:A:258:SER:OG	1:A:287:LYS:HE3	2.18	0.43
1:B:182:SER:OG	1:B:184:ILE:HG22	2.19	0.43
1:A:237:PHE:CD1	1:B:98:GLU:HB2	2.53	0.43
1:B:265:ALA:O	1:B:266:ASP:C	2.57	0.43
1:A:182:SER:HA	1:B:124:GLU:O	2.18	0.43
1:B:24:ARG:O	1:B:24:ARG:CG	2.66	0.43
1:B:128:ILE:HD12	1:B:129:THR:N	2.33	0.43
1:A:213:GLU:OE2	1:A:219:ARG:HD3	2.19	0.43
1:B:33:LEU:HD13	1:B:60:MET:SD	2.58	0.43
1:A:31:HIS:CG	1:A:32:PRO:HD2	2.54	0.42
1:A:89:THR:HG23	1:A:93:TYR:HE1	1.84	0.42



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:265:ALA:O	1:A:266:ASP:C	2.57	0.42
1:B:117:LEU:HD22	1:B:118:ARG:H	1.82	0.42
1:A:36:VAL:HG21	1:A:63:PHE:HZ	1.84	0.42
1:A:199:ASN:H	1:A:199:ASN:ND2	2.15	0.42
1:B:156:GLU:O	1:B:183:LEU:HD13	2.19	0.42
1:A:8:VAL:HG12	1:A:29:TYR:CD2	2.55	0.42
1:A:128:ILE:HD11	1:A:130:TYR:CE2	2.55	0.42
1:A:149:ILE:CB	1:A:162:GLN:HG3	2.42	0.42
1:B:285:VAL:O	1:B:285:VAL:HG22	2.19	0.42
1:A:24:ARG:HH11	1:A:24:ARG:CB	2.25	0.42
1:A:117:LEU:HD22	1:A:118:ARG:H	1.84	0.42
1:B:31:HIS:CG	1:B:32:PRO:HD2	2.54	0.42
1:B:36:VAL:HG21	1:B:63:PHE:CZ	2.55	0.42
1:A:146:LEU:HB2	1:A:194:LYS:HD3	2.02	0.42
1:A:154:SER:O	1:A:155:ASP:O	2.37	0.42
1:B:15:LEU:HD23	1:B:18:ARG:HH22	1.83	0.42
1:B:175:LYS:O	1:B:176:GLY:O	2.38	0.42
1:A:225:ASN:O	1:A:229:ARG:HG3	2.19	0.42
1:B:256:PRO:HG2	1:B:257:HIS:CE1	2.55	0.42
1:A:31:HIS:ND1	1:A:33:LEU:HB2	2.35	0.42
1:A:142:GLN:HE21	1:A:248:LYS:HA	1.85	0.42
1:B:128:ILE:HD11	1:B:130:TYR:CD2	2.54	0.42
1:B:190:LEU:HD13	1:B:190:LEU:C	2.41	0.42
1:B:213:GLU:OE2	1:B:219:ARG:HD3	2.19	0.42
1:B:184:ILE:CG2	1:B:185:GLU:N	2.82	0.42
1:A:11:ALA:HA	1:A:28:ILE:HG13	2.02	0.41
1:B:31:HIS:CG	1:B:82:ILE:HD13	2.56	0.41
1:B:142:GLN:HE22	1:B:249:VAL:N	2.14	0.41
1:A:104:MET:HE1	1:A:300:PHE:HE1	1.86	0.41
1:A:231:PHE:HE2	1:A:247:ARG:HG2	1.86	0.41
1:B:146:LEU:HB2	1:B:194:LYS:HD3	2.02	0.41
1:A:13:LYS:HA	1:A:13:LYS:HD3	1.68	0.41
1:A:26:ASP:OD1	1:A:26:ASP:N	2.51	0.41
1:B:166:PHE:CE2	1:B:174:GLU:HB2	2.55	0.41
1:B:121:VAL:CG1	1:B:272:LEU:HD13	2.51	0.41
1:A:10:LYS:O	1:A:12:LYS:HG3	2.20	0.41
1:A:183:LEU:HD12	1:A:183:LEU:HA	1.86	0.41
1:A:266:ASP:O	1:A:267:SER:HB3	2.20	0.41
1:B:11:ALA:HA	1:B:28:ILE:HG13	2.03	0.41
1:B:298:LEU:HD23	1:B:298:LEU:HA	1.80	0.41
1:A:31:HIS:CG	1:A:82:ILE:HD13	2.56	0.41



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:190:LEU:HD13	1:A:190:LEU:C	2.42	0.41
1:B:156:GLU:HB3	1:B:157:TYR:CD1	2.56	0.41
1:B:226:LEU:HB3	1:B:233:VAL:CG2	2.49	0.41
1:A:107:ILE:CD1	1:A:133:VAL:HG11	2.47	0.40
1:A:156:GLU:HB3	1:A:157:TYR:CD1	2.56	0.40
1:B:304:LYS:HE2	1:B:305:VAL:CG2	2.51	0.40
1:A:83:GLN:O	1:A:84:GLY:O	2.38	0.40
1:A:121:VAL:CG1	1:A:272:LEU:HD13	2.51	0.40
1:A:128:ILE:HD12	1:A:129:THR:N	2.36	0.40
1:A:153:LEU:CD1	1:A:158:VAL:HG12	2.50	0.40
1:A:116:GLU:O	1:A:117:LEU:C	2.60	0.40
1:A:170:PHE:O	1:A:234:LYS:HE2	2.22	0.40
1:B:241:SER:HA	1:B:263:ASP:OD1	2.21	0.40
1:A:46:PHE:CD1	1:A:46:PHE:N	2.89	0.40
1:B:10:LYS:O	1:B:12:LYS:HG3	2.22	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	Perce	entiles
1	А	302/305~(99%)	265~(88%)	30 (10%)	7 (2%)	6	30
1	В	302/305~(99%)	266 (88%)	28~(9%)	8(3%)	5	27
All	All	604/610~(99%)	531 (88%)	58 (10%)	15 (2%)	5	28

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	115	ASP
1	А	266	ASP
1	В	115	ASP



Mol	Chain	Res	Type
1	В	155	ASP
1	В	266	ASP
1	А	84	GLY
1	А	155	ASP
1	А	176	GLY
1	В	84	GLY
1	В	176	GLY
1	А	89	THR
1	В	89	THR
1	А	146	LEU
1	В	146	LEU
1	В	63	PHE

### 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	Pe	erce	en	til	es
1	А	272/273~(100%)	203~(75%)	69~(25%)		0		3	
1	В	272/273~(100%)	204~(75%)	68~(25%)		0		3	
All	All	544/546~(100%)	407~(75%)	137~(25%)		0		3	

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	10	LYS
1	А	13	LYS
1	А	18	ARG
1	А	22	VAL
1	А	23	LYS
1	А	24	ARG
1	А	26	ASP
1	А	27	LYS
1	А	33	LEU
1	А	59	ARG
1	А	65	THR



Mol	Chain	Res	Type
1	А	89	THR
1	А	90	LYS
1	А	91	LYS
1	А	98	GLU
1	А	103	ARG
1	А	107	ILE
1	А	115	ASP
1	А	116	GLU
1	А	117	LEU
1	А	118	ARG
1	А	119	LEU
1	А	121	VAL
1	А	122	VAL
1	А	127	GLU
1	А	128	ILE
1	А	129	THR
1	А	135	GLU
1	А	137	ASP
1	А	142	GLN
1	А	148	GLU
1	А	152	VAL
1	А	155	ASP
1	А	158	VAL
1	А	162	GLN
1	А	164	GLU
1	А	175	LYS
1	А	177	ASP
1	А	178	LEU
1	А	183	LEU
1	А	194	LYS
1	А	196	ASN
1	А	197	LEU
1	А	199	ASN
1	А	202	ARG
1	А	203	GLU
1	А	207	LYS
1	А	208	ARG
1	А	219	ARG
1	А	222	VAL
1	А	224	ARG
1	А	226	LEU
1	А	227	LYS



Mol	Chain	Res	Type
1	А	234	LYS
1	А	244	ARG
1	А	248	LYS
1	А	250	GLU
1	А	251	SER
1	А	259	GLU
1	А	261	LEU
1	А	269	GLU
1	А	271	ARG
1	А	275	LEU
1	А	281	LEU
1	А	283	GLN
1	А	286	ARG
1	А	298	LEU
1	А	304	LYS
1	А	305	VAL
1	В	10	LYS
1	В	13	LYS
1	В	18	ARG
1	В	22	VAL
1	В	23	LYS
1	В	24	ARG
1	В	26	ASP
1	В	27	LYS
1	В	33	LEU
1	В	59	ARG
1	В	65	THR
1	В	89	THR
1	В	90	LYS
1	В	91	LYS
1	В	98	GLU
1	В	103	ARG
1	В	107	ILE
1	В	115	ASP
1	В	116	GLU
1	В	117	LEU
1	В	118	ARG
1	В	119	LEU
1	В	121	VAL
1	В	122	VAL
1	В	127	GLU
1	В	128	ILE



Continued from previous page					
Mol	Chain	Res	Type		
1	В	129	THR		
1	В	135	GLU		
1	В	137	ASP		
1	В	142	GLN		
1	В	148	GLU		
1	В	152	VAL		
1	В	155	ASP		
1	В	158	VAL		
1	В	162	GLN		
1	В	164	GLU		
1	В	175	LYS		
1	В	177	ASP		
1	В	178	LEU		
1	В	183	LEU		
1	В	194	LYS		
1	В	196	ASN		
1	В	197	LEU		
1	В	199	ASN		
1	В	202	ARG		
1	В	203	GLU		
1	В	207	LYS		
1	В	208	ARG		
1	В	219	ARG		
1	В	222	VAL		
1	В	224	ARG		
1	В	226	LEU		
1	В	227	LYS		
1	В	234	LYS		
1	В	244	ARG		
1	В	248	LYS		
1	В	250	GLU		
1	В	251	SER		
1	В	259	GLU		
1	В	261	LEU		
1	В	271	ARG		
1	В	275	LEU		
1	В	281	LEU		
1	В	283	GLN		
1	В	286	ARG		
1	В	298	LEU		
1	В	304	LYS		
1	В	305	VAL		



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	39	GLN
1	А	78	ASN
1	А	113	ASN
1	А	142	GLN
1	А	162	GLN
1	А	196	ASN
1	А	199	ASN
1	А	257	HIS
1	А	284	ASN
1	В	39	GLN
1	В	78	ASN
1	В	113	ASN
1	В	142	GLN
1	В	162	GLN
1	В	196	ASN
1	В	199	ASN
1	В	257	HIS
1	В	284	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 monosaccharides 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,  $95^{th}$  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	А	304/305~(99%)	-0.14	4 (1%) 77	51	21, 44, 70, 84	0
1	В	304/305~(99%)	-0.32	2 (0%) 87	69	18, 43, 69, 84	0
All	All	608/610~(99%)	-0.23	6 (0%) 82	59	18, 44, 69, 84	0

All (6) RSRZ outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	RSRZ
1	А	214	ARG	3.3
1	А	115	ASP	3.0
1	В	60	MET	3.0
1	В	138	MET	2.4
1	А	2	ILE	2.4
1	А	138	MET	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 monosaccharides 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.

