



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 05:21 pm GMT

PDB ID : 2G04  
Title : Crystal structure of fatty acid-CoA racemase from Mycobacterium tuberculosis H37Rv  
Authors : Lee, K.S.; Park, S.M.; Rhee, K.H.; Bang, W.G.; Hwang, K.Y.; Chi, Y.M.  
Deposited on : 2006-02-11  
Resolution : 2.70 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 : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

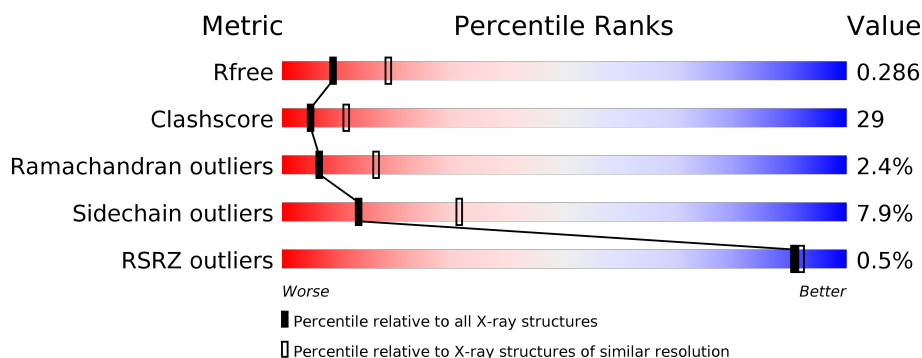
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	111664	2449 (2.70-2.70)
Clashscore	122126	2756 (2.70-2.70)
Ramachandran outliers	120053	2716 (2.70-2.70)
Sidechain outliers	120020	2716 (2.70-2.70)
RSRZ outliers	108989	2376 (2.70-2.70)

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	359	<div> <div>%</div> <div> <div></div> <div>55%</div> <div>37%</div> <div>5%</div> <div>••</div> </div> </div>
1	B	359	<div> <div>%</div> <div> <div></div> <div>52%</div> <div>41%</div> <div>5%</div> <div>••</div> </div> </div>
1	C	359	<div> <div>%</div> <div> <div></div> <div>52%</div> <div>41%</div> <div>5%</div> <div>•</div> </div> </div>
1	D	359	<div> <div></div> <div> <div></div> <div>54%</div> <div>39%</div> <div>5%</div> <div>••</div> </div> </div>
1	E	359	<div> <div>%</div> <div> <div></div> <div>47%</div> <div>45%</div> <div>6%</div> <div>••</div> </div> </div>
1	F	359	<div> <div></div> <div> <div></div> <div>54%</div> <div>40%</div> <div></div> <div>•••</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16228 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 PROBABLE FATTY-ACID-CoA RACEMASE FAR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	0	0
			2626	1658	463	489	16			
1	B	353	Total	C	N	O	S	0	0	0
			2626	1658	463	489	16			
1	C	353	Total	C	N	O	S	0	0	0
			2626	1658	463	489	16			
1	D	353	Total	C	N	O	S	0	0	0
			2626	1658	463	489	16			
1	E	353	Total	C	N	O	S	0	0	0
			2626	1658	463	489	16			
1	F	353	Total	C	N	O	S	0	0	0
			2626	1658	463	489	16			

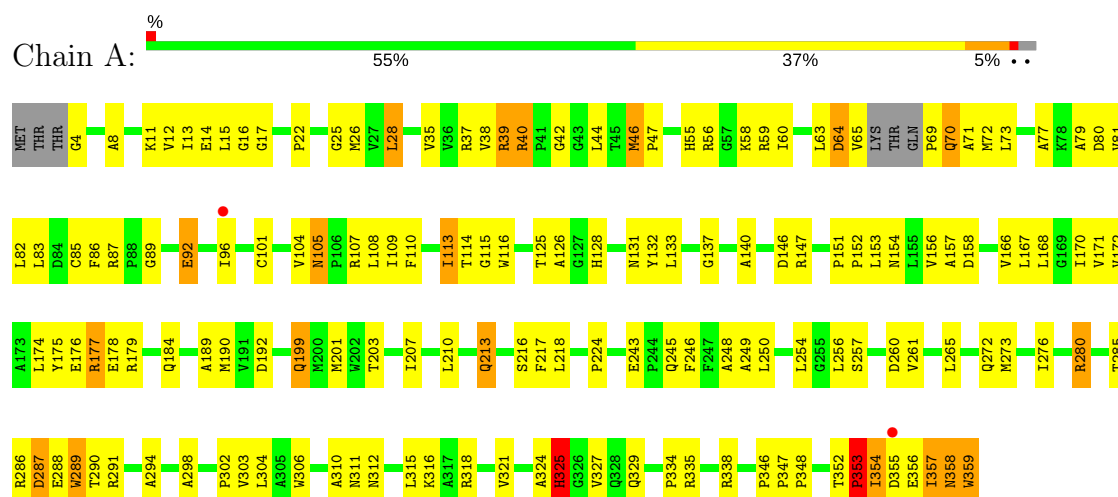
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	100	Total	O	0	0
			100	100		
2	B	81	Total	O	0	0
			81	81		
2	C	98	Total	O	0	0
			98	98		
2	D	89	Total	O	0	0
			89	89		
2	E	58	Total	O	0	0
			58	58		
2	F	46	Total	O	0	0
			46	46		

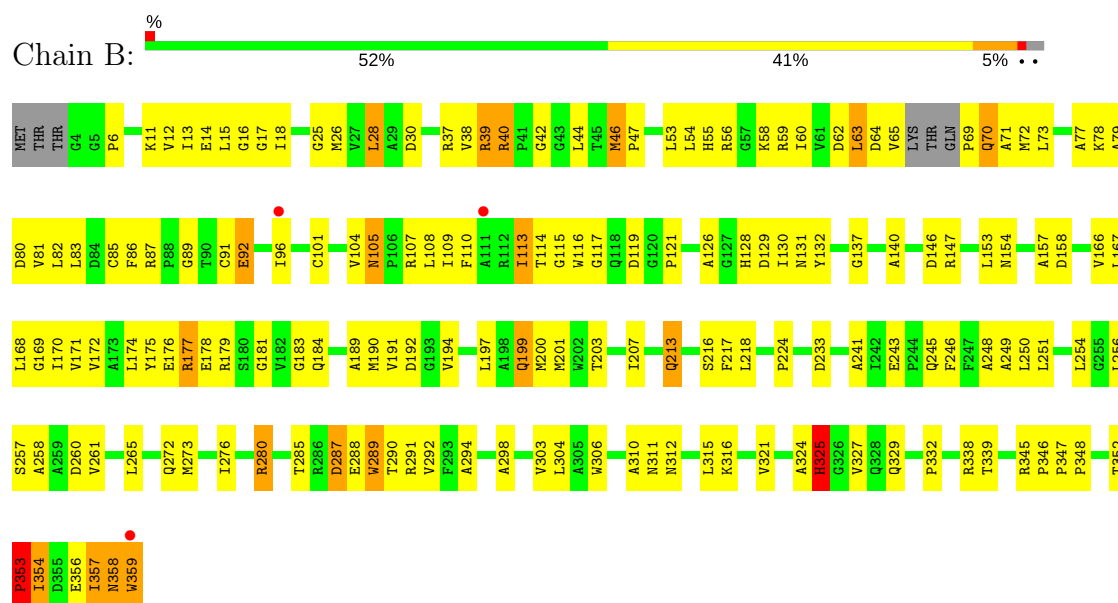
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: PROBABLE FATTY-ACID-CoA RACEMASE FAR

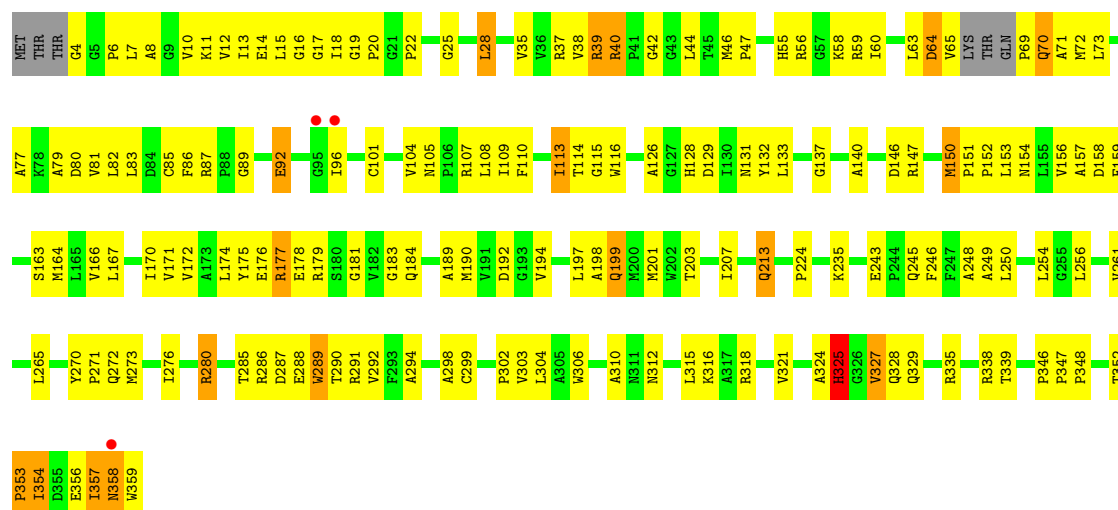


#### • Molecule 1: PROBABLE FATTY-ACID-CoA RACEMASE FAR



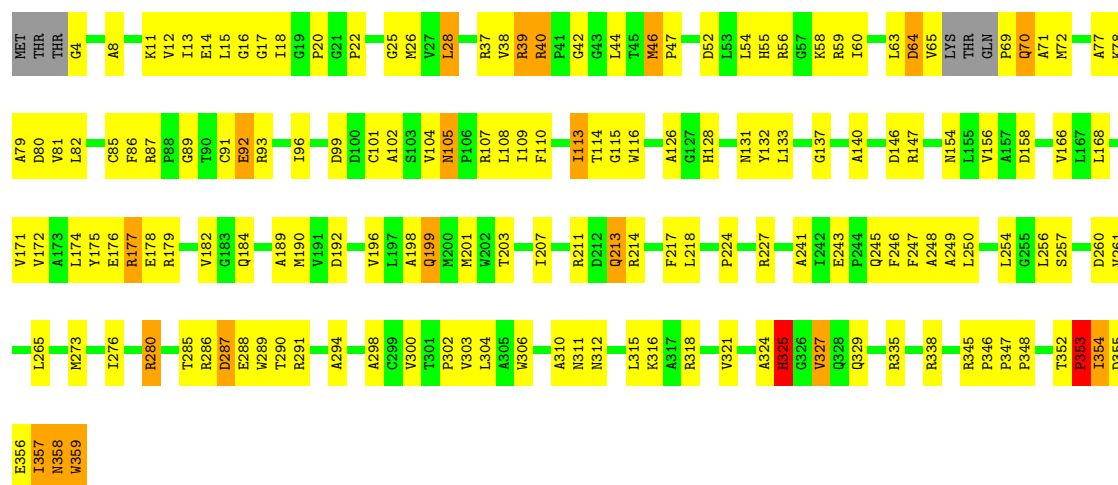
#### • Molecule 1: PROBABLE FATTY-ACID-CoA RACEMASE FAR





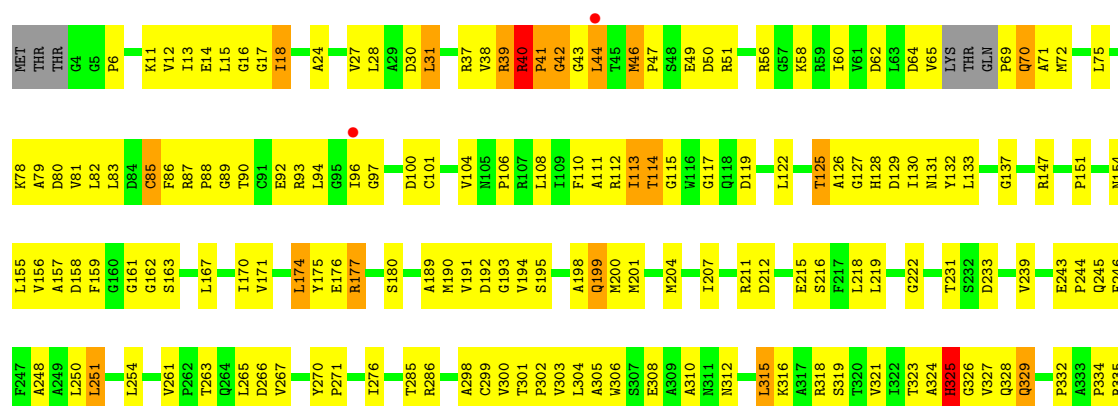
• Molecule 1: PROBABLE FATTY-ACID-CoA RACEMASE FAR

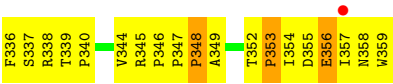
Chain D: 54% 39% 5% ..



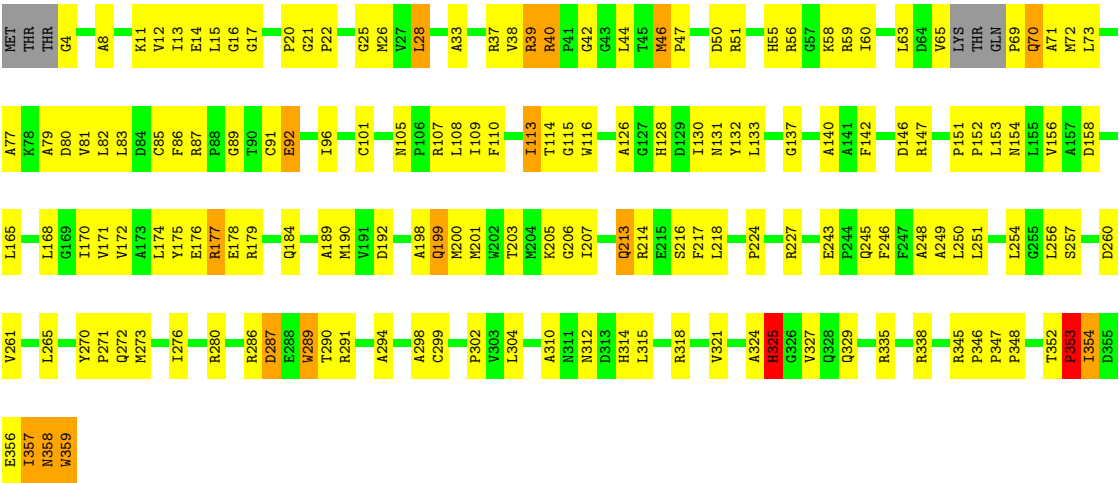
• Molecule 1: PROBABLE FATTY-ACID-CoA RACEMASE FAR

Chain E: 47% 45% 6% ..





● Molecule 1: PROBABLE FATTY-ACID-CoA RACEMASE FAR



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.56Å 109.56Å 147.97Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.70 36.66 – 2.51	Depositor EDS
% Data completeness (in resolution range)	95.9 (30.00-2.70) 92.1 (36.66-2.51)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.52 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.240 , 0.290 0.242 , 0.286	Depositor DCC
$R_{free}$ test set	2668 reflections (4.24%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.9	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 33.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.004 for -h,-k,l 0.056 for h,-h-k,-l 0.156 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	16228	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.61 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.6440e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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](#)

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	0.39	0/2686	0.59	0/3656
1	B	0.43	0/2686	0.61	0/3656
1	C	0.41	0/2686	0.62	0/3656
1	D	0.43	0/2686	0.62	0/3656
1	E	0.43	0/2686	0.63	0/3656
1	F	0.41	0/2686	0.61	0/3656
All	All	0.42	0/16116	0.61	0/21936

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	2626	0	2599	151	0
1	B	2626	0	2599	178	0
1	C	2626	0	2599	164	0
1	D	2626	0	2599	150	0
1	E	2626	0	2599	190	0
1	F	2626	0	2599	153	0
2	A	100	0	0	9	0
2	B	81	0	0	18	0
2	C	98	0	0	11	0
2	D	89	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	58	0	0	6	0
2	F	46	0	0	3	0
All	All	16228	0	15594	904	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 29.

All (904) 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:14:GLU:HG2	2:A:453:HOH:O	1.59	1.02
1:E:171:VAL:HG12	1:F:171:VAL:HG12	1.46	0.97
1:C:199:GLN:HE21	1:C:199:GLN:HA	1.29	0.97
1:E:199:GLN:HA	1:E:199:GLN:HE21	1.28	0.96
1:A:171:VAL:HG12	1:B:171:VAL:HG12	1.47	0.96
1:B:56:ARG:HH11	1:B:329:GLN:HE21	1.11	0.95
1:A:199:GLN:HA	1:A:199:GLN:HE21	1.28	0.95
1:B:199:GLN:HA	1:B:199:GLN:HE21	1.29	0.94
1:F:199:GLN:HE21	1:F:199:GLN:HA	1.31	0.94
1:E:40:ARG:HB2	1:E:41:PRO:HD2	1.47	0.94
1:D:199:GLN:HA	1:D:199:GLN:HE21	1.32	0.93
1:D:69:PRO:HB3	2:D:374:HOH:O	1.69	0.92
1:C:56:ARG:HH11	1:C:329:GLN:HE21	1.17	0.90
1:E:40:ARG:HE	1:E:40:ARG:H	1.11	0.90
1:B:59:ARG:HD2	1:B:352:THR:HG21	1.54	0.90
1:A:201:MET:HG2	1:B:306:TRP:CZ2	2.09	0.88
1:E:15:LEU:HD21	1:E:96:ILE:HD13	1.58	0.86
1:A:56:ARG:HH11	1:A:329:GLN:HE21	1.26	0.84
1:C:171:VAL:HG12	1:D:171:VAL:HG12	1.59	0.84
1:D:56:ARG:HH11	1:D:329:GLN:HE21	1.25	0.84
1:E:115:GLY:HA2	1:E:190:MET:HB2	1.58	0.83
1:A:355:ASP:HB2	2:A:407:HOH:O	1.79	0.82
1:B:55:HIS:HA	1:B:58:LYS:HD3	1.59	0.82
1:E:114:THR:HB	1:E:117:GLY:H	1.45	0.81
1:E:312:ASN:HD22	1:E:315:LEU:HB2	1.45	0.81
1:F:55:HIS:HA	1:F:58:LYS:HD3	1.63	0.80
1:C:16:GLY:HA3	1:C:85:CYS:HB2	1.60	0.80
1:A:128:HIS:H	1:A:131:ASN:HD22	1.30	0.79
1:B:128:HIS:H	1:B:131:ASN:HD22	1.29	0.79
1:E:115:GLY:HA3	1:E:132:TYR:CE1	2.18	0.79
1:C:128:HIS:H	1:C:131:ASN:HD22	1.31	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:HIS:HA	1:A:58:LYS:HD3	1.65	0.78
1:E:113:ILE:H	1:E:113:ILE:HD12	1.46	0.78
1:F:40:ARG:H	1:F:40:ARG:HE	1.32	0.78
1:F:16:GLY:HA3	1:F:85:CYS:HB2	1.65	0.77
1:A:16:GLY:HA3	1:A:85:CYS:HB2	1.64	0.77
1:B:44:LEU:HA	2:B:420:HOH:O	1.84	0.76
1:C:47:PRO:HG3	1:D:207:ILE:HD11	1.67	0.76
1:B:40:ARG:HE	1:B:40:ARG:H	1.32	0.76
1:C:55:HIS:HA	1:C:58:LYS:HD3	1.68	0.76
1:C:201:MET:HG2	1:D:306:TRP:CZ2	2.21	0.76
1:F:59:ARG:HD2	1:F:352:THR:HG21	1.68	0.76
1:B:14:GLU:OE2	1:B:37:ARG:HD3	1.86	0.76
1:E:207:ILE:HD11	1:F:47:PRO:HG3	1.66	0.76
1:C:306:TRP:CZ2	1:D:201:MET:HG2	2.21	0.75
1:D:17:GLY:CA	1:D:37:ARG:HH12	2.00	0.75
1:E:306:TRP:CZ2	1:F:201:MET:HG2	2.21	0.75
1:A:59:ARG:HD2	1:A:352:THR:HG21	1.69	0.75
1:D:59:ARG:HD2	1:D:352:THR:HG21	1.68	0.75
1:E:327:VAL:HG11	1:F:206:GLY:HA3	1.68	0.75
1:F:128:HIS:H	1:F:131:ASN:HD22	1.35	0.75
1:A:40:ARG:HE	1:A:40:ARG:H	1.33	0.75
1:F:17:GLY:CA	1:F:37:ARG:HH12	2.00	0.74
1:C:40:ARG:H	1:C:40:ARG:HE	1.32	0.74
1:B:357:ILE:HA	2:B:416:HOH:O	1.87	0.74
1:A:17:GLY:CA	1:A:37:ARG:HH12	2.02	0.73
1:E:250:LEU:O	1:E:254:LEU:HB2	1.89	0.73
1:D:14:GLU:OE2	1:D:37:ARG:HD3	1.89	0.73
1:E:14:GLU:OE2	1:E:37:ARG:HD3	1.87	0.73
1:B:357:ILE:HG22	2:B:416:HOH:O	1.88	0.72
1:E:17:GLY:O	1:E:18:ILE:HG23	1.88	0.72
1:B:115:GLY:HA2	1:B:190:MET:HB2	1.71	0.72
1:C:287:ASP:HB3	1:C:291:ARG:HH12	1.53	0.72
1:B:170:ILE:HG22	2:B:437:HOH:O	1.88	0.72
1:E:245:GLN:O	1:E:248:ALA:HB3	1.90	0.72
1:B:199:GLN:CA	1:B:199:GLN:HE21	1.99	0.72
1:E:312:ASN:ND2	1:E:315:LEU:H	1.88	0.72
1:D:114:THR:HG21	2:D:448:HOH:O	1.89	0.71
1:D:128:HIS:H	1:D:131:ASN:HD22	1.38	0.71
1:A:47:PRO:HG3	1:B:207:ILE:HD11	1.72	0.71
1:C:312:ASN:HD22	1:C:315:LEU:H	1.37	0.71
1:E:325:HIS:NE2	1:E:346:PRO:HD3	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:56:ARG:HH11	1:E:329:GLN:HE21	1.38	0.71
1:F:345:ARG:HD2	2:F:388:HOH:O	1.89	0.70
1:E:337:SER:OG	1:F:184:GLN:HB2	1.92	0.70
1:B:325:HIS:NE2	1:B:346:PRO:HD3	2.07	0.70
1:F:115:GLY:HA3	1:F:132:TYR:CZ	2.26	0.70
1:D:115:GLY:HA3	1:D:132:TYR:CZ	2.26	0.70
1:E:50:ASP:HB3	1:E:349:ALA:HA	1.72	0.70
1:A:115:GLY:HA3	1:A:132:TYR:CZ	2.26	0.70
1:C:359:TRP:HA	2:C:425:HOH:O	1.92	0.69
1:A:125:THR:HG21	2:A:416:HOH:O	1.91	0.69
1:A:306:TRP:CZ2	1:B:201:MET:HG2	2.27	0.69
1:C:207:ILE:HD11	1:D:47:PRO:HG3	1.75	0.69
1:B:17:GLY:CA	1:B:37:ARG:HH12	2.05	0.69
1:F:290:THR:O	1:F:294:ALA:HB2	1.92	0.69
1:B:115:GLY:HA3	1:B:132:TYR:CZ	2.28	0.69
1:E:13:ILE:HB	1:E:82:LEU:HD13	1.73	0.69
1:D:40:ARG:H	1:D:40:ARG:HE	1.41	0.69
1:A:287:ASP:HB3	1:A:291:ARG:HH12	1.58	0.69
1:B:56:ARG:NH1	1:B:329:GLN:HE21	1.90	0.69
1:D:11:LYS:HB2	1:D:80:ASP:H	1.57	0.69
1:E:115:GLY:HA3	1:E:132:TYR:CZ	2.28	0.69
1:B:16:GLY:HA3	1:B:85:CYS:HB2	1.74	0.68
1:E:303:VAL:HG12	1:F:140:ALA:HB2	1.76	0.68
1:C:14:GLU:OE2	1:C:37:ARG:HD3	1.93	0.68
1:D:16:GLY:HA3	1:D:85:CYS:HB2	1.73	0.68
1:E:312:ASN:HD22	1:E:315:LEU:H	1.40	0.68
1:B:113:ILE:HG13	1:B:166:VAL:HG21	1.76	0.68
1:D:55:HIS:HA	1:D:58:LYS:HD3	1.75	0.67
1:A:140:ALA:HB2	1:B:303:VAL:HG12	1.77	0.67
1:B:312:ASN:HD22	1:B:315:LEU:H	1.42	0.67
1:D:287:ASP:HB3	1:D:291:ARG:HH12	1.59	0.67
1:E:189:ALA:O	1:E:192:ASP:HB2	1.95	0.67
1:F:287:ASP:HB3	1:F:291:ARG:HH12	1.59	0.67
1:A:207:ILE:HD11	1:B:47:PRO:HG3	1.77	0.67
1:C:77:ALA:HA	1:C:105:ASN:HB2	1.76	0.67
1:F:189:ALA:O	1:F:192:ASP:HB2	1.94	0.67
1:E:199:GLN:HG3	1:F:26:MET:SD	2.35	0.67
1:E:44:LEU:HD12	1:E:44:LEU:H	1.60	0.66
1:C:59:ARG:HD2	1:C:352:THR:HG21	1.78	0.66
1:A:199:GLN:HA	1:A:199:GLN:NE2	2.08	0.66
1:C:199:GLN:CA	1:C:199:GLN:HE21	2.07	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:GLU:OE2	1:A:37:ARG:HD3	1.96	0.66
1:A:303:VAL:HG12	1:B:140:ALA:HB2	1.77	0.66
1:C:140:ALA:HB2	1:D:303:VAL:HG12	1.78	0.66
1:D:77:ALA:HA	1:D:105:ASN:HB2	1.78	0.66
1:B:199:GLN:HA	1:B:199:GLN:NE2	2.05	0.65
1:C:115:GLY:HA3	1:C:132:TYR:CZ	2.31	0.65
1:D:199:GLN:CA	1:D:199:GLN:HE21	2.09	0.65
1:B:287:ASP:HB3	1:B:291:ARG:HH12	1.61	0.65
1:E:353:PRO:HD2	1:E:356:GLU:HG3	1.78	0.65
1:D:81:VAL:HG13	1:D:109:ILE:HB	1.79	0.65
1:E:154:ASN:O	1:E:158:ASP:HB2	1.96	0.65
1:D:290:THR:O	1:D:294:ALA:HB2	1.95	0.65
1:F:312:ASN:HD22	1:F:315:LEU:H	1.42	0.65
1:D:93:ARG:HD2	2:D:445:HOH:O	1.97	0.65
1:C:324:ALA:HB3	1:C:329:GLN:OE1	1.96	0.65
1:B:77:ALA:HA	1:B:105:ASN:HB2	1.78	0.65
1:E:17:GLY:C	1:E:18:ILE:HG13	2.16	0.65
1:D:250:LEU:O	1:D:254:LEU:HB2	1.97	0.64
1:A:312:ASN:HD22	1:A:315:LEU:H	1.43	0.64
1:E:39:ARG:CZ	1:E:60:ILE:HG21	2.28	0.64
1:A:115:GLY:HA2	1:A:190:MET:HB2	1.80	0.64
1:F:56:ARG:HH11	1:F:329:GLN:HE21	1.46	0.64
1:A:77:ALA:HA	1:A:105:ASN:HB2	1.77	0.64
1:E:159:PHE:HA	1:E:163:SER:HB3	1.80	0.64
1:E:56:ARG:NH1	1:E:329:GLN:HE21	1.95	0.64
1:C:11:LYS:HB2	1:C:80:ASP:H	1.61	0.64
1:D:325:HIS:NE2	1:D:346:PRO:HD3	2.13	0.64
1:C:115:GLY:HA2	1:C:190:MET:HB2	1.78	0.63
1:C:245:GLN:O	1:C:248:ALA:HB3	1.98	0.63
1:D:13:ILE:HB	1:D:82:LEU:HD12	1.80	0.63
1:B:261:VAL:HG22	1:B:276:ILE:HG21	1.80	0.63
1:B:65:VAL:CG2	2:B:421:HOH:O	2.46	0.63
1:B:254:LEU:HD23	1:B:256:LEU:HD12	1.81	0.63
1:C:113:ILE:HG13	1:C:166:VAL:HG21	1.81	0.63
1:C:40:ARG:H	1:C:40:ARG:NE	1.97	0.63
1:E:298:ALA:O	1:E:300:VAL:HG23	1.98	0.63
1:F:77:ALA:HA	1:F:105:ASN:HB2	1.79	0.63
1:C:17:GLY:N	2:C:364:HOH:O	2.31	0.62
1:D:89:GLY:O	1:D:92:GLU:HG2	1.99	0.62
1:D:4:GLY:O	1:D:8:ALA:HB2	1.98	0.62
1:C:17:GLY:CA	1:C:37:ARG:HH12	2.12	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:199:GLN:NE2	1:C:199:GLN:HA	2.09	0.62
1:C:304:LEU:O	1:D:137:GLY:HA2	1.98	0.62
1:B:101:CYS:HB3	1:B:108:LEU:HD23	1.81	0.62
1:D:17:GLY:HA2	1:D:37:ARG:HH12	1.63	0.62
1:F:353:PRO:HB2	1:F:356:GLU:HG3	1.82	0.62
1:B:113:ILE:H	1:B:113:ILE:HD12	1.65	0.62
1:B:40:ARG:H	1:B:40:ARG:NE	1.97	0.62
1:D:133:LEU:HD21	1:D:156:VAL:CG1	2.29	0.62
1:A:137:GLY:HA2	1:B:304:LEU:O	1.99	0.61
1:F:81:VAL:HG13	1:F:109:ILE:HB	1.81	0.61
1:C:47:PRO:HG3	1:D:207:ILE:CD1	2.30	0.61
1:E:171:VAL:HG12	1:F:171:VAL:CG1	2.26	0.61
1:C:113:ILE:H	1:C:113:ILE:HD12	1.65	0.61
1:C:353:PRO:HB2	1:C:356:GLU:HG3	1.82	0.61
1:C:101:CYS:HB3	1:C:108:LEU:HD23	1.83	0.61
1:E:177:ARG:HA	1:E:180:SER:OG	2.01	0.61
1:E:304:LEU:O	1:F:137:GLY:HA2	1.99	0.60
1:A:189:ALA:O	1:A:192:ASP:HB2	2.02	0.60
1:E:89:GLY:HA2	1:E:92:GLU:OE1	2.02	0.60
1:D:20:PRO:HG3	1:D:190:MET:HE1	1.84	0.60
1:C:207:ILE:CD1	1:D:47:PRO:HG3	2.30	0.60
1:F:38:VAL:HG11	1:F:72:MET:SD	2.41	0.60
1:A:40:ARG:NE	1:A:40:ARG:H	1.98	0.60
1:B:14:GLU:OE1	1:B:25:GLY:HA3	2.02	0.60
1:D:14:GLU:OE1	1:D:25:GLY:HA3	2.02	0.60
1:D:199:GLN:HA	1:D:199:GLN:NE2	2.12	0.60
1:A:69:PRO:HB3	2:A:368:HOH:O	2.02	0.59
1:B:11:LYS:HE3	2:B:418:HOH:O	2.02	0.59
1:E:147:ARG:HH12	1:F:147:ARG:CG	2.15	0.59
1:C:12:VAL:HG11	1:C:28:LEU:HD23	1.84	0.59
1:D:115:GLY:HA2	1:D:190:MET:HB2	1.84	0.59
1:D:58:LYS:O	1:D:348:PRO:HG3	2.02	0.59
1:E:17:GLY:HA3	1:E:37:ARG:HH12	1.68	0.59
1:E:39:ARG:HH21	1:E:49:GLU:HG3	1.67	0.59
1:C:87:ARG:NH2	1:C:126:ALA:HB2	2.18	0.59
1:F:21:GLY:HA3	1:F:85:CYS:SG	2.43	0.59
1:A:17:GLY:HA2	1:A:37:ARG:HH12	1.68	0.58
1:E:58:LYS:O	1:E:348:PRO:HG3	2.03	0.58
1:C:56:ARG:NH1	1:C:329:GLN:HE21	1.96	0.58
1:F:199:GLN:NE2	1:F:199:GLN:HA	2.11	0.58
1:C:7:LEU:O	1:C:10:VAL:HG23	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:312:ASN:HD22	1:D:315:LEU:H	1.50	0.58
1:E:147:ARG:HH12	1:F:147:ARG:HG3	1.68	0.58
1:E:261:VAL:HG12	1:E:276:ILE:HG21	1.86	0.58
1:B:12:VAL:HG11	1:B:28:LEU:HD23	1.85	0.58
1:C:189:ALA:O	1:C:192:ASP:HB2	2.04	0.58
1:D:174:LEU:O	1:D:178:GLU:HB2	2.03	0.58
1:E:127:GLY:HA2	1:F:299:CYS:SG	2.43	0.58
1:E:65:VAL:HG11	1:E:96:ILE:HD11	1.85	0.58
1:F:115:GLY:HA3	1:F:132:TYR:CE1	2.39	0.58
1:F:14:GLU:OE1	1:F:25:GLY:HA3	2.03	0.58
1:B:114:THR:HG22	1:B:116:TRP:H	1.68	0.58
1:D:15:LEU:HB3	1:D:86:PHE:CE1	2.39	0.58
1:E:156:VAL:O	1:E:161:GLY:N	2.35	0.58
1:A:199:GLN:CA	1:A:199:GLN:HE21	2.06	0.57
1:A:304:LEU:O	1:B:137:GLY:HA2	2.04	0.57
1:F:174:LEU:O	1:F:178:GLU:HB2	2.04	0.57
1:F:40:ARG:H	1:F:40:ARG:NE	2.01	0.57
1:B:178:GLU:HG2	2:B:425:HOH:O	2.03	0.57
1:E:110:PHE:HE2	1:E:112:ARG:HE	1.52	0.57
1:E:215:GLU:O	1:E:222:GLY:HA2	2.04	0.57
1:E:335:ARG:HG2	1:E:335:ARG:HH11	1.68	0.57
1:E:96:ILE:HG22	1:E:97:GLY:N	2.19	0.57
1:C:243:GLU:HB2	1:C:246:PHE:CD2	2.38	0.57
1:D:147:ARG:HG3	1:D:147:ARG:HH11	1.69	0.57
1:F:92:GLU:HA	1:F:96:ILE:O	2.05	0.57
1:B:17:GLY:HA2	1:B:37:ARG:HH12	1.70	0.57
1:B:38:VAL:HG11	1:B:72:MET:SD	2.44	0.57
1:C:114:THR:HG22	1:C:116:TRP:H	1.70	0.57
1:C:174:LEU:HB3	1:D:175:TYR:CD1	2.40	0.57
1:E:56:ARG:HH12	1:E:329:GLN:HG3	1.68	0.57
1:C:16:GLY:CA	1:C:85:CYS:HB2	2.32	0.57
1:F:13:ILE:HB	1:F:82:LEU:HD12	1.86	0.57
1:A:12:VAL:HG11	1:A:28:LEU:HD23	1.86	0.57
1:A:243:GLU:HB2	1:A:246:PHE:CD2	2.40	0.57
1:A:290:THR:O	1:A:294:ALA:HB2	2.04	0.57
1:A:58:LYS:O	1:A:348:PRO:HG3	2.04	0.57
1:E:325:HIS:HE1	1:E:344:VAL:O	1.88	0.57
1:A:176:GLU:OE1	1:B:338:ARG:NH2	2.27	0.57
1:B:357:ILE:HD12	1:B:359:TRP:OXT	2.05	0.57
1:B:55:HIS:CA	1:B:58:LYS:HD3	2.33	0.57
1:C:235:LYS:HE3	2:C:444:HOH:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:83:LEU:HD11	1:C:113:ILE:HD11	1.86	0.56
1:A:250:LEU:O	1:A:254:LEU:HB2	2.06	0.56
1:A:47:PRO:HG3	1:B:207:ILE:CD1	2.35	0.56
1:F:310:ALA:HA	1:F:321:VAL:HG21	1.87	0.56
1:F:101:CYS:HB3	1:F:108:LEU:HD23	1.87	0.56
1:F:107:ARG:HG3	2:F:368:HOH:O	2.04	0.56
1:C:203:THR:HG22	1:C:207:ILE:HD12	1.87	0.56
1:D:357:ILE:HG13	1:D:358:ASN:H	1.71	0.56
1:E:357:ILE:HG22	1:E:359:TRP:HB2	1.86	0.56
1:F:11:LYS:HG2	1:F:80:ASP:OD2	2.05	0.56
1:B:82:LEU:HD23	1:B:110:PHE:CE1	2.41	0.56
1:C:175:TYR:CD1	1:D:174:LEU:HB3	2.40	0.56
1:A:101:CYS:HB3	1:A:108:LEU:HD23	1.88	0.56
1:A:14:GLU:OE1	1:A:25:GLY:HA3	2.05	0.56
1:A:207:ILE:CD1	1:B:47:PRO:HG3	2.36	0.56
1:F:243:GLU:HB2	1:F:246:PHE:CD2	2.41	0.56
1:A:11:LYS:HB2	1:A:80:ASP:H	1.70	0.56
1:B:324:ALA:O	1:B:325:HIS:C	2.43	0.56
1:C:82:LEU:HD23	1:C:110:PHE:CE1	2.41	0.56
1:C:327:VAL:HG21	2:D:386:HOH:O	2.05	0.56
1:E:50:ASP:OD1	1:E:51:ARG:HD3	2.06	0.56
1:F:250:LEU:O	1:F:254:LEU:HB2	2.06	0.56
1:D:38:VAL:HG11	1:D:72:MET:SD	2.45	0.56
1:A:174:LEU:O	1:A:178:GLU:HB2	2.06	0.55
1:A:89:GLY:O	1:A:92:GLU:HG2	2.07	0.55
1:E:299:CYS:HB3	1:F:131:ASN:HD21	1.71	0.55
1:A:113:ILE:HG13	1:A:166:VAL:HG21	1.88	0.55
1:A:353:PRO:HB2	1:A:356:GLU:HG3	1.88	0.55
1:C:272:GLN:O	1:C:276:ILE:HD13	2.06	0.55
1:B:54:LEU:HG	2:B:440:HOH:O	2.06	0.55
1:C:114:THR:HG22	1:C:115:GLY:N	2.21	0.55
1:E:101:CYS:HA	1:E:104:VAL:HG22	1.88	0.55
1:B:17:GLY:O	1:B:18:ILE:HG23	2.06	0.55
1:E:114:THR:HB	1:E:117:GLY:N	2.17	0.55
1:C:303:VAL:HG12	1:D:140:ALA:HB2	1.88	0.55
1:D:37:ARG:HB2	1:D:60:ILE:HD13	1.89	0.55
1:E:18:ILE:O	1:E:18:ILE:HD12	2.06	0.55
1:E:327:VAL:HG11	1:F:206:GLY:CA	2.34	0.55
1:F:17:GLY:HA2	1:F:37:ARG:HH12	1.72	0.55
1:F:321:VAL:HG23	1:F:321:VAL:O	2.07	0.55
1:B:87:ARG:HH21	1:B:126:ALA:HB2	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:325:HIS:NE2	1:C:346:PRO:HD3	2.22	0.55
1:D:243:GLU:HB2	1:D:246:PHE:CD2	2.42	0.55
1:E:93:ARG:HG3	1:E:93:ARG:HH11	1.72	0.55
1:E:96:ILE:HG22	1:E:97:GLY:H	1.72	0.55
1:B:310:ALA:HA	1:B:321:VAL:HG21	1.89	0.54
1:B:353:PRO:HB2	1:B:356:GLU:HG3	1.90	0.54
1:B:357:ILE:HG13	2:B:415:HOH:O	2.07	0.54
1:E:122:LEU:HD22	1:E:125:THR:HG21	1.89	0.54
1:E:199:GLN:HA	1:E:199:GLN:NE2	2.09	0.54
1:A:115:GLY:HA3	1:A:132:TYR:CE1	2.42	0.54
1:B:11:LYS:HB2	1:B:80:ASP:H	1.72	0.54
1:E:50:ASP:CB	1:E:349:ALA:HA	2.37	0.54
1:F:14:GLU:OE2	1:F:37:ARG:HD3	2.07	0.54
1:E:176:GLU:HG3	1:E:177:ARG:N	2.22	0.54
1:A:170:ILE:HD12	2:A:455:HOH:O	2.07	0.54
1:B:11:LYS:HG2	1:B:80:ASP:OD2	2.07	0.54
1:B:87:ARG:NH2	1:B:126:ALA:HB2	2.22	0.54
1:B:170:ILE:CG2	2:B:437:HOH:O	2.52	0.54
1:E:12:VAL:HA	1:E:81:VAL:O	2.06	0.54
1:E:133:LEU:HD23	1:E:194:VAL:HG11	1.88	0.54
1:A:38:VAL:HG11	1:A:72:MET:SD	2.47	0.54
1:B:357:ILE:HG13	1:B:358:ASN:H	1.72	0.54
1:C:87:ARG:HH21	1:C:126:ALA:HB2	1.72	0.54
1:F:176:GLU:HG3	1:F:177:ARG:N	2.22	0.54
1:B:243:GLU:HB2	1:B:246:PHE:CD2	2.42	0.54
1:C:128:HIS:HE1	1:D:243:GLU:OE1	1.91	0.54
1:E:337:SER:HG	1:F:184:GLN:HB2	1.72	0.54
1:A:81:VAL:HG13	1:A:109:ILE:HB	1.90	0.54
1:A:357:ILE:HG13	1:A:358:ASN:H	1.73	0.54
1:C:194:VAL:HA	1:C:197:LEU:HD12	1.90	0.54
1:D:254:LEU:HD23	1:D:256:LEU:HD12	1.90	0.54
1:E:80:ASP:O	1:E:108:LEU:HD12	2.07	0.54
1:A:324:ALA:O	1:A:325:HIS:C	2.46	0.54
1:C:176:GLU:HG3	1:C:177:ARG:N	2.23	0.54
1:D:40:ARG:NE	1:D:40:ARG:H	2.03	0.54
1:F:83:LEU:HD11	1:F:113:ILE:HD11	1.89	0.54
1:A:16:GLY:CA	1:A:85:CYS:HB2	2.35	0.54
1:C:11:LYS:HB2	1:C:79:ALA:HA	1.88	0.54
1:D:56:ARG:NH1	1:D:329:GLN:HE21	2.00	0.54
1:F:55:HIS:CA	1:F:58:LYS:HD3	2.35	0.54
1:D:92:GLU:HA	1:D:96:ILE:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:324:ALA:O	1:F:325:HIS:C	2.45	0.54
1:F:289:TRP:HA	1:F:289:TRP:CE3	2.43	0.53
1:B:213:GLN:H	1:B:213:GLN:NE2	2.06	0.53
1:C:133:LEU:HD21	1:C:156:VAL:CG1	2.39	0.53
1:C:153:LEU:HD13	1:D:201:MET:CE	2.38	0.53
1:E:87:ARG:NH2	1:E:126:ALA:HB2	2.23	0.53
1:A:201:MET:CE	1:B:153:LEU:HD13	2.38	0.53
1:E:83:LEU:HA	1:E:111:ALA:HB3	1.90	0.53
1:D:101:CYS:HB3	1:D:108:LEU:HD23	1.91	0.53
1:F:261:VAL:HG22	1:F:276:ILE:HG21	1.91	0.53
1:A:147:ARG:HG3	1:A:147:ARG:HH11	1.73	0.53
1:C:37:ARG:HB2	1:C:60:ILE:HD13	1.89	0.53
1:D:113:ILE:HG12	1:D:166:VAL:HG11	1.90	0.53
1:E:40:ARG:HE	1:E:40:ARG:N	1.93	0.53
1:F:199:GLN:CA	1:F:199:GLN:HE21	2.12	0.53
1:A:213:GLN:H	1:A:213:GLN:NE2	2.06	0.53
1:B:114:THR:HG22	1:B:115:GLY:N	2.24	0.53
1:B:194:VAL:HA	1:B:197:LEU:HD12	1.91	0.53
1:C:249:ALA:HB3	1:C:298:ALA:HA	1.91	0.53
1:A:289:TRP:CE3	1:A:289:TRP:HA	2.44	0.53
1:E:176:GLU:OE1	1:F:338:ARG:NH2	2.33	0.53
1:A:174:LEU:HB3	1:B:175:TYR:CD1	2.44	0.52
1:B:58:LYS:O	1:B:348:PRO:HG3	2.08	0.52
1:C:15:LEU:HD23	1:C:86:PHE:HE1	1.74	0.52
1:D:65:VAL:O	1:D:69:PRO:HD2	2.09	0.52
1:B:46:MET:SD	1:B:46:MET:C	2.87	0.52
1:C:115:GLY:HA3	1:C:132:TYR:CE1	2.43	0.52
1:E:345:ARG:HG2	1:E:346:PRO:HD2	1.91	0.52
1:F:114:THR:HG22	1:F:115:GLY:N	2.23	0.52
1:F:114:THR:HG22	1:F:116:TRP:H	1.74	0.52
1:F:177:ARG:C	1:F:179:ARG:H	2.12	0.52
1:B:250:LEU:O	1:B:254:LEU:HB2	2.08	0.52
1:E:128:HIS:H	1:E:131:ASN:HD22	1.55	0.52
1:F:17:GLY:HA3	1:F:37:ARG:HH12	1.72	0.52
1:A:261:VAL:HG22	1:A:276:ILE:HG21	1.90	0.52
1:A:56:ARG:NH1	1:A:329:GLN:HE21	2.01	0.52
1:F:115:GLY:HA2	1:F:190:MET:HB2	1.91	0.52
1:C:72:MET:HE2	1:C:96:ILE:HG21	1.91	0.52
1:E:56:ARG:HB2	1:E:345:ARG:O	2.09	0.52
1:F:286:ARG:HD2	1:F:302:PRO:HB2	1.92	0.52
1:B:65:VAL:HG21	2:B:421:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:250:LEU:O	1:C:254:LEU:HB2	2.10	0.52
1:E:318:ARG:O	1:E:319:SER:HB2	2.10	0.52
1:E:336:PHE:HB2	1:E:340:PRO:HA	1.90	0.52
1:F:65:VAL:O	1:F:69:PRO:HD2	2.09	0.52
1:A:11:LYS:HG2	1:A:80:ASP:OD2	2.10	0.52
1:A:153:LEU:HD13	1:B:201:MET:CE	2.40	0.52
1:A:249:ALA:HB3	1:A:298:ALA:HA	1.92	0.52
1:F:16:GLY:CA	1:F:85:CYS:HB2	2.36	0.52
1:C:6:PRO:HD3	1:C:339:THR:O	2.09	0.52
1:E:270:TYR:N	1:E:271:PRO:CD	2.73	0.52
1:B:115:GLY:HA3	1:B:132:TYR:CE1	2.45	0.52
1:B:65:VAL:HG22	2:B:421:HOH:O	2.08	0.52
1:E:56:ARG:NH1	1:E:329:GLN:HG3	2.25	0.52
1:A:92:GLU:HA	1:A:96:ILE:O	2.10	0.51
1:C:4:GLY:O	1:C:8:ALA:HB2	2.10	0.51
1:D:12:VAL:HG11	1:D:28:LEU:HD23	1.93	0.51
1:F:357:ILE:HG13	1:F:358:ASN:H	1.75	0.51
1:C:14:GLU:OE2	1:C:22:PRO:HA	2.10	0.51
1:E:27:VAL:HG12	1:E:31:LEU:HD23	1.93	0.51
1:E:324:ALA:O	1:E:326:GLY:N	2.43	0.51
1:A:177:ARG:C	1:A:179:ARG:H	2.14	0.51
1:A:13:ILE:HB	1:A:82:LEU:HD12	1.92	0.51
1:B:168:LEU:O	1:B:172:VAL:HG23	2.11	0.51
1:C:310:ALA:HA	1:C:321:VAL:HG21	1.92	0.51
1:D:39:ARG:HD3	1:D:39:ARG:O	2.10	0.51
1:D:16:GLY:CA	1:D:85:CYS:HB2	2.41	0.51
1:E:16:GLY:HA3	1:E:85:CYS:HB2	1.92	0.51
1:E:250:LEU:HD23	1:E:300:VAL:HG21	1.91	0.51
1:A:357:ILE:HD12	1:A:359:TRP:OXT	2.10	0.51
1:C:261:VAL:HG22	1:C:276:ILE:HG21	1.92	0.51
1:C:89:GLY:O	1:C:92:GLU:HG2	2.10	0.51
1:D:321:VAL:O	1:D:321:VAL:HG23	2.10	0.51
1:E:122:LEU:O	1:E:125:THR:HG22	2.10	0.51
1:E:303:VAL:O	1:E:304:LEU:HD23	2.11	0.51
1:A:254:LEU:HD23	1:A:256:LEU:HD12	1.92	0.51
1:A:37:ARG:HB2	1:A:60:ILE:HD13	1.92	0.51
1:C:39:ARG:HD3	1:C:39:ARG:O	2.11	0.51
1:F:213:GLN:H	1:F:213:GLN:NE2	2.08	0.51
1:C:291:ARG:NE	2:C:435:HOH:O	2.43	0.51
1:C:55:HIS:CA	1:C:58:LYS:HD3	2.40	0.51
1:D:289:TRP:CE3	1:D:289:TRP:HA	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:42:GLY:O	1:D:44:LEU:HD12	2.11	0.51
1:E:303:VAL:HB	2:E:402:HOH:O	2.10	0.51
1:F:113:ILE:H	1:F:113:ILE:HD12	1.75	0.51
1:E:88:PRO:HG3	1:E:114:THR:HG21	1.91	0.51
1:A:113:ILE:HD12	1:A:113:ILE:H	1.76	0.51
1:B:39:ARG:HD2	1:B:60:ILE:HG23	1.92	0.51
1:D:113:ILE:HG13	1:D:166:VAL:HG21	1.93	0.51
1:E:17:GLY:CA	1:E:37:ARG:HH12	2.24	0.51
1:A:114:THR:HG22	1:A:115:GLY:N	2.26	0.50
1:B:128:HIS:HD2	2:B:427:HOH:O	1.94	0.50
1:F:12:VAL:HG13	1:F:81:VAL:HB	1.94	0.50
1:B:354:ILE:O	1:B:357:ILE:HG23	2.11	0.50
1:C:289:TRP:HA	1:C:289:TRP:CE3	2.46	0.50
1:D:249:ALA:HB3	1:D:298:ALA:HA	1.93	0.50
1:E:86:PHE:HB3	1:E:90:THR:OG1	2.10	0.50
1:A:310:ALA:HA	1:A:321:VAL:HG21	1.93	0.50
1:C:11:LYS:HG2	1:C:80:ASP:OD2	2.11	0.50
1:F:11:LYS:HB2	1:F:80:ASP:H	1.77	0.50
1:A:245:GLN:O	1:A:248:ALA:HB3	2.10	0.50
1:B:42:GLY:O	1:B:44:LEU:HD12	2.12	0.50
1:C:58:LYS:O	1:C:348:PRO:HG3	2.11	0.50
1:D:114:THR:CG2	2:D:448:HOH:O	2.55	0.50
1:D:115:GLY:HA3	1:D:132:TYR:CE1	2.47	0.50
1:D:147:ARG:HG3	1:D:147:ARG:NH1	2.27	0.50
1:E:78:LYS:HD2	1:E:359:TRP:OXT	2.11	0.50
1:A:133:LEU:HD21	1:A:156:VAL:CG1	2.41	0.50
1:A:11:LYS:HB2	1:A:79:ALA:HA	1.93	0.50
1:D:213:GLN:NE2	1:D:213:GLN:H	2.09	0.50
1:E:305:ALA:N	1:E:308:GLU:HB2	2.26	0.50
1:E:329:GLN:NE2	2:E:394:HOH:O	2.42	0.50
1:B:39:ARG:HD2	1:B:60:ILE:CG2	2.41	0.50
1:D:11:LYS:HD2	1:D:359:TRP:CD1	2.47	0.50
1:B:11:LYS:HD2	1:B:359:TRP:CD1	2.47	0.50
1:D:324:ALA:O	1:D:325:HIS:C	2.49	0.50
1:B:254:LEU:HG	1:B:280:ARG:HG2	1.94	0.50
1:B:289:TRP:HA	1:B:289:TRP:CE3	2.46	0.50
1:C:324:ALA:O	1:C:325:HIS:C	2.50	0.50
1:D:203:THR:HG22	1:D:207:ILE:HD12	1.93	0.50
1:A:114:THR:HG22	1:A:116:TRP:H	1.76	0.49
1:A:176:GLU:HG3	1:A:177:ARG:N	2.26	0.49
1:B:290:THR:O	1:B:294:ALA:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:14:GLU:OE1	1:C:25:GLY:HA3	2.11	0.49
1:C:15:LEU:HB3	1:C:86:PHE:CE1	2.47	0.49
1:D:177:ARG:C	1:D:179:ARG:H	2.15	0.49
1:A:325:HIS:NE2	1:A:346:PRO:HD3	2.27	0.49
1:B:83:LEU:HD11	1:B:113:ILE:HD11	1.93	0.49
1:E:325:HIS:CE1	1:E:344:VAL:O	2.65	0.49
1:F:89:GLY:O	1:F:92:GLU:HG2	2.11	0.49
1:A:176:GLU:HG2	1:A:184:GLN:NE2	2.27	0.49
1:D:64:ASP:O	1:D:69:PRO:HB2	2.12	0.49
1:A:15:LEU:HB3	1:A:86:PHE:CE1	2.48	0.49
1:C:213:GLN:NE2	1:C:213:GLN:H	2.09	0.49
1:C:137:GLY:HA2	1:D:304:LEU:O	2.11	0.49
1:D:327:VAL:HG12	2:D:433:HOH:O	2.12	0.49
1:E:130:ILE:HG23	1:E:131:ASN:N	2.27	0.49
1:E:175:TYR:CE1	1:F:178:GLU:HG3	2.47	0.49
1:A:321:VAL:HG23	1:A:321:VAL:O	2.12	0.49
1:B:174:LEU:O	1:B:178:GLU:HB2	2.12	0.49
1:B:189:ALA:O	1:B:192:ASP:HB2	2.11	0.49
1:C:243:GLU:OE1	1:D:128:HIS:HE1	1.95	0.49
1:A:203:THR:HG22	1:A:207:ILE:HD12	1.94	0.49
1:A:39:ARG:HD2	1:A:60:ILE:HG23	1.94	0.49
1:B:176:GLU:HG2	1:B:184:GLN:NE2	2.28	0.49
1:E:327:VAL:HG12	1:E:328:GLN:N	2.28	0.49
1:F:176:GLU:HG2	1:F:184:GLN:NE2	2.27	0.49
1:F:46:MET:SD	1:F:46:MET:C	2.90	0.49
1:C:44:LEU:N	1:C:44:LEU:HD12	2.28	0.49
1:D:211:ARG:NH2	2:D:369:HOH:O	2.43	0.49
1:E:263:THR:HG23	1:E:266:ASP:HB2	1.94	0.49
1:A:82:LEU:HD23	1:A:110:PHE:CE1	2.48	0.49
1:C:177:ARG:C	1:C:179:ARG:H	2.14	0.49
1:C:175:TYR:CE1	1:D:178:GLU:HG3	2.48	0.49
1:F:200:MET:O	1:F:203:THR:HB	2.13	0.49
1:A:83:LEU:HD11	1:A:113:ILE:HD11	1.95	0.49
1:D:17:GLY:HA2	1:D:37:ARG:NH1	2.27	0.49
1:C:321:VAL:O	2:C:410:HOH:O	2.20	0.49
1:F:82:LEU:HD23	1:F:110:PHE:CE1	2.48	0.49
1:A:338:ARG:NH1	1:B:183:GLY:O	2.44	0.48
1:E:231:THR:HG21	1:E:286:ARG:HA	1.95	0.48
1:F:37:ARG:HB2	1:F:60:ILE:HD13	1.95	0.48
1:A:128:HIS:HE1	1:B:243:GLU:OE1	1.95	0.48
1:C:147:ARG:HG3	1:C:147:ARG:HH11	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:GLY:O	1:C:44:LEU:HD12	2.13	0.48
1:D:286:ARG:HD2	1:D:302:PRO:HB2	1.96	0.48
1:E:243:GLU:HB2	1:E:246:PHE:CD2	2.49	0.48
1:E:65:VAL:O	1:E:69:PRO:HD2	2.13	0.48
1:A:55:HIS:CA	1:A:58:LYS:HD3	2.40	0.48
1:A:87:ARG:NH2	1:A:126:ALA:HB2	2.28	0.48
1:B:92:GLU:HA	1:B:96:ILE:O	2.14	0.48
1:E:119:ASP:O	1:F:318:ARG:HD2	2.12	0.48
1:E:251:LEU:HD11	1:E:261:VAL:HG21	1.94	0.48
1:F:11:LYS:HB2	1:F:79:ALA:HA	1.95	0.48
1:B:37:ARG:HB2	1:B:60:ILE:HD13	1.95	0.48
1:C:290:THR:O	1:C:294:ALA:HB2	2.13	0.48
1:D:353:PRO:HB2	1:D:356:GLU:HG3	1.96	0.48
1:A:210:LEU:N	2:A:382:HOH:O	2.42	0.48
1:B:272:GLN:HG3	2:B:430:HOH:O	2.14	0.48
1:D:133:LEU:HD21	1:D:156:VAL:HG12	1.96	0.48
1:D:15:LEU:HD23	1:D:86:PHE:HE1	1.79	0.48
1:E:15:LEU:HD13	1:E:82:LEU:HD11	1.96	0.48
1:E:56:ARG:HH11	1:E:329:GLN:NE2	2.10	0.48
1:E:47:PRO:HG2	1:F:207:ILE:CD1	2.43	0.48
1:F:217:PHE:CG	1:F:218:LEU:N	2.81	0.48
1:F:55:HIS:HA	1:F:58:LYS:CD	2.40	0.48
1:A:39:ARG:O	1:A:39:ARG:HD3	2.13	0.48
1:C:174:LEU:O	1:C:178:GLU:HB2	2.14	0.48
1:F:87:ARG:NH2	1:F:126:ALA:HB2	2.28	0.48
1:E:130:ILE:CG2	1:E:131:ASN:N	2.76	0.48
1:C:357:ILE:HG13	1:C:358:ASN:H	1.78	0.48
1:D:357:ILE:HD12	1:D:359:TRP:OXT	2.14	0.48
1:E:106:PRO:C	1:E:108:LEU:H	2.16	0.48
1:E:47:PRO:CG	1:F:207:ILE:HD13	2.44	0.48
1:E:65:VAL:HG23	2:E:401:HOH:O	2.12	0.48
1:B:107:ARG:NH1	2:B:383:HOH:O	2.47	0.48
1:B:89:GLY:O	1:B:92:GLU:HG2	2.14	0.48
1:D:11:LYS:HB2	1:D:79:ALA:HA	1.95	0.48
1:D:11:LYS:HG2	1:D:80:ASP:OD2	2.14	0.48
1:C:133:LEU:HD21	1:C:156:VAL:HG12	1.96	0.47
1:D:176:GLU:HG2	1:D:184:GLN:NE2	2.29	0.47
1:E:338:ARG:HH12	1:F:184:GLN:HB3	1.79	0.47
1:E:70:GLN:HG2	1:E:70:GLN:O	2.14	0.47
1:F:151:PRO:HA	1:F:152:PRO:HD3	1.77	0.47
1:F:15:LEU:HB3	1:F:86:PHE:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:VAL:O	1:B:170:ILE:HG13	2.14	0.47
1:D:56:ARG:HB2	1:D:345:ARG:O	2.14	0.47
1:F:357:ILE:HD12	1:F:359:TRP:OXT	2.13	0.47
1:A:87:ARG:HH21	1:A:126:ALA:HB2	1.79	0.47
1:B:15:LEU:HD23	1:B:86:PHE:HE1	1.79	0.47
1:E:13:ILE:HB	1:E:82:LEU:CD1	2.42	0.47
1:E:321:VAL:HG23	1:E:321:VAL:O	2.14	0.47
1:F:17:GLY:HA2	1:F:37:ARG:NH1	2.29	0.47
1:A:39:ARG:HD2	1:A:60:ILE:CG2	2.44	0.47
1:B:147:ARG:HH11	1:B:147:ARG:HG3	1.80	0.47
1:B:203:THR:HG22	1:B:207:ILE:HD12	1.96	0.47
1:C:177:ARG:O	1:C:181:GLY:N	2.48	0.47
1:D:217:PHE:CG	1:D:218:LEU:N	2.83	0.47
1:E:81:VAL:HG22	1:E:174:LEU:HD11	1.95	0.47
1:B:357:ILE:CD1	2:B:414:HOH:O	2.63	0.47
1:F:154:ASN:O	1:F:158:ASP:HB2	2.13	0.47
1:A:11:LYS:HD2	1:A:359:TRP:CD1	2.49	0.47
1:A:147:ARG:NH1	1:A:147:ARG:HG3	2.30	0.47
1:A:14:GLU:OE2	1:A:22:PRO:HA	2.15	0.47
1:A:17:GLY:HA2	1:A:37:ARG:NH1	2.28	0.47
1:C:83:LEU:CD1	1:C:113:ILE:HD11	2.44	0.47
1:D:261:VAL:HG22	1:D:276:ILE:HG21	1.97	0.47
1:E:261:VAL:CG1	1:E:276:ILE:HG21	2.45	0.47
1:F:133:LEU:HD21	1:F:156:VAL:CG1	2.45	0.47
1:B:213:GLN:HG2	1:B:216:SER:OG	2.14	0.47
1:D:176:GLU:HG3	1:D:177:ARG:N	2.30	0.47
1:A:40:ARG:N	1:A:40:ARG:HE	2.09	0.47
1:C:299:CYS:HB3	1:D:131:ASN:HD21	1.80	0.47
1:C:92:GLU:HA	1:C:96:ILE:O	2.15	0.47
1:E:114:THR:O	1:E:189:ALA:HA	2.14	0.47
1:E:87:ARG:HB2	1:E:90:THR:HG23	1.96	0.47
1:F:58:LYS:O	1:F:348:PRO:HG3	2.15	0.47
1:A:280:ARG:NH1	2:A:435:HOH:O	2.48	0.47
1:D:114:THR:HG22	1:D:115:GLY:N	2.30	0.47
1:F:318:ARG:NH1	1:F:318:ARG:HB3	2.30	0.47
1:B:114:THR:HB	2:B:374:HOH:O	2.15	0.47
1:B:272:GLN:O	1:B:276:ILE:HD13	2.14	0.46
1:D:46:MET:C	1:D:46:MET:SD	2.94	0.46
1:F:70:GLN:C	1:F:72:MET:H	2.19	0.46
1:F:70:GLN:HG2	1:F:73:LEU:HD12	1.97	0.46
1:B:311:ASN:O	1:B:316:LYS:HE2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:60:ILE:HG12	1:C:348:PRO:HG2	1.96	0.46
1:E:338:ARG:NH1	1:F:184:GLN:HB3	2.30	0.46
1:F:168:LEU:O	1:F:172:VAL:HG23	2.15	0.46
1:A:224:PRO:HG2	1:A:273:MET:SD	2.56	0.46
1:D:168:LEU:O	1:D:172:VAL:HG23	2.16	0.46
1:F:254:LEU:HD23	1:F:256:LEU:HD12	1.97	0.46
1:F:56:ARG:HA	1:F:347:PRO:HA	1.97	0.46
1:B:249:ALA:HB3	1:B:298:ALA:HA	1.98	0.46
1:C:171:VAL:HG11	1:D:172:VAL:HA	1.98	0.46
1:E:244:PRO:HD3	2:E:415:HOH:O	2.15	0.46
1:F:39:ARG:HD3	1:F:39:ARG:O	2.16	0.46
1:A:217:PHE:CG	1:A:218:LEU:N	2.83	0.46
1:B:177:ARG:C	1:B:179:ARG:H	2.18	0.46
1:C:318:ARG:NH1	1:C:318:ARG:HB3	2.30	0.46
1:C:38:VAL:HG11	1:C:72:MET:SD	2.56	0.46
1:D:189:ALA:O	1:D:192:ASP:HB2	2.15	0.46
1:E:358:ASN:HB3	2:E:404:HOH:O	2.15	0.46
1:A:42:GLY:O	1:A:44:LEU:HD12	2.16	0.46
1:C:312:ASN:ND2	1:C:315:LEU:H	2.10	0.46
1:E:325:HIS:CD2	1:E:346:PRO:HD3	2.50	0.46
1:E:46:MET:CG	2:E:366:HOH:O	2.64	0.46
1:D:107:ARG:HH11	1:D:107:ARG:HG3	1.81	0.46
1:F:133:LEU:HD21	1:F:156:VAL:HG12	1.97	0.46
1:F:15:LEU:HD23	1:F:86:PHE:HE1	1.80	0.46
1:D:285:THR:OG1	1:D:288:GLU:HG3	2.16	0.46
1:E:122:LEU:HB2	1:F:314:HIS:CG	2.51	0.46
1:E:286:ARG:HH12	1:E:308:GLU:CD	2.19	0.46
1:F:257:SER:HB3	1:F:260:ASP:OD2	2.16	0.46
1:B:39:ARG:O	1:B:39:ARG:HD3	2.16	0.46
1:C:316:LYS:HA	2:C:410:HOH:O	2.16	0.46
1:A:168:LEU:O	1:A:172:VAL:HG23	2.16	0.46
1:B:101:CYS:HA	1:B:104:VAL:HG22	1.97	0.46
1:C:35:VAL:HB	1:C:58:LYS:HG2	1.98	0.46
1:D:192:ASP:O	1:D:196:VAL:HG23	2.17	0.46
1:A:154:ASN:O	1:A:158:ASP:HB2	2.15	0.45
1:B:109:ILE:HG13	1:B:174:LEU:HD12	1.99	0.45
1:C:321:VAL:HG23	1:C:321:VAL:O	2.17	0.45
1:C:14:GLU:CD	1:C:58:LYS:HZ2	2.19	0.45
1:D:99:ASP:O	1:D:102:ALA:HB3	2.16	0.45
1:A:15:LEU:HD23	1:A:86:PHE:HE1	1.82	0.45
1:C:81:VAL:HG13	1:C:109:ILE:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:224:PRO:HG2	1:F:273:MET:SD	2.56	0.45
1:A:4:GLY:O	1:A:8:ALA:HB2	2.17	0.45
1:B:257:SER:HB3	1:B:260:ASP:OD2	2.17	0.45
1:D:91:CYS:O	1:D:96:ILE:HG13	2.16	0.45
1:E:250:LEU:C	1:E:250:LEU:HD13	2.37	0.45
1:B:17:GLY:HA3	1:B:37:ARG:HH12	1.81	0.45
1:C:39:ARG:HD2	1:C:60:ILE:HG23	1.98	0.45
1:E:24:ALA:HA	1:E:167:LEU:HD11	1.98	0.45
1:F:60:ILE:HG12	1:F:348:PRO:HG2	1.98	0.45
1:A:175:TYR:CD1	1:B:174:LEU:HB3	2.52	0.45
1:E:40:ARG:HB2	1:E:41:PRO:CD	2.33	0.45
1:A:286:ARG:HD2	1:A:302:PRO:HB2	1.99	0.45
1:C:28:LEU:HD13	1:C:167:LEU:CD2	2.46	0.45
1:D:345:ARG:HD2	2:D:372:HOH:O	2.16	0.45
1:D:52:ASP:OD2	2:D:446:HOH:O	2.21	0.45
1:E:30:ASP:HB3	1:E:332:PRO:HB3	1.99	0.45
1:F:107:ARG:HH11	1:F:107:ARG:HG3	1.82	0.45
1:A:46:MET:C	1:A:46:MET:SD	2.95	0.45
1:B:11:LYS:HB2	1:B:79:ALA:HA	1.97	0.45
1:C:270:TYR:N	1:C:271:PRO:CD	2.80	0.45
1:C:276:ILE:N	1:C:276:ILE:HD12	2.31	0.45
1:C:353:PRO:HG2	1:C:356:GLU:CD	2.37	0.45
1:E:251:LEU:HD21	1:E:261:VAL:CG2	2.47	0.45
1:B:321:VAL:HG23	1:B:321:VAL:O	2.17	0.45
1:C:318:ARG:O	1:C:335:ARG:NH1	2.45	0.45
1:F:50:ASP:OD1	1:F:51:ARG:HD3	2.16	0.45
1:F:12:VAL:HG11	1:F:28:LEU:HD23	1.98	0.45
1:E:129:ASP:O	1:E:130:ILE:C	2.56	0.44
1:F:87:ARG:HH21	1:F:126:ALA:HB2	1.82	0.44
1:A:107:ARG:HH11	1:A:107:ARG:HG3	1.82	0.44
1:B:13:ILE:HB	1:B:82:LEU:HD12	1.99	0.44
1:B:154:ASN:O	1:B:158:ASP:HB2	2.16	0.44
1:D:245:GLN:O	1:D:248:ALA:HB3	2.17	0.44
1:C:70:GLN:HG2	1:C:73:LEU:HD12	2.00	0.44
1:D:116:TRP:HB2	2:D:448:HOH:O	2.17	0.44
1:B:56:ARG:HB2	1:B:345:ARG:O	2.18	0.44
1:C:338:ARG:NH2	1:D:176:GLU:OE1	2.39	0.44
1:D:310:ALA:HA	1:D:321:VAL:HG21	1.99	0.44
1:D:39:ARG:HD2	1:D:60:ILE:CG2	2.48	0.44
1:D:78:LYS:HD3	1:D:359:TRP:OXT	2.17	0.44
1:E:190:MET:O	1:E:191:VAL:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:250:LEU:HD23	1:E:300:VAL:CG2	2.47	0.44
1:C:154:ASN:O	1:C:158:ASP:HB2	2.17	0.44
1:D:39:ARG:HD2	1:D:60:ILE:HG23	1.98	0.44
1:C:286:ARG:HD2	1:C:302:PRO:HB2	2.00	0.44
1:D:318:ARG:O	1:D:335:ARG:NH1	2.46	0.44
1:E:218:LEU:O	1:E:219:LEU:HD23	2.17	0.44
1:F:176:GLU:HG2	1:F:184:GLN:HE21	1.83	0.44
1:F:28:LEU:O	1:F:33:ALA:HB3	2.18	0.44
1:A:243:GLU:OE1	1:B:128:HIS:HE1	2.00	0.44
1:B:114:THR:CG2	1:B:117:GLY:H	2.31	0.44
1:B:147:ARG:NH1	1:B:147:ARG:HG3	2.33	0.44
1:D:359:TRP:CD1	1:D:359:TRP:N	2.84	0.44
1:E:65:VAL:HG11	1:E:96:ILE:CD1	2.47	0.44
1:F:359:TRP:CD1	1:F:359:TRP:N	2.83	0.44
1:A:44:LEU:N	1:A:44:LEU:HD12	2.32	0.44
1:A:65:VAL:O	1:A:69:PRO:HD2	2.18	0.44
1:B:65:VAL:O	1:B:69:PRO:HD2	2.18	0.44
1:C:107:ARG:HH11	1:C:107:ARG:HG3	1.82	0.44
1:D:70:GLN:C	1:D:72:MET:H	2.21	0.44
1:E:200:MET:O	1:E:204:MET:HG2	2.18	0.44
1:F:147:ARG:HG3	1:F:147:ARG:HH11	1.83	0.44
1:F:72:MET:HE2	1:F:96:ILE:HG21	2.00	0.44
1:B:107:ARG:HG3	1:B:107:ARG:HH11	1.82	0.44
1:E:170:ILE:O	1:E:174:LEU:HD13	2.18	0.44
1:E:211:ARG:HH21	1:E:216:SER:CB	2.31	0.44
1:F:357:ILE:CG1	1:F:358:ASN:H	2.31	0.44
1:A:17:GLY:HA3	1:A:37:ARG:HH12	1.78	0.43
1:B:170:ILE:O	1:B:174:LEU:HD13	2.18	0.43
1:B:56:ARG:HA	1:B:347:PRO:HA	2.00	0.43
1:B:15:LEU:HB3	1:B:86:PHE:CE1	2.53	0.43
1:E:315:LEU:HD12	1:E:315:LEU:HA	1.78	0.43
1:E:347:PRO:HA	1:E:348:PRO:HD3	1.89	0.43
1:F:353:PRO:O	1:F:354:ILE:HB	2.18	0.43
1:A:285:THR:OG1	1:A:288:GLU:HG3	2.18	0.43
1:A:318:ARG:HB3	1:A:318:ARG:NH1	2.33	0.43
1:B:17:GLY:HA2	1:B:37:ARG:NH1	2.32	0.43
1:C:224:PRO:HG2	1:C:273:MET:SD	2.58	0.43
1:E:305:ALA:H	1:E:308:GLU:HB2	1.83	0.43
1:A:113:ILE:HG12	1:A:166:VAL:HG11	2.00	0.43
1:B:44:LEU:HD12	1:B:44:LEU:N	2.33	0.43
1:C:176:GLU:HG2	1:C:184:GLN:NE2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:6:PRO:HD3	1:E:339:THR:O	2.19	0.43
1:E:93:ARG:HB2	1:E:93:ARG:CZ	2.46	0.43
1:F:14:GLU:OE2	1:F:22:PRO:HA	2.18	0.43
1:F:214:ARG:HG3	1:F:214:ARG:HH11	1.83	0.43
1:A:354:ILE:O	1:A:357:ILE:HG23	2.19	0.43
2:A:409:HOH:O	1:B:121:PRO:HG3	2.18	0.43
1:B:55:HIS:HA	1:B:58:LYS:CD	2.42	0.43
1:C:101:CYS:HA	1:C:104:VAL:HG22	1.99	0.43
1:C:156:VAL:HB	2:C:387:HOH:O	2.18	0.43
1:D:140:ALA:O	1:D:214:ARG:HD3	2.18	0.43
1:E:310:ALA:HA	1:E:321:VAL:HG21	2.00	0.43
1:A:151:PRO:HA	1:A:152:PRO:HD3	1.75	0.43
1:C:11:LYS:CB	1:C:79:ALA:HA	2.48	0.43
1:C:147:ARG:NH1	1:C:147:ARG:HG3	2.34	0.43
1:E:39:ARG:O	1:E:62:ASP:HA	2.19	0.43
1:B:105:ASN:ND2	1:B:107:ARG:H	2.16	0.43
1:B:81:VAL:HG13	1:B:109:ILE:HB	1.99	0.43
1:B:16:GLY:CA	1:B:85:CYS:HB2	2.44	0.43
1:D:224:PRO:HG2	1:D:273:MET:SD	2.59	0.43
1:E:115:GLY:HA3	1:E:132:TYR:CD1	2.53	0.43
1:E:219:LEU:O	1:F:153:LEU:HA	2.18	0.43
1:B:101:CYS:HB3	1:B:108:LEU:CD2	2.46	0.43
1:B:359:TRP:N	1:B:359:TRP:CD1	2.86	0.43
1:B:62:ASP:O	1:B:63:LEU:HB2	2.17	0.43
1:E:171:VAL:HA	1:E:174:LEU:HD22	2.00	0.43
1:E:212:ASP:O	1:E:212:ASP:OD2	2.37	0.43
1:A:70:GLN:C	1:A:72:MET:H	2.22	0.43
1:C:183:GLY:O	1:D:338:ARG:NH1	2.48	0.43
1:C:12:VAL:HG13	1:C:81:VAL:HB	2.01	0.43
1:D:357:ILE:CG1	1:D:358:ASN:H	2.29	0.43
1:F:272:GLN:O	1:F:276:ILE:HD13	2.19	0.43
1:A:334:PRO:HG3	1:B:169:GLY:HA3	2.01	0.43
1:B:289:TRP:HA	1:B:289:TRP:HE3	1.84	0.43
1:B:40:ARG:HE	1:B:40:ARG:N	2.09	0.43
1:F:205:LYS:NZ	2:F:399:HOH:O	2.51	0.43
1:F:40:ARG:N	1:F:40:ARG:HE	2.09	0.43
1:B:207:ILE:O	1:B:207:ILE:HG22	2.17	0.43
1:B:357:ILE:O	1:B:358:ASN:HB2	2.18	0.43
1:C:254:LEU:HD23	1:C:256:LEU:HD12	2.00	0.43
1:C:289:TRP:HE3	1:C:289:TRP:HA	1.84	0.43
1:C:359:TRP:CD1	1:C:359:TRP:N	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:GLN:C	1:C:72:MET:H	2.22	0.43
1:D:113:ILE:H	1:D:113:ILE:HD12	1.84	0.43
1:E:137:GLY:HA2	1:F:304:LEU:O	2.18	0.43
1:E:70:GLN:O	1:E:70:GLN:NE2	2.52	0.43
1:F:39:ARG:HD2	1:F:60:ILE:CG2	2.49	0.43
1:C:256:LEU:HD13	1:C:261:VAL:HG21	2.01	0.42
1:C:354:ILE:O	1:C:357:ILE:HG23	2.19	0.42
1:D:15:LEU:HD11	1:D:82:LEU:HD11	1.99	0.42
1:D:352:THR:O	1:D:353:PRO:O	2.37	0.42
1:E:312:ASN:HB3	1:E:315:LEU:HB2	2.01	0.42
1:E:89:GLY:O	1:E:92:GLU:N	2.37	0.42
1:A:166:VAL:O	1:A:170:ILE:HG13	2.19	0.42
1:A:289:TRP:HA	1:A:289:TRP:HE3	1.84	0.42
1:A:26:MET:SD	1:B:199:GLN:HG3	2.59	0.42
1:B:91:CYS:O	1:B:96:ILE:HG13	2.19	0.42
1:C:105:ASN:HD21	1:C:107:ARG:HB2	1.84	0.42
1:C:13:ILE:HB	1:C:82:LEU:HD12	2.02	0.42
1:C:285:THR:OG1	1:C:288:GLU:HG3	2.19	0.42
1:D:14:GLU:OE2	1:D:22:PRO:HA	2.19	0.42
1:E:157:ALA:HB2	1:E:194:VAL:HG21	2.01	0.42
1:E:267:VAL:HA	1:E:270:TYR:CD2	2.54	0.42
1:E:334:PRO:HB3	1:F:165:LEU:HG	2.00	0.42
1:E:13:ILE:O	1:E:82:LEU:HD12	2.18	0.42
1:F:20:PRO:O	1:F:21:GLY:C	2.58	0.42
1:A:70:GLN:HG2	1:A:73:LEU:HD12	2.00	0.42
1:B:12:VAL:HG13	1:B:81:VAL:HB	2.02	0.42
1:C:56:ARG:HA	1:C:347:PRO:HA	2.00	0.42
1:C:172:VAL:CG2	1:D:171:VAL:HG11	2.50	0.42
1:A:318:ARG:O	1:A:335:ARG:NH1	2.46	0.42
1:B:249:ALA:HB1	1:B:298:ALA:HB2	2.02	0.42
1:C:353:PRO:O	1:C:354:ILE:HB	2.19	0.42
1:D:198:ALA:O	1:D:199:GLN:C	2.56	0.42
1:F:318:ARG:O	1:F:335:ARG:NH1	2.47	0.42
1:A:28:LEU:HD13	1:A:167:LEU:CD2	2.49	0.42
1:A:213:GLN:HG2	1:A:216:SER:OG	2.19	0.42
1:A:311:ASN:O	1:A:316:LYS:HE2	2.18	0.42
1:B:176:GLU:HG3	1:B:177:ARG:N	2.34	0.42
1:C:17:GLY:HA2	1:C:37:ARG:HH12	1.83	0.42
1:D:357:ILE:HG13	1:D:358:ASN:N	2.34	0.42
1:D:54:LEU:O	1:D:58:LYS:NZ	2.52	0.42
1:E:233:ASP:HB3	1:E:285:THR:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:251:LEU:HA	1:E:251:LEU:HD12	1.87	0.42
1:E:263:THR:CG2	1:E:266:ASP:HB2	2.50	0.42
1:B:28:LEU:HD13	1:B:167:LEU:CD2	2.49	0.42
1:C:19:GLY:HA3	1:C:20:PRO:HD2	1.89	0.42
1:C:40:ARG:N	1:C:40:ARG:HE	2.06	0.42
1:F:198:ALA:O	1:F:199:GLN:C	2.57	0.42
1:E:353:PRO:HD2	1:E:356:GLU:CG	2.46	0.42
1:F:11:LYS:HD2	1:F:359:TRP:CD1	2.54	0.42
1:F:170:ILE:O	1:F:174:LEU:HD13	2.19	0.42
1:A:153:LEU:HD13	1:B:201:MET:HE3	2.00	0.42
1:A:170:ILE:CD1	2:A:455:HOH:O	2.64	0.42
1:B:254:LEU:HD23	1:B:256:LEU:CD1	2.49	0.42
1:F:312:ASN:ND2	1:F:315:LEU:H	2.14	0.42
1:A:133:LEU:HD21	1:A:156:VAL:HG12	2.01	0.42
1:B:129:ASP:OD2	1:B:157:ALA:HB3	2.20	0.42
1:B:217:PHE:CG	1:B:218:LEU:N	2.87	0.42
1:B:285:THR:OG1	1:B:288:GLU:HG3	2.19	0.42
1:B:288:GLU:O	1:B:291:ARG:HB2	2.19	0.42
1:B:357:ILE:HG13	1:B:358:ASN:N	2.34	0.42
1:B:55:HIS:O	1:B:58:LYS:HB2	2.20	0.42
1:E:191:VAL:CG2	1:F:315:LEU:HD11	2.50	0.42
1:E:56:ARG:HD2	1:E:344:VAL:CG1	2.49	0.42
1:B:130:ILE:HG23	1:B:131:ASN:N	2.34	0.42
1:A:199:GLN:HG3	1:B:26:MET:HE1	2.02	0.41
1:B:78:LYS:HE3	2:B:414:HOH:O	2.20	0.41
1:C:150:MET:HG3	1:C:151:PRO:HD2	2.02	0.41
1:C:39:ARG:HD2	1:C:60:ILE:CG2	2.49	0.41
1:D:257:SER:HB3	1:D:260:ASP:OD2	2.20	0.41
1:E:335:ARG:CG	1:E:335:ARG:HH11	2.32	0.41
1:F:130:ILE:HG23	1:F:131:ASN:N	2.34	0.41
1:F:44:LEU:HD12	1:F:44:LEU:N	2.35	0.41
1:B:70:GLN:HG2	1:B:73:LEU:HD12	2.01	0.41
1:C:328:GLN:NE2	2:C:446:HOH:O	2.53	0.41
1:D:56:ARG:HA	1:D:347:PRO:HA	2.02	0.41
1:E:97:GLY:HA3	1:E:100:ASP:OD2	2.20	0.41
1:E:162:GLY:HA3	1:E:190:MET:HG2	2.02	0.41
1:F:249:ALA:HB3	1:F:298:ALA:HA	2.02	0.41
1:A:257:SER:HB3	1:A:260:ASP:OD2	2.20	0.41
1:A:56:ARG:HA	1:A:347:PRO:HA	2.02	0.41
1:A:353:PRO:O	1:A:354:ILE:HB	2.20	0.41
1:B:280:ARG:O	1:B:289:TRP:HZ2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:GLY:CA	2:C:364:HOH:O	2.68	0.41
1:C:198:ALA:O	1:C:199:GLN:C	2.59	0.41
1:C:249:ALA:HB1	1:C:298:ALA:HB2	2.02	0.41
1:F:325:HIS:NE2	1:F:346:PRO:HD3	2.35	0.41
1:F:42:GLY:O	1:F:44:LEU:HD12	2.20	0.41
1:F:91:CYS:O	1:F:96:ILE:HG13	2.20	0.41
1:B:233:ASP:N	1:B:233:ASP:OD2	2.53	0.41
1:B:30:ASP:HB3	1:B:332:PRO:HB3	2.02	0.41
1:B:6:PRO:HD3	1:B:339:THR:O	2.20	0.41
1:B:353:PRO:O	1:B:354:ILE:HB	2.20	0.41
1:C:14:GLU:OE2	1:C:58:LYS:NZ	2.52	0.41
1:E:122:LEU:HB2	1:F:314:HIS:ND1	2.35	0.41
1:E:174:LEU:HB3	1:F:175:TYR:CD1	2.56	0.41
1:E:90:THR:O	1:E:94:LEU:HG	2.19	0.41
1:A:315:LEU:HD11	1:B:191:VAL:HG21	2.03	0.41
1:B:315:LEU:HB3	1:B:321:VAL:HG22	2.02	0.41
1:C:64:ASP:O	1:C:69:PRO:HB2	2.21	0.41
1:C:65:VAL:O	1:C:69:PRO:HD2	2.21	0.41
1:D:177:ARG:HB2	1:D:182:VAL:O	2.21	0.41
1:D:249:ALA:HB1	1:D:298:ALA:HB2	2.02	0.41
1:E:207:ILE:HD11	1:F:47:PRO:CG	2.43	0.41
1:E:64:ASP:O	1:E:69:PRO:HB2	2.21	0.41
1:E:191:VAL:HG21	1:F:315:LEU:HD11	2.01	0.41
1:F:39:ARG:HD2	1:F:60:ILE:HG23	2.00	0.41
1:A:157:ALA:O	1:A:190:MET:HG2	2.20	0.41
1:A:12:VAL:HG13	1:A:81:VAL:HB	2.03	0.41
1:B:14:GLU:HG3	1:B:83:LEU:HD23	2.03	0.41
1:C:114:THR:CG2	1:C:115:GLY:N	2.84	0.41
1:E:11:LYS:HB2	1:E:79:ALA:HA	2.02	0.41
1:E:192:ASP:O	1:E:193:GLY:C	2.58	0.41
1:E:41:PRO:O	1:E:42:GLY:C	2.58	0.41
1:A:201:MET:HE3	1:B:153:LEU:HD13	2.02	0.41
1:B:224:PRO:HG2	1:B:273:MET:SD	2.61	0.41
1:C:159:PHE:HA	1:C:163:SER:HB3	2.03	0.41
1:D:82:LEU:HD23	1:D:110:PHE:CE1	2.56	0.41
1:D:288:GLU:O	1:D:291:ARG:HB2	2.20	0.41
1:D:315:LEU:HB3	1:D:321:VAL:HG22	2.01	0.41
1:B:353:PRO:HG2	1:B:356:GLU:CD	2.40	0.41
1:C:101:CYS:HB3	1:C:108:LEU:CD2	2.49	0.41
1:D:87:ARG:HH21	1:D:126:ALA:HB2	1.86	0.41
1:D:280:ARG:O	1:D:289:TRP:HZ2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:239:VAL:HG22	1:E:300:VAL:HG22	2.02	0.41
1:E:312:ASN:O	1:E:316:LYS:HG3	2.20	0.41
1:E:38:VAL:HG11	1:E:72:MET:CE	2.51	0.41
1:E:70:GLN:O	1:E:72:MET:N	2.54	0.41
1:F:289:TRP:HA	1:F:289:TRP:HE3	1.84	0.41
1:F:353:PRO:HG2	1:F:356:GLU:CD	2.41	0.41
1:A:199:GLN:HG3	1:B:26:MET:SD	2.61	0.41
1:C:166:VAL:O	1:C:170:ILE:HG13	2.21	0.41
1:C:18:ILE:HD12	1:C:18:ILE:O	2.21	0.41
1:D:176:GLU:HG2	1:D:184:GLN:HE21	1.86	0.41
1:D:214:ARG:HH11	1:D:214:ARG:HG3	1.86	0.41
1:E:211:ARG:HH21	1:E:216:SER:HB2	1.86	0.41
1:F:245:GLN:O	1:F:248:ALA:HB3	2.20	0.41
1:F:4:GLY:O	1:F:8:ALA:HB2	2.21	0.41
1:A:359:TRP:CD1	1:A:359:TRP:N	2.86	0.41
1:A:318:ARG:HD2	1:B:119:ASP:O	2.21	0.41
1:B:245:GLN:O	1:B:248:ALA:HB3	2.21	0.41
1:B:251:LEU:HD23	1:B:258:ALA:HA	2.02	0.41
1:C:129:ASP:OD2	1:C:157:ALA:HB3	2.21	0.41
1:D:133:LEU:HD21	1:D:156:VAL:HG11	2.01	0.41
1:E:130:ILE:HD12	1:E:151:PRO:HG3	2.02	0.41
1:A:101:CYS:HA	1:A:104:VAL:HG22	2.03	0.40
1:A:64:ASP:O	1:A:69:PRO:HB2	2.21	0.40
1:B:113:ILE:HG12	1:B:166:VAL:HG11	2.02	0.40
1:D:101:CYS:HA	1:D:104:VAL:HG22	2.03	0.40
1:C:199:GLN:HG3	1:D:26:MET:SD	2.60	0.40
1:F:270:TYR:HB2	1:F:271:PRO:HD3	2.03	0.40
1:A:272:GLN:O	1:A:276:ILE:HD13	2.22	0.40
1:B:200:MET:O	1:B:203:THR:HB	2.21	0.40
1:C:151:PRO:HA	1:C:152:PRO:HD3	1.82	0.40
1:C:164:MET:HA	1:C:167:LEU:HD12	2.03	0.40
1:D:311:ASN:O	1:D:316:LYS:HE2	2.22	0.40
1:D:318:ARG:HB3	1:D:318:ARG:NH1	2.37	0.40
1:D:354:ILE:HG23	1:D:355:ASP:N	2.36	0.40
1:E:198:ALA:O	1:E:201:MET:HB2	2.22	0.40
1:E:318:ARG:O	1:E:319:SER:CB	2.68	0.40
1:E:87:ARG:HB2	1:E:90:THR:CG2	2.51	0.40
1:F:213:GLN:HG2	1:F:216:SER:OG	2.21	0.40
1:A:353:PRO:HG2	1:A:356:GLU:CD	2.42	0.40
1:A:35:VAL:HB	1:A:58:LYS:HG2	2.03	0.40
1:B:177:ARG:O	1:B:181:GLY:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:250:LEU:HD23	1:D:300:VAL:CG2	2.52	0.40
1:F:357:ILE:HG13	1:F:358:ASN:N	2.36	0.40
1:C:280:ARG:HD3	2:C:401:HOH:O	2.21	0.40
1:D:154:ASN:O	1:D:158:ASP:HB2	2.21	0.40
1:E:155:LEU:HD12	1:F:142:PHE:HZ	1.86	0.40
1:E:285:THR:O	1:E:286:ARG:C	2.59	0.40
1:A:60:ILE:HG12	1:A:348:PRO:HG2	2.02	0.40
1:A:357:ILE:HG13	1:A:358:ASN:N	2.35	0.40
1:C:156:VAL:N	2:C:387:HOH:O	2.53	0.40
1:C:357:ILE:HD12	1:C:359:TRP:OXT	2.21	0.40
1:D:241:ALA:HB1	1:D:247:PHE:HA	2.03	0.40
1:E:301:THR:HB	1:E:302:PRO:HD2	2.03	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	349/359 (97%)	304 (87%)	38 (11%)	7 (2%)	8	21
1	B	349/359 (97%)	304 (87%)	35 (10%)	10 (3%)	5	12
1	C	349/359 (97%)	307 (88%)	34 (10%)	8 (2%)	7	18
1	D	349/359 (97%)	302 (86%)	40 (12%)	7 (2%)	8	21
1	E	349/359 (97%)	278 (80%)	60 (17%)	11 (3%)	4	10
1	F	349/359 (97%)	307 (88%)	35 (10%)	7 (2%)	8	21
All	All	2094/2154 (97%)	1802 (86%)	242 (12%)	50 (2%)	6	16

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	353	PRO

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Mol	Chain	Res	Type
1	A	354	ILE
1	A	357	ILE
1	A	358	ASN
1	B	353	PRO
1	B	354	ILE
1	B	357	ILE
1	B	358	ASN
1	C	325	HIS
1	C	353	PRO
1	C	354	ILE
1	C	357	ILE
1	C	358	ASN
1	D	353	PRO
1	D	354	ILE
1	D	357	ILE
1	D	358	ASN
1	E	70	GLN
1	E	353	PRO
1	E	354	ILE
1	F	353	PRO
1	F	354	ILE
1	F	357	ILE
1	F	358	ASN
1	A	325	HIS
1	B	325	HIS
1	C	71	ALA
1	D	325	HIS
1	E	18	ILE
1	E	71	ALA
1	F	71	ALA
1	F	325	HIS
1	A	63	LEU
1	A	71	ALA
1	B	63	LEU
1	B	71	ALA
1	C	63	LEU
1	D	71	ALA
1	E	41	PRO
1	F	63	LEU
1	B	241	ALA
1	D	63	LEU
1	E	325	HIS

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Mol	Chain	Res	Type
1	B	53	LEU
1	E	40	ARG
1	E	42	GLY
1	E	348	PRO
1	B	292	VAL
1	C	292	VAL
1	E	43	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	268/274 (98%)	247 (92%)	21 (8%)	14	32
1	B	268/274 (98%)	247 (92%)	21 (8%)	14	32
1	C	268/274 (98%)	250 (93%)	18 (7%)	18	40
1	D	268/274 (98%)	246 (92%)	22 (8%)	12	29
1	E	268/274 (98%)	244 (91%)	24 (9%)	10	24
1	F	268/274 (98%)	247 (92%)	21 (8%)	14	32
All	All	1608/1644 (98%)	1481 (92%)	127 (8%)	13	31

All (127) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	39	ARG
1	A	40	ARG
1	A	46	MET
1	A	64	ASP
1	A	70	GLN
1	A	92	GLU
1	A	105	ASN
1	A	113	ILE
1	A	146	ASP
1	A	177	ARG

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Mol	Chain	Res	Type
1	A	199	GLN
1	A	213	GLN
1	A	265	LEU
1	A	280	ARG
1	A	287	ASP
1	A	289	TRP
1	A	325	HIS
1	A	327	VAL
1	A	353	PRO
1	A	359	TRP
1	B	28	LEU
1	B	39	ARG
1	B	40	ARG
1	B	46	MET
1	B	64	ASP
1	B	70	GLN
1	B	92	GLU
1	B	105	ASN
1	B	113	ILE
1	B	146	ASP
1	B	177	ARG
1	B	199	GLN
1	B	213	GLN
1	B	265	LEU
1	B	280	ARG
1	B	287	ASP
1	B	289	TRP
1	B	325	HIS
1	B	327	VAL
1	B	353	PRO
1	B	359	TRP
1	C	28	LEU
1	C	39	ARG
1	C	40	ARG
1	C	46	MET
1	C	64	ASP
1	C	70	GLN
1	C	92	GLU
1	C	113	ILE
1	C	146	ASP
1	C	150	MET
1	C	177	ARG

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Mol	Chain	Res	Type
1	C	199	GLN
1	C	213	GLN
1	C	265	LEU
1	C	280	ARG
1	C	289	TRP
1	C	325	HIS
1	C	327	VAL
1	D	18	ILE
1	D	28	LEU
1	D	39	ARG
1	D	40	ARG
1	D	46	MET
1	D	64	ASP
1	D	70	GLN
1	D	92	GLU
1	D	105	ASN
1	D	113	ILE
1	D	146	ASP
1	D	177	ARG
1	D	199	GLN
1	D	213	GLN
1	D	227	ARG
1	D	265	LEU
1	D	280	ARG
1	D	287	ASP
1	D	325	HIS
1	D	327	VAL
1	D	353	PRO
1	D	359	TRP
1	E	28	LEU
1	E	31	LEU
1	E	39	ARG
1	E	40	ARG
1	E	44	LEU
1	E	46	MET
1	E	75	LEU
1	E	85	CYS
1	E	113	ILE
1	E	114	THR
1	E	125	THR
1	E	174	LEU
1	E	177	ARG

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Mol	Chain	Res	Type
1	E	195	SER
1	E	199	GLN
1	E	251	LEU
1	E	265	LEU
1	E	315	LEU
1	E	323	THR
1	E	325	HIS
1	E	329	GLN
1	E	352	THR
1	E	355	ASP
1	E	356	GLU
1	F	28	LEU
1	F	39	ARG
1	F	40	ARG
1	F	46	MET
1	F	70	GLN
1	F	92	GLU
1	F	113	ILE
1	F	146	ASP
1	F	177	ARG
1	F	199	GLN
1	F	213	GLN
1	F	227	ARG
1	F	251	LEU
1	F	265	LEU
1	F	280	ARG
1	F	287	ASP
1	F	289	TRP
1	F	325	HIS
1	F	327	VAL
1	F	353	PRO
1	F	359	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	105	ASN
1	A	128	HIS
1	A	131	ASN
1	A	199	GLN
1	A	213	GLN

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Mol	Chain	Res	Type
1	A	245	GLN
1	A	312	ASN
1	A	329	GLN
1	B	70	GLN
1	B	105	ASN
1	B	128	HIS
1	B	131	ASN
1	B	199	GLN
1	B	213	GLN
1	B	245	GLN
1	B	312	ASN
1	B	329	GLN
1	C	70	GLN
1	C	105	ASN
1	C	128	HIS
1	C	131	ASN
1	C	199	GLN
1	C	213	GLN
1	C	245	GLN
1	C	312	ASN
1	C	329	GLN
1	D	70	GLN
1	D	105	ASN
1	D	128	HIS
1	D	131	ASN
1	D	199	GLN
1	D	213	GLN
1	D	245	GLN
1	D	312	ASN
1	D	329	GLN
1	E	55	HIS
1	E	70	GLN
1	E	105	ASN
1	E	128	HIS
1	E	131	ASN
1	E	199	GLN
1	E	245	GLN
1	E	312	ASN
1	E	329	GLN
1	F	70	GLN
1	F	105	ASN
1	F	128	HIS

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Mol	Chain	Res	Type
1	F	131	ASN
1	F	135	GLN
1	F	199	GLN
1	F	213	GLN
1	F	245	GLN
1	F	312	ASN
1	F	329	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 ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

### 5.7 Other polymers ⓘ

There are no such residues in this entry.

### 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	353/359 (98%)	-0.33	2 (0%) 89 90	28, 54, 85, 101	0
1	B	353/359 (98%)	-0.27	3 (0%) 86 87	29, 54, 86, 102	0
1	C	353/359 (98%)	-0.19	3 (0%) 86 87	27, 54, 86, 102	0
1	D	353/359 (98%)	-0.25	0 100 100	28, 54, 85, 101	0
1	E	353/359 (98%)	-0.31	3 (0%) 86 87	27, 52, 82, 103	0
1	F	353/359 (98%)	-0.29	0 100 100	28, 54, 85, 101	0
All	All	2118/2154 (98%)	-0.27	11 (0%) 90 92	27, 54, 85, 103	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	358	ASN	4.4
1	C	96	ILE	3.9
1	E	44	LEU	3.7
1	A	355	ASP	2.6
1	A	96	ILE	2.5
1	B	96	ILE	2.5
1	B	111	ALA	2.4
1	B	359	TRP	2.4
1	E	96	ILE	2.2
1	E	357	ILE	2.2
1	C	95	GLY	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.