



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:37 AM GMT

PDB ID : 2XQ7  
Title : PENTAMERIC LIGAND GATED ION CHANNEL GLIC IN COMPLEX  
WITH CADMIUM ION (CD2+)  
Authors : Hilf, R.J.C.; Bertozzi, C.; Zimmermann, I.; Reiter, A.; Trauner, D.; Dutzler,  
R.  
Deposited on : 2010-09-01  
Resolution : 3.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

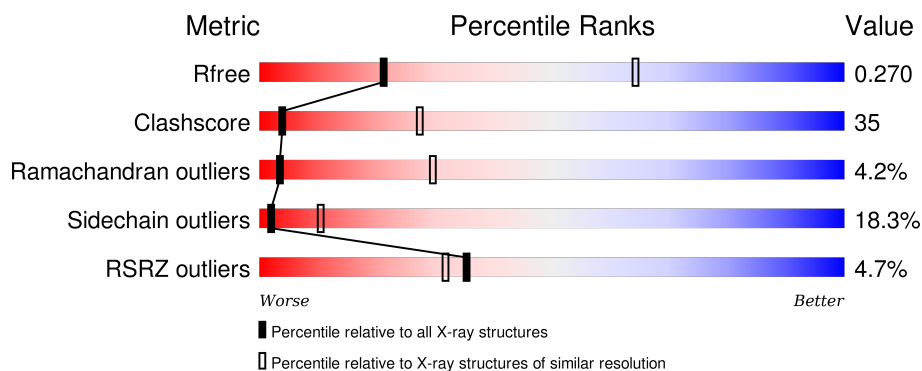
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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))
$R_{free}$	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	317	<div> <div>3%</div> <div> <div>41%</div> <div>43%</div> <div>13%</div> <div>..</div> </div> </div>
1	B	317	<div> <div>3%</div> <div> <div>40%</div> <div>44%</div> <div>13%</div> <div>..</div> </div> </div>
1	C	317	<div> <div>6%</div> <div> <div>42%</div> <div>42%</div> <div>13%</div> <div>..</div> </div> </div>
1	D	317	<div> <div>4%</div> <div> <div>41%</div> <div>43%</div> <div>13%</div> <div>..</div> </div> </div>
1	E	317	<div> <div>7%</div> <div> <div>43%</div> <div>41%</div> <div>13%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12655 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 GLR4197 PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	1	0
			2530	1667	404	455	4			
1	B	310	Total	C	N	O	S	0	1	0
			2530	1667	404	455	4			
1	C	310	Total	C	N	O	S	0	1	0
			2530	1667	404	455	4			
1	D	310	Total	C	N	O	S	0	1	0
			2530	1667	404	455	4			
1	E	310	Total	C	N	O	S	0	1	0
			2530	1667	404	455	4			

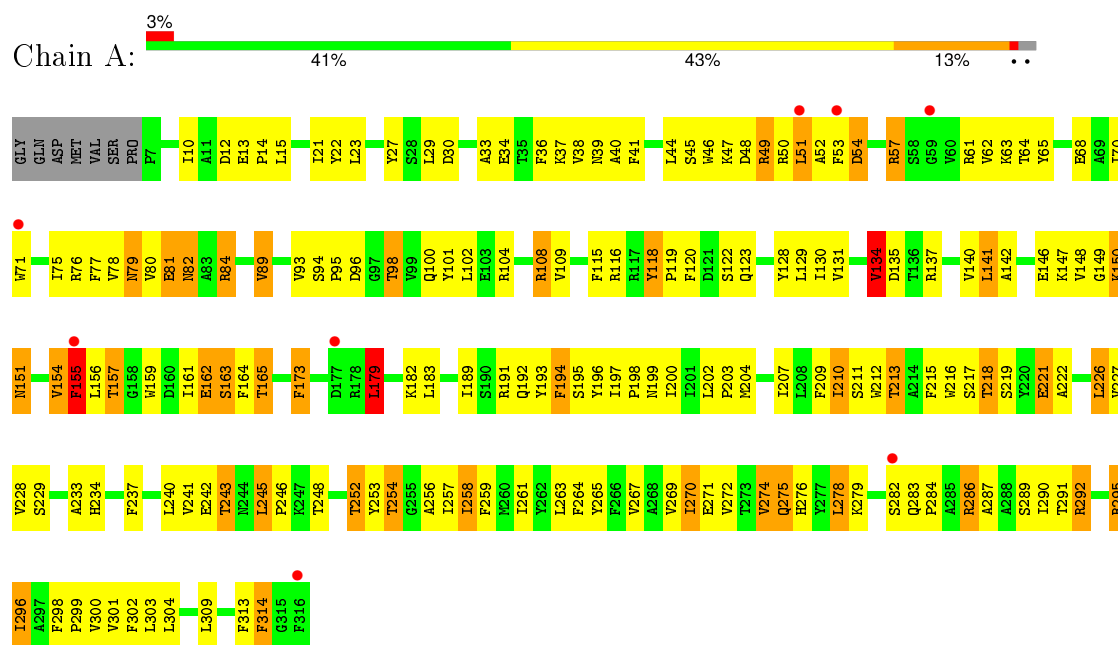
- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Cd	0	0
			3	3		
2	C	2	Total	Cd	0	0
			2	2		

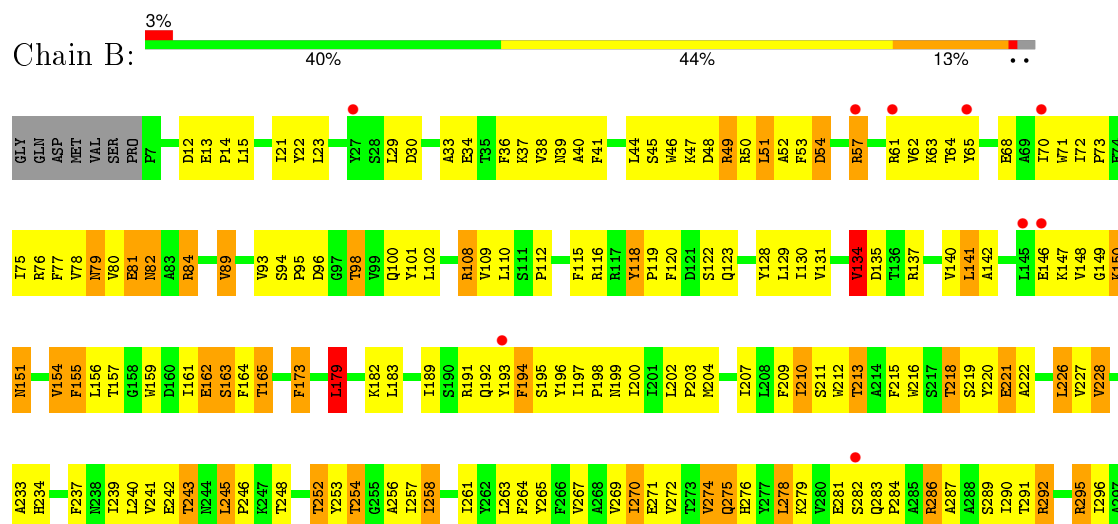
### 3 Residue-property plots

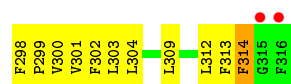
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: GLR4197 PROTEIN

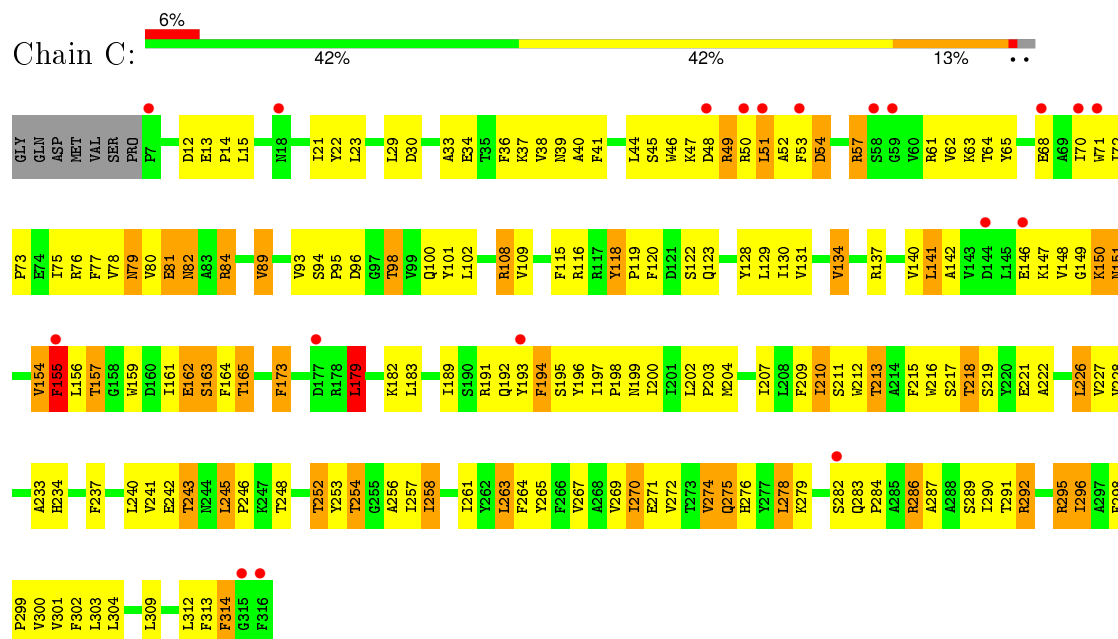


#### • Molecule 1: GLR4197 PROTEIN

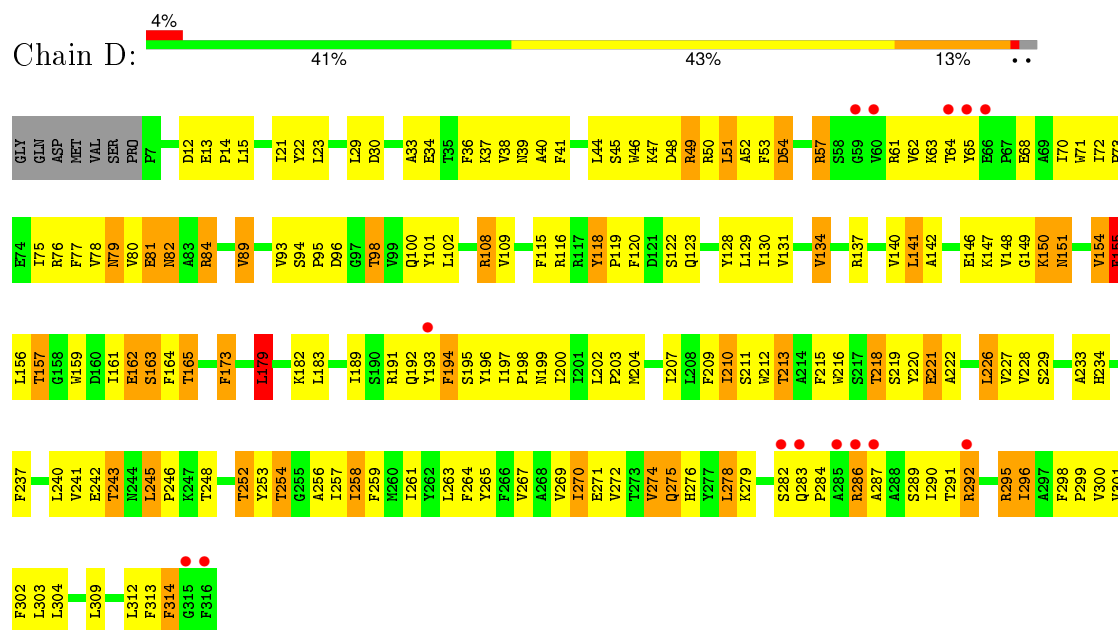




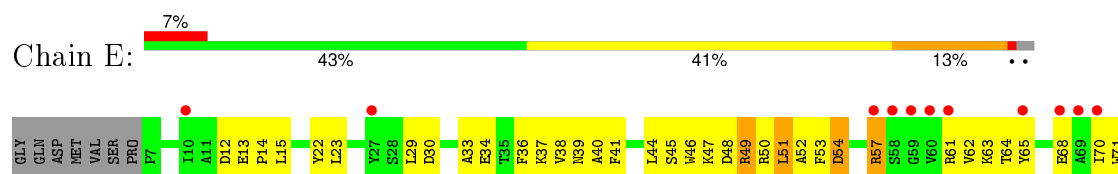
• Molecule 1: GLR4197 PROTEIN

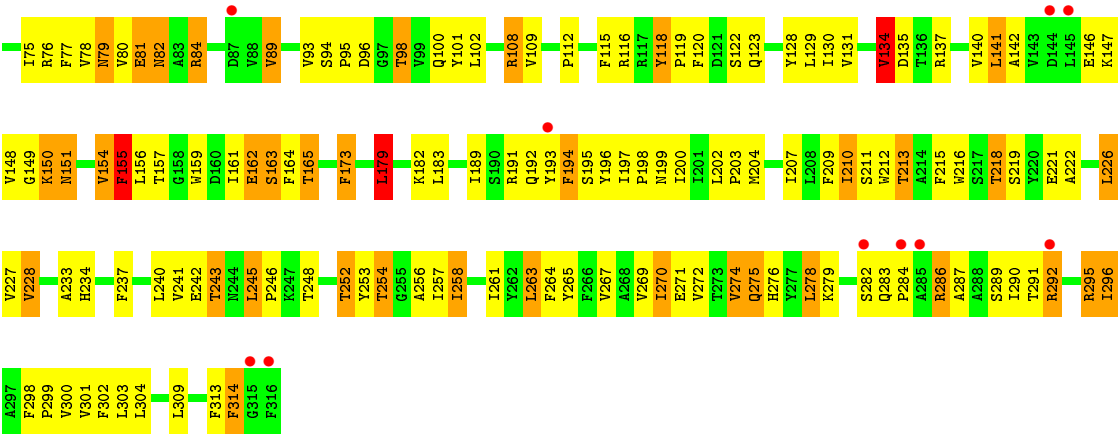


• Molecule 1: GLR4197 PROTEIN



• Molecule 1: GLR4197 PROTEIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	183.31Å 128.31Å 164.37Å 90.00° 104.04° 90.00°	Depositor
Resolution (Å)	40.20 – 3.40 40.20 – 3.40	Depositor EDS
% Data completeness (in resolution range)	98.0 (40.20-3.40) 98.1 (40.20-3.40)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.06 (at 3.40Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.242 , 0.266 0.254 , 0.270	Depositor DCC
$R_{free}$ test set	2497 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	93.1	Xtriage
Anisotropy	0.437	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 55.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 50801 reflections	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	12655	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

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

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	0.48	0/2598	0.66	2/3547 (0.1%)
1	B	0.48	0/2598	0.66	2/3547 (0.1%)
1	C	0.49	0/2598	0.66	2/3547 (0.1%)
1	D	0.49	0/2598	0.66	2/3547 (0.1%)
1	E	0.47	0/2598	0.66	2/3547 (0.1%)
All	All	0.48	0/12990	0.66	10/17735 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	179	LEU	CA-CB-CG	5.68	128.37	115.30
1	D	179	LEU	CA-CB-CG	5.68	128.36	115.30
1	E	179	LEU	CA-CB-CG	5.68	128.36	115.30
1	A	179	LEU	CA-CB-CG	5.67	128.34	115.30
1	C	179	LEU	CA-CB-CG	5.65	128.29	115.30
1	A	134	VAL	N-CA-CB	-5.26	99.92	111.50
1	E	134	VAL	N-CA-CB	-5.26	99.93	111.50
1	B	134	VAL	N-CA-CB	-5.26	99.93	111.50
1	C	134	VAL	N-CA-CB	-5.26	99.93	111.50
1	D	134	VAL	N-CA-CB	-5.25	99.94	111.50

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	2530	0	2542	192	0
1	B	2530	0	2542	189	0
1	C	2530	0	2542	179	0
1	D	2530	0	2542	183	0
1	E	2530	0	2542	172	0
2	A	3	0	0	0	0
2	C	2	0	0	0	0
All	All	12655	0	12710	880	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 35.

All (880) 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:A:283:GLN:HG2	1:A:283:GLN:O	1.45	1.13
1:D:283:GLN:O	1:D:283:GLN:HG2	1.45	1.13
1:B:283:GLN:O	1:B:283:GLN:HG2	1.45	1.12
1:E:283:GLN:O	1:E:283:GLN:HG2	1.45	1.11
1:C:283:GLN:O	1:C:283:GLN:HG2	1.45	1.06
1:D:147:LYS:C	1:D:149:GLY:H	1.68	0.95
1:E:147:LYS:C	1:E:149:GLY:H	1.66	0.94
1:C:147:LYS:C	1:C:149:GLY:H	1.68	0.93
1:D:22:TYR:HA	1:D:149:GLY:HA3	1.51	0.93
1:B:22:TYR:HA	1:B:149:GLY:HA3	1.51	0.92
1:A:22:TYR:HA	1:A:149:GLY:HA3	1.51	0.92
1:A:147:LYS:C	1:A:149:GLY:H	1.68	0.91
1:C:22:TYR:HA	1:C:149:GLY:HA3	1.51	0.91
1:B:147:LYS:C	1:B:149:GLY:H	1.69	0.89
1:E:22:TYR:HA	1:E:149:GLY:HA3	1.55	0.88
1:C:13:GLU:HB3	1:C:14:PRO:HD2	1.56	0.88
1:E:13:GLU:HB3	1:E:14:PRO:HD2	1.56	0.88
1:D:13:GLU:HB3	1:D:14:PRO:HD2	1.56	0.88
1:B:13:GLU:HB3	1:B:14:PRO:HD2	1.56	0.86
1:A:13:GLU:HB3	1:A:14:PRO:HD2	1.56	0.85
1:D:278:LEU:HD21	1:D:286:ARG:HB3	1.59	0.85
1:E:22:TYR:HA	1:E:149:GLY:CA	2.07	0.84
1:B:278:LEU:HD21	1:B:286:ARG:HB3	1.59	0.84
1:B:22:TYR:HA	1:B:149:GLY:CA	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:TYR:HA	1:D:149:GLY:CA	2.07	0.84
1:A:278:LEU:HD21	1:A:286:ARG:HB3	1.59	0.83
1:C:278:LEU:HD21	1:C:286:ARG:HB3	1.59	0.83
1:A:22:TYR:HA	1:A:149:GLY:CA	2.07	0.83
1:E:278:LEU:HD21	1:E:286:ARG:HB3	1.59	0.83
1:C:22:TYR:HA	1:C:149:GLY:CA	2.07	0.83
1:A:283:GLN:O	1:A:283:GLN:CG	2.30	0.78
1:E:197:ILE:HB	1:E:198:PRO:HD3	1.65	0.78
1:C:13:GLU:HB3	1:C:14:PRO:CD	2.14	0.78
1:E:253:TYR:HA	1:E:313:PHE:CE2	2.19	0.78
1:D:253:TYR:HA	1:D:313:PHE:CE2	2.19	0.78
1:C:197:ILE:HB	1:C:198:PRO:HD3	1.65	0.77
1:B:253:TYR:HA	1:B:313:PHE:CE2	2.19	0.77
1:A:253:TYR:HA	1:A:313:PHE:CE2	2.19	0.77
1:A:197:ILE:HB	1:A:198:PRO:HD3	1.65	0.77
1:D:13:GLU:HB3	1:D:14:PRO:CD	2.14	0.77
1:B:13:GLU:HB3	1:B:14:PRO:CD	2.14	0.77
1:C:253:TYR:HA	1:C:313:PHE:CE2	2.19	0.77
1:D:197:ILE:HB	1:D:198:PRO:HD3	1.65	0.77
1:D:119:PRO:O	1:D:193:TYR:HB3	1.85	0.76
1:E:147:LYS:C	1:E:149:GLY:N	2.39	0.76
1:D:61:ARG:HG2	1:D:62:VAL:HG23	1.67	0.76
1:B:197:ILE:HB	1:B:198:PRO:HD3	1.65	0.76
1:B:119:PRO:O	1:B:193:TYR:HB3	1.85	0.76
1:B:77:PHE:H	1:B:84:ARG:HD3	1.51	0.76
1:C:119:PRO:O	1:C:193:TYR:HB3	1.85	0.76
1:D:314:PHE:N	1:D:314:PHE:HD1	1.84	0.76
1:E:314:PHE:HD1	1:E:314:PHE:N	1.84	0.76
1:A:61:ARG:HG2	1:A:62:VAL:HG23	1.68	0.76
1:E:119:PRO:O	1:E:193:TYR:HB3	1.85	0.76
1:A:119:PRO:O	1:A:193:TYR:HB3	1.85	0.75
1:A:13:GLU:HB3	1:A:14:PRO:CD	2.14	0.75
1:D:77:PHE:H	1:D:84:ARG:HD3	1.51	0.75
1:D:78:VAL:HG22	1:D:130:ILE:HG12	1.68	0.75
1:A:314:PHE:HD1	1:A:314:PHE:N	1.84	0.75
1:C:314:PHE:HD1	1:C:314:PHE:N	1.84	0.75
1:A:77:PHE:H	1:A:84:ARG:HD3	1.51	0.75
1:B:314:PHE:N	1:B:314:PHE:HD1	1.84	0.75
1:E:13:GLU:HB3	1:E:14:PRO:CD	2.14	0.74
1:A:78:VAL:HG22	1:A:130:ILE:HG12	1.68	0.74
1:E:253:TYR:HA	1:E:313:PHE:HE2	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:253:TYR:HA	1:C:313:PHE:HE2	1.52	0.74
1:B:61:ARG:HG2	1:B:62:VAL:HG23	1.68	0.74
1:E:78:VAL:HG22	1:E:130:ILE:HG12	1.68	0.74
1:E:61:ARG:HG2	1:E:62:VAL:HG23	1.68	0.74
1:E:77:PHE:H	1:E:84:ARG:HD3	1.51	0.74
1:C:61:ARG:HG2	1:C:62:VAL:HG23	1.68	0.73
1:D:253:TYR:HA	1:D:313:PHE:HE2	1.52	0.73
1:B:253:TYR:HA	1:B:313:PHE:HE2	1.52	0.73
1:C:77:PHE:H	1:C:84:ARG:HD3	1.51	0.73
1:B:147:LYS:C	1:B:149:GLY:N	2.40	0.73
1:B:78:VAL:HG22	1:B:130:ILE:HG12	1.68	0.73
1:C:13:GLU:OE1	1:C:14:PRO:HD3	1.89	0.73
1:E:314:PHE:CD1	1:E:314:PHE:N	2.57	0.73
1:A:253:TYR:HA	1:A:313:PHE:HE2	1.52	0.73
1:B:13:GLU:OE1	1:B:14:PRO:HD3	1.89	0.72
1:D:13:GLU:OE1	1:D:14:PRO:HD3	1.89	0.72
1:C:78:VAL:HG22	1:C:130:ILE:HG12	1.68	0.72
1:E:13:GLU:OE1	1:E:14:PRO:HD3	1.89	0.72
1:B:173:PHE:HZ	1:B:182:LYS:HE3	1.54	0.72
1:C:173:PHE:HZ	1:C:182:LYS:HE3	1.54	0.72
1:D:173:PHE:HZ	1:D:182:LYS:HE3	1.54	0.72
1:B:267:VAL:HG23	1:B:298:PHE:CZ	2.25	0.72
1:A:13:GLU:OE1	1:A:14:PRO:HD3	1.89	0.72
1:A:173:PHE:HZ	1:A:182:LYS:HE3	1.54	0.72
1:B:79:ASN:H	1:B:79:ASN:HD22	1.38	0.71
1:C:79:ASN:HD22	1:C:79:ASN:H	1.38	0.71
1:A:267:VAL:HG23	1:A:298:PHE:CZ	2.25	0.71
1:E:173:PHE:HZ	1:E:182:LYS:HE3	1.54	0.71
1:D:267:VAL:HG23	1:D:298:PHE:CZ	2.25	0.71
1:C:267:VAL:HG23	1:C:298:PHE:CZ	2.25	0.71
1:B:76:ARG:NH2	1:B:130:ILE:HD12	2.06	0.71
1:E:267:VAL:HG23	1:E:298:PHE:CZ	2.25	0.71
1:A:314:PHE:CD1	1:A:314:PHE:N	2.57	0.70
1:C:76:ARG:NH2	1:C:130:ILE:HD12	2.06	0.70
1:C:314:PHE:CD1	1:C:314:PHE:N	2.57	0.70
1:D:79:ASN:HD22	1:D:79:ASN:H	1.38	0.70
1:E:76:ARG:NH2	1:E:130:ILE:HD12	2.06	0.70
1:D:76:ARG:NH2	1:D:130:ILE:HD12	2.06	0.70
1:A:147:LYS:C	1:A:149:GLY:N	2.40	0.69
1:D:314:PHE:N	1:D:314:PHE:CD1	2.57	0.69
1:B:314:PHE:N	1:B:314:PHE:CD1	2.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ASN:HD22	1:A:79:ASN:H	1.38	0.69
1:D:257:ILE:HG22	1:D:309:LEU:HD23	1.75	0.69
1:A:286:ARG:HH11	1:A:286:ARG:HG2	1.58	0.69
1:C:286:ARG:HG2	1:C:286:ARG:HH11	1.58	0.69
1:E:49:ARG:HH11	1:E:49:ARG:HB3	1.58	0.69
1:A:257:ILE:HG22	1:A:309:LEU:HD23	1.75	0.69
1:B:286:ARG:HH11	1:B:286:ARG:HG2	1.58	0.69
1:A:76:ARG:NH2	1:A:130:ILE:HD12	2.06	0.69
1:A:49:ARG:HH11	1:A:49:ARG:HB3	1.58	0.69
1:E:147:LYS:O	1:E:149:GLY:N	2.24	0.69
1:C:147:LYS:C	1:C:149:GLY:N	2.40	0.69
1:E:286:ARG:HH11	1:E:286:ARG:HG2	1.58	0.69
1:D:147:LYS:O	1:D:149:GLY:N	2.26	0.69
1:C:22:TYR:CD1	1:C:149:GLY:HA2	2.28	0.69
1:E:79:ASN:HD22	1:E:79:ASN:H	1.38	0.69
1:C:49:ARG:HH11	1:C:49:ARG:HB3	1.58	0.69
1:D:283:GLN:CG	1:D:283:GLN:O	2.30	0.68
1:B:22:TYR:CD1	1:B:149:GLY:HA2	2.28	0.68
1:C:283:GLN:HE21	1:C:286:ARG:HB2	1.58	0.68
1:E:257:ILE:HG22	1:E:309:LEU:HD23	1.75	0.68
1:E:283:GLN:HE21	1:E:286:ARG:HB2	1.58	0.68
1:A:283:GLN:HE21	1:A:286:ARG:HB2	1.58	0.68
1:C:257:ILE:HG22	1:C:309:LEU:HD23	1.75	0.68
1:B:49:ARG:HB3	1:B:49:ARG:HH11	1.58	0.68
1:D:286:ARG:HG2	1:D:286:ARG:HH11	1.58	0.68
1:C:147:LYS:O	1:C:149:GLY:N	2.26	0.68
1:B:147:LYS:O	1:B:149:GLY:N	2.26	0.68
1:A:147:LYS:O	1:A:149:GLY:N	2.26	0.68
1:D:22:TYR:CD1	1:D:149:GLY:HA2	2.28	0.68
1:B:257:ILE:HG22	1:B:309:LEU:HD23	1.75	0.68
1:D:283:GLN:HE21	1:D:286:ARG:HB2	1.58	0.67
1:A:22:TYR:CD1	1:A:149:GLY:HA2	2.28	0.67
1:A:283:GLN:NE2	1:A:286:ARG:HB2	2.10	0.67
1:D:245:LEU:HD12	1:D:246:PRO:HD2	1.77	0.67
1:D:283:GLN:NE2	1:D:286:ARG:HB2	2.10	0.66
1:B:283:GLN:NE2	1:B:286:ARG:HB2	2.10	0.66
1:D:49:ARG:HH11	1:D:49:ARG:HB3	1.58	0.66
1:C:227:VAL:HG11	1:C:269:VAL:HG23	1.77	0.66
1:B:227:VAL:HG11	1:B:269:VAL:HG23	1.77	0.66
1:E:245:LEU:HD12	1:E:246:PRO:HD2	1.77	0.66
1:C:245:LEU:HD12	1:C:246:PRO:HD2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:283:GLN:NE2	1:E:286:ARG:HB2	2.10	0.66
1:E:227:VAL:HG11	1:E:269:VAL:HG23	1.77	0.66
1:A:245:LEU:HD12	1:A:246:PRO:HD2	1.77	0.66
1:B:245:LEU:HD12	1:B:246:PRO:HD2	1.77	0.66
1:B:283:GLN:HE21	1:B:286:ARG:HB2	1.58	0.65
1:A:157:THR:CG2	1:B:34:GLU:OE1	2.44	0.65
1:C:283:GLN:NE2	1:C:286:ARG:HB2	2.10	0.65
1:E:128:TYR:O	1:E:129:LEU:HB2	1.97	0.65
1:E:278:LEU:CD2	1:E:286:ARG:HB3	2.27	0.65
1:D:227:VAL:HG11	1:D:269:VAL:HG23	1.77	0.65
1:A:227:VAL:CG1	1:A:269:VAL:HG23	2.27	0.65
1:A:227:VAL:HG11	1:A:269:VAL:HG23	1.77	0.65
1:D:278:LEU:CD2	1:D:286:ARG:HB3	2.26	0.64
1:C:278:LEU:CD2	1:C:286:ARG:HB3	2.26	0.64
1:E:283:GLN:O	1:E:283:GLN:CG	2.30	0.64
1:D:147:LYS:C	1:D:149:GLY:N	2.40	0.64
1:C:227:VAL:CG1	1:C:269:VAL:HG23	2.27	0.64
1:D:227:VAL:CG1	1:D:269:VAL:HG23	2.27	0.64
1:D:141:LEU:HD23	1:D:142:ALA:H	1.62	0.64
1:B:278:LEU:CD2	1:B:286:ARG:HB3	2.27	0.64
1:B:227:VAL:CG1	1:B:269:VAL:HG23	2.27	0.64
1:A:278:LEU:CD2	1:A:286:ARG:HB3	2.26	0.64
1:C:128:TYR:O	1:C:129:LEU:HB2	1.97	0.64
1:E:227:VAL:CG1	1:E:269:VAL:HG23	2.27	0.64
1:A:141:LEU:HD23	1:A:142:ALA:H	1.62	0.63
1:E:141:LEU:HD23	1:E:142:ALA:H	1.62	0.63
1:C:141:LEU:HD23	1:C:142:ALA:H	1.62	0.63
1:B:141:LEU:HD23	1:B:142:ALA:H	1.62	0.63
1:E:22:TYR:CD1	1:E:149:GLY:HA2	2.32	0.63
1:B:128:TYR:O	1:B:129:LEU:HB2	1.97	0.63
1:A:128:TYR:O	1:A:129:LEU:HB2	1.97	0.63
1:A:155:PHE:CE1	1:B:112:PRO:HB3	2.33	0.62
1:B:79:ASN:H	1:B:79:ASN:ND2	1.98	0.62
1:C:286:ARG:HG2	1:C:286:ARG:NH1	2.14	0.62
1:D:128:TYR:O	1:D:129:LEU:HB2	1.97	0.62
1:B:115:PHE:O	1:B:252:THR:HG22	2.00	0.62
1:D:147:LYS:O	1:D:147:LYS:HG2	2.00	0.62
1:B:286:ARG:NH1	1:B:286:ARG:HG2	2.14	0.62
1:A:157:THR:HG21	1:B:34:GLU:OE1	2.00	0.62
1:B:242:GLU:O	1:B:242:GLU:HG2	2.00	0.62
1:C:79:ASN:H	1:C:79:ASN:ND2	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:PHE:O	1:C:252:THR:HG22	2.00	0.61
1:D:242:GLU:O	1:D:242:GLU:HG2	2.00	0.61
1:E:286:ARG:HG2	1:E:286:ARG:NH1	2.14	0.61
1:A:242:GLU:O	1:A:242:GLU:HG2	2.00	0.61
1:E:147:LYS:O	1:E:147:LYS:HG2	2.00	0.61
1:E:84:ARG:CB	1:E:84:ARG:HH11	2.14	0.61
1:B:49:ARG:HB3	1:B:49:ARG:NH1	2.15	0.61
1:A:15:LEU:HD11	1:A:46:TRP:HB2	1.83	0.61
1:A:115:PHE:O	1:A:252:THR:HG22	2.00	0.61
1:A:286:ARG:HG2	1:A:286:ARG:NH1	2.14	0.61
1:A:147:LYS:O	1:A:147:LYS:HG2	2.00	0.61
1:E:115:PHE:O	1:E:252:THR:HG22	2.00	0.61
1:E:15:LEU:HD11	1:E:46:TRP:HB2	1.83	0.61
1:C:84:ARG:CB	1:C:84:ARG:HH11	2.14	0.61
1:E:49:ARG:NH1	1:E:49:ARG:HB3	2.15	0.61
1:B:147:LYS:HG2	1:B:147:LYS:O	2.00	0.61
1:D:131:VAL:HG11	1:D:140:VAL:HG13	1.83	0.61
1:D:79:ASN:ND2	1:D:79:ASN:H	1.98	0.61
1:A:49:ARG:NH1	1:A:49:ARG:HB3	2.15	0.61
1:E:242:GLU:HG2	1:E:242:GLU:O	2.00	0.61
1:E:79:ASN:ND2	1:E:79:ASN:H	1.98	0.61
1:D:115:PHE:O	1:D:252:THR:HG22	2.00	0.61
1:C:147:LYS:O	1:C:147:LYS:HG2	2.00	0.61
1:B:84:ARG:CB	1:B:84:ARG:HH11	2.14	0.61
1:D:49:ARG:NH1	1:D:49:ARG:HB3	2.16	0.61
1:D:15:LEU:HD11	1:D:46:TRP:HB2	1.83	0.61
1:A:79:ASN:ND2	1:A:79:ASN:H	1.98	0.60
1:B:15:LEU:HD11	1:B:46:TRP:HB2	1.83	0.60
1:C:242:GLU:HG2	1:C:242:GLU:O	2.00	0.60
1:A:274:VAL:C	1:A:276:HIS:H	2.04	0.60
1:D:286:ARG:HG2	1:D:286:ARG:NH1	2.14	0.60
1:A:84:ARG:HH11	1:A:84:ARG:CB	2.14	0.60
1:C:131:VAL:HG11	1:C:140:VAL:HG13	1.83	0.60
1:C:15:LEU:HD11	1:C:46:TRP:HB2	1.83	0.60
1:C:274:VAL:C	1:C:276:HIS:H	2.04	0.60
1:B:23:LEU:HA	1:B:40:ALA:HB2	1.83	0.60
1:A:131:VAL:HG11	1:A:140:VAL:HG13	1.83	0.60
1:E:274:VAL:C	1:E:276:HIS:H	2.04	0.60
1:D:274:VAL:C	1:D:276:HIS:H	2.04	0.60
1:D:23:LEU:HA	1:D:40:ALA:HB2	1.83	0.60
1:B:274:VAL:C	1:B:276:HIS:H	2.04	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:ARG:NH1	1:C:49:ARG:HB3	2.15	0.60
1:D:84:ARG:CB	1:D:84:ARG:HH11	2.14	0.59
1:E:131:VAL:HG11	1:E:140:VAL:HG13	1.83	0.59
1:A:23:LEU:HA	1:A:40:ALA:HB2	1.83	0.59
1:B:131:VAL:HG11	1:B:140:VAL:HG13	1.82	0.59
1:B:298:PHE:HB2	1:B:299:PRO:HD3	1.84	0.59
1:D:298:PHE:HB2	1:D:299:PRO:HD3	1.84	0.59
1:E:23:LEU:HA	1:E:40:ALA:HB2	1.83	0.59
1:C:23:LEU:HA	1:C:40:ALA:HB2	1.83	0.59
1:C:54:ASP:HB2	1:C:57:ARG:HG3	1.85	0.59
1:A:298:PHE:HB2	1:A:299:PRO:HD3	1.84	0.59
1:B:283:GLN:O	1:B:283:GLN:CG	2.30	0.59
1:C:151:ASN:O	1:C:154:VAL:HG22	2.03	0.59
1:D:151:ASN:O	1:D:154:VAL:HG22	2.03	0.59
1:C:267:VAL:HG23	1:C:298:PHE:HZ	1.68	0.59
1:E:151:ASN:O	1:E:154:VAL:HG22	2.03	0.58
1:C:298:PHE:HB2	1:C:299:PRO:HD3	1.84	0.58
1:E:298:PHE:HB2	1:E:299:PRO:HD3	1.84	0.58
1:D:84:ARG:NH1	1:D:84:ARG:HB2	2.19	0.58
1:A:84:ARG:HB2	1:A:84:ARG:NH1	2.19	0.58
1:D:254:THR:O	1:D:258:ILE:HB	2.04	0.58
1:B:254:THR:O	1:B:258:ILE:HB	2.04	0.58
1:C:84:ARG:NH1	1:C:84:ARG:HB2	2.19	0.58
1:E:22:TYR:HA	1:E:149:GLY:HA2	1.86	0.58
1:E:267:VAL:HG23	1:E:298:PHE:HZ	1.68	0.58
1:B:44:LEU:HB2	1:B:101:TYR:HB3	1.86	0.58
1:A:151:ASN:O	1:A:154:VAL:HG22	2.03	0.58
1:D:54:ASP:HB2	1:D:57:ARG:HG3	1.85	0.58
1:E:254:THR:O	1:E:258:ILE:HB	2.04	0.58
1:E:141:LEU:HD23	1:E:142:ALA:N	2.19	0.58
1:E:44:LEU:HB2	1:E:101:TYR:HB3	1.86	0.58
1:B:84:ARG:NH1	1:B:84:ARG:HB2	2.19	0.58
1:C:141:LEU:HD23	1:C:142:ALA:N	2.19	0.58
1:B:141:LEU:HD23	1:B:142:ALA:N	2.19	0.58
1:A:44:LEU:HB2	1:A:101:TYR:HB3	1.86	0.58
1:D:89:VAL:CG1	1:D:102:LEU:HD23	2.34	0.58
1:B:89:VAL:CG1	1:B:102:LEU:HD23	2.34	0.58
1:A:89:VAL:CG1	1:A:102:LEU:HD23	2.34	0.57
1:C:254:THR:O	1:C:258:ILE:HB	2.04	0.57
1:E:89:VAL:CG1	1:E:102:LEU:HD23	2.34	0.57
1:B:267:VAL:HG23	1:B:298:PHE:HZ	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:141:LEU:HD23	1:D:142:ALA:N	2.19	0.57
1:A:141:LEU:HD23	1:A:142:ALA:N	2.19	0.57
1:B:151:ASN:O	1:B:154:VAL:HG22	2.03	0.57
1:B:54:ASP:HB2	1:B:57:ARG:HG3	1.85	0.57
1:E:84:ARG:HB2	1:E:84:ARG:NH1	2.19	0.57
1:C:89:VAL:CG1	1:C:102:LEU:HD23	2.34	0.57
1:C:159:TRP:CE3	1:C:189:ILE:HD12	2.39	0.57
1:D:159:TRP:CE3	1:D:189:ILE:HD12	2.40	0.57
1:A:202:LEU:HB2	1:A:203:PRO:HD3	1.87	0.57
1:A:254:THR:O	1:A:258:ILE:HB	2.04	0.57
1:D:202:LEU:HB2	1:D:203:PRO:HD3	1.87	0.57
1:B:202:LEU:HB2	1:B:203:PRO:HD3	1.87	0.57
1:C:44:LEU:HB2	1:C:101:TYR:HB3	1.86	0.57
1:A:54:ASP:HB2	1:A:57:ARG:HG3	1.85	0.57
1:E:54:ASP:HB2	1:E:57:ARG:HG3	1.84	0.57
1:B:159:TRP:CE3	1:B:189:ILE:HD12	2.40	0.57
1:E:159:TRP:CE3	1:E:189:ILE:HD12	2.40	0.57
1:A:267:VAL:HG23	1:A:298:PHE:HZ	1.68	0.57
1:B:47:LYS:HD2	1:B:49:ARG:NH2	2.20	0.57
1:D:44:LEU:HB2	1:D:101:TYR:HB3	1.86	0.57
1:E:149:GLY:O	1:E:150:LYS:HB2	2.05	0.56
1:A:240:LEU:HD22	1:B:239:ILE:HG12	1.87	0.56
1:A:298:PHE:CB	1:A:299:PRO:HD3	2.35	0.56
1:C:75:ILE:HD13	1:C:131:VAL:HB	1.87	0.56
1:A:159:TRP:CE3	1:A:189:ILE:HD12	2.40	0.56
1:C:202:LEU:HB2	1:C:203:PRO:HD3	1.87	0.56
1:D:47:LYS:HD2	1:D:49:ARG:NH2	2.20	0.56
1:B:298:PHE:CB	1:B:299:PRO:HD3	2.35	0.56
1:D:298:PHE:CB	1:D:299:PRO:HD3	2.36	0.56
1:E:75:ILE:HD13	1:E:131:VAL:HB	1.87	0.56
1:C:286:ARG:O	1:C:289:SER:HB3	2.06	0.56
1:A:47:LYS:HD2	1:A:49:ARG:NH2	2.20	0.56
1:C:120:PHE:CE2	1:C:193:TYR:CD2	2.94	0.56
1:B:75:ILE:HD13	1:B:131:VAL:HB	1.87	0.56
1:C:47:LYS:HD2	1:C:49:ARG:NH2	2.20	0.56
1:E:202:LEU:HB2	1:E:203:PRO:HD3	1.87	0.56
1:A:76:ARG:NH2	1:A:130:ILE:CD1	2.69	0.56
1:E:47:LYS:HD2	1:E:49:ARG:NH2	2.20	0.56
1:B:286:ARG:O	1:B:289:SER:HB3	2.06	0.55
1:E:286:ARG:O	1:E:289:SER:HB3	2.06	0.55
1:C:76:ARG:NH2	1:C:130:ILE:CD1	2.69	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:ARG:O	1:A:289:SER:HB3	2.06	0.55
1:D:286:ARG:O	1:D:289:SER:HB3	2.06	0.55
1:E:76:ARG:NH2	1:E:130:ILE:CD1	2.69	0.55
1:D:120:PHE:CE2	1:D:193:TYR:CD2	2.95	0.55
1:B:76:ARG:NH2	1:B:130:ILE:CD1	2.69	0.55
1:E:298:PHE:CB	1:E:299:PRO:HD3	2.36	0.55
1:D:75:ILE:HD13	1:D:131:VAL:HB	1.88	0.55
1:A:53:PHE:CE2	1:A:94:SER:C	2.80	0.55
1:C:298:PHE:CB	1:C:299:PRO:HD3	2.36	0.55
1:E:222:ALA:O	1:E:226:LEU:HB2	2.07	0.55
1:B:65:TYR:CD2	1:B:70:ILE:HD11	2.42	0.55
1:A:75:ILE:HD13	1:A:131:VAL:HB	1.87	0.55
1:C:222:ALA:O	1:C:226:LEU:HB2	2.07	0.55
1:D:222:ALA:O	1:D:226:LEU:HB2	2.07	0.55
1:A:65:TYR:CD2	1:A:70:ILE:HD11	2.42	0.55
1:B:120:PHE:CE2	1:B:193:TYR:CD2	2.94	0.55
1:A:120:PHE:CE2	1:A:193:TYR:CD2	2.94	0.55
1:A:200:ILE:HD11	1:A:240:LEU:HD23	1.89	0.55
1:D:76:ARG:NH2	1:D:130:ILE:CD1	2.69	0.55
1:A:229:SER:CB	1:B:228:VAL:HG11	2.37	0.55
1:B:197:ILE:CB	1:B:198:PRO:HD3	2.37	0.55
1:D:215:PHE:HB2	1:D:216:TRP:CZ3	2.42	0.55
1:C:215:PHE:HB2	1:C:216:TRP:CZ3	2.42	0.55
1:D:65:TYR:CD2	1:D:70:ILE:HD11	2.42	0.55
1:E:65:TYR:CD2	1:E:70:ILE:HD11	2.42	0.55
1:A:215:PHE:HB2	1:A:216:TRP:CZ3	2.42	0.54
1:C:29:LEU:HB2	1:C:156:LEU:HD11	1.90	0.54
1:E:29:LEU:HB2	1:E:156:LEU:HD11	1.89	0.54
1:E:120:PHE:CE2	1:E:193:TYR:CD2	2.94	0.54
1:B:200:ILE:HD11	1:B:240:LEU:HD23	1.89	0.54
1:C:65:TYR:CD2	1:C:70:ILE:HD11	2.42	0.54
1:C:197:ILE:CB	1:C:198:PRO:HD3	2.37	0.54
1:D:155:PHE:CE1	1:E:112:PRO:HB3	2.41	0.54
1:B:222:ALA:O	1:B:226:LEU:HB2	2.07	0.54
1:B:215:PHE:HB2	1:B:216:TRP:CZ3	2.42	0.54
1:D:149:GLY:O	1:D:164:PHE:HD1	1.91	0.54
1:D:267:VAL:HG23	1:D:298:PHE:HZ	1.68	0.54
1:E:89:VAL:HG11	1:E:102:LEU:HD23	1.90	0.54
1:A:222:ALA:O	1:A:226:LEU:HB2	2.07	0.54
1:C:149:GLY:O	1:C:164:PHE:HD1	1.91	0.54
1:B:149:GLY:O	1:B:164:PHE:HD1	1.91	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:215:PHE:HB2	1:E:216:TRP:CZ3	2.42	0.54
1:A:29:LEU:HB2	1:A:156:LEU:HD11	1.89	0.54
1:A:197:ILE:CB	1:A:198:PRO:HD3	2.37	0.54
1:A:191:ARG:HG3	1:A:192:GLN:N	2.23	0.54
1:E:191:ARG:HG3	1:E:192:GLN:N	2.23	0.54
1:A:149:GLY:O	1:A:164:PHE:HD1	1.91	0.54
1:D:29:LEU:HB2	1:D:156:LEU:HD11	1.90	0.54
1:D:89:VAL:HG11	1:D:102:LEU:HD23	1.90	0.53
1:A:276:HIS:C	1:A:278:LEU:H	2.12	0.53
1:A:13:GLU:CB	1:A:14:PRO:CD	2.86	0.53
1:D:200:ILE:HD11	1:D:240:LEU:HD23	1.89	0.53
1:C:200:ILE:HD11	1:C:240:LEU:HD23	1.89	0.53
1:B:276:HIS:C	1:B:278:LEU:H	2.12	0.53
1:D:197:ILE:CB	1:D:198:PRO:HD3	2.37	0.53
1:B:29:LEU:HB2	1:B:156:LEU:HD11	1.89	0.53
1:B:191:ARG:HG3	1:B:192:GLN:N	2.23	0.53
1:E:200:ILE:HD11	1:E:240:LEU:HD23	1.89	0.53
1:D:276:HIS:C	1:D:278:LEU:H	2.12	0.53
1:B:89:VAL:HG11	1:B:102:LEU:HD23	1.90	0.53
1:C:191:ARG:HG3	1:C:192:GLN:N	2.23	0.53
1:C:89:VAL:HG11	1:C:102:LEU:HD23	1.90	0.53
1:C:276:HIS:C	1:C:278:LEU:H	2.12	0.53
1:E:197:ILE:CB	1:E:198:PRO:HD3	2.37	0.53
1:D:191:ARG:HG3	1:D:192:GLN:N	2.23	0.53
1:E:276:HIS:C	1:E:278:LEU:H	2.12	0.53
1:D:218:THR:HG22	1:D:279:LYS:HE2	1.91	0.53
1:E:128:TYR:O	1:E:183:LEU:O	2.27	0.53
1:D:267:VAL:HA	1:D:270:ILE:HB	1.92	0.52
1:B:218:THR:HG22	1:B:279:LYS:HE2	1.91	0.52
1:A:89:VAL:HG11	1:A:102:LEU:HD23	1.90	0.52
1:C:218:THR:HG22	1:C:279:LYS:HE2	1.91	0.52
1:E:13:GLU:CB	1:E:14:PRO:CD	2.86	0.52
1:E:253:TYR:HD1	1:E:313:PHE:CD2	2.28	0.52
1:A:218:THR:HG22	1:A:279:LYS:HE2	1.91	0.52
1:C:207:ILE:HD11	1:C:234:HIS:HB2	1.92	0.51
1:D:157:THR:CG2	1:E:34:GLU:OE1	2.58	0.51
1:D:22:TYR:HA	1:D:149:GLY:HA2	1.91	0.51
1:D:13:GLU:CB	1:D:14:PRO:CD	2.86	0.51
1:A:267:VAL:HA	1:A:270:ILE:HB	1.92	0.51
1:C:267:VAL:HA	1:C:270:ILE:HB	1.91	0.51
1:C:37:LYS:HG2	1:C:108:ARG:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:179:LEU:C	1:C:179:LEU:HD12	2.31	0.51
1:C:253:TYR:HD1	1:C:313:PHE:CD2	2.28	0.51
1:B:207:ILE:HD11	1:B:234:HIS:HB2	1.92	0.51
1:B:253:TYR:HD1	1:B:313:PHE:CD2	2.28	0.51
1:C:217:SER:HG	1:D:220:TYR:HE2	1.52	0.51
1:A:207:ILE:HD11	1:A:234:HIS:HB2	1.92	0.51
1:A:253:TYR:HD1	1:A:313:PHE:CD2	2.28	0.51
1:B:37:LYS:HG2	1:B:108:ARG:HB2	1.92	0.51
1:C:84:ARG:NH1	1:C:84:ARG:CB	2.74	0.51
1:B:267:VAL:HA	1:B:270:ILE:HB	1.92	0.51
1:E:218:THR:HG22	1:E:279:LYS:HE2	1.91	0.51
1:A:84:ARG:NH1	1:A:84:ARG:CB	2.74	0.51
1:B:13:GLU:CB	1:B:14:PRO:CD	2.86	0.50
1:D:253:TYR:HD1	1:D:313:PHE:CD2	2.28	0.50
1:D:84:ARG:NH1	1:D:84:ARG:CB	2.74	0.50
1:E:207:ILE:HD11	1:E:234:HIS:HB2	1.92	0.50
1:E:179:LEU:HD12	1:E:179:LEU:C	2.31	0.50
1:E:65:TYR:CG	1:E:70:ILE:HD11	2.47	0.50
1:E:37:LYS:HG2	1:E:108:ARG:HB2	1.93	0.50
1:B:179:LEU:HD12	1:B:179:LEU:C	2.31	0.50
1:B:65:TYR:CG	1:B:70:ILE:HD11	2.47	0.50
1:A:65:TYR:CG	1:A:70:ILE:HD11	2.47	0.50
1:D:37:LYS:HG2	1:D:108:ARG:HB2	1.92	0.50
1:E:267:VAL:HA	1:E:270:ILE:HB	1.92	0.50
1:A:37:LYS:HG2	1:A:108:ARG:HB2	1.92	0.50
1:D:179:LEU:C	1:D:179:LEU:HD12	2.31	0.50
1:D:207:ILE:HD11	1:D:234:HIS:HB2	1.92	0.50
1:A:179:LEU:HD12	1:A:179:LEU:C	2.31	0.50
1:A:22:TYR:HA	1:A:149:GLY:HA2	1.91	0.50
1:E:84:ARG:CB	1:E:84:ARG:NH1	2.74	0.50
1:C:222:ALA:HB2	1:D:221[B]:GLU:HG2	1.91	0.50
1:B:94:SER:OG	1:B:95:PRO:HD2	2.12	0.50
1:C:53:PHE:CE2	1:C:94:SER:C	2.85	0.50
1:C:65:TYR:CG	1:C:70:ILE:HD11	2.47	0.50
1:A:283:GLN:N	1:A:284:PRO:HD3	2.27	0.50
1:C:261:ILE:O	1:C:265:TYR:HD1	1.95	0.50
1:C:13:GLU:CB	1:C:14:PRO:CD	2.86	0.50
1:D:157:THR:HG21	1:E:34:GLU:OE1	2.12	0.50
1:D:283:GLN:N	1:D:284:PRO:HD3	2.27	0.49
1:D:53:PHE:CE2	1:D:94:SER:C	2.85	0.49
1:C:215:PHE:HB2	1:C:216:TRP:CE3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:TYR:CB	1:B:110:LEU:HD11	2.42	0.49
1:B:283:GLN:N	1:B:284:PRO:HD3	2.27	0.49
1:E:283:GLN:N	1:E:284:PRO:HD3	2.27	0.49
1:D:94:SER:OG	1:D:95:PRO:HD2	2.12	0.49
1:B:84:ARG:CB	1:B:84:ARG:NH1	2.74	0.49
1:C:94:SER:OG	1:C:95:PRO:HD2	2.12	0.49
1:B:261:ILE:O	1:B:265:TYR:HD1	1.95	0.49
1:D:215:PHE:HB2	1:D:216:TRP:CE3	2.47	0.49
1:D:65:TYR:CG	1:D:70:ILE:HD11	2.47	0.49
1:C:217:SER:OG	1:D:220:TYR:HE2	1.93	0.49
1:A:173:PHE:CZ	1:A:182:LYS:HE3	2.43	0.49
1:B:194:PHE:C	1:B:196:TYR:N	2.65	0.49
1:A:128:TYR:O	1:A:183:LEU:O	2.31	0.49
1:C:53:PHE:O	1:C:54:ASP:C	2.51	0.49
1:D:241:VAL:C	1:D:243:THR:H	2.16	0.49
1:C:22:TYR:HA	1:C:149:GLY:HA2	1.91	0.49
1:D:194:PHE:C	1:D:196:TYR:N	2.65	0.49
1:B:215:PHE:HB2	1:B:216:TRP:CE3	2.47	0.49
1:E:215:PHE:HB2	1:E:216:TRP:CE3	2.47	0.49
1:C:256:ALA:HB1	1:C:309:LEU:HD21	1.95	0.49
1:D:261:ILE:O	1:D:265:TYR:HD1	1.95	0.49
1:C:241:VAL:C	1:C:243:THR:H	2.16	0.49
1:E:173:PHE:CZ	1:E:182:LYS:HE3	2.43	0.49
1:C:194:PHE:C	1:C:196:TYR:N	2.65	0.49
1:E:147:LYS:HE2	1:E:165:THR:HA	1.95	0.49
1:A:94:SER:OG	1:A:95:PRO:HD2	2.12	0.49
1:C:215:PHE:HZ	1:C:298:PHE:CE1	2.31	0.49
1:E:94:SER:OG	1:E:95:PRO:HD2	2.12	0.49
1:D:147:LYS:HE2	1:D:165:THR:HA	1.95	0.49
1:A:53:PHE:CZ	1:A:95:PRO:N	2.81	0.49
1:B:128:TYR:O	1:B:183:LEU:O	2.31	0.49
1:C:173:PHE:CZ	1:C:182:LYS:HE3	2.43	0.49
1:B:215:PHE:HZ	1:B:298:PHE:CE1	2.31	0.49
1:E:256:ALA:HB1	1:E:309:LEU:HD21	1.95	0.49
1:E:70:ILE:HG22	1:E:71:TRP:N	2.28	0.49
1:A:215:PHE:HB2	1:A:216:TRP:CE3	2.47	0.49
1:A:256:ALA:HB1	1:A:309:LEU:HD21	1.94	0.49
1:C:70:ILE:HG22	1:C:71:TRP:N	2.28	0.49
1:A:241:VAL:C	1:A:243:THR:H	2.16	0.49
1:B:70:ILE:HG22	1:B:71:TRP:N	2.28	0.48
1:C:283:GLN:N	1:C:284:PRO:HD3	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:LYS:HE2	1:B:165:THR:HA	1.95	0.48
1:A:53:PHE:O	1:A:54:ASP:C	2.50	0.48
1:A:194:PHE:C	1:A:196:TYR:N	2.65	0.48
1:D:256:ALA:HB1	1:D:309:LEU:HD21	1.95	0.48
1:B:36:PHE:CE1	1:B:109:VAL:HB	2.49	0.48
1:C:48:ASP:O	1:C:51:LEU:HD23	2.14	0.48
1:C:36:PHE:CE1	1:C:109:VAL:HB	2.48	0.48
1:A:104:ARG:HD2	1:B:76:ARG:HH11	1.78	0.48
1:D:215:PHE:HZ	1:D:298:PHE:CE1	2.31	0.48
1:E:261:ILE:O	1:E:265:TYR:HD1	1.95	0.48
1:D:48:ASP:O	1:D:51:LEU:HD23	2.14	0.48
1:D:128:TYR:O	1:D:183:LEU:O	2.31	0.48
1:B:256:ALA:HB1	1:B:309:LEU:HD21	1.95	0.48
1:A:221[B]:GLU:HG2	1:E:222:ALA:HB2	1.94	0.48
1:C:264:PHE:HE2	1:C:302:PHE:CA	2.26	0.48
1:D:53:PHE:O	1:D:54:ASP:C	2.50	0.48
1:A:120:PHE:HE2	1:A:193:TYR:CD2	2.32	0.48
1:A:259:PHE:CZ	1:E:202:LEU:HD12	2.49	0.48
1:A:70:ILE:HG22	1:A:71:TRP:N	2.28	0.48
1:E:48:ASP:O	1:E:51:LEU:HD23	2.14	0.48
1:A:38:VAL:HG22	1:A:39:ASN:N	2.29	0.48
1:D:264:PHE:HE2	1:D:302:PHE:CA	2.26	0.48
1:C:283:GLN:O	1:C:283:GLN:CG	2.30	0.48
1:A:147:LYS:HE2	1:A:165:THR:HA	1.95	0.48
1:D:120:PHE:HE2	1:D:193:TYR:CD2	2.32	0.48
1:E:53:PHE:O	1:E:54:ASP:C	2.52	0.48
1:B:241:VAL:C	1:B:243:THR:H	2.16	0.48
1:A:261:ILE:O	1:A:265:TYR:HD1	1.95	0.48
1:E:36:PHE:CE1	1:E:109:VAL:HB	2.49	0.48
1:C:38:VAL:HG22	1:C:39:ASN:N	2.29	0.48
1:E:241:VAL:C	1:E:243:THR:H	2.16	0.48
1:D:36:PHE:CE1	1:D:109:VAL:HB	2.48	0.48
1:E:120:PHE:HE2	1:E:193:TYR:CD2	2.32	0.48
1:A:131:VAL:CG1	1:A:140:VAL:HG13	2.44	0.48
1:A:221[A]:GLU:OE2	1:B:221[A]:GLU:CD	2.53	0.48
1:A:36:PHE:CE1	1:A:109:VAL:HB	2.48	0.48
1:D:229:SER:CB	1:E:228:VAL:HG11	2.44	0.48
1:C:147:LYS:HE2	1:C:165:THR:HA	1.95	0.48
1:E:215:PHE:HZ	1:E:298:PHE:CE1	2.31	0.48
1:B:131:VAL:CG1	1:B:140:VAL:HG13	2.44	0.48
1:E:264:PHE:HE2	1:E:302:PHE:CA	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:TYR:O	1:C:183:LEU:O	2.31	0.47
1:B:173:PHE:CZ	1:B:182:LYS:HE3	2.43	0.47
1:A:215:PHE:HZ	1:A:298:PHE:CE1	2.31	0.47
1:A:27:TYR:CG	1:B:110:LEU:HD11	2.49	0.47
1:E:194:PHE:C	1:E:196:TYR:N	2.65	0.47
1:D:149:GLY:O	1:D:150:LYS:HB2	2.14	0.47
1:A:216:TRP:CH2	1:A:295:ARG:HB3	2.49	0.47
1:D:216:TRP:CH2	1:D:295:ARG:HB3	2.49	0.47
1:B:38:VAL:HG22	1:B:39:ASN:N	2.28	0.47
1:C:157:THR:CG2	1:D:34:GLU:OE1	2.62	0.47
1:B:264:PHE:HE2	1:B:302:PHE:CA	2.26	0.47
1:E:38:VAL:HG22	1:E:39:ASN:N	2.29	0.47
1:A:149:GLY:O	1:A:150:LYS:HB2	2.14	0.47
1:D:131:VAL:CG1	1:D:140:VAL:HG13	2.44	0.47
1:E:131:VAL:CG1	1:E:140:VAL:HG13	2.44	0.47
1:D:38:VAL:HG22	1:D:39:ASN:N	2.29	0.47
1:C:120:PHE:HE2	1:C:193:TYR:CD2	2.32	0.47
1:D:70:ILE:HG22	1:D:71:TRP:N	2.28	0.47
1:B:53:PHE:O	1:B:54:ASP:C	2.53	0.47
1:A:48:ASP:O	1:A:51:LEU:HD23	2.14	0.47
1:E:216:TRP:CH2	1:E:295:ARG:HB3	2.49	0.47
1:D:81:GLU:HG3	1:D:108:ARG:HG2	1.97	0.47
1:B:48:ASP:O	1:B:51:LEU:HD23	2.14	0.47
1:A:217:SER:OG	1:B:220:TYR:CE2	2.67	0.47
1:B:149:GLY:O	1:B:150:LYS:HB2	2.14	0.47
1:B:216:TRP:CH2	1:B:295:ARG:HB3	2.49	0.47
1:A:221[B]:GLU:HB2	1:B:221[B]:GLU:OE2	2.15	0.47
1:C:149:GLY:O	1:C:150:LYS:HB2	2.14	0.47
1:C:216:TRP:CH2	1:C:295:ARG:HB3	2.50	0.47
1:A:155:PHE:CZ	1:B:112:PRO:HB3	2.50	0.47
1:A:81:GLU:HG3	1:A:108:ARG:HG2	1.97	0.47
1:A:33:ALA:O	1:A:34:GLU:HB2	2.15	0.47
1:C:33:ALA:O	1:C:34:GLU:HB2	2.15	0.47
1:A:219:SER:OG	1:A:222:ALA:HB3	2.15	0.47
1:B:219:SER:OG	1:B:222:ALA:HB3	2.15	0.47
1:A:264:PHE:HE2	1:A:302:PHE:CA	2.26	0.47
1:B:22:TYR:HA	1:B:149:GLY:HA2	1.91	0.46
1:D:173:PHE:CZ	1:D:182:LYS:HE3	2.43	0.46
1:A:34:GLU:OE1	1:E:155:PHE:CZ	2.68	0.46
1:E:147:LYS:CG	1:E:147:LYS:O	2.64	0.46
1:C:245:LEU:HD12	1:C:245:LEU:HA	1.77	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:131:VAL:CG1	1:C:140:VAL:HG13	2.44	0.46
1:A:222:ALA:HB2	1:B:221[B]:GLU:HG2	1.97	0.46
1:C:219:SER:OG	1:C:222:ALA:HB3	2.15	0.46
1:C:81:GLU:HG3	1:C:108:ARG:HG2	1.97	0.46
1:B:33:ALA:O	1:B:34:GLU:HB2	2.15	0.46
1:C:202:LEU:HD12	1:D:259:PHE:CZ	2.50	0.46
1:E:263:LEU:HD12	1:E:263:LEU:HA	1.67	0.46
1:A:274:VAL:C	1:A:276:HIS:N	2.69	0.46
1:D:291:THR:O	1:D:295:ARG:HG3	2.16	0.46
1:E:291:THR:O	1:E:295:ARG:HG3	2.16	0.46
1:C:199:ASN:O	1:C:200:ILE:HD13	2.16	0.46
1:E:199:ASN:O	1:E:200:ILE:HD13	2.16	0.46
1:C:217:SER:OG	1:D:220:TYR:CE2	2.60	0.46
1:A:27:TYR:HB3	1:B:110:LEU:HD11	1.98	0.46
1:A:210:ILE:O	1:A:213:THR:HB	2.16	0.46
1:B:210:ILE:O	1:B:213:THR:HB	2.16	0.46
1:D:84:ARG:HB3	1:D:84:ARG:HH11	1.81	0.46
1:B:291:THR:O	1:B:295:ARG:HG3	2.16	0.46
1:A:75:ILE:CD1	1:A:131:VAL:HB	2.45	0.46
1:A:199:ASN:O	1:A:200:ILE:HD13	2.16	0.46
1:C:274:VAL:C	1:C:276:HIS:N	2.69	0.46
1:D:219:SER:OG	1:D:222:ALA:HB3	2.15	0.46
1:D:33:ALA:O	1:D:34:GLU:HB2	2.15	0.46
1:A:217:SER:OG	1:B:220:TYR:HE2	1.99	0.46
1:E:75:ILE:CD1	1:E:131:VAL:HB	2.45	0.46
1:E:33:ALA:O	1:E:34:GLU:HB2	2.15	0.46
1:C:204:MET:HE3	1:C:261:ILE:HD12	1.98	0.46
1:B:120:PHE:HE2	1:B:193:TYR:CD2	2.32	0.46
1:D:314:PHE:H	1:D:314:PHE:HD1	1.62	0.46
1:E:219:SER:OG	1:E:222:ALA:HB3	2.15	0.46
1:A:229:SER:HB3	1:B:228:VAL:CG1	2.45	0.46
1:B:81:GLU:HG3	1:B:108:ARG:HG2	1.97	0.46
1:E:81:GLU:HG3	1:E:108:ARG:HG2	1.97	0.46
1:B:274:VAL:C	1:B:276:HIS:N	2.69	0.45
1:E:274:VAL:C	1:E:276:HIS:N	2.69	0.45
1:B:253:TYR:CA	1:B:313:PHE:HE2	2.27	0.45
1:E:119:PRO:HD3	1:E:254:THR:OG1	2.16	0.45
1:D:75:ILE:CD1	1:D:131:VAL:HB	2.46	0.45
1:C:75:ILE:CD1	1:C:131:VAL:HB	2.45	0.45
1:D:199:ASN:O	1:D:200:ILE:HD13	2.16	0.45
1:E:118:TYR:CE2	1:E:196:TYR:HE2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:84:ARG:HH11	1:C:84:ARG:HB3	1.81	0.45
1:C:291:THR:O	1:C:295:ARG:HG3	2.16	0.45
1:A:147:LYS:O	1:A:147:LYS:CG	2.64	0.45
1:B:79:ASN:ND2	1:B:128:TYR:HB2	2.32	0.45
1:A:291:THR:O	1:A:295:ARG:HG3	2.16	0.45
1:E:179:LEU:CD1	1:E:179:LEU:C	2.85	0.45
1:B:179:LEU:CD1	1:B:179:LEU:C	2.85	0.45
1:A:204:MET:HE3	1:A:261:ILE:HD12	1.98	0.45
1:D:119:PRO:HD3	1:D:254:THR:OG1	2.16	0.45
1:C:79:ASN:ND2	1:C:128:TYR:HB2	2.32	0.45
1:B:75:ILE:CD1	1:B:131:VAL:HB	2.45	0.45
1:B:199:ASN:O	1:B:200:ILE:HD13	2.16	0.45
1:D:179:LEU:C	1:D:179:LEU:CD1	2.85	0.45
1:D:274:VAL:C	1:D:276:HIS:N	2.69	0.45
1:B:281:GLU:O	1:B:283:GLN:N	2.43	0.45
1:D:62:VAL:HG13	1:D:93:VAL:O	2.16	0.45
1:D:77:PHE:CG	1:D:84:ARG:HD2	2.52	0.45
1:E:79:ASN:ND2	1:E:128:TYR:HB2	2.32	0.45
1:C:179:LEU:C	1:C:179:LEU:CD1	2.85	0.45
1:D:210:ILE:O	1:D:213:THR:HB	2.16	0.45
1:B:162:GLU:O	1:B:163:SER:HB3	2.17	0.45
1:B:147:LYS:CG	1:B:147:LYS:O	2.64	0.45
1:B:118:TYR:HD2	1:B:254:THR:HG1	1.64	0.45
1:A:62:VAL:HG13	1:A:93:VAL:O	2.16	0.45
1:C:275:GLN:HG2	1:C:275:GLN:O	2.17	0.45
1:E:51:LEU:N	1:E:51:LEU:HD23	2.32	0.45
1:E:210:ILE:O	1:E:213:THR:HB	2.16	0.45
1:D:147:LYS:CG	1:D:147:LYS:O	2.64	0.45
1:B:77:PHE:CG	1:B:84:ARG:HD2	2.52	0.45
1:A:259:PHE:CE1	1:E:202:LEU:HD12	2.52	0.45
1:D:51:LEU:N	1:D:51:LEU:HD23	2.32	0.45
1:E:162:GLU:O	1:E:163:SER:HB3	2.17	0.45
1:C:119:PRO:HD3	1:C:254:THR:OG1	2.16	0.45
1:A:118:TYR:CE2	1:A:196:TYR:HE2	2.35	0.45
1:B:314:PHE:H	1:B:314:PHE:HD1	1.62	0.45
1:E:77:PHE:CG	1:E:84:ARG:HD2	2.52	0.45
1:B:137:ARG:HA	1:B:137:ARG:HD3	1.61	0.45
1:B:51:LEU:N	1:B:51:LEU:HD23	2.32	0.45
1:C:147:LYS:O	1:C:147:LYS:CG	2.64	0.45
1:E:78:VAL:CG2	1:E:128:TYR:HB3	2.47	0.45
1:C:62:VAL:HG13	1:C:93:VAL:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:118:TYR:CE2	1:C:196:TYR:HE2	2.35	0.45
1:A:162:GLU:O	1:A:163:SER:HB3	2.17	0.45
1:E:195:SER:O	1:E:199:ASN:HB2	2.18	0.44
1:D:118:TYR:CE2	1:D:196:TYR:HE2	2.35	0.44
1:B:62:VAL:HG13	1:B:93:VAL:O	2.16	0.44
1:E:62:VAL:HG13	1:E:93:VAL:O	2.16	0.44
1:C:77:PHE:CG	1:C:84:ARG:HD2	2.52	0.44
1:E:275:GLN:O	1:E:275:GLN:HG2	2.17	0.44
1:A:195:SER:O	1:A:199:ASN:HB2	2.18	0.44
1:A:179:LEU:CD1	1:A:179:LEU:C	2.85	0.44
1:A:253:TYR:CA	1:A:313:PHE:HE2	2.27	0.44
1:B:118:TYR:CE2	1:B:196:TYR:HE2	2.35	0.44
1:B:119:PRO:HD3	1:B:254:THR:OG1	2.17	0.44
1:A:79:ASN:ND2	1:A:128:TYR:HB2	2.32	0.44
1:E:292:ARG:HD2	1:E:292:ARG:O	2.18	0.44
1:D:79:ASN:ND2	1:D:128:TYR:HB2	2.32	0.44
1:A:314:PHE:HD1	1:A:314:PHE:H	1.62	0.44
1:A:77:PHE:CG	1:A:84:ARG:HD2	2.52	0.44
1:C:162:GLU:O	1:C:163:SER:HB3	2.17	0.44
1:D:162:GLU:O	1:D:163:SER:HB3	2.17	0.44
1:A:104:ARG:HD2	1:B:76:ARG:NH1	2.32	0.44
1:A:51:LEU:N	1:A:51:LEU:HD23	2.32	0.44
1:C:210:ILE:O	1:C:213:THR:HB	2.16	0.44
1:A:119:PRO:HD3	1:A:254:THR:OG1	2.16	0.44
1:C:51:LEU:N	1:C:51:LEU:HD23	2.32	0.44
1:E:233:ALA:O	1:E:237:PHE:HD1	2.01	0.44
1:C:292:ARG:O	1:C:292:ARG:HD2	2.18	0.44
1:A:118:TYR:HD2	1:A:254:THR:HG1	1.66	0.44
1:C:183:LEU:HD23	1:C:183:LEU:HA	1.85	0.44
1:B:275:GLN:HG2	1:B:275:GLN:O	2.17	0.44
1:A:275:GLN:HG2	1:A:275:GLN:O	2.17	0.44
1:D:233:ALA:O	1:D:237:PHE:HD1	2.01	0.44
1:C:296:ILE:HA	1:C:296:ILE:HD13	1.66	0.44
1:E:149:GLY:O	1:E:164:PHE:HD1	2.01	0.44
1:B:159:TRP:CD2	1:B:189:ILE:HD12	2.53	0.44
1:B:84:ARG:HH11	1:B:84:ARG:HB3	1.81	0.44
1:A:155:PHE:HB3	1:A:156:LEU:H	1.65	0.44
1:C:195:SER:O	1:C:199:ASN:HB2	2.18	0.44
1:D:292:ARG:O	1:D:292:ARG:HD2	2.18	0.44
1:B:292:ARG:HD2	1:B:292:ARG:O	2.18	0.44
1:C:287:ALA:C	1:C:289:SER:H	2.22	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:22:TYR:CG	1:C:149:GLY:HA2	2.53	0.43
1:E:62:VAL:HG12	1:E:63:LYS:N	2.33	0.43
1:B:78:VAL:HG23	1:B:128:TYR:HB3	2.00	0.43
1:D:275:GLN:O	1:D:275:GLN:HG2	2.17	0.43
1:E:159:TRP:CD2	1:E:189:ILE:HD12	2.53	0.43
1:A:233:ALA:O	1:A:237:PHE:HD1	2.01	0.43
1:D:287:ALA:C	1:D:289:SER:H	2.22	0.43
1:E:287:ALA:C	1:E:289:SER:H	2.22	0.43
1:B:62:VAL:HG12	1:B:63:LYS:N	2.33	0.43
1:C:62:VAL:HG12	1:C:63:LYS:N	2.33	0.43
1:D:195:SER:O	1:D:199:ASN:HB2	2.18	0.43
1:D:204:MET:HE3	1:D:261:ILE:HD12	2.00	0.43
1:C:286:ARG:CG	1:C:286:ARG:HH11	2.29	0.43
1:E:78:VAL:HG23	1:E:128:TYR:HB3	2.00	0.43
1:A:292:ARG:HD2	1:A:292:ARG:O	2.18	0.43
1:E:84:ARG:HB3	1:E:84:ARG:HH11	1.81	0.43
1:B:287:ALA:C	1:B:289:SER:H	2.22	0.43
1:A:22:TYR:CG	1:A:149:GLY:HA2	2.53	0.43
1:A:44:LEU:HA	1:A:44:LEU:HD23	1.82	0.43
1:E:296:ILE:HA	1:E:296:ILE:HD13	1.66	0.43
1:B:233:ALA:O	1:B:237:PHE:HD1	2.01	0.43
1:B:89:VAL:HG12	1:B:102:LEU:HD23	2.01	0.43
1:E:137:ARG:HD2	1:E:179:LEU:HG	2.01	0.43
1:D:137:ARG:HA	1:D:137:ARG:HD3	1.61	0.43
1:B:22:TYR:CG	1:B:149:GLY:HA2	2.53	0.43
1:E:253:TYR:CA	1:E:313:PHE:HE2	2.27	0.43
1:C:53:PHE:CZ	1:C:95:PRO:N	2.87	0.43
1:C:233:ALA:O	1:C:237:PHE:HD1	2.01	0.43
1:D:22:TYR:CG	1:D:149:GLY:HA2	2.53	0.43
1:D:53:PHE:CZ	1:D:95:PRO:N	2.87	0.43
1:A:62:VAL:HG12	1:A:63:LYS:N	2.33	0.43
1:C:159:TRP:CD2	1:C:189:ILE:HD12	2.53	0.43
1:A:159:TRP:CD2	1:A:189:ILE:HD12	2.53	0.43
1:D:72:ILE:HA	1:D:73:PRO:HD3	1.84	0.43
1:B:134:VAL:HB	1:B:135:ASP:H	1.61	0.43
1:A:78:VAL:HG23	1:A:128:TYR:HB3	2.00	0.43
1:D:151:ASN:HA	1:D:151:ASN:HD22	1.66	0.43
1:D:89:VAL:HG12	1:D:102:LEU:HD23	2.00	0.43
1:E:89:VAL:HG12	1:E:102:LEU:HD23	2.00	0.43
1:B:195:SER:O	1:B:199:ASN:HB2	2.18	0.43
1:D:209:PHE:O	1:D:210:ILE:C	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:ASP:OD1	1:C:98:THR:HB	2.19	0.43
1:A:290:ILE:HG22	1:A:291:THR:N	2.34	0.42
1:D:137:ARG:HD2	1:D:179:LEU:HG	2.01	0.42
1:A:296:ILE:HD13	1:A:296:ILE:HA	1.66	0.42
1:A:53:PHE:CZ	1:A:93:VAL:O	2.72	0.42
1:A:84:ARG:HB3	1:A:84:ARG:HH11	1.81	0.42
1:A:216:TRP:CZ2	1:A:295:ARG:HB3	2.54	0.42
1:E:30:ASP:HB3	1:E:33:ALA:HB3	2.02	0.42
1:C:209:PHE:O	1:C:210:ILE:C	2.58	0.42
1:D:96:ASP:OD1	1:D:98:THR:HB	2.19	0.42
1:A:173:PHE:HZ	1:A:182:LYS:CE	2.29	0.42
1:D:216:TRP:CZ2	1:D:295:ARG:HB3	2.55	0.42
1:D:30:ASP:HB3	1:D:33:ALA:HB3	2.02	0.42
1:B:22:TYR:HB3	1:B:41:PHE:HB2	2.02	0.42
1:E:314:PHE:HD1	1:E:314:PHE:H	1.62	0.42
1:D:78:VAL:HG23	1:D:128:TYR:HB3	2.00	0.42
1:D:183:LEU:HA	1:D:183:LEU:HD23	1.85	0.42
1:E:216:TRP:CZ2	1:E:295:ARG:HB3	2.54	0.42
1:E:290:ILE:HG22	1:E:291:THR:N	2.34	0.42
1:C:227:VAL:HG12	1:C:269:VAL:HG23	2.01	0.42
1:B:30:ASP:HB3	1:B:33:ALA:HB3	2.02	0.42
1:A:229:SER:HB2	1:B:228:VAL:HG11	2.00	0.42
1:A:34:GLU:OE1	1:E:155:PHE:HZ	2.02	0.42
1:C:30:ASP:HB3	1:C:33:ALA:HB3	2.02	0.42
1:D:53:PHE:CZ	1:D:93:VAL:O	2.72	0.42
1:E:173:PHE:HZ	1:E:182:LYS:CE	2.29	0.42
1:B:44:LEU:HD23	1:B:44:LEU:HA	1.82	0.42
1:C:155:PHE:HB3	1:C:156:LEU:H	1.65	0.42
1:A:137:ARG:HD2	1:A:179:LEU:HG	2.01	0.42
1:B:209:PHE:O	1:B:210:ILE:C	2.58	0.42
1:E:96:ASP:OD1	1:E:98:THR:HB	2.19	0.42
1:B:72:ILE:HA	1:B:73:PRO:HD3	1.84	0.42
1:C:22:TYR:HB3	1:C:41:PHE:HB2	2.01	0.42
1:D:62:VAL:HG12	1:D:63:LYS:N	2.33	0.42
1:C:78:VAL:HG23	1:C:128:TYR:HB3	2.00	0.42
1:D:159:TRP:CD2	1:D:189:ILE:HD12	2.53	0.42
1:C:222:ALA:HB2	1:D:221[B]:GLU:HA	2.02	0.42
1:E:52:ALA:HA	1:E:95:PRO:O	2.19	0.42
1:A:209:PHE:O	1:A:210:ILE:C	2.58	0.42
1:D:123:GLN:NE2	1:D:123:GLN:HA	2.35	0.42
1:B:290:ILE:HG22	1:B:291:THR:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:216:TRP:CZ2	1:C:295:ARG:HB3	2.55	0.42
1:E:227:VAL:HG12	1:E:269:VAL:HG23	2.01	0.42
1:A:151:ASN:HA	1:A:151:ASN:HD22	1.66	0.42
1:A:287:ALA:C	1:A:289:SER:H	2.22	0.42
1:D:286:ARG:HH11	1:D:286:ARG:CG	2.29	0.42
1:B:286:ARG:HH11	1:B:286:ARG:CG	2.29	0.42
1:E:22:TYR:HB3	1:E:41:PHE:HB2	2.02	0.42
1:D:78:VAL:CG2	1:D:128:TYR:HB3	2.50	0.42
1:C:53:PHE:CZ	1:C:93:VAL:O	2.72	0.42
1:B:52:ALA:HA	1:B:95:PRO:O	2.19	0.42
1:B:312:LEU:HA	1:B:312:LEU:HD12	1.87	0.42
1:E:271:GLU:OE2	1:E:272:VAL:N	2.53	0.42
1:D:22:TYR:HB3	1:D:41:PHE:HB2	2.01	0.42
1:A:52:ALA:HA	1:A:95:PRO:O	2.20	0.42
1:D:76:ARG:HH22	1:D:130:ILE:CD1	2.33	0.42
1:B:216:TRP:CZ2	1:B:295:ARG:HB3	2.54	0.42
1:D:290:ILE:HG22	1:D:291:THR:N	2.34	0.42
1:A:89:VAL:HG12	1:A:102:LEU:HD23	2.00	0.42
1:C:161:ILE:HA	1:C:189:ILE:HG22	2.02	0.42
1:D:161:ILE:HA	1:D:189:ILE:HG22	2.02	0.42
1:A:271:GLU:OE2	1:A:272:VAL:N	2.53	0.42
1:C:271:GLU:OE2	1:C:272:VAL:N	2.53	0.42
1:D:52:ALA:HA	1:D:95:PRO:O	2.20	0.41
1:C:120:PHE:HE2	1:C:193:TYR:CE2	2.38	0.41
1:A:78:VAL:CG2	1:A:128:TYR:HB3	2.50	0.41
1:B:271:GLU:OE2	1:B:272:VAL:N	2.53	0.41
1:E:53:PHE:O	1:E:53:PHE:CD1	2.73	0.41
1:B:80:VAL:HG12	1:B:81:GLU:N	2.35	0.41
1:B:264:PHE:HZ	1:B:301:VAL:HG12	1.85	0.41
1:B:123:GLN:HA	1:B:123:GLN:NE2	2.35	0.41
1:B:96:ASP:OD1	1:B:98:THR:HB	2.19	0.41
1:B:137:ARG:HD2	1:B:179:LEU:HG	2.01	0.41
1:D:80:VAL:HG12	1:D:81:GLU:N	2.35	0.41
1:A:30:ASP:HB3	1:A:33:ALA:HB3	2.02	0.41
1:A:134:VAL:HB	1:A:135:ASP:H	1.62	0.41
1:A:286:ARG:HH11	1:A:286:ARG:CG	2.29	0.41
1:B:78:VAL:CG2	1:B:128:TYR:HB3	2.50	0.41
1:B:53:PHE:CD1	1:B:53:PHE:O	2.73	0.41
1:E:204:MET:HE3	1:E:261:ILE:HD12	2.02	0.41
1:C:312:LEU:HD12	1:C:312:LEU:HA	1.87	0.41
1:E:22:TYR:CG	1:E:149:GLY:HA2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:120:PHE:HE2	1:E:193:TYR:CE2	2.39	0.41
1:C:52:ALA:HA	1:C:95:PRO:O	2.20	0.41
1:C:290:ILE:HG22	1:C:291:THR:N	2.34	0.41
1:C:89:VAL:HG12	1:C:102:LEU:HD23	2.00	0.41
1:C:80:VAL:HG12	1:C:81:GLU:N	2.35	0.41
1:C:137:ARG:HD2	1:C:179:LEU:HG	2.01	0.41
1:D:296:ILE:HA	1:D:296:ILE:HD13	1.66	0.41
1:D:312:LEU:HA	1:D:312:LEU:HD12	1.87	0.41
1:C:21:ILE:O	1:C:149:GLY:HA3	2.21	0.41
1:C:78:VAL:CG2	1:C:128:TYR:HB3	2.50	0.41
1:B:227:VAL:HG12	1:B:269:VAL:HG23	2.02	0.41
1:D:80:VAL:HG12	1:D:82:ASN:O	2.21	0.41
1:D:264:PHE:HZ	1:D:301:VAL:HG12	1.85	0.41
1:C:123:GLN:NE2	1:C:123:GLN:HA	2.35	0.41
1:C:263:LEU:HA	1:C:263:LEU:HD12	1.67	0.41
1:D:120:PHE:HE2	1:D:193:TYR:CE2	2.39	0.41
1:B:120:PHE:HE2	1:B:193:TYR:CE2	2.39	0.41
1:B:76:ARG:HH22	1:B:130:ILE:CD1	2.33	0.41
1:D:215:PHE:HB3	1:D:295:ARG:HG2	2.03	0.41
1:B:80:VAL:HG12	1:B:82:ASN:O	2.21	0.41
1:A:264:PHE:HZ	1:A:301:VAL:HG12	1.85	0.41
1:E:134:VAL:HB	1:E:135:ASP:H	1.61	0.41
1:E:123:GLN:NE2	1:E:123:GLN:HA	2.35	0.41
1:A:96:ASP:OD1	1:A:98:THR:HB	2.19	0.41
1:D:147:LYS:C	1:D:147:LYS:HD3	2.41	0.41
1:D:21:ILE:O	1:D:149:GLY:HA3	2.20	0.41
1:C:147:LYS:C	1:C:147:LYS:HD3	2.41	0.41
1:A:53:PHE:CD1	1:A:53:PHE:O	2.74	0.41
1:E:209:PHE:O	1:E:210:ILE:C	2.58	0.41
1:B:21:ILE:O	1:B:149:GLY:HA3	2.21	0.41
1:A:21:ILE:O	1:A:149:GLY:HA3	2.21	0.41
1:A:76:ARG:HH22	1:A:130:ILE:CD1	2.33	0.41
1:D:202:LEU:HD23	1:D:202:LEU:HA	1.83	0.41
1:A:80:VAL:HG12	1:A:81:GLU:N	2.35	0.41
1:E:276:HIS:C	1:E:278:LEU:N	2.74	0.41
1:C:276:HIS:C	1:C:278:LEU:N	2.74	0.41
1:B:147:LYS:HD3	1:B:147:LYS:C	2.41	0.41
1:D:54:ASP:HB2	1:D:57:ARG:CG	2.50	0.41
1:B:215:PHE:HB3	1:B:295:ARG:HG2	2.03	0.41
1:D:270:ILE:HA	1:D:270:ILE:HD13	1.73	0.41
1:C:49:ARG:HG2	1:C:49:ARG:H	1.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:VAL:HG12	1:C:82:ASN:O	2.21	0.41
1:A:80:VAL:HG12	1:A:82:ASN:O	2.21	0.41
1:B:204:MET:HE3	1:B:261:ILE:HD12	2.02	0.41
1:E:264:PHE:HZ	1:E:301:VAL:HG12	1.85	0.41
1:D:271:GLU:OE2	1:D:272:VAL:N	2.53	0.41
1:A:123:GLN:HA	1:A:123:GLN:NE2	2.35	0.41
1:A:227:VAL:HG12	1:A:269:VAL:HG23	2.01	0.41
1:B:151:ASN:HD22	1:B:151:ASN:HA	1.66	0.41
1:A:10:ILE:H	1:A:10:ILE:HG13	1.56	0.41
1:D:275:GLN:HG3	1:D:291:THR:OG1	2.21	0.40
1:E:215:PHE:HB3	1:E:295:ARG:HG2	2.03	0.40
1:E:54:ASP:HB2	1:E:57:ARG:CG	2.50	0.40
1:E:80:VAL:HG12	1:E:82:ASN:O	2.21	0.40
1:D:53:PHE:O	1:D:53:PHE:CD1	2.74	0.40
1:C:314:PHE:H	1:C:314:PHE:HD1	1.62	0.40
1:C:53:PHE:CD1	1:C:53:PHE:O	2.74	0.40
1:B:183:LEU:HD23	1:B:183:LEU:HA	1.85	0.40
1:A:275:GLN:HG3	1:A:291:THR:OG1	2.21	0.40
1:E:275:GLN:HG3	1:E:291:THR:OG1	2.21	0.40
1:E:161:ILE:HA	1:E:189:ILE:HG22	2.02	0.40
1:C:222:ALA:HB2	1:D:221[A]:GLU:HA	2.04	0.40
1:E:147:LYS:HD3	1:E:147:LYS:C	2.41	0.40
1:A:147:LYS:HD3	1:A:147:LYS:C	2.41	0.40
1:A:22:TYR:HB3	1:A:41:PHE:HB2	2.02	0.40
1:B:77:PHE:N	1:B:84:ARG:HD3	2.29	0.40
1:B:275:GLN:HG3	1:B:291:THR:OG1	2.21	0.40
1:B:161:ILE:HA	1:B:189:ILE:HG22	2.02	0.40
1:C:137:ARG:HA	1:C:137:ARG:HD3	1.61	0.40
1:E:80:VAL:HG12	1:E:81:GLU:N	2.35	0.40
1:C:72:ILE:HA	1:C:73:PRO:HD3	1.84	0.40
1:C:54:ASP:HB2	1:C:57:ARG:CG	2.50	0.40
1:C:275:GLN:HG3	1:C:291:THR:OG1	2.21	0.40
1:A:161:ILE:HA	1:A:189:ILE:HG22	2.02	0.40
1:C:264:PHE:HZ	1:C:301:VAL:HG12	1.85	0.40
1:D:194:PHE:O	1:D:198:PRO:HD2	2.22	0.40
1:B:270:ILE:HG22	1:B:271:GLU:N	2.37	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	309/317 (98%)	247 (80%)	49 (16%)	13 (4%)	3	29
1	B	309/317 (98%)	247 (80%)	49 (16%)	13 (4%)	3	29
1	C	309/317 (98%)	247 (80%)	49 (16%)	13 (4%)	3	29
1	D	309/317 (98%)	247 (80%)	49 (16%)	13 (4%)	3	29
1	E	309/317 (98%)	246 (80%)	50 (16%)	13 (4%)	3	29
All	All	1545/1585 (98%)	1234 (80%)	246 (16%)	65 (4%)	3	29

All (65) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	148	VAL
1	A	194	PHE
1	B	148	VAL
1	B	194	PHE
1	C	148	VAL
1	C	194	PHE
1	D	148	VAL
1	D	194	PHE
1	E	148	VAL
1	E	150	LYS
1	E	194	PHE
1	A	50	ARG
1	A	150	LYS
1	B	50	ARG
1	B	150	LYS
1	C	50	ARG
1	C	150	LYS
1	D	50	ARG
1	D	150	LYS
1	E	50	ARG
1	A	81	GLU

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Mol	Chain	Res	Type
1	A	163	SER
1	A	275	GLN
1	A	295	ARG
1	B	81	GLU
1	B	163	SER
1	B	275	GLN
1	B	295	ARG
1	C	81	GLU
1	C	163	SER
1	C	275	GLN
1	D	81	GLU
1	D	163	SER
1	D	275	GLN
1	E	81	GLU
1	E	163	SER
1	E	275	GLN
1	E	295	ARG
1	C	295	ARG
1	D	295	ARG
1	A	118	TYR
1	B	118	TYR
1	C	118	TYR
1	D	118	TYR
1	E	118	TYR
1	A	155	PHE
1	A	278	LEU
1	A	303	LEU
1	B	155	PHE
1	B	278	LEU
1	B	303	LEU
1	C	155	PHE
1	C	278	LEU
1	C	303	LEU
1	D	155	PHE
1	D	278	LEU
1	D	303	LEU
1	E	155	PHE
1	E	278	LEU
1	E	303	LEU
1	A	210	ILE
1	B	210	ILE
1	C	210	ILE

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Mol	Chain	Res	Type
1	D	210	ILE
1	E	210	ILE

### 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	279/284 (98%)	227 (81%)	52 (19%)	2	10
1	B	279/284 (98%)	227 (81%)	52 (19%)	2	10
1	C	279/284 (98%)	227 (81%)	52 (19%)	2	10
1	D	279/284 (98%)	227 (81%)	52 (19%)	2	10
1	E	279/284 (98%)	227 (81%)	52 (19%)	2	10
All	All	1395/1420 (98%)	1135 (81%)	260 (19%)	2	10

All (260) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ASP
1	A	45	SER
1	A	49	ARG
1	A	51	LEU
1	A	54	ASP
1	A	57	ARG
1	A	64	THR
1	A	68	GLU
1	A	79	ASN
1	A	82	ASN
1	A	84	ARG
1	A	89	VAL
1	A	98	THR
1	A	100	GLN
1	A	108	ARG
1	A	116	ARG
1	A	122	SER

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Mol	Chain	Res	Type
1	A	134	VAL
1	A	141	LEU
1	A	146	GLU
1	A	151	ASN
1	A	154	VAL
1	A	155	PHE
1	A	157	THR
1	A	162	GLU
1	A	165	THR
1	A	173	PHE
1	A	179	LEU
1	A	211	SER
1	A	212	TRP
1	A	213	THR
1	A	218	THR
1	A	221[A]	GLU
1	A	221[B]	GLU
1	A	226	LEU
1	A	228	VAL
1	A	243	THR
1	A	245	LEU
1	A	248	THR
1	A	252	THR
1	A	254	THR
1	A	258	ILE
1	A	263	LEU
1	A	270	ILE
1	A	274	VAL
1	A	282	SER
1	A	286	ARG
1	A	292	ARG
1	A	296	ILE
1	A	300	VAL
1	A	304	LEU
1	A	314	PHE
1	B	12	ASP
1	B	45	SER
1	B	49	ARG
1	B	51	LEU
1	B	54	ASP
1	B	57	ARG
1	B	64	THR

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Mol	Chain	Res	Type
1	B	68	GLU
1	B	79	ASN
1	B	82	ASN
1	B	84	ARG
1	B	89	VAL
1	B	98	THR
1	B	100	GLN
1	B	108	ARG
1	B	116	ARG
1	B	122	SER
1	B	134	VAL
1	B	141	LEU
1	B	146	GLU
1	B	151	ASN
1	B	154	VAL
1	B	155	PHE
1	B	157	THR
1	B	162	GLU
1	B	165	THR
1	B	173	PHE
1	B	179	LEU
1	B	211	SER
1	B	212	TRP
1	B	213	THR
1	B	218	THR
1	B	221[A]	GLU
1	B	221[B]	GLU
1	B	226	LEU
1	B	228	VAL
1	B	243	THR
1	B	245	LEU
1	B	248	THR
1	B	252	THR
1	B	254	THR
1	B	258	ILE
1	B	263	LEU
1	B	270	ILE
1	B	274	VAL
1	B	282	SER
1	B	286	ARG
1	B	292	ARG
1	B	296	ILE

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Mol	Chain	Res	Type
1	B	300	VAL
1	B	304	LEU
1	B	314	PHE
1	C	12	ASP
1	C	45	SER
1	C	49	ARG
1	C	51	LEU
1	C	54	ASP
1	C	57	ARG
1	C	64	THR
1	C	68	GLU
1	C	79	ASN
1	C	82	ASN
1	C	84	ARG
1	C	89	VAL
1	C	98	THR
1	C	100	GLN
1	C	108	ARG
1	C	116	ARG
1	C	122	SER
1	C	134	VAL
1	C	141	LEU
1	C	146	GLU
1	C	151	ASN
1	C	154	VAL
1	C	155	PHE
1	C	157	THR
1	C	162	GLU
1	C	165	THR
1	C	173	PHE
1	C	179	LEU
1	C	211	SER
1	C	212	TRP
1	C	213	THR
1	C	218	THR
1	C	221[A]	GLU
1	C	221[B]	GLU
1	C	226	LEU
1	C	228	VAL
1	C	243	THR
1	C	245	LEU
1	C	248	THR

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Mol	Chain	Res	Type
1	C	252	THR
1	C	254	THR
1	C	258	ILE
1	C	263	LEU
1	C	270	ILE
1	C	274	VAL
1	C	282	SER
1	C	286	ARG
1	C	292	ARG
1	C	296	ILE
1	C	300	VAL
1	C	304	LEU
1	C	314	PHE
1	D	12	ASP
1	D	45	SER
1	D	49	ARG
1	D	51	LEU
1	D	54	ASP
1	D	57	ARG
1	D	64	THR
1	D	68	GLU
1	D	79	ASN
1	D	82	ASN
1	D	84	ARG
1	D	89	VAL
1	D	98	THR
1	D	100	GLN
1	D	108	ARG
1	D	116	ARG
1	D	122	SER
1	D	134	VAL
1	D	141	LEU
1	D	146	GLU
1	D	151	ASN
1	D	154	VAL
1	D	155	PHE
1	D	157	THR
1	D	162	GLU
1	D	165	THR
1	D	173	PHE
1	D	179	LEU
1	D	211	SER

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Mol	Chain	Res	Type
1	D	212	TRP
1	D	213	THR
1	D	218	THR
1	D	221[A]	GLU
1	D	221[B]	GLU
1	D	226	LEU
1	D	228	VAL
1	D	243	THR
1	D	245	LEU
1	D	248	THR
1	D	252	THR
1	D	254	THR
1	D	258	ILE
1	D	263	LEU
1	D	270	ILE
1	D	274	VAL
1	D	282	SER
1	D	286	ARG
1	D	292	ARG
1	D	296	ILE
1	D	300	VAL
1	D	304	LEU
1	D	314	PHE
1	E	12	ASP
1	E	45	SER
1	E	49	ARG
1	E	51	LEU
1	E	54	ASP
1	E	57	ARG
1	E	64	THR
1	E	68	GLU
1	E	79	ASN
1	E	82	ASN
1	E	84	ARG
1	E	89	VAL
1	E	98	THR
1	E	100	GLN
1	E	108	ARG
1	E	116	ARG
1	E	122	SER
1	E	134	VAL
1	E	141	LEU

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Mol	Chain	Res	Type
1	E	146	GLU
1	E	151	ASN
1	E	154	VAL
1	E	155	PHE
1	E	157	THR
1	E	162	GLU
1	E	165	THR
1	E	173	PHE
1	E	179	LEU
1	E	211	SER
1	E	212	TRP
1	E	213	THR
1	E	218	THR
1	E	221[A]	GLU
1	E	221[B]	GLU
1	E	226	LEU
1	E	228	VAL
1	E	243	THR
1	E	245	LEU
1	E	248	THR
1	E	252	THR
1	E	254	THR
1	E	258	ILE
1	E	263	LEU
1	E	270	ILE
1	E	274	VAL
1	E	282	SER
1	E	286	ARG
1	E	292	ARG
1	E	296	ILE
1	E	300	VAL
1	E	304	LEU
1	E	314	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	79	ASN
1	A	100	GLN
1	A	138	ASN
1	A	151	ASN

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Mol	Chain	Res	Type
1	A	234	HIS
1	A	244	ASN
1	A	283	GLN
1	B	39	ASN
1	B	79	ASN
1	B	100	GLN
1	B	151	ASN
1	B	234	HIS
1	B	244	ASN
1	B	283	GLN
1	C	39	ASN
1	C	79	ASN
1	C	100	GLN
1	C	138	ASN
1	C	151	ASN
1	C	234	HIS
1	C	244	ASN
1	C	283	GLN
1	D	39	ASN
1	D	79	ASN
1	D	100	GLN
1	D	138	ASN
1	D	151	ASN
1	D	234	HIS
1	D	244	ASN
1	D	283	GLN
1	E	39	ASN
1	E	79	ASN
1	E	138	ASN
1	E	151	ASN
1	E	234	HIS
1	E	244	ASN
1	E	283	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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



## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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 [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	310/317 (97%)	0.13	8 (2%) 59 54	69, 100, 157, 271	0
1	B	310/317 (97%)	0.14	11 (3%) 48 42	69, 100, 157, 271	0
1	C	310/317 (97%)	0.18	19 (6%) 25 23	69, 100, 157, 271	0
1	D	310/317 (97%)	0.17	14 (4%) 37 33	69, 100, 157, 271	0
1	E	310/317 (97%)	0.21	21 (6%) 20 19	69, 100, 157, 271	0
All	All	1550/1585 (97%)	0.17	73 (4%) 35 32	69, 100, 158, 271	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	316	PHE	6.0
1	C	59	GLY	5.5
1	E	316	PHE	5.1
1	C	58	SER	4.6
1	D	282	SER	4.3
1	A	282	SER	4.3
1	C	316	PHE	4.3
1	B	316	PHE	4.3
1	D	286	ARG	4.2
1	B	282	SER	4.1
1	B	65	TYR	3.9
1	C	50	ARG	3.9
1	B	145	LEU	3.7
1	D	285	ALA	3.6
1	D	60	VAL	3.6
1	D	287	ALA	3.5
1	E	315	GLY	3.5
1	E	284	PRO	3.5
1	B	315	GLY	3.5
1	A	59	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	E	282	SER	3.4
1	E	57	ARG	3.3
1	C	144	ASP	3.3
1	E	285	ALA	3.3
1	E	60	VAL	3.2
1	B	57	ARG	3.1
1	C	315	GLY	3.1
1	C	193	TYR	3.1
1	A	53	PHE	3.1
1	D	65	TYR	3.0
1	E	87	ASP	3.0
1	C	282	SER	3.0
1	E	193	TYR	2.9
1	D	64	THR	2.9
1	D	316	PHE	2.8
1	E	65	TYR	2.8
1	E	58	SER	2.8
1	E	144	ASP	2.8
1	B	27	TYR	2.8
1	A	177	ASP	2.7
1	E	61	ARG	2.7
1	D	283	GLN	2.7
1	A	51	LEU	2.6
1	E	59	GLY	2.6
1	E	292	ARG	2.6
1	C	177	ASP	2.5
1	C	51	LEU	2.5
1	A	155	PHE	2.5
1	C	53	PHE	2.5
1	D	59	GLY	2.5
1	B	193	TYR	2.5
1	C	7	PRO	2.4
1	D	66	GLU	2.4
1	C	48	ASP	2.4
1	C	68	GLU	2.4
1	E	70	ILE	2.3
1	E	69	ALA	2.2
1	C	155	PHE	2.2
1	B	146	GLU	2.2
1	A	71	TRP	2.1
1	C	71	TRP	2.1
1	D	193	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	315	GLY	2.1
1	E	10	ILE	2.1
1	C	18	ASN	2.1
1	B	70	ILE	2.1
1	C	70	ILE	2.1
1	D	292	ARG	2.1
1	B	61	ARG	2.1
1	C	146	GLU	2.1
1	E	145	LEU	2.0
1	E	68	GLU	2.0
1	E	27	TYR	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CD	A	1318	1/1	0.99	0.23	0.15	137,137,137,137	0
2	CD	A	1317	1/1	0.97	0.19	-1.17	120,120,120,120	0
2	CD	C	1317	1/1	1.00	0.08	-	111,111,111,111	0
2	CD	C	1318	1/1	0.99	0.11	-	146,146,146,146	0
2	CD	A	1319	1/1	0.99	0.06	-	109,109,109,109	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.