



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:32 AM UTC

PDB ID : 3OBY / pdb\_00003oby  
Title : Crystal structure of Archaeoglobus fulgidus Pelota reveals inter-domain structural plasticity  
Authors : Lee, H.H.; Jang, J.Y.; Yoon, H.-J.; Kim, S.J.; Suh, S.W.  
Deposited on : 2010-08-09  
Resolution : 2.90 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

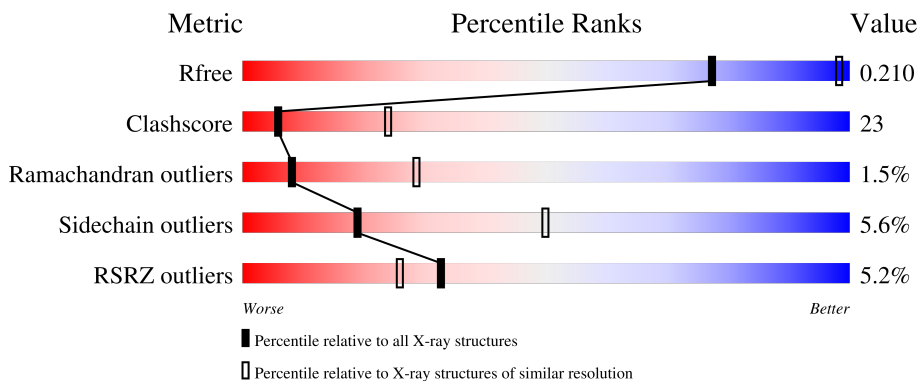
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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  $\geq 3$ , 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	352	 2% 59% 29% 10%
1	B	352	 7% 48% 36% 10%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5312 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 Protein pelota homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	317	2553	1633	441	473	6	0	0	0
1	B	316	2547	1631	437	473	6	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	345	LEU	-	expression tag	UNP O29421
A	346	GLU	-	expression tag	UNP O29421
A	347	HIS	-	expression tag	UNP O29421
A	348	HIS	-	expression tag	UNP O29421
A	349	HIS	-	expression tag	UNP O29421
A	350	HIS	-	expression tag	UNP O29421
A	351	HIS	-	expression tag	UNP O29421
A	352	HIS	-	expression tag	UNP O29421
B	345	LEU	-	expression tag	UNP O29421
B	346	GLU	-	expression tag	UNP O29421
B	347	HIS	-	expression tag	UNP O29421
B	348	HIS	-	expression tag	UNP O29421
B	349	HIS	-	expression tag	UNP O29421
B	350	HIS	-	expression tag	UNP O29421
B	351	HIS	-	expression tag	UNP O29421
B	352	HIS	-	expression tag	UNP O29421

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	146	Total	O	0	0
			146	146		
2	B	66	Total	O	0	0
			66	66		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.24Å 66.69Å 98.38Å 90.00° 107.29° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90 15.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (15.00-2.90) 95.1 (15.00-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	39.31 (at 2.91Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.209 , 0.279 0.218 , 0.210	Depositor DCC
$R_{free}$ test set	1778 reflections (9.84%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.9	Xtrriage
Anisotropy	0.382	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 71.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	5312	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.58% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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	0.47	1/2590 (0.0%)	0.96	8/3477 (0.2%)
1	B	0.61	5/2585 (0.2%)	1.14	27/3471 (0.8%)
All	All	0.55	6/5175 (0.1%)	1.06	35/6948 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	1	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	195	PHE	CA-CB	-8.23	1.41	1.53
1	B	196	ALA	CA-CB	-7.64	1.40	1.53
1	B	153	GLU	C-O	-7.34	1.14	1.24
1	A	196	ALA	CA-CB	-7.13	1.42	1.53
1	B	195	PHE	C-O	6.90	1.33	1.24
1	B	196	ALA	CA-C	6.45	1.61	1.52

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	61	VAL	N-CA-CB	-15.94	84.92	111.23
1	B	170	LYS	CA-CB-CG	-13.92	86.25	114.10
1	B	149	TRP	N-CA-C	-12.82	97.16	112.92
1	A	42	THR	CA-C-N	-11.21	101.52	121.70
1	A	42	THR	C-N-CA	-11.21	101.52	121.70
1	B	172	PHE	N-CA-C	-10.22	100.83	113.20
1	A	172	PHE	N-CA-C	-9.21	101.32	111.36
1	B	61	VAL	CA-CB-CG2	9.18	126.01	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	153	GLU	CA-C-N	8.62	137.48	121.97
1	B	153	GLU	C-N-CA	8.62	137.48	121.97
1	A	269	GLY	N-CA-C	-7.88	101.62	112.18
1	B	170	LYS	CB-CA-C	7.59	124.52	110.10
1	B	171	GLU	N-CA-CB	7.47	123.11	110.49
1	B	195	PHE	N-CA-C	-7.13	102.91	113.61
1	B	175	GLU	CA-C-N	-6.81	109.72	121.97
1	B	175	GLU	C-N-CA	-6.81	109.72	121.97
1	B	63	LEU	N-CA-C	6.62	120.32	110.52
1	B	175	GLU	N-CA-C	-6.44	105.28	113.01
1	A	110	LYS	N-CA-C	-6.19	98.64	108.73
1	B	62	ARG	CA-C-O	6.00	129.09	120.51
1	B	195	PHE	CA-C-O	-5.84	112.28	119.18
1	B	338	LEU	N-CA-C	5.83	118.42	110.55
1	A	338	LEU	N-CA-C	5.58	118.78	110.52
1	B	62	ARG	N-CA-CB	5.52	119.81	110.49
1	B	154	ILE	CA-CB-CG1	5.48	119.72	110.40
1	B	150	GLY	N-CA-C	-5.45	106.06	111.56
1	B	157	GLU	N-CA-C	5.44	118.43	109.72
1	B	154	ILE	CB-CA-C	5.44	120.21	111.29
1	A	265	ARG	N-CA-C	5.44	118.94	111.54
1	B	195	PHE	CA-C-N	-5.37	112.55	120.28
1	B	195	PHE	C-N-CA	-5.37	112.55	120.28
1	B	282	ILE	N-CA-C	5.33	115.88	108.84
1	B	235	ARG	N-CA-C	5.26	118.85	111.90
1	A	43	LYS	CA-CB-CG	5.10	124.30	114.10
1	B	61	VAL	CA-CB-CG1	5.04	118.97	110.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	154	ILE	CA

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	154	ILE	Mainchain
1	B	170	LYS	Mainchain

## 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	2553	0	2599	94	0
1	B	2547	0	2586	143	0
2	A	146	0	0	6	0
2	B	66	0	0	5	0
All	All	5312	0	5185	237	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 23.

All (237) 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:175:GLU:O	1:B:179:LYS:HG3	1.20	1.34
1:B:60:THR:CB	1:B:61:VAL:HG12	1.70	1.22
1:B:60:THR:HB	1:B:61:VAL:CG1	1.73	1.18
1:B:42:THR:HB	1:B:61:VAL:HG11	1.26	1.14
1:B:143:ALA:O	1:B:153:GLU:O	1.65	1.13
1:B:175:GLU:O	1:B:179:LYS:CG	2.00	1.08
1:B:42:THR:HB	1:B:61:VAL:CG1	1.84	1.08
1:B:343:LYS:HE3	1:B:343:LYS:HA	1.39	1.00
1:B:144:GLY:HA2	1:B:153:GLU:O	1.64	0.98
1:A:157:GLU:OE1	1:A:179:LYS:NZ	1.97	0.97
1:B:342:VAL:HG23	1:B:343:LYS:H	1.29	0.97
1:A:14:GLU:HB2	1:A:108:ILE:HG12	1.46	0.95
1:B:60:THR:HB	1:B:61:VAL:HG12	0.94	0.92
1:B:60:THR:O	1:B:61:VAL:HB	1.54	0.92
1:B:42:THR:O	1:B:43:LYS:HG3	1.69	0.92
1:A:201:LEU:HG	1:A:205:LYS:HE3	1.49	0.91
1:B:41:THR:HA	1:B:62:ARG:HB2	1.52	0.90
1:B:171:GLU:HA	1:B:171:GLU:OE1	1.72	0.90
1:A:42:THR:HG21	1:A:95:HIS:NE2	1.88	0.87
1:B:170:LYS:HD3	1:B:171:GLU:H	1.40	0.84
1:A:171:GLU:OE1	1:A:171:GLU:HA	1.75	0.83
1:B:175:GLU:HB3	1:B:179:LYS:HE3	1.59	0.83
1:B:42:THR:CB	1:B:61:VAL:HG11	2.09	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:PRO:HB3	1:B:221:SER:HA	1.64	0.79
1:B:306:ARG:O	1:B:310:GLU:HG3	1.82	0.79
1:A:129:PRO:HG2	1:A:131:ILE:HD11	1.65	0.79
1:A:142:VAL:HG22	1:A:156:GLU:HG2	1.64	0.78
1:B:197:LYS:NZ	1:B:219:ASP:HA	2.00	0.77
1:B:155:PHE:C	1:B:155:PHE:CD2	2.64	0.75
1:A:43:LYS:HG3	1:A:60:THR:HG22	1.69	0.74
1:B:220:VAL:HG22	1:B:222:SER:H	1.52	0.74
1:A:222:SER:HB2	1:A:227:GLY:HA2	1.70	0.73
1:A:43:LYS:HG3	1:A:60:THR:CG2	2.19	0.73
1:B:155:PHE:C	1:B:155:PHE:HD2	1.97	0.73
1:B:277:HIS:O	1:B:280:ARG:HD2	1.88	0.73
1:B:73:HIS:CE1	1:B:80:ARG:HB2	2.24	0.72
1:A:129:PRO:HB2	1:A:186:LYS:HD2	1.71	0.72
1:B:78:ARG:HG2	1:B:100:THR:HG22	1.70	0.72
1:A:129:PRO:CB	1:A:186:LYS:HD2	2.19	0.72
1:B:133:MET:HE3	1:B:231:ILE:HB	1.73	0.71
1:A:195:PHE:HA	1:A:198:ASN:HD22	1.53	0.71
1:B:42:THR:O	1:B:43:LYS:CG	2.39	0.71
1:B:342:VAL:HG23	1:B:343:LYS:N	2.03	0.71
1:B:154:ILE:O	1:B:155:PHE:HB3	1.91	0.70
1:B:171:GLU:OE1	1:B:171:GLU:CA	2.40	0.70
1:B:175:GLU:O	1:B:179:LYS:CD	2.40	0.70
1:B:254:ASP:O	1:B:258:GLU:HG3	1.93	0.69
1:B:144:GLY:CA	1:B:153:GLU:O	2.41	0.68
1:B:201:LEU:HD22	1:B:217:VAL:HG23	1.75	0.68
1:B:170:LYS:HD3	1:B:171:GLU:N	2.03	0.67
1:B:133:MET:CE	1:B:231:ILE:HB	2.24	0.67
1:B:42:THR:HB	1:B:61:VAL:HG13	1.75	0.66
1:A:139:GLY:HA3	1:A:159:MET:HB2	1.76	0.66
1:B:154:ILE:HD11	1:B:183:PHE:CD1	2.30	0.66
1:A:220:VAL:HG21	1:A:231:ILE:HD13	1.78	0.65
1:B:126:SER:HB2	2:B:401:HOH:O	1.94	0.65
1:A:43:LYS:HD2	1:A:43:LYS:N	2.11	0.65
1:A:139:GLY:CA	1:A:159:MET:HB2	2.27	0.65
1:B:197:LYS:HZ2	1:B:219:ASP:HA	1.60	0.65
1:A:129:PRO:HB2	1:A:186:LYS:HG3	1.80	0.64
1:B:42:THR:H	1:B:61:VAL:HG13	1.62	0.64
1:B:134:LEU:HD12	1:B:143:ALA:HB2	1.78	0.64
1:B:143:ALA:C	1:B:153:GLU:O	2.39	0.64
1:B:85:ILE:HD11	1:B:95:HIS:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLU:HG3	1:A:83:GLY:HA2	1.82	0.62
1:B:171:GLU:OE1	1:B:171:GLU:N	2.33	0.62
1:B:175:GLU:C	1:B:179:LYS:HG3	2.16	0.62
1:A:151:VAL:HG21	1:A:228:PHE:HB3	1.82	0.61
1:A:201:LEU:HD22	1:A:217:VAL:HG23	1.82	0.61
1:A:282:ILE:HG12	2:A:479:HOH:O	1.99	0.61
1:B:148:GLN:C	1:B:150:GLY:H	2.07	0.60
1:A:41:THR:HA	1:A:62:ARG:HA	1.83	0.59
1:B:317:ILE:HD12	1:B:317:ILE:N	2.17	0.59
1:B:275:GLU:O	1:B:279:TYR:HD2	1.85	0.59
1:A:218:VAL:HG12	1:A:220:VAL:H	1.67	0.59
1:A:29:ARG:HD3	1:A:29:ARG:C	2.28	0.58
1:B:343:LYS:HE3	1:B:343:LYS:CA	2.24	0.58
1:B:180:LEU:C	1:B:182:SER:H	2.11	0.58
1:A:129:PRO:HB2	1:A:186:LYS:CD	2.33	0.58
1:A:254:ASP:O	1:A:258:GLU:HG3	2.04	0.58
1:B:219:ASP:O	1:B:220:VAL:HB	2.03	0.58
1:B:133:MET:HE3	1:B:231:ILE:CB	2.35	0.57
1:B:129:PRO:O	1:B:131:ILE:HG13	2.05	0.57
1:B:237:VAL:O	1:B:241:VAL:HG23	2.05	0.57
1:B:135:THR:OG1	1:B:142:VAL:HG13	2.04	0.56
1:B:119:LEU:O	1:B:123:VAL:HG23	2.05	0.56
1:B:154:ILE:HD11	1:B:183:PHE:HD1	1.70	0.56
1:B:27:HIS:HE1	1:B:309:GLU:OE2	1.89	0.56
1:B:60:THR:C	1:B:61:VAL:CG1	2.73	0.56
1:A:219:ASP:HB3	1:A:234:ARG:HH12	1.69	0.56
1:B:200:PHE:O	1:B:203:PHE:HB3	2.05	0.55
1:A:302:ASP:O	1:A:306:ARG:HG3	2.06	0.55
1:B:134:LEU:CD1	1:B:143:ALA:HB2	2.37	0.55
1:B:175:GLU:O	1:B:179:LYS:HD2	2.06	0.55
1:B:189:ILE:HD12	1:B:189:ILE:N	2.22	0.55
1:A:129:PRO:HB2	1:A:186:LYS:CG	2.37	0.54
1:B:343:LYS:HA	1:B:343:LYS:CE	2.25	0.54
1:A:130:GLU:H	1:A:186:LYS:NZ	2.05	0.54
1:B:14:GLU:HB2	1:B:108:ILE:HG12	1.89	0.54
1:B:133:MET:HE2	1:B:231:ILE:HD12	1.90	0.54
1:A:130:GLU:H	1:A:186:LYS:HZ2	1.56	0.53
1:B:187:TYR:HE1	1:B:214:ASN:HD22	1.56	0.53
1:A:78:ARG:HG2	1:A:100:THR:HG22	1.90	0.53
1:A:227:GLY:O	1:A:231:ILE:HG12	2.09	0.53
1:B:42:THR:O	1:B:43:LYS:CB	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:ILE:N	1:A:189:ILE:HD12	2.24	0.53
1:A:195:PHE:HA	1:A:198:ASN:ND2	2.23	0.53
1:B:225:SER:O	1:B:229:ILE:HG12	2.09	0.52
1:A:73:HIS:CE1	1:A:80:ARG:HB2	2.45	0.52
1:B:39:PHE:HB2	1:B:106:SER:HB2	1.91	0.52
1:B:38:VAL:HB	1:B:65:ILE:HD11	1.92	0.52
1:A:42:THR:O	1:A:60:THR:HG22	2.09	0.51
1:B:109:LYS:HZ1	1:B:115:GLN:HE22	1.57	0.51
1:B:342:VAL:CG2	1:B:343:LYS:H	2.11	0.51
1:B:60:THR:C	1:B:61:VAL:HG12	2.32	0.51
1:B:20:GLU:OE1	1:B:126:SER:OG	2.28	0.51
1:B:78:ARG:HG2	1:B:100:THR:CG2	2.40	0.51
1:A:42:THR:CG2	1:A:95:HIS:NE2	2.67	0.51
1:A:267:ALA:HA	1:A:272:GLU:OE1	2.11	0.51
1:A:225:SER:O	1:A:229:ILE:HG12	2.12	0.50
1:B:65:ILE:O	1:B:65:ILE:HD12	2.11	0.50
1:A:282:ILE:HD12	1:A:282:ILE:N	2.26	0.50
1:A:86:VAL:HG13	1:A:87:ALA:N	2.26	0.49
1:B:2:GLN:HG3	1:B:20:GLU:OE2	2.11	0.49
1:B:210:GLU:O	1:B:213:LYS:HG3	2.12	0.49
1:B:245:ARG:HD3	2:B:403:HOH:O	2.13	0.49
1:A:40:ALA:O	1:A:62:ARG:HA	2.13	0.49
1:B:2:GLN:HB2	1:B:18:ILE:HB	1.95	0.49
1:A:120:ARG:HD2	2:A:357:HOH:O	2.13	0.49
1:B:281:ALA:O	1:B:339:ARG:HG3	2.13	0.49
1:A:61:VAL:HG13	1:A:63:LEU:HD13	1.94	0.49
1:A:201:LEU:CG	1:A:205:LYS:HE3	2.33	0.48
1:A:29:ARG:HD3	1:A:29:ARG:O	2.13	0.48
1:A:123:VAL:C	1:A:125:ASP:H	2.21	0.48
1:A:200:PHE:O	1:A:203:PHE:HB3	2.13	0.48
1:A:40:ALA:HB3	1:A:97:LEU:HD22	1.96	0.48
1:B:191:ALA:HB2	1:B:218:VAL:CG2	2.43	0.48
1:B:226:ARG:HG3	1:B:226:ARG:HH11	1.78	0.48
1:B:66:GLU:HB2	1:B:86:VAL:CG1	2.44	0.48
1:A:27:HIS:HE1	1:A:309:GLU:OE2	1.96	0.48
1:A:31:ILE:HD12	1:A:115:GLN:HB3	1.94	0.48
1:A:42:THR:O	1:A:60:THR:HA	2.14	0.48
1:B:276:ALA:HA	1:B:342:VAL:HG11	1.95	0.48
1:A:322:PHE:O	1:A:326:LYS:HG3	2.14	0.48
1:A:41:THR:HG22	1:A:62:ARG:HB2	1.95	0.48
1:B:222:SER:OG	1:B:227:GLY:HA2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:LEU:C	1:B:182:SER:N	2.72	0.47
1:A:19:PRO:HB3	1:A:28:LEU:HD11	1.96	0.47
1:A:277:HIS:HB2	2:A:479:HOH:O	2.13	0.47
1:A:43:LYS:HG3	1:A:60:THR:HG23	1.94	0.47
1:B:42:THR:HG23	1:B:43:LYS:N	2.28	0.47
1:A:270:LEU:HG	1:A:274:ARG:HD2	1.96	0.47
1:B:40:ALA:C	1:B:62:ARG:HG3	2.40	0.47
1:B:85:ILE:HD11	1:B:95:HIS:CB	2.45	0.47
1:B:265:ARG:NH1	1:B:340:PHE:HA	2.29	0.47
1:A:131:ILE:CD1	1:A:187:TYR:HB2	2.44	0.47
1:B:133:MET:CE	1:B:231:ILE:HD12	2.45	0.47
1:A:74:ARG:HD3	1:A:297:GLU:OE2	2.15	0.46
1:B:94:TYR:N	1:B:94:TYR:CD1	2.82	0.46
1:B:29:ARG:C	1:B:29:ARG:HD3	2.40	0.46
1:B:153:GLU:HG2	1:B:155:PHE:H	1.80	0.46
1:B:222:SER:OG	1:B:226:ARG:HG2	2.15	0.46
1:B:225:SER:HA	1:B:228:PHE:CD2	2.49	0.46
1:B:42:THR:C	1:B:43:LYS:HG3	2.39	0.46
1:B:283:GLU:HG2	1:B:284:VAL:HG23	1.97	0.46
1:A:15:ILE:HD12	1:A:111:TRP:CZ2	2.51	0.46
1:A:129:PRO:HG2	1:A:131:ILE:CD1	2.41	0.46
1:A:218:VAL:HG12	1:A:219:ASP:N	2.31	0.46
1:B:195:PHE:O	1:B:196:ALA:C	2.58	0.45
1:A:131:ILE:HD12	1:A:187:TYR:HB2	1.98	0.45
1:A:119:LEU:O	1:A:123:VAL:HG23	2.16	0.45
1:B:281:ALA:HB2	1:B:340:PHE:CE2	2.51	0.45
1:B:285:LEU:HD11	1:B:334:ILE:HD11	1.99	0.45
1:A:42:THR:HG21	1:A:95:HIS:CD2	2.49	0.45
1:B:109:LYS:NZ	1:B:115:GLN:HE22	2.14	0.45
1:A:72:PHE:HB3	2:A:415:HOH:O	2.17	0.45
1:A:277:HIS:HA	1:A:282:ILE:HD13	1.98	0.44
1:B:181:GLU:N	1:B:211:MET:HE1	2.31	0.44
1:B:209:PRO:O	1:B:213:LYS:HG2	2.17	0.44
1:A:124:GLU:C	2:A:475:HOH:O	2.60	0.44
1:B:197:LYS:HZ1	1:B:219:ASP:HA	1.82	0.44
1:A:170:LYS:C	1:A:172:PHE:H	2.26	0.44
1:B:193:PRO:HD3	1:B:222:SER:O	2.17	0.44
1:B:231:ILE:HG23	1:B:236:VAL:HG21	1.99	0.44
1:A:265:ARG:HG3	1:A:265:ARG:HH21	1.83	0.44
1:B:152:GLU:O	1:B:153:GLU:C	2.60	0.44
1:B:133:MET:CE	1:B:228:PHE:HA	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:HIS:CE1	1:B:98:ASN:ND2	2.85	0.44
1:B:101:VAL:O	1:B:101:VAL:HG23	2.18	0.44
1:A:175:GLU:O	1:A:179:LYS:HG2	2.18	0.43
1:B:42:THR:CG2	1:B:61:VAL:HG11	2.47	0.43
1:A:39:PHE:HB2	1:A:106:SER:HB2	2.00	0.43
1:A:42:THR:O	1:A:43:LYS:CB	2.65	0.43
1:B:15:ILE:HD12	1:B:111:TRP:CZ2	2.53	0.43
1:A:84:LYS:NZ	1:A:84:LYS:HB3	2.34	0.43
1:A:323:GLU:HB2	1:A:324:PRO:HD3	2.01	0.43
1:B:133:MET:HE3	1:B:231:ILE:CG2	2.49	0.43
1:B:118:ARG:O	1:B:118:ARG:HD3	2.17	0.43
1:B:149:TRP:CD1	1:B:149:TRP:C	2.97	0.43
1:A:319:SER:C	1:A:321:GLU:H	2.27	0.43
1:B:37:VAL:HA	1:B:65:ILE:O	2.19	0.43
1:A:86:VAL:CG1	1:A:87:ALA:N	2.81	0.42
1:A:155:PHE:CD2	1:A:179:LYS:HD2	2.54	0.42
1:A:1:MET:N	1:A:20:GLU:OE1	2.53	0.42
1:B:315:VAL:HG12	1:B:317:ILE:CD1	2.49	0.42
1:B:197:LYS:HG3	1:B:198:ASN:N	2.34	0.42
1:B:17:LEU:C	1:B:17:LEU:HD12	2.44	0.42
1:B:69:LYS:HE2	1:B:71:GLU:OE1	2.19	0.41
1:A:155:PHE:CD2	1:A:179:LYS:CD	3.03	0.41
1:A:210:GLU:O	1:A:213:LYS:HG2	2.21	0.41
1:B:14:GLU:CB	1:B:108:ILE:HG12	2.50	0.41
1:A:19:PRO:HB3	1:A:28:LEU:CD1	2.51	0.41
1:A:127:ASN:HB2	2:A:476:HOH:O	2.20	0.41
1:B:137:GLU:O	1:B:138:GLU:C	2.63	0.41
1:B:185:PHE:HE2	1:B:188:LEU:HB2	1.84	0.41
1:B:190:VAL:O	1:B:217:VAL:HA	2.20	0.41
1:B:241:VAL:O	1:B:244:VAL:HB	2.20	0.41
1:A:19:PRO:HD2	1:A:103:LYS:O	2.20	0.41
1:A:39:PHE:CZ	1:A:87:ALA:HB3	2.55	0.41
1:A:170:LYS:C	1:A:172:PHE:N	2.77	0.41
1:B:27:HIS:HD2	2:B:365:HOH:O	2.02	0.41
1:A:129:PRO:O	1:A:131:ILE:HG12	2.21	0.41
1:B:315:VAL:HG12	1:B:317:ILE:HD12	2.02	0.41
1:A:195:PHE:O	1:A:196:ALA:C	2.59	0.41
1:B:133:MET:HE2	1:B:228:PHE:HA	2.03	0.41
1:B:204:LEU:O	1:B:208:TYR:N	2.44	0.41
1:B:220:VAL:HG12	2:B:415:HOH:O	2.20	0.41
1:B:269:GLY:O	1:B:273:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:HIS:O	1:A:31:ILE:HG12	2.20	0.41
1:B:19:PRO:HD2	1:B:103:LYS:O	2.21	0.41
1:B:314:LYS:HD3	2:B:394:HOH:O	2.20	0.41
1:A:137:GLU:O	1:A:138:GLU:C	2.63	0.41
1:B:179:LYS:O	1:B:182:SER:OG	2.31	0.40
1:B:188:LEU:C	1:B:189:ILE:HD12	2.46	0.40
1:A:119:LEU:HD23	1:A:119:LEU:HA	1.93	0.40
1:B:73:HIS:HE1	1:B:80:ARG:HB2	1.79	0.40
1:B:175:GLU:HB3	1:B:179:LYS:CE	2.42	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	309/352 (88%)	291 (94%)	16 (5%)	2 (1%)	21	51
1	B	308/352 (88%)	289 (94%)	12 (4%)	7 (2%)	5	19
All	All	617/704 (88%)	580 (94%)	28 (4%)	9 (2%)	8	28

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	61	VAL
1	B	220	VAL
1	B	138	GLU
1	B	171	GLU
1	B	155	PHE
1	A	222	SER
1	A	62	ARG
1	B	67	VAL
1	B	154	ILE

### 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	270/300 (90%)	260 (96%)	10 (4%)	30	64
1	B	269/300 (90%)	249 (93%)	20 (7%)	13	38
All	All	539/600 (90%)	509 (94%)	30 (6%)	19	50

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LYS
1	A	59	VAL
1	A	65	ILE
1	A	84	LYS
1	A	116	LEU
1	A	126	SER
1	A	128	ARG
1	A	171	GLU
1	A	207	ARG
1	A	257	LEU
1	B	42	THR
1	B	60	THR
1	B	62	ARG
1	B	85	ILE
1	B	142	VAL
1	B	151	VAL
1	B	154	ILE
1	B	155	PHE
1	B	170	LYS
1	B	171	GLU
1	B	172	PHE
1	B	207	ARG
1	B	213	LYS
1	B	223	VAL
1	B	233	LYS
1	B	239	LYS
1	B	243	GLU

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Mol	Chain	Res	Type
1	B	257	LEU
1	B	341	ASN
1	B	343	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	HIS
1	A	77	ASN
1	A	148	GLN
1	A	198	ASN
1	A	214	ASN
1	A	278	ASN
1	B	2	GLN
1	B	11	ASN
1	B	27	HIS
1	B	73	HIS
1	B	77	ASN
1	B	95	HIS
1	B	98	ASN
1	B	115	GLN
1	B	198	ASN
1	B	214	ASN
1	B	278	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

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	317/352 (90%)	-0.21	7 (2%) 62 53	6, 27, 75, 119	0
1	B	316/352 (89%)	0.15	26 (8%) 17 14	7, 35, 94, 137	0
All	All	633/704 (89%)	-0.03	33 (5%) 33 26	6, 31, 86, 137	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	60	THR	5.2
1	A	59	VAL	4.0
1	B	220	VAL	3.9
1	B	181	GLU	3.7
1	B	150	GLY	3.6
1	B	152	GLU	3.5
1	A	195	PHE	3.5
1	B	194	GLY	3.4
1	B	92	SER	3.1
1	B	222	SER	2.9
1	B	154	ILE	2.9
1	B	196	ALA	2.7
1	B	144	GLY	2.7
1	B	170	LYS	2.7
1	B	178	ALA	2.7
1	B	223	VAL	2.6
1	B	235	ARG	2.6
1	B	179	LYS	2.4
1	B	344	GLY	2.4
1	B	153	GLU	2.4
1	B	43	LYS	2.3
1	B	207	ARG	2.3
1	A	194	GLY	2.3
1	A	169	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	42	THR	2.3
1	B	342	VAL	2.2
1	B	229	ILE	2.2
1	A	219	ASP	2.2
1	A	61	VAL	2.1
1	B	195	PHE	2.1
1	B	62	ARG	2.1
1	B	206	GLU	2.0
1	A	140	TYR	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.