



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2014 – 05:39 PM EDT

PDB ID : 3P83  
Title : Structure of the PCNA:RNase HII complex from *Archaeoglobus fulgidus*.  
Authors : Bubeck, D.; Reijns, M.A.; Graham, S.C.; Astell, K.R.; Jones, E.Y.; Jackson, A.P.  
Deposited on : 2010-10-13  
Resolution : 3.05 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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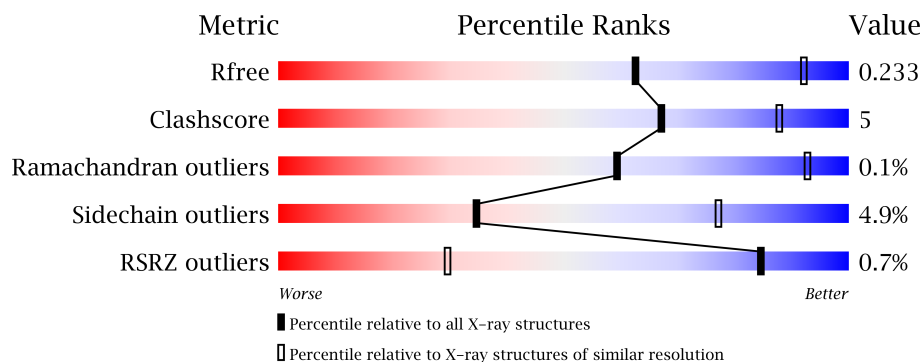
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.16 November 2013
Xtriage (Phenix)	:	dev-1439
EDS	:	stable23828
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)	:	stable23828

# 1 Overall quality at a glance

The reported resolution of this entry is 3.05 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	2079 (3.12-3.00)
Clashscore	79885	2629 (3.12-3.00)
Ramachandran outliers	78287	2536 (3.12-3.00)
Sidechain outliers	78261	2539 (3.12-3.00)
RSRZ outliers	66119	2081 (3.12-3.00)

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 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	245	
1	B	245	
1	C	245	
2	D	217	
2	E	217	
2	F	217	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10465 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 DNA polymerase sliding clamp.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	0	0
			1895	1214	311	362	8			
1	B	244	Total	C	N	O	S	0	0	0
			1894	1214	306	366	8			
1	C	243	Total	C	N	O	S	0	0	0
			1881	1206	305	362	8			

- Molecule 2 is a protein called Ribonuclease HII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	213	Total	C	N	O	S	0	0	0
			1665	1043	302	312	8			
2	E	202	Total	C	N	O	S	0	0	0
			1564	977	277	302	8			
2	F	205	Total	C	N	O	S	0	0	0
			1566	978	284	297	7			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-11	GLY	-	EXPRESSION TAG	UNP O29634
D	-10	PRO	-	EXPRESSION TAG	UNP O29634
D	-9	LEU	-	EXPRESSION TAG	UNP O29634
D	-8	GLY	-	EXPRESSION TAG	UNP O29634
D	-7	SER	-	EXPRESSION TAG	UNP O29634
D	-6	PRO	-	EXPRESSION TAG	UNP O29634
D	-5	GLU	-	EXPRESSION TAG	UNP O29634
D	-4	PHE	-	EXPRESSION TAG	UNP O29634
D	-3	PRO	-	EXPRESSION TAG	UNP O29634
D	-2	GLY	-	EXPRESSION TAG	UNP O29634
D	-1	ARG	-	EXPRESSION TAG	UNP O29634
D	0	LEU	-	EXPRESSION TAG	UNP O29634

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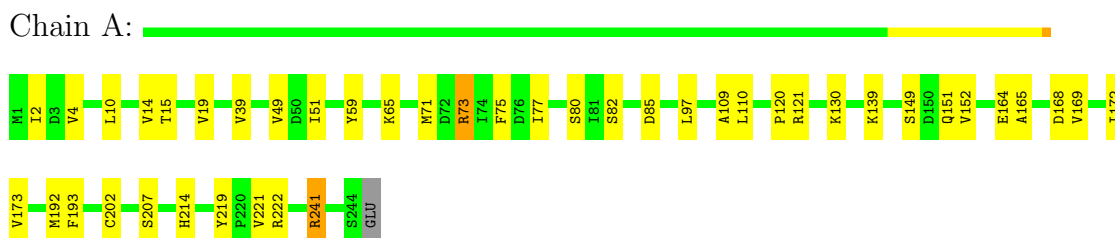
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Chain	Residue	Modelled	Actual	Comment	Reference
E	-11	GLY	-	EXPRESSION TAG	UNP O29634
E	-10	PRO	-	EXPRESSION TAG	UNP O29634
E	-9	LEU	-	EXPRESSION TAG	UNP O29634
E	-8	GLY	-	EXPRESSION TAG	UNP O29634
E	-7	SER	-	EXPRESSION TAG	UNP O29634
E	-6	PRO	-	EXPRESSION TAG	UNP O29634
E	-5	GLU	-	EXPRESSION TAG	UNP O29634
E	-4	PHE	-	EXPRESSION TAG	UNP O29634
E	-3	PRO	-	EXPRESSION TAG	UNP O29634
E	-2	GLY	-	EXPRESSION TAG	UNP O29634
E	-1	ARG	-	EXPRESSION TAG	UNP O29634
E	0	LEU	-	EXPRESSION TAG	UNP O29634
F	-11	GLY	-	EXPRESSION TAG	UNP O29634
F	-10	PRO	-	EXPRESSION TAG	UNP O29634
F	-9	LEU	-	EXPRESSION TAG	UNP O29634
F	-8	GLY	-	EXPRESSION TAG	UNP O29634
F	-7	SER	-	EXPRESSION TAG	UNP O29634
F	-6	PRO	-	EXPRESSION TAG	UNP O29634
F	-5	GLU	-	EXPRESSION TAG	UNP O29634
F	-4	PHE	-	EXPRESSION TAG	UNP O29634
F	-3	PRO	-	EXPRESSION TAG	UNP O29634
F	-2	GLY	-	EXPRESSION TAG	UNP O29634
F	-1	ARG	-	EXPRESSION TAG	UNP O29634
F	0	LEU	-	EXPRESSION TAG	UNP O29634

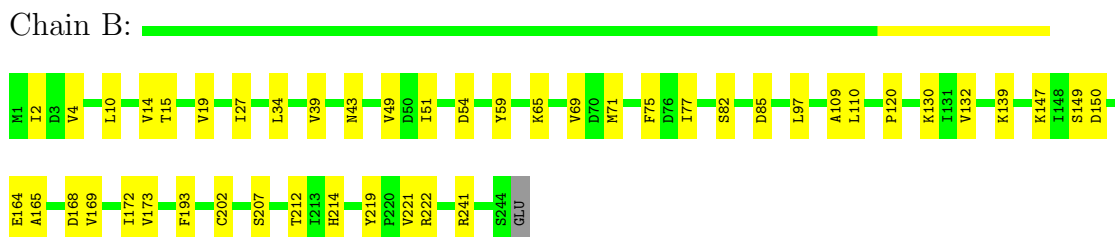
### 3 Residue-property plots

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.

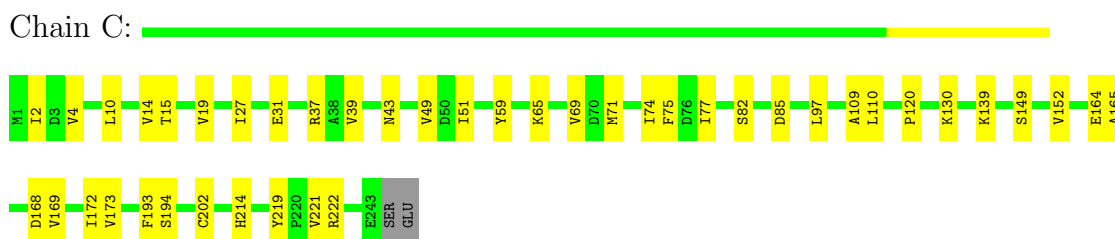
- Molecule 1: DNA polymerase sliding clamp



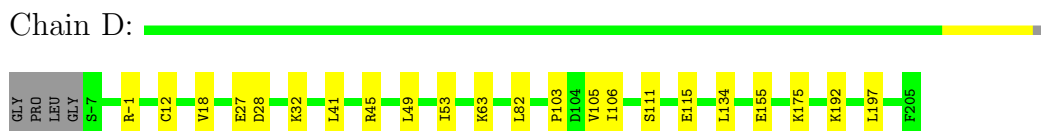
- Molecule 1: DNA polymerase sliding clamp



- Molecule 1: DNA polymerase sliding clamp

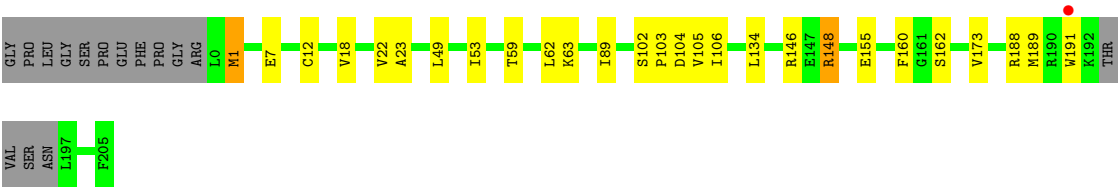


- Molecule 2: Ribonuclease HII



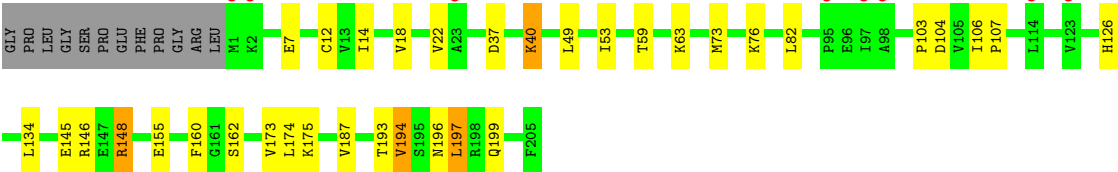
- Molecule 2: Ribonuclease HII





● Molecule 2: Ribonuclease HII

Chain F: GLY PRO LEU GLY SER PRO GLU PHE PRO GLY ARG LEU M1 K2 E7 C12 V13 I14 V18 V22 A23 D37 K40 L49 I53 T59 K63 M73 K76 L82 P95 E96 I97 A98 P103 D104 V105 I106 P107 L114 V123 H126



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	149.67Å 152.03Å 90.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.54 – 3.05 67.77 – 3.05	Depositor EDS
% Data completeness (in resolution range)	(Not available) (44.54-3.05) 99.6 (67.77-3.05)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.23 (at 3.07Å)	Xtriage
Refinement program	BUSTER 2.9.2	Depositor
R, $R_{free}$	0.187 , 0.216 0.198 , 0.233	Depositor DCC
$R_{free}$ test set	1996 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	72.8	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.0	EDS
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 39748 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	10465	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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	0.43	0/1923	0.63	0/2595
1	B	0.41	0/1922	0.63	0/2594
1	C	0.40	0/1909	0.63	0/2577
2	D	0.49	0/1687	0.67	0/2268
2	E	0.47	0/1582	0.67	0/2127
2	F	0.44	0/1585	0.66	0/2135
All	All	0.44	0/10608	0.65	0/14296

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	1895	0	1941	23	0
1	B	1894	0	1936	27	0
1	C	1881	0	1918	23	0
2	D	1665	0	1715	10	0
2	E	1564	0	1576	14	0
2	F	1566	0	1574	14	0
All	All	10465	0	10660	102	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 5.

All (102) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:19:VAL:HG12	2:E:106:ILE:HG13	1.46	0.97
2:F:82:LEU:HD23	2:F:103:PRO:HG3	1.61	0.82
1:A:214:HIS:HB2	1:A:222:ARG:HB2	1.61	0.81
1:B:109:ALA:HB3	1:C:169:VAL:HG22	1.65	0.79
1:C:214:HIS:HB2	1:C:222:ARG:HB2	1.67	0.77
1:B:214:HIS:HB2	1:B:222:ARG:HB2	1.66	0.77
1:A:82:SER:HB3	1:A:85:ASP:HB2	1.68	0.74
1:B:82:SER:HB3	1:B:85:ASP:HB2	1.70	0.74
1:C:82:SER:HB3	1:C:85:ASP:HB2	1.73	0.71
2:D:41:LEU:HD22	2:D:45:ARG:HG2	1.76	0.68
1:A:151:GLN:OE1	1:A:241:ARG:NH1	2.28	0.66
1:B:19:VAL:HG21	1:B:75:PHE:HB2	1.78	0.65
2:D:41:LEU:HD13	2:D:45:ARG:HG3	1.79	0.64
1:B:15:THR:O	1:B:19:VAL:HG23	2.00	0.61
1:C:19:VAL:HG21	1:C:75:PHE:HB2	1.82	0.61
1:C:15:THR:O	1:C:19:VAL:HG23	2.00	0.61
2:E:1:MET:HE1	2:E:23:ALA:HB1	1.84	0.60
1:A:15:THR:O	1:A:19:VAL:HG23	2.02	0.60
1:A:19:VAL:HG21	1:A:75:PHE:HB2	1.84	0.59
2:F:14:ILE:HG12	2:F:187:VAL:HG22	1.87	0.56
2:D:111:SER:O	2:D:115:GLU:HG3	2.04	0.56
1:C:2:ILE:HD11	1:C:65:LYS:HB3	1.90	0.54
1:B:2:ILE:HD11	1:B:65:LYS:HB3	1.90	0.53
1:A:2:ILE:HD11	1:A:65:LYS:HB3	1.90	0.52
1:A:139:LYS:HG3	1:A:202:CYS:HB3	1.92	0.51
1:B:19:VAL:CG1	2:E:106:ILE:HG13	2.29	0.51
1:A:14:VAL:HG23	1:A:49:VAL:HG11	1.93	0.51
2:D:28:ASP:O	2:D:32:LYS:HG2	2.11	0.50
1:C:139:LYS:HG3	1:C:202:CYS:HB3	1.93	0.50
2:E:49:LEU:O	2:E:53:ILE:HG12	2.11	0.50
1:C:37:ARG:HG3	1:C:120:PRO:HG2	1.94	0.49
1:C:39:VAL:HG23	1:C:120:PRO:HB3	1.93	0.49
2:D:82:LEU:HD23	2:D:103:PRO:HG3	1.93	0.49
1:A:39:VAL:HG23	1:A:120:PRO:HB3	1.95	0.49
2:D:49:LEU:O	2:D:53:ILE:HG12	2.13	0.49
1:B:150:ASP:OD2	1:B:241:ARG:NH2	2.44	0.49
1:A:19:VAL:HG22	1:A:71:MET:HB3	1.93	0.49
1:B:39:VAL:HG23	1:B:120:PRO:HB3	1.95	0.49
2:D:175:LYS:HG3	2:D:197:LEU:HD22	1.95	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:E:18:VAL:HG22	2:E:63:LYS:HG2	1.94	0.48
1:B:139:LYS:HG3	1:B:202:CYS:HB3	1.95	0.48
2:E:188:ARG:O	2:E:191:TRP:HD1	1.97	0.48
1:C:19:VAL:HG22	1:C:71:MET:HB3	1.95	0.48
1:A:4:VAL:HG12	1:A:59:TYR:HA	1.96	0.47
1:A:97:LEU:HB2	1:A:110:LEU:HD21	1.96	0.47
1:B:19:VAL:HG22	1:B:71:MET:HB3	1.97	0.47
2:F:40:LYS:HB3	2:F:40:LYS:HE3	1.64	0.47
2:F:49:LEU:O	2:F:53:ILE:HG12	2.13	0.47
2:F:194:VAL:HG13	2:F:197:LEU:HD22	1.96	0.47
1:A:14:VAL:HB	1:A:51:ILE:HD11	1.97	0.47
1:B:14:VAL:HG23	1:B:49:VAL:HG11	1.96	0.47
1:B:4:VAL:HG12	1:B:59:TYR:HA	1.97	0.46
1:C:193:PHE:CZ	1:C:221:VAL:HB	2.50	0.46
2:D:106:ILE:HG12	2:E:148:ARG:HB2	1.96	0.46
1:C:14:VAL:HG23	1:C:49:VAL:HG11	1.96	0.46
2:E:1:MET:CE	2:E:23:ALA:HB1	2.45	0.46
2:F:106:ILE:HA	2:F:107:PRO:HD3	1.76	0.46
1:B:193:PHE:CZ	1:B:221:VAL:HB	2.50	0.46
1:B:164:GLU:HB3	1:B:173:VAL:HG22	1.98	0.46
1:A:80:SER:OG	1:B:147:LYS:HE3	2.16	0.46
2:F:18:VAL:HG22	2:F:63:LYS:HG2	1.96	0.45
1:C:165:ALA:HB3	1:C:172:ILE:HG22	1.99	0.45
2:D:18:VAL:HG22	2:D:63:LYS:HG2	1.98	0.45
1:A:39:VAL:CG2	1:A:120:PRO:HB3	2.46	0.45
1:C:39:VAL:CG2	1:C:120:PRO:HB3	2.46	0.45
2:E:160:PHE:HA	2:E:173:VAL:HG21	1.99	0.45
1:A:169:VAL:HG22	1:C:109:ALA:HB3	1.98	0.44
1:B:14:VAL:HB	1:B:51:ILE:HD11	1.98	0.44
2:E:146:ARG:NH2	2:E:162:SER:O	2.43	0.44
1:B:27:ILE:HD12	1:B:69:VAL:HG21	1.98	0.44
1:C:14:VAL:HB	1:C:51:ILE:HD11	1.99	0.44
1:A:193:PHE:CZ	1:A:221:VAL:HB	2.53	0.44
1:B:165:ALA:HB3	1:B:172:ILE:HG22	1.99	0.44
2:F:22:VAL:HG22	2:F:59:THR:HG22	1.99	0.44
1:C:164:GLU:HB3	1:C:173:VAL:HG22	1.99	0.44
1:A:152:VAL:HG12	1:A:165:ALA:HB2	1.99	0.44
1:C:27:ILE:HD12	1:C:69:VAL:HG21	1.99	0.44
1:A:164:GLU:HB3	1:A:173:VAL:HG22	1.99	0.44
1:A:165:ALA:HB3	1:A:172:ILE:HG22	1.99	0.44
1:C:152:VAL:HG12	1:C:165:ALA:HB2	2.00	0.44
2:D:41:LEU:HD22	2:D:45:ARG:CG	2.46	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:4:VAL:HG12	1:C:59:TYR:HA	2.00	0.43
2:E:22:VAL:HG22	2:E:59:THR:HG22	2.00	0.43
2:F:146:ARG:NH2	2:F:162:SER:O	2.48	0.43
2:F:160:PHE:HA	2:F:173:VAL:HG21	2.00	0.43
1:A:109:ALA:HB3	1:B:169:VAL:HG22	2.01	0.42
2:E:105:VAL:HG12	2:E:106:ILE:HG12	2.01	0.42
1:B:97:LEU:HB2	1:B:110:LEU:HD21	2.00	0.42
1:C:97:LEU:HB2	1:C:110:LEU:HD21	2.01	0.42
1:C:39:VAL:CG1	1:C:43:ASN:HA	2.48	0.42
1:B:39:VAL:CG2	1:B:120:PRO:HB3	2.50	0.42
1:A:192:MET:HG2	1:A:241:ARG:HG3	2.01	0.42
1:B:241:ARG:HG3	2:F:199:GLN:HA	2.02	0.41
2:E:102:SER:HA	2:E:103:PRO:HD3	1.96	0.41
2:F:145:GLU:O	2:F:148:ARG:HG2	2.20	0.41
1:B:132:VAL:HG22	1:B:212:THR:HG23	2.03	0.41
2:F:174:LEU:HD13	2:F:197:LEU:HD21	2.03	0.41
1:A:73:ARG:NH2	1:B:147:LYS:O	2.54	0.40
2:E:62:LEU:HB2	2:E:89:ILE:HD11	2.03	0.40
1:B:34:LEU:HB3	1:B:51:ILE:HB	2.04	0.40
2:F:73:MET:HA	2:F:76:LYS:O	2.22	0.40
1:C:15:THR:HG21	1:C:74:ILE:HG22	2.04	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	242/245 (99%)	235 (97%)	7 (3%)	0	100	100
1	B	242/245 (99%)	236 (98%)	6 (2%)	0	100	100
1	C	241/245 (98%)	234 (97%)	7 (3%)	0	100	100
2	D	211/217 (97%)	207 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	198/217 (91%)	191 (96%)	6 (3%)	1 (0%)	38	82
2	F	203/217 (94%)	199 (98%)	4 (2%)	0	100	100
All	All	1337/1386 (96%)	1302 (97%)	34 (2%)	1 (0%)	59	93

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	1	MET

### 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	208/212 (98%)	198 (95%)	10 (5%)	35	78
1	B	209/212 (99%)	200 (96%)	9 (4%)	40	81
1	C	206/212 (97%)	198 (96%)	8 (4%)	43	84
2	D	177/185 (96%)	170 (96%)	7 (4%)	42	84
2	E	164/185 (89%)	157 (96%)	7 (4%)	40	81
2	F	161/185 (87%)	147 (91%)	14 (9%)	15	49
All	All	1125/1191 (94%)	1070 (95%)	55 (5%)	35	77

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LEU
1	A	73	ARG
1	A	77	ILE
1	A	121	ARG
1	A	130	LYS
1	A	149	SER
1	A	168	ASP
1	A	207	SER
1	A	219	TYR
1	A	241	ARG

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Mol	Chain	Res	Type
1	B	10	LEU
1	B	43	ASN
1	B	54	ASP
1	B	77	ILE
1	B	130	LYS
1	B	149	SER
1	B	168	ASP
1	B	207	SER
1	B	219	TYR
1	C	10	LEU
1	C	31	GLU
1	C	77	ILE
1	C	130	LYS
1	C	149	SER
1	C	168	ASP
1	C	194	SER
1	C	219	TYR
2	D	-1	ARG
2	D	12	CYS
2	D	27	GLU
2	D	105	VAL
2	D	134	LEU
2	D	155	GLU
2	D	192	LYS
2	E	7	GLU
2	E	12	CYS
2	E	104	ASP
2	E	134	LEU
2	E	148	ARG
2	E	155	GLU
2	E	189	MET
2	F	7	GLU
2	F	12	CYS
2	F	37	ASP
2	F	40	LYS
2	F	104	ASP
2	F	126	HIS
2	F	134	LEU
2	F	148	ARG
2	F	155	GLU
2	F	175	LYS
2	F	193	THR

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Mol	Chain	Res	Type
2	F	194	VAL
2	F	196	ASN
2	F	197	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	43	ASN
2	D	68	ASN
2	D	126	HIS
2	E	68	ASN
2	F	68	ASN
2	F	196	ASN
2	F	199	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	244/245 (99%)	-0.18	0	100 100	34, 59, 90, 102	0
1	B	244/245 (99%)	-0.07	0	100 100	50, 75, 110, 128	0
1	C	243/245 (99%)	0.15	0	100 100	58, 85, 113, 139	0
2	D	213/217 (98%)	-0.12	0	100 100	38, 57, 100, 140	0
2	E	202/217 (93%)	-0.11	1 (0%)	88 37	43, 74, 129, 146	0
2	F	205/217 (94%)	0.14	8 (3%)	37 6	41, 90, 145, 170	0
All	All	1351/1386 (97%)	-0.03	9 (0%)	84 30	34, 72, 126, 170	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	97	ILE	3.6
2	F	1	MET	3.4
2	F	2	LYS	3.0
2	E	191	TRP	2.8
2	F	114	LEU	2.3
2	F	23	ALA	2.3
2	F	98	ALA	2.1
2	F	95	PRO	2.1
2	F	123	VAL	2.1

### 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.