



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 03:54 am BST

PDB ID : 3U5M  
Title : Crystal structure of TRIM33 PHD-Bromo in the free state  
Authors : Wang, Z.; Patel, D.J.  
Deposited on : 2011-10-11  
Resolution : 3.08 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

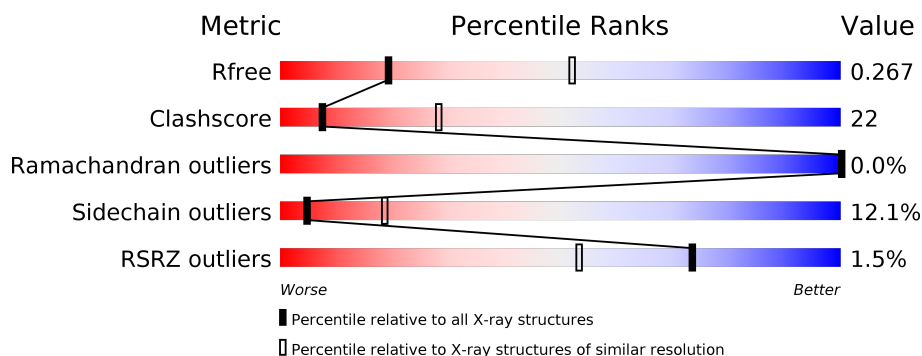
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.08 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))
$R_{free}$	130704	1447 (3.10-3.06)
Clashscore	141614	1546 (3.10-3.06)
Ramachandran outliers	138981	1487 (3.10-3.06)
Sidechain outliers	138945	1486 (3.10-3.06)
RSRZ outliers	127900	1416 (3.10-3.06)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	207	<div> <div>%</div> <div> <div></div> <div>50%</div> <div>30%</div> <div>6%</div> <div>14%</div> </div> </div>
1	B	207	<div> <div>2%</div> <div> <div></div> <div>52%</div> <div>28%</div> <div>6%</div> <div>14%</div> </div> </div>
1	C	207	<div> <div>%</div> <div> <div></div> <div>49%</div> <div>29%</div> <div>6%</div> <div>16%</div> </div> </div>
1	D	207	<div> <div>%</div> <div> <div></div> <div>51%</div> <div>31%</div> <div>•</div> <div>14%</div> </div> </div>
1	E	207	<div> <div></div> <div> <div>48%</div> <div>33%</div> <div>•</div> <div>16%</div> </div> </div>
1	F	207	<div> <div>2%</div> <div> <div></div> <div>57%</div> <div>26%</div> <div>•</div> <div>14%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	207	<div><div><div>%</div><div><div></div><div>46%</div><div>35%</div><div>5%</div><div>13%</div></div></div></div>
1	H	207	<div><div><div>2%</div><div><div></div><div>50%</div><div>30%</div><div>6%</div><div>14%</div></div></div></div>
1	I	207	<div><div><div></div><div><div></div><div>48%</div><div>30%</div><div>5%</div><div>16%</div></div></div></div>
1	J	207	<div><div><div>%</div><div><div></div><div>53%</div><div>27%</div><div></div><div>16%</div></div></div></div>
1	K	207	<div><div><div>%</div><div><div></div><div>48%</div><div>29%</div><div>7%</div><div>15%</div></div></div></div>
1	L	207	<div><div><div>%</div><div><div></div><div>48%</div><div>30%</div><div>6%</div><div>15%</div></div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17117 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 E3 ubiquitin-protein ligase TRIM33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1441	923	238	265	15			
1	B	178	Total	C	N	O	S	0	0	0
			1440	923	238	265	14			
1	C	174	Total	C	N	O	S	0	0	0
			1402	899	233	256	14			
1	D	177	Total	C	N	O	S	0	0	0
			1435	920	237	264	14			
1	E	173	Total	C	N	O	S	0	0	0
			1399	897	233	255	14			
1	F	179	Total	C	N	O	S	0	0	0
			1447	925	239	268	15			
1	G	180	Total	C	N	O	S	0	0	0
			1454	930	240	269	15			
1	H	178	Total	C	N	O	S	0	0	0
			1439	921	238	265	15			
1	I	173	Total	C	N	O	S	0	0	0
			1397	895	233	255	14			
1	J	174	Total	C	N	O	S	0	0	0
			1404	900	234	256	14			
1	K	175	Total	C	N	O	S	0	0	0
			1411	905	235	257	14			
1	L	175	Total	C	N	O	S	0	0	0
			1412	904	235	259	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
B	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
C	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
D	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
E	881	SER	-	EXPRESSION TAG	UNP Q9UPN9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
G	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
H	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
I	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
J	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
K	881	SER	-	EXPRESSION TAG	UNP Q9UPN9
L	881	SER	-	EXPRESSION TAG	UNP Q9UPN9

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	2	Total Zn 2 2	0	0
2	J	2	Total Zn 2 2	0	0
2	D	2	Total Zn 2 2	0	0
2	K	2	Total Zn 2 2	0	0
2	E	2	Total Zn 2 2	0	0
2	H	2	Total Zn 2 2	0	0
2	B	2	Total Zn 2 2	0	0
2	I	2	Total Zn 2 2	0	0
2	C	2	Total Zn 2 2	0	0
2	A	2	Total Zn 2 2	0	0
2	L	2	Total Zn 2 2	0	0
2	F	2	Total Zn 2 2	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	2	Total Ca 2 2	0	0
3	B	2	Total Ca 2 2	0	0

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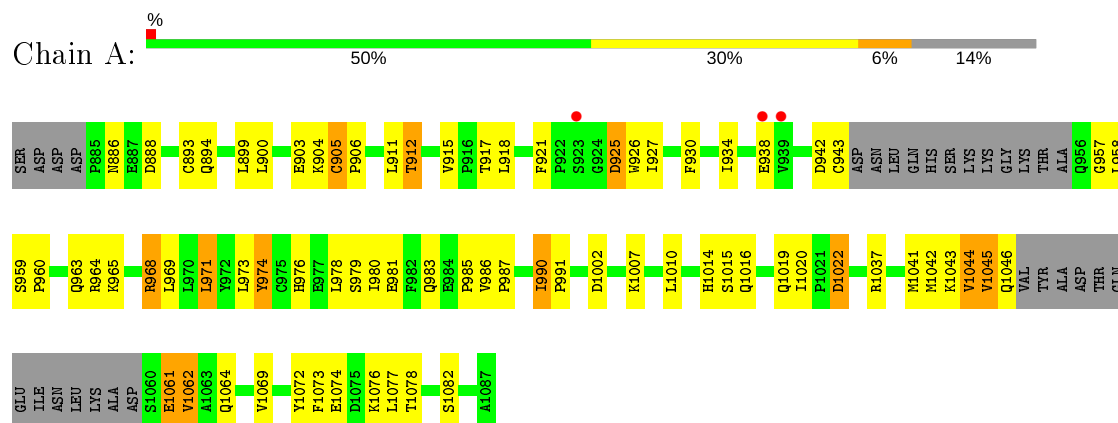
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	I	2	Total 2	Ca 2	0	0
3	C	2	Total 2	Ca 2	0	0
3	A	2	Total 2	Ca 2	0	0
3	F	2	Total 2	Ca 2	0	0

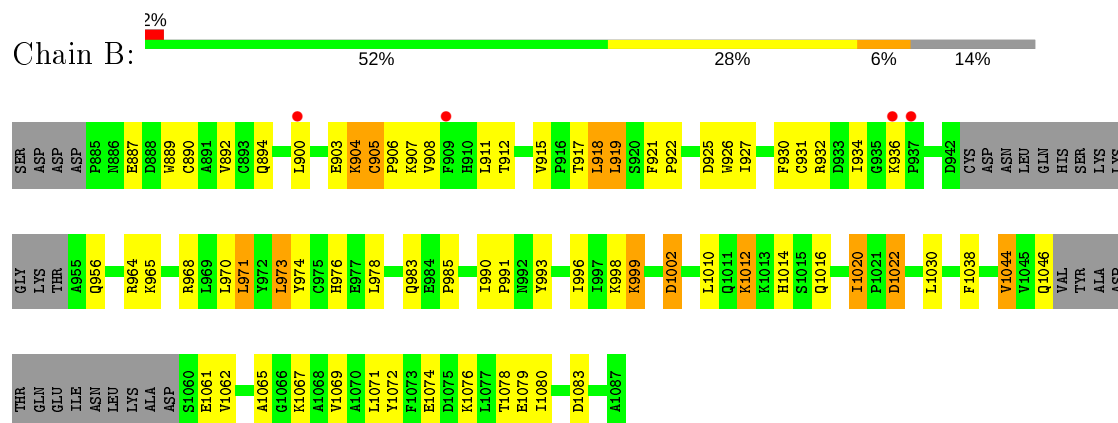
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

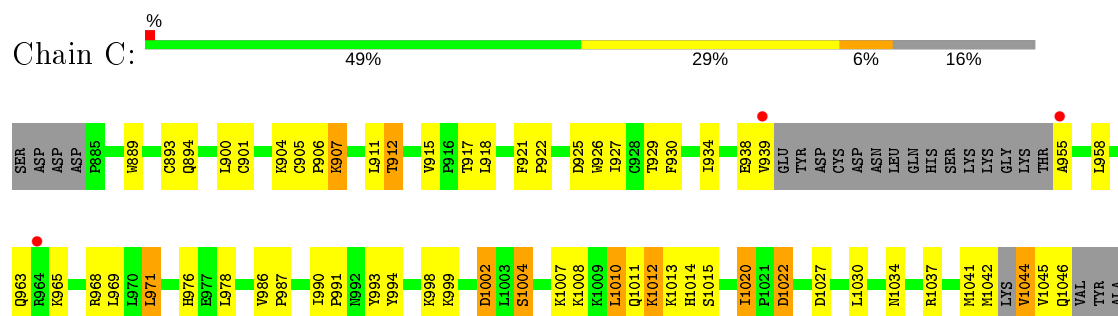
#### • Molecule 1: E3 ubiquitin-protein ligase TRIM33

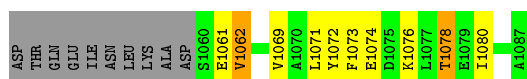


#### • Molecule 1: E3 ubiquitin-protein ligase TRIM33

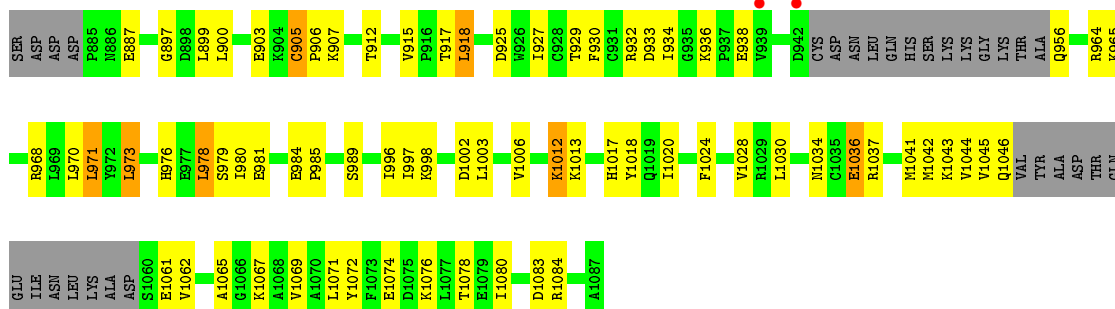


#### • Molecule 1: E3 ubiquitin-protein ligase TRIM33

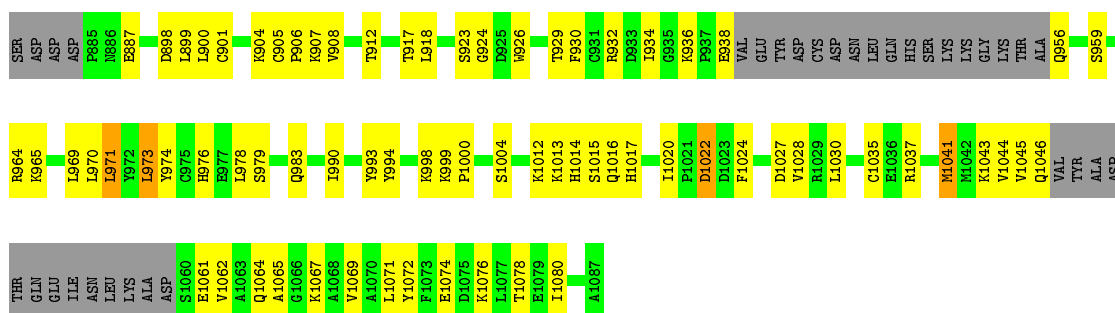




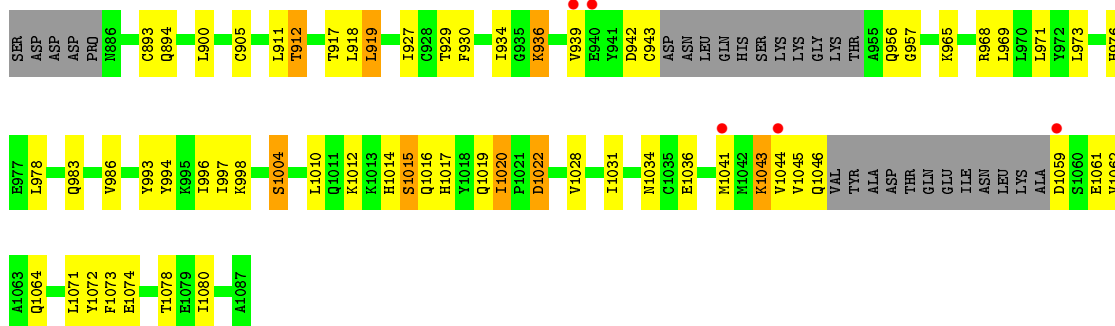
• Molecule 1: E3 ubiquitin-protein ligase TRIM33



• Molecule 1: E3 ubiquitin-protein ligase TRIM33



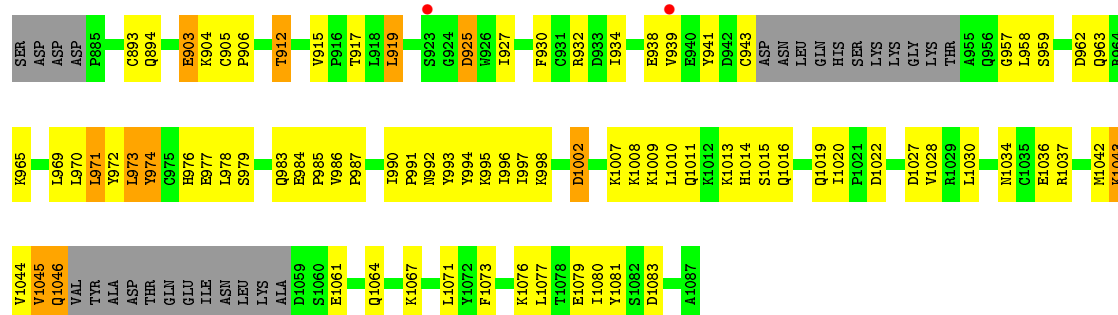
• Molecule 1: E3 ubiquitin-protein ligase TRIM33



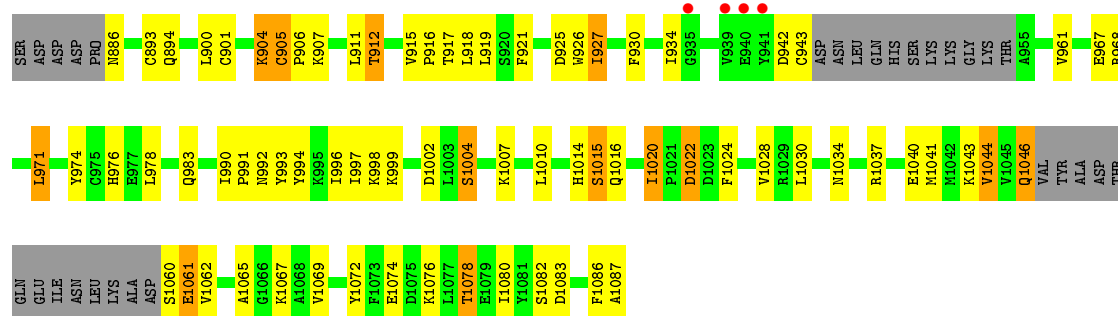
• Molecule 1: E3 ubiquitin-protein ligase TRIM33



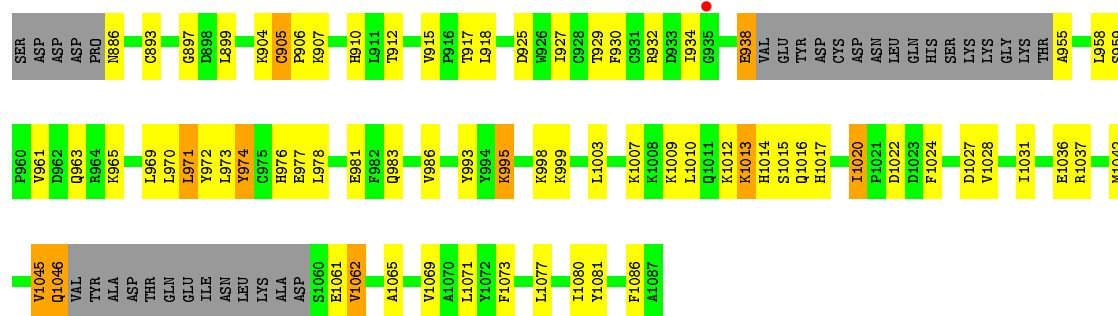




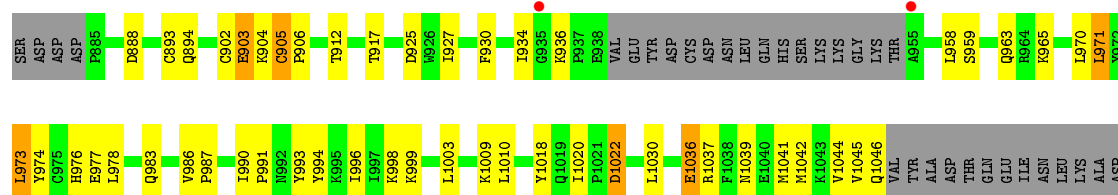
• Molecule 1: E3 ubiquitin-protein ligase TRIM33



• Molecule 1: E3 ubiquitin-protein ligase TRIM33

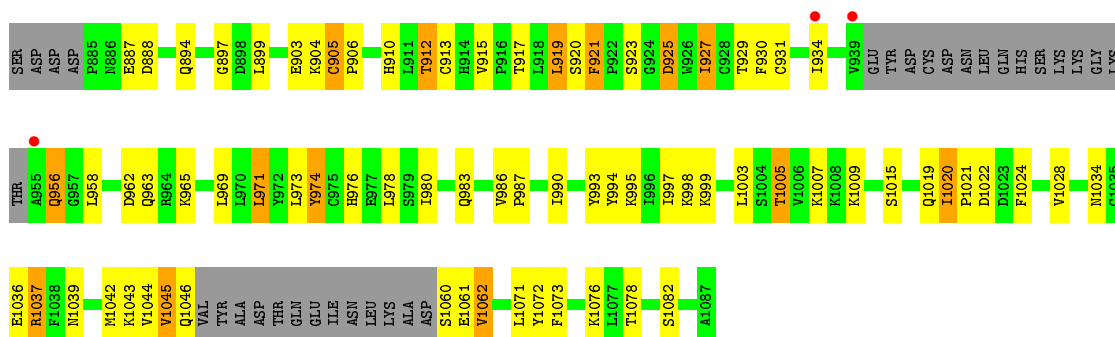


• Molecule 1: E3 ubiquitin-protein ligase TRIM33

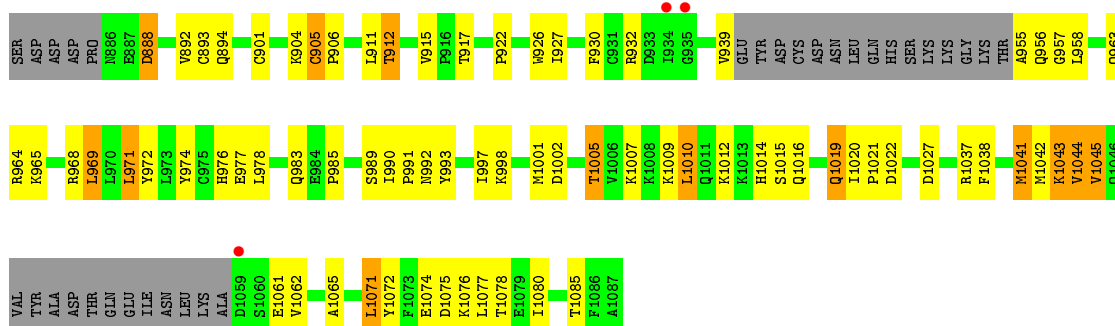




• Molecule 1: E3 ubiquitin-protein ligase TRIM33



• Molecule 1: E3 ubiquitin-protein ligase TRIM33



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.53Å 79.78Å 134.16Å 89.90° 89.96° 59.97°	Depositor
Resolution (Å)	27.36 – 3.08 27.36 – 3.08	Depositor EDS
% Data completeness (in resolution range)	95.9 (27.36-3.08) 90.8 (27.36-3.08)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.49 (at 3.11Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.207 , 0.293 0.192 , 0.267	Depositor DCC
$R_{free}$ test set	1963 reflections (3.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	122.2	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 83.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.397 for k,-h+k,l 0.397 for h-k,h,l 0.387 for -h+k,-h,l 0.387 for -k,h-k,l 0.389 for h,h-k,-l 0.407 for -k,-h,-l 0.417 for -h,-k,l 0.429 for -h+k,k,-l 0.426 for h-k,-k,-l 0.400 for -h,-h+k,-l 0.387 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	17117	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	147.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.46	0/1475	0.62	0/1991
1	B	0.44	0/1474	0.61	0/1990
1	C	0.47	0/1434	0.62	0/1935
1	D	0.46	0/1469	0.61	0/1983
1	E	0.45	0/1432	0.61	0/1932
1	F	0.43	0/1480	0.61	0/1998
1	G	0.47	0/1488	0.62	0/2009
1	H	0.45	0/1472	0.63	0/1987
1	I	0.44	0/1429	0.63	0/1928
1	J	0.46	0/1437	0.61	0/1939
1	K	0.47	0/1444	0.63	0/1949
1	L	0.46	0/1444	0.61	0/1949
All	All	0.46	0/17478	0.62	0/23590

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 [i](#)

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	1441	0	1415	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1440	0	1415	62	0
1	C	1402	0	1381	67	0
1	D	1435	0	1410	58	0
1	E	1399	0	1382	59	0
1	F	1447	0	1415	54	0
1	G	1454	0	1423	76	0
1	H	1439	0	1411	65	0
1	I	1397	0	1379	51	0
1	J	1404	0	1388	60	0
1	K	1411	0	1396	64	0
1	L	1412	0	1392	81	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	I	2	0	0	0	0
All	All	17117	0	16807	751	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 22.

All (751) 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:L:1019:GLN:OE1	1:L:1019:GLN:HA	1.43	1.10
1:A:912:THR:HA	1:A:917:THR:HG23	1.37	1.06
1:G:998:LYS:HA	1:G:998:LYS:HE2	1.39	1.05
1:J:912:THR:HA	1:J:917:THR:HG23	1.41	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:976:HIS:HD2	1:J:1072:TYR:CD2	1.79	1.00
1:G:919:LEU:HD12	1:G:919:LEU:H	1.25	0.99
1:L:1020:ILE:HG23	1:L:1021:PRO:HD2	1.45	0.98
1:K:912:THR:HA	1:K:917:THR:HG23	1.46	0.95
1:K:1042:MET:HA	1:K:1045:VAL:HG23	1.48	0.95
1:C:1042:MET:O	1:C:1044:VAL:N	2.01	0.94
1:I:1014:HIS:HD2	1:I:1016:GLN:H	1.12	0.92
1:A:1014:HIS:HD2	1:A:1016:GLN:H	1.15	0.91
1:B:998:LYS:HE2	1:B:998:LYS:HA	1.50	0.91
1:A:1014:HIS:CD2	1:A:1016:GLN:H	1.88	0.90
1:K:919:LEU:HD12	1:K:919:LEU:H	1.37	0.90
1:F:912:THR:HA	1:F:917:THR:HG23	1.54	0.90
1:K:998:LYS:HE2	1:K:998:LYS:HA	1.53	0.90
1:G:976:HIS:CE1	1:G:978:LEU:HB2	2.07	0.88
1:C:1061:GLU:HG2	1:C:1062:VAL:H	1.40	0.86
1:I:1014:HIS:CD2	1:I:1016:GLN:H	1.93	0.86
1:K:956:GLN:HA	1:K:956:GLN:HE21	1.41	0.85
1:H:912:THR:HA	1:H:917:THR:HG23	1.59	0.84
1:F:919:LEU:HD12	1:F:919:LEU:H	1.40	0.84
1:E:905:CYS:HB2	1:E:906:PRO:HD2	1.58	0.84
1:H:915:VAL:HG22	1:H:1007:LYS:HD3	1.57	0.84
1:I:912:THR:HA	1:I:917:THR:HG23	1.57	0.84
1:G:1045:VAL:O	1:G:1046:GLN:NE2	2.11	0.83
1:L:976:HIS:HE1	1:L:978:LEU:HD23	1.45	0.82
1:H:1020:ILE:CG2	1:H:1022:ASP:HB2	2.10	0.82
1:G:934:ILE:HD13	1:G:965:LYS:HG2	1.60	0.81
1:L:969:LEU:HD22	1:L:1080:ILE:HD13	1.61	0.81
1:D:934:ILE:HG13	1:D:968:ARG:NH2	1.96	0.81
1:G:969:LEU:CD1	1:G:1080:ILE:HD13	2.11	0.81
1:L:1020:ILE:HG23	1:L:1021:PRO:CD	2.11	0.80
1:B:976:HIS:HE1	1:B:978:LEU:HD23	1.47	0.80
1:G:905:CYS:HB2	1:G:906:PRO:HD2	1.62	0.79
1:A:1041:MET:O	1:A:1044:VAL:HG13	1.83	0.79
1:C:1046:GLN:N	1:C:1046:GLN:OE1	2.15	0.79
1:D:976:HIS:HD2	1:D:1072:TYR:CD2	2.00	0.79
1:J:1061:GLU:HG2	1:J:1062:VAL:H	1.48	0.78
1:L:969:LEU:CD2	1:L:1080:ILE:HD13	2.14	0.78
1:C:1012:LYS:H	1:C:1012:LYS:NZ	1.82	0.78
1:D:1037:ARG:HH21	1:J:1037:ARG:HE	1.28	0.78
1:L:976:HIS:HD2	1:L:1072:TYR:CD2	2.02	0.78
1:B:1012:LYS:NZ	1:B:1012:LYS:H	1.81	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1014:HIS:CD2	1:F:1016:GLN:H	2.02	0.77
1:G:1014:HIS:CD2	1:G:1016:GLN:H	2.01	0.77
1:C:905:CYS:HB2	1:C:906:PRO:HD2	1.66	0.77
1:A:1014:HIS:CD2	1:A:1015:SER:N	2.52	0.77
1:L:1014:HIS:CD2	1:L:1016:GLN:H	2.03	0.77
1:H:1037:ARG:HH21	1:K:1037:ARG:HE	1.30	0.77
1:F:1014:HIS:CD2	1:F:1015:SER:N	2.54	0.76
1:F:965:LYS:HD3	1:F:1080:ILE:HG22	1.67	0.76
1:F:976:HIS:HE1	1:F:978:LEU:HD23	1.51	0.76
1:H:1014:HIS:CD2	1:H:1016:GLN:H	2.04	0.76
1:G:974:TYR:CE2	1:G:983:GLN:HG2	2.21	0.75
1:D:1037:ARG:HH21	1:J:1037:ARG:NE	1.84	0.75
1:J:976:HIS:HE1	1:J:978:LEU:HD23	1.51	0.75
1:K:919:LEU:N	1:K:919:LEU:HD12	2.02	0.75
1:D:976:HIS:CD2	1:D:1072:TYR:CD2	2.75	0.75
1:L:930:PHE:CZ	1:L:971:LEU:HB3	2.22	0.75
1:B:1012:LYS:HZ1	1:B:1012:LYS:H	1.34	0.75
1:F:934:ILE:HG12	1:F:968:ARG:HH22	1.50	0.75
1:F:993:TYR:HD2	1:F:994:TYR:CE2	2.05	0.74
1:J:1046:GLN:OE1	1:J:1046:GLN:N	2.21	0.74
1:L:957:GLY:HA2	1:L:1019:GLN:OE1	1.88	0.74
1:G:919:LEU:HD12	1:G:919:LEU:N	2.00	0.74
1:J:998:LYS:HE2	1:J:998:LYS:HA	1.70	0.74
1:B:932:ARG:NH2	1:B:964:ARG:HG2	2.02	0.73
1:F:998:LYS:HA	1:F:998:LYS:HE2	1.70	0.73
1:H:1020:ILE:HG22	1:H:1022:ASP:HB2	1.71	0.73
1:C:1012:LYS:H	1:C:1012:LYS:HZ1	1.34	0.73
1:K:930:PHE:CE1	1:K:971:LEU:HB3	2.24	0.73
1:D:1030:LEU:O	1:D:1034:ASN:HB2	1.89	0.73
1:J:976:HIS:CD2	1:J:1072:TYR:CD2	2.71	0.72
1:B:930:PHE:CZ	1:B:971:LEU:HD22	2.24	0.72
1:F:1014:HIS:HD2	1:F:1016:GLN:H	1.36	0.72
1:J:905:CYS:HB2	1:J:906:PRO:HD2	1.71	0.72
1:D:1067:LYS:O	1:D:1071:LEU:HG	1.90	0.72
1:G:915:VAL:HG22	1:G:1007:LYS:HE3	1.71	0.72
1:A:1042:MET:HA	1:A:1045:VAL:HG23	1.71	0.72
1:I:974:TYR:HE2	1:I:983:GLN:HG2	1.55	0.72
1:A:985:PRO:HA	1:A:1002:ASP:OD2	1.90	0.72
1:A:900:LEU:HD11	1:A:918:LEU:HD22	1.71	0.72
1:F:1014:HIS:HD2	1:F:1015:SER:N	1.86	0.72
1:E:1014:HIS:CD2	1:E:1016:GLN:H	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:930:PHE:CE1	1:F:971:LEU:HB3	2.25	0.72
1:B:934:ILE:HD13	1:B:965:LYS:HG2	1.70	0.71
1:G:1014:HIS:HD2	1:G:1015:SER:N	1.88	0.71
1:G:1014:HIS:HD2	1:G:1016:GLN:H	1.38	0.71
1:I:1014:HIS:HD2	1:I:1016:GLN:N	1.88	0.71
1:G:976:HIS:HE1	1:G:978:LEU:HD23	1.54	0.71
1:K:974:TYR:HE2	1:K:983:GLN:HG2	1.55	0.71
1:L:976:HIS:CE1	1:L:978:LEU:HD23	2.25	0.71
1:D:956:GLN:OE1	1:D:956:GLN:HA	1.91	0.70
1:H:1014:HIS:HD2	1:H:1015:SER:N	1.89	0.70
1:J:976:HIS:HD2	1:J:1072:TYR:HD2	1.34	0.70
1:F:957:GLY:HA2	1:F:1019:GLN:HA	1.74	0.70
1:L:976:HIS:CD2	1:L:1072:TYR:CD2	2.79	0.70
1:H:930:PHE:CE1	1:H:971:LEU:HB3	2.26	0.70
1:G:969:LEU:HD13	1:G:1080:ILE:HD13	1.72	0.70
1:E:1046:GLN:OE1	1:E:1046:GLN:N	2.25	0.70
1:H:1002:ASP:OD2	1:H:1004:SER:HB3	1.92	0.70
1:C:934:ILE:HD13	1:C:965:LYS:HG2	1.74	0.69
1:C:976:HIS:HE1	1:C:978:LEU:HD23	1.57	0.69
1:E:1024:PHE:O	1:E:1028:VAL:HG23	1.92	0.69
1:H:904:LYS:HB2	1:H:927:ILE:HG22	1.74	0.69
1:B:905:CYS:CB	1:B:906:PRO:HD2	2.22	0.69
1:E:912:THR:HA	1:E:917:THR:HG23	1.73	0.69
1:K:976:HIS:HD2	1:K:1072:TYR:CD2	2.10	0.69
1:B:965:LYS:HD3	1:B:1080:ILE:HG22	1.74	0.69
1:I:1012:LYS:HA	1:I:1017:HIS:CD2	2.28	0.69
1:I:905:CYS:HB2	1:I:906:PRO:HD2	1.74	0.69
1:K:956:GLN:CA	1:K:956:GLN:HE21	2.05	0.69
1:G:979:SER:OG	1:G:983:GLN:NE2	2.25	0.69
1:E:905:CYS:SG	1:E:907:LYS:HB2	2.32	0.68
1:H:1037:ARG:HH21	1:K:1037:ARG:NE	1.90	0.68
1:F:996:ILE:HD13	1:F:1041:MET:HG2	1.75	0.68
1:G:927:ILE:HD11	1:G:938:GLU:HB2	1.75	0.68
1:E:1014:HIS:CD2	1:E:1015:SER:N	2.62	0.68
1:G:974:TYR:HE2	1:G:983:GLN:HG2	1.57	0.68
1:E:905:CYS:CB	1:E:906:PRO:HD2	2.24	0.68
1:L:1014:HIS:HD2	1:L:1015:SER:N	1.91	0.68
1:C:998:LYS:HE2	1:C:998:LYS:HA	1.75	0.67
1:H:1020:ILE:HG22	1:H:1022:ASP:H	1.59	0.67
1:K:956:GLN:NE2	1:K:956:GLN:HA	2.09	0.67
1:L:892:VAL:HG12	1:L:893:CYS:N	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:915:VAL:HG22	1:L:1007:LYS:HE3	1.77	0.67
1:G:1014:HIS:CD2	1:G:1015:SER:N	2.62	0.67
1:I:934:ILE:HD13	1:I:965:LYS:HG2	1.75	0.67
1:F:1014:HIS:CD2	1:F:1015:SER:H	2.13	0.67
1:I:974:TYR:CE2	1:I:983:GLN:HG2	2.29	0.67
1:A:930:PHE:CE1	1:A:971:LEU:HB3	2.30	0.66
1:F:1043:LYS:HZ3	1:F:1043:LYS:HB3	1.60	0.66
1:J:905:CYS:CB	1:J:906:PRO:HD2	2.25	0.66
1:D:929:THR:HB	1:D:971:LEU:HD12	1.76	0.66
1:E:1014:HIS:HD2	1:E:1016:GLN:H	1.43	0.66
1:A:1014:HIS:HD2	1:A:1016:GLN:N	1.89	0.66
1:G:912:THR:HA	1:G:917:THR:HG23	1.77	0.66
1:C:912:THR:HA	1:C:917:THR:HG23	1.76	0.66
1:A:1061:GLU:HG2	1:A:1062:VAL:H	1.59	0.66
1:F:1043:LYS:HB3	1:F:1043:LYS:NZ	2.11	0.66
1:B:1074:GLU:O	1:B:1078:THR:HG23	1.96	0.66
1:G:919:LEU:H	1:G:919:LEU:CD1	2.07	0.65
1:G:998:LYS:CA	1:G:998:LYS:HE2	2.22	0.65
1:A:1014:HIS:CD2	1:A:1015:SER:H	2.14	0.65
1:A:979:SER:OG	1:A:983:GLN:NE2	2.28	0.65
1:A:973:LEU:O	1:A:979:SER:HB3	1.97	0.65
1:L:901:CYS:O	1:L:926:TRP:HE3	1.79	0.65
1:A:912:THR:HA	1:A:917:THR:CG2	2.22	0.64
1:B:892:VAL:HG13	1:B:974:TYR:HB3	1.79	0.64
1:A:1072:TYR:CE1	1:A:1076:LYS:HE3	2.32	0.64
1:D:897:GLY:O	1:D:899:LEU:HG	1.97	0.64
1:F:993:TYR:HD2	1:F:994:TYR:CD2	2.16	0.64
1:L:990:ILE:HG23	1:L:991:PRO:HD2	1.79	0.64
1:A:1014:HIS:HD2	1:A:1015:SER:N	1.94	0.64
1:A:976:HIS:CD2	1:A:1072:TYR:CD2	2.85	0.64
1:A:1042:MET:HA	1:A:1045:VAL:CG2	2.28	0.64
1:J:1065:ALA:O	1:J:1069:VAL:HG23	1.97	0.64
1:B:905:CYS:SG	1:B:906:PRO:HD2	2.37	0.64
1:G:976:HIS:CE1	1:G:978:LEU:HD23	2.32	0.64
1:A:976:HIS:HD2	1:A:1072:TYR:CD2	2.16	0.64
1:J:1072:TYR:HE1	1:J:1076:LYS:HG3	1.63	0.64
1:A:976:HIS:HE1	1:A:978:LEU:HD23	1.62	0.63
1:F:993:TYR:CD2	1:F:994:TYR:CE2	2.86	0.63
1:G:976:HIS:HE1	1:G:978:LEU:HB2	1.59	0.63
1:L:893:CYS:O	1:L:894:GLN:HB2	1.98	0.63
1:L:930:PHE:CE1	1:L:971:LEU:HB3	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1072:TYR:CZ	1:C:1076:LYS:HE3	2.33	0.63
1:A:1022:ASP:N	1:A:1022:ASP:OD1	2.32	0.63
1:B:904:LYS:HB2	1:B:927:ILE:HG22	1.79	0.63
1:H:1014:HIS:CD2	1:H:1015:SER:N	2.66	0.63
1:D:1065:ALA:O	1:D:1069:VAL:HG23	1.99	0.63
1:E:976:HIS:HD2	1:E:1072:TYR:CD2	2.17	0.63
1:I:930:PHE:CZ	1:I:971:LEU:HB3	2.33	0.63
1:K:976:HIS:CD2	1:K:1072:TYR:CD2	2.86	0.63
1:K:969:LEU:HD22	1:K:1073:PHE:CE1	2.34	0.62
1:K:974:TYR:CE2	1:K:983:GLN:HG2	2.33	0.62
1:L:1014:HIS:HD2	1:L:1016:GLN:H	1.46	0.62
1:I:1024:PHE:O	1:I:1028:VAL:HG23	2.00	0.62
1:G:1030:LEU:O	1:G:1034:ASN:HB2	1.98	0.62
1:J:1044:VAL:O	1:J:1044:VAL:HG12	1.99	0.62
1:H:993:TYR:HD2	1:H:994:TYR:CD2	2.17	0.62
1:D:912:THR:HA	1:D:917:THR:HG23	1.80	0.62
1:J:1041:MET:HE2	1:J:1041:MET:HA	1.82	0.62
1:K:934:ILE:HD13	1:K:965:LYS:HG2	1.82	0.62
1:D:905:CYS:HB2	1:D:906:PRO:HD2	1.82	0.62
1:K:1042:MET:HA	1:K:1045:VAL:CG2	2.26	0.62
1:K:903:GLU:OE1	1:K:925:ASP:HA	2.00	0.62
1:H:976:HIS:HE1	1:H:978:LEU:HD23	1.66	0.61
1:C:990:ILE:HG23	1:C:991:PRO:HD2	1.83	0.61
1:E:976:HIS:CD2	1:E:1072:TYR:CD2	2.87	0.61
1:I:1046:GLN:OE1	1:I:1046:GLN:N	2.33	0.61
1:L:1076:LYS:O	1:L:1080:ILE:HD12	2.00	0.61
1:D:1061:GLU:HG2	1:D:1062:VAL:H	1.66	0.61
1:L:1020:ILE:HG22	1:L:1022:ASP:N	2.15	0.61
1:E:1041:MET:O	1:E:1045:VAL:HG23	2.01	0.61
1:H:901:CYS:O	1:H:926:TRP:HE3	1.84	0.60
1:F:956:GLN:OE1	1:F:956:GLN:HA	2.00	0.60
1:G:1037:ARG:HE	1:L:1037:ARG:HH21	1.49	0.60
1:D:905:CYS:CB	1:D:906:PRO:HD2	2.31	0.60
1:E:930:PHE:CZ	1:E:971:LEU:HB3	2.35	0.60
1:K:987:PRO:HD2	1:K:990:ILE:HG13	1.84	0.60
1:G:1009:LYS:NZ	1:G:1027:ASP:OD2	2.31	0.60
1:I:976:HIS:HE1	1:I:978:LEU:HD23	1.66	0.60
1:C:915:VAL:HG22	1:C:1007:LYS:HE3	1.82	0.60
1:J:930:PHE:CE1	1:J:971:LEU:HB3	2.36	0.60
1:I:938:GLU:N	1:I:938:GLU:OE1	2.35	0.60
1:B:976:HIS:CE1	1:B:978:LEU:HD23	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1061:GLU:HG2	1:J:1062:VAL:N	2.16	0.60
1:D:984:GLU:HG3	1:D:985:PRO:HD2	1.84	0.60
1:I:1014:HIS:CD2	1:I:1015:SER:N	2.70	0.60
1:K:915:VAL:HG22	1:K:1007:LYS:HE3	1.84	0.59
1:E:905:CYS:SG	1:E:907:LYS:HD3	2.42	0.59
1:C:969:LEU:HD21	1:C:1080:ILE:HD13	1.83	0.59
1:E:1014:HIS:HD2	1:E:1015:SER:N	1.99	0.59
1:E:1076:LYS:O	1:E:1080:ILE:HG13	2.02	0.59
1:J:976:HIS:HE1	1:J:978:LEU:CD2	2.15	0.59
1:L:912:THR:HA	1:L:917:THR:HG23	1.84	0.59
1:B:1014:HIS:HD2	1:B:1016:GLN:H	1.51	0.59
1:L:955:ALA:HB3	1:L:1012:LYS:HE2	1.85	0.59
1:F:969:LEU:HD22	1:F:1073:PHE:CE1	2.38	0.59
1:L:1014:HIS:CD2	1:L:1015:SER:N	2.70	0.58
1:C:969:LEU:CD2	1:C:1080:ILE:HD13	2.33	0.58
1:A:1041:MET:HE2	1:A:1041:MET:HA	1.84	0.58
1:L:1020:ILE:HG22	1:L:1022:ASP:H	1.68	0.58
1:C:1012:LYS:HB2	1:C:1012:LYS:HZ2	1.69	0.58
1:H:1014:HIS:HD2	1:H:1016:GLN:H	1.48	0.58
1:G:905:CYS:CB	1:G:906:PRO:HD2	2.32	0.58
1:L:1020:ILE:CG2	1:L:1021:PRO:N	2.67	0.58
1:C:1061:GLU:HG2	1:C:1062:VAL:N	2.13	0.58
1:E:1022:ASP:OD1	1:E:1022:ASP:N	2.35	0.58
1:C:993:TYR:HD2	1:C:994:TYR:CD1	2.21	0.58
1:E:976:HIS:CE1	1:E:978:LEU:HB2	2.39	0.58
1:E:930:PHE:CE2	1:E:971:LEU:HD13	2.38	0.58
1:L:894:GLN:OE1	1:L:894:GLN:HA	2.03	0.58
1:H:996:ILE:HD11	1:K:1044:VAL:HG11	1.86	0.57
1:B:903:GLU:OE1	1:B:925:ASP:HA	2.04	0.57
1:A:1061:GLU:HG2	1:A:1062:VAL:N	2.20	0.57
1:J:1045:VAL:O	1:J:1045:VAL:HG12	2.03	0.57
1:K:921:PHE:N	1:K:921:PHE:CD2	2.72	0.57
1:H:976:HIS:CE1	1:H:978:LEU:HD23	2.40	0.57
1:G:1042:MET:HA	1:G:1045:VAL:HG13	1.87	0.57
1:H:1074:GLU:O	1:H:1078:THR:HG23	2.03	0.57
1:A:904:LYS:HG3	1:A:927:ILE:CG2	2.35	0.57
1:I:1042:MET:HA	1:I:1045:VAL:HG22	1.87	0.57
1:L:985:PRO:HA	1:L:1002:ASP:CG	2.24	0.57
1:E:1014:HIS:HD2	1:E:1016:GLN:N	2.03	0.57
1:H:1061:GLU:HG2	1:H:1062:VAL:H	1.70	0.57
1:C:976:HIS:CE1	1:C:978:LEU:HD23	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:965:LYS:O	1:L:969:LEU:HD23	2.05	0.56
1:H:1014:HIS:C	1:H:1014:HIS:CD2	2.78	0.56
1:K:969:LEU:HD22	1:K:1073:PHE:HE1	1.70	0.56
1:L:978:LEU:HB3	1:L:1065:ALA:HB1	1.87	0.56
1:B:905:CYS:SG	1:B:907:LYS:HG3	2.45	0.56
1:C:1042:MET:HA	1:C:1045:VAL:HG23	1.87	0.56
1:F:900:LEU:HD11	1:F:918:LEU:HD22	1.86	0.56
1:D:1046:GLN:OE1	1:D:1046:GLN:N	2.37	0.56
1:D:976:HIS:CE1	1:D:978:LEU:HB2	2.41	0.56
1:H:992:ASN:O	1:H:996:ILE:HG12	2.06	0.56
1:I:981:GLU:OE1	1:I:1062:VAL:HG11	2.05	0.56
1:J:930:PHE:CZ	1:J:971:LEU:HB3	2.40	0.56
1:B:965:LYS:O	1:B:968:ARG:HB2	2.06	0.56
1:H:1020:ILE:HG22	1:H:1022:ASP:N	2.20	0.56
1:I:1042:MET:HA	1:I:1045:VAL:CG2	2.36	0.56
1:B:1012:LYS:HB2	1:B:1012:LYS:HZ2	1.71	0.55
1:K:1044:VAL:HG12	1:K:1044:VAL:O	2.05	0.55
1:K:987:PRO:HG2	1:K:990:ILE:HD11	1.88	0.55
1:E:976:HIS:HE1	1:E:978:LEU:HD23	1.70	0.55
1:G:1028:VAL:HG11	1:G:1073:PHE:CE1	2.41	0.55
1:E:1074:GLU:O	1:E:1078:THR:HG23	2.07	0.55
1:H:990:ILE:HG23	1:H:991:PRO:HD2	1.89	0.55
1:H:1065:ALA:O	1:H:1069:VAL:HG23	2.06	0.55
1:F:919:LEU:HD11	1:F:943:CYS:HB2	1.87	0.55
1:G:1045:VAL:O	1:G:1046:GLN:CD	2.45	0.55
1:E:1065:ALA:O	1:E:1069:VAL:HG23	2.07	0.55
1:E:887:GLU:HG2	1:E:906:PRO:O	2.07	0.55
1:D:1037:ARG:NH2	1:J:1037:ARG:HE	2.03	0.55
1:L:932:ARG:HH21	1:L:964:ARG:HG2	1.71	0.55
1:B:973:LEU:N	1:B:973:LEU:HD23	2.22	0.55
1:C:1072:TYR:OH	1:C:1076:LYS:HE3	2.07	0.55
1:D:903:GLU:OE1	1:D:925:ASP:HA	2.07	0.55
1:E:993:TYR:HD2	1:E:994:TYR:CD2	2.25	0.55
1:E:999:LYS:O	1:E:1030:LEU:HD21	2.07	0.55
1:A:985:PRO:HA	1:A:1002:ASP:CG	2.27	0.55
1:J:930:PHE:CE2	1:J:971:LEU:HD13	2.42	0.55
1:E:929:THR:HB	1:E:971:LEU:HD12	1.88	0.55
1:K:1020:ILE:HG23	1:K:1022:ASP:H	1.72	0.55
1:D:1072:TYR:CE1	1:D:1076:LYS:HD3	2.43	0.54
1:I:965:LYS:HD2	1:I:1081:TYR:CE1	2.43	0.54
1:F:976:HIS:CE1	1:F:978:LEU:HD23	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:976:HIS:CE1	1:A:978:LEU:HD23	2.43	0.54
1:D:1061:GLU:HG2	1:D:1062:VAL:N	2.22	0.54
1:G:1042:MET:HA	1:G:1045:VAL:CG1	2.38	0.54
1:A:1069:VAL:O	1:A:1072:TYR:HB3	2.08	0.54
1:C:963:GLN:NE2	1:C:1010:LEU:O	2.34	0.54
1:F:930:PHE:CZ	1:F:971:LEU:HB3	2.42	0.54
1:B:922:PRO:O	1:J:1083:ASP:OD1	2.25	0.54
1:F:1074:GLU:O	1:F:1078:THR:HG23	2.07	0.54
1:E:936:LYS:HG3	1:E:936:LYS:O	2.07	0.54
1:J:976:HIS:CE1	1:J:978:LEU:HD23	2.38	0.53
1:C:1074:GLU:O	1:C:1078:THR:HG23	2.09	0.53
1:E:976:HIS:CE1	1:E:978:LEU:HD23	2.43	0.53
1:J:1042:MET:HA	1:J:1045:VAL:HG23	1.90	0.53
1:K:929:THR:HB	1:K:971:LEU:HD12	1.90	0.53
1:I:976:HIS:CE1	1:I:978:LEU:HB2	2.43	0.53
1:I:1065:ALA:O	1:I:1069:VAL:HG23	2.09	0.53
1:L:985:PRO:HA	1:L:1002:ASP:OD1	2.08	0.53
1:D:1024:PHE:O	1:D:1028:VAL:HG23	2.09	0.53
1:G:972:TYR:CE2	1:G:1076:LYS:HD2	2.44	0.53
1:L:927:ILE:HD12	1:L:932:ARG:HB2	1.91	0.53
1:D:1036:GLU:HG3	1:D:1037:ARG:N	2.24	0.53
1:E:905:CYS:HB2	1:E:906:PRO:CD	2.34	0.53
1:F:919:LEU:HD12	1:F:919:LEU:N	2.17	0.53
1:K:976:HIS:HE1	1:K:978:LEU:HD23	1.73	0.53
1:B:905:CYS:SG	1:B:906:PRO:CD	2.97	0.52
1:G:1014:HIS:CD2	1:G:1015:SER:H	2.26	0.52
1:K:921:PHE:HD2	1:K:921:PHE:H	1.55	0.52
1:I:976:HIS:CE1	1:I:978:LEU:HD23	2.44	0.52
1:F:983:GLN:O	1:F:1004:SER:HB2	2.10	0.52
1:G:903:GLU:OE1	1:G:925:ASP:HA	2.09	0.52
1:I:934:ILE:CG2	1:I:961:VAL:HG13	2.40	0.52
1:G:1073:PHE:CE2	1:G:1077:LEU:HD22	2.45	0.52
1:H:1020:ILE:HG22	1:H:1022:ASP:CB	2.40	0.52
1:G:957:GLY:HA2	1:G:1019:GLN:HA	1.91	0.52
1:L:1001:MET:SD	1:L:1005:THR:HB	2.50	0.52
1:B:911:LEU:HD11	1:B:921:PHE:CE2	2.45	0.52
1:D:1074:GLU:O	1:D:1078:THR:HG23	2.10	0.52
1:K:905:CYS:HB2	1:K:906:PRO:HD2	1.90	0.52
1:E:905:CYS:CB	1:E:906:PRO:CD	2.88	0.52
1:F:912:THR:HA	1:F:917:THR:CG2	2.34	0.52
1:H:893:CYS:O	1:H:894:GLN:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:1005:THR:O	1:K:1009:LYS:HB2	2.10	0.52
1:A:911:LEU:HD11	1:A:921:PHE:CE2	2.45	0.52
1:B:1065:ALA:O	1:B:1069:VAL:HG23	2.10	0.52
1:B:1083:ASP:OD2	1:B:1083:ASP:N	2.42	0.52
1:G:919:LEU:HD11	1:G:943:CYS:HB2	1.92	0.52
1:B:889:TRP:HB3	1:B:894:GLN:O	2.09	0.51
1:C:1011:GLN:OE1	1:C:1013:LYS:HE3	2.09	0.51
1:D:930:PHE:CE1	1:D:971:LEU:HB3	2.44	0.51
1:E:1067:LYS:O	1:E:1071:LEU:HD23	2.10	0.51
1:F:1043:LYS:CB	1:F:1043:LYS:NZ	2.72	0.51
1:C:934:ILE:HD13	1:C:965:LYS:CG	2.40	0.51
1:H:1024:PHE:O	1:H:1028:VAL:HG23	2.10	0.51
1:J:983:GLN:HA	1:J:1003:LEU:HB2	1.92	0.51
1:C:927:ILE:HG12	1:C:939:VAL:CG2	2.40	0.51
1:H:1060:SER:OG	1:H:1061:GLU:N	2.44	0.51
1:I:893:CYS:SG	1:I:910:HIS:CE1	3.03	0.51
1:J:996:ILE:HD13	1:J:1041:MET:CG	2.41	0.51
1:L:1061:GLU:HG2	1:L:1062:VAL:N	2.25	0.51
1:L:976:HIS:CD2	1:L:1072:TYR:HD2	2.28	0.51
1:K:905:CYS:CB	1:K:906:PRO:HD2	2.40	0.51
1:B:1014:HIS:CD2	1:B:1016:GLN:H	2.27	0.51
1:D:976:HIS:HE1	1:D:978:LEU:HD23	1.75	0.51
1:H:974:TYR:CE2	1:H:983:GLN:HG2	2.46	0.51
1:D:933:ASP:HB3	1:D:936:LYS:O	2.11	0.51
1:E:900:LEU:CD1	1:E:918:LEU:HD22	2.41	0.51
1:I:995:LYS:HD2	1:I:995:LYS:N	2.26	0.51
1:K:912:THR:HA	1:K:917:THR:CG2	2.31	0.51
1:K:905:CYS:HB3	1:K:931:CYS:SG	2.51	0.51
1:H:901:CYS:O	1:H:926:TRP:CE3	2.64	0.51
1:C:905:CYS:SG	1:C:907:LYS:HB2	2.50	0.51
1:C:900:LEU:HD11	1:C:918:LEU:HD22	1.93	0.51
1:F:893:CYS:C	1:F:894:GLN:HG2	2.30	0.51
1:C:934:ILE:HD11	1:C:968:ARG:CD	2.41	0.50
1:E:1014:HIS:C	1:E:1014:HIS:CD2	2.85	0.50
1:G:985:PRO:HA	1:G:1002:ASP:CG	2.31	0.50
1:J:934:ILE:HD13	1:J:965:LYS:HG3	1.93	0.50
1:B:985:PRO:HA	1:B:1002:ASP:OD1	2.11	0.50
1:J:996:ILE:HD13	1:J:1041:MET:HG2	1.92	0.50
1:L:1020:ILE:CG2	1:L:1022:ASP:H	2.24	0.50
1:H:1020:ILE:HG21	1:H:1022:ASP:HB2	1.89	0.50
1:H:916:PRO:HD3	1:H:967:GLU:OE1	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1009:LYS:HB3	1:J:1018:TYR:CE2	2.47	0.50
1:C:955:ALA:CB	1:C:1012:LYS:HG2	2.42	0.50
1:H:900:LEU:HD11	1:H:918:LEU:HD22	1.93	0.50
1:L:927:ILE:HD11	1:L:939:VAL:HG22	1.92	0.50
1:B:1067:LYS:O	1:B:1071:LEU:HG	2.12	0.50
1:B:973:LEU:H	1:B:973:LEU:HD23	1.76	0.50
1:D:1043:LYS:CB	1:D:1043:LYS:NZ	2.75	0.50
1:L:985:PRO:HA	1:L:1002:ASP:OD2	2.12	0.50
1:C:934:ILE:HD11	1:C:968:ARG:HD2	1.94	0.50
1:D:915:VAL:HG11	1:D:970:LEU:HD23	1.94	0.50
1:C:905:CYS:CB	1:C:906:PRO:HD2	2.38	0.50
1:J:1072:TYR:CD1	1:J:1072:TYR:C	2.85	0.50
1:C:930:PHE:CE1	1:C:971:LEU:HB3	2.47	0.49
1:I:905:CYS:CB	1:I:906:PRO:HD2	2.41	0.49
1:K:1024:PHE:O	1:K:1028:VAL:HG23	2.12	0.49
1:L:1020:ILE:HG23	1:L:1021:PRO:N	2.26	0.49
1:B:930:PHE:CE2	1:B:971:LEU:HD22	2.47	0.49
1:E:998:LYS:O	1:E:1000:PRO:HD3	2.11	0.49
1:G:965:LYS:HD3	1:G:1080:ILE:CG2	2.43	0.49
1:A:900:LEU:CD1	1:A:918:LEU:HD22	2.42	0.49
1:C:929:THR:HB	1:C:971:LEU:HD12	1.93	0.49
1:H:934:ILE:HD11	1:H:968:ARG:CD	2.42	0.49
1:C:900:LEU:CD1	1:C:918:LEU:HD22	2.42	0.49
1:E:976:HIS:HE1	1:E:978:LEU:HB2	1.75	0.49
1:A:974:TYR:CE2	1:A:983:GLN:HG2	2.47	0.49
1:D:997:ILE:HG21	1:D:1034:ASN:ND2	2.28	0.49
1:G:990:ILE:HG23	1:G:991:PRO:HD2	1.95	0.49
1:A:957:GLY:HA2	1:A:1019:GLN:HA	1.94	0.49
1:A:934:ILE:HG12	1:A:968:ARG:NH2	2.28	0.49
1:A:987:PRO:HD2	1:A:990:ILE:HG13	1.93	0.49
1:C:1041:MET:HA	1:C:1041:MET:HE2	1.93	0.49
1:C:965:LYS:O	1:C:968:ARG:HB2	2.12	0.49
1:E:976:HIS:HB2	1:E:1072:TYR:CE2	2.47	0.49
1:G:985:PRO:HA	1:G:1002:ASP:OD2	2.12	0.49
1:C:1061:GLU:HG2	1:C:1062:VAL:HG22	1.94	0.49
1:A:960:PRO:O	1:A:964:ARG:HG3	2.13	0.49
1:E:934:ILE:HD13	1:E:965:LYS:HG2	1.93	0.49
1:F:1020:ILE:HG22	1:F:1022:ASP:HB2	1.93	0.49
1:F:927:ILE:HG12	1:F:939:VAL:HG21	1.95	0.49
1:I:905:CYS:SG	1:I:907:LYS:HB2	2.53	0.49
1:L:965:LYS:HD3	1:L:1080:ILE:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:974:TYR:CE2	1:L:983:GLN:HG2	2.48	0.49
1:A:969:LEU:HD11	1:A:1077:LEU:HD13	1.94	0.49
1:C:1069:VAL:O	1:C:1072:TYR:HB3	2.13	0.49
1:L:958:LEU:HD13	1:L:963:GLN:HA	1.95	0.49
1:I:986:VAL:HG11	1:I:993:TYR:CG	2.47	0.48
1:J:974:TYR:CE2	1:J:983:GLN:HG2	2.48	0.48
1:L:972:TYR:CE2	1:L:1076:LYS:HD2	2.48	0.48
1:A:900:LEU:HD13	1:A:926:TRP:CZ2	2.49	0.48
1:A:965:LYS:O	1:A:968:ARG:HB3	2.14	0.48
1:B:1044:VAL:HG13	1:B:1044:VAL:O	2.12	0.48
1:D:934:ILE:HG13	1:D:968:ARG:HH21	1.75	0.48
1:D:1083:ASP:OD2	1:E:924:GLY:O	2.30	0.48
1:F:976:HIS:CD2	1:F:1072:TYR:CD2	3.02	0.48
1:K:904:LYS:HB2	1:K:927:ILE:HG22	1.95	0.48
1:L:904:LYS:HB3	1:L:904:LYS:HE3	1.67	0.48
1:D:1006:VAL:HG13	1:D:1018:TYR:OH	2.14	0.48
1:D:887:GLU:HG2	1:D:906:PRO:O	2.14	0.48
1:E:900:LEU:HD11	1:E:918:LEU:HD22	1.95	0.48
1:H:919:LEU:HD12	1:H:942:ASP:HB3	1.96	0.48
1:I:1077:LEU:HD11	1:I:1086:PHE:CE1	2.48	0.48
1:H:905:CYS:SG	1:H:907:LYS:HG3	2.54	0.48
1:H:993:TYR:HD2	1:H:994:TYR:CE2	2.31	0.48
1:J:1073:PHE:CE2	1:J:1077:LEU:HD22	2.48	0.48
1:L:957:GLY:CA	1:L:1019:GLN:OE1	2.59	0.48
1:B:993:TYR:HA	1:B:1038:PHE:CE1	2.48	0.48
1:G:965:LYS:HD2	1:G:1081:TYR:CE1	2.49	0.48
1:G:958:LEU:HD22	1:G:962:ASP:HB3	1.96	0.48
1:K:998:LYS:HE2	1:K:998:LYS:CA	2.34	0.48
1:L:990:ILE:HG23	1:L:991:PRO:CD	2.44	0.48
1:K:1078:THR:O	1:K:1082:SER:HA	2.14	0.47
1:F:900:LEU:CD1	1:F:918:LEU:HD22	2.44	0.47
1:K:1060:SER:HB2	1:K:1062:VAL:HG23	1.96	0.47
1:B:1020:ILE:HG22	1:B:1022:ASP:H	1.79	0.47
1:C:894:GLN:OE1	1:C:894:GLN:HA	2.13	0.47
1:G:1067:LYS:O	1:G:1071:LEU:HD23	2.14	0.47
1:J:1072:TYR:HD1	1:J:1072:TYR:C	2.18	0.47
1:L:1061:GLU:HG2	1:L:1062:VAL:H	1.79	0.47
1:F:1041:MET:HE2	1:F:1041:MET:HA	1.96	0.47
1:J:976:HIS:CD2	1:J:1072:TYR:HD2	2.20	0.47
1:B:934:ILE:CD1	1:B:965:LYS:HG2	2.42	0.47
1:B:973:LEU:N	1:B:973:LEU:CD2	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:934:ILE:HG12	1:F:968:ARG:NH2	2.25	0.47
1:L:956:GLN:HA	1:L:956:GLN:OE1	2.15	0.47
1:B:1061:GLU:CD	1:B:1061:GLU:H	2.18	0.47
1:G:1046:GLN:HE21	1:G:1046:GLN:HA	1.79	0.47
1:H:997:ILE:HG21	1:H:1034:ASN:ND2	2.30	0.47
1:B:998:LYS:HE2	1:B:998:LYS:CA	2.33	0.47
1:H:1067:LYS:HB3	1:H:1067:LYS:HE2	1.69	0.47
1:B:1076:LYS:HD3	1:B:1079:GLU:OE2	2.15	0.47
1:I:1020:ILE:CG2	1:I:1022:ASP:HB2	2.45	0.47
1:K:1039:ASN:O	1:K:1043:LYS:HG3	2.14	0.47
1:G:1067:LYS:HB3	1:G:1067:LYS:HE2	1.70	0.47
1:G:1076:LYS:HD3	1:G:1079:GLU:OE1	2.14	0.47
1:F:1020:ILE:HG22	1:F:1022:ASP:H	1.80	0.47
1:H:934:ILE:HG22	1:H:961:VAL:HG13	1.96	0.47
1:I:915:VAL:HG22	1:I:1007:LYS:HE3	1.97	0.47
1:J:986:VAL:HG13	1:J:987:PRO:HD2	1.97	0.47
1:L:1019:GLN:CA	1:L:1019:GLN:OE1	2.32	0.47
1:B:905:CYS:HB2	1:B:906:PRO:HD2	1.97	0.46
1:D:905:CYS:CB	1:D:906:PRO:CD	2.93	0.46
1:F:936:LYS:HE2	1:F:936:LYS:HB2	1.69	0.46
1:A:930:PHE:CZ	1:A:971:LEU:HB3	2.50	0.46
1:E:1012:LYS:HA	1:E:1017:HIS:CD2	2.50	0.46
1:E:974:TYR:CE2	1:E:983:GLN:HG2	2.49	0.46
1:F:1014:HIS:HD2	1:F:1016:GLN:N	2.08	0.46
1:B:905:CYS:CB	1:B:906:PRO:CD	2.93	0.46
1:C:893:CYS:O	1:C:894:GLN:HB2	2.15	0.46
1:I:886:ASN:HA	1:I:906:PRO:HA	1.97	0.46
1:A:958:LEU:HD13	1:A:963:GLN:HA	1.96	0.46
1:G:974:TYR:CD2	1:G:983:GLN:HG2	2.50	0.46
1:C:1020:ILE:HG22	1:C:1022:ASP:HB2	1.97	0.46
1:G:930:PHE:CZ	1:G:971:LEU:HB3	2.50	0.46
1:H:1076:LYS:O	1:H:1080:ILE:HD12	2.16	0.46
1:H:886:ASN:HA	1:H:906:PRO:HA	1.98	0.46
1:I:1061:GLU:HB3	1:I:1062:VAL:H	1.54	0.46
1:J:990:ILE:HG23	1:J:991:PRO:HD2	1.97	0.46
1:K:910:HIS:HB2	1:K:913:CYS:SG	2.55	0.46
1:D:1042:MET:HA	1:D:1045:VAL:HG23	1.98	0.46
1:G:930:PHE:CE1	1:G:971:LEU:HB3	2.51	0.46
1:K:986:VAL:HG21	1:K:993:TYR:CZ	2.50	0.46
1:L:1044:VAL:HG13	1:L:1044:VAL:O	2.15	0.46
1:F:986:VAL:HB	1:F:993:TYR:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:971:LEU:HD23	1:H:971:LEU:HA	1.63	0.46
1:J:905:CYS:CB	1:J:906:PRO:CD	2.93	0.46
1:L:969:LEU:H	1:L:969:LEU:CD2	2.29	0.46
1:C:1041:MET:CE	1:C:1041:MET:HA	2.45	0.46
1:F:930:PHE:HA	1:F:968:ARG:HD2	1.97	0.46
1:L:965:LYS:O	1:L:968:ARG:HB2	2.16	0.46
1:A:904:LYS:HG3	1:A:927:ILE:HG22	1.96	0.46
1:B:919:LEU:HG	1:B:919:LEU:H	1.47	0.46
1:K:993:TYR:HD2	1:K:994:TYR:CD1	2.33	0.46
1:K:904:LYS:HD3	1:K:904:LYS:C	2.36	0.45
1:G:969:LEU:HA	1:G:969:LEU:HD12	1.63	0.45
1:J:1036:GLU:OE1	1:J:1067:LYS:HE2	2.16	0.45
1:A:903:GLU:OE1	1:A:925:ASP:HA	2.17	0.45
1:A:986:VAL:HG13	1:A:987:PRO:HD2	1.99	0.45
1:G:993:TYR:HD2	1:G:994:TYR:CD2	2.35	0.45
1:H:915:VAL:HG22	1:H:1007:LYS:CD	2.38	0.45
1:H:978:LEU:HB3	1:H:1065:ALA:HB1	1.98	0.45
1:L:969:LEU:HD21	1:L:1080:ILE:HD13	1.95	0.45
1:C:904:LYS:HE3	1:C:904:LYS:HB3	1.78	0.45
1:F:969:LEU:HD22	1:F:1073:PHE:HE1	1.79	0.45
1:L:969:LEU:N	1:L:969:LEU:CD2	2.78	0.45
1:C:958:LEU:HD13	1:C:963:GLN:HA	1.99	0.45
1:G:932:ARG:NH1	1:G:941:TYR:CE2	2.85	0.45
1:K:969:LEU:O	1:K:973:LEU:HD23	2.16	0.45
1:K:998:LYS:CE	1:K:998:LYS:HA	2.37	0.45
1:L:971:LEU:HD23	1:L:971:LEU:HA	1.78	0.45
1:J:893:CYS:O	1:J:894:GLN:HB2	2.17	0.45
1:J:973:LEU:HD23	1:J:973:LEU:HA	1.69	0.45
1:L:1044:VAL:CG1	1:L:1044:VAL:O	2.62	0.45
1:L:969:LEU:HD23	1:L:969:LEU:H	1.81	0.45
1:A:973:LEU:H	1:A:973:LEU:HD22	1.81	0.45
1:A:978:LEU:HA	1:A:978:LEU:HD13	1.80	0.45
1:F:934:ILE:CG1	1:F:968:ARG:HH22	2.25	0.45
1:G:976:HIS:HE1	1:G:978:LEU:CD2	2.27	0.45
1:H:893:CYS:O	1:H:894:GLN:CB	2.65	0.45
1:D:905:CYS:SG	1:D:907:LYS:HB2	2.56	0.45
1:H:900:LEU:CD1	1:H:918:LEU:HD22	2.46	0.45
1:I:1036:GLU:HG3	1:I:1037:ARG:N	2.32	0.45
1:J:999:LYS:HD2	1:J:1030:LEU:HD22	1.98	0.45
1:H:1020:ILE:CG2	1:H:1022:ASP:H	2.30	0.45
1:I:917:THR:HG22	1:I:918:LEU:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:897:GLY:O	1:K:899:LEU:HG	2.17	0.45
1:A:934:ILE:CG1	1:A:968:ARG:NH2	2.79	0.45
1:B:990:ILE:CG2	1:B:991:PRO:HD2	2.48	0.45
1:C:889:TRP:HB3	1:C:894:GLN:O	2.17	0.45
1:F:996:ILE:O	1:F:996:ILE:HG22	2.17	0.45
1:K:1022:ASP:N	1:K:1022:ASP:OD1	2.50	0.45
1:K:934:ILE:CD1	1:K:965:LYS:HG2	2.47	0.45
1:L:969:LEU:HD11	1:L:1077:LEU:HA	1.99	0.45
1:A:904:LYS:HG3	1:A:927:ILE:HG21	1.98	0.44
1:A:905:CYS:CB	1:A:906:PRO:HD2	2.46	0.44
1:C:911:LEU:HD11	1:C:921:PHE:CE2	2.52	0.44
1:G:986:VAL:HG21	1:G:993:TYR:CZ	2.51	0.44
1:K:887:GLU:CG	1:K:888:ASP:H	2.29	0.44
1:L:963:GLN:NE2	1:L:1010:LEU:O	2.38	0.44
1:L:993:TYR:CZ	1:L:997:ILE:HD12	2.52	0.44
1:J:1072:TYR:CE1	1:J:1076:LYS:HG3	2.47	0.44
1:K:958:LEU:HD13	1:K:963:GLN:HA	1.98	0.44
1:C:999:LYS:O	1:C:1030:LEU:HD21	2.18	0.44
1:C:934:ILE:CD1	1:C:965:LYS:HG2	2.46	0.44
1:G:963:GLN:NE2	1:G:1010:LEU:O	2.45	0.44
1:I:934:ILE:HG22	1:I:961:VAL:HG13	1.99	0.44
1:L:1014:HIS:CD2	1:L:1015:SER:H	2.35	0.44
1:E:904:LYS:HE3	1:E:904:LYS:HB3	1.78	0.44
1:H:911:LEU:HD11	1:H:921:PHE:CE2	2.52	0.44
1:L:1014:HIS:HD2	1:L:1015:SER:H	1.62	0.44
1:A:973:LEU:O	1:A:979:SER:CB	2.63	0.44
1:B:996:ILE:HG22	1:B:996:ILE:O	2.17	0.44
1:K:973:LEU:HD21	1:K:1073:PHE:HD1	1.83	0.44
1:L:888:ASP:N	1:L:888:ASP:OD1	2.51	0.44
1:B:927:ILE:HD12	1:B:932:ARG:HA	1.99	0.44
1:H:900:LEU:HD11	1:H:918:LEU:CD2	2.48	0.44
1:I:1020:ILE:HG23	1:I:1022:ASP:HB2	2.00	0.44
1:A:990:ILE:HG22	1:A:991:PRO:HD2	2.00	0.44
1:G:1014:HIS:HD2	1:G:1016:GLN:N	2.12	0.44
1:I:904:LYS:HE3	1:I:904:LYS:HB3	1.63	0.44
1:L:893:CYS:O	1:L:894:GLN:CB	2.63	0.44
1:L:997:ILE:HD11	1:L:1038:PHE:HB2	2.00	0.44
1:B:915:VAL:HG11	1:B:970:LEU:HD23	1.99	0.44
1:E:990:ILE:HG22	1:E:993:TYR:HB2	2.00	0.44
1:B:1014:HIS:HD2	1:B:1016:GLN:N	2.13	0.44
1:E:1061:GLU:N	1:E:1061:GLU:OE2	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1072:TYR:OH	1:E:1076:LYS:HE2	2.18	0.44
1:C:1014:HIS:ND1	1:C:1015:SER:N	2.65	0.43
1:C:901:CYS:O	1:C:926:TRP:HE3	2.01	0.43
1:D:965:LYS:HD3	1:D:1080:ILE:HG22	2.00	0.43
1:I:972:TYR:HE2	1:I:1080:ILE:HD11	1.83	0.43
1:B:1072:TYR:OH	1:B:1076:LYS:NZ	2.51	0.43
1:F:969:LEU:HG	1:F:1080:ILE:HG13	2.00	0.43
1:H:1040:GLU:HA	1:H:1043:LYS:HE2	1.99	0.43
1:K:986:VAL:HG11	1:K:993:TYR:CG	2.53	0.43
1:I:973:LEU:HD21	1:I:1073:PHE:HB2	2.00	0.43
1:J:971:LEU:HD23	1:J:971:LEU:HA	1.65	0.43
1:K:919:LEU:CD1	1:K:919:LEU:N	2.71	0.43
1:C:1030:LEU:O	1:C:1034:ASN:HB2	2.19	0.43
1:G:997:ILE:HD13	1:G:997:ILE:HA	1.80	0.43
1:J:1044:VAL:O	1:J:1044:VAL:CG1	2.66	0.43
1:A:976:HIS:CE1	1:A:978:LEU:HB2	2.54	0.43
1:A:990:ILE:CG2	1:A:991:PRO:HD2	2.48	0.43
1:D:1084:ARG:HA	1:E:899:LEU:O	2.18	0.43
1:E:969:LEU:HG	1:E:1080:ILE:HD12	2.00	0.43
1:B:974:TYR:CE2	1:B:983:GLN:HG2	2.53	0.43
1:E:973:LEU:O	1:E:979:SER:HB3	2.18	0.43
1:G:974:TYR:HE2	1:G:983:GLN:CG	2.29	0.43
1:J:930:PHE:CZ	1:J:971:LEU:HD13	2.53	0.43
1:L:1043:LYS:HB3	1:L:1043:LYS:HE2	1.58	0.43
1:L:927:ILE:HD11	1:L:939:VAL:HG13	1.99	0.43
1:F:1012:LYS:HA	1:F:1017:HIS:CD2	2.54	0.43
1:G:1061:GLU:O	1:G:1064:GLN:HG2	2.19	0.43
1:C:927:ILE:HG12	1:C:939:VAL:HG22	2.01	0.43
1:D:1069:VAL:O	1:D:1072:TYR:HB3	2.18	0.43
1:F:934:ILE:CG1	1:F:968:ARG:NH2	2.82	0.43
1:G:1008:LYS:O	1:G:1011:GLN:HB2	2.19	0.43
1:A:915:VAL:HG22	1:A:1007:LYS:HE3	2.01	0.43
1:D:930:PHE:CZ	1:D:971:LEU:HB3	2.54	0.43
1:D:936:LYS:HG3	1:D:936:LYS:O	2.18	0.43
1:I:1009:LYS:NZ	1:I:1027:ASP:OD2	2.47	0.43
1:K:997:ILE:HG21	1:K:1034:ASN:ND2	2.33	0.43
1:K:887:GLU:CG	1:K:888:ASP:N	2.82	0.43
1:K:962:ASP:CG	1:K:1021:PRO:HG3	2.39	0.43
1:A:1074:GLU:O	1:A:1078:THR:HG23	2.19	0.42
1:D:973:LEU:N	1:D:973:LEU:HD23	2.34	0.42
1:J:903:GLU:OE1	1:J:903:GLU:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:971:LEU:HD23	1:A:971:LEU:HA	1.90	0.42
1:B:900:LEU:HD13	1:B:926:TRP:CZ2	2.54	0.42
1:D:978:LEU:HD13	1:D:978:LEU:HA	1.81	0.42
1:G:905:CYS:CB	1:G:906:PRO:CD	2.97	0.42
1:H:905:CYS:HB2	1:H:906:PRO:HD2	2.00	0.42
1:C:969:LEU:HD13	1:C:1073:PHE:CE1	2.54	0.42
1:G:1071:LEU:HA	1:G:1071:LEU:HD13	1.72	0.42
1:G:915:VAL:HG22	1:G:1007:LYS:CE	2.46	0.42
1:H:905:CYS:CB	1:H:906:PRO:HD2	2.49	0.42
1:I:969:LEU:CD2	1:I:1080:ILE:HD12	2.50	0.42
1:I:930:PHE:CE1	1:I:971:LEU:HB3	2.53	0.42
1:L:1020:ILE:CG2	1:L:1021:PRO:CD	2.91	0.42
1:L:927:ILE:HD12	1:L:932:ARG:CB	2.48	0.42
1:A:927:ILE:HD11	1:A:938:GLU:HB2	2.01	0.42
1:B:900:LEU:HD11	1:B:918:LEU:HD23	2.00	0.42
1:B:918:LEU:HD21	1:B:926:TRP:HE1	1.85	0.42
1:H:999:LYS:NZ	1:H:1030:LEU:HD22	2.35	0.42
1:J:1069:VAL:O	1:J:1072:TYR:HB3	2.20	0.42
1:E:971:LEU:HA	1:E:971:LEU:HD23	1.69	0.42
1:L:1074:GLU:O	1:L:1078:THR:HG23	2.19	0.42
1:A:1072:TYR:CZ	1:A:1076:LYS:HE3	2.54	0.42
1:A:905:CYS:SG	1:A:906:PRO:N	2.93	0.42
1:D:973:LEU:O	1:D:979:SER:HB3	2.20	0.42
1:E:1043:LYS:HE2	1:E:1043:LYS:HB3	1.62	0.42
1:H:993:TYR:CD2	1:H:994:TYR:CE2	3.07	0.42
1:L:1009:LYS:NZ	1:L:1027:ASP:OD2	2.39	0.42
1:D:1041:MET:CE	1:D:1041:MET:HA	2.50	0.42
1:D:996:ILE:O	1:D:996:ILE:HG22	2.19	0.42
1:A:973:LEU:HD21	1:A:1073:PHE:CD1	2.54	0.42
1:I:1013:LYS:HB3	1:I:1013:LYS:HE3	1.84	0.42
1:J:976:HIS:CE1	1:J:978:LEU:CD2	3.00	0.42
1:G:1043:LYS:NZ	1:G:1043:LYS:HB3	2.35	0.42
1:H:934:ILE:CG2	1:H:961:VAL:HG13	2.50	0.42
1:I:972:TYR:CE2	1:I:1080:ILE:HD11	2.54	0.42
1:J:1022:ASP:N	1:J:1022:ASP:OD1	2.53	0.42
1:J:993:TYR:HD2	1:J:994:TYR:CD2	2.38	0.42
1:L:1041:MET:O	1:L:1045:VAL:HB	2.20	0.42
1:D:1012:LYS:HA	1:D:1017:HIS:CD2	2.55	0.42
1:D:933:ASP:HB2	1:D:938:GLU:OE2	2.20	0.42
1:D:927:ILE:CD1	1:D:938:GLU:HB2	2.50	0.42
1:K:904:LYS:HD3	1:K:904:LYS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:890:CYS:HA	1:B:908:VAL:O	2.19	0.41
1:D:1030:LEU:HG	1:D:1030:LEU:O	2.20	0.41
1:F:1028:VAL:O	1:F:1031:ILE:HB	2.20	0.41
1:G:984:GLU:HB3	1:G:985:PRO:HD2	2.02	0.41
1:I:929:THR:HB	1:I:971:LEU:HD12	2.02	0.41
1:J:1074:GLU:O	1:J:1078:THR:HG23	2.19	0.41
1:K:1003:LEU:HA	1:K:1003:LEU:HD23	1.89	0.41
1:B:1020:ILE:CG2	1:B:1022:ASP:H	2.33	0.41
1:B:905:CYS:SG	1:B:906:PRO:N	2.93	0.41
1:B:912:THR:HA	1:B:917:THR:HG23	2.02	0.41
1:C:1004:SER:O	1:C:1008:LYS:HG3	2.21	0.41
1:C:1020:ILE:CG2	1:C:1022:ASP:HB2	2.51	0.41
1:C:927:ILE:HG12	1:C:939:VAL:HG21	2.00	0.41
1:D:900:LEU:HD11	1:D:918:LEU:HD23	2.02	0.41
1:G:927:ILE:HG12	1:G:939:VAL:CG2	2.50	0.41
1:K:990:ILE:H	1:K:990:ILE:HG12	1.66	0.41
1:L:957:GLY:HA2	1:L:1019:GLN:HA	2.03	0.41
1:F:1020:ILE:CG2	1:F:1022:ASP:HB2	2.50	0.41
1:J:1071:LEU:HD13	1:J:1071:LEU:HA	1.81	0.41
1:C:1002:ASP:OD2	1:C:1004:SER:HB3	2.20	0.41
1:C:927:ILE:HD11	1:C:938:GLU:HB2	2.01	0.41
1:E:932:ARG:HH21	1:E:964:ARG:HG2	1.85	0.41
1:G:986:VAL:HA	1:G:987:PRO:HD3	1.93	0.41
1:G:996:ILE:HG22	1:G:996:ILE:O	2.20	0.41
1:K:1044:VAL:O	1:K:1044:VAL:CG1	2.67	0.41
1:A:1042:MET:CA	1:A:1045:VAL:HG23	2.43	0.41
1:C:986:VAL:HA	1:C:987:PRO:HD3	1.90	0.41
1:E:1037:ARG:HG3	1:E:1037:ARG:HH11	1.84	0.41
1:G:904:LYS:HE3	1:G:904:LYS:HB3	1.90	0.41
1:H:1041:MET:HE2	1:H:1041:MET:HA	2.02	0.41
1:I:897:GLY:O	1:I:899:LEU:HG	2.21	0.41
1:C:927:ILE:CG1	1:C:939:VAL:HG22	2.50	0.41
1:A:905:CYS:SG	1:A:906:PRO:HD2	2.61	0.41
1:B:911:LEU:HB3	1:B:918:LEU:O	2.20	0.41
1:C:900:LEU:HB3	1:C:926:TRP:CZ3	2.55	0.41
1:D:1037:ARG:HH21	1:J:1037:ARG:CZ	2.31	0.41
1:D:932:ARG:NH2	1:D:964:ARG:HG2	2.36	0.41
1:I:955:ALA:HB1	1:I:1012:LYS:HD3	2.03	0.41
1:J:1041:MET:CE	1:J:1041:MET:HA	2.49	0.41
1:J:1065:ALA:O	1:J:1068:ALA:HB3	2.21	0.41
1:B:931:CYS:O	1:B:932:ARG:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:900:LEU:HD13	1:C:926:TRP:CZ2	2.56	0.41
1:C:930:PHE:CZ	1:C:971:LEU:HB3	2.56	0.41
1:E:917:THR:HG22	1:E:918:LEU:N	2.35	0.41
1:E:973:LEU:O	1:E:979:SER:CB	2.68	0.41
1:H:1069:VAL:O	1:H:1072:TYR:HB3	2.21	0.41
1:K:930:PHE:CZ	1:K:971:LEU:HB3	2.56	0.41
1:A:899:LEU:HB2	1:L:1085:THR:OG1	2.21	0.41
1:A:957:GLY:HA2	1:A:1019:GLN:OE1	2.20	0.41
1:H:1014:HIS:C	1:H:1014:HIS:HD2	2.22	0.41
1:H:1041:MET:O	1:H:1044:VAL:HG12	2.20	0.41
1:H:1046:GLN:N	1:H:1046:GLN:OE1	2.54	0.41
1:J:976:HIS:ND1	1:J:977:GLU:N	2.68	0.41
1:K:1076:LYS:HA	1:K:1076:LYS:HD3	1.76	0.41
1:A:893:CYS:O	1:A:894:GLN:HB2	2.21	0.41
1:E:899:LEU:HD13	1:E:908:VAL:CG2	2.50	0.41
1:F:919:LEU:CD1	1:F:919:LEU:H	2.19	0.41
1:G:973:LEU:N	1:G:973:LEU:HD23	2.36	0.41
1:G:992:ASN:O	1:G:996:ILE:HG13	2.21	0.41
1:H:1086:PHE:O	1:H:1087:ALA:C	2.60	0.41
1:I:983:GLN:HA	1:I:1003:LEU:HB2	2.03	0.41
1:I:958:LEU:HD13	1:I:963:GLN:HA	2.02	0.41
1:A:981:GLU:OE1	1:A:1062:VAL:HG13	2.21	0.40
1:C:993:TYR:HD2	1:C:994:TYR:HD1	1.65	0.40
1:D:976:HIS:CD2	1:D:1072:TYR:HD2	2.35	0.40
1:F:997:ILE:HG21	1:F:1034:ASN:ND2	2.36	0.40
1:L:1045:VAL:HG13	1:L:1045:VAL:O	2.20	0.40
1:A:1061:GLU:HG2	1:A:1062:VAL:CG2	2.51	0.40
1:B:999:LYS:HB3	1:B:1030:LEU:HD21	2.02	0.40
1:B:990:ILE:HG22	1:B:991:PRO:HD2	2.03	0.40
1:C:1072:TYR:CE1	1:C:1076:LYS:HE3	2.56	0.40
1:D:1003:LEU:O	1:D:1006:VAL:N	2.54	0.40
1:D:981:GLU:OE1	1:D:1062:VAL:HG13	2.22	0.40
1:E:901:CYS:O	1:E:926:TRP:HE3	2.04	0.40
1:E:930:PHE:CE1	1:E:971:LEU:HB3	2.56	0.40
1:E:936:LYS:O	1:E:936:LYS:CG	2.70	0.40
1:G:1083:ASP:N	1:G:1083:ASP:OD2	2.48	0.40
1:I:1028:VAL:O	1:I:1031:ILE:HB	2.22	0.40
1:J:978:LEU:HD13	1:J:978:LEU:HA	1.84	0.40
1:L:1071:LEU:HD13	1:L:1071:LEU:HA	1.72	0.40
1:L:905:CYS:CB	1:L:906:PRO:HD2	2.52	0.40
1:B:1010:LEU:HD12	1:B:1010:LEU:HA	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:919:LEU:HD11	1:F:943:CYS:CB	2.52	0.40
1:F:973:LEU:HD23	1:F:973:LEU:HA	1.69	0.40
1:G:973:LEU:O	1:G:979:SER:CB	2.68	0.40
1:A:886:ASN:HA	1:A:906:PRO:HA	2.03	0.40
1:B:918:LEU:HD21	1:B:926:TRP:NE1	2.37	0.40
1:G:893:CYS:C	1:G:894:GLN:HG2	2.41	0.40
1:C:922:PRO:O	1:H:1083:ASP:OD1	2.40	0.40
1:J:958:LEU:HD13	1:J:963:GLN:HA	2.02	0.40
1:L:901:CYS:O	1:L:926:TRP:CE3	2.67	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	172/207 (83%)	162 (94%)	10 (6%)	0	100	100
1	B	172/207 (83%)	166 (96%)	6 (4%)	0	100	100
1	C	166/207 (80%)	156 (94%)	10 (6%)	0	100	100
1	D	171/207 (83%)	164 (96%)	7 (4%)	0	100	100
1	E	167/207 (81%)	163 (98%)	4 (2%)	0	100	100
1	F	173/207 (84%)	164 (95%)	9 (5%)	0	100	100
1	G	174/207 (84%)	162 (93%)	12 (7%)	0	100	100
1	H	172/207 (83%)	162 (94%)	10 (6%)	0	100	100
1	I	167/207 (81%)	157 (94%)	10 (6%)	0	100	100
1	J	168/207 (81%)	161 (96%)	7 (4%)	0	100	100
1	K	169/207 (82%)	164 (97%)	5 (3%)	0	100	100
1	L	169/207 (82%)	160 (95%)	8 (5%)	1 (1%)	25	57
All	All	2040/2484 (82%)	1941 (95%)	98 (5%)	1 (0%)	100	100



All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	922	PRO

### 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	164/189 (87%)	140 (85%)	24 (15%)	3	13
1	B	163/189 (86%)	146 (90%)	17 (10%)	7	25
1	C	159/189 (84%)	143 (90%)	16 (10%)	7	26
1	D	163/189 (86%)	149 (91%)	14 (9%)	10	36
1	E	159/189 (84%)	141 (89%)	18 (11%)	6	22
1	F	164/189 (87%)	142 (87%)	22 (13%)	4	15
1	G	165/189 (87%)	145 (88%)	20 (12%)	5	19
1	H	163/189 (86%)	145 (89%)	18 (11%)	6	23
1	I	158/189 (84%)	138 (87%)	20 (13%)	4	17
1	J	159/189 (84%)	139 (87%)	20 (13%)	4	17
1	K	160/189 (85%)	134 (84%)	26 (16%)	2	9
1	L	160/189 (85%)	140 (88%)	20 (12%)	4	17
All	All	1937/2268 (85%)	1702 (88%)	235 (12%)	5	19

All (235) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	888	ASP
1	A	905	CYS
1	A	912	THR
1	A	925	ASP
1	A	942	ASP
1	A	943	CYS
1	A	959	SER
1	A	968	ARG

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Mol	Chain	Res	Type
1	A	971	LEU
1	A	974	TYR
1	A	980	ILE
1	A	990	ILE
1	A	1010	LEU
1	A	1020	ILE
1	A	1022	ASP
1	A	1037	ARG
1	A	1043	LYS
1	A	1044	VAL
1	A	1045	VAL
1	A	1046	GLN
1	A	1061	GLU
1	A	1062	VAL
1	A	1064	GLN
1	A	1082	SER
1	B	887	GLU
1	B	904	LYS
1	B	905	CYS
1	B	918	LEU
1	B	919	LEU
1	B	936	LYS
1	B	956	GLN
1	B	971	LEU
1	B	973	LEU
1	B	999	LYS
1	B	1002	ASP
1	B	1012	LYS
1	B	1020	ILE
1	B	1022	ASP
1	B	1044	VAL
1	B	1046	GLN
1	B	1062	VAL
1	C	907	LYS
1	C	912	THR
1	C	925	ASP
1	C	971	LEU
1	C	1002	ASP
1	C	1004	SER
1	C	1010	LEU
1	C	1012	LYS
1	C	1020	ILE

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Mol	Chain	Res	Type
1	C	1022	ASP
1	C	1027	ASP
1	C	1037	ARG
1	C	1044	VAL
1	C	1062	VAL
1	C	1071	LEU
1	C	1078	THR
1	D	905	CYS
1	D	918	LEU
1	D	971	LEU
1	D	973	LEU
1	D	978	LEU
1	D	980	ILE
1	D	989	SER
1	D	998	LYS
1	D	1002	ASP
1	D	1012	LYS
1	D	1013	LYS
1	D	1020	ILE
1	D	1036	GLU
1	D	1044	VAL
1	E	898	ASP
1	E	923	SER
1	E	938	GLU
1	E	956	GLN
1	E	959	SER
1	E	970	LEU
1	E	971	LEU
1	E	973	LEU
1	E	1004	SER
1	E	1013	LYS
1	E	1020	ILE
1	E	1022	ASP
1	E	1027	ASP
1	E	1035	CYS
1	E	1041	MET
1	E	1044	VAL
1	E	1062	VAL
1	E	1064	GLN
1	F	905	CYS
1	F	911	LEU
1	F	912	THR

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Mol	Chain	Res	Type
1	F	919	LEU
1	F	929	THR
1	F	936	LYS
1	F	942	ASP
1	F	1004	SER
1	F	1010	LEU
1	F	1015	SER
1	F	1020	ILE
1	F	1022	ASP
1	F	1036	GLU
1	F	1043	LYS
1	F	1044	VAL
1	F	1045	VAL
1	F	1046	GLN
1	F	1059	ASP
1	F	1061	GLU
1	F	1062	VAL
1	F	1064	GLN
1	F	1071	LEU
1	G	903	GLU
1	G	912	THR
1	G	919	LEU
1	G	925	ASP
1	G	959	SER
1	G	970	LEU
1	G	971	LEU
1	G	973	LEU
1	G	974	TYR
1	G	977	GLU
1	G	995	LYS
1	G	1002	ASP
1	G	1013	LYS
1	G	1020	ILE
1	G	1022	ASP
1	G	1036	GLU
1	G	1043	LYS
1	G	1044	VAL
1	G	1045	VAL
1	G	1046	GLN
1	H	904	LYS
1	H	905	CYS
1	H	912	THR

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Mol	Chain	Res	Type
1	H	925	ASP
1	H	927	ILE
1	H	943	CYS
1	H	971	LEU
1	H	998	LYS
1	H	1004	SER
1	H	1010	LEU
1	H	1015	SER
1	H	1020	ILE
1	H	1022	ASP
1	H	1044	VAL
1	H	1046	GLN
1	H	1061	GLU
1	H	1078	THR
1	H	1082	SER
1	I	905	CYS
1	I	925	ASP
1	I	927	ILE
1	I	932	ARG
1	I	938	GLU
1	I	959	SER
1	I	970	LEU
1	I	971	LEU
1	I	974	TYR
1	I	977	GLU
1	I	995	LYS
1	I	998	LYS
1	I	999	LYS
1	I	1010	LEU
1	I	1013	LYS
1	I	1020	ILE
1	I	1045	VAL
1	I	1046	GLN
1	I	1062	VAL
1	I	1071	LEU
1	J	888	ASP
1	J	902	CYS
1	J	903	GLU
1	J	904	LYS
1	J	905	CYS
1	J	925	ASP
1	J	927	ILE

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Mol	Chain	Res	Type
1	J	936	LYS
1	J	959	SER
1	J	970	LEU
1	J	971	LEU
1	J	973	LEU
1	J	1010	LEU
1	J	1020	ILE
1	J	1022	ASP
1	J	1036	GLU
1	J	1039	ASN
1	J	1062	VAL
1	J	1071	LEU
1	J	1072	TYR
1	K	894	GLN
1	K	905	CYS
1	K	912	THR
1	K	919	LEU
1	K	920	SER
1	K	921	PHE
1	K	923	SER
1	K	925	ASP
1	K	927	ILE
1	K	956	GLN
1	K	971	LEU
1	K	974	TYR
1	K	980	ILE
1	K	995	LYS
1	K	999	LYS
1	K	1005	THR
1	K	1015	SER
1	K	1019	GLN
1	K	1020	ILE
1	K	1036	GLU
1	K	1037	ARG
1	K	1045	VAL
1	K	1046	GLN
1	K	1061	GLU
1	K	1062	VAL
1	K	1071	LEU
1	L	888	ASP
1	L	905	CYS
1	L	911	LEU

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Mol	Chain	Res	Type
1	L	912	THR
1	L	969	LEU
1	L	971	LEU
1	L	977	GLU
1	L	989	SER
1	L	992	ASN
1	L	998	LYS
1	L	1005	THR
1	L	1010	LEU
1	L	1019	GLN
1	L	1041	MET
1	L	1042	MET
1	L	1043	LYS
1	L	1044	VAL
1	L	1045	VAL
1	L	1071	LEU
1	L	1075	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	976	HIS
1	A	983	GLN
1	A	1014	HIS
1	A	1016	GLN
1	A	1064	GLN
1	B	1014	HIS
1	D	976	HIS
1	E	956	GLN
1	E	976	HIS
1	E	1014	HIS
1	F	976	HIS
1	F	983	GLN
1	F	1014	HIS
1	F	1016	GLN
1	G	983	GLN
1	G	1014	HIS
1	G	1046	GLN
1	G	1064	GLN
1	H	1014	HIS
1	H	1016	GLN
1	I	1014	HIS

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Mol	Chain	Res	Type
1	I	1016	GLN
1	I	1064	GLN
1	J	976	HIS
1	J	983	GLN
1	K	886	ASN
1	K	894	GLN
1	K	956	GLN
1	K	976	HIS
1	K	983	GLN
1	L	886	ASN
1	L	976	HIS
1	L	1014	HIS

### 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](#)

Of 36 ligands modelled in this entry, 36 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.



## 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	178/207 (85%)	-0.28	3 (1%) 70 48	106, 144, 198, 220	0
1	B	178/207 (85%)	-0.23	4 (2%) 62 39	110, 142, 200, 223	0
1	C	174/207 (84%)	-0.24	3 (1%) 70 48	105, 141, 189, 210	0
1	D	177/207 (85%)	-0.25	2 (1%) 80 63	108, 141, 196, 217	0
1	E	173/207 (83%)	-0.33	0 100 100	108, 143, 188, 217	0
1	F	179/207 (86%)	-0.22	5 (2%) 53 28	112, 144, 205, 239	0
1	G	180/207 (86%)	-0.28	2 (1%) 80 63	111, 145, 202, 235	0
1	H	178/207 (85%)	-0.21	4 (2%) 62 39	108, 145, 197, 237	0
1	I	173/207 (83%)	-0.28	1 (0%) 89 77	104, 144, 191, 211	0
1	J	174/207 (84%)	-0.22	2 (1%) 80 63	106, 142, 191, 219	0
1	K	175/207 (84%)	-0.24	3 (1%) 70 48	109, 142, 190, 213	0
1	L	175/207 (84%)	-0.24	3 (1%) 70 48	106, 143, 198, 233	0
All	All	2114/2484 (85%)	-0.25	32 (1%) 73 53	104, 143, 196, 239	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	939	VAL	5.9
1	A	939	VAL	4.6
1	H	940	GLU	4.4
1	F	1059	ASP	4.1
1	K	939	VAL	4.0
1	C	955	ALA	3.7
1	L	935	GLY	3.6
1	F	939	VAL	3.3
1	H	939	VAL	3.1
1	L	1059	ASP	3.1
1	H	941	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	900	LEU	2.9
1	J	955	ALA	2.7
1	B	937	PRO	2.6
1	K	955	ALA	2.4
1	C	939	VAL	2.4
1	F	940	GLU	2.4
1	B	936	LYS	2.3
1	H	935	GLY	2.3
1	B	909	PHE	2.2
1	L	934	ILE	2.2
1	A	938	GLU	2.2
1	F	1041	MET	2.2
1	F	1044	VAL	2.2
1	K	934	ILE	2.1
1	I	935	GLY	2.1
1	G	939	VAL	2.1
1	D	942	ASP	2.1
1	C	964	ARG	2.1
1	G	923	SER	2.1
1	A	923	SER	2.1
1	J	935	GLY	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CA	I	3	1/1	0.73	0.16	132,132,132,132	0
2	ZN	L	2	1/1	0.85	0.12	155,155,155,155	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	I	1	1/1	0.86	0.11	149,149,149,149	0
2	ZN	E	1	1/1	0.87	0.15	149,149,149,149	0
3	CA	F	3	1/1	0.89	0.23	142,142,142,142	0
3	CA	A	1088	1/1	0.91	0.31	133,133,133,133	0
2	ZN	A	1	1/1	0.92	0.11	149,149,149,149	0
2	ZN	A	2	1/1	0.92	0.14	148,148,148,148	0
3	CA	B	1088	1/1	0.92	0.26	127,127,127,127	0
2	ZN	G	2	1/1	0.92	0.15	156,156,156,156	0
2	ZN	F	1	1/1	0.94	0.15	150,150,150,150	0
3	CA	B	3	1/1	0.94	0.25	138,138,138,138	0
3	CA	F	1088	1/1	0.95	0.25	135,135,135,135	0
2	ZN	K	2	1/1	0.95	0.17	147,147,147,147	0
2	ZN	K	1	1/1	0.95	0.12	148,148,148,148	0
2	ZN	E	2	1/1	0.96	0.13	146,146,146,146	0
2	ZN	J	1	1/1	0.96	0.14	149,149,149,149	0
2	ZN	B	2	1/1	0.96	0.21	148,148,148,148	0
3	CA	A	3	1/1	0.96	0.25	129,129,129,129	0
3	CA	E	3	1/1	0.97	0.18	138,138,138,138	0
3	CA	I	1088	1/1	0.97	0.26	142,142,142,142	0
2	ZN	L	1	1/1	0.97	0.17	160,160,160,160	0
2	ZN	B	1	1/1	0.97	0.14	156,156,156,156	0
2	ZN	J	2	1/1	0.97	0.17	154,154,154,154	0
2	ZN	H	1	1/1	0.97	0.14	151,151,151,151	0
2	ZN	D	2	1/1	0.98	0.12	147,147,147,147	0
2	ZN	G	1	1/1	0.98	0.11	154,154,154,154	0
3	CA	C	3	1/1	0.98	0.30	134,134,134,134	0
2	ZN	C	2	1/1	0.98	0.15	146,146,146,146	0
2	ZN	I	2	1/1	0.98	0.17	149,149,149,149	0
2	ZN	C	1	1/1	0.98	0.15	151,151,151,151	0
3	CA	C	1088	1/1	0.99	0.18	135,135,135,135	0
2	ZN	D	1	1/1	0.99	0.12	147,147,147,147	0
2	ZN	F	2	1/1	0.99	0.10	144,144,144,144	0
2	ZN	H	2	1/1	0.99	0.12	153,153,153,153	0
3	CA	E	1088	1/1	0.99	0.23	129,129,129,129	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.