



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 05:11 am GMT

PDB ID : 3IWP  
Title : Crystal structure of human copper homeostasis protein CutC  
Authors : Li, Y.; Du, J.; Zhang, P.; Ding, J.  
Deposited on : 2009-09-03  
Resolution : 2.50 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

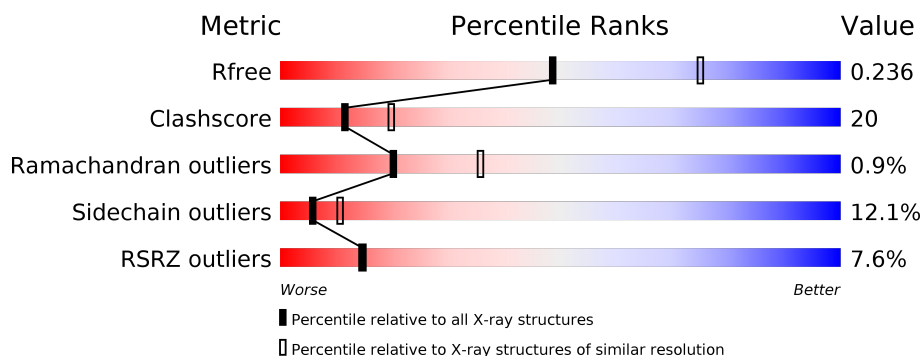
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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	287	<div> <div>4%</div> <div> <div>47%</div> <div>32%</div> <div>8%</div> <div>13%</div> </div> </div>
1	B	287	<div> <div>%</div> <div> <div>57%</div> <div>23%</div> <div>6%</div> <div>15%</div> </div> </div>
1	C	287	<div> <div>%</div> <div> <div>58%</div> <div>23%</div> <div>•</div> <div>14%</div> </div> </div>
1	D	287	<div> <div>%</div> <div> <div>48%</div> <div>28%</div> <div>9%</div> <div>15%</div> </div> </div>
1	E	287	<div> <div>7%</div> <div> <div>55%</div> <div>25%</div> <div>5%</div> <div>16%</div> </div> </div>
1	F	287	<div> <div>5%</div> <div> <div>47%</div> <div>31%</div> <div>5%</div> <div>•</div> <div>16%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	287	
1	H	287	
1	I	287	
1	J	287	
1	K	287	
1	L	287	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22740 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 Copper homeostasis protein cutC homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	0	0
			1870	1166	329	357	18			
1	B	244	Total	C	N	O	S	0	0	0
			1837	1145	324	350	18			
1	C	247	Total	C	N	O	S	0	0	0
			1856	1157	327	354	18			
1	D	245	Total	C	N	O	S	0	0	0
			1843	1150	324	351	18			
1	E	242	Total	C	N	O	S	0	0	0
			1825	1138	322	348	17			
1	F	241	Total	C	N	O	S	0	0	0
			1817	1135	320	345	17			
1	G	237	Total	C	N	O	S	0	0	0
			1792	1119	317	340	16			
1	H	236	Total	C	N	O	S	0	0	0
			1779	1111	315	337	16			
1	I	241	Total	C	N	O	S	0	0	0
			1822	1138	321	347	16			
1	J	239	Total	C	N	O	S	0	0	0
			1807	1129	318	344	16			
1	K	238	Total	C	N	O	S	0	0	0
			1800	1127	317	340	16			
1	L	239	Total	C	N	O	S	0	0	0
			1804	1129	318	341	16			

There are 168 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
A	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
A	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
A	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
A	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
A	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
A	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
A	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
A	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
A	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
A	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
A	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
A	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
B	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
B	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
B	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
B	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
B	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
B	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
B	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
B	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
B	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
B	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
B	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
B	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
B	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
B	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
C	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
C	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
C	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
C	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
C	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
C	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
C	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
C	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
C	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
C	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
C	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
C	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
C	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
C	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
D	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
D	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
D	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
D	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
D	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
D	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
D	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
D	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
D	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
D	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
D	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
D	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
D	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
E	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
E	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
E	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
E	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
E	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
E	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
E	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
E	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
E	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
E	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
E	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
E	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
E	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
E	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
F	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
F	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
F	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
F	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
F	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
F	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
F	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
F	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
F	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
F	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
F	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
F	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
F	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
F	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
G	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
G	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
G	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
G	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
G	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
G	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
G	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
G	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
G	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
G	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
G	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
G	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
G	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
H	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
H	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
H	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
H	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
H	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
H	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
H	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
H	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
H	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
H	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
H	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
H	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
H	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
H	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
I	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
I	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
I	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
I	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
I	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
I	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
I	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
I	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
I	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
I	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
I	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
I	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
I	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
I	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
J	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
J	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
J	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
J	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
J	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
J	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
J	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
J	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
J	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
J	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
J	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
J	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
J	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
K	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
K	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
K	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
K	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
K	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
K	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
K	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
K	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
K	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
K	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
K	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
K	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
K	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
K	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9
L	-13	MET	-	EXPRESSION TAG	UNP Q9NTM9
L	-12	ARG	-	EXPRESSION TAG	UNP Q9NTM9
L	-11	GLY	-	EXPRESSION TAG	UNP Q9NTM9
L	-10	SER	-	EXPRESSION TAG	UNP Q9NTM9
L	-9	HIS	-	EXPRESSION TAG	UNP Q9NTM9
L	-8	HIS	-	EXPRESSION TAG	UNP Q9NTM9
L	-7	HIS	-	EXPRESSION TAG	UNP Q9NTM9
L	-6	HIS	-	EXPRESSION TAG	UNP Q9NTM9
L	-5	HIS	-	EXPRESSION TAG	UNP Q9NTM9
L	-4	HIS	-	EXPRESSION TAG	UNP Q9NTM9
L	-3	GLY	-	EXPRESSION TAG	UNP Q9NTM9
L	-2	SER	-	EXPRESSION TAG	UNP Q9NTM9
L	-1	ALA	-	EXPRESSION TAG	UNP Q9NTM9
L	0	CYS	-	EXPRESSION TAG	UNP Q9NTM9

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	145	Total O 145 145	0	0

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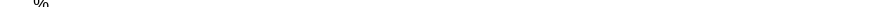
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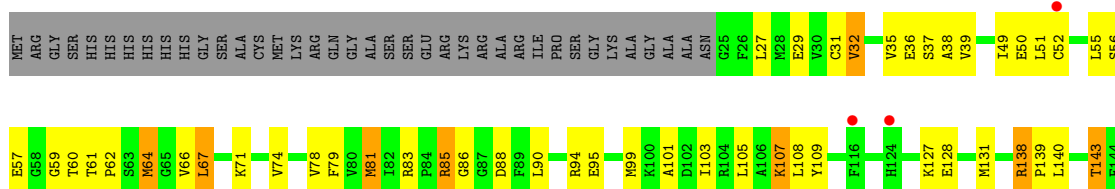
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	134	Total 134	O 134	0	0
2	C	137	Total 137	O 137	0	0
2	D	157	Total 157	O 157	0	0
2	E	58	Total 58	O 58	0	0
2	F	47	Total 47	O 47	0	0
2	G	25	Total 25	O 25	0	0
2	H	33	Total 33	O 33	0	0
2	I	56	Total 56	O 56	0	0
2	J	43	Total 43	O 43	0	0
2	K	26	Total 26	O 26	0	0
2	L	27	Total 27	O 27	0	0

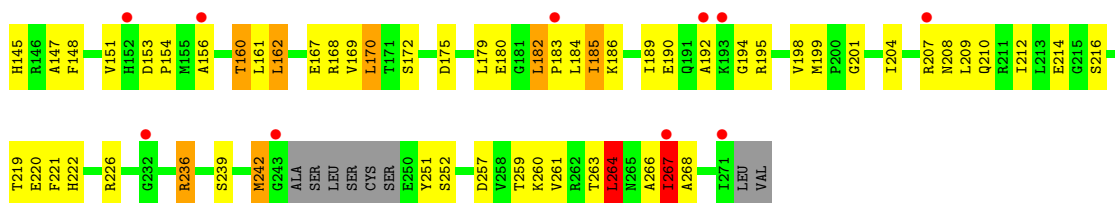
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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.

- Chain A:
- 
- 4% 47% 32% 8% 13%
- MET ARG GLY SER HIS HIS HIS HIS GLY SER ALA CYS MET LYS ARG GLN GLY ALA SER SER SER GLU ARG LYS ARG ALA ARG ARG ILE PRO SER GLY LYS GLY ALA ALA ALA N24 N25 F26 L27 N28 C31 V32 D33 S37 A38 S37 A38 A46 I49 E50 L51 L51 S53 S53 G54 L55 G59 T60 T61 P62 S63 R63 G65 V66 L67 Q68 K71 V74 W75 I76 M81 I82 R83 P84 R85 L90 Y91 S92 D93 E94 E95 I96 E97 V98 M99 K100 A101 D102 I103 R104 L105 A106 K107 L108 Y109 G110 L114 V115 F116 G117 A118 L119 T120 G123 H124 L125 E128 G127 R138 V142 T143 F144 H145 M150 V151 M155 E159 T160 L161 L162 T163 L164 E167 R168 V169 L170 T171 L179 E180 G181 L182 T185 Q191 A192 R195 T196 V197 P200 G201 T204 T205 D206 R207 N208 L209 L212 L213 S216 T219 E220 C223 R228 T229 D230 S231 F235 R236 N237 G243 A244 S245 L246 S247 C248 S249 E250 Y251 S252 L253 T256 D257 V258 T259 R260 V261 R262 T263 L272 VAL

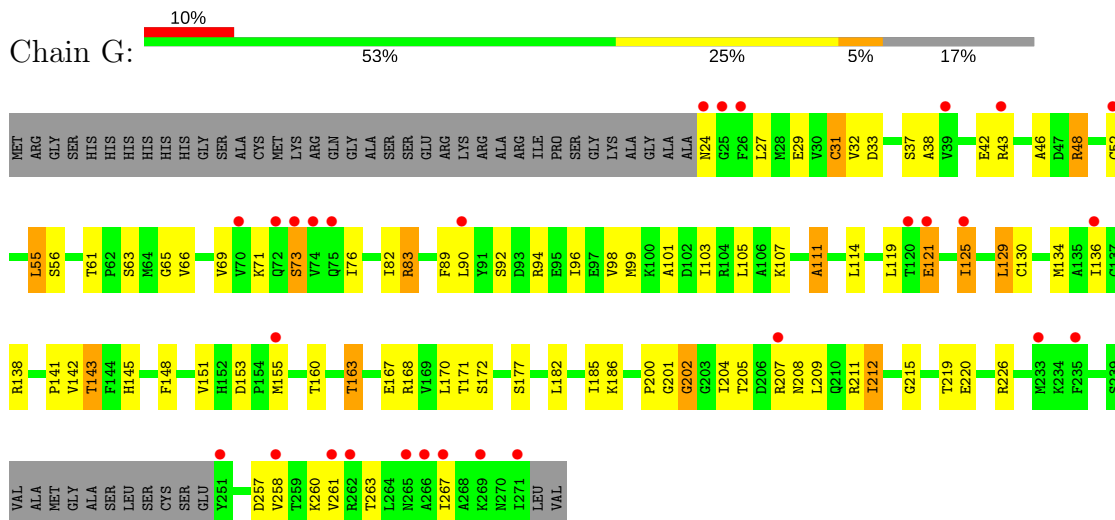
- [illegible]

- Chain C: 
- | Residue | Category |
|---------|----------|
| MET     | Green    |
| ARG     | Green    |
| GLY     | Green    |
| SER     | Green    |
| HIS     | Green    |
| HIS     | Green    |
| HIS     | Green    |
| HIS     | Green    |
| HIS     | Green    |
| HIS     | Green    |
| GLY     | Green    |
| SER     | Green    |
| ALA     | Green    |
| CYS     | Green    |
| MET     | Green    |
| MET     | Green    |
| LYS     | Green    |
| ARG     | Green    |
| GLN     | Green    |
| GLY     | Green    |
| ALA     | Green    |
| SER     | Green    |
| SER     | Green    |
| SER     | Green    |
| GLU     | Green    |
| ARG     | Green    |
| LYS     | Green    |
| ARG     | Green    |
| ALA     | Green    |
| ALA     | Green    |
| ILE     | Green    |
| PRO     | Green    |
| SER     | Green    |
| GLY     | Green    |
| LYS     | Green    |
| ALA     | Green    |
| GLY     | Green    |
| ALA     | Green    |
| N24     | Green    |
| L27     | Yellow   |
| M28     | Yellow   |
| E29     | Yellow   |
| V30     | Yellow   |
| C31     | Yellow   |
| V32     | Yellow   |
| D33     | Yellow   |
| S37     | Yellow   |
| A46     | Grey     |
| D47     | Grey     |
| R48     | Grey     |
| S53     | Grey     |
| G54     | Grey     |
| L55     | Grey     |
| G59     | Grey     |
| T60     | Grey     |
| T61     | Grey     |

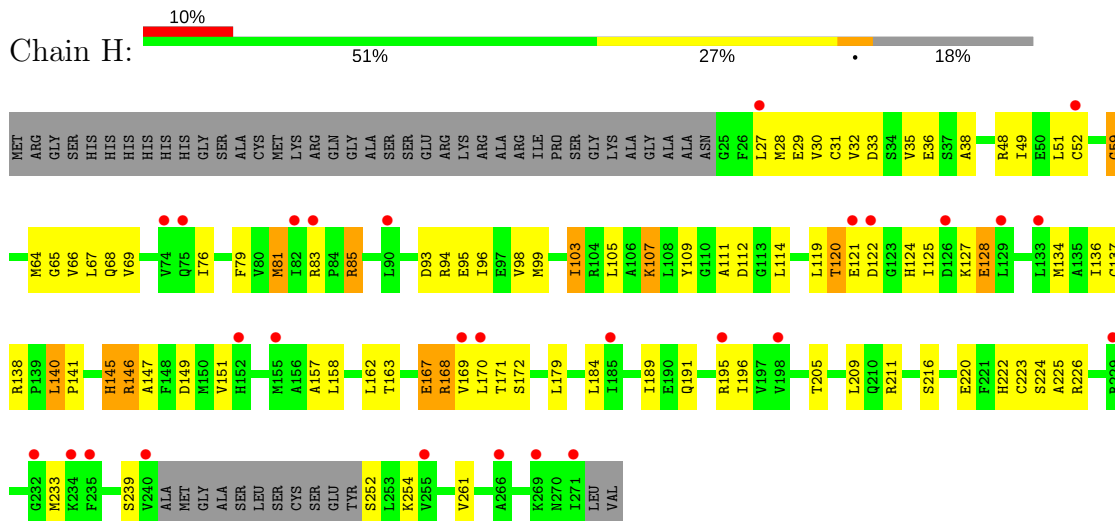




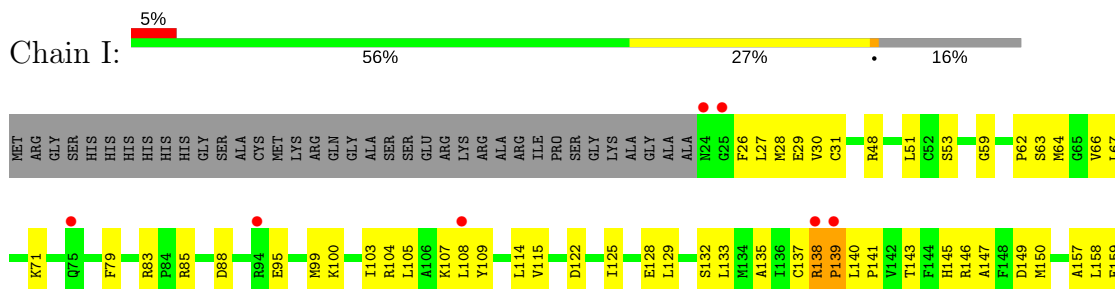
• Molecule 1: Copper homeostasis protein cutC homolog

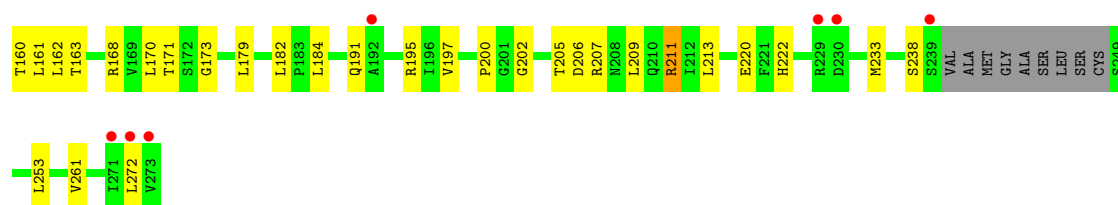


• Molecule 1: Copper homeostasis protein cutC homolog

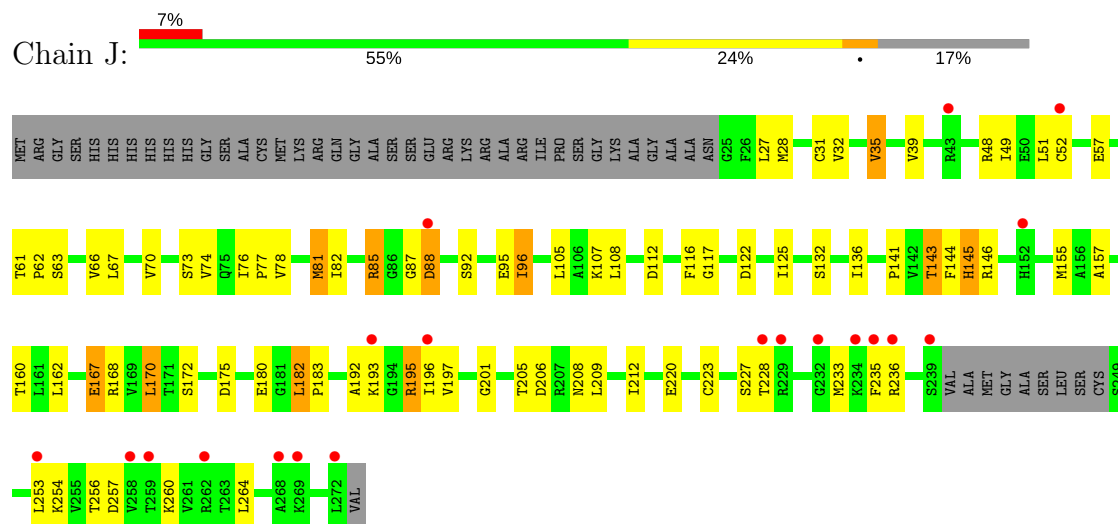


• Molecule 1: Copper homeostasis protein cutC homolog

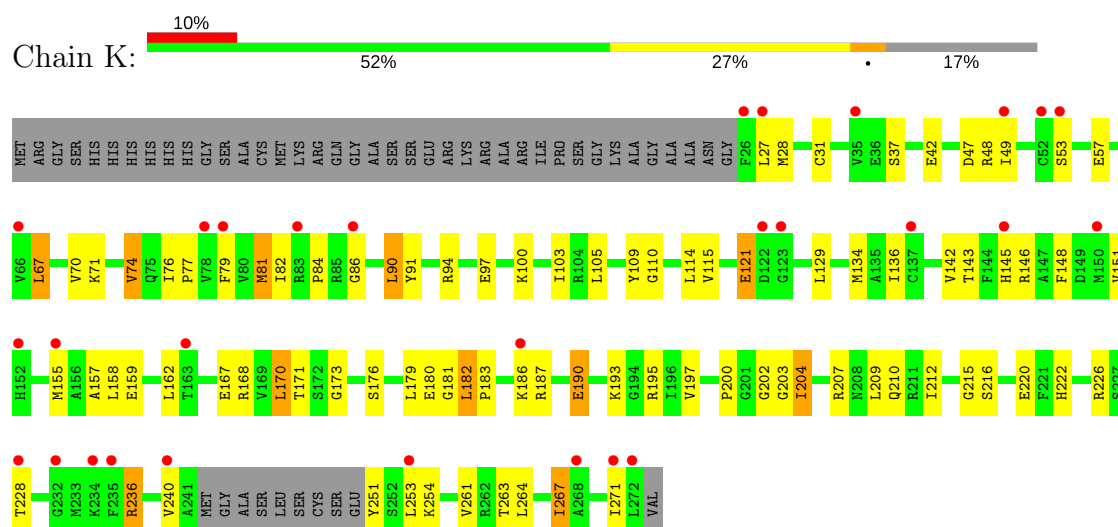




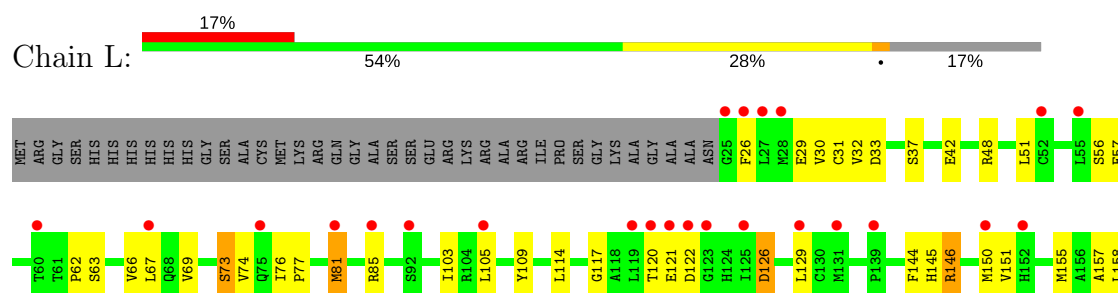
• Molecule 1: Copper homeostasis protein cutC homolog

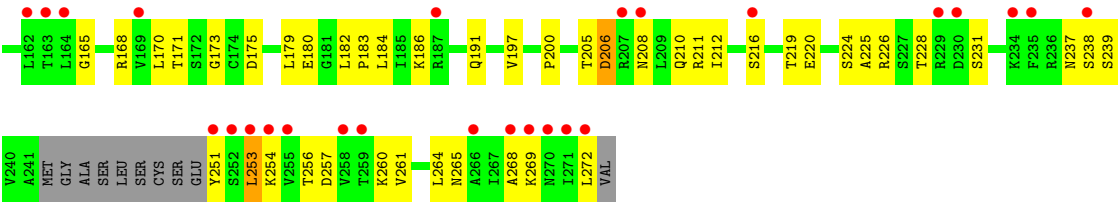


• Molecule 1: Copper homeostasis protein cutC homolog



• Molecule 1: Copper homeostasis protein cutC homolog





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.16Å 78.41Å 170.35Å 76.84° 87.88° 71.86°	Depositor
Resolution (Å)	50.00 – 2.50 40.13 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.5 (50.00-2.50) 90.7 (40.13-2.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.74 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.233 , 0.283 0.233 , 0.236	Depositor DCC
$R_{free}$ test set	6413 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.8	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 57.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.054 for -h,-k,-k+l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	22740	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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

### 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	0.64	0/1893	0.82	2/2549 (0.1%)
1	B	0.67	0/1859	0.78	0/2501
1	C	0.69	0/1878	0.84	1/2527 (0.0%)
1	D	0.69	1/1865 (0.1%)	0.83	3/2509 (0.1%)
1	E	0.46	0/1847	0.63	0/2486
1	F	0.49	0/1839	0.67	2/2474 (0.1%)
1	G	0.39	0/1814	0.58	0/2441
1	H	0.36	0/1800	0.58	0/2422
1	I	0.44	0/1844	0.61	0/2482
1	J	0.44	0/1829	0.61	0/2461
1	K	0.36	0/1822	0.57	0/2453
1	L	0.37	0/1826	0.55	0/2458
All	All	0.52	1/22116 (0.0%)	0.68	8/29763 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	52	CYS	CB-SG	6.06	1.92	1.82

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	27	LEU	CA-CB-CG	6.59	130.46	115.30
1	F	264	LEU	CA-CB-CG	6.18	129.51	115.30
1	A	85	ARG	NE-CZ-NH2	-6.01	117.29	120.30
1	C	105	LEU	CA-CB-CG	5.72	128.46	115.30
1	D	64	MET	CG-SD-CE	5.46	108.94	100.20
1	F	162	LEU	CA-CB-CG	5.42	127.77	115.30
1	A	64	MET	CG-SD-CE	5.39	108.83	100.20
1	D	90	LEU	CA-CB-CG	5.23	127.33	115.30

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	1870	0	1905	125	0
1	B	1837	0	1867	70	0
1	C	1856	0	1888	70	0
1	D	1843	0	1877	107	0
1	E	1825	0	1855	67	0
1	F	1817	0	1851	73	0
1	G	1792	0	1825	74	0
1	H	1779	0	1819	69	0
1	I	1822	0	1856	63	0
1	J	1807	0	1841	61	0
1	K	1800	0	1841	75	0
1	L	1804	0	1844	50	0
2	A	145	0	0	14	0
2	B	134	0	0	9	0
2	C	137	0	0	12	0
2	D	157	0	0	17	0
2	E	58	0	0	8	0
2	F	47	0	0	4	0
2	G	25	0	0	4	0
2	H	33	0	0	3	0
2	I	56	0	0	9	0
2	J	43	0	0	4	0
2	K	26	0	0	6	0
2	L	27	0	0	5	0
All	All	22740	0	22269	863	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 20.

All (863) 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:61:THR:HG21	2:B:280:HOH:O	1.38	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:SER:CB	1:A:250:GLU:HA	1.68	1.18
1:J:88:ASP:HB2	2:J:294:HOH:O	1.50	1.08
1:I:138:ARG:HB3	1:I:139:PRO:HD2	1.38	1.04
1:C:61:THR:HG21	2:C:276:HOH:O	1.57	1.02
1:A:249:SER:HB3	1:A:250:GLU:HA	1.40	1.01
1:A:231:SER:HB2	1:A:251:TYR:O	1.61	1.00
1:C:143:THR:HG21	2:C:274:HOH:O	1.61	0.98
1:I:107:LYS:NZ	1:I:138:ARG:HB2	1.79	0.97
1:D:31:CYS:HB2	2:D:792:HOH:O	1.63	0.97
1:G:55:LEU:H	1:G:55:LEU:HD13	1.30	0.96
1:A:27:LEU:HB3	1:A:220:GLU:HG2	1.49	0.95
1:G:125:ILE:H	1:G:125:ILE:HD13	1.30	0.94
1:I:145:HIS:HD2	1:I:147:ALA:H	1.15	0.94
1:D:61:THR:HG21	2:D:275:HOH:O	1.67	0.94
1:K:48:ARG:NH2	1:K:168:ARG:HH12	1.65	0.94
1:G:48:ARG:HB3	1:G:48:ARG:HH11	1.33	0.93
1:D:185:ILE:HG21	2:D:277:HOH:O	1.66	0.93
1:F:101:ALA:O	1:F:105:LEU:HD23	1.67	0.93
1:J:175:ASP:OD2	1:J:180:GLU:HB3	1.69	0.91
1:A:231:SER:HB3	1:A:251:TYR:HB3	1.51	0.90
1:I:27:LEU:HB2	1:I:220:GLU:HG2	1.53	0.90
1:B:104:ARG:HG3	1:B:104:ARG:HH11	1.36	0.89
1:L:171:THR:HG22	1:L:173:GLY:H	1.35	0.89
1:D:48:ARG:NH1	1:D:168:ARG:HH12	1.71	0.89
1:A:250:GLU:HB3	2:A:363:HOH:O	1.72	0.89
1:D:159:GLU:HG2	2:D:332:HOH:O	1.72	0.87
1:I:138:ARG:HA	2:I:755:HOH:O	1.74	0.87
1:A:249:SER:OG	1:A:250:GLU:HA	1.75	0.87
1:G:55:LEU:CB	1:G:226:ARG:HH22	1.88	0.86
1:I:128:GLU:HG2	2:I:737:HOH:O	1.76	0.86
1:A:37:SER:HB3	1:A:256:THR:HG23	1.58	0.86
1:I:108:LEU:HB3	2:I:811:HOH:O	1.75	0.85
1:A:249:SER:CB	1:A:250:GLU:CA	2.54	0.85
1:F:143:THR:HG22	2:F:276:HOH:O	1.76	0.85
1:A:143:THR:HG22	2:A:331:HOH:O	1.76	0.85
1:C:206:ASP:HB2	2:C:782:HOH:O	1.76	0.84
1:J:205:THR:H	1:J:208:ASN:HB2	1.40	0.84
1:C:143:THR:HB	1:C:168:ARG:HB2	1.60	0.84
1:B:143:THR:HG21	2:B:292:HOH:O	1.75	0.84
1:G:55:LEU:HB2	1:G:226:ARG:HH22	1.43	0.84
1:A:115:VAL:HG13	1:A:143:THR:O	1.78	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:171:THR:HG22	1:K:173:GLY:H	1.39	0.84
1:I:107:LYS:HZ2	1:I:138:ARG:HB2	1.43	0.83
1:B:63:SER:OG	1:B:66:VAL:HG23	1.78	0.83
1:D:162:LEU:HD21	1:D:195:ARG:HB2	1.60	0.83
1:E:94:ARG:HB2	1:E:94:ARG:HH11	1.41	0.83
1:K:162:LEU:HD13	1:K:195:ARG:HD2	1.59	0.83
1:H:85:ARG:HG3	1:H:85:ARG:HH11	1.44	0.83
1:A:61:THR:HG21	2:A:277:HOH:O	1.77	0.82
1:B:248:CYS:N	1:C:248:CYS:SG	2.53	0.82
1:A:24:ASN:N	1:A:219:THR:HG1	1.76	0.82
1:G:27:LEU:HB2	1:G:220:GLU:HG2	1.62	0.82
1:C:251:TYR:OH	1:D:150:MET:HE2	1.81	0.81
1:E:195:ARG:HD2	2:E:281:HOH:O	1.81	0.81
1:I:105:LEU:O	1:I:109:TYR:HD1	1.62	0.81
1:B:182:LEU:HD23	1:B:182:LEU:O	1.81	0.81
1:C:55:LEU:H	1:C:55:LEU:CD2	1.94	0.80
1:I:114:LEU:HB2	2:I:282:HOH:O	1.79	0.80
1:L:42:GLU:HG3	1:L:76:ILE:HD12	1.63	0.80
1:A:118:ALA:O	1:A:119:LEU:HD23	1.80	0.80
1:J:63:SER:OG	1:J:66:VAL:HG23	1.81	0.80
1:A:249:SER:OG	1:A:250:GLU:CA	2.30	0.80
1:E:31:CYS:HB2	2:E:453:HOH:O	1.82	0.80
1:G:143:THR:HG21	2:G:275:HOH:O	1.82	0.80
1:K:115:VAL:HG13	1:K:145:HIS:CD2	2.17	0.80
1:A:31:CYS:SG	1:A:55:LEU:HD21	2.22	0.79
1:F:31:CYS:SG	1:F:55:LEU:HD21	2.22	0.79
1:J:208:ASN:HB3	1:J:212:ILE:HD12	1.64	0.79
1:F:192:ALA:HA	1:F:195:ARG:HH11	1.47	0.79
1:A:231:SER:CB	1:A:251:TYR:HB3	2.13	0.79
1:I:122:ASP:HA	1:J:235:PHE:CD1	2.18	0.79
1:A:116:PHE:O	1:A:145:HIS:CD2	2.36	0.78
1:H:27:LEU:HB3	1:H:220:GLU:HG2	1.64	0.78
1:A:28:MET:HE3	1:A:261:VAL:HG13	1.65	0.78
1:A:168:ARG:HG2	1:A:197:VAL:HB	1.65	0.78
1:K:263:THR:O	1:K:267:ILE:HG22	1.84	0.78
1:B:248:CYS:N	1:C:248:CYS:HG	1.82	0.78
1:E:27:LEU:HB2	1:E:220:GLU:HG2	1.66	0.77
1:E:61:THR:HG21	2:E:449:HOH:O	1.84	0.77
1:J:27:LEU:HB3	1:J:220:GLU:HG2	1.66	0.77
1:D:82:ILE:HD13	1:D:103:ILE:CG1	2.14	0.77
1:E:101:ALA:HA	1:E:104:ARG:HH11	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:29:GLU:OE2	1:B:222:HIS:HD2	1.65	0.77
1:A:143:THR:HG21	2:A:275:HOH:O	1.83	0.76
1:A:250:GLU:CB	2:A:363:HOH:O	2.32	0.76
1:B:205:THR:H	1:B:208:ASN:HD21	1.34	0.76
1:D:48:ARG:NH1	1:D:168:ARG:NH1	2.33	0.76
1:A:101:ALA:O	1:A:105:LEU:HD23	1.86	0.75
1:E:99:MET:O	1:E:103:ILE:HG12	1.86	0.75
1:G:141:PRO:HA	1:G:167:GLU:OE2	1.86	0.75
1:G:99:MET:O	1:G:103:ILE:HG12	1.86	0.75
1:I:138:ARG:O	1:I:140:LEU:N	2.20	0.75
1:D:59:GLY:O	1:D:83:ARG:HD3	1.86	0.75
1:A:116:PHE:HD1	1:A:117:GLY:H	1.32	0.74
2:A:342:HOH:O	1:B:250:GLU:HG3	1.87	0.74
1:I:171:THR:HG22	1:I:173:GLY:H	1.51	0.74
1:A:226:ARG:HH11	1:A:256:THR:HG22	1.51	0.74
1:D:152:HIS:CD2	2:D:645:HOH:O	2.41	0.74
1:I:145:HIS:CD2	1:I:147:ALA:H	2.05	0.73
1:A:231:SER:CB	1:A:251:TYR:O	2.35	0.73
1:B:143:THR:HB	1:B:168:ARG:HB2	1.71	0.72
1:D:82:ILE:HD13	1:D:103:ILE:HG13	1.71	0.72
1:E:105:LEU:HD23	2:F:784:HOH:O	1.90	0.72
1:K:42:GLU:OE2	1:K:76:ILE:HG12	1.90	0.72
1:B:143:THR:HG22	2:B:302:HOH:O	1.88	0.71
1:D:81:MET:CE	1:D:145:HIS:HD2	2.03	0.71
1:D:185:ILE:CG2	2:D:277:HOH:O	2.28	0.71
1:D:82:ILE:CD1	1:D:114:LEU:HD22	2.19	0.71
1:F:145:HIS:HD2	1:F:147:ALA:H	1.36	0.71
1:D:143:THR:HG22	2:D:328:HOH:O	1.88	0.71
1:E:130:CYS:O	1:E:134:MET:HB2	1.91	0.71
1:C:28:MET:HE1	1:C:261:VAL:HG13	1.72	0.70
1:H:81:MET:HB3	2:H:402:HOH:O	1.89	0.70
1:A:114:LEU:CD1	1:A:137:CYS:SG	2.79	0.70
1:A:250:GLU:HG3	1:A:250:GLU:O	1.92	0.70
1:K:228:THR:HG22	2:K:666:HOH:O	1.89	0.70
1:L:105:LEU:O	1:L:109:TYR:HD1	1.73	0.70
1:F:175:ASP:OD2	1:F:180:GLU:HB3	1.90	0.70
1:C:251:TYR:OH	1:D:150:MET:CE	2.40	0.70
1:K:168:ARG:HG2	1:K:197:VAL:HB	1.73	0.70
1:A:32:VAL:HG13	1:A:37:SER:HB2	1.74	0.70
1:D:32:VAL:HG22	1:D:37:SER:HB3	1.74	0.70
1:B:104:ARG:HH11	1:B:104:ARG:CG	2.03	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:125:ILE:CD1	1:G:125:ILE:H	2.05	0.69
1:I:53:SER:HB2	1:I:62:PRO:HA	1.75	0.69
1:A:53:SER:HB3	1:A:60:THR:HG22	1.71	0.69
1:B:155:MET:SD	2:B:492:HOH:O	2.51	0.69
1:F:59:GLY:O	1:F:83:ARG:HD3	1.93	0.69
1:H:169:VAL:HG23	1:H:196:ILE:HG21	1.75	0.69
1:A:32:VAL:HG22	1:A:256:THR:HG21	1.74	0.69
1:D:209:LEU:HD22	1:D:213:LEU:HG	1.75	0.69
1:A:96:ILE:HA	1:A:99:MET:HE3	1.74	0.69
1:D:81:MET:HE3	1:D:145:HIS:HD2	1.58	0.69
1:K:204:ILE:CG2	1:K:212:ILE:HD13	2.23	0.69
1:A:259:THR:O	1:A:263:THR:HG23	1.93	0.69
1:E:158:LEU:HD13	1:E:188:LEU:CD1	2.24	0.68
1:D:143:THR:HG21	2:D:647:HOH:O	1.93	0.68
1:C:146:ARG:HD2	1:C:149:ASP:OD2	1.94	0.68
1:A:114:LEU:HD13	1:A:137:CYS:SG	2.33	0.68
1:G:55:LEU:H	1:G:55:LEU:CD1	2.01	0.68
1:A:207:ARG:HH22	1:D:239:SER:HB3	1.59	0.68
1:K:42:GLU:HG3	2:K:458:HOH:O	1.93	0.68
1:G:208:ASN:ND2	1:G:211:ARG:HH21	1.91	0.68
1:H:162:LEU:HD21	1:H:195:ARG:HB3	1.76	0.68
1:I:26:PHE:HE1	1:I:272:LEU:HD21	1.59	0.67
1:D:185:ILE:HD12	1:D:200:PRO:HB3	1.75	0.67
1:G:48:ARG:HB3	1:G:48:ARG:NH1	2.08	0.67
1:J:162:LEU:HD23	1:J:196:ILE:HG23	1.76	0.67
1:J:208:ASN:HB3	1:J:212:ILE:CD1	2.24	0.67
1:F:27:LEU:HB2	1:F:220:GLU:HG2	1.75	0.67
1:K:48:ARG:HH22	1:K:168:ARG:HH12	1.42	0.67
1:H:99:MET:O	1:H:103:ILE:HG22	1.94	0.67
1:C:55:LEU:H	1:C:55:LEU:HD23	1.57	0.67
1:A:114:LEU:HD12	1:A:137:CYS:CB	2.25	0.66
1:A:160:THR:O	1:A:163:THR:HG22	1.96	0.66
1:B:265:ASN:HD21	1:B:269:LYS:HE3	1.59	0.66
1:C:143:THR:HG22	2:C:302:HOH:O	1.94	0.66
1:H:103:ILE:O	1:H:107:LYS:HG2	1.94	0.66
1:F:192:ALA:HA	1:F:195:ARG:HD3	1.78	0.66
1:F:266:ALA:O	1:F:267:ILE:HG12	1.96	0.66
1:H:85:ARG:CG	1:H:85:ARG:HH11	2.09	0.66
1:L:269:LYS:H	1:L:272:LEU:HD12	1.61	0.66
1:J:85:ARG:HG2	1:J:87:GLY:H	1.60	0.66
1:B:104:ARG:NH1	2:B:345:HOH:O	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:THR:H	1:B:208:ASN:ND2	1.92	0.65
1:F:260:LYS:O	1:F:264:LEU:HD22	1.96	0.65
1:A:28:MET:CE	1:A:261:VAL:HG13	2.25	0.65
1:H:27:LEU:HB3	1:H:220:GLU:CG	2.27	0.65
1:I:28:MET:CE	1:I:261:VAL:HG13	2.26	0.65
1:B:204:ILE:HB	1:B:212:ILE:CD1	2.26	0.65
1:K:48:ARG:HD3	1:K:79:PHE:CD2	2.31	0.65
1:E:170:LEU:HD21	1:E:222:HIS:HB3	1.79	0.65
1:J:257:ASP:OD2	1:J:260:LYS:HG2	1.96	0.65
1:E:143:THR:HB	1:E:168:ARG:HB2	1.77	0.65
1:H:134:MET:HG2	1:H:138:ARG:NH2	2.10	0.65
1:B:48:ARG:NH2	1:B:220:GLU:OE1	2.28	0.65
1:A:53:SER:HB2	1:A:62:PRO:HA	1.79	0.65
1:D:82:ILE:HD13	1:D:103:ILE:HG12	1.79	0.65
1:E:172:SER:HB3	1:E:201:GLY:O	1.97	0.65
1:G:151:VAL:HG12	1:G:153:ASP:H	1.60	0.65
1:G:107:LYS:NZ	1:G:136:ILE:O	2.25	0.64
1:E:115:VAL:HG22	1:E:143:THR:HG23	1.79	0.64
1:H:83:ARG:HE	1:H:145:HIS:CE1	2.16	0.64
1:C:206:ASP:CB	2:C:782:HOH:O	2.39	0.64
1:E:118:ALA:HB1	1:E:129:LEU:HD13	1.80	0.64
1:L:165:GLY:N	2:L:783:HOH:O	2.29	0.64
1:K:28:MET:CE	1:K:261:VAL:HG13	2.28	0.64
1:H:103:ILE:CD1	1:H:137:CYS:SG	2.86	0.64
1:L:197:VAL:HG11	1:L:220:GLU:OE1	1.98	0.64
1:K:42:GLU:OE2	1:K:74:VAL:HG13	1.97	0.64
1:C:27:LEU:HB2	1:C:220:GLU:HG2	1.80	0.63
1:G:148:PHE:O	1:G:151:VAL:HG23	1.99	0.63
1:E:49:ILE:HD12	1:E:76:ILE:HD11	1.79	0.63
1:H:107:LYS:HE3	1:H:136:ILE:O	1.99	0.63
1:K:27:LEU:HB2	1:K:220:GLU:HG3	1.81	0.63
1:B:29:GLU:OE1	1:B:48:ARG:NH1	2.27	0.63
1:C:265:ASN:O	1:C:269:LYS:HG2	1.99	0.63
1:K:48:ARG:CZ	1:K:168:ARG:HH12	2.11	0.63
1:D:192:ALA:O	1:D:195:ARG:HG3	1.99	0.62
1:E:60:THR:O	1:E:61:THR:C	2.37	0.62
1:B:125:ILE:HD12	1:B:160:THR:CG2	2.30	0.62
1:F:185:ILE:HG13	1:F:186:LYS:N	2.14	0.62
1:G:32:VAL:HG13	1:G:37:SER:HB2	1.81	0.62
1:I:205:THR:HG22	1:I:206:ASP:H	1.65	0.62
1:A:114:LEU:HD12	1:A:137:CYS:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:148:PHE:O	1:F:151:VAL:HG22	2.00	0.62
1:A:179:LEU:HD13	1:C:179:LEU:HG	1.82	0.62
1:J:28:MET:CE	1:J:223:CYS:SG	2.88	0.62
1:K:209:LEU:HD12	1:K:264:LEU:HD23	1.81	0.62
1:A:116:PHE:CD1	1:A:117:GLY:N	2.58	0.62
1:D:53:SER:HB2	1:D:62:PRO:HA	1.81	0.62
1:I:138:ARG:CB	1:I:139:PRO:HD2	2.20	0.62
1:E:101:ALA:HA	1:E:104:ARG:NH1	2.14	0.62
1:F:64:MET:HG2	1:F:109:TYR:CD1	2.35	0.61
1:G:105:LEU:HD21	1:H:68:GLN:HE22	1.65	0.61
1:A:94:ARG:HA	1:A:97:GLU:HG2	1.81	0.61
1:B:204:ILE:HB	1:B:212:ILE:HD12	1.80	0.61
1:I:28:MET:HE3	1:I:261:VAL:HG13	1.83	0.61
1:A:231:SER:HB3	1:A:251:TYR:CB	2.26	0.61
1:C:32:VAL:HG22	1:C:37:SER:CB	2.30	0.61
1:C:150:MET:SD	1:D:240:VAL:HG22	2.40	0.61
1:F:32:VAL:CG2	1:F:37:SER:HB3	2.31	0.61
1:K:253:LEU:HD12	1:L:85:ARG:HD3	1.82	0.61
1:L:51:LEU:HB3	1:L:62:PRO:HG3	1.81	0.61
1:A:185:ILE:HD13	1:A:200:PRO:HB3	1.81	0.61
1:A:205:THR:HG22	1:A:208:ASN:ND2	2.15	0.61
1:B:225:ALA:N	2:B:308:HOH:O	2.34	0.61
1:D:82:ILE:HD12	1:D:114:LEU:HD22	1.81	0.61
1:D:61:THR:HG22	1:D:83:ARG:H	1.65	0.61
1:E:94:ARG:HB2	1:E:94:ARG:NH1	2.15	0.61
1:K:143:THR:HG23	1:K:168:ARG:HB2	1.83	0.61
1:A:116:PHE:O	1:A:145:HIS:NE2	2.33	0.61
1:I:205:THR:HG22	1:I:206:ASP:N	2.15	0.61
1:C:33:ASP:OD1	1:C:55:LEU:HD21	2.01	0.60
1:A:114:LEU:HD12	1:A:137:CYS:SG	2.40	0.60
1:E:120:THR:HG22	1:E:124:HIS:H	1.66	0.60
1:G:145:HIS:HA	1:G:170:LEU:HB2	1.84	0.60
1:L:117:GLY:HA2	1:L:144:PHE:CE1	2.36	0.60
1:B:61:THR:HG22	1:B:83:ARG:O	2.01	0.60
1:A:59:GLY:O	1:A:83:ARG:HD3	2.02	0.60
1:H:103:ILE:HD11	1:H:137:CYS:SG	2.42	0.60
1:L:126:ASP:OD2	1:L:129:LEU:HB2	2.02	0.60
1:G:55:LEU:HB3	1:G:226:ARG:HH22	1.65	0.60
1:G:31:CYS:HB2	2:G:544:HOH:O	2.01	0.60
1:H:179:LEU:HD11	1:H:211:ARG:HH21	1.67	0.60
1:J:162:LEU:HD21	1:J:195:ARG:HB3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:159:GLU:OE1	1:K:159:GLU:HA	2.01	0.60
1:G:182:LEU:HA	1:G:185:ILE:HG12	1.83	0.60
1:H:225:ALA:HB3	1:H:261:VAL:HG23	1.82	0.60
1:D:182:LEU:HA	1:D:185:ILE:CG2	2.32	0.60
1:E:105:LEU:HD13	1:E:109:TYR:HE2	1.67	0.60
1:J:132:SER:O	1:J:136:ILE:HD12	2.02	0.60
1:D:143:THR:HG22	1:D:168:ARG:HB2	1.82	0.60
1:K:236:ARG:HH22	1:K:251:TYR:HB2	1.67	0.59
1:G:63:SER:OG	1:G:66:VAL:HG23	2.01	0.59
1:J:162:LEU:CD2	1:J:195:ARG:HB3	2.33	0.59
1:B:168:ARG:HG2	1:B:197:VAL:HB	1.85	0.59
1:J:143:THR:HG21	2:J:457:HOH:O	2.01	0.59
1:C:207:ARG:NH2	2:C:808:HOH:O	2.35	0.59
1:K:182:LEU:HB3	1:K:186:LYS:HE3	1.84	0.59
1:F:204:ILE:HA	1:F:208:ASN:HD21	1.68	0.59
1:G:257:ASP:O	1:G:261:VAL:HG23	2.02	0.59
1:H:151:VAL:HG11	1:H:157:ALA:HB2	1.85	0.59
1:D:61:THR:HG22	1:D:83:ARG:O	2.02	0.59
1:G:29:GLU:HA	1:G:48:ARG:O	2.03	0.59
1:G:55:LEU:HD22	1:G:56:SER:H	1.68	0.59
1:H:49:ILE:HG12	1:H:76:ILE:HD11	1.84	0.59
1:B:204:ILE:HD13	1:B:209:LEU:HD13	1.85	0.59
1:D:190:GLU:O	1:D:193:LYS:HD2	2.02	0.59
1:J:92:SER:O	1:J:96:ILE:HG23	2.02	0.59
1:F:143:THR:HG21	2:F:275:HOH:O	2.03	0.59
1:J:146:ARG:HH12	1:J:172:SER:HB3	1.68	0.58
2:E:446:HOH:O	1:G:205:THR:HG21	2.02	0.58
1:G:257:ASP:HB3	1:G:260:LYS:HB2	1.85	0.58
1:H:140:LEU:HD23	1:H:140:LEU:H	1.68	0.58
1:A:249:SER:H	1:A:250:GLU:HB2	1.69	0.58
1:B:127:LYS:O	1:B:131:MET:HG3	2.04	0.58
1:K:204:ILE:HG22	1:K:212:ILE:CD1	2.34	0.58
1:C:150:MET:SD	1:D:240:VAL:CG2	2.91	0.58
1:G:186:LYS:HA	2:G:781:HOH:O	2.02	0.58
1:K:134:MET:HG3	1:K:142:VAL:HG21	1.86	0.58
1:I:132:SER:O	1:I:135:ALA:HB3	2.03	0.58
1:C:61:THR:HG22	1:C:83:ARG:O	2.04	0.58
1:F:261:VAL:HA	1:F:264:LEU:CD2	2.34	0.58
1:K:182:LEU:O	1:K:186:LYS:HG3	2.04	0.58
1:A:103:ILE:HG23	1:A:114:LEU:HD11	1.85	0.58
1:B:125:ILE:HD12	1:B:160:THR:HG21	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:ARG:CZ	1:D:168:ARG:NH1	2.67	0.57
1:E:63:SER:OG	1:E:66:VAL:HG23	2.03	0.57
1:A:237:ASN:N	1:A:251:TYR:OH	2.36	0.57
1:C:28:MET:CE	1:C:261:VAL:HG13	2.34	0.57
1:D:226:ARG:NE	2:D:573:HOH:O	2.37	0.57
1:I:105:LEU:O	1:I:109:TYR:CD1	2.52	0.57
1:J:85:ARG:CG	1:J:87:GLY:H	2.18	0.57
1:E:107:LYS:NZ	2:E:793:HOH:O	2.37	0.57
1:A:192:ALA:O	1:A:195:ARG:HD3	2.05	0.57
1:A:31:CYS:HB2	1:A:50:GLU:HB3	1.86	0.57
1:B:83:ARG:HG2	2:B:282:HOH:O	2.04	0.57
1:I:146:ARG:NH2	1:I:202:GLY:HA2	2.19	0.57
1:F:167:GLU:HG3	2:F:509:HOH:O	2.04	0.57
1:F:168:ARG:NH1	1:F:220:GLU:OE1	2.38	0.57
1:A:32:VAL:HG13	1:A:37:SER:CB	2.35	0.57
1:B:29:GLU:OE2	1:B:222:HIS:CD2	2.54	0.57
1:G:204:ILE:HG13	1:G:212:ILE:HD12	1.86	0.57
1:C:28:MET:HE2	1:C:46:ALA:HA	1.86	0.56
1:H:103:ILE:HD12	1:H:137:CYS:SG	2.45	0.56
1:D:82:ILE:HD11	1:D:114:LEU:HD22	1.86	0.56
1:I:64:MET:HE3	2:I:481:HOH:O	2.04	0.56
1:J:182:LEU:HB3	1:J:183:PRO:HD3	1.86	0.56
1:A:114:LEU:O	1:A:142:VAL:HA	2.05	0.56
1:E:158:LEU:HD13	1:E:188:LEU:HD11	1.88	0.56
1:H:189:ILE:HD12	1:H:216:SER:HB2	1.87	0.56
1:L:48:ARG:HB3	1:L:77:PRO:HG2	1.87	0.56
1:A:37:SER:CB	1:A:256:THR:HG23	2.30	0.56
1:A:64:MET:CE	1:A:64:MET:HA	2.36	0.56
1:G:143:THR:HB	1:G:168:ARG:HB2	1.88	0.56
1:J:51:LEU:HB3	1:J:62:PRO:HG3	1.88	0.56
1:A:206:ASP:HB3	2:A:322:HOH:O	2.04	0.56
1:H:226:ARG:HH21	1:H:254:LYS:HD3	1.70	0.56
1:C:32:VAL:HG22	1:C:37:SER:HB3	1.88	0.56
1:D:64:MET:HG2	1:D:109:TYR:CD1	2.41	0.56
1:L:257:ASP:O	1:L:261:VAL:HG23	2.05	0.56
1:C:237:ASN:HB3	1:D:150:MET:HE3	1.88	0.56
1:E:57:GLU:O	1:E:83:ARG:NH2	2.39	0.56
1:F:85:ARG:HD2	1:F:86:GLY:O	2.05	0.56
1:G:182:LEU:CD1	1:G:212:ILE:HA	2.36	0.56
1:K:145:HIS:HB2	2:K:274:HOH:O	2.06	0.56
1:A:245:SER:O	1:A:246:LEU:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:205:THR:HG22	1:J:206:ASP:H	1.71	0.56
1:A:245:SER:O	1:C:245:SER:HB2	2.06	0.56
1:F:259:THR:O	1:F:263:THR:HG23	2.06	0.56
1:K:28:MET:HE3	1:K:261:VAL:HG13	1.87	0.56
1:A:116:PHE:O	1:A:145:HIS:CE1	2.59	0.55
1:G:92:SER:O	1:G:96:ILE:HG23	2.06	0.55
1:D:151:VAL:HG11	1:D:157:ALA:HB2	1.87	0.55
1:I:99:MET:O	1:I:103:ILE:HG13	2.06	0.55
1:L:105:LEU:O	1:L:109:TYR:CD1	2.58	0.55
1:L:205:THR:HG22	1:L:206:ASP:H	1.71	0.55
1:H:107:LYS:HD2	1:H:140:LEU:HD11	1.88	0.55
1:A:25:GLY:HA3	2:A:305:HOH:O	2.06	0.55
1:L:74:VAL:HG12	1:L:76:ILE:H	1.71	0.55
1:C:206:ASP:CG	2:C:782:HOH:O	2.44	0.55
1:C:29:GLU:OE1	1:C:48:ARG:NH1	2.35	0.55
1:E:134:MET:HE1	1:E:138:ARG:HG2	1.89	0.55
1:A:68:GLN:OE1	1:B:105:LEU:HD21	2.07	0.55
1:C:168:ARG:HG2	1:C:197:VAL:HB	1.88	0.55
1:C:53:SER:O	1:C:59:GLY:HA2	2.06	0.55
1:J:28:MET:HE2	1:J:223:CYS:SG	2.47	0.55
1:D:64:MET:CE	1:D:64:MET:HA	2.37	0.55
1:E:159:GLU:O	1:E:163:THR:HG22	2.07	0.55
1:H:179:LEU:HD11	1:H:211:ARG:NH2	2.22	0.55
1:I:29:GLU:OE2	1:I:222:HIS:HD2	1.89	0.55
1:J:85:ARG:NH1	1:J:95:GLU:OE1	2.39	0.55
1:K:90:LEU:HD11	1:K:121:GLU:HG2	1.89	0.55
1:H:30:VAL:HG13	1:H:224:SER:HA	1.88	0.54
1:B:146:ARG:HD2	1:B:149:ASP:OD1	2.07	0.54
1:G:200:PRO:HD2	1:G:220:GLU:O	2.07	0.54
1:G:204:ILE:HG13	1:G:212:ILE:CD1	2.37	0.54
1:H:134:MET:HG2	1:H:138:ARG:HH21	1.71	0.54
1:B:182:LEU:HD23	1:B:182:LEU:C	2.28	0.54
1:C:127:LYS:HD2	2:C:475:HOH:O	2.07	0.54
1:F:210:GLN:O	1:F:214:GLU:HG2	2.08	0.54
1:A:26:PHE:HA	1:A:219:THR:O	2.08	0.54
1:E:158:LEU:CD1	1:E:196:ILE:HD11	2.38	0.54
1:F:192:ALA:CA	1:F:195:ARG:HH11	2.20	0.54
1:I:128:GLU:HG3	2:I:281:HOH:O	2.07	0.54
1:J:125:ILE:HD11	1:J:157:ALA:HB1	1.88	0.54
1:D:152:HIS:HD2	2:D:645:HOH:O	1.86	0.54
1:D:269:LYS:C	2:D:407:HOH:O	2.46	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:VAL:HG22	1:B:37:SER:HB3	1.90	0.53
1:J:35:VAL:O	1:J:39:VAL:HG23	2.09	0.53
1:A:205:THR:HG23	1:A:207:ARG:H	1.73	0.53
1:C:71:LYS:HE2	1:C:110:GLY:O	2.08	0.53
1:E:61:THR:HG22	1:E:83:ARG:O	2.09	0.53
1:E:51:LEU:HB3	1:E:62:PRO:HG3	1.91	0.53
1:E:67:LEU:O	1:E:71:LYS:HB2	2.08	0.53
1:G:177:SER:HB2	1:G:202:GLY:O	2.09	0.53
1:H:105:LEU:O	1:H:109:TYR:HD1	1.91	0.53
1:H:122:ASP:HB2	1:H:124:HIS:CE1	2.44	0.53
1:I:162:LEU:HD11	1:I:195:ARG:HB2	1.90	0.53
1:A:128:GLU:HB2	2:A:552:HOH:O	2.09	0.53
1:D:182:LEU:HA	1:D:185:ILE:HG23	1.90	0.53
1:F:127:LYS:O	1:F:131:MET:HG3	2.08	0.53
1:H:94:ARG:O	1:H:98:VAL:HG23	2.08	0.53
1:F:143:THR:HB	1:F:168:ARG:CB	2.39	0.53
1:I:103:ILE:HG23	1:I:114:LEU:HD13	1.90	0.53
1:K:204:ILE:HG21	1:K:212:ILE:HD13	1.90	0.53
1:A:209:LEU:HD22	1:A:213:LEU:HG	1.91	0.53
1:C:192:ALA:O	1:C:195:ARG:HD3	2.09	0.53
1:G:151:VAL:HG12	1:G:153:ASP:N	2.24	0.53
1:K:210:GLN:HB2	1:K:267:ILE:HD11	1.90	0.53
1:D:155:MET:SD	1:D:191:GLN:OE1	2.67	0.53
1:K:48:ARG:NH2	1:K:168:ARG:NH1	2.47	0.53
1:B:208:ASN:HD22	1:B:208:ASN:C	2.12	0.53
1:D:160:THR:HA	1:D:163:THR:CG2	2.39	0.53
1:I:141:PRO:HA	2:I:279:HOH:O	2.09	0.53
1:G:260:LYS:HA	1:G:263:THR:HG22	1.91	0.52
1:B:175:ASP:OD1	1:D:207:ARG:NH2	2.42	0.52
1:C:143:THR:CG2	2:C:274:HOH:O	2.35	0.52
1:I:125:ILE:HD13	1:I:161:LEU:HD21	1.91	0.52
1:J:183:PRO:HG2	1:L:211:ARG:NH1	2.24	0.52
1:A:208:ASN:OD1	1:A:208:ASN:C	2.48	0.52
1:C:53:SER:HB2	1:C:62:PRO:HA	1.90	0.52
1:I:107:LYS:HG2	1:I:140:LEU:CD1	2.39	0.52
1:J:233:MET:O	1:J:236:ARG:HD3	2.09	0.52
1:J:27:LEU:CB	1:J:220:GLU:HG2	2.36	0.52
1:F:266:ALA:C	1:F:268:ALA:H	2.13	0.52
1:F:50:GLU:OE1	1:F:81:MET:HG2	2.10	0.52
1:I:59:GLY:O	1:I:83:ARG:HD3	2.10	0.52
1:K:28:MET:HE1	1:K:261:VAL:HG13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:145:HIS:CG	1:L:146:ARG:H	2.28	0.52
1:D:61:THR:HB	1:D:81:MET:O	2.09	0.52
1:K:167:GLU:HB2	2:K:621:HOH:O	2.08	0.52
1:B:134:MET:HE3	1:B:142:VAL:HG21	1.91	0.52
1:E:166:PHE:O	1:E:196:ILE:HG22	2.08	0.52
1:I:129:LEU:O	1:I:133:LEU:HG	2.09	0.52
1:I:149:ASP:OD1	1:I:171:THR:HG23	2.09	0.52
1:G:94:ARG:HH11	1:H:36:GLU:HG3	1.75	0.52
1:K:82:ILE:HD12	1:K:114:LEU:HD22	1.91	0.52
1:L:120:THR:O	1:L:122:ASP:N	2.43	0.52
1:B:192:ALA:O	1:B:195:ARG:HD3	2.10	0.52
1:H:127:LYS:HB2	1:H:128:GLU:OE1	2.10	0.52
1:K:204:ILE:CG2	1:K:212:ILE:CD1	2.88	0.52
1:K:267:ILE:HG13	1:K:267:ILE:O	2.10	0.52
1:C:55:LEU:H	1:C:55:LEU:HD22	1.74	0.51
1:D:162:LEU:HD11	1:D:195:ARG:HE	1.74	0.51
1:A:117:GLY:HA2	1:A:144:PHE:CE1	2.46	0.51
1:F:32:VAL:HG23	1:F:37:SER:HB3	1.90	0.51
1:G:42:GLU:HG3	1:G:76:ILE:HD12	1.92	0.51
1:H:138:ARG:HD3	2:H:796:HOH:O	2.11	0.51
1:C:99:MET:O	1:C:103:ILE:HG12	2.10	0.51
1:C:127:LYS:HD2	1:C:127:LYS:H	1.76	0.51
1:C:32:VAL:HG22	1:C:37:SER:HB2	1.91	0.51
1:K:148:PHE:O	1:K:151:VAL:HG23	2.10	0.51
1:L:155:MET:HG2	1:L:191:GLN:HE22	1.75	0.51
1:D:94:ARG:HA	1:D:97:GLU:HG2	1.92	0.51
1:F:161:LEU:HD13	1:F:169:VAL:CG2	2.41	0.51
1:H:28:MET:HE1	1:H:261:VAL:HG13	1.91	0.51
1:J:175:ASP:OD2	1:J:180:GLU:CB	2.50	0.51
1:A:81:MET:CE	1:A:145:HIS:HD2	2.24	0.51
1:I:107:LYS:HG2	1:I:140:LEU:HD12	1.93	0.51
1:I:138:ARG:C	1:I:140:LEU:H	2.12	0.51
1:K:151:VAL:HG11	1:K:157:ALA:HB2	1.91	0.51
1:G:101:ALA:O	1:G:105:LEU:HD23	2.11	0.51
1:G:61:THR:HG22	1:G:83:ARG:O	2.11	0.51
1:E:35:VAL:HG22	1:E:70:VAL:HG23	1.93	0.51
1:G:43:ARG:HH11	1:G:258:VAL:HG21	1.75	0.51
1:K:186:LYS:O	1:K:190:GLU:HG2	2.10	0.51
1:A:115:VAL:HG13	1:A:143:THR:C	2.31	0.51
1:C:32:VAL:CG2	1:C:37:SER:HB3	2.41	0.51
1:G:46:ALA:O	1:G:76:ILE:HD13	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:51:LEU:O	1:L:81:MET:HB2	2.11	0.51
1:D:170:LEU:HD21	1:D:222:HIS:HB3	1.93	0.50
1:E:146:ARG:NH2	1:E:172:SER:HB3	2.26	0.50
1:G:55:LEU:HD13	1:G:55:LEU:N	2.13	0.50
1:K:186:LYS:HG2	1:K:216:SER:HA	1.93	0.50
1:L:30:VAL:HG13	1:L:224:SER:HA	1.93	0.50
1:A:258:VAL:CG1	1:A:262:ARG:HH21	2.24	0.50
1:C:143:THR:HB	1:C:168:ARG:CB	2.37	0.50
1:G:182:LEU:HD11	1:G:215:GLY:HA3	1.93	0.50
1:K:71:LYS:HG3	1:K:110:GLY:O	2.11	0.50
1:A:223:CYS:HA	2:A:312:HOH:O	2.10	0.50
1:A:71:LYS:HE2	1:A:110:GLY:O	2.11	0.50
1:E:89:PHE:HB2	1:E:119:LEU:HB2	1.93	0.50
1:F:145:HIS:CD2	1:F:147:ALA:H	2.24	0.50
1:J:32:VAL:HG12	1:J:256:THR:HG21	1.92	0.50
1:L:26:PHE:HB2	1:L:269:LYS:HE2	1.92	0.50
1:B:210:GLN:HA	1:B:271:ILE:HD11	1.93	0.50
1:B:53:SER:HB3	1:B:62:PRO:HA	1.94	0.50
1:C:257:ASP:OD2	1:C:259:THR:HG23	2.12	0.50
1:F:67:LEU:O	1:F:71:LYS:HB2	2.11	0.50
1:A:115:VAL:CG1	1:A:143:THR:OG1	2.60	0.50
1:J:107:LYS:NZ	1:J:136:ILE:O	2.37	0.50
1:J:61:THR:HA	1:J:81:MET:O	2.12	0.50
1:D:81:MET:HE2	1:D:115:VAL:O	2.12	0.50
1:G:125:ILE:N	1:G:125:ILE:HD13	2.12	0.50
1:I:125:ILE:HD11	1:I:157:ALA:HB1	1.93	0.50
1:G:209:LEU:HD22	1:G:267:ILE:HG13	1.94	0.50
1:C:82:ILE:HG13	1:C:103:ILE:HD13	1.94	0.50
1:D:44:GLY:HA2	1:D:262:ARG:HG3	1.93	0.50
1:D:272:LEU:HB2	2:D:885:HOH:O	2.12	0.50
1:E:94:ARG:NH1	1:F:36:GLU:HB2	2.27	0.50
1:A:115:VAL:HG22	1:A:143:THR:HG23	1.92	0.49
1:E:204:ILE:HD11	1:E:221:PHE:HD2	1.77	0.49
1:J:49:ILE:HG22	1:J:78:VAL:HG13	1.93	0.49
1:L:151:VAL:HG11	1:L:157:ALA:HB2	1.94	0.49
1:A:205:THR:OG1	1:A:206:ASP:N	2.45	0.49
1:F:257:ASP:O	1:F:261:VAL:HG23	2.11	0.49
1:G:73:SER:HB2	2:G:579:HOH:O	2.11	0.49
1:K:197:VAL:HG11	1:K:220:GLU:OE1	2.12	0.49
1:B:209:LEU:HD22	1:B:264:LEU:CD2	2.43	0.49
1:E:168:ARG:HG2	1:E:197:VAL:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:61:THR:HG22	1:F:83:ARG:O	2.12	0.49
1:L:182:LEU:N	1:L:183:PRO:HD2	2.28	0.49
1:C:209:LEU:HD22	1:C:213:LEU:HG	1.94	0.49
1:J:27:LEU:HD13	1:J:220:GLU:OE2	2.13	0.49
1:A:123:GLY:O	1:A:151:VAL:HG22	2.13	0.49
1:D:127:LYS:NZ	2:D:561:HOH:O	2.45	0.49
1:F:172:SER:HB3	1:F:201:GLY:O	2.12	0.49
1:B:125:ILE:HD13	1:B:125:ILE:C	2.32	0.49
1:B:259:THR:HG22	2:B:310:HOH:O	2.13	0.49
1:G:182:LEU:O	1:G:185:ILE:HG12	2.12	0.49
1:J:116:PHE:O	1:J:144:PHE:HA	2.11	0.49
1:L:182:LEU:HD11	1:L:212:ILE:HA	1.95	0.49
1:A:114:LEU:O	1:A:115:VAL:HG22	2.13	0.49
1:A:115:VAL:HG13	1:A:143:THR:OG1	2.12	0.49
1:D:48:ARG:HH12	1:D:168:ARG:HH12	1.56	0.49
1:E:24:ASN:HB2	2:E:700:HOH:O	2.13	0.49
1:J:205:THR:HB	1:J:208:ASN:HD22	1.78	0.49
1:L:206:ASP:HB2	2:L:745:HOH:O	2.12	0.49
1:A:103:ILE:HG23	1:A:114:LEU:CD1	2.42	0.49
1:J:146:ARG:HG3	1:J:170:LEU:HD13	1.95	0.49
1:K:115:VAL:HG13	1:K:145:HIS:NE2	2.27	0.49
1:E:226:ARG:HA	1:E:256:THR:HA	1.94	0.49
1:F:236:ARG:HH21	1:F:251:TYR:HB3	1.77	0.49
1:A:247:SER:O	1:A:248:CYS:O	2.30	0.48
1:A:251:TYR:N	1:A:251:TYR:CD1	2.81	0.48
1:C:55:LEU:HD23	1:C:55:LEU:N	2.27	0.48
1:E:146:ARG:HH21	1:E:202:GLY:CA	2.26	0.48
1:J:192:ALA:O	1:J:195:ARG:HD2	2.12	0.48
1:L:208:ASN:OD1	1:L:211:ARG:NE	2.45	0.48
1:A:105:LEU:HD21	1:B:68:GLN:OE1	2.13	0.48
1:I:85:ARG:HH21	1:I:88:ASP:CG	2.15	0.48
1:L:210:GLN:NE2	2:L:777:HOH:O	2.46	0.48
1:L:56:SER:HB3	1:L:254:LYS:NZ	2.27	0.48
1:A:171:THR:O	1:A:200:PRO:HA	2.13	0.48
1:C:127:LYS:O	1:C:131:MET:HG3	2.12	0.48
1:J:48:ARG:NH2	1:J:168:ARG:HH11	2.11	0.48
1:K:105:LEU:O	1:K:109:TYR:HD1	1.95	0.48
1:L:205:THR:HG22	1:L:206:ASP:N	2.28	0.48
1:B:204:ILE:CD1	1:B:209:LEU:HD13	2.42	0.48
1:G:208:ASN:HD21	1:G:211:ARG:HH21	1.59	0.48
1:A:116:PHE:O	1:A:145:HIS:CG	2.65	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:LEU:HG	1:D:179:LEU:HD13	1.96	0.48
1:H:114:LEU:HD13	1:H:137:CYS:SG	2.53	0.48
1:H:32:VAL:HG11	1:H:38:ALA:HB2	1.94	0.48
1:I:160:THR:HA	1:I:163:THR:HG22	1.95	0.48
1:E:26:PHE:HA	1:E:219:THR:O	2.14	0.48
1:I:211:ARG:HD2	1:I:211:ARG:H	1.78	0.48
1:K:155:MET:SD	1:K:187:ARG:NH2	2.83	0.48
1:B:105:LEU:HD12	1:B:109:TYR:HE1	1.78	0.48
1:B:26:PHE:HA	1:B:219:THR:O	2.13	0.48
1:K:103:ILE:HG23	1:K:114:LEU:HD13	1.95	0.48
1:A:236:ARG:HB3	1:A:251:TYR:CZ	2.48	0.48
1:D:205:THR:OG1	1:D:206:ASP:N	2.47	0.48
1:E:71:LYS:NZ	1:E:112:ASP:OD2	2.46	0.48
1:K:81:MET:HA	1:K:115:VAL:HB	1.95	0.48
1:K:82:ILE:CD1	1:K:114:LEU:HD22	2.44	0.48
1:B:51:LEU:HB3	1:B:62:PRO:HG3	1.95	0.48
1:C:69:VAL:HA	1:C:72:GLN:HG2	1.94	0.48
1:A:219:THR:HG21	2:A:541:HOH:O	2.13	0.48
1:D:234:LYS:HG2	2:D:661:HOH:O	2.14	0.48
1:G:71:LYS:HD2	1:G:111:ALA:H	1.79	0.48
1:K:200:PRO:HD2	1:K:220:GLU:O	2.14	0.48
1:A:229:ARG:O	1:A:253:LEU:HD23	2.14	0.47
1:B:209:LEU:HD22	1:B:264:LEU:HD23	1.96	0.47
1:F:239:SER:OG	1:G:207:ARG:NH2	2.47	0.47
1:J:81:MET:HE1	1:J:145:HIS:CD2	2.49	0.47
1:K:100:LYS:HG2	1:K:136:ILE:HD13	1.96	0.47
1:A:200:PRO:HD2	1:A:220:GLU:O	2.15	0.47
1:E:68:GLN:O	1:E:72:GLN:HG2	2.14	0.47
1:K:145:HIS:ND1	1:K:170:LEU:HD12	2.28	0.47
1:K:42:GLU:OE1	2:K:458:HOH:O	2.20	0.47
1:L:186:LYS:HG2	1:L:216:SER:HA	1.95	0.47
1:H:95:GLU:O	1:H:99:MET:HG3	2.13	0.47
1:C:101:ALA:O	1:C:105:LEU:HD22	2.14	0.47
1:C:182:LEU:O	1:C:183:PRO:C	2.51	0.47
1:C:243:GLY:HA2	1:D:57:GLU:C	2.35	0.47
1:D:160:THR:HA	1:D:163:THR:HG22	1.96	0.47
1:F:208:ASN:O	1:F:212:ILE:HG23	2.14	0.47
1:H:167:GLU:C	1:H:168:ARG:HG2	2.35	0.47
1:J:167:GLU:HG2	2:J:660:HOH:O	2.14	0.47
1:A:201:GLY:O	2:A:312:HOH:O	2.20	0.47
1:A:185:ILE:HD11	1:A:216:SER:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:VAL:CG1	1:D:145:HIS:HB3	2.45	0.47
1:E:105:LEU:HD13	1:E:109:TYR:CE2	2.48	0.47
1:E:127:LYS:H	1:E:127:LYS:HD2	1.80	0.47
1:J:27:LEU:O	1:J:220:GLU:HA	2.15	0.47
1:L:251:TYR:N	2:L:277:HOH:O	2.47	0.47
1:B:100:LYS:HG2	1:B:136:ILE:HD12	1.97	0.47
1:F:99:MET:O	1:F:103:ILE:HG12	2.14	0.47
1:H:85:ARG:CG	1:H:85:ARG:NH1	2.74	0.47
1:K:94:ARG:O	1:K:97:GLU:HB2	2.14	0.47
1:C:243:GLY:HA2	1:D:58:GLY:N	2.30	0.47
1:D:193:LYS:HB2	1:D:195:ARG:HH11	1.80	0.47
1:D:168:ARG:HG2	1:D:197:VAL:HB	1.96	0.47
1:F:161:LEU:HD13	1:F:169:VAL:HG21	1.97	0.47
1:G:130:CYS:O	1:G:134:MET:HB2	2.14	0.47
1:B:259:THR:O	1:B:263:THR:HG22	2.15	0.47
1:D:151:VAL:HG12	1:D:153:ASP:H	1.80	0.47
1:I:85:ARG:NH1	1:I:95:GLU:OE1	2.48	0.47
1:A:150:MET:SD	1:B:240:VAL:HB	2.55	0.46
1:A:207:ARG:HH22	1:D:239:SER:CB	2.27	0.46
1:A:81:MET:CE	1:A:145:HIS:CD2	2.98	0.46
1:E:68:GLN:HE22	1:F:105:LEU:HD21	1.80	0.46
1:H:49:ILE:HG12	1:H:76:ILE:CD1	2.45	0.46
1:J:81:MET:CE	1:J:145:HIS:HD2	2.28	0.46
1:D:125:ILE:HD13	1:D:161:LEU:HD23	1.97	0.46
1:H:162:LEU:CD2	1:H:195:ARG:HB3	2.45	0.46
1:A:226:ARG:NH1	1:A:256:THR:HG22	2.26	0.46
1:D:48:ARG:HD2	1:D:79:PHE:CD2	2.51	0.46
1:F:49:ILE:HD11	1:F:78:VAL:HG22	1.97	0.46
1:I:205:THR:HG21	1:I:207:ARG:NH1	2.31	0.46
1:F:257:ASP:HB3	1:F:260:LYS:HB2	1.97	0.46
1:A:155:MET:SD	1:A:191:GLN:NE2	2.89	0.46
1:C:205:THR:H	1:C:208:ASN:HB2	1.80	0.46
1:D:115:VAL:HG12	1:D:145:HIS:HB3	1.97	0.46
1:H:51:LEU:O	1:H:81:MET:HB2	2.16	0.46
1:K:27:LEU:HA	1:K:47:ASP:OD2	2.16	0.46
1:E:158:LEU:HD13	1:E:188:LEU:HD13	1.97	0.46
1:E:60:THR:O	1:E:61:THR:O	2.34	0.46
1:K:253:LEU:HD23	1:K:253:LEU:H	1.80	0.46
1:A:31:CYS:HA	1:A:50:GLU:O	2.15	0.46
1:C:259:THR:HG22	2:C:420:HOH:O	2.15	0.46
1:D:96:ILE:HG21	1:D:129:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:103:ILE:HG23	1:G:114:LEU:HD13	1.97	0.46
1:H:168:ARG:HH11	1:H:168:ARG:HG3	1.80	0.46
1:A:37:SER:HB3	1:A:256:THR:CG2	2.39	0.46
1:B:125:ILE:HD12	1:B:160:THR:HG22	1.97	0.46
1:D:204:ILE:HG12	1:D:212:ILE:HD13	1.98	0.46
1:E:94:ARG:CB	1:E:94:ARG:HH11	2.20	0.46
1:F:182:LEU:HB3	1:F:183:PRO:HD3	1.98	0.46
1:D:159:GLU:O	1:D:163:THR:HG22	2.16	0.46
1:G:65:GLY:O	1:G:69:VAL:HG23	2.16	0.46
1:L:200:PRO:HD2	1:L:220:GLU:O	2.15	0.46
1:A:49:ILE:HG23	1:A:76:ILE:HD11	1.98	0.45
1:A:92:SER:O	1:A:96:ILE:HG23	2.16	0.45
1:D:104:ARG:NE	2:D:343:HOH:O	2.40	0.45
1:F:185:ILE:HD11	1:F:216:SER:CB	2.47	0.45
1:E:253:LEU:HD21	1:F:88:ASP:HB3	1.98	0.45
1:H:167:GLU:H	1:H:167:GLU:HG2	1.53	0.45
1:I:138:ARG:HB3	1:I:139:PRO:CD	2.28	0.45
1:J:193:LYS:HA	2:J:858:HOH:O	2.15	0.45
1:B:120:THR:HB	1:B:124:HIS:O	2.17	0.45
1:C:120:THR:HG22	1:C:121:GLU:H	1.81	0.45
1:D:48:ARG:CZ	1:D:168:ARG:HH11	2.29	0.45
1:D:269:LYS:HA	2:D:407:HOH:O	2.16	0.45
1:D:35:VAL:HG21	1:D:69:VAL:CG1	2.47	0.45
1:F:32:VAL:HG21	1:F:38:ALA:N	2.31	0.45
1:G:98:VAL:HG11	1:H:66:VAL:HG22	1.97	0.45
1:K:182:LEU:HD11	1:K:212:ILE:HA	1.98	0.45
1:L:145:HIS:CG	1:L:146:ARG:N	2.84	0.45
1:F:156:ALA:O	1:F:160:THR:HG22	2.17	0.45
1:F:35:VAL:O	1:F:39:VAL:HG23	2.15	0.45
1:A:64:MET:HG2	1:A:109:TYR:CD1	2.51	0.45
1:D:259:THR:O	1:D:263:THR:HG23	2.17	0.45
1:D:55:LEU:HD13	1:D:226:ARG:CZ	2.47	0.45
1:H:111:ALA:O	1:H:140:LEU:HD13	2.17	0.45
1:H:112:ASP:O	1:H:141:PRO:HD2	2.17	0.45
1:L:225:ALA:HB1	1:L:260:LYS:HB3	1.98	0.45
1:I:159:GLU:OE2	1:I:191:GLN:NE2	2.50	0.45
1:J:28:MET:HE3	1:J:223:CYS:SG	2.57	0.45
1:K:170:LEU:HD21	1:K:222:HIS:HB3	1.99	0.45
1:B:134:MET:CE	1:B:142:VAL:HG21	2.47	0.45
1:E:94:ARG:NE	2:E:739:HOH:O	2.34	0.45
1:J:197:VAL:HG11	1:J:220:GLU:OE1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:66:VAL:O	1:J:70:VAL:HG23	2.17	0.45
1:C:146:ARG:C	1:C:148:PHE:N	2.70	0.45
1:I:149:ASP:OD1	1:I:171:THR:CG2	2.64	0.45
1:I:205:THR:HG22	1:I:206:ASP:OD1	2.17	0.45
1:A:107:LYS:NZ	1:A:138:ARG:O	2.50	0.45
1:A:181:GLY:O	1:A:185:ILE:HG23	2.17	0.44
1:B:257:ASP:HB3	1:B:260:LYS:HB2	1.99	0.44
1:C:55:LEU:HD23	2:C:315:HOH:O	2.17	0.44
1:D:237:ASN:ND2	1:D:239:SER:H	2.15	0.44
1:G:82:ILE:HG13	1:G:103:ILE:HD13	1.99	0.44
1:H:28:MET:CE	1:H:261:VAL:HG13	2.47	0.44
1:A:114:LEU:C	1:A:115:VAL:CG2	2.85	0.44
1:D:146:ARG:HG2	1:D:170:LEU:HD13	2.00	0.44
1:D:168:ARG:NH1	1:D:220:GLU:OE1	2.50	0.44
1:F:128:GLU:HA	1:F:131:MET:HE2	1.98	0.44
1:H:105:LEU:O	1:H:109:TYR:CD1	2.71	0.44
1:D:71:LYS:NZ	1:D:112:ASP:OD2	2.51	0.44
1:F:85:ARG:NH1	1:F:95:GLU:OE1	2.51	0.44
1:K:226:ARG:HH21	1:K:254:LYS:HB2	1.81	0.44
1:D:49:ILE:HD11	1:D:78:VAL:HG22	1.99	0.44
1:F:143:THR:HB	1:F:168:ARG:HB2	2.00	0.44
1:F:51:LEU:HB3	1:F:62:PRO:HG3	2.00	0.44
1:H:134:MET:SD	1:H:138:ARG:NH2	2.90	0.44
1:K:204:ILE:HD11	1:K:222:HIS:O	2.18	0.44
1:C:242:MET:SD	1:D:89:PHE:HZ	2.41	0.44
1:E:185:ILE:CD1	1:E:200:PRO:HB3	2.47	0.44
1:K:173:GLY:HA3	1:K:181:GLY:HA3	2.00	0.44
1:C:237:ASN:HB3	1:D:150:MET:CE	2.48	0.44
1:D:171:THR:O	1:D:200:PRO:HA	2.18	0.44
1:I:100:LYS:O	1:I:104:ARG:HG3	2.17	0.44
1:K:84:PRO:HD2	1:K:91:TYR:CE2	2.53	0.44
1:L:237:ASN:O	1:L:239:SER:N	2.49	0.44
1:D:170:LEU:HD21	1:D:222:HIS:CB	2.47	0.44
1:E:44:GLY:HA3	1:E:261:VAL:HG23	1.99	0.44
1:L:103:ILE:HG23	1:L:114:LEU:HD13	1.99	0.44
1:A:207:ARG:HB2	1:A:207:ARG:HE	1.67	0.44
1:C:159:GLU:O	1:C:162:LEU:HD12	2.17	0.43
1:C:200:PRO:HD2	1:C:220:GLU:O	2.18	0.43
1:F:143:THR:HB	1:F:168:ARG:HB3	2.00	0.43
1:K:49:ILE:HG13	1:K:76:ILE:HD11	1.98	0.43
1:C:55:LEU:CD2	1:C:55:LEU:N	2.68	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:200:PRO:HD2	1:E:220:GLU:O	2.17	0.43
1:G:55:LEU:CD2	1:G:56:SER:H	2.29	0.43
1:K:240:VAL:HG11	1:L:150:MET:HG3	1.99	0.43
1:E:116:PHE:CE2	1:E:142:VAL:HG11	2.54	0.43
1:F:103:ILE:O	1:F:107:LYS:HG2	2.19	0.43
1:F:138:ARG:HG2	1:F:139:PRO:HA	1.99	0.43
1:L:69:VAL:O	1:L:73:SER:OG	2.37	0.43
1:C:125:ILE:HD12	1:C:130:CYS:SG	2.59	0.43
1:I:168:ARG:HG2	1:I:197:VAL:HB	2.00	0.43
1:K:180:GLU:HG2	2:K:469:HOH:O	2.18	0.43
1:A:116:PHE:CE2	1:A:142:VAL:HG11	2.53	0.43
1:D:265:ASN:OD1	1:D:269:LYS:HE3	2.19	0.43
1:F:29:GLU:HG2	1:F:222:HIS:HD1	1.84	0.43
1:G:105:LEU:HD21	1:H:68:GLN:NE2	2.33	0.43
1:J:146:ARG:NH1	1:J:172:SER:HB3	2.32	0.43
1:J:260:LYS:O	1:J:264:LEU:HD23	2.18	0.43
1:L:268:ALA:O	1:L:269:LYS:HB2	2.18	0.43
1:A:114:LEU:C	1:A:115:VAL:HG23	2.39	0.43
1:A:228:THR:HG22	2:A:320:HOH:O	2.18	0.43
1:C:130:CYS:O	1:C:134:MET:HG3	2.18	0.43
1:I:200:PRO:HD2	1:I:220:GLU:O	2.18	0.43
1:I:28:MET:HE1	1:I:261:VAL:HG13	1.97	0.43
1:L:63:SER:OG	1:L:66:VAL:HG23	2.18	0.43
1:A:116:PHE:CG	1:A:117:GLY:N	2.85	0.43
1:D:182:LEU:O	1:D:182:LEU:HD23	2.19	0.43
1:H:93:ASP:HA	1:H:96:ILE:HD12	2.00	0.43
1:J:85:ARG:HH11	1:J:95:GLU:CD	2.21	0.43
1:L:208:ASN:HB2	2:L:473:HOH:O	2.19	0.43
1:B:122:ASP:OD2	1:B:124:HIS:ND1	2.52	0.43
1:D:205:THR:HG22	1:D:208:ASN:ND2	2.34	0.43
1:F:60:THR:CG2	1:F:61:THR:N	2.82	0.43
1:G:153:ASP:OD1	1:G:155:MET:HB2	2.18	0.43
1:G:172:SER:HB3	1:G:202:GLY:H	1.83	0.43
1:A:114:LEU:O	1:A:115:VAL:CG2	2.66	0.43
1:D:118:ALA:O	1:D:119:LEU:HD23	2.19	0.43
1:G:138:ARG:HE	1:G:142:VAL:HG23	1.83	0.43
1:I:115:VAL:HG22	1:I:143:THR:HB	2.00	0.43
1:J:117:GLY:HA2	1:J:144:PHE:CE1	2.54	0.43
1:A:235:PHE:CE1	1:B:152:HIS:ND1	2.86	0.43
1:A:81:MET:HE1	1:A:145:HIS:CD2	2.53	0.43
1:E:146:ARG:HH11	1:E:146:ARG:HB3	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:95:GLU:O	1:F:99:MET:HG3	2.19	0.43
1:H:59:GLY:O	1:H:83:ARG:HD2	2.19	0.43
1:J:205:THR:HG22	1:J:206:ASP:OD1	2.19	0.43
1:D:151:VAL:HG12	1:D:153:ASP:N	2.33	0.42
1:D:91:TYR:CG	1:D:99:MET:HE1	2.54	0.42
1:G:90:LEU:HD21	1:G:121:GLU:N	2.34	0.42
1:I:85:ARG:NH2	1:I:88:ASP:OD2	2.52	0.42
1:J:81:MET:HE2	1:J:82:ILE:N	2.34	0.42
1:K:70:VAL:O	1:K:74:VAL:HB	2.19	0.42
1:D:85:ARG:NH2	1:D:88:ASP:OD2	2.50	0.42
1:K:121:GLU:HG3	1:K:121:GLU:H	1.57	0.42
1:A:249:SER:OG	1:A:250:GLU:N	2.50	0.42
1:E:158:LEU:HD11	1:E:196:ILE:HD11	2.01	0.42
1:G:170:LEU:HD23	1:G:170:LEU:HA	1.91	0.42
1:G:89:PHE:HB2	1:G:119:LEU:HD23	2.01	0.42
1:I:63:SER:OG	1:I:66:VAL:HG23	2.19	0.42
1:K:48:ARG:HA	1:K:76:ILE:HD12	2.01	0.42
1:A:258:VAL:HG12	1:A:262:ARG:HH21	1.84	0.42
1:B:170:LEU:HD21	1:B:222:HIS:HB3	2.00	0.42
1:F:209:LEU:HD21	1:F:221:PHE:CE2	2.54	0.42
1:H:120:THR:HG22	1:H:121:GLU:H	1.83	0.42
1:J:235:PHE:C	1:J:236:ARG:HG2	2.40	0.42
1:B:210:GLN:HE21	1:B:210:GLN:HB2	1.57	0.42
1:F:182:LEU:HD11	1:F:212:ILE:HA	2.02	0.42
1:H:107:LYS:HD3	1:H:114:LEU:HD11	2.00	0.42
1:H:146:ARG:H	1:H:146:ARG:HG2	1.68	0.42
1:H:252:SER:N	2:H:289:HOH:O	2.52	0.42
1:K:186:LYS:HG2	1:K:215:GLY:O	2.18	0.42
1:E:116:PHE:O	1:E:144:PHE:HA	2.19	0.42
1:G:182:LEU:HD12	1:G:212:ILE:HA	2.01	0.42
1:B:71:LYS:HD2	1:B:71:LYS:HA	1.83	0.42
1:C:94:ARG:NH1	1:D:36:GLU:HG3	2.34	0.42
1:D:61:THR:CG2	2:D:275:HOH:O	2.45	0.42
1:G:55:LEU:HB3	1:G:226:ARG:NH2	2.34	0.42
1:K:37:SER:HG	1:L:85:ARG:HH22	1.68	0.42
1:B:182:LEU:HD21	1:B:215:GLY:O	2.18	0.42
1:E:37:SER:HB3	1:E:256:THR:HG23	2.01	0.42
1:I:26:PHE:CE2	1:I:213:LEU:HD13	2.55	0.42
1:L:103:ILE:HG23	1:L:114:LEU:CD1	2.50	0.42
1:H:48:ARG:HD2	1:H:79:PHE:CE1	2.55	0.42
1:I:79:PHE:HE2	2:I:284:HOH:O	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:112:ASP:O	1:J:141:PRO:HD2	2.19	0.42
1:D:48:ARG:HD2	1:D:79:PHE:CE2	2.55	0.42
1:L:226:ARG:HA	1:L:256:THR:HA	2.00	0.42
1:A:160:THR:O	1:A:164:LEU:HG	2.20	0.41
1:C:150:MET:SD	1:D:240:VAL:HG21	2.59	0.41
1:H:137:CYS:O	1:H:140:LEU:HG	2.20	0.41
1:H:29:GLU:OE2	1:H:222:HIS:CD2	2.73	0.41
1:A:60:THR:CG2	1:A:61:THR:N	2.83	0.41
1:C:127:LYS:CD	2:C:475:HOH:O	2.67	0.41
1:F:199:MET:HG3	1:F:221:PHE:HA	2.00	0.41
1:J:76:ILE:HB	1:J:77:PRO:HD2	2.02	0.41
1:D:236:ARG:HG2	1:D:251:TYR:CE2	2.55	0.41
1:E:39:VAL:HG11	1:F:94:ARG:HH11	1.86	0.41
1:G:160:THR:O	1:G:163:THR:HG22	2.20	0.41
1:G:94:ARG:HD2	1:H:36:GLU:HG3	2.02	0.41
1:K:210:GLN:HG3	1:K:271:ILE:HD11	2.03	0.41
1:D:81:MET:HE1	1:D:145:HIS:HD2	1.84	0.41
1:E:39:VAL:HG11	1:F:94:ARG:NH1	2.34	0.41
1:E:41:ALA:HB3	1:E:49:ILE:HD11	2.02	0.41
1:F:81:MET:CE	1:F:145:HIS:ND1	2.84	0.41
1:F:153:ASP:HA	1:F:154:PRO:HD2	1.80	0.41
1:H:223:CYS:SG	1:H:224:SER:N	2.93	0.41
1:G:94:ARG:HD3	1:H:35:VAL:HG12	2.03	0.41
1:H:65:GLY:O	1:H:69:VAL:HG23	2.20	0.41
1:I:140:LEU:HA	1:I:141:PRO:HD2	1.73	0.41
1:K:71:LYS:CG	1:K:110:GLY:O	2.69	0.41
1:B:201:GLY:O	1:B:202:GLY:C	2.58	0.41
1:I:137:CYS:O	1:I:138:ARG:O	2.38	0.41
1:K:67:LEU:O	1:K:71:LYS:HB2	2.21	0.41
1:A:33:ASP:OD2	1:A:55:LEU:HD12	2.21	0.41
1:B:170:LEU:HD21	1:B:222:HIS:CB	2.51	0.41
1:H:149:ASP:CG	1:H:172:SER:H	2.24	0.41
1:I:205:THR:CG2	1:I:206:ASP:N	2.83	0.41
1:I:29:GLU:HA	1:I:48:ARG:O	2.21	0.41
1:A:182:LEU:HD21	1:A:216:SER:HB3	2.03	0.41
1:A:250:GLU:HB2	2:A:363:HOH:O	2.12	0.41
1:A:253:LEU:HD23	1:A:253:LEU:N	2.35	0.41
1:C:151:VAL:HG11	1:C:157:ALA:HB2	2.02	0.41
1:C:125:ILE:HD11	1:C:164:LEU:CD1	2.51	0.41
1:D:91:TYR:CG	1:D:99:MET:CE	3.04	0.41
1:E:226:ARG:HG3	1:E:256:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:32:VAL:HG13	1:L:37:SER:OG	2.21	0.41
1:A:32:VAL:HG11	1:A:38:ALA:N	2.35	0.41
1:F:261:VAL:HA	1:F:264:LEU:HD22	2.02	0.41
1:H:79:PHE:CZ	1:H:141:PRO:HG2	2.55	0.41
1:L:261:VAL:HA	1:L:264:LEU:HD12	2.03	0.41
1:L:29:GLU:HB2	1:L:48:ARG:O	2.21	0.41
1:D:167:GLU:H	1:D:167:GLU:HG2	1.63	0.41
1:D:193:LYS:HB2	1:D:195:ARG:NH1	2.36	0.41
1:E:40:ASN:ND2	2:E:640:HOH:O	2.40	0.41
1:E:83:ARG:HH12	1:F:242:MET:HG2	1.86	0.41
1:G:257:ASP:CB	1:G:260:LYS:HD3	2.50	0.41
1:J:172:SER:HB3	1:J:201:GLY:O	2.20	0.41
1:D:64:MET:CG	1:D:109:TYR:CD1	3.04	0.41
1:F:50:GLU:HA	1:F:79:PHE:O	2.21	0.41
1:G:32:VAL:HG11	1:G:38:ALA:HB2	2.02	0.41
1:H:119:LEU:HD23	1:H:125:ILE:HA	2.03	0.41
1:H:149:ASP:OD1	1:H:171:THR:HG23	2.21	0.41
1:K:76:ILE:HB	1:K:77:PRO:HD2	2.03	0.41
1:B:104:ARG:HG3	1:B:104:ARG:NH1	2.14	0.41
1:B:67:LEU:O	1:B:71:LYS:HB2	2.20	0.41
1:I:205:THR:CG2	1:I:206:ASP:H	2.33	0.41
1:A:28:MET:HE2	1:A:46:ALA:HA	2.02	0.40
1:D:88:ASP:C	1:D:88:ASP:OD2	2.60	0.40
1:J:205:THR:HG22	1:J:206:ASP:N	2.35	0.40
1:J:228:THR:HA	1:J:253:LEU:O	2.20	0.40
1:K:57:GLU:HG3	1:K:86:GLY:HA3	2.03	0.40
1:L:168:ARG:HG2	1:L:197:VAL:HB	2.04	0.40
1:B:224:SER:HA	2:B:308:HOH:O	2.20	0.40
1:D:60:THR:CG2	1:D:61:THR:N	2.83	0.40
1:E:162:LEU:HB3	1:E:196:ILE:HD13	2.01	0.40
1:F:55:LEU:C	1:F:57:GLU:H	2.25	0.40
1:I:168:ARG:NH1	2:I:284:HOH:O	2.48	0.40
1:A:204:ILE:HG12	1:A:212:ILE:HD13	2.02	0.40
1:F:170:LEU:HD21	1:F:222:HIS:HB3	2.04	0.40
1:H:145:HIS:CD2	1:H:147:ALA:H	2.38	0.40
1:B:259:THR:O	1:B:263:THR:CG2	2.70	0.40
1:B:35:VAL:HG21	1:B:69:VAL:HG12	2.04	0.40
1:F:189:ILE:HG12	1:F:198:VAL:HB	2.03	0.40
1:G:96:ILE:HG21	1:G:129:LEU:HD11	2.03	0.40
1:J:81:MET:CE	1:J:145:HIS:CD2	3.04	0.40
1:K:182:LEU:N	1:K:183:PRO:HD2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:228:THR:HG23	1:L:253:LEU:H	1.87	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	247/287 (86%)	231 (94%)	13 (5%)	3 (1%)	15	27
1	B	240/287 (84%)	228 (95%)	10 (4%)	2 (1%)	22	39
1	C	243/287 (85%)	237 (98%)	5 (2%)	1 (0%)	38	59
1	D	241/287 (84%)	235 (98%)	6 (2%)	0	100	100
1	E	238/287 (83%)	217 (91%)	18 (8%)	3 (1%)	14	25
1	F	237/287 (83%)	214 (90%)	20 (8%)	3 (1%)	14	25
1	G	233/287 (81%)	208 (89%)	21 (9%)	4 (2%)	11	18
1	H	232/287 (81%)	211 (91%)	20 (9%)	1 (0%)	38	59
1	I	237/287 (83%)	225 (95%)	10 (4%)	2 (1%)	22	39
1	J	235/287 (82%)	216 (92%)	18 (8%)	1 (0%)	38	59
1	K	234/287 (82%)	213 (91%)	17 (7%)	4 (2%)	11	18
1	L	235/287 (82%)	210 (89%)	22 (9%)	3 (1%)	14	25
All	All	2852/3444 (83%)	2645 (93%)	180 (6%)	27 (1%)	20	36

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	CYS
1	F	267	ILE
1	I	138	ARG

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Mol	Chain	Res	Type
1	I	139	PRO
1	L	121	GLU
1	A	26	PHE
1	B	53	SER
1	C	243	GLY
1	G	121	GLU
1	H	59	GLY
1	K	176	SER
1	K	203	GLY
1	L	238	SER
1	B	201	GLY
1	E	215	GLY
1	F	56	SER
1	G	202	GLY
1	K	146	ARG
1	K	202	GLY
1	E	54	GLY
1	E	61	THR
1	F	194	GLY
1	G	111	ALA
1	J	195	ARG
1	L	146	ARG
1	A	201	GLY
1	G	201	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	206/233 (88%)	172 (84%)	34 (16%)	2	4
1	B	202/233 (87%)	176 (87%)	26 (13%)	5	9
1	C	204/233 (88%)	179 (88%)	25 (12%)	5	10
1	D	203/233 (87%)	165 (81%)	38 (19%)	2	3
1	E	201/233 (86%)	179 (89%)	22 (11%)	7	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	199/233 (85%)	169 (85%)	30 (15%)	3	6
1	G	197/233 (84%)	182 (92%)	15 (8%)	15	29
1	H	196/233 (84%)	171 (87%)	25 (13%)	5	9
1	I	201/233 (86%)	185 (92%)	16 (8%)	14	27
1	J	199/233 (85%)	175 (88%)	24 (12%)	6	11
1	K	198/233 (85%)	180 (91%)	18 (9%)	11	21
1	L	198/233 (85%)	180 (91%)	18 (9%)	11	21
All	All	2404/2796 (86%)	2113 (88%)	291 (12%)	6	11

All (291) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	31	CYS
1	A	51	LEU
1	A	60	THR
1	A	64	MET
1	A	66	VAL
1	A	67	LEU
1	A	74	VAL
1	A	81	MET
1	A	85	ARG
1	A	90	LEU
1	A	96	ILE
1	A	120	THR
1	A	125	ILE
1	A	143	THR
1	A	145	HIS
1	A	151	VAL
1	A	159	GLU
1	A	160	THR
1	A	162	LEU
1	A	167	GLU
1	A	169	VAL
1	A	170	LEU
1	A	179	LEU
1	A	182	LEU
1	A	185	ILE
1	A	209	LEU
1	A	228	THR

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Mol	Chain	Res	Type
1	A	249	SER
1	A	251	TYR
1	A	256	THR
1	A	259	THR
1	A	263	THR
1	A	272	LEU
1	B	31	CYS
1	B	33	ASP
1	B	43	ARG
1	B	52	CYS
1	B	55	LEU
1	B	57	GLU
1	B	61	THR
1	B	67	LEU
1	B	74	VAL
1	B	83	ARG
1	B	90	LEU
1	B	104	ARG
1	B	120	THR
1	B	125	ILE
1	B	134	MET
1	B	143	THR
1	B	145	HIS
1	B	163	THR
1	B	170	LEU
1	B	176	SER
1	B	204	ILE
1	B	208	ASN
1	B	250	GLU
1	B	258	VAL
1	B	263	THR
1	B	265	ASN
1	C	31	CYS
1	C	32	VAL
1	C	55	LEU
1	C	61	THR
1	C	66	VAL
1	C	67	LEU
1	C	74	VAL
1	C	83	ARG
1	C	90	LEU
1	C	105	LEU

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Mol	Chain	Res	Type
1	C	108	LEU
1	C	125	ILE
1	C	127	LYS
1	C	129	LEU
1	C	143	THR
1	C	145	HIS
1	C	162	LEU
1	C	170	LEU
1	C	186	LYS
1	C	209	LEU
1	C	248	CYS
1	C	253	LEU
1	C	259	THR
1	C	263	THR
1	C	271	ILE
1	D	27	LEU
1	D	31	CYS
1	D	32	VAL
1	D	43	ARG
1	D	51	LEU
1	D	52	CYS
1	D	60	THR
1	D	61	THR
1	D	64	MET
1	D	66	VAL
1	D	67	LEU
1	D	81	MET
1	D	85	ARG
1	D	90	LEU
1	D	96	ILE
1	D	105	LEU
1	D	108	LEU
1	D	122	ASP
1	D	125	ILE
1	D	128	GLU
1	D	129	LEU
1	D	145	HIS
1	D	160	THR
1	D	162	LEU
1	D	163	THR
1	D	167	GLU
1	D	170	LEU

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Mol	Chain	Res	Type
1	D	175	ASP
1	D	179	LEU
1	D	185	ILE
1	D	190	GLU
1	D	193	LYS
1	D	209	LEU
1	D	228	THR
1	D	237	ASN
1	D	240	VAL
1	D	248	CYS
1	D	263	THR
1	E	31	CYS
1	E	39	VAL
1	E	49	ILE
1	E	61	THR
1	E	71	LYS
1	E	90	LEU
1	E	104	ARG
1	E	105	LEU
1	E	119	LEU
1	E	125	ILE
1	E	127	LYS
1	E	134	MET
1	E	143	THR
1	E	145	HIS
1	E	146	ARG
1	E	151	VAL
1	E	170	LEU
1	E	175	ASP
1	E	186	LYS
1	E	188	LEU
1	E	209	LEU
1	E	259	THR
1	F	32	VAL
1	F	52	CYS
1	F	64	MET
1	F	66	VAL
1	F	67	LEU
1	F	74	VAL
1	F	81	MET
1	F	85	ARG
1	F	90	LEU

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Mol	Chain	Res	Type
1	F	107	LYS
1	F	108	LEU
1	F	138	ARG
1	F	140	LEU
1	F	143	THR
1	F	160	THR
1	F	162	LEU
1	F	170	LEU
1	F	179	LEU
1	F	182	LEU
1	F	184	LEU
1	F	185	ILE
1	F	190	GLU
1	F	207	ARG
1	F	219	THR
1	F	226	ARG
1	F	236	ARG
1	F	242	MET
1	F	252	SER
1	F	264	LEU
1	F	267	ILE
1	G	24	ASN
1	G	31	CYS
1	G	33	ASP
1	G	48	ARG
1	G	52	CYS
1	G	55	LEU
1	G	73	SER
1	G	83	ARG
1	G	125	ILE
1	G	129	LEU
1	G	143	THR
1	G	163	THR
1	G	171	THR
1	G	212	ILE
1	G	219	THR
1	H	31	CYS
1	H	33	ASP
1	H	52	CYS
1	H	64	MET
1	H	67	LEU
1	H	81	MET

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Mol	Chain	Res	Type
1	H	85	ARG
1	H	103	ILE
1	H	107	LYS
1	H	120	THR
1	H	128	GLU
1	H	140	LEU
1	H	145	HIS
1	H	146	ARG
1	H	158	LEU
1	H	163	THR
1	H	167	GLU
1	H	168	ARG
1	H	170	LEU
1	H	184	LEU
1	H	191	GLN
1	H	205	THR
1	H	209	LEU
1	H	233	MET
1	H	239	SER
1	I	30	VAL
1	I	31	CYS
1	I	51	LEU
1	I	67	LEU
1	I	71	LYS
1	I	150	MET
1	I	158	LEU
1	I	170	LEU
1	I	179	LEU
1	I	182	LEU
1	I	184	LEU
1	I	209	LEU
1	I	211	ARG
1	I	233	MET
1	I	238	SER
1	I	253	LEU
1	J	31	CYS
1	J	35	VAL
1	J	52	CYS
1	J	57	GLU
1	J	67	LEU
1	J	73	SER
1	J	74	VAL

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Mol	Chain	Res	Type
1	J	81	MET
1	J	85	ARG
1	J	88	ASP
1	J	96	ILE
1	J	105	LEU
1	J	108	LEU
1	J	122	ASP
1	J	143	THR
1	J	145	HIS
1	J	155	MET
1	J	160	THR
1	J	167	GLU
1	J	170	LEU
1	J	182	LEU
1	J	209	LEU
1	J	227	SER
1	J	254	LYS
1	K	31	CYS
1	K	53	SER
1	K	67	LEU
1	K	74	VAL
1	K	81	MET
1	K	90	LEU
1	K	121	GLU
1	K	129	LEU
1	K	158	LEU
1	K	170	LEU
1	K	179	LEU
1	K	182	LEU
1	K	190	GLU
1	K	193	LYS
1	K	204	ILE
1	K	207	ARG
1	K	236	ARG
1	K	267	ILE
1	L	31	CYS
1	L	33	ASP
1	L	57	GLU
1	L	67	LEU
1	L	73	SER
1	L	81	MET
1	L	126	ASP

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Mol	Chain	Res	Type
1	L	158	LEU
1	L	170	LEU
1	L	175	ASP
1	L	179	LEU
1	L	180	GLU
1	L	184	LEU
1	L	206	ASP
1	L	219	THR
1	L	231	SER
1	L	253	LEU
1	L	265	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	124	HIS
1	A	145	HIS
1	A	191	GLN
1	B	24	ASN
1	B	72	GLN
1	B	208	ASN
1	B	210	GLN
1	B	222	HIS
1	B	265	ASN
1	C	75	GLN
1	C	210	GLN
1	D	72	GLN
1	D	124	HIS
1	D	152	HIS
1	D	237	ASN
1	E	24	ASN
1	E	68	GLN
1	G	68	GLN
1	H	68	GLN
1	H	222	HIS
1	I	145	HIS
1	I	191	GLN
1	I	222	HIS
1	J	68	GLN
1	J	208	ASN
1	K	124	HIS

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Mol	Chain	Res	Type
1	L	191	GLN
1	L	270	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 carbohydrates 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	249/287 (86%)	0.07	11 (4%) 35 37	9, 25, 57, 151	0
1	B	244/287 (85%)	-0.25	2 (0%) 86 86	9, 24, 48, 100	0
1	C	247/287 (86%)	-0.23	3 (1%) 79 80	12, 22, 50, 91	0
1	D	245/287 (85%)	-0.14	2 (0%) 86 86	9, 23, 48, 89	0
1	E	242/287 (84%)	0.56	19 (7%) 13 13	36, 60, 94, 119	0
1	F	241/287 (83%)	0.29	13 (5%) 26 27	26, 55, 89, 113	0
1	G	237/287 (82%)	0.88	29 (12%) 5 4	52, 77, 99, 134	0
1	H	236/287 (82%)	0.82	28 (11%) 5 4	52, 79, 103, 120	0
1	I	241/287 (83%)	0.52	14 (5%) 24 24	37, 57, 91, 136	0
1	J	239/287 (83%)	0.39	20 (8%) 12 11	35, 57, 92, 113	0
1	K	238/287 (82%)	0.92	29 (12%) 5 4	54, 80, 108, 125	0
1	L	239/287 (83%)	1.20	50 (20%) 1 1	61, 87, 121, 143	0
All	All	2898/3444 (84%)	0.41	220 (7%) 15 14	9, 58, 100, 151	0

All (220) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	273	VAL	11.6
1	A	245	SER	9.3
1	L	271	ILE	7.3
1	A	246	LEU	7.2
1	K	145	HIS	6.9
1	K	272	LEU	6.5
1	I	24	ASN	6.2
1	G	271	ILE	6.0
1	G	269	LYS	5.9
1	I	272	LEU	5.6
1	K	27	LEU	5.6

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Mol	Chain	Res	Type	RSRZ
1	L	52	CYS	5.4
1	J	272	LEU	5.2
1	K	86	GLY	5.2
1	L	26	PHE	5.1
1	G	258	VAL	5.0
1	H	90	LEU	5.0
1	L	25	GLY	4.9
1	L	254	LYS	4.8
1	L	266	ALA	4.6
1	A	24	ASN	4.5
1	L	27	LEU	4.5
1	J	196	ILE	4.4
1	I	25	GLY	4.3
1	H	152	HIS	4.3
1	G	24	ASN	4.3
1	H	52	CYS	4.3
1	A	244	ALA	4.2
1	K	83	ARG	4.1
1	H	155	MET	4.1
1	E	152	HIS	4.1
1	L	60	THR	4.1
1	G	52	CYS	4.0
1	I	271	ILE	4.0
1	L	162	LEU	4.0
1	K	26	PHE	3.9
1	K	122	ASP	3.8
1	K	152	HIS	3.8
1	K	271	ILE	3.8
1	F	52	CYS	3.8
1	G	26	PHE	3.7
1	J	235	PHE	3.7
1	E	187	ARG	3.6
1	L	272	LEU	3.6
1	K	234	LYS	3.6
1	I	138	ARG	3.6
1	L	85	ARG	3.6
1	L	269	LYS	3.6
1	K	79	PHE	3.5
1	L	129	LEU	3.5
1	L	234	LYS	3.5
1	K	155	MET	3.4
1	L	268	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	E	248	CYS	3.4
1	L	208	ASN	3.3
1	K	163	THR	3.3
1	H	240	VAL	3.3
1	H	234	LYS	3.3
1	K	123	GLY	3.2
1	L	230	ASP	3.2
1	J	152	HIS	3.2
1	B	24	ASN	3.2
1	H	129	LEU	3.2
1	D	247	SER	3.2
1	A	115	VAL	3.2
1	G	73	SER	3.2
1	E	264	LEU	3.1
1	G	39	VAL	3.1
1	H	74	VAL	3.1
1	H	195	ARG	3.1
1	J	234	LYS	3.1
1	E	24	ASN	3.1
1	G	262	ARG	3.1
1	H	83	ARG	3.1
1	K	53	SER	3.1
1	F	271	ILE	3.0
1	J	88	ASP	3.0
1	J	229	ARG	3.0
1	L	163	THR	2.9
1	G	25	GLY	2.9
1	L	121	GLU	2.9
1	G	70	VAL	2.9
1	H	229	ARG	2.9
1	J	193	LYS	2.9
1	G	136	ILE	2.9
1	H	266	ALA	2.9
1	A	249	SER	2.9
1	L	139	PRO	2.9
1	L	253	LEU	2.9
1	L	270	ASN	2.8
1	L	169	VAL	2.8
1	A	251	TYR	2.8
1	F	193	LYS	2.8
1	J	269	LYS	2.8
1	K	52	CYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	245	SER	2.8
1	F	192	ALA	2.7
1	H	269	LYS	2.7
1	J	262	ARG	2.7
1	E	257	ASP	2.7
1	J	228	THR	2.7
1	L	122	ASP	2.7
1	K	253	LEU	2.7
1	L	238	SER	2.7
1	G	43	ARG	2.7
1	G	207	ARG	2.7
1	L	152	HIS	2.6
1	G	261	VAL	2.6
1	L	75	GLN	2.6
1	G	74	VAL	2.6
1	H	126	ASP	2.6
1	G	121	GLU	2.6
1	H	170	LEU	2.6
1	L	67	LEU	2.6
1	G	265	ASN	2.6
1	L	123	GLY	2.6
1	H	121	GLU	2.6
1	L	229	ARG	2.5
1	K	232	GLY	2.5
1	L	150	MET	2.5
1	L	252	SER	2.5
1	I	108	LEU	2.5
1	A	248	CYS	2.5
1	J	52	CYS	2.5
1	E	188	LEU	2.5
1	G	251	TYR	2.5
1	E	235	PHE	2.5
1	F	124	HIS	2.5
1	L	120	THR	2.5
1	F	152	HIS	2.4
1	H	255	VAL	2.4
1	K	35	VAL	2.4
1	G	267	ILE	2.4
1	E	229	ARG	2.4
1	I	192	ALA	2.4
1	H	27	LEU	2.4
1	H	235	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	H	271	ILE	2.4
1	E	128	GLU	2.4
1	K	66	VAL	2.4
1	F	243	GLY	2.4
1	H	133	LEU	2.4
1	I	94	ARG	2.4
1	G	120	THR	2.4
1	E	258	VAL	2.4
1	H	75	GLN	2.4
1	K	150	MET	2.4
1	G	125	ILE	2.4
1	G	155	MET	2.4
1	I	229	ARG	2.4
1	L	207	ARG	2.4
1	K	49	ILE	2.3
1	J	232	GLY	2.3
1	E	262	ARG	2.3
1	L	258	VAL	2.3
1	L	216	SER	2.3
1	H	232	GLY	2.3
1	E	43	ARG	2.3
1	K	268	ALA	2.3
1	L	187	ARG	2.3
1	L	259	THR	2.3
1	G	90	LEU	2.3
1	B	243	GLY	2.3
1	L	235	PHE	2.3
1	J	259	THR	2.3
1	E	234	LYS	2.2
1	H	122	ASP	2.2
1	I	230	ASP	2.2
1	E	200	PRO	2.2
1	G	233	MET	2.2
1	K	137	CYS	2.2
1	L	92	SER	2.2
1	G	266	ALA	2.2
1	G	235	PHE	2.2
1	K	235	PHE	2.2
1	J	253	LEU	2.2
1	L	119	LEU	2.2
1	A	247	SER	2.2
1	C	248	CYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	116	PHE	2.2
1	K	228	THR	2.2
1	L	125	ILE	2.2
1	E	90	LEU	2.2
1	I	139	PRO	2.2
1	J	43	ARG	2.2
1	L	251	TYR	2.2
1	H	169	VAL	2.2
1	C	272	LEU	2.2
1	A	243	GLY	2.2
1	G	72	GLN	2.1
1	G	75	GLN	2.1
1	J	236	ARG	2.1
1	L	28	MET	2.1
1	L	131	MET	2.1
1	F	267	ILE	2.1
1	F	232	GLY	2.1
1	I	75	GLN	2.1
1	K	78	VAL	2.1
1	L	255	VAL	2.1
1	E	121	GLU	2.1
1	F	156	ALA	2.1
1	F	207	ARG	2.1
1	D	248	CYS	2.1
1	J	239	SER	2.1
1	L	55	LEU	2.1
1	L	81	MET	2.1
1	E	261	VAL	2.1
1	E	122	ASP	2.1
1	J	268	ALA	2.0
1	H	198	VAL	2.0
1	I	239	SER	2.0
1	H	82	ILE	2.0
1	H	185	ILE	2.0
1	K	186	LYS	2.0
1	J	258	VAL	2.0
1	K	240	VAL	2.0
1	A	25	GLY	2.0
1	L	105	LEU	2.0
1	L	164	LEU	2.0
1	F	183	PRO	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 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.