



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:54 PM GMT

PDB ID : 4AU2  
Title : Crystal Structure of a Hsp47-collagen complex  
Authors : Widmer, C.; Gebauer, J.M.; Brunstein, E.; Drogemuller, C.; Leeb, T.; Baumann, U.  
Deposited on : 2012-05-13  
Resolution : 2.30 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

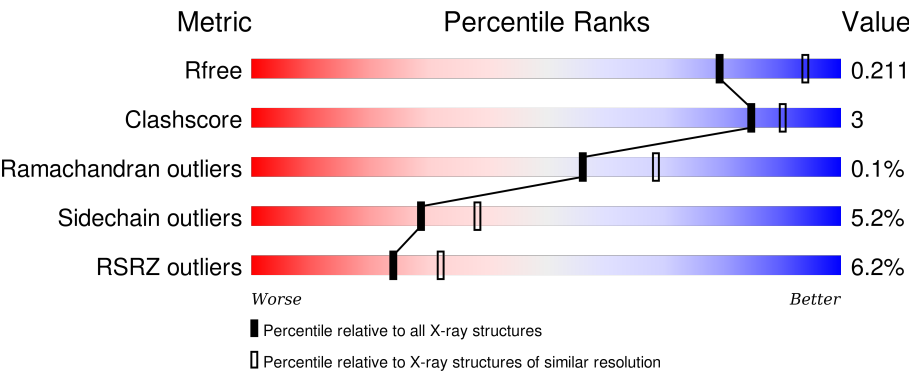
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

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 <sub>free</sub>	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (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. 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	392	<div><div>100%</div><div>82%10%6%</div></div>
1	B	392	<div><div>10%</div><div>81%9%10%</div></div>
1	C	392	<div><div>9%</div><div>77%8%14%</div></div>
1	D	392	<div><div>4%</div><div>81%10%8%</div></div>
2	E	16	<div><div></div><div>75%13%13%</div></div>

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Mol	Chain	Length	Quality of chain
2	F	16	 81% 13% 6%
2	G	16	 75% 13% 13%
2	H	16	 75% 13% 13%
2	I	16	 75% 19% 6%
2	J	16	 63% 19% 19%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11897 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 SERPIN PEPTIDASE INHIBITOR, CLADE H (HEAT SHOCK PROTEIN 47), MEMBER 1, (COLLAGEN BINDING PROTEIN 1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			2886	1839	501	532	14			
1	B	354	Total	C	N	O	S	0	0	0
			2778	1769	487	510	12			
1	C	338	Total	C	N	O	S	0	0	0
			2654	1692	461	488	13			
1	D	359	Total	C	N	O	S	0	0	0
			2814	1789	493	520	12			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	35	MET	-	EXPRESSION TAG	UNP C7C419
A	419	LEU	-	EXPRESSION TAG	UNP C7C419
A	420	GLU	-	EXPRESSION TAG	UNP C7C419
A	421	HIS	-	EXPRESSION TAG	UNP C7C419
A	422	HIS	-	EXPRESSION TAG	UNP C7C419
A	423	HIS	-	EXPRESSION TAG	UNP C7C419
A	424	HIS	-	EXPRESSION TAG	UNP C7C419
A	425	HIS	-	EXPRESSION TAG	UNP C7C419
A	426	HIS	-	EXPRESSION TAG	UNP C7C419
B	35	MET	-	EXPRESSION TAG	UNP C7C419
B	419	LEU	-	EXPRESSION TAG	UNP C7C419
B	420	GLU	-	EXPRESSION TAG	UNP C7C419
B	421	HIS	-	EXPRESSION TAG	UNP C7C419
B	422	HIS	-	EXPRESSION TAG	UNP C7C419
B	423	HIS	-	EXPRESSION TAG	UNP C7C419
B	424	HIS	-	EXPRESSION TAG	UNP C7C419
B	425	HIS	-	EXPRESSION TAG	UNP C7C419
B	426	HIS	-	EXPRESSION TAG	UNP C7C419
C	35	MET	-	EXPRESSION TAG	UNP C7C419
C	419	LEU	-	EXPRESSION TAG	UNP C7C419

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Chain	Residue	Modelled	Actual	Comment	Reference
C	420	GLU	-	EXPRESSION TAG	UNP C7C419
C	421	HIS	-	EXPRESSION TAG	UNP C7C419
C	422	HIS	-	EXPRESSION TAG	UNP C7C419
C	423	HIS	-	EXPRESSION TAG	UNP C7C419
C	424	HIS	-	EXPRESSION TAG	UNP C7C419
C	425	HIS	-	EXPRESSION TAG	UNP C7C419
C	426	HIS	-	EXPRESSION TAG	UNP C7C419
D	35	MET	-	EXPRESSION TAG	UNP C7C419
D	419	LEU	-	EXPRESSION TAG	UNP C7C419
D	420	GLU	-	EXPRESSION TAG	UNP C7C419
D	421	HIS	-	EXPRESSION TAG	UNP C7C419
D	422	HIS	-	EXPRESSION TAG	UNP C7C419
D	423	HIS	-	EXPRESSION TAG	UNP C7C419
D	424	HIS	-	EXPRESSION TAG	UNP C7C419
D	425	HIS	-	EXPRESSION TAG	UNP C7C419
D	426	HIS	-	EXPRESSION TAG	UNP C7C419

- Molecule 2 is a protein called 15ER COLLAGEN MODEL PEPTIDE 15-R8.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	14	Total	C	N	O	0	0	0
			90	59	17	14			
2	F	15	Total	C	N	O	0	0	0
			93	61	17	15			
2	G	14	Total	C	N	O	0	0	0
			86	56	16	14			
2	H	14	Total	C	N	O	0	0	0
			90	59	17	14			
2	I	15	Total	C	N	O	0	0	0
			93	61	17	15			
2	J	13	Total	C	N	O	0	0	0
			79	51	15	13			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	77	Total	O	0	0
			77	77		
3	B	28	Total	O	0	0
			28	28		
3	C	43	Total	O	0	0
			43	43		

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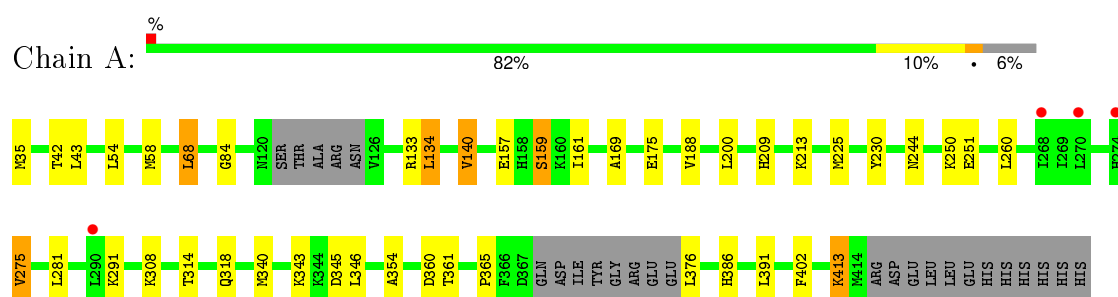
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	62	Total 62	O 62	0	0
3	E	1	Total 1	O 1	0	0
3	F	1	Total 1	O 1	0	0
3	G	1	Total 1	O 1	0	0
3	H	1	Total 1	O 1	0	0
3	I	20	Total 20	O 20	0	0

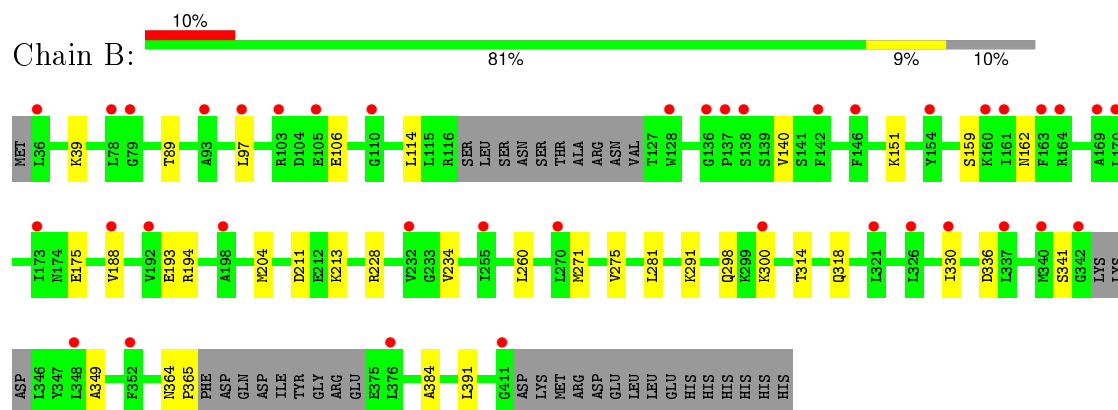
### 3 Residue-property plots

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.

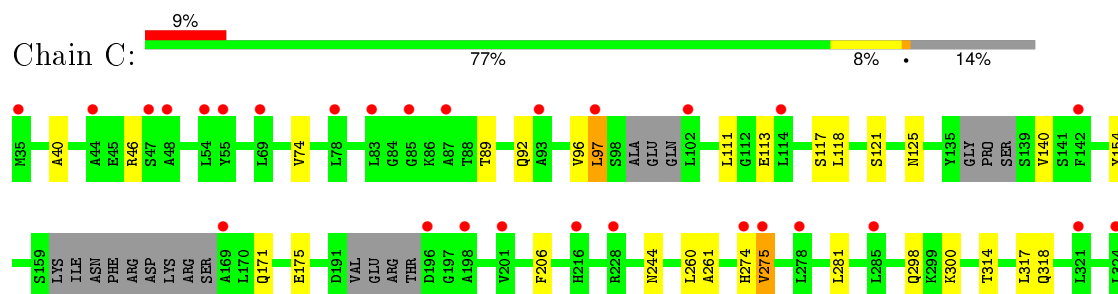
- Molecule 1: SERPIN PEPTIDASE INHIBITOR, CLADE H (HEAT SHOCK PROTEIN 47), MEMBER 1, (COLLAGEN BINDING PROTEIN 1)

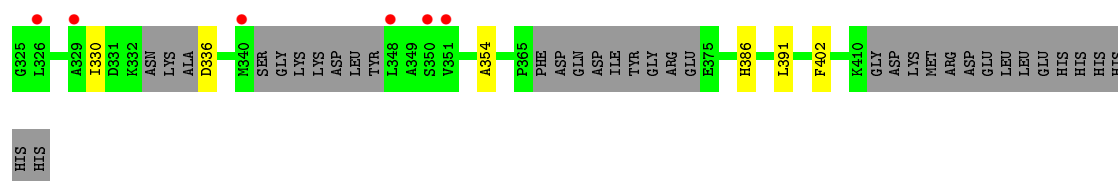


- Molecule 1: SERPIN PEPTIDASE INHIBITOR, CLADE H (HEAT SHOCK PROTEIN 47), MEMBER 1, (COLLAGEN BINDING PROTEIN 1)

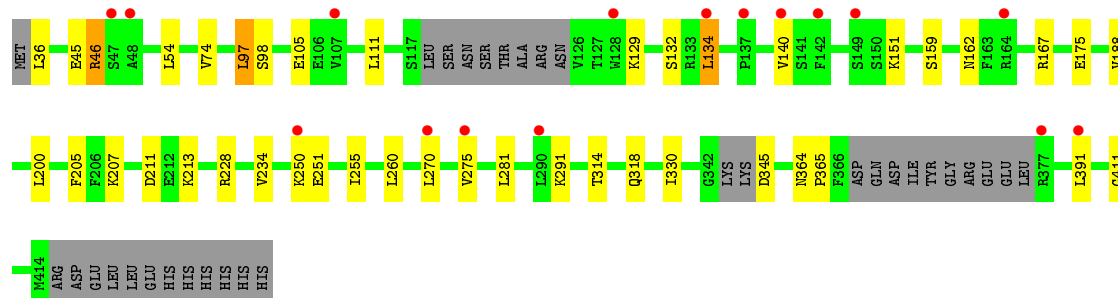
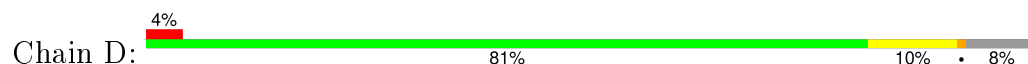


- Molecule 1: SERPIN PEPTIDASE INHIBITOR, CLADE H (HEAT SHOCK PROTEIN 47), MEMBER 1, (COLLAGEN BINDING PROTEIN 1)





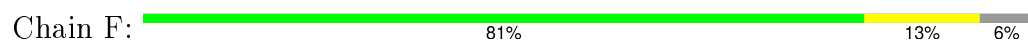
- Molecule 1: SERPIN PEPTIDASE INHIBITOR, CLADE H (HEAT SHOCK PROTEIN 47), MEMBER 1, (COLLAGEN BINDING PROTEIN 1)



- Molecule 2: 15ER COLLAGEN MODEL PEPTIDE 15-R8



- Molecule 2: 15ER COLLAGEN MODEL PEPTIDE 15-R8



- Molecule 2: 15ER COLLAGEN MODEL PEPTIDE 15-R8



- Molecule 2: 15ER COLLAGEN MODEL PEPTIDE 15-R8



- Molecule 2: 15ER COLLAGEN MODEL PEPTIDE 15-R8







- Molecule 2: 15ER COLLAGEN MODEL PEPTIDE 15-R8

Chain J:   
63% 19% 19%

A horizontal bar chart showing the coverage of residues for Chain J. The bar is divided into three segments: a green segment representing 63% coverage, a yellow segment representing 19% coverage, and a grey segment representing 19% coverage.



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.50 Å   92.78 Å   100.46 Å 95.24°   98.95°   96.73°	Depositor
Resolution (Å)	98.62 – 2.30 98.61 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.4 (98.62-2.30) 92.9 (98.61-2.30)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.54 (at 2.29 Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.203   ,   0.240 0.213   ,   0.211	Depositor DCC
$R_{free}$ test set	2801 reflections (4.16%)	DCC
Wilson B-factor (Å <sup>2</sup> )	50.4	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 51.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 70113 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11897	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACE

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	0.51	0/2944	0.69	0/3968
1	B	0.42	0/2834	0.67	0/3821
1	C	0.43	0/2703	0.70	0/3641
1	D	0.44	0/2870	0.69	0/3869
2	E	0.48	0/98	0.44	0/138
2	F	0.48	0/99	0.41	0/141
2	G	0.46	0/91	0.43	0/129
2	H	0.49	0/98	0.39	0/138
2	I	0.50	0/99	0.41	0/141
2	J	0.46	0/83	0.43	0/117
All	All	0.45	0/11919	0.68	0/16103

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

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	2886	0	2919	23	0
1	B	2778	0	2799	11	0
1	C	2654	0	2678	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2814	0	2827	14	0
2	E	90	0	90	2	0
2	F	93	0	91	2	0
2	G	86	0	84	2	0
2	H	90	0	90	2	0
2	I	93	0	91	3	0
2	J	79	0	77	3	0
3	A	77	0	0	2	0
3	B	28	0	0	0	0
3	C	43	0	0	0	0
3	D	62	0	0	1	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	20	0	0	0	0
All	All	11897	0	11746	68	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 3.

All (68) 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:89:THR:HG21	1:B:336:ASP:H	1.37	0.88
1:B:89:THR:HG21	1:B:336:ASP:N	2.07	0.69
1:D:54:LEU:HD22	1:D:74:VAL:HG11	1.75	0.68
1:D:188:VAL:O	1:D:314:THR:HG21	1.95	0.67
1:A:42:THR:HG22	3:A:2003:HOH:O	1.97	0.64
1:D:134:LEU:HD12	1:D:200:LEU:HD13	1.80	0.63
1:B:188:VAL:O	1:B:314:THR:HG21	2.00	0.62
1:A:275:VAL:HG13	1:A:386:HIS:HB2	1.83	0.60
1:C:275:VAL:HG13	1:C:386:HIS:HB2	1.84	0.59
1:C:298:GLN:HG3	1:C:300:LYS:HE2	1.88	0.56
1:A:209:HIS:HD2	3:A:2030:HOH:O	1.90	0.55
1:A:230:TYR:CE1	1:A:413:LYS:HB3	2.42	0.55
2:H:13:PRO:HG2	2:J:11:PRO:HB3	1.89	0.55
1:D:228:ARG:HG2	1:D:275:VAL:HG13	1.90	0.54
1:B:271:MET:CE	1:B:384:ALA:HA	2.38	0.54
1:C:125:ASN:HA	1:C:261:ALA:HB3	1.90	0.53
1:B:213:LYS:HD3	1:B:365:PRO:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:8:ARG:HE	2:G:10:PRO:HD3	1.74	0.52
1:D:97:LEU:HD11	1:D:111:LEU:HD11	1.90	0.52
1:C:89:THR:HG1	1:C:336:ASP:N	2.07	0.52
1:B:298:GLN:HG3	1:B:300:LYS:HE2	1.92	0.52
1:A:225:MET:HE3	1:A:275:VAL:HG22	1.92	0.52
1:A:84:GLY:HA3	1:A:340:MET:HG3	1.92	0.51
1:D:318:GLN:HG2	1:D:330:ILE:HD12	1.90	0.51
1:D:255:ILE:HD12	1:D:270:LEU:HD11	1.91	0.51
1:B:318:GLN:HG2	1:B:330:ILE:HD12	1.92	0.51
1:D:255:ILE:HB	1:D:270:LEU:HD13	1.93	0.51
1:B:228:ARG:HG2	1:B:275:VAL:HG13	1.92	0.51
1:D:213:LYS:HD3	1:D:365:PRO:HA	1.93	0.50
1:A:213:LYS:HD3	1:A:365:PRO:HA	1.92	0.50
1:A:54:LEU:O	1:A:58:MET:HG3	2.10	0.50
1:A:134:LEU:HG	1:A:200:LEU:HD13	1.94	0.50
1:D:250:LYS:HD3	1:D:251:GLU:HG2	1.94	0.50
2:E:11:PRO:HB3	2:F:10:PRO:HG2	1.95	0.49
1:C:97:LEU:HD21	1:C:111:LEU:HD11	1.94	0.48
1:C:318:GLN:HG2	1:C:330:ILE:HD12	1.95	0.47
1:C:111:LEU:HB3	1:C:154:TYR:HE1	1.78	0.47
1:A:133:ARG:HE	1:A:159:SER:HB2	1.79	0.47
1:A:250:LYS:HD3	1:A:251:GLU:HG2	1.97	0.46
1:A:308:LYS:HZ2	1:A:361:THR:HG23	1.81	0.46
1:C:74:VAL:HG22	1:C:317:LEU:HD21	1.98	0.45
1:A:314:THR:HG23	1:A:354:ALA:HB2	1.99	0.45
1:D:207:LYS:HE2	3:D:2031:HOH:O	2.16	0.44
1:B:194:ARG:HB2	1:B:349:ALA:HB1	1.98	0.44
1:C:206:PHE:CD1	1:C:402:PHE:CE2	3.06	0.44
1:C:206:PHE:CD1	1:C:402:PHE:HE2	2.36	0.44
1:A:188:VAL:O	1:A:314:THR:HG21	2.17	0.44
1:C:40:ALA:HB2	1:C:113:GLU:HB3	1.99	0.44
1:A:133:ARG:NH1	1:A:157:GLU:OE1	2.50	0.44
2:H:11:PRO:HB3	2:I:10:PRO:HG2	2.00	0.44
1:A:68:LEU:HD12	1:A:402:PHE:HD1	1.83	0.43
1:A:140:VAL:HG23	1:A:345:ASP:OD2	2.19	0.43
1:A:68:LEU:HA	1:A:68:LEU:HD13	1.68	0.42
2:I:12:GLY:O	2:J:12:GLY:HA3	2.19	0.42
2:E:13:PRO:HG2	2:G:11:PRO:HB3	2.01	0.42
1:B:211:ASP:O	1:B:364:ASN:HB2	2.19	0.42
2:I:11:PRO:HA	2:J:10:PRO:O	2.20	0.42
1:D:46:ARG:HG3	1:D:98:SER:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:MET:HE3	1:A:225:MET:HB2	1.96	0.41
1:A:340:MET:HE2	1:A:346:LEU:HD23	2.02	0.41
1:A:161:ILE:HD11	1:A:169:ALA:HA	2.03	0.41
1:C:314:THR:HG23	1:C:354:ALA:HB2	2.01	0.41
1:A:68:LEU:HD12	1:A:402:PHE:CD1	2.55	0.41
1:D:211:ASP:O	1:D:364:ASN:HB2	2.21	0.40
1:C:92:GLN:O	1:C:96:VAL:HG23	2.22	0.40
1:D:129:LYS:HB2	1:D:205:PHE:HB3	2.04	0.40
1:B:39:LYS:HE2	1:B:106:GLU:HG2	2.02	0.40
1:A:308:LYS:NZ	1:A:360:ASP:OD1	2.49	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	361/392 (92%)	351 (97%)	10 (3%)	0	100	100
1	B	346/392 (88%)	336 (97%)	10 (3%)	0	100	100
1	C	322/392 (82%)	307 (95%)	15 (5%)	0	100	100
1	D	351/392 (90%)	340 (97%)	10 (3%)	1 (0%)	46	57
2	E	12/16 (75%)	12 (100%)	0	0	100	100
2	F	13/16 (81%)	13 (100%)	0	0	100	100
2	G	12/16 (75%)	12 (100%)	0	0	100	100
2	H	12/16 (75%)	12 (100%)	0	0	100	100
2	I	13/16 (81%)	13 (100%)	0	0	100	100
2	J	11/16 (69%)	11 (100%)	0	0	100	100
All	All	1453/1664 (87%)	1407 (97%)	45 (3%)	1 (0%)	56	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	411	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	313/337 (93%)	296 (95%)	17 (5%)	27	36
1	B	298/337 (88%)	283 (95%)	15 (5%)	30	41
1	C	288/337 (86%)	274 (95%)	14 (5%)	31	41
1	D	302/337 (90%)	283 (94%)	19 (6%)	22	29
2	E	10/10 (100%)	10 (100%)	0	100	100
2	F	10/10 (100%)	10 (100%)	0	100	100
2	G	9/10 (90%)	9 (100%)	0	100	100
2	H	10/10 (100%)	10 (100%)	0	100	100
2	I	10/10 (100%)	10 (100%)	0	100	100
2	J	8/10 (80%)	8 (100%)	0	100	100
All	All	1258/1408 (89%)	1193 (95%)	65 (5%)	29	38

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	MET
1	A	43	LEU
1	A	68	LEU
1	A	134	LEU
1	A	140	VAL
1	A	159	SER
1	A	175	GLU
1	A	244	ASN
1	A	260	LEU
1	A	275	VAL
1	A	281	LEU

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Mol	Chain	Res	Type
1	A	291	LYS
1	A	318	GLN
1	A	343	LYS
1	A	376	LEU
1	A	391	LEU
1	A	413	LYS
1	B	97	LEU
1	B	114	LEU
1	B	140	VAL
1	B	151	LYS
1	B	159	SER
1	B	162	ASN
1	B	175	GLU
1	B	193	GLU
1	B	204	MET
1	B	234	VAL
1	B	260	LEU
1	B	281	LEU
1	B	291	LYS
1	B	341	SER
1	B	391	LEU
1	C	46	ARG
1	C	97	LEU
1	C	117	SER
1	C	118	LEU
1	C	121	SER
1	C	140	VAL
1	C	171	GLN
1	C	175	GLU
1	C	244	ASN
1	C	260	LEU
1	C	274	HIS
1	C	275	VAL
1	C	281	LEU
1	C	391	LEU
1	D	36	LEU
1	D	45	GLU
1	D	46	ARG
1	D	97	LEU
1	D	105	GLU
1	D	132	SER
1	D	134	LEU

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Mol	Chain	Res	Type
1	D	140	VAL
1	D	151	LYS
1	D	159	SER
1	D	162	ASN
1	D	167	ARG
1	D	175	GLU
1	D	234	VAL
1	D	260	LEU
1	D	281	LEU
1	D	291	LYS
1	D	345	ASP
1	D	391	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	GLN
1	C	108	HIS
1	C	364	ASN
1	C	396	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	367/392 (93%)	0.17	4 (1%) 82 86	30, 53, 89, 111	0
1	B	354/392 (90%)	0.56	39 (11%) 7 11	42, 84, 135, 168	0
1	C	338/392 (86%)	0.70	34 (10%) 9 13	45, 82, 131, 179	0
1	D	359/392 (91%)	0.26	16 (4%) 37 46	45, 66, 102, 134	0
2	E	14/16 (87%)	-0.04	0 100 100	47, 56, 82, 89	0
2	F	14/16 (87%)	0.23	0 100 100	48, 56, 84, 89	0
2	G	13/16 (81%)	-0.10	0 100 100	47, 52, 85, 95	0
2	H	14/16 (87%)	0.01	0 100 100	49, 57, 76, 85	0
2	I	14/16 (87%)	-0.02	0 100 100	49, 55, 92, 105	0
2	J	12/16 (75%)	-0.08	0 100 100	47, 54, 81, 101	0
All	All	1499/1664 (90%)	0.39	93 (6%) 24 32	30, 68, 123, 179	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	198	ALA	7.8
1	C	48	ALA	7.7
1	C	348	LEU	7.3
1	C	321	LEU	6.5
1	D	142	PHE	6.0
1	C	83	LEU	5.3
1	B	142	PHE	5.2
1	C	97	LEU	5.2
1	D	140	VAL	5.2
1	C	47	SER	5.0
1	C	274	HIS	4.8
1	C	102	LEU	4.7
1	C	326	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	169	ALA	4.5
1	B	192	VAL	4.4
1	C	324	LEU	4.0
1	B	198	ALA	3.9
1	B	163	PHE	3.9
1	B	136	GLY	3.8
1	D	47	SER	3.7
1	C	351	VAL	3.7
1	B	105	GLU	3.6
1	C	275	VAL	3.6
1	B	137	PRO	3.6
1	C	285	LEU	3.4
1	C	228	ARG	3.4
1	B	110	GLY	3.3
1	C	78	LEU	3.3
1	C	87	ALA	3.3
1	B	170	LEU	3.3
1	B	161	ILE	3.2
1	B	160	LYS	3.2
1	B	342	GLY	3.2
1	B	154	TYR	3.2
1	B	146	PHE	3.2
1	C	54	LEU	3.2
1	D	377	ARG	3.2
1	D	137	PRO	3.1
1	B	348	LEU	3.1
1	B	79	GLY	3.0
1	B	128	TRP	3.0
1	B	337	LEU	3.0
1	B	93	ALA	3.0
1	C	55	TYR	3.0
1	B	97	LEU	2.9
1	D	134	LEU	2.9
1	D	48	ALA	2.9
1	B	376	LEU	2.9
1	D	290	LEU	2.8
1	C	142	PHE	2.8
1	B	36	LEU	2.8
1	A	274	HIS	2.7
1	B	326	LEU	2.7
1	C	350	SER	2.6
1	B	340	MET	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	201	VAL	2.6
1	B	188	VAL	2.6
1	D	391	LEU	2.6
1	C	44	ALA	2.6
1	B	321	LEU	2.6
1	C	69	LEU	2.5
1	B	330	ILE	2.5
1	B	164	ARG	2.5
1	A	290	LEU	2.5
1	D	107	VAL	2.5
1	B	103	ARG	2.5
1	B	173	ILE	2.4
1	D	275	VAL	2.4
1	D	128	TRP	2.4
1	D	164	ARG	2.4
1	B	300	LYS	2.4
1	C	114	LEU	2.3
1	D	270	LEU	2.3
1	C	216	HIS	2.3
1	C	35	MET	2.3
1	C	340	MET	2.2
1	B	411	GLY	2.2
1	C	278	LEU	2.2
1	B	169	ALA	2.2
1	C	196	ASP	2.2
1	B	270	LEU	2.1
1	C	329	ALA	2.1
1	B	255	ILE	2.1
1	D	250	LYS	2.1
1	C	85	GLY	2.1
1	C	93	ALA	2.1
1	B	138	SER	2.1
1	A	268	ILE	2.1
1	B	232	VAL	2.1
1	B	352	PHE	2.0
1	A	270	LEU	2.0
1	B	78	LEU	2.0
1	D	149	SER	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 [i](#)

There are no carbohydrates 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.