



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 03:29 AM GMT

PDB ID : 1GD8  
Title : THE CRYSTAL STRUCTURE OF BACTERIA-SPECIFIC L17 RIBOSOMAL PROTEIN.  
Authors : Vassilyev, D.G.; Shirouzu, M.; Wada, T.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2000-09-22  
Resolution : 2.30 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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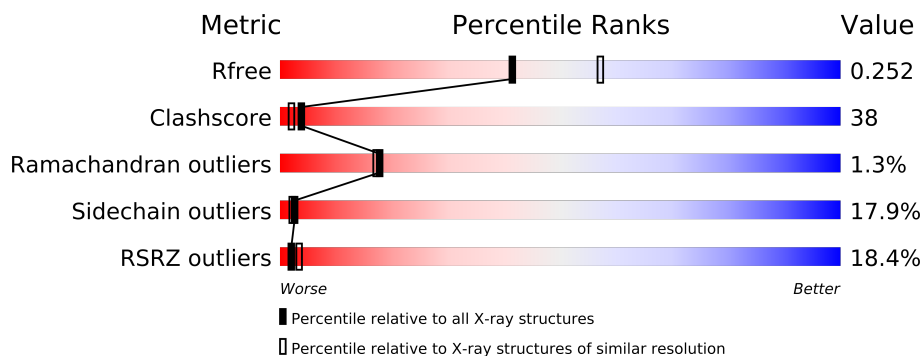
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.30 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))
$R_{free}$	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	118	
1	B	118	
1	C	118	
1	D	118	
1	E	118	
1	F	118	
1	G	118	
1	H	118	
1	I	118	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7852 atoms, of which 0 are hydrogen and 0 are deuterium.

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 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	B	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	C	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	D	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	E	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	F	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	G	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	H	105	Total	C	N	O	0	0	0
			855	536	174	145			
1	I	105	Total	C	N	O	0	0	0
			855	536	174	145			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	36	Total	O	0	0
			36	36		
2	B	15	Total	O	0	0
			15	15		
2	C	16	Total	O	0	0
			16	16		
2	D	27	Total	O	0	0
			27	27		
2	E	13	Total	O	0	0
			13	13		

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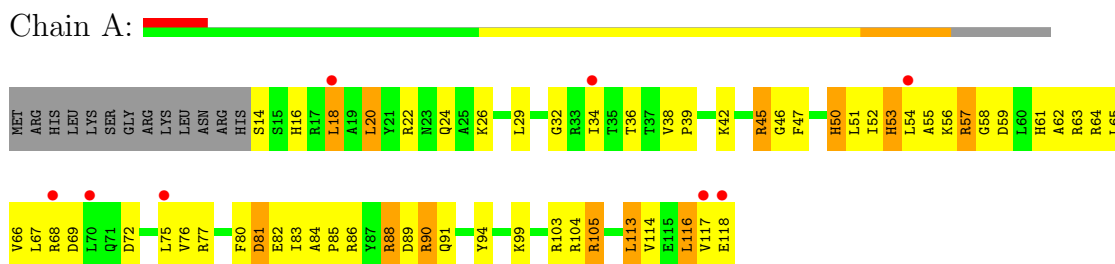
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	4	Total 4	O 4	0	0
2	G	19	Total 19	O 19	0	0
2	H	13	Total 13	O 13	0	0
2	I	14	Total 14	O 14	0	0

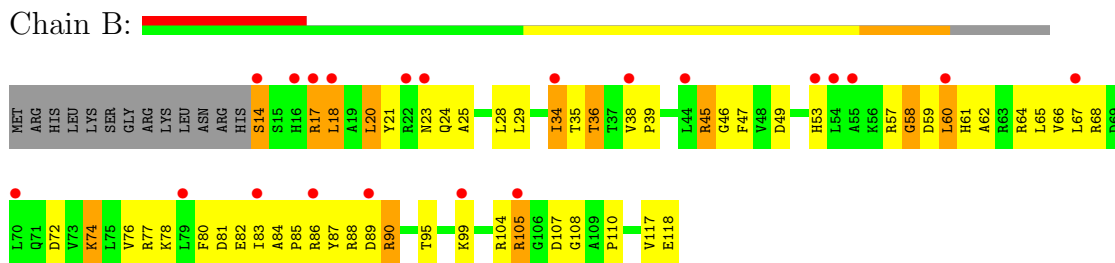
### 3 Residue-property plots

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.

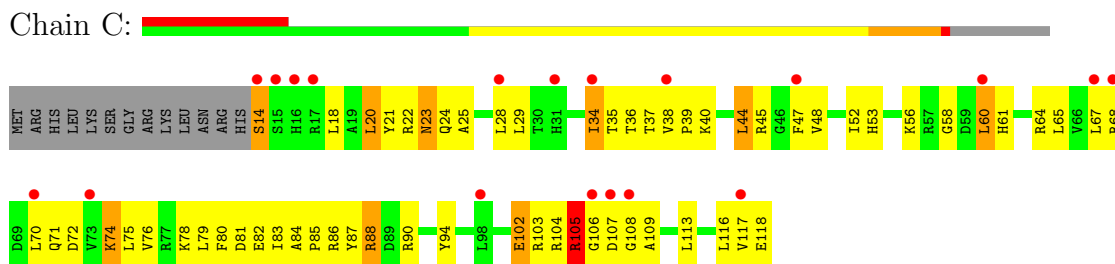
#### • Molecule 1: 50S RIBOSOMAL PROTEIN L17



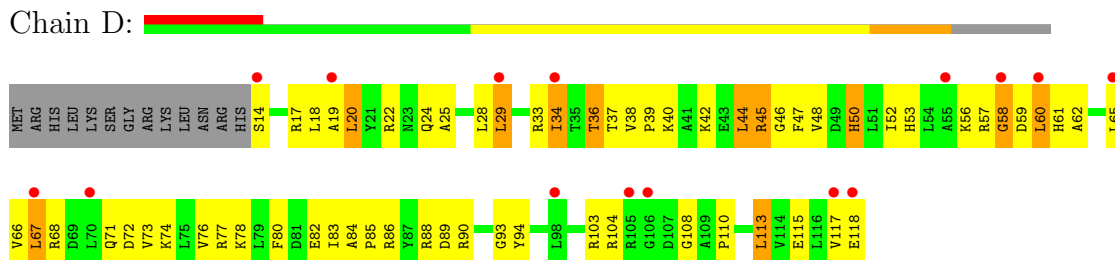
#### • Molecule 1: 50S RIBOSOMAL PROTEIN L17



#### • Molecule 1: 50S RIBOSOMAL PROTEIN L17

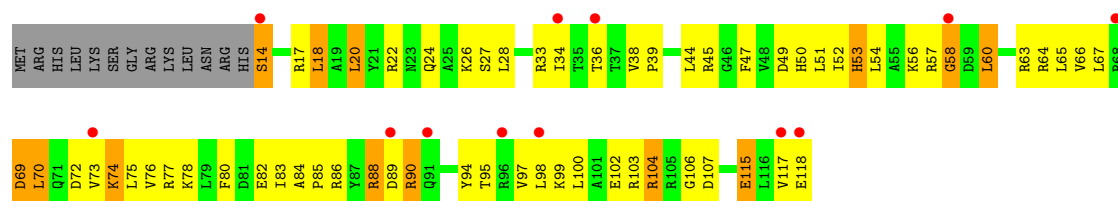


#### • Molecule 1: 50S RIBOSOMAL PROTEIN L17



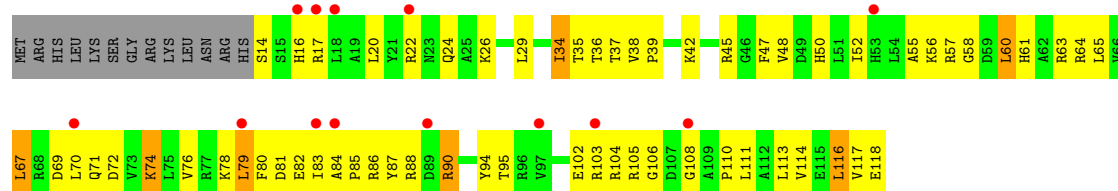
- Molecule 1: 50S RIBOSOMAL PROTEIN L17

Chain E:



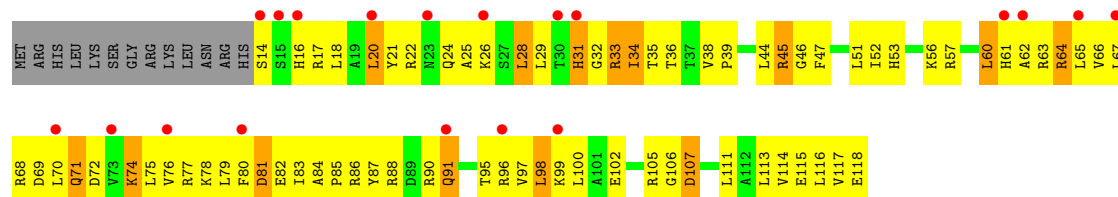
- Molecule 1: 50S RIBOSOMAL PROTEIN L17

Chain F:



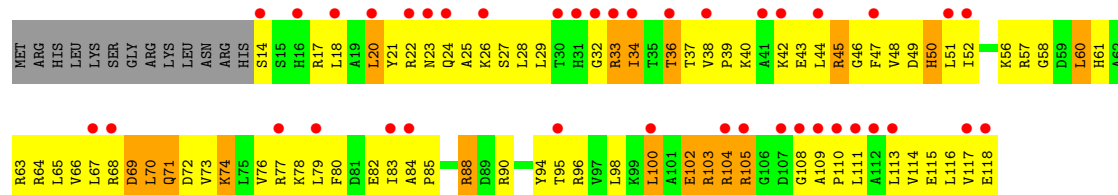
- Molecule 1: 50S RIBOSOMAL PROTEIN L17

Chain G:



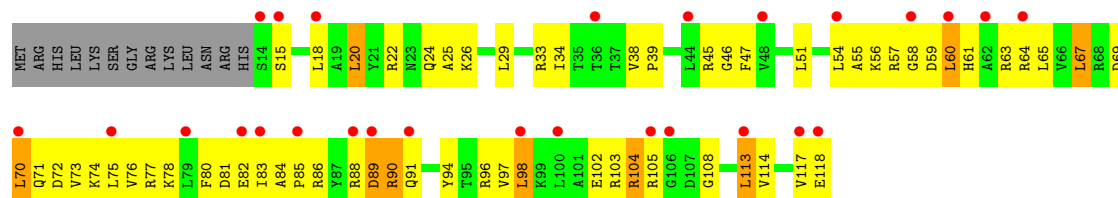
- Molecule 1: 50S RIBOSOMAL PROTEIN L17

Chain H:



- Molecule 1: 50S RIBOSOMAL PROTEIN L17

Chain I:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.24Å 109.24Å 128.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 39.97 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.2 (50.00-2.30) 97.2 (39.97-2.30)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	11276.44 (at 2.29Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.210 , 0.254 0.211 , 0.252	Depositor DCC
$R_{free}$ test set	3065 reflections (4.94%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.7	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 38.0	EDS
Estimated twinning fraction	0.337 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 65159 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7852	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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	0.39	0/867	0.70	0/1162
1	B	0.41	0/867	0.72	0/1162
1	C	0.38	0/867	0.72	0/1162
1	D	0.42	0/867	0.73	0/1162
1	E	0.39	0/867	0.65	0/1162
1	F	0.39	0/867	0.64	0/1162
1	G	0.42	0/867	0.69	0/1162
1	H	0.39	0/867	0.66	0/1162
1	I	0.38	0/867	0.62	0/1162
All	All	0.40	0/7803	0.68	0/10458

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	855	0	906	62	0
1	B	855	0	906	57	0
1	C	855	0	906	67	0
1	D	855	0	906	55	0
1	E	855	0	906	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	855	0	906	65	0
1	G	855	0	906	101	0
1	H	855	0	906	110	0
1	I	855	0	906	71	0
2	A	36	0	0	5	0
2	B	15	0	0	1	0
2	C	16	0	0	0	0
2	D	27	0	0	3	0
2	E	13	0	0	5	0
2	F	4	0	0	0	0
2	G	19	0	0	5	0
2	H	13	0	0	1	0
2	I	14	0	0	0	0
All	All	7852	0	8154	603	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 38.

All (603) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:68:ARG:HD2	1:H:68:ARG:HD3	1.36	1.05
1:F:74:LYS:HD3	1:F:74:LYS:H	1.17	1.05
1:C:78:LYS:HE2	1:C:83:ILE:HD11	1.34	1.04
1:G:26:LYS:HG3	1:G:75:LEU:HD11	1.35	1.03
1:E:60:LEU:HD23	1:E:60:LEU:H	1.23	1.03
1:A:105:ARG:H	1:A:105:ARG:HD3	1.19	1.03
1:B:105:ARG:HB3	1:B:105:ARG:HH11	1.24	1.02
1:H:60:LEU:HD23	1:H:60:LEU:H	1.18	1.01
1:D:34:ILE:HD11	2:D:139:HOH:O	1.62	0.97
1:E:45:ARG:HG3	1:E:95:THR:HG23	1.47	0.97
1:C:36:THR:HG22	1:C:37:THR:H	1.31	0.95
1:C:106:GLY:HA2	1:E:38:VAL:HG11	1.48	0.93
1:G:64:ARG:HH11	1:G:64:ARG:HB3	1.33	0.93
1:G:111:LEU:HD12	2:G:135:HOH:O	1.68	0.92
1:G:25:ALA:O	1:G:29:LEU:HD23	1.68	0.92
1:A:26:LYS:HB3	2:A:139:HOH:O	1.68	0.92
1:B:87:TYR:HD2	1:B:90:ARG:HG3	1.35	0.92
1:G:38:VAL:HG21	1:G:99:LYS:HE3	1.54	0.89
1:F:60:LEU:HD23	1:F:60:LEU:H	1.35	0.89
1:A:116:LEU:HD12	1:A:116:LEU:H	1.36	0.88
1:I:67:LEU:HD11	1:I:73:VAL:HG22	1.53	0.88
1:F:38:VAL:HG12	1:F:42:LYS:HZ2	1.39	0.88

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:14:SER:OG	1:I:89:ASP:HB2	1.73	0.88
1:F:24:GLN:HE21	1:F:36:THR:HG21	1.39	0.88
1:G:56:LYS:HE3	1:G:88:ARG:HA	1.55	0.87
1:G:98:LEU:HD12	1:G:113:LEU:HD12	1.54	0.87
1:B:62:ALA:O	1:B:66:VAL:HG23	1.73	0.86
1:G:67:LEU:HD23	1:G:76:VAL:HG21	1.57	0.86
1:G:68:ARG:CD	1:H:68:ARG:HD3	2.06	0.85
1:H:61:HIS:O	1:H:65:LEU:HD23	1.76	0.85
1:I:104:ARG:HG2	1:I:105:ARG:H	1.40	0.85
1:D:33:ARG:HD3	1:D:113:LEU:HD21	1.60	0.84
1:E:45:ARG:HD3	1:E:97:VAL:HG23	1.59	0.84
1:G:79:LEU:HD22	2:G:134:HOH:O	1.78	0.84
1:G:105:ARG:HG2	1:G:105:ARG:HH11	1.42	0.83
1:F:61:HIS:O	1:F:65:LEU:HD23	1.78	0.83
1:B:17:ARG:HH11	1:B:17:ARG:HG3	1.43	0.82
1:H:72:ASP:OD2	1:H:74:LYS:HG3	1.79	0.82
1:H:105:ARG:H	1:H:105:ARG:HD3	1.44	0.82
1:A:105:ARG:H	1:A:105:ARG:CD	1.89	0.82
1:E:45:ARG:HG3	1:E:95:THR:CG2	2.09	0.81
1:D:60:LEU:HD23	1:D:60:LEU:H	1.43	0.81
1:A:26:LYS:HA	1:A:75:LEU:HD11	1.63	0.81
1:F:14:SER:N	1:F:17:ARG:HG3	1.95	0.81
1:I:90:ARG:HH22	1:I:118:GLU:HA	1.46	0.80
1:A:57:ARG:HG2	1:A:57:ARG:HH11	1.46	0.80
1:C:37:THR:OG1	1:C:40:LYS:HG2	1.83	0.79
1:A:26:LYS:HD3	2:A:139:HOH:O	1.81	0.79
1:C:53:HIS:CE1	1:D:53:HIS:HE1	1.99	0.79
1:C:22:ARG:HD3	1:C:71:GLN:HG2	1.64	0.79
1:A:14:SER:HA	2:A:147:HOH:O	1.81	0.79
1:I:22:ARG:O	1:I:26:LYS:HG3	1.83	0.79
1:C:74:LYS:HE3	1:F:88:ARG:HH21	1.48	0.79
1:F:38:VAL:HG12	1:F:42:LYS:NZ	1.97	0.79
1:C:105:ARG:N	1:C:105:ARG:HD2	1.98	0.79
1:B:60:LEU:H	1:B:60:LEU:HD23	1.49	0.78
1:C:104:ARG:HB2	1:C:105:ARG:HH11	1.48	0.78
1:I:96:ARG:HG2	1:I:98:LEU:HD11	1.64	0.78
1:H:18:LEU:HB3	1:H:22:ARG:HH21	1.46	0.78
1:H:73:VAL:HG12	1:H:77:ARG:HD3	1.63	0.78
1:C:53:HIS:HE1	1:D:53:HIS:HE1	1.32	0.78
1:G:117:VAL:O	1:G:118:GLU:HG3	1.83	0.78
1:G:14:SER:N	1:G:17:ARG:HG3	1.98	0.77
1:H:44:LEU:HD12	1:H:114:VAL:HG11	1.66	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:45:ARG:HG3	1:I:46:GLY:N	1.98	0.77
1:H:60:LEU:H	1:H:60:LEU:CD2	1.91	0.77
1:C:34:ILE:HD13	1:C:35:THR:N	2.00	0.77
1:F:24:GLN:NE2	1:F:36:THR:HG21	2.00	0.77
1:B:34:ILE:HD13	1:B:35:THR:H	1.50	0.77
1:I:57:ARG:HG2	1:I:59:ASP:OD1	1.85	0.77
1:C:21:TYR:HB3	1:C:47:PHE:CD2	2.19	0.76
1:E:64:ARG:NH2	1:F:69:ASP:OD2	2.18	0.76
1:A:85:PRO:HA	1:A:88:ARG:HD3	1.66	0.76
1:I:72:ASP:HB3	1:I:75:LEU:HD12	1.67	0.75
1:C:34:ILE:HD13	1:C:35:THR:H	1.50	0.75
1:C:105:ARG:H	1:C:105:ARG:HD2	1.48	0.75
1:E:94:TYR:O	1:E:117:VAL:HG12	1.87	0.75
1:B:90:ARG:HD2	2:B:133:HOH:O	1.85	0.75
1:E:63:ARG:HH21	1:E:77:ARG:HA	1.51	0.74
1:D:117:VAL:O	1:D:118:GLU:HB2	1.85	0.74
1:I:25:ALA:O	1:I:29:LEU:HD23	1.87	0.74
1:G:87:TYR:HD2	1:G:90:ARG:HE	1.34	0.74
1:C:74:LYS:HE3	1:F:88:ARG:NH2	2.03	0.73
1:D:67:LEU:HD23	1:D:76:VAL:HG21	1.71	0.73
1:H:22:ARG:O	1:H:26:LYS:HG3	1.88	0.73
1:I:103:ARG:HB3	1:I:108:GLY:O	1.90	0.72
1:H:25:ALA:O	1:H:29:LEU:HD23	1.89	0.72
1:H:26:LYS:NZ	1:H:72:ASP:HB2	2.05	0.72
1:A:38:VAL:HB	1:A:39:PRO:HD3	1.72	0.72
1:A:22:ARG:O	1:A:26:LYS:HG3	1.89	0.71
1:H:74:LYS:HA	1:H:77:ARG:NE	2.06	0.71
1:F:38:VAL:HG23	1:F:110:PRO:O	1.91	0.71
1:H:104:ARG:HB2	1:H:111:LEU:HD21	1.72	0.71
1:E:14:SER:O	1:E:18:LEU:HD12	1.90	0.71
1:C:118:GLU:OXT	1:C:118:GLU:HG2	1.90	0.71
1:B:38:VAL:HB	1:B:39:PRO:HD3	1.72	0.71
1:C:60:LEU:H	1:C:60:LEU:HD23	1.55	0.71
1:G:35:THR:HG22	1:G:113:LEU:HD23	1.73	0.71
1:H:82:GLU:HG2	1:H:83:ILE:HD13	1.73	0.70
1:E:60:LEU:H	1:E:60:LEU:CD2	1.94	0.70
1:G:51:LEU:HD13	1:G:70:LEU:HD11	1.74	0.70
1:D:33:ARG:CD	1:D:113:LEU:HD21	2.21	0.70
1:G:64:ARG:HE	1:H:18:LEU:HD11	1.55	0.70
1:C:53:HIS:HE1	1:D:53:HIS:CE1	2.10	0.70
1:I:70:LEU:HD11	1:I:75:LEU:HD13	1.73	0.70
1:E:104:ARG:HD2	1:E:107:ASP:OD2	1.91	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:96:ARG:HG2	1:I:98:LEU:CD1	2.23	0.69
1:E:27:SER:HB2	1:E:34:ILE:HD11	1.74	0.69
1:F:38:VAL:HB	1:F:39:PRO:HD3	1.74	0.69
1:G:65:LEU:HD22	1:H:65:LEU:HD12	1.75	0.69
1:D:94:TYR:O	1:D:117:VAL:HG12	1.93	0.69
1:A:53:HIS:NE2	1:B:53:HIS:HE1	1.91	0.68
1:G:64:ARG:NH2	1:H:69:ASP:OD2	2.27	0.68
1:I:94:TYR:O	1:I:117:VAL:HG12	1.93	0.68
1:I:90:ARG:NH2	1:I:118:GLU:HA	2.08	0.68
1:E:56:LYS:HG2	2:E:127:HOH:O	1.94	0.68
1:H:102:GLU:HB3	1:H:111:LEU:HD12	1.76	0.68
1:A:57:ARG:NH1	1:A:57:ARG:HG2	2.07	0.68
1:C:105:ARG:CD	1:C:105:ARG:H	2.07	0.68
1:B:88:ARG:HH22	1:G:22:ARG:NH1	1.92	0.68
1:G:65:LEU:HD13	1:H:65:LEU:HB3	1.75	0.67
1:G:64:ARG:CB	1:G:64:ARG:HH11	2.08	0.67
1:I:63:ARG:HA	1:I:80:PHE:CZ	2.29	0.67
1:E:72:ASP:OD2	1:E:74:LYS:HD3	1.93	0.67
1:C:45:ARG:HH11	1:C:45:ARG:HG2	1.60	0.67
1:I:104:ARG:HG2	1:I:105:ARG:N	2.10	0.67
1:F:103:ARG:HD3	1:F:108:GLY:O	1.95	0.67
1:E:33:ARG:CD	1:G:33:ARG:HH22	2.07	0.67
1:B:86:ARG:NH1	1:B:118:GLU:HB2	2.10	0.67
1:C:103:ARG:HB3	1:C:108:GLY:O	1.95	0.66
1:G:24:GLN:NE2	1:G:36:THR:HG21	2.09	0.66
1:D:58:GLY:HA2	1:D:80:PHE:CE2	2.29	0.66
1:H:96:ARG:HG2	1:H:98:LEU:HD11	1.76	0.66
1:H:28:LEU:HD21	1:H:115:GLU:HA	1.77	0.66
1:H:104:ARG:HB3	1:H:109:ALA:HB3	1.77	0.66
1:A:45:ARG:HG3	1:A:46:GLY:N	2.11	0.66
1:A:62:ALA:O	1:A:66:VAL:HG23	1.95	0.66
1:F:67:LEU:O	1:F:67:LEU:HD22	1.95	0.66
1:C:72:ASP:OD1	1:C:75:LEU:HG	1.96	0.66
1:I:102:GLU:HG2	1:I:103:ARG:N	2.11	0.66
1:A:53:HIS:HB2	2:A:119:HOH:O	1.96	0.66
1:H:105:ARG:H	1:H:105:ARG:CD	2.10	0.65
1:D:38:VAL:HB	1:D:39:PRO:HD3	1.78	0.65
1:H:94:TYR:O	1:H:117:VAL:HG12	1.96	0.65
1:G:105:ARG:HG2	1:G:105:ARG:NH1	2.10	0.65
1:B:87:TYR:CD2	1:B:90:ARG:HG3	2.24	0.65
1:A:105:ARG:N	1:A:105:ARG:HD3	2.03	0.65
1:G:62:ALA:O	1:G:66:VAL:HG23	1.97	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:56:LYS:HE2	1:A:94:TYR:OH	1.97	0.65
1:C:36:THR:HG22	1:C:37:THR:N	2.08	0.65
1:C:106:GLY:CA	1:E:38:VAL:HG11	2.25	0.64
1:I:104:ARG:CG	1:I:105:ARG:H	2.10	0.64
1:B:105:ARG:HB3	1:B:105:ARG:NH1	2.05	0.64
1:H:47:PHE:CE2	1:H:51:LEU:HD11	2.32	0.64
1:H:118:GLU:OXT	1:H:118:GLU:HG2	1.97	0.64
1:A:69:ASP:OD2	1:B:64:ARG:NH2	2.30	0.64
1:B:72:ASP:O	1:B:76:VAL:HG23	1.97	0.64
1:B:84:ALA:HB3	1:B:85:PRO:HD3	1.80	0.64
1:G:60:LEU:HD23	1:G:60:LEU:H	1.61	0.64
1:B:118:GLU:HG2	1:B:118:GLU:OXT	1.98	0.64
1:I:98:LEU:N	1:I:98:LEU:HD12	2.13	0.64
1:F:117:VAL:O	1:F:118:GLU:HB2	1.97	0.64
1:B:78:LYS:O	1:B:82:GLU:HB3	1.98	0.64
1:H:74:LYS:HA	1:H:77:ARG:CZ	2.28	0.63
1:E:20:LEU:HD22	1:E:24:GLN:HG3	1.80	0.63
1:F:60:LEU:CD2	1:F:60:LEU:H	2.00	0.63
1:D:45:ARG:HG3	1:D:46:GLY:N	2.13	0.63
1:H:84:ALA:HB3	1:H:85:PRO:HD3	1.81	0.63
1:D:84:ALA:HB3	1:D:85:PRO:HD3	1.81	0.63
1:A:47:PHE:CE2	1:A:51:LEU:HD11	2.34	0.62
1:A:20:LEU:O	1:A:24:GLN:HG3	2.00	0.62
1:I:117:VAL:O	1:I:118:GLU:HB2	2.00	0.62
1:C:78:LYS:O	1:C:82:GLU:HB3	2.00	0.61
1:I:22:ARG:HG2	1:I:70:LEU:HD23	1.82	0.61
1:C:60:LEU:H	1:C:60:LEU:CD2	2.10	0.61
1:H:14:SER:O	1:H:18:LEU:HD23	2.00	0.61
1:H:74:LYS:HA	1:H:77:ARG:HE	1.66	0.61
1:B:17:ARG:NH1	1:B:17:ARG:HG3	2.13	0.61
1:F:94:TYR:O	1:F:117:VAL:HG12	2.00	0.61
1:H:45:ARG:HG3	1:H:46:GLY:N	2.15	0.61
1:H:78:LYS:O	1:H:82:GLU:HB3	2.01	0.61
1:F:102:GLU:HG2	1:F:103:ARG:N	2.16	0.61
1:D:58:GLY:HA2	1:D:80:PHE:HE2	1.66	0.61
1:F:60:LEU:HD23	1:F:60:LEU:N	2.12	0.61
1:A:63:ARG:HG2	1:A:80:PHE:CE2	2.36	0.61
1:H:95:THR:HG22	1:H:116:LEU:HD23	1.83	0.61
1:I:78:LYS:HE3	1:I:82:GLU:OE2	2.01	0.61
1:H:74:LYS:HA	1:H:77:ARG:NH2	2.16	0.60
1:I:26:LYS:HG2	1:I:75:LEU:HD11	1.83	0.60
1:E:63:ARG:NH2	1:E:77:ARG:HA	2.15	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:74:LYS:HA	1:I:77:ARG:HH21	1.65	0.60
1:H:73:VAL:O	1:H:77:ARG:HG3	2.01	0.60
1:H:105:ARG:HD2	2:H:122:HOH:O	2.02	0.60
1:C:84:ALA:HB3	1:C:85:PRO:HD3	1.83	0.60
1:E:117:VAL:O	1:E:118:GLU:HB2	2.01	0.60
1:A:76:VAL:O	1:A:80:PHE:HD1	1.85	0.60
1:G:67:LEU:CD2	1:G:76:VAL:HG21	2.30	0.59
1:I:98:LEU:HD13	1:I:113:LEU:CD1	2.32	0.59
1:E:33:ARG:CB	1:G:33:ARG:HH22	2.14	0.59
1:C:104:ARG:HB2	1:C:105:ARG:NH1	2.17	0.59
1:I:20:LEU:HD22	1:I:24:GLN:HG3	1.83	0.59
1:E:33:ARG:HD2	1:G:33:ARG:NH2	2.17	0.59
1:H:21:TYR:HA	1:H:24:GLN:OE1	2.01	0.59
1:E:118:GLU:OXT	1:E:118:GLU:HG2	2.03	0.59
1:F:45:ARG:HG2	1:F:45:ARG:HH11	1.67	0.59
1:H:72:ASP:OD1	1:H:74:LYS:HE2	2.03	0.59
1:E:60:LEU:HD23	1:E:60:LEU:N	2.06	0.59
1:G:38:VAL:HB	1:G:39:PRO:HD3	1.83	0.59
1:G:102:GLU:HB3	2:G:135:HOH:O	2.02	0.59
1:G:52:ILE:HA	2:G:134:HOH:O	2.02	0.59
1:A:53:HIS:NE2	1:B:53:HIS:CE1	2.70	0.58
1:G:14:SER:HB3	1:I:89:ASP:HA	1.86	0.58
1:E:24:GLN:NE2	1:E:36:THR:HG21	2.18	0.58
1:G:78:LYS:O	1:G:82:GLU:HB3	2.02	0.58
1:G:14:SER:O	1:G:18:LEU:HD23	2.03	0.58
1:E:78:LYS:O	1:E:82:GLU:HB3	2.04	0.58
1:D:33:ARG:HD3	1:D:113:LEU:CD2	2.33	0.58
1:E:100:LEU:HD23	1:G:100:LEU:HD23	1.85	0.58
1:B:72:ASP:OD2	1:B:74:LYS:HG3	2.03	0.58
1:C:74:LYS:CE	1:F:88:ARG:HH21	2.16	0.57
1:E:27:SER:CB	1:E:34:ILE:HD11	2.33	0.57
1:E:85:PRO:HA	1:E:88:ARG:HD3	1.86	0.57
1:A:84:ALA:HB3	1:A:85:PRO:HD3	1.87	0.57
1:H:63:ARG:HA	1:H:80:PHE:CZ	2.40	0.57
1:A:113:LEU:C	1:A:113:LEU:HD13	2.25	0.57
1:C:25:ALA:O	1:C:29:LEU:HD23	2.05	0.57
1:B:88:ARG:NH2	1:G:22:ARG:HH11	2.03	0.56
1:H:100:LEU:HD21	1:H:113:LEU:N	2.20	0.56
1:E:33:ARG:HD2	1:G:33:ARG:HH22	1.70	0.56
1:F:71:GLN:HA	1:F:71:GLN:HE21	1.70	0.56
1:C:117:VAL:O	1:C:118:GLU:HB2	2.05	0.56
1:D:72:ASP:OD2	1:D:72:ASP:C	2.43	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:68:ARG:HB3	1:H:68:ARG:NH1	2.21	0.56
1:H:20:LEU:HD22	1:H:24:GLN:CD	2.25	0.56
1:F:34:ILE:HD13	1:F:35:THR:H	1.70	0.55
1:D:44:LEU:HD22	1:D:48:VAL:HG23	1.87	0.55
1:A:18:LEU:HD13	1:A:18:LEU:O	2.06	0.55
1:G:98:LEU:CD1	1:G:113:LEU:HD12	2.31	0.55
1:F:48:VAL:O	1:F:52:ILE:HG13	2.07	0.55
1:I:84:ALA:HB3	1:I:85:PRO:HD3	1.88	0.55
1:H:104:ARG:CB	1:H:109:ALA:HB3	2.36	0.55
1:D:38:VAL:O	1:D:42:LYS:HG2	2.06	0.55
1:F:118:GLU:OXT	1:F:118:GLU:HG2	2.06	0.55
1:E:84:ALA:HA	2:E:127:HOH:O	2.07	0.55
1:H:90:ARG:HG3	1:H:90:ARG:HH11	1.72	0.55
1:E:67:LEU:O	1:E:67:LEU:HD23	2.06	0.55
1:H:103:ARG:O	1:H:108:GLY:HA2	2.07	0.55
1:D:73:VAL:O	1:D:77:ARG:HG3	2.07	0.55
1:C:74:LYS:H	1:C:74:LYS:HD3	1.72	0.55
1:G:81:ASP:OD2	1:G:81:ASP:N	2.39	0.55
1:G:83:ILE:HG23	1:G:87:TYR:HE1	1.72	0.54
1:A:105:ARG:N	1:A:105:ARG:CD	2.62	0.54
1:H:79:LEU:HA	1:H:83:ILE:HG12	1.88	0.54
1:G:67:LEU:HD23	1:G:76:VAL:CG2	2.34	0.54
1:B:57:ARG:HG2	1:B:59:ASP:OD1	2.08	0.54
1:B:14:SER:O	1:B:18:LEU:HD22	2.07	0.54
1:B:104:ARG:O	1:B:108:GLY:HA2	2.07	0.54
1:H:56:LYS:O	1:H:88:ARG:NH2	2.39	0.54
1:I:64:ARG:NH1	1:I:64:ARG:HB3	2.22	0.54
1:D:40:LYS:HE3	2:D:138:HOH:O	2.07	0.54
1:G:31:HIS:ND1	1:G:31:HIS:N	2.56	0.54
1:C:106:GLY:HA2	1:E:38:VAL:CG1	2.30	0.54
1:I:72:ASP:O	1:I:76:VAL:HG23	2.08	0.54
1:F:38:VAL:HG23	1:F:110:PRO:HG2	1.90	0.54
1:H:61:HIS:HA	1:H:64:ARG:HH12	1.73	0.54
1:C:102:GLU:HB2	1:G:105:ARG:NH1	2.22	0.54
1:E:53:HIS:CE1	1:F:57:ARG:HE	2.26	0.54
1:C:104:ARG:HG2	1:C:109:ALA:HB3	1.89	0.54
1:C:64:ARG:HD2	1:C:68:ARG:HH22	1.73	0.54
1:H:38:VAL:CG1	1:H:42:LYS:HE3	2.37	0.54
1:B:25:ALA:O	1:B:29:LEU:HD23	2.08	0.54
1:E:47:PHE:O	1:E:51:LEU:HG	2.07	0.53
1:H:96:ARG:HG2	1:H:98:LEU:CD1	2.38	0.53
1:C:117:VAL:O	1:C:118:GLU:CB	2.56	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:113:LEU:HD13	1:A:113:LEU:O	2.08	0.53
1:E:28:LEU:HD21	1:E:115:GLU:HA	1.91	0.53
1:G:53:HIS:CD2	1:H:57:ARG:HD3	2.44	0.53
1:F:72:ASP:O	1:F:76:VAL:HG23	2.09	0.53
1:E:24:GLN:HE21	1:E:36:THR:HG21	1.74	0.53
1:I:86:ARG:HH11	1:I:86:ARG:CB	2.22	0.53
1:F:34:ILE:CD1	1:F:35:THR:H	2.22	0.53
1:F:78:LYS:O	1:F:82:GLU:HB3	2.08	0.53
1:B:88:ARG:HH22	1:G:22:ARG:HH11	1.57	0.53
1:D:83:ILE:HD13	1:D:86:ARG:NH2	2.24	0.53
1:G:57:ARG:NH2	1:H:50:HIS:ND1	2.48	0.53
1:B:86:ARG:NH1	1:B:87:TYR:OH	2.42	0.52
1:I:22:ARG:CZ	1:I:71:GLN:HG2	2.38	0.52
1:I:56:LYS:NZ	1:I:88:ARG:HA	2.24	0.52
1:A:57:ARG:HG2	1:A:59:ASP:OD1	2.09	0.52
1:C:14:SER:O	1:C:18:LEU:HD23	2.08	0.52
1:G:66:VAL:HG12	1:G:76:VAL:HG22	1.91	0.52
1:D:72:ASP:O	1:D:76:VAL:HG23	2.09	0.52
1:H:98:LEU:O	1:H:100:LEU:HD23	2.09	0.52
1:D:37:THR:HB	1:D:39:PRO:HD2	1.91	0.52
1:H:39:PRO:O	1:H:43:GLU:HG2	2.09	0.52
1:C:28:LEU:HD13	1:C:28:LEU:O	2.10	0.52
1:I:26:LYS:CG	1:I:75:LEU:HD11	2.39	0.52
1:H:34:ILE:HG22	1:H:114:VAL:HB	1.91	0.52
1:G:20:LEU:HD22	1:G:24:GLN:CD	2.30	0.52
1:A:18:LEU:HD12	1:A:22:ARG:NH2	2.25	0.52
1:C:44:LEU:O	1:C:48:VAL:HG23	2.08	0.52
1:D:19:ALA:HA	1:D:22:ARG:NH1	2.24	0.52
1:G:29:LEU:N	1:G:29:LEU:HD22	2.25	0.52
1:E:65:LEU:HD12	1:F:65:LEU:HD12	1.90	0.51
1:B:49:ASP:OD2	1:B:95:THR:HG23	2.10	0.51
1:H:58:GLY:HA2	1:H:80:PHE:CE2	2.45	0.51
1:D:60:LEU:HD23	1:D:60:LEU:N	2.21	0.51
1:B:77:ARG:HH21	1:I:88:ARG:NH2	2.09	0.51
1:H:48:VAL:O	1:H:52:ILE:HG13	2.10	0.51
1:F:78:LYS:HG3	1:F:82:GLU:OE2	2.10	0.51
1:D:78:LYS:O	1:D:82:GLU:HB3	2.11	0.51
1:H:105:ARG:HD3	1:H:105:ARG:N	2.18	0.51
1:F:74:LYS:N	1:F:74:LYS:HD3	2.02	0.51
1:A:56:LYS:NZ	1:A:90:ARG:O	2.43	0.51
1:I:61:HIS:O	1:I:65:LEU:HD23	2.11	0.51
1:E:38:VAL:HB	1:E:39:PRO:HD3	1.92	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:78:LYS:HE3	1:H:82:GLU:OE1	2.10	0.51
1:E:18:LEU:HD21	1:F:64:ARG:CZ	2.40	0.51
1:H:103:ARG:C	1:H:108:GLY:HA2	2.31	0.51
1:F:55:ALA:CB	1:F:79:LEU:HD22	2.40	0.51
1:F:84:ALA:HB3	1:F:85:PRO:HD3	1.93	0.51
1:G:97:VAL:HG22	1:G:114:VAL:HG22	1.92	0.51
1:A:72:ASP:O	1:A:76:VAL:HG23	2.11	0.51
1:A:50:HIS:O	1:A:54:LEU:HD12	2.11	0.51
1:C:45:ARG:NH1	1:C:45:ARG:HG2	2.25	0.51
1:G:117:VAL:O	1:G:118:GLU:CG	2.56	0.50
1:F:71:GLN:HA	1:F:71:GLN:NE2	2.25	0.50
1:A:53:HIS:HD1	1:A:54:LEU:N	2.09	0.50
1:F:102:GLU:CG	1:F:103:ARG:N	2.74	0.50
1:D:61:HIS:O	1:D:65:LEU:HD23	2.12	0.50
1:G:102:GLU:CB	2:G:135:HOH:O	2.59	0.50
1:D:89:ASP:OD2	1:D:90:ARG:N	2.45	0.50
1:F:45:ARG:HG3	1:F:95:THR:OG1	2.12	0.50
1:C:23:ASN:OD1	1:C:24:GLN:HG3	2.12	0.50
1:B:117:VAL:O	1:B:118:GLU:HB2	2.12	0.50
1:C:83:ILE:O	1:C:86:ARG:HB3	2.12	0.49
1:E:74:LYS:H	1:E:74:LYS:HD3	1.76	0.49
1:A:113:LEU:HD22	1:A:114:VAL:N	2.27	0.49
1:D:65:LEU:HD22	1:D:65:LEU:N	2.26	0.49
1:A:42:LYS:HE2	1:G:107:ASP:OD2	2.12	0.49
1:G:96:ARG:NE	1:G:115:GLU:OE1	2.45	0.49
1:I:70:LEU:CD1	1:I:75:LEU:HD13	2.40	0.49
1:F:103:ARG:HD3	1:F:108:GLY:C	2.33	0.49
1:B:34:ILE:HD13	1:B:35:THR:N	2.23	0.49
1:F:22:ARG:HD3	1:F:71:GLN:HG2	1.94	0.49
1:C:60:LEU:N	1:C:60:LEU:HD23	2.25	0.49
1:E:52:ILE:O	1:E:56:LYS:HG3	2.13	0.49
1:H:26:LYS:HE2	1:H:70:LEU:CD2	2.42	0.49
1:H:73:VAL:CG1	1:H:77:ARG:HD3	2.39	0.49
1:H:56:LYS:HE2	1:H:94:TYR:OH	2.13	0.49
1:A:63:ARG:HA	1:A:80:PHE:CZ	2.47	0.49
1:C:36:THR:CG2	1:C:37:THR:H	2.12	0.49
1:I:90:ARG:NH2	1:I:118:GLU:HG3	2.28	0.49
1:B:83:ILE:HG23	1:B:87:TYR:HE1	1.78	0.49
1:I:20:LEU:O	1:I:24:GLN:HG3	2.13	0.49
1:G:68:ARG:HD2	1:H:68:ARG:CD	2.26	0.49
1:E:99:LYS:HB3	1:G:102:GLU:OE2	2.13	0.49
1:E:70:LEU:CD2	1:E:72:ASP:HB3	2.42	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:76:VAL:O	1:G:80:PHE:HD1	1.96	0.48
1:H:36:THR:CG2	1:H:40:LYS:HD3	2.43	0.48
1:F:63:ARG:HA	1:F:80:PHE:CZ	2.48	0.48
1:A:32:GLY:HA2	1:A:116:LEU:HD11	1.95	0.48
1:H:48:VAL:HB	1:H:95:THR:HG21	1.95	0.48
1:C:65:LEU:HD12	1:D:65:LEU:HD12	1.95	0.48
1:D:89:ASP:OD2	1:D:90:ARG:HG2	2.13	0.48
1:E:49:ASP:OD2	1:E:95:THR:HG22	2.13	0.48
1:H:63:ARG:NH2	1:H:77:ARG:HA	2.28	0.48
1:H:74:LYS:HB3	1:H:77:ARG:NH2	2.28	0.48
1:D:56:LYS:HE2	1:D:94:TYR:OH	2.14	0.48
1:G:72:ASP:OD1	1:G:74:LYS:HE3	2.12	0.48
1:H:18:LEU:HB3	1:H:22:ARG:NH2	2.22	0.48
1:H:37:THR:HG22	1:H:109:ALA:HB1	1.95	0.48
1:H:90:ARG:HG3	1:H:90:ARG:NH1	2.28	0.48
1:B:61:HIS:O	1:B:65:LEU:CD2	2.61	0.48
1:A:117:VAL:O	1:A:118:GLU:CG	2.61	0.48
1:I:67:LEU:HD12	1:I:76:VAL:HG21	1.94	0.48
1:I:113:LEU:HD22	1:I:114:VAL:N	2.29	0.48
1:D:62:ALA:O	1:D:66:VAL:HG23	2.13	0.48
1:I:26:LYS:HG2	1:I:75:LEU:CD1	2.43	0.48
1:G:83:ILE:O	1:G:86:ARG:HB3	2.13	0.48
1:I:55:ALA:HB1	1:I:84:ALA:HB2	1.95	0.48
1:G:96:ARG:HG3	1:G:115:GLU:HG3	1.96	0.48
1:D:28:LEU:HD21	1:D:115:GLU:HA	1.96	0.48
1:F:63:ARG:NH1	1:F:76:VAL:HG12	2.29	0.48
1:E:56:LYS:NZ	1:E:90:ARG:O	2.47	0.48
1:E:69:ASP:OD2	1:F:64:ARG:NH2	2.47	0.48
1:E:53:HIS:CE1	1:E:54:LEU:HG	2.49	0.48
1:D:20:LEU:O	1:D:24:GLN:HG3	2.13	0.48
1:A:52:ILE:O	1:A:56:LYS:HG3	2.14	0.47
1:I:74:LYS:HA	1:I:77:ARG:NH2	2.29	0.47
1:A:68:ARG:HG2	1:B:68:ARG:HH11	1.79	0.47
1:I:60:LEU:HD23	1:I:60:LEU:H	1.79	0.47
1:E:75:LEU:HD23	1:E:75:LEU:HA	1.71	0.47
1:H:64:ARG:HB3	1:H:64:ARG:NH1	2.29	0.47
1:F:22:ARG:O	1:F:26:LYS:HG3	2.15	0.47
1:A:117:VAL:O	1:A:118:GLU:HG2	2.15	0.47
1:B:67:LEU:C	1:B:67:LEU:HD13	2.34	0.47
1:G:35:THR:CG2	1:G:113:LEU:HD23	2.43	0.47
1:C:85:PRO:HA	1:C:88:ARG:HD3	1.97	0.47
1:C:20:LEU:O	1:C:23:ASN:OD1	2.33	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:52:ILE:O	1:C:56:LYS:HG3	2.15	0.47
1:E:102:GLU:HG2	1:E:103:ARG:N	2.30	0.47
1:D:60:LEU:CD2	1:D:60:LEU:H	2.14	0.47
1:I:29:LEU:HD12	1:I:83:ILE:HG13	1.96	0.47
1:C:72:ASP:O	1:C:76:VAL:HG23	2.14	0.47
1:G:64:ARG:NE	1:H:18:LEU:HD11	2.27	0.47
1:H:26:LYS:HZ1	1:H:72:ASP:HB2	1.76	0.47
1:G:113:LEU:C	1:G:113:LEU:HD13	2.34	0.47
1:D:52:ILE:HD12	1:D:94:TYR:HB2	1.95	0.47
1:E:45:ARG:NH2	2:E:130:HOH:O	2.48	0.47
1:I:67:LEU:CD1	1:I:73:VAL:HG22	2.37	0.47
1:H:28:LEU:HD11	1:H:116:LEU:HG	1.97	0.47
1:F:47:PHE:O	1:F:50:HIS:HB3	2.15	0.47
1:C:37:THR:OG1	1:C:39:PRO:HD2	2.14	0.47
1:E:33:ARG:HB3	1:G:33:ARG:HH22	1.80	0.47
1:H:38:VAL:HG23	1:H:110:PRO:O	2.15	0.47
1:D:17:ARG:HA	1:D:17:ARG:HD3	1.75	0.47
1:I:96:ARG:CG	1:I:98:LEU:HD11	2.39	0.47
1:B:45:ARG:HG3	1:B:46:GLY:N	2.27	0.47
1:I:86:ARG:HD3	1:I:118:GLU:OE1	2.15	0.46
1:C:53:HIS:CE1	1:D:53:HIS:CE1	2.87	0.46
1:E:67:LEU:C	1:E:67:LEU:HD23	2.36	0.46
1:B:59:ASP:HB2	1:B:60:LEU:HD23	1.97	0.46
1:H:20:LEU:HD22	1:H:24:GLN:NE2	2.31	0.46
1:H:38:VAL:HG13	1:H:42:LYS:HE3	1.97	0.46
1:C:52:ILE:HD12	1:C:94:TYR:HB2	1.97	0.46
1:E:66:VAL:HG12	1:E:76:VAL:HG22	1.97	0.46
1:B:58:GLY:HA2	1:B:80:PHE:HE2	1.79	0.46
1:I:33:ARG:HE	1:I:113:LEU:HD21	1.80	0.46
1:I:74:LYS:CA	1:I:77:ARG:HH21	2.27	0.46
1:E:83:ILE:HD13	1:E:86:ARG:HH22	1.79	0.46
1:G:28:LEU:O	1:G:32:GLY:HA2	2.14	0.46
1:E:45:ARG:NH1	1:E:97:VAL:HB	2.31	0.46
1:B:77:ARG:HH12	1:I:57:ARG:HA	1.80	0.46
1:B:61:HIS:O	1:B:65:LEU:HD23	2.15	0.46
1:H:71:GLN:H	1:H:71:GLN:HG2	1.59	0.46
1:A:32:GLY:O	1:A:116:LEU:HD12	2.15	0.46
1:F:37:THR:HG21	1:F:104:ARG:NH2	2.31	0.46
1:G:35:THR:HG22	1:G:113:LEU:CD2	2.42	0.46
1:B:60:LEU:H	1:B:60:LEU:CD2	2.23	0.46
1:H:20:LEU:O	1:H:23:ASN:HB3	2.15	0.46
1:H:26:LYS:HZ3	1:H:72:ASP:HB2	1.78	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:72:ASP:C	1:H:72:ASP:OD2	2.53	0.46
1:H:29:LEU:HD11	1:H:79:LEU:HD21	1.98	0.46
1:A:53:HIS:C	1:A:53:HIS:ND1	2.68	0.46
1:F:74:LYS:H	1:F:74:LYS:CD	1.99	0.46
1:B:105:ARG:CB	1:B:105:ARG:HH11	2.10	0.46
1:H:14:SER:N	1:H:17:ARG:HG3	2.31	0.46
1:E:104:ARG:CD	1:E:107:ASP:OD2	2.62	0.46
1:A:64:ARG:HG2	1:A:68:ARG:NH2	2.31	0.46
1:D:33:ARG:NE	1:D:113:LEU:HD21	2.30	0.46
1:F:37:THR:HG21	1:F:104:ARG:HH21	1.80	0.45
1:F:103:ARG:HA	1:F:111:LEU:HG	1.98	0.45
1:H:103:ARG:HH21	1:H:110:PRO:HA	1.80	0.45
1:F:72:ASP:OD2	1:F:74:LYS:HE2	2.15	0.45
1:C:22:ARG:HD3	1:C:71:GLN:CG	2.41	0.45
1:F:22:ARG:NE	1:F:69:ASP:O	2.50	0.45
1:G:84:ALA:HB3	1:G:85:PRO:HD3	1.99	0.45
1:E:45:ARG:HD3	1:E:97:VAL:CG2	2.37	0.45
1:G:64:ARG:NH1	1:G:64:ARG:HB3	2.15	0.45
1:E:78:LYS:HE2	1:E:83:ILE:HD11	1.97	0.45
1:D:25:ALA:O	1:D:29:LEU:HD22	2.16	0.45
1:B:20:LEU:HD22	1:B:24:GLN:HG3	1.99	0.45
1:D:104:ARG:O	1:D:108:GLY:HA2	2.17	0.45
1:G:65:LEU:HB3	1:H:65:LEU:HD12	1.98	0.45
1:B:60:LEU:N	1:B:60:LEU:HD23	2.25	0.45
1:F:56:LYS:HE2	1:F:94:TYR:OH	2.16	0.45
1:D:93:GLY:HA2	2:D:119:HOH:O	2.16	0.45
1:H:98:LEU:HD13	1:H:113:LEU:HD12	1.98	0.45
1:F:45:ARG:HG2	1:F:45:ARG:NH1	2.31	0.45
1:I:97:VAL:HG22	1:I:114:VAL:HG22	1.98	0.45
1:C:88:ARG:HH11	1:C:88:ARG:HG3	1.81	0.45
1:I:102:GLU:CG	1:I:103:ARG:N	2.80	0.45
1:G:69:ASP:OD2	1:H:65:LEU:HD11	2.17	0.44
1:E:117:VAL:O	1:E:118:GLU:CB	2.65	0.44
1:G:83:ILE:CG2	1:G:87:TYR:HE1	2.30	0.44
1:H:74:LYS:HA	1:H:77:ARG:HH21	1.81	0.44
1:A:116:LEU:HD12	1:A:116:LEU:N	2.17	0.44
1:A:57:ARG:CG	1:A:57:ARG:HH11	2.22	0.44
1:G:22:ARG:CZ	1:G:71:GLN:HG3	2.48	0.44
1:G:24:GLN:HE21	1:G:36:THR:HG21	1.79	0.44
1:F:67:LEU:C	1:F:67:LEU:HD22	2.38	0.44
1:G:45:ARG:HG3	1:G:46:GLY:N	2.31	0.44
1:F:34:ILE:HG22	1:F:114:VAL:HB	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:14:SER:O	1:D:18:LEU:HD23	2.18	0.44
1:H:38:VAL:O	1:H:42:LYS:HG3	2.17	0.44
1:I:64:ARG:HH11	1:I:64:ARG:HB3	1.82	0.44
1:C:61:HIS:O	1:C:65:LEU:CD2	2.65	0.44
1:A:86:ARG:NH1	1:A:118:GLU:HG3	2.33	0.44
1:G:14:SER:N	1:G:17:ARG:CG	2.77	0.44
1:G:63:ARG:HA	1:G:80:PHE:CZ	2.53	0.44
1:H:78:LYS:HG2	1:H:83:ILE:HD11	2.00	0.44
1:E:72:ASP:OD2	1:E:74:LYS:HE2	2.18	0.44
1:C:28:LEU:HD13	1:C:28:LEU:C	2.38	0.44
1:A:117:VAL:O	1:A:118:GLU:CB	2.66	0.44
1:I:102:GLU:HG2	1:I:103:ARG:H	1.82	0.44
1:A:91:GLN:HG2	1:A:91:GLN:O	2.17	0.44
1:A:99:LYS:HB2	1:G:106:GLY:O	2.17	0.44
1:E:98:LEU:HD22	1:G:102:GLU:HG3	2.00	0.44
1:B:38:VAL:CB	1:B:39:PRO:HD3	2.44	0.44
1:E:33:ARG:NE	1:G:33:ARG:HH22	2.16	0.44
1:G:69:ASP:CG	1:H:64:ARG:HH21	2.22	0.43
1:H:28:LEU:O	1:H:32:GLY:N	2.51	0.43
1:D:61:HIS:O	1:D:65:LEU:CD2	2.66	0.43
1:I:47:PHE:O	1:I:51:LEU:HG	2.18	0.43
1:D:47:PHE:O	1:D:50:HIS:HB3	2.17	0.43
1:B:77:ARG:NH2	1:I:88:ARG:NH2	2.66	0.43
1:I:67:LEU:HD11	1:I:73:VAL:CG2	2.34	0.43
1:H:78:LYS:CG	1:H:83:ILE:HD11	2.48	0.43
1:G:51:LEU:CD1	1:G:70:LEU:HD11	2.46	0.43
1:F:52:ILE:O	1:F:56:LYS:HG3	2.19	0.43
1:D:68:ARG:O	1:D:71:GLN:OE1	2.36	0.43
1:E:70:LEU:C	1:E:70:LEU:CD2	2.86	0.43
1:F:90:ARG:HB2	1:F:90:ARG:HE	1.50	0.43
1:H:95:THR:HG22	1:H:116:LEU:CD2	2.48	0.43
1:D:38:VAL:N	1:D:39:PRO:CD	2.82	0.43
1:E:56:LYS:HE2	1:E:94:TYR:OH	2.19	0.43
1:A:29:LEU:HD12	1:A:83:ILE:HG13	2.00	0.43
1:F:87:TYR:OH	1:F:116:LEU:HD23	2.18	0.43
1:F:83:ILE:CD1	1:F:86:ARG:NH2	2.82	0.43
1:H:38:VAL:HB	1:H:39:PRO:HD3	2.00	0.43
1:B:89:ASP:HB2	1:G:74:LYS:NZ	2.34	0.43
1:H:66:VAL:HG12	1:H:76:VAL:HG22	2.00	0.43
1:D:57:ARG:NH2	1:D:59:ASP:OD1	2.43	0.43
1:C:37:THR:HG1	1:C:40:LYS:HG2	1.84	0.43
1:H:83:ILE:N	1:H:83:ILE:HD13	2.34	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:83:ILE:HD12	1:F:86:ARG:NH2	2.34	0.43
1:D:74:LYS:HB2	1:D:74:LYS:HE2	1.64	0.43
1:G:26:LYS:HE2	1:G:75:LEU:HD12	2.00	0.42
1:C:36:THR:CG2	1:C:37:THR:N	2.77	0.42
1:A:53:HIS:ND1	1:A:54:LEU:N	2.68	0.42
1:A:64:ARG:HE	1:A:68:ARG:HH22	1.67	0.42
1:A:61:HIS:O	1:A:65:LEU:HG	2.18	0.42
1:F:65:LEU:HD22	1:F:65:LEU:N	2.34	0.42
1:E:84:ALA:CB	2:E:127:HOH:O	2.66	0.42
1:E:22:ARG:HG2	1:E:26:LYS:HE3	2.00	0.42
1:I:113:LEU:HD13	1:I:113:LEU:O	2.20	0.42
1:I:98:LEU:N	1:I:98:LEU:CD1	2.81	0.42
1:E:14:SER:N	1:E:17:ARG:HG3	2.35	0.42
1:E:22:ARG:O	1:E:26:LYS:HG3	2.19	0.42
1:B:99:LYS:HE3	1:B:110:PRO:HB2	2.00	0.42
1:D:103:ARG:HG2	1:D:110:PRO:HA	2.02	0.42
1:B:58:GLY:HA2	1:B:80:PHE:CE2	2.55	0.42
1:C:61:HIS:O	1:C:65:LEU:HD22	2.20	0.42
1:G:29:LEU:CD2	1:G:29:LEU:N	2.83	0.42
1:B:90:ARG:HG2	1:B:90:ARG:H	1.59	0.42
1:G:22:ARG:NH1	1:G:71:GLN:HG3	2.34	0.42
1:E:33:ARG:CD	1:G:33:ARG:NH2	2.76	0.42
1:A:61:HIS:ND1	1:A:64:ARG:NH1	2.61	0.42
1:G:91:GLN:O	1:G:91:GLN:NE2	2.52	0.42
1:A:55:ALA:HA	1:A:80:PHE:CE2	2.55	0.42
1:H:113:LEU:C	1:H:113:LEU:HD13	2.40	0.42
1:E:98:LEU:HD13	1:G:100:LEU:HD13	2.01	0.42
1:I:56:LYS:HZ3	1:I:88:ARG:HA	1.85	0.42
1:E:70:LEU:HD22	1:E:72:ASP:HB3	2.01	0.42
1:H:104:ARG:HB3	1:H:109:ALA:CB	2.48	0.41
1:B:21:TYR:HB3	1:B:47:PHE:CD2	2.55	0.41
1:I:22:ARG:NH2	1:I:71:GLN:HG2	2.35	0.41
1:C:104:ARG:CB	1:C:105:ARG:HH11	2.25	0.41
1:E:84:ALA:HB3	1:E:85:PRO:HD3	2.02	0.41
1:B:88:ARG:NH2	1:G:22:ARG:NH1	2.60	0.41
1:A:90:ARG:HD3	2:A:151:HOH:O	2.19	0.41
1:B:107:ASP:OD2	1:B:107:ASP:N	2.49	0.41
1:A:77:ARG:O	1:A:81:ASP:OD1	2.38	0.41
1:E:33:ARG:HB3	1:G:33:ARG:NH2	2.35	0.41
1:C:76:VAL:O	1:C:80:PHE:HD1	2.03	0.41
1:G:61:HIS:CE1	1:H:47:PHE:HD1	2.38	0.41
1:H:103:ARG:HB3	1:H:108:GLY:CA	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:38:VAL:N	1:C:39:PRO:CD	2.84	0.41
1:G:116:LEU:HA	1:G:116:LEU:HD23	1.86	0.41
1:A:59:ASP:O	1:A:63:ARG:HG3	2.21	0.41
1:E:56:LYS:CG	2:E:127:HOH:O	2.62	0.41
1:H:38:VAL:N	1:H:110:PRO:O	2.51	0.41
1:A:68:ARG:HG2	1:B:68:ARG:NH1	2.35	0.41
1:G:95:THR:HG22	1:G:116:LEU:HD23	2.02	0.41
1:E:58:GLY:HA2	1:E:80:PHE:CE2	2.55	0.41
1:D:52:ILE:O	1:D:56:LYS:HG3	2.20	0.41
1:E:72:ASP:OD2	1:E:74:LYS:CD	2.65	0.41
1:H:73:VAL:HG12	1:H:77:ARG:CD	2.43	0.41
1:F:37:THR:OG1	1:F:39:PRO:HD2	2.20	0.41
1:G:34:ILE:HG23	1:G:35:THR:N	2.35	0.41
1:B:17:ARG:NH1	1:B:17:ARG:CG	2.79	0.41
1:H:78:LYS:CE	1:H:83:ILE:HD11	2.51	0.41
1:I:38:VAL:HB	1:I:39:PRO:HD3	2.02	0.41
1:I:54:LEU:HD23	1:I:54:LEU:HA	1.89	0.41
1:G:21:TYR:HB3	1:G:47:PHE:CD2	2.55	0.41
1:C:36:THR:HG22	1:C:37:THR:HG23	2.03	0.41
1:I:98:LEU:HD13	1:I:113:LEU:HD13	2.00	0.41
1:E:33:ARG:HD2	1:G:33:ARG:CZ	2.51	0.40
1:D:36:THR:HB	1:D:37:THR:H	1.55	0.40
1:H:33:ARG:HG3	1:H:33:ARG:HH11	1.87	0.40
1:F:38:VAL:N	1:F:39:PRO:CD	2.84	0.40
1:H:61:HIS:HA	1:H:64:ARG:NH1	2.35	0.40
1:I:98:LEU:HD13	1:I:113:LEU:HD12	2.01	0.40
1:D:73:VAL:HG12	1:D:77:ARG:HE	1.87	0.40
1:I:64:ARG:HH11	1:I:64:ARG:CB	2.33	0.40
1:B:24:GLN:NE2	1:B:36:THR:HG21	2.36	0.40
1:C:87:TYR:OH	1:C:116:LEU:HB3	2.22	0.40
1:H:117:VAL:O	1:H:118:GLU:CB	2.69	0.40
1:C:104:ARG:HA	1:C:105:ARG:NH1	2.37	0.40
1:I:97:VAL:C	1:I:98:LEU:HD12	2.41	0.40
1:I:57:ARG:NH1	1:I:59:ASP:OD1	2.54	0.40
1:C:44:LEU:HD22	1:C:48:VAL:CG2	2.52	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	103/118 (87%)	99 (96%)	3 (3%)	1 (1%)	22	23
1	B	103/118 (87%)	98 (95%)	4 (4%)	1 (1%)	22	23
1	C	103/118 (87%)	96 (93%)	5 (5%)	2 (2%)	12	9
1	D	103/118 (87%)	94 (91%)	8 (8%)	1 (1%)	22	23
1	E	103/118 (87%)	97 (94%)	4 (4%)	2 (2%)	12	9
1	F	103/118 (87%)	98 (95%)	3 (3%)	2 (2%)	12	9
1	G	103/118 (87%)	98 (95%)	5 (5%)	0	100	100
1	H	103/118 (87%)	92 (89%)	10 (10%)	1 (1%)	22	23
1	I	103/118 (87%)	96 (93%)	5 (5%)	2 (2%)	12	9
All	All	927/1062 (87%)	868 (94%)	47 (5%)	12 (1%)	18	17

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	105	ARG
1	F	58	GLY
1	I	104	ARG
1	I	58	GLY
1	H	104	ARG
1	A	58	GLY
1	E	58	GLY
1	B	58	GLY
1	E	106	GLY
1	F	106	GLY
1	D	58	GLY
1	C	58	GLY

### 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	89/101 (88%)	69 (78%)	20 (22%)	1	1
1	B	89/101 (88%)	75 (84%)	14 (16%)	4	3
1	C	89/101 (88%)	72 (81%)	17 (19%)	2	2
1	D	89/101 (88%)	78 (88%)	11 (12%)	7	7
1	E	89/101 (88%)	72 (81%)	17 (19%)	2	2
1	F	89/101 (88%)	75 (84%)	14 (16%)	4	3
1	G	89/101 (88%)	72 (81%)	17 (19%)	2	2
1	H	89/101 (88%)	70 (79%)	19 (21%)	1	1
1	I	89/101 (88%)	75 (84%)	14 (16%)	4	3
All	All	801/909 (88%)	658 (82%)	143 (18%)	2	2

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	HIS
1	A	18	LEU
1	A	20	LEU
1	A	34	ILE
1	A	36	THR
1	A	45	ARG
1	A	50	HIS
1	A	53	HIS
1	A	57	ARG
1	A	67	LEU
1	A	81	ASP
1	A	82	GLU
1	A	88	ARG
1	A	89	ASP
1	A	90	ARG
1	A	103	ARG
1	A	104	ARG
1	A	105	ARG
1	A	113	LEU
1	A	116	LEU
1	B	14	SER
1	B	17	ARG
1	B	18	LEU

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Mol	Chain	Res	Type
1	B	20	LEU
1	B	23	ASN
1	B	28	LEU
1	B	34	ILE
1	B	36	THR
1	B	45	ARG
1	B	60	LEU
1	B	74	LYS
1	B	81	ASP
1	B	90	ARG
1	B	105	ARG
1	C	14	SER
1	C	20	LEU
1	C	23	ASN
1	C	34	ILE
1	C	44	LEU
1	C	60	LEU
1	C	67	LEU
1	C	70	LEU
1	C	74	LYS
1	C	79	LEU
1	C	81	ASP
1	C	88	ARG
1	C	90	ARG
1	C	102	GLU
1	C	105	ARG
1	C	107	ASP
1	C	113	LEU
1	D	20	LEU
1	D	29	LEU
1	D	34	ILE
1	D	36	THR
1	D	44	LEU
1	D	45	ARG
1	D	50	HIS
1	D	60	LEU
1	D	67	LEU
1	D	88	ARG
1	D	113	LEU
1	E	14	SER
1	E	18	LEU
1	E	20	LEU

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Mol	Chain	Res	Type
1	E	44	LEU
1	E	50	HIS
1	E	53	HIS
1	E	57	ARG
1	E	60	LEU
1	E	69	ASP
1	E	70	LEU
1	E	73	VAL
1	E	74	LYS
1	E	88	ARG
1	E	89	ASP
1	E	90	ARG
1	E	104	ARG
1	E	115	GLU
1	F	16	HIS
1	F	20	LEU
1	F	29	LEU
1	F	34	ILE
1	F	60	LEU
1	F	67	LEU
1	F	70	LEU
1	F	74	LYS
1	F	79	LEU
1	F	81	ASP
1	F	90	ARG
1	F	105	ARG
1	F	113	LEU
1	F	116	LEU
1	G	16	HIS
1	G	20	LEU
1	G	28	LEU
1	G	31	HIS
1	G	33	ARG
1	G	34	ILE
1	G	44	LEU
1	G	45	ARG
1	G	60	LEU
1	G	64	ARG
1	G	71	GLN
1	G	74	LYS
1	G	77	ARG
1	G	81	ASP

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Mol	Chain	Res	Type
1	G	91	GLN
1	G	98	LEU
1	G	107	ASP
1	H	20	LEU
1	H	27	SER
1	H	33	ARG
1	H	34	ILE
1	H	36	THR
1	H	45	ARG
1	H	49	ASP
1	H	50	HIS
1	H	60	LEU
1	H	67	LEU
1	H	69	ASP
1	H	70	LEU
1	H	71	GLN
1	H	74	LYS
1	H	88	ARG
1	H	100	LEU
1	H	102	GLU
1	H	103	ARG
1	H	105	ARG
1	I	15	SER
1	I	18	LEU
1	I	20	LEU
1	I	34	ILE
1	I	60	LEU
1	I	67	LEU
1	I	69	ASP
1	I	70	LEU
1	I	81	ASP
1	I	89	ASP
1	I	90	ARG
1	I	91	GLN
1	I	98	LEU
1	I	113	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	GLN
1	B	23	ASN

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Mol	Chain	Res	Type
1	B	53	HIS
1	B	71	GLN
1	C	53	HIS
1	C	71	GLN
1	D	31	HIS
1	D	53	HIS
1	E	24	GLN
1	F	24	GLN
1	F	53	HIS
1	F	71	GLN
1	G	24	GLN
1	G	61	HIS
1	G	71	GLN
1	G	91	GLN
1	H	53	HIS
1	H	71	GLN
1	I	71	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

### 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	105/118 (88%)	1.05	8 (7%) 14 20	28, 44, 59, 71	0
1	B	105/118 (88%)	1.22	21 (20%) 2 3	36, 50, 63, 67	0
1	C	105/118 (88%)	1.40	19 (18%) 2 3	34, 51, 63, 71	0
1	D	105/118 (88%)	1.23	15 (14%) 3 5	25, 42, 54, 66	0
1	E	105/118 (88%)	1.03	12 (11%) 6 9	37, 52, 63, 70	0
1	F	105/118 (88%)	1.16	13 (12%) 5 7	44, 55, 63, 68	0
1	G	105/118 (88%)	1.37	19 (18%) 2 3	37, 55, 65, 67	0
1	H	105/118 (88%)	1.83	40 (38%) 1 1	37, 58, 68, 70	0
1	I	105/118 (88%)	1.48	27 (25%) 1 2	37, 54, 65, 76	0
All	All	945/1062 (88%)	1.31	174 (18%) 2 3	25, 52, 65, 76	0

All (174) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	16	HIS	8.0
1	C	16	HIS	7.1
1	C	107	ASP	7.0
1	I	60	LEU	6.7
1	B	16	HIS	6.3
1	F	70	LEU	5.7
1	H	32	GLY	5.7
1	G	65	LEU	5.5
1	H	22	ARG	5.0
1	F	17	ARG	4.9
1	H	14	SER	4.8
1	D	106	GLY	4.8
1	F	18	LEU	4.7
1	C	14	SER	4.6
1	I	75	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
1	H	112	ALA	4.2
1	H	31	HIS	4.2
1	D	105	ARG	4.2
1	G	70	LEU	4.1
1	H	16	HIS	4.1
1	G	67	LEU	4.1
1	C	34	ILE	4.0
1	I	85	PRO	4.0
1	H	23	ASN	4.0
1	I	89	ASP	3.9
1	C	60	LEU	3.9
1	G	30	THR	3.9
1	H	38	VAL	3.8
1	H	77	ARG	3.8
1	G	14	SER	3.8
1	H	84	ALA	3.7
1	F	53	HIS	3.6
1	H	34	ILE	3.6
1	B	89	ASP	3.6
1	I	14	SER	3.6
1	C	31	HIS	3.5
1	I	113	LEU	3.5
1	H	30	THR	3.4
1	C	108	GLY	3.4
1	I	15	SER	3.4
1	G	76	VAL	3.3
1	I	118	GLU	3.3
1	I	70	LEU	3.3
1	D	14	SER	3.3
1	D	60	LEU	3.3
1	H	44	LEU	3.3
1	E	118	GLU	3.2
1	D	19	ALA	3.2
1	D	118	GLU	3.2
1	I	117	VAL	3.2
1	I	100	LEU	3.1
1	I	106	GLY	3.1
1	F	89	ASP	3.1
1	G	15	SER	3.1
1	B	54	LEU	3.1
1	H	113	LEU	3.1
1	F	103	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	28	LEU	3.0
1	E	98	LEU	3.0
1	F	79	LEU	3.0
1	G	62	ALA	3.0
1	H	111	LEU	2.9
1	H	117	VAL	2.9
1	G	20	LEU	2.9
1	B	70	LEU	2.9
1	C	73	VAL	2.9
1	G	73	VAL	2.8
1	G	31	HIS	2.8
1	D	70	LEU	2.8
1	I	98	LEU	2.8
1	B	17	ARG	2.8
1	F	84	ALA	2.8
1	A	18	LEU	2.8
1	E	34	ILE	2.8
1	I	62	ALA	2.7
1	C	70	LEU	2.7
1	G	96	ARG	2.7
1	H	42	LYS	2.7
1	F	83	ILE	2.7
1	C	47	PHE	2.7
1	I	64	ARG	2.7
1	H	51	LEU	2.7
1	I	36	THR	2.7
1	H	118	GLU	2.6
1	A	68	ARG	2.6
1	F	22	ARG	2.6
1	C	106	GLY	2.6
1	A	117	VAL	2.6
1	E	91	GLN	2.6
1	C	17	ARG	2.6
1	B	60	LEU	2.6
1	B	34	ILE	2.6
1	H	83	ILE	2.5
1	I	83	ILE	2.5
1	F	16	HIS	2.5
1	E	117	VAL	2.5
1	C	68	ARG	2.5
1	I	82	GLU	2.5
1	A	70	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	75	LEU	2.5
1	C	67	LEU	2.5
1	E	89	ASP	2.5
1	D	29	LEU	2.5
1	H	41	ALA	2.5
1	C	117	VAL	2.4
1	B	86	ARG	2.4
1	G	23	ASN	2.4
1	H	104	ARG	2.4
1	E	14	SER	2.4
1	H	107	ASP	2.4
1	D	58	GLY	2.4
1	H	18	LEU	2.4
1	H	100	LEU	2.4
1	B	44	LEU	2.4
1	C	38	VAL	2.4
1	E	73	VAL	2.4
1	B	83	ILE	2.4
1	G	61	HIS	2.4
1	A	54	LEU	2.4
1	D	117	VAL	2.4
1	H	109	ALA	2.3
1	B	14	SER	2.3
1	B	53	HIS	2.3
1	H	26	LYS	2.3
1	G	99	LYS	2.3
1	H	79	LEU	2.3
1	I	105	ARG	2.3
1	F	97	VAL	2.3
1	H	24	GLN	2.3
1	E	68	ARG	2.2
1	E	96	ARG	2.2
1	H	36	THR	2.3
1	H	68	ARG	2.2
1	H	95	THR	2.3
1	E	58	GLY	2.2
1	D	98	LEU	2.2
1	C	15	SER	2.2
1	B	99	LYS	2.2
1	I	58	GLY	2.2
1	D	67	LEU	2.2
1	H	20	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	I	79	LEU	2.2
1	B	105	ARG	2.2
1	H	105	ARG	2.2
1	B	22	ARG	2.2
1	I	88	ARG	2.2
1	B	55	ALA	2.2
1	C	98	LEU	2.2
1	B	67	LEU	2.1
1	H	108	GLY	2.1
1	E	36	THR	2.1
1	G	26	LYS	2.1
1	A	34	ILE	2.1
1	D	65	LEU	2.1
1	G	91	GLN	2.1
1	H	33	ARG	2.1
1	I	48	VAL	2.1
1	D	34	ILE	2.1
1	D	55	ALA	2.1
1	G	80	PHE	2.1
1	H	47	PHE	2.1
1	H	67	LEU	2.0
1	I	44	LEU	2.0
1	I	54	LEU	2.0
1	B	38	VAL	2.0
1	H	52	ILE	2.0
1	A	118	GLU	2.0
1	B	79	LEU	2.0
1	I	18	LEU	2.0
1	F	108	GLY	2.0
1	B	23	ASN	2.0
1	B	18	LEU	2.0
1	H	110	PRO	2.0
1	I	91	GLN	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.