



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:03 AM GMT

PDB ID : 3NOG
Title : Designed ankyrin repeat protein (DARPin) Binders to AcrB: Plasticity of the Interface
Authors : Monroe, N.; Briand, C.; Gruetter, M.G.
Deposited on : 2010-06-25
Resolution : 3.34 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

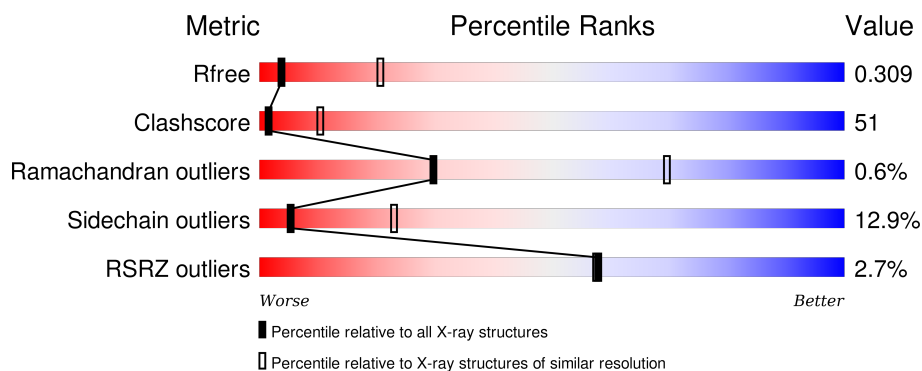
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.34 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	1004 (3.40-3.28)
Clashscore	102246	1072 (3.40-3.28)
Ramachandran outliers	100387	1055 (3.40-3.28)
Sidechain outliers	100360	1054 (3.40-3.28)
RSRZ outliers	91569	1009 (3.40-3.28)

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 ≥ 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	1049	<div> <div></div> <div> <div></div> <div>50%</div> <div>40%</div> <div>7%</div> <div>.</div> </div> </div>
1	B	1049	<div> <div>2%</div> <div> <div></div> <div>41%</div> <div>47%</div> <div>9%</div> <div>.</div> </div> </div>
1	C	1049	<div> <div></div> <div> <div></div> <div>45%</div> <div>45%</div> <div>9%</div> <div>.</div> </div> </div>
2	D	169	<div> <div>6%</div> <div> <div></div> <div>44%</div> <div>40%</div> <div>7%</div> <div>9%</div> </div> </div>
2	E	169	<div> <div>24%</div> <div> <div></div> <div>48%</div> <div>37%</div> <div>.</div> <div>.</div> <div>11%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	FME	B	1	-	-	X	-
1	FME	C	1	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 24874 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 Acriflavine resistance protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1012	Total	C	N	O	S	27	0	0
			7464	4806	1218	1399	41			
1	B	1028	Total	C	N	O	S	0	0	0
			7547	4853	1237	1414	43			
1	C	1040	Total	C	N	O	S	20	0	0
			7736	4979	1270	1444	43			

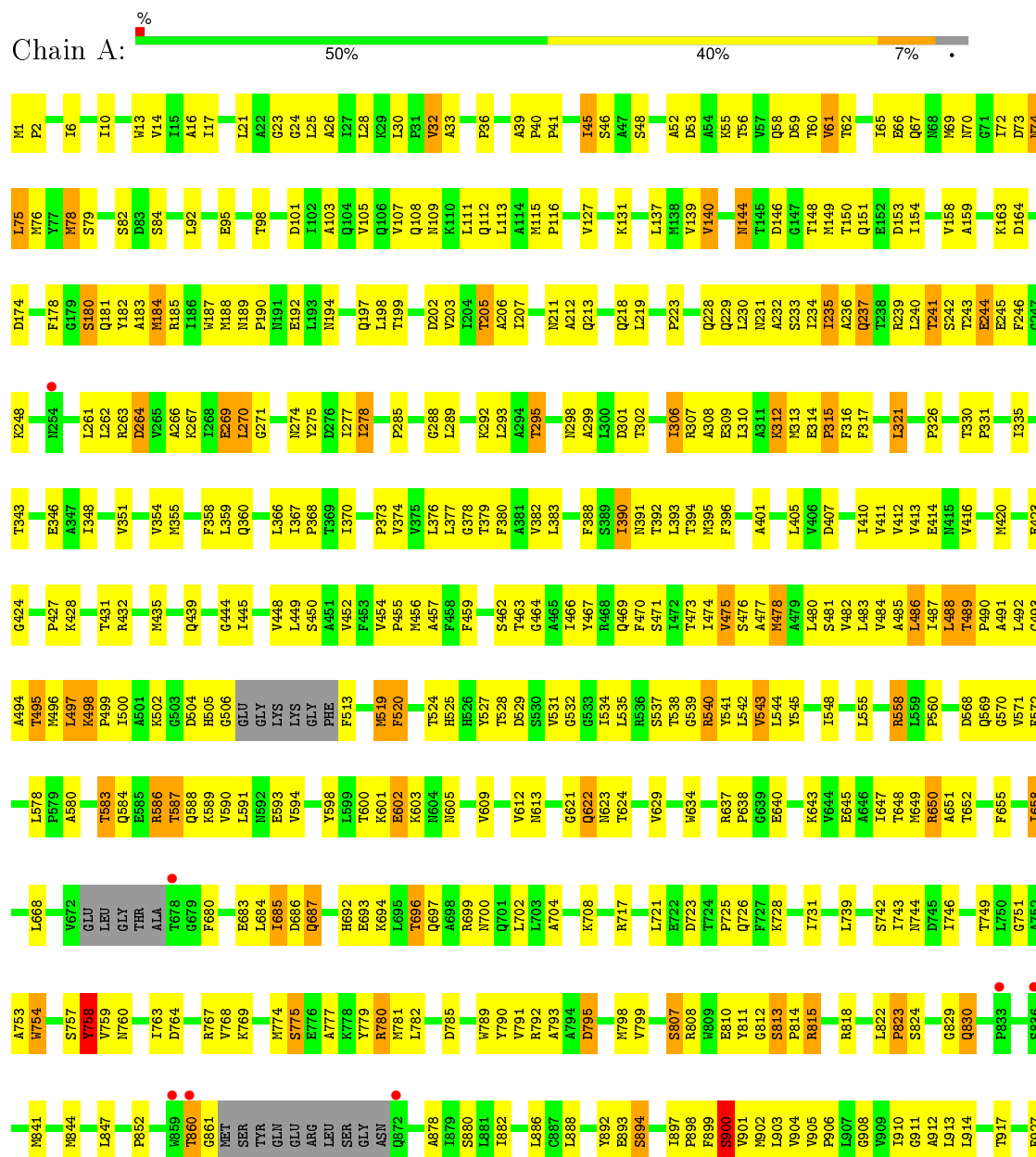
- Molecule 2 is a protein called Designed ankyrin repeat protein.

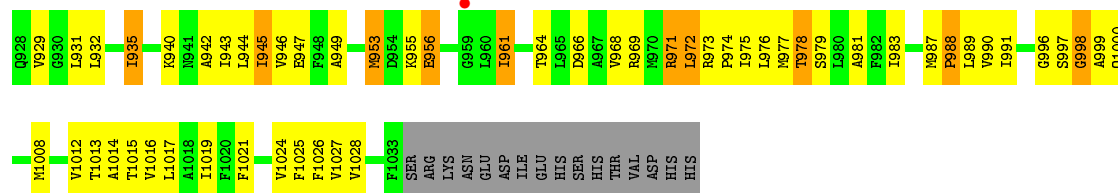
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	154	Total	C	N	O	S	4	0	0
			1097	686	194	216	1			
2	E	151	Total	C	N	O	S	21	0	0
			1030	641	185	203	1			

3 Residue-property plots

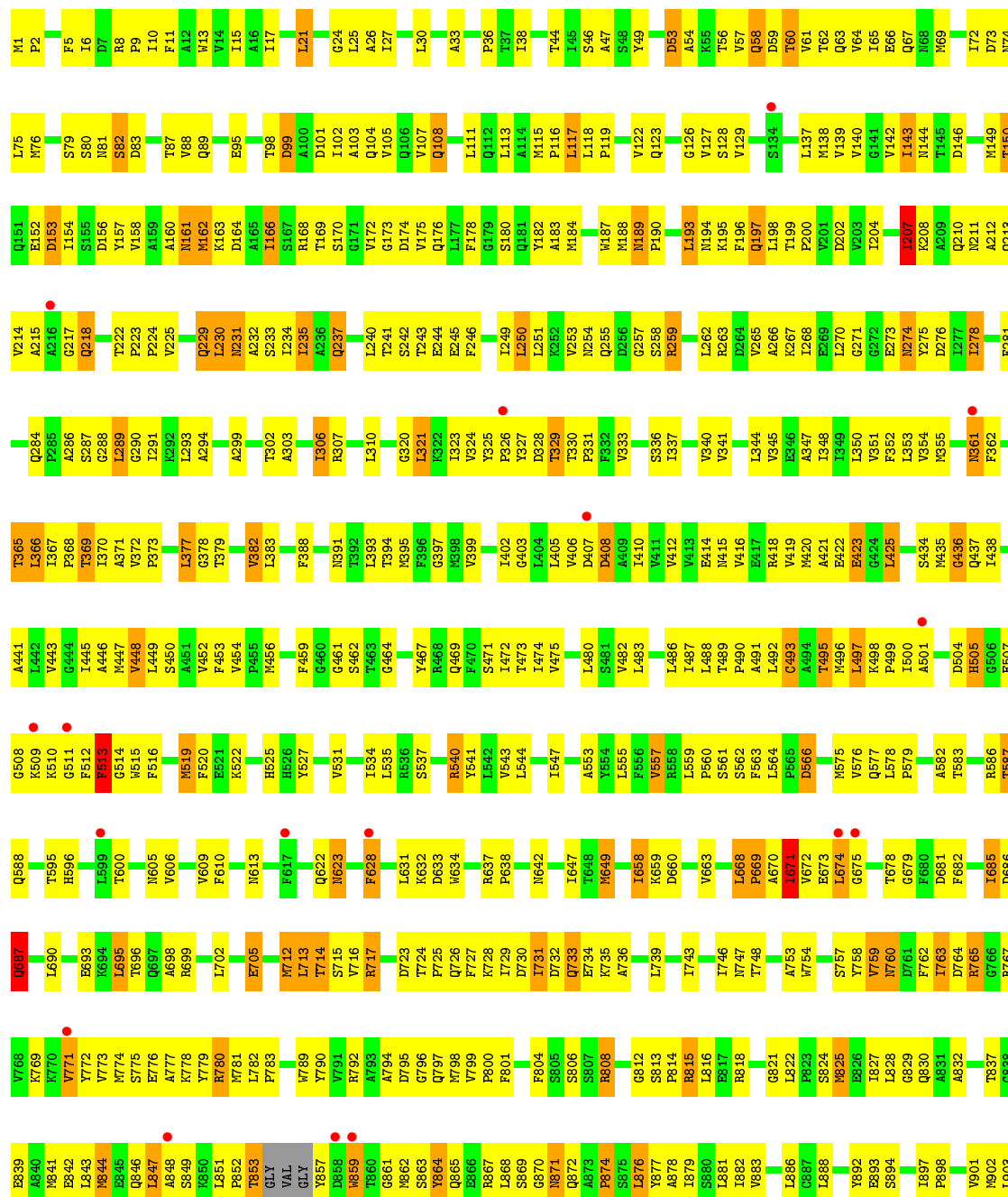
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

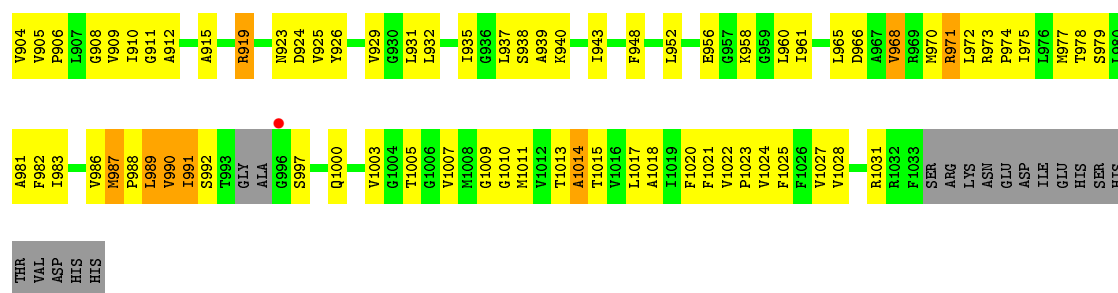
• Molecule 1: Acriflavine resistance protein B



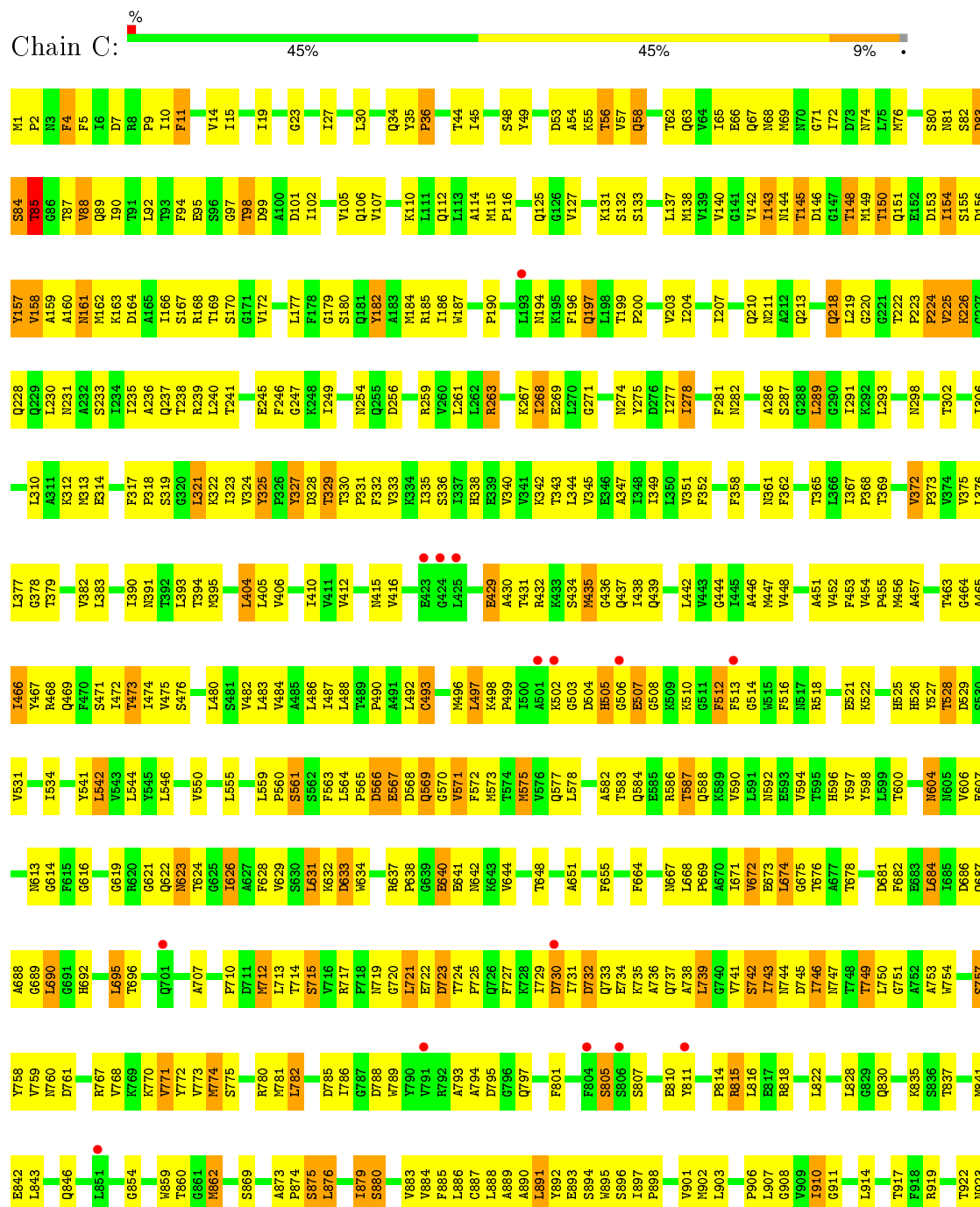


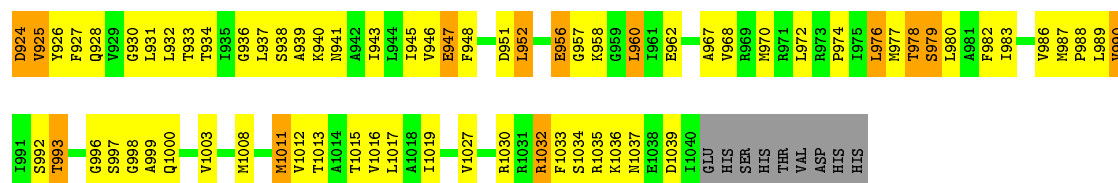
• Molecule 1: Acriflavine resistance protein B



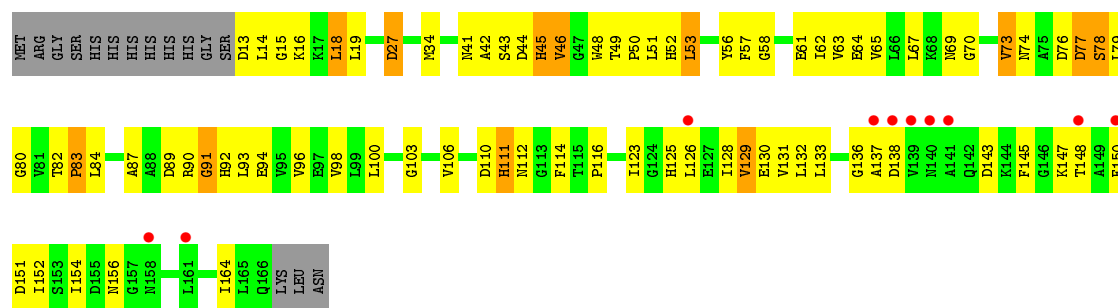


• Molecule 1: Acriflavine resistance protein B

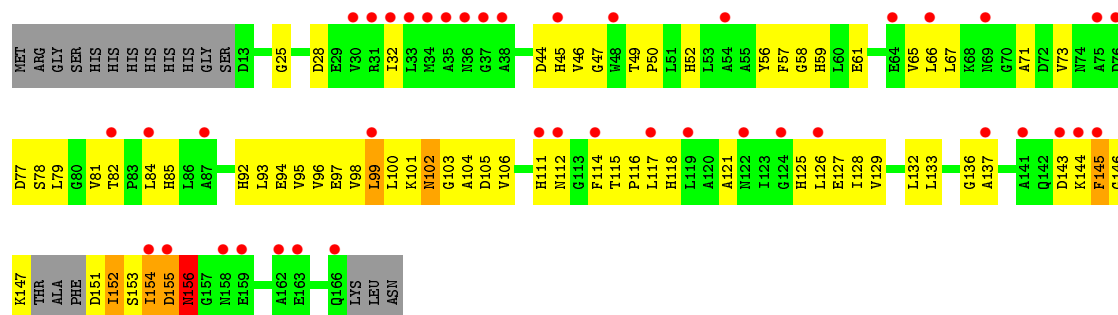




• Molecule 2: Designed ankyrin repeat protein



• Molecule 2: Designed ankyrin repeat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	145.40 Å 158.00 Å 258.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.78 – 3.34 49.15 – 3.34	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.78-3.34) 99.8 (49.15-3.34)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.46 (at 3.33 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.2_432)	Depositor
R, R_{free}	0.257 , 0.307 0.249 , 0.309	Depositor DCC
R_{free} test set	1041 reflections (1.20%)	DCC
Wilson B-factor (Å ²)	70.8	Xtriage
Anisotropy	0.506	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 49.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	2 of 86836 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	24874	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.77	2/7591 (0.0%)	0.74	9/10342 (0.1%)
1	B	0.77	0/7675	0.79	15/10467 (0.1%)
1	C	0.82	2/7874 (0.0%)	0.79	12/10720 (0.1%)
2	D	0.87	0/1115	0.89	3/1525 (0.2%)
2	E	0.40	0/1046	0.62	2/1434 (0.1%)
All	All	0.78	4/25301 (0.0%)	0.77	41/34488 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	493	CYS	CB-SG	-5.86	1.72	1.81
1	C	225	VAL	CA-CB	-5.37	1.43	1.54
1	A	475	VAL	CA-CB	-5.18	1.43	1.54
1	A	758	TYR	CD2-CE2	-5.09	1.31	1.39

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	138	ASP	N-CA-C	-8.41	88.30	111.00
1	A	945	ILE	CB-CA-C	-7.27	97.07	111.60
1	B	668	LEU	C-N-CD	-7.16	104.85	120.60
1	B	259	ARG	N-CA-CB	-7.06	97.90	110.60
1	C	85	THR	N-CA-C	-6.79	92.65	111.00
2	E	156	ASN	N-CA-C	6.78	129.30	111.00
1	A	61	VAL	CB-CA-C	-6.76	98.55	111.40
1	C	83	ASP	N-CA-C	6.75	129.21	111.00
1	C	1032	ARG	N-CA-C	-6.61	93.16	111.00
2	D	42	ALA	N-CA-C	-6.51	93.43	111.00
1	B	679	GLY	N-CA-C	-6.46	96.96	113.10
1	C	97	GLY	N-CA-C	-6.40	97.10	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	952	LEU	CA-CB-CG	-6.28	100.85	115.30
1	B	760	ASN	CB-CA-C	-6.24	97.92	110.40
1	A	270	LEU	N-CA-C	-6.22	94.22	111.00
1	B	685	ILE	N-CA-C	6.14	127.58	111.00
1	C	925	VAL	CB-CA-C	-6.04	99.92	111.40
1	C	327	TYR	N-CA-C	6.03	127.29	111.00
1	A	540	ARG	N-CA-C	-5.91	95.04	111.00
1	B	685	ILE	CB-CA-C	-5.88	99.84	111.60
1	B	847	LEU	CA-CB-CG	5.80	128.64	115.30
1	B	861	GLY	N-CA-C	-5.78	98.65	113.10
2	E	156	ASN	C-N-CA	5.76	134.40	122.30
1	B	514	GLY	N-CA-C	-5.72	98.79	113.10
1	A	759	VAL	N-CA-C	5.63	126.20	111.00
1	C	57	VAL	CB-CA-C	-5.50	100.95	111.40
1	B	207	ILE	CB-CA-C	-5.49	100.61	111.60
1	A	759	VAL	CB-CA-C	-5.44	101.06	111.40
1	A	61	VAL	N-CA-C	5.35	125.44	111.00
1	B	505	HIS	N-CA-C	-5.29	96.71	111.00
1	A	900	SER	N-CA-C	-5.26	96.79	111.00
1	B	687	GLN	N-CA-C	5.24	125.15	111.00
1	C	672	VAL	N-CA-C	5.17	124.97	111.00
1	C	131	LYS	N-CA-C	-5.16	97.06	111.00
1	B	671	ILE	CB-CA-C	-5.15	101.31	111.60
2	D	91	GLY	N-CA-C	5.14	125.96	113.10
1	C	158	VAL	CB-CA-C	-5.13	101.65	111.40
1	A	45	ILE	CB-CA-C	-5.06	101.47	111.60
1	B	513	PHE	N-CA-C	-5.05	97.36	111.00
1	B	509	LYS	N-CA-C	-5.02	97.45	111.00
1	C	746	ILE	CB-CA-C	-5.01	101.58	111.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7464	0	7440	661	0
1	B	7547	0	7469	863	0
1	C	7736	0	7730	828	0
2	D	1097	0	1008	142	0
2	E	1030	0	896	94	0
All	All	24874	0	24543	2520	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 51.

All (2520) 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:234:ILE:C	1:A:235:ILE:HD13	1.18	1.50
1:C:314:GLU:HA	1:C:317:PHE:CE1	1.48	1.48
1:B:563:PHE:C	1:B:564:LEU:HD12	1.33	1.48
1:B:705:GLU:HG2	1:B:847:LEU:CD2	1.40	1.47
1:C:689:GLY:C	1:C:690:LEU:HD23	1.36	1.39
1:B:919:ARG:NH1	1:B:919:ARG:HB3	1.39	1.38
1:A:496:MET:C	1:A:497:LEU:HD23	1.44	1.36
1:B:222:THR:CG2	1:C:275:TYR:HB2	1.55	1.35
1:A:75:LEU:HD12	1:A:76:MET:N	1.39	1.34
1:A:808:ARG:NH1	1:A:808:ARG:HB2	1.42	1.34
1:C:671:ILE:CD1	1:C:674:LEU:HD11	1.59	1.33
1:B:250:LEU:HD23	1:B:251:LEU:N	1.43	1.32
2:D:56:TYR:CE1	2:D:90:ARG:HD3	1.64	1.31
1:B:270:LEU:HD23	1:B:271:GLY:N	1.46	1.30
1:B:799:VAL:HG13	1:B:800:PRO:CD	1.59	1.30
1:A:482:VAL:O	1:A:486:LEU:HD21	1.28	1.30
1:B:197:GLN:HA	1:B:798:MET:CE	1.61	1.29
1:A:721:LEU:CD1	1:A:814:PRO:HG3	1.62	1.29
1:C:185:ARG:HH12	1:C:774:MET:CE	1.48	1.27
1:B:960:LEU:HD23	1:B:960:LEU:O	1.33	1.27
1:C:879:ILE:O	1:C:879:ILE:HD12	1.35	1.26
1:C:741:VAL:CG1	1:C:746:ILE:HD11	1.64	1.25
1:A:234:ILE:C	1:A:235:ILE:CD1	2.05	1.24
2:D:56:TYR:CE1	2:D:90:ARG:CD	2.21	1.23
1:B:919:ARG:CB	1:B:919:ARG:HH11	1.51	1.23
2:D:51:LEU:HD23	2:D:51:LEU:O	1.34	1.23
1:C:154:ILE:C	1:C:154:ILE:HD12	1.56	1.22
2:D:56:TYR:HE1	2:D:90:ARG:CD	1.51	1.22
1:B:230:LEU:O	1:B:230:LEU:HD23	1.33	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:GLN:CA	1:B:798:MET:HE3	1.70	1.21
1:C:671:ILE:CG1	1:C:674:LEU:HD21	1.71	1.21
1:B:270:LEU:C	1:B:270:LEU:HD23	1.49	1.21
1:C:750:LEU:HD23	1:C:750:LEU:C	1.59	1.21
1:B:799:VAL:CG1	1:B:800:PRO:HD2	1.70	1.20
2:E:152:ILE:HD12	2:E:152:ILE:C	1.62	1.20
1:B:562:SER:O	1:B:924:ASP:HA	1.39	1.19
1:B:960:LEU:C	1:B:960:LEU:HD23	1.59	1.19
1:C:750:LEU:HD23	1:C:750:LEU:O	1.34	1.19
1:B:668:LEU:O	1:B:668:LEU:HD12	1.39	1.19
2:D:18:LEU:HD23	2:D:18:LEU:O	1.42	1.19
2:D:129:VAL:O	2:D:133:LEU:HD12	1.38	1.19
1:A:488:LEU:HD12	1:A:488:LEU:O	1.40	1.19
1:A:428:LYS:O	1:A:431:THR:HG22	1.39	1.19
1:C:671:ILE:HD11	1:C:674:LEU:CD1	1.71	1.18
1:C:607:GLU:OE2	1:C:632:LYS:HG2	1.38	1.18
1:C:154:ILE:O	1:C:154:ILE:HD12	1.37	1.18
2:E:46:VAL:HG13	2:E:47:GLY:H	1.02	1.18
1:C:674:LEU:H	1:C:674:LEU:CD2	1.52	1.17
1:C:314:GLU:HA	1:C:317:PHE:CD1	1.79	1.16
1:C:688:ALA:HB3	1:C:690:LEU:HD21	1.20	1.16
1:B:188:MET:CE	1:B:773:VAL:HG22	1.74	1.16
1:A:423:GLU:CA	1:A:502:LYS:HE3	1.76	1.16
1:A:486:LEU:H	1:A:486:LEU:CD2	1.52	1.16
1:A:721:LEU:CD1	1:A:814:PRO:CG	2.24	1.16
1:C:960:LEU:O	1:C:960:LEU:HD13	1.43	1.16
1:B:254:ASN:HD22	1:B:258:SER:HB3	1.11	1.16
1:A:498:LYS:HE3	1:A:498:LYS:O	1.45	1.15
1:B:668:LEU:C	1:B:668:LEU:HD12	1.67	1.15
1:B:989:LEU:HD23	1:B:1000:GLN:HG2	1.26	1.15
1:B:705:GLU:HG2	1:B:847:LEU:HD22	1.26	1.14
1:A:808:ARG:CB	1:A:808:ARG:HH11	1.61	1.14
2:D:53:LEU:H	2:D:53:LEU:CD2	1.58	1.14
1:A:478:MET:O	1:A:482:VAL:HG23	1.45	1.14
1:C:575:MET:HG3	1:C:575:MET:O	1.43	1.14
1:B:197:GLN:CA	1:B:798:MET:CE	2.22	1.13
1:C:144:ASN:HD22	1:C:149:MET:CB	1.60	1.13
1:A:486:LEU:HD22	1:A:486:LEU:N	1.60	1.13
1:C:879:ILE:C	1:C:879:ILE:HD12	1.62	1.13
1:C:674:LEU:HD22	1:C:674:LEU:N	1.59	1.13
1:B:230:LEU:C	1:B:230:LEU:HD23	1.60	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:LEU:HD23	1:B:193:LEU:N	1.52	1.13
1:B:991:ILE:HD12	1:B:991:ILE:O	1.49	1.12
1:B:222:THR:HG21	1:C:275:TYR:HB2	1.26	1.12
2:D:61:GLU:O	2:D:65:VAL:HG23	1.49	1.12
1:C:739:LEU:N	1:C:739:LEU:HD13	1.50	1.11
1:A:931:LEU:O	1:A:935:ILE:HG22	1.50	1.11
1:B:705:GLU:CG	1:B:847:LEU:CD2	2.28	1.11
1:B:848:ALA:HA	1:B:851:LEU:CD1	1.79	1.11
1:A:486:LEU:HD13	1:A:486:LEU:N	1.59	1.11
1:B:188:MET:HE2	1:B:773:VAL:HG22	1.11	1.11
1:A:360:GLN:HG2	1:A:513:PHE:CZ	1.84	1.11
2:E:112:ASN:O	2:E:144:LYS:HG2	1.51	1.11
1:C:83:ASP:HB3	1:C:85:THR:HG23	1.24	1.10
1:B:222:THR:CG2	1:C:275:TYR:CB	2.28	1.10
1:C:879:ILE:HD11	1:C:883:VAL:HG23	1.30	1.10
1:C:671:ILE:HG13	1:C:671:ILE:O	1.41	1.10
1:A:519:MET:SD	1:A:519:MET:C	2.30	1.10
1:C:200:PRO:CD	1:C:749:THR:HG23	1.79	1.10
1:C:447:MET:SD	1:C:891:LEU:HD21	1.91	1.09
1:A:971:ARG:O	1:A:974:PRO:HD2	1.52	1.09
1:B:534:ILE:HG13	1:B:541:TYR:CE2	1.87	1.09
1:C:741:VAL:HG13	1:C:746:ILE:CD1	1.81	1.09
1:A:234:ILE:O	1:A:235:ILE:CD1	2.00	1.09
1:B:563:PHE:C	1:B:564:LEU:CD1	2.19	1.08
1:C:671:ILE:HD11	1:C:674:LEU:HD11	1.10	1.08
1:A:971:ARG:HH11	1:A:971:ARG:HG3	1.06	1.08
1:C:497:LEU:HD23	1:C:498:LYS:H	1.03	1.08
1:B:182:TYR:HB3	1:B:270:LEU:HD11	1.31	1.08
1:A:721:LEU:HD12	1:A:814:PRO:HG3	1.31	1.08
2:E:152:ILE:HD12	2:E:152:ILE:O	1.53	1.08
1:C:144:ASN:ND2	1:C:149:MET:HB2	1.68	1.08
1:C:435:MET:CE	1:C:435:MET:HA	1.84	1.08
1:A:971:ARG:HH11	1:A:971:ARG:CG	1.67	1.08
1:B:871:ASN:HB3	1:B:872:GLN:HG2	1.35	1.07
1:A:235:ILE:N	1:A:235:ILE:HD13	1.57	1.07
1:C:919:ARG:HH12	1:C:990:VAL:HG12	1.20	1.07
1:A:379:THR:O	1:A:383:LEU:HD23	1.50	1.07
1:B:649:MET:HA	1:B:649:MET:CE	1.82	1.07
1:B:671:ILE:HD13	1:B:671:ILE:O	1.52	1.07
1:A:498:LYS:HD3	1:A:498:LYS:H	1.14	1.07
1:A:808:ARG:HB2	1:A:808:ARG:HH11	0.91	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:534:ILE:HG13	1:B:541:TYR:CZ	1.89	1.07
1:A:721:LEU:HD12	1:A:814:PRO:CG	1.84	1.06
1:B:717:ARG:HH11	1:B:717:ARG:HG2	0.95	1.06
1:B:194:ASN:ND2	1:B:790:TYR:CG	2.22	1.06
1:B:658:ILE:H	1:B:658:ILE:CD1	1.67	1.06
1:A:519:MET:SD	1:A:520:PHE:N	2.29	1.06
1:B:182:TYR:CB	1:B:270:LEU:HD11	1.84	1.06
1:C:11:PHE:HD1	1:C:11:PHE:O	1.38	1.05
1:C:54:ALA:HB2	1:C:814:PRO:O	1.55	1.05
1:A:411:VAL:HG21	1:A:971:ARG:HH21	1.09	1.05
1:C:435:MET:HE3	1:C:435:MET:HA	1.05	1.05
2:E:92:HIS:O	2:E:96:VAL:HG23	1.55	1.05
1:B:712:MET:O	1:B:713:LEU:HD12	1.56	1.05
2:D:51:LEU:HD23	2:D:51:LEU:C	1.71	1.04
1:C:200:PRO:HD2	1:C:749:THR:HG23	1.08	1.04
2:E:112:ASN:HA	2:E:144:LYS:HE2	1.40	1.04
1:B:207:ILE:HG22	1:B:760:ASN:ND2	1.72	1.04
1:C:570:GLY:O	1:C:571:VAL:HG12	1.55	1.04
1:C:44:THR:HB	1:C:132:SER:OG	1.57	1.03
1:A:527:TYR:CE1	1:A:972:LEU:HD23	1.92	1.03
1:C:497:LEU:CD2	1:C:498:LYS:H	1.69	1.03
1:B:874:PRO:HB2	1:B:877:TYR:HD2	1.22	1.03
1:C:567:GLU:OE1	1:C:998:GLY:HA3	1.59	1.03
1:B:874:PRO:CB	1:B:877:TYR:HD2	1.70	1.03
1:A:498:LYS:H	1:A:498:LYS:CD	1.64	1.03
1:B:222:THR:HG22	1:C:275:TYR:HB2	1.39	1.03
1:C:314:GLU:CA	1:C:317:PHE:CE1	2.43	1.02
1:B:197:GLN:HA	1:B:798:MET:HE3	1.04	1.02
1:A:935:ILE:HD12	1:A:935:ILE:O	1.59	1.02
1:B:119:PRO:O	1:B:123:GLN:HG3	1.59	1.02
1:C:671:ILE:HG13	1:C:674:LEU:HD21	1.05	1.02
1:A:240:LEU:N	1:A:240:LEU:HD12	1.68	1.02
1:B:250:LEU:HD23	1:B:250:LEU:C	1.76	1.02
2:D:56:TYR:HE1	2:D:90:ARG:HD3	0.97	1.02
1:B:156:ASP:CB	1:B:182:TYR:CE2	2.43	1.02
1:B:194:ASN:ND2	1:B:790:TYR:CD2	2.25	1.02
1:A:360:GLN:HG2	1:A:513:PHE:HZ	1.15	1.02
1:B:158:VAL:HA	1:B:162:MET:HG3	1.40	1.02
1:B:705:GLU:CG	1:B:847:LEU:HD22	1.88	1.01
2:D:56:TYR:CE1	2:D:90:ARG:NE	2.26	1.01
1:C:989:LEU:HD22	1:C:1000:GLN:HB3	1.42	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:53:LEU:HD23	2:D:53:LEU:H	1.18	1.01
2:E:152:ILE:HG13	2:E:153:SER:N	1.73	1.01
1:B:204:ILE:O	1:B:208:LYS:HG3	1.58	1.01
1:B:471:SER:O	1:B:475:VAL:HG12	1.61	1.01
1:C:185:ARG:HH12	1:C:774:MET:HE3	1.19	1.01
1:B:672:VAL:O	1:B:672:VAL:HG22	1.53	1.01
1:C:879:ILE:CD1	1:C:883:VAL:HG23	1.90	1.01
1:C:83:ASP:HB3	1:C:85:THR:CG2	1.91	1.01
1:C:689:GLY:C	1:C:690:LEU:CD2	2.29	1.00
1:B:250:LEU:CD2	1:B:250:LEU:C	2.30	1.00
1:A:73:ASP:HB3	1:A:74:ASN:OD1	1.60	1.00
1:C:497:LEU:HD23	1:C:498:LYS:N	1.74	1.00
1:B:712:MET:C	1:B:713:LEU:CD1	2.30	1.00
1:C:896:SER:OG	1:C:897:ILE:HD12	1.61	1.00
1:C:671:ILE:HG13	1:C:674:LEU:CD2	1.91	1.00
2:E:93:LEU:CD2	2:E:128:ILE:HG12	1.92	1.00
1:B:799:VAL:CG1	1:B:800:PRO:CD	2.33	1.00
1:C:434:SER:O	1:C:438:ILE:HG12	1.60	1.00
1:B:164:ASP:O	1:B:168:ARG:HG3	1.62	1.00
1:B:960:LEU:CD2	1:B:960:LEU:C	2.30	0.99
1:A:423:GLU:HA	1:A:502:LYS:HE3	1.01	0.99
1:A:497:LEU:HD23	1:A:497:LEU:N	1.58	0.99
1:C:568:ASP:OD2	1:C:644:VAL:HG13	1.61	0.99
1:B:758:TYR:HB2	1:B:772:TYR:CE1	1.97	0.99
1:C:741:VAL:HG13	1:C:746:ILE:HD11	1.00	0.99
1:C:623:ASN:C	1:C:623:ASN:HD22	1.65	0.99
1:C:314:GLU:O	1:C:317:PHE:HD1	1.42	0.99
1:B:270:LEU:CD2	1:B:270:LEU:C	2.29	0.99
2:D:44:ASP:OD1	2:D:45:HIS:CB	2.10	0.99
1:B:726:GLN:HE22	1:B:812:GLY:HA3	1.25	0.99
1:A:519:MET:O	1:A:519:MET:HE1	1.62	0.98
1:B:222:THR:HG21	1:C:275:TYR:CB	1.90	0.98
1:C:325:TYR:N	1:C:325:TYR:CD1	2.30	0.98
1:C:146:ASP:CB	1:C:148:THR:CG2	2.40	0.98
1:C:721:LEU:N	1:C:721:LEU:HD23	1.77	0.98
1:C:688:ALA:CB	1:C:690:LEU:HD21	1.94	0.98
1:C:144:ASN:HD22	1:C:149:MET:HB2	0.84	0.98
1:C:200:PRO:HD2	1:C:749:THR:CG2	1.93	0.98
1:B:658:ILE:N	1:B:658:ILE:HD12	1.78	0.98
1:B:197:GLN:C	1:B:798:MET:CE	2.32	0.98
2:D:18:LEU:HD23	2:D:18:LEU:C	1.81	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:736:ALA:O	1:C:741:VAL:HB	1.63	0.98
1:B:190:PRO:HG3	1:B:789:TRP:CH2	1.99	0.97
2:E:100:LEU:HD21	2:E:106:VAL:HG12	1.47	0.97
1:B:193:LEU:HD23	1:B:193:LEU:H	1.29	0.97
1:B:511:GLY:HA2	1:B:513:PHE:O	1.64	0.96
1:C:879:ILE:HD11	1:C:883:VAL:CG2	1.95	0.96
1:A:527:TYR:CE1	1:A:972:LEU:CD2	2.48	0.96
1:B:207:ILE:CG2	1:B:760:ASN:ND2	2.27	0.96
1:C:673:GLU:H	1:C:673:GLU:CD	1.69	0.96
1:A:32:VAL:HG12	1:A:390:ILE:HB	1.47	0.96
1:B:948:PHE:HE2	1:B:971:ARG:HE	1.02	0.96
1:B:61:VAL:O	1:B:65:ILE:HG13	1.66	0.96
1:B:69:MET:CE	1:B:72:ILE:HD11	1.96	0.96
1:C:741:VAL:CG1	1:C:746:ILE:CD1	2.38	0.96
1:C:435:MET:HE3	1:C:435:MET:CA	1.96	0.96
1:A:411:VAL:CG2	1:A:971:ARG:HH21	1.79	0.95
1:B:685:ILE:HG22	1:B:686:ASP:N	1.80	0.95
1:C:671:ILE:HD11	1:C:674:LEU:CG	1.95	0.95
1:A:498:LYS:CE	1:A:498:LYS:N	2.30	0.95
2:D:44:ASP:OD1	2:D:45:HIS:HB3	1.65	0.95
1:C:314:GLU:CA	1:C:317:PHE:HE1	1.77	0.95
1:B:459:PHE:HB2	1:B:464:GLY:HA2	1.48	0.95
1:B:207:ILE:CG2	1:B:760:ASN:HD22	1.79	0.95
1:A:527:TYR:O	1:A:531:VAL:HG23	1.64	0.95
1:B:361:ASN:H	1:B:361:ASN:HD22	1.01	0.95
1:C:671:ILE:CD1	1:C:674:LEU:HD21	1.96	0.95
1:C:750:LEU:CD2	1:C:750:LEU:C	2.30	0.95
1:A:423:GLU:HA	1:A:502:LYS:CE	1.95	0.95
2:E:46:VAL:HG13	2:E:47:GLY:N	1.82	0.94
1:C:196:PHE:C	1:C:197:GLN:HG2	1.87	0.94
2:D:14:LEU:H	2:D:14:LEU:HD12	1.31	0.94
1:C:919:ARG:HG3	1:C:919:ARG:O	1.67	0.94
1:B:649:MET:HA	1:B:649:MET:HE3	1.49	0.94
1:B:717:ARG:HH11	1:B:717:ARG:CG	1.77	0.94
1:B:799:VAL:HG13	1:B:800:PRO:HD2	0.96	0.94
1:C:875:SER:O	1:C:879:ILE:HG22	1.68	0.94
1:B:361:ASN:N	1:B:361:ASN:HD22	1.60	0.94
1:C:976:LEU:O	1:C:980:LEU:HD23	1.66	0.94
1:C:1:FME:N	1:C:2:PRO:CD	2.30	0.94
1:B:685:ILE:CG2	1:B:686:ASP:N	2.29	0.94
1:C:506:GLY:C	1:C:507:GLU:HG2	1.88	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:496:MET:C	1:A:497:LEU:CD2	2.36	0.94
1:C:960:LEU:HD11	1:C:1027:VAL:HG22	1.47	0.93
1:C:447:MET:SD	1:C:891:LEU:CD2	2.55	0.93
1:A:973:ARG:O	1:A:977:MET:HG3	1.68	0.93
1:A:480:LEU:O	1:A:484:VAL:HG23	1.67	0.93
1:B:196:PHE:HA	1:B:197:GLN:HE22	1.34	0.93
1:C:739:LEU:N	1:C:739:LEU:CD1	2.30	0.93
1:C:439:GLN:HA	1:C:442:LEU:HD12	1.49	0.93
1:B:717:ARG:NH1	1:B:717:ARG:HG2	1.76	0.93
1:B:102:ILE:CG2	1:B:103:ALA:N	2.32	0.93
1:B:229:GLN:CD	1:B:229:GLN:H	1.64	0.93
1:C:4:PHE:O	1:C:4:PHE:HD2	1.49	0.93
1:B:678:THR:O	1:B:678:THR:HG22	1.65	0.93
1:C:690:LEU:HD23	1:C:690:LEU:N	1.84	0.93
1:C:733:GLN:HE22	1:C:743:ILE:HG21	1.34	0.93
2:E:152:ILE:CD1	2:E:152:ILE:C	2.30	0.93
1:C:185:ARG:NH1	1:C:774:MET:CE	2.32	0.92
1:B:705:GLU:HG2	1:B:847:LEU:HD23	1.47	0.92
1:C:144:ASN:ND2	1:C:149:MET:CB	2.28	0.92
1:B:1:FME:CE	1:B:487:ILE:HD11	1.98	0.92
1:B:422:GLU:C	1:B:423:GLU:HG2	1.87	0.92
1:C:896:SER:OG	1:C:897:ILE:N	1.98	0.92
1:B:117:LEU:CD1	1:B:117:LEU:N	2.30	0.92
1:A:486:LEU:H	1:A:486:LEU:HD22	0.76	0.92
1:B:726:GLN:NE2	1:B:812:GLY:HA3	1.84	0.92
1:C:68:ASN:HD22	1:C:114:ALA:HB2	1.35	0.92
1:B:352:PHE:HD1	1:B:365:THR:HG1	0.97	0.92
1:B:563:PHE:O	1:B:564:LEU:HG	1.69	0.92
1:C:960:LEU:C	1:C:960:LEU:HD13	1.90	0.92
1:B:1:FME:HE1	1:B:487:ILE:HD11	1.52	0.92
1:C:327:TYR:HD2	1:C:327:TYR:O	1.53	0.92
1:C:200:PRO:CD	1:C:749:THR:CG2	2.46	0.92
1:B:234:ILE:O	1:B:235:ILE:CD1	2.18	0.92
1:A:901:VAL:O	1:A:901:VAL:HG12	1.68	0.92
1:B:188:MET:CE	1:B:773:VAL:CG2	2.48	0.92
1:B:117:LEU:HD13	1:B:117:LEU:N	1.84	0.91
1:B:739:LEU:HD13	1:B:799:VAL:HG21	1.52	0.91
1:A:754:TRP:HZ3	1:C:219:LEU:HD23	1.32	0.91
1:B:240:LEU:HD23	1:B:245:GLU:HB3	1.48	0.91
1:A:971:ARG:HG3	1:A:971:ARG:NH1	1.76	0.91
1:B:765:ARG:HB3	1:B:765:ARG:HH11	1.34	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:712:MET:C	1:B:713:LEU:HD13	1.91	0.91
1:B:190:PRO:HG3	1:B:789:TRP:CZ2	2.06	0.91
1:C:447:MET:CE	1:C:891:LEU:CD2	2.48	0.91
1:C:146:ASP:CB	1:C:148:THR:HG23	2.01	0.91
1:B:563:PHE:O	1:B:564:LEU:CD1	2.17	0.91
1:A:904:VAL:HG22	1:A:904:VAL:O	1.67	0.91
1:A:240:LEU:N	1:A:240:LEU:CD1	2.33	0.91
1:C:185:ARG:NH1	1:C:774:MET:HE3	1.86	0.90
1:B:874:PRO:O	1:B:874:PRO:HG2	1.68	0.90
2:D:53:LEU:N	2:D:53:LEU:CD2	2.30	0.90
2:E:152:ILE:CG1	2:E:153:SER:N	2.33	0.90
1:B:705:GLU:HG2	1:B:847:LEU:HD21	1.50	0.90
1:C:879:ILE:C	1:C:879:ILE:CD1	2.38	0.90
1:C:83:ASP:CB	1:C:85:THR:HG23	2.01	0.90
1:C:674:LEU:H	1:C:674:LEU:HD22	0.73	0.90
1:C:497:LEU:CD2	1:C:498:LYS:N	2.30	0.90
1:B:361:ASN:ND2	1:B:361:ASN:H	1.66	0.90
1:B:563:PHE:O	1:B:564:LEU:CG	2.19	0.90
1:B:250:LEU:CD2	1:B:251:LEU:N	2.34	0.90
1:C:154:ILE:CD1	1:C:154:ILE:C	2.32	0.90
1:B:362:PHE:O	1:B:365:THR:HG22	1.72	0.90
1:A:298:ASN:ND2	1:A:301:ASP:H	1.70	0.89
1:C:268:ILE:HD13	1:C:268:ILE:N	1.85	0.89
1:C:84:SER:HB3	1:C:814:PRO:O	1.72	0.89
1:A:721:LEU:HD11	1:A:814:PRO:CG	2.02	0.89
1:B:193:LEU:CD2	1:B:193:LEU:N	2.30	0.89
2:D:125:HIS:ND1	2:D:128:ILE:HG13	1.88	0.89
1:B:874:PRO:HB2	1:B:877:TYR:CD2	2.07	0.89
1:A:248:LYS:O	1:A:261:LEU:HD23	1.73	0.89
1:B:815:ARG:HH11	1:B:815:ARG:HG2	1.38	0.89
1:B:197:GLN:CA	1:B:798:MET:HE2	2.01	0.89
1:A:431:THR:HG23	1:A:432:ARG:N	1.87	0.89
1:A:431:THR:CG2	1:A:432:ARG:N	2.36	0.88
1:C:54:ALA:CB	1:C:814:PRO:O	2.21	0.88
1:B:69:MET:HE3	1:B:72:ILE:HD11	1.55	0.88
2:D:49:THR:O	2:D:53:LEU:CD2	2.20	0.88
2:D:18:LEU:C	2:D:18:LEU:CD2	2.40	0.88
1:C:896:SER:OG	1:C:897:ILE:CD1	2.20	0.88
1:C:993:THR:HG23	1:C:993:THR:O	1.73	0.88
1:B:150:THR:HG23	1:B:153:ASP:OD2	1.72	0.88
2:E:94:GLU:O	2:E:98:VAL:HG23	1.73	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:GLN:HB2	1:A:233:SER:HA	1.56	0.88
1:C:447:MET:HE1	1:C:891:LEU:HD23	1.56	0.88
2:E:97:GLU:OE1	2:E:97:GLU:HA	1.71	0.88
1:A:534:ILE:HA	1:A:541:TYR:HE1	1.39	0.88
1:C:689:GLY:O	1:C:690:LEU:HD23	1.73	0.88
1:C:291:ILE:HD13	1:C:306:ILE:HD13	1.52	0.88
1:A:234:ILE:O	1:A:235:ILE:HD12	1.74	0.88
1:A:75:LEU:HD12	1:A:76:MET:H	0.98	0.88
1:B:712:MET:C	1:B:713:LEU:HD12	1.91	0.88
1:B:169:THR:HG22	1:B:172:VAL:HG13	1.56	0.87
1:A:67:GLN:HE21	1:C:767:ARG:NH1	1.72	0.87
1:B:564:LEU:N	1:B:564:LEU:HD12	1.89	0.87
1:A:519:MET:SD	1:A:520:PHE:CA	2.61	0.87
1:A:32:VAL:CG1	1:A:390:ILE:HB	2.04	0.87
1:A:758:TYR:CD1	1:A:758:TYR:C	2.46	0.87
1:A:482:VAL:O	1:A:486:LEU:CD2	2.21	0.87
1:A:491:ALA:O	1:A:495:THR:HG23	1.75	0.87
2:D:73:VAL:CG1	2:D:74:ASN:N	2.37	0.87
1:B:705:GLU:CB	1:B:847:LEU:HD22	2.04	0.87
1:C:158:VAL:HG22	1:C:162:MET:HE3	1.55	0.87
1:C:738:ALA:C	1:C:739:LEU:HD13	1.95	0.87
1:A:524:THR:O	1:A:528:THR:HG23	1.75	0.87
2:D:126:LEU:HA	2:D:129:VAL:HG21	1.56	0.86
1:B:166:ILE:HG22	1:B:175:VAL:HG21	1.57	0.86
1:C:74:ASN:HB3	1:C:95:GLU:HB2	1.57	0.86
1:A:488:LEU:HD12	1:A:488:LEU:C	1.93	0.86
1:B:658:ILE:N	1:B:658:ILE:CD1	2.30	0.86
1:C:960:LEU:CD1	1:C:960:LEU:C	2.43	0.86
1:C:144:ASN:ND2	1:C:149:MET:HG3	1.90	0.86
1:A:519:MET:SD	1:A:520:PHE:HA	2.16	0.86
1:C:325:TYR:N	1:C:325:TYR:HD1	1.73	0.86
1:A:496:MET:O	1:A:497:LEU:HD23	1.73	0.86
1:B:234:ILE:C	1:B:235:ILE:HD13	1.96	0.86
1:B:445:ILE:HG21	1:B:940:LYS:HG3	1.55	0.86
1:C:200:PRO:HG2	1:C:749:THR:HG22	1.56	0.86
1:C:989:LEU:CD2	1:C:1000:GLN:HB3	2.06	0.86
1:B:137:LEU:HD22	1:B:293:LEU:HD12	1.58	0.86
1:A:780:ARG:O	1:A:780:ARG:HG3	1.74	0.86
1:A:358:PHE:HB2	1:A:977:MET:HE1	1.58	0.86
1:B:563:PHE:CA	1:B:564:LEU:HD12	2.06	0.85
1:A:498:LYS:CD	1:A:498:LYS:N	2.35	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:735:LYS:O	1:C:739:LEU:HD22	1.76	0.85
1:A:75:LEU:CD1	1:A:76:MET:N	2.33	0.85
1:C:15:ILE:O	1:C:19:ILE:HG12	1.76	0.85
2:D:56:TYR:O	2:D:56:TYR:CD1	2.29	0.85
2:D:49:THR:O	2:D:53:LEU:HD21	1.77	0.85
1:B:762:PHE:HE1	1:B:764:ASP:HB2	1.40	0.85
1:A:758:TYR:CD1	1:A:758:TYR:O	2.29	0.85
1:C:211:ASN:HD22	1:C:760:ASN:ND2	1.74	0.85
1:B:348:ILE:HG21	1:B:369:THR:HG23	1.58	0.85
1:C:671:ILE:O	1:C:674:LEU:CD2	2.25	0.85
1:B:154:ILE:O	1:B:158:VAL:HG23	1.77	0.85
1:B:196:PHE:C	1:B:197:GLN:NE2	2.30	0.85
1:C:158:VAL:HA	1:C:162:MET:HE2	1.55	0.85
1:C:154:ILE:HD11	1:C:287:SER:HB3	1.56	0.85
1:C:4:PHE:O	1:C:4:PHE:CD2	2.30	0.85
1:C:237:GLN:O	1:C:238:THR:HG23	1.77	0.85
1:A:749:THR:HG21	1:A:791:VAL:HG11	1.57	0.84
1:C:671:ILE:HD12	1:C:674:LEU:HD11	1.59	0.84
1:B:948:PHE:HE2	1:B:971:ARG:NE	1.73	0.84
2:E:73:VAL:HG12	2:E:104:ALA:HB2	1.58	0.84
1:B:495:THR:HG22	1:B:496:MET:N	1.92	0.84
1:C:447:MET:CE	1:C:891:LEU:HD23	2.07	0.84
2:E:56:TYR:CD1	2:E:56:TYR:O	2.30	0.84
2:E:144:LYS:O	2:E:145:PHE:CG	2.31	0.84
1:A:790:TYR:HB3	1:A:798:MET:HB3	1.59	0.84
1:A:75:LEU:CD1	1:A:76:MET:H	1.87	0.84
1:B:561:SER:HB2	1:B:923:ASN:HB3	1.58	0.84
1:B:207:ILE:HG22	1:B:760:ASN:HD21	1.42	0.84
1:C:327:TYR:O	1:C:327:TYR:CD2	2.30	0.84
2:E:46:VAL:CG1	2:E:47:GLY:H	1.87	0.84
1:B:658:ILE:H	1:B:658:ILE:HD13	1.42	0.84
1:B:713:LEU:CD1	1:B:713:LEU:N	2.41	0.84
1:B:563:PHE:O	1:B:564:LEU:HD12	1.75	0.84
1:A:758:TYR:HD1	1:A:758:TYR:C	1.80	0.84
1:B:197:GLN:N	1:B:197:GLN:CD	2.30	0.83
2:E:144:LYS:O	2:E:145:PHE:CD2	2.30	0.83
1:B:281:PHE:HD1	1:B:610:PHE:HD1	1.26	0.83
2:D:56:TYR:CD1	2:D:90:ARG:NE	2.45	0.83
1:A:486:LEU:N	1:A:486:LEU:CD1	2.30	0.83
1:A:367:ILE:HB	1:A:368:PRO:HD3	1.60	0.83
1:B:1027:VAL:O	1:B:1031:ARG:HG2	1.78	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:GLN:OE1	1:B:230:LEU:N	2.11	0.83
2:D:125:HIS:O	2:D:129:VAL:HG22	1.78	0.83
1:A:974:PRO:O	1:A:978:THR:HG23	1.77	0.83
1:A:190:PRO:HG2	1:A:779:TYR:HB3	1.59	0.83
1:C:810:GLU:C	1:C:811:TYR:HD2	1.81	0.83
1:B:837:THR:O	1:B:841:MET:HG3	1.78	0.83
1:C:11:PHE:CD1	1:C:11:PHE:O	2.30	0.83
1:B:53:ASP:O	1:B:57:VAL:HG23	1.78	0.83
1:A:411:VAL:HG21	1:A:971:ARG:NH2	1.94	0.83
1:B:102:ILE:HG22	1:B:103:ALA:H	1.44	0.83
1:A:488:LEU:CD1	1:A:492:LEU:HD13	2.09	0.83
2:D:56:TYR:CD1	2:D:90:ARG:HG3	2.13	0.82
1:B:182:TYR:CG	1:B:270:LEU:HD11	2.13	0.82
1:B:254:ASN:ND2	1:B:258:SER:HB3	1.93	0.82
1:B:671:ILE:HG23	1:B:671:ILE:O	1.77	0.82
1:C:758:TYR:CE2	1:C:770:LYS:HB3	2.14	0.82
1:B:562:SER:O	1:B:924:ASP:CA	2.25	0.82
1:A:498:LYS:HE3	1:A:498:LYS:N	1.94	0.82
1:A:488:LEU:HD12	1:A:492:LEU:HD13	1.59	0.82
1:C:200:PRO:HG2	1:C:749:THR:CG2	2.09	0.82
1:A:971:ARG:C	1:A:974:PRO:HD2	1.99	0.82
2:D:44:ASP:OD1	2:D:45:HIS:CA	2.28	0.82
1:B:234:ILE:O	1:B:235:ILE:HD12	1.79	0.82
1:B:853:THR:C	1:B:857:TYR:N	2.33	0.82
1:B:989:LEU:CD2	1:B:1000:GLN:HG2	2.09	0.82
1:C:733:GLN:NE2	1:C:743:ILE:HG21	1.94	0.82
1:A:558:ARG:HD2	1:A:558:ARG:O	1.79	0.82
1:B:563:PHE:CB	1:B:564:LEU:HD12	2.10	0.81
1:C:671:ILE:CD1	1:C:674:LEU:CD1	2.42	0.81
1:A:445:ILE:HG21	1:A:940:LYS:HE2	1.62	0.81
1:A:519:MET:C	1:A:519:MET:CE	2.48	0.81
1:B:605:ASN:O	1:B:631:LEU:HD22	1.79	0.81
1:A:680:PHE:CZ	1:A:829:GLY:HA3	2.15	0.81
1:B:731:ILE:O	1:B:731:ILE:HG12	1.79	0.81
2:D:56:TYR:CD1	2:D:90:ARG:CD	2.63	0.81
2:D:51:LEU:CD2	2:D:51:LEU:C	2.47	0.81
1:B:160:ALA:C	1:B:161:ASN:HD22	1.83	0.81
1:B:354:VAL:HG21	1:B:981:ALA:HB2	1.63	0.81
1:C:733:GLN:OE1	1:C:743:ILE:HD13	1.81	0.81
1:C:71:GLY:O	1:C:72:ILE:HG12	1.81	0.81
1:B:674:LEU:HD13	1:B:674:LEU:O	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:587:THR:HG21	1:B:622:GLN:O	1.81	0.81
1:B:230:LEU:CD2	1:B:230:LEU:C	2.37	0.81
1:C:980:LEU:HD22	1:C:980:LEU:N	1.95	0.81
1:A:1:FME:N	1:A:2:PRO:CD	2.43	0.81
1:A:685:ILE:HD13	1:A:685:ILE:H	1.45	0.81
1:C:512:PHE:O	1:C:512:PHE:CD1	2.34	0.81
1:B:527:TYR:HE2	1:B:968:VAL:HG13	1.45	0.81
1:A:485:ALA:O	1:A:490:PRO:CD	2.29	0.80
1:B:649:MET:HE2	1:B:649:MET:HA	1.62	0.80
1:B:775:SER:OG	1:B:780:ARG:HG2	1.80	0.80
1:A:182:TYR:CD2	1:A:270:LEU:HD23	2.14	0.80
1:B:671:ILE:O	1:B:672:VAL:CG1	2.30	0.80
1:B:561:SER:CB	1:B:923:ASN:HB3	2.10	0.80
1:C:85:THR:OG1	1:C:87:THR:HG23	1.80	0.80
1:B:362:PHE:O	1:B:365:THR:CG2	2.30	0.80
2:D:73:VAL:CG1	2:D:74:ASN:OD1	2.28	0.80
1:A:483:LEU:O	1:A:486:LEU:CD2	2.30	0.80
1:A:379:THR:O	1:A:383:LEU:CD2	2.30	0.80
1:B:668:LEU:C	1:B:668:LEU:CD1	2.46	0.80
1:A:534:ILE:HA	1:A:541:TYR:CE1	2.16	0.80
2:D:46:VAL:CG2	2:D:46:VAL:O	2.30	0.80
1:C:83:ASP:O	1:C:84:SER:CB	2.29	0.80
1:C:570:GLY:O	1:C:571:VAL:CG1	2.30	0.80
1:A:188:MET:HG2	1:A:774:MET:O	1.82	0.80
1:C:568:ASP:OD2	1:C:644:VAL:HG22	1.82	0.80
1:C:672:VAL:CG2	1:C:673:GLU:OE1	2.30	0.80
1:C:496:MET:CG	1:C:496:MET:O	2.30	0.80
1:B:278:ILE:HG12	1:B:278:ILE:O	1.82	0.80
1:A:498:LYS:CE	1:A:498:LYS:H	1.93	0.80
1:B:848:ALA:O	1:B:851:LEU:CD1	2.29	0.80
1:C:88:VAL:HG23	1:C:89:GLN:N	1.95	0.80
1:C:976:LEU:O	1:C:980:LEU:CD2	2.30	0.80
1:C:927:PHE:CE2	1:C:931:LEU:HD11	2.16	0.80
1:B:188:MET:HE2	1:B:773:VAL:CG2	2.02	0.80
1:B:671:ILE:CD1	1:B:671:ILE:O	2.30	0.80
1:A:647:ILE:O	1:A:650:ARG:HG2	1.81	0.80
1:B:848:ALA:HA	1:B:851:LEU:HD13	1.62	0.79
2:D:53:LEU:N	2:D:53:LEU:HD22	1.95	0.79
1:B:848:ALA:HA	1:B:851:LEU:HD11	1.63	0.79
1:A:73:ASP:CB	1:A:74:ASN:OD1	2.30	0.79
1:C:71:GLY:O	1:C:72:ILE:CG1	2.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:441:ALA:O	1:B:445:ILE:HG13	1.81	0.79
1:B:501:ALA:O	1:B:504:ASP:HB3	1.82	0.79
1:A:558:ARG:O	1:A:558:ARG:CD	2.30	0.79
1:B:182:TYR:HB3	1:B:270:LEU:CD1	2.10	0.79
1:C:11:PHE:C	1:C:11:PHE:HD1	1.85	0.79
2:D:73:VAL:HG12	2:D:74:ASN:N	1.96	0.79
1:A:558:ARG:C	1:A:558:ARG:CD	2.50	0.79
1:C:566:ASP:OD2	1:C:678:THR:HG21	1.82	0.79
1:C:876:LEU:C	1:C:876:LEU:CD2	2.50	0.79
1:C:923:ASN:OD1	1:C:927:PHE:CD2	2.35	0.79
1:C:314:GLU:CA	1:C:317:PHE:CD1	2.65	0.79
1:C:144:ASN:ND2	1:C:149:MET:CG	2.45	0.79
2:E:93:LEU:HD21	2:E:128:ILE:CG1	2.13	0.79
1:B:966:ASP:O	1:B:970:MET:HG3	1.80	0.79
1:B:991:ILE:CD1	1:B:991:ILE:O	2.30	0.79
1:A:931:LEU:O	1:A:935:ILE:CG2	2.30	0.79
1:C:88:VAL:CG2	1:C:89:GLN:N	2.45	0.79
1:A:519:MET:O	1:A:519:MET:CE	2.30	0.78
1:A:376:LEU:O	1:A:380:PHE:HD1	1.64	0.78
1:B:874:PRO:CB	1:B:877:TYR:CD2	2.61	0.78
1:B:218:GLN:HB3	1:B:232:ALA:O	1.82	0.78
1:A:935:ILE:CD1	1:A:935:ILE:O	2.30	0.78
1:B:24:GLY:O	1:B:27:ILE:HG22	1.83	0.78
2:D:56:TYR:HE1	2:D:90:ARG:NE	1.72	0.78
1:C:149:MET:SD	1:C:321:LEU:CD1	2.72	0.78
1:C:758:TYR:HE2	1:C:770:LYS:HB3	1.48	0.78
1:A:263:ARG:HG3	1:A:264:ASP:OD2	1.83	0.78
1:B:182:TYR:CD1	1:B:270:LEU:CD1	2.66	0.78
1:C:960:LEU:O	1:C:960:LEU:CD1	2.30	0.78
1:B:848:ALA:CA	1:B:851:LEU:CD1	2.60	0.78
2:E:93:LEU:HD21	2:E:128:ILE:HG12	1.64	0.78
1:A:956:GLU:CA	1:A:956:GLU:OE2	2.30	0.78
1:B:449:LEU:O	1:B:453:PHE:HD1	1.66	0.78
1:B:302:THR:O	1:B:306:ILE:HG22	1.83	0.78
2:D:56:TYR:HD1	2:D:90:ARG:HG3	1.49	0.78
1:B:196:PHE:C	1:B:197:GLN:CD	2.42	0.78
1:B:919:ARG:HH11	1:B:919:ARG:HB3	0.67	0.78
1:A:485:ALA:C	1:A:486:LEU:HD13	2.03	0.78
1:A:10:ILE:O	1:A:14:VAL:HG23	1.83	0.78
1:C:156:ASP:OD1	1:C:182:TYR:HB2	1.84	0.78
1:B:156:ASP:CB	1:B:182:TYR:HE2	1.96	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:724:THR:CB	1:C:725:PRO:CD	2.63	0.78
1:C:68:ASN:ND2	1:C:114:ALA:HB2	1.98	0.78
1:B:575:MET:HG3	1:B:576:VAL:N	1.99	0.77
1:B:534:ILE:HA	1:B:541:TYR:CZ	2.19	0.77
1:A:67:GLN:NE2	1:C:767:ARG:NH1	2.32	0.77
1:C:927:PHE:CE2	1:C:931:LEU:CD1	2.67	0.77
1:A:181:GLN:HE21	1:A:769:LYS:HE3	1.49	0.77
1:A:496:MET:O	1:A:497:LEU:CD2	2.30	0.77
1:C:568:ASP:OD2	1:C:644:VAL:CG1	2.32	0.77
1:A:348:ILE:O	1:A:351:VAL:HG12	1.84	0.77
2:E:146:GLY:HA2	2:E:147:LYS:CB	2.15	0.77
1:C:1:FME:CN	1:C:2:PRO:HD2	2.15	0.77
1:C:157:TYR:CD2	1:C:157:TYR:C	2.58	0.77
1:C:185:ARG:HH12	1:C:774:MET:HE2	1.46	0.77
1:B:762:PHE:HD2	1:B:771:VAL:HG23	1.48	0.77
1:B:218:GLN:NE2	1:B:231:ASN:HD21	1.82	0.77
1:A:150:THR:O	1:A:154:ILE:HG13	1.85	0.77
1:B:103:ALA:O	1:B:107:VAL:HG23	1.84	0.77
2:D:126:LEU:O	2:D:129:VAL:HG23	1.85	0.77
1:C:669:PRO:HA	1:C:678:THR:HG22	1.66	0.77
1:A:498:LYS:CE	1:A:498:LYS:O	2.30	0.76
1:C:155:SER:HB3	1:C:287:SER:HB2	1.64	0.76
1:B:713:LEU:N	1:B:713:LEU:HD13	1.99	0.76
1:B:559:LEU:HD12	1:B:560:PRO:HD2	1.66	0.76
1:A:75:LEU:HD12	1:A:75:LEU:C	1.86	0.76
1:C:671:ILE:O	1:C:674:LEU:HD21	1.85	0.76
1:B:5:PHE:O	1:B:491:ALA:HB2	1.85	0.76
1:B:204:ILE:HG23	1:B:759:VAL:CG1	2.16	0.76
1:C:502:LYS:HG2	1:C:503:GLY:N	2.00	0.76
1:B:270:LEU:CD2	1:B:271:GLY:N	2.39	0.76
1:B:974:PRO:O	1:B:978:THR:HG23	1.85	0.76
1:B:674:LEU:CD1	1:B:674:LEU:O	2.34	0.76
2:D:126:LEU:HA	2:D:129:VAL:CG2	2.15	0.76
1:B:874:PRO:CG	1:B:874:PRO:O	2.30	0.76
1:C:570:GLY:C	1:C:571:VAL:CG1	2.53	0.76
1:C:623:ASN:C	1:C:623:ASN:ND2	2.34	0.76
1:B:234:ILE:O	1:B:235:ILE:HD13	1.85	0.76
1:B:196:PHE:HA	1:B:197:GLN:NE2	2.00	0.76
1:C:607:GLU:OE2	1:C:632:LYS:CG	2.29	0.76
1:B:102:ILE:HG22	1:B:103:ALA:N	1.97	0.76
1:B:72:ILE:HG22	1:B:73:ASP:N	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:196:PHE:C	1:C:197:GLN:CG	2.54	0.76
1:A:904:VAL:CG2	1:A:904:VAL:O	2.34	0.76
1:C:669:PRO:CA	1:C:678:THR:HG22	2.15	0.76
2:D:19:LEU:HD23	2:D:50:PRO:HG3	1.67	0.75
1:B:712:MET:O	1:B:713:LEU:CD1	2.30	0.75
1:B:501:ALA:HB3	1:B:504:ASP:CB	2.17	0.75
1:A:235:ILE:O	1:B:728:LYS:HA	1.87	0.75
1:C:369:THR:O	1:C:372:VAL:HG13	1.86	0.75
1:C:144:ASN:HD21	1:C:149:MET:HG3	1.52	0.75
1:B:1:FME:N	1:B:2:PRO:CD	2.49	0.75
1:C:876:LEU:O	1:C:876:LEU:CD2	2.34	0.75
1:C:34:GLN:HB2	1:C:333:VAL:HG13	1.67	0.75
1:C:724:THR:HB	1:C:725:PRO:CD	2.16	0.75
1:B:178:PHE:HB2	1:B:287:SER:O	1.86	0.75
1:B:848:ALA:O	1:B:851:LEU:HD12	1.86	0.75
1:B:415:ASN:O	1:B:419:VAL:HG23	1.87	0.75
1:C:689:GLY:CA	1:C:690:LEU:HD23	2.17	0.75
1:B:988:PRO:O	1:B:991:ILE:CG2	2.35	0.75
1:B:204:ILE:HG23	1:B:759:VAL:HG12	1.69	0.75
1:C:327:TYR:HD1	1:C:628:PHE:HB3	1.50	0.75
1:C:160:ALA:C	1:C:161:ASN:OD1	2.25	0.75
1:A:101:ASP:O	1:A:105:VAL:HG23	1.87	0.75
1:C:314:GLU:HA	1:C:317:PHE:HE1	1.01	0.75
1:C:200:PRO:CG	1:C:749:THR:CG2	2.65	0.75
1:B:799:VAL:HG13	1:B:800:PRO:HD3	1.68	0.74
1:B:853:THR:CG2	1:B:853:THR:O	2.34	0.74
1:B:224:PRO:HA	1:C:781:MET:HE1	1.70	0.74
1:B:10:ILE:HB	1:C:893:GLU:OE2	1.87	0.74
1:A:542:LEU:O	1:A:545:TYR:HB3	1.87	0.74
1:B:161:ASN:N	1:B:161:ASN:ND2	2.29	0.74
2:D:18:LEU:CD2	2:D:18:LEU:O	2.30	0.74
1:C:4:PHE:CD2	1:C:4:PHE:C	2.51	0.74
1:A:62:THR:O	1:A:66:GLU:HG3	1.86	0.74
2:E:152:ILE:HG13	2:E:153:SER:H	1.51	0.74
1:C:102:ILE:O	1:C:106:GLN:HG3	1.87	0.74
1:C:742:SER:HB3	1:C:745:ASP:H	1.53	0.74
1:B:668:LEU:O	1:B:668:LEU:CD1	2.30	0.74
1:B:188:MET:HE1	1:B:773:VAL:CG2	2.16	0.74
2:E:112:ASN:CA	2:E:144:LYS:HE2	2.17	0.74
1:C:891:LEU:HD12	1:C:892:TYR:CD1	2.23	0.74
1:C:587:THR:HG21	1:C:622:GLN:O	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:GLN:CA	1:B:229:GLN:OE1	2.34	0.74
1:A:428:LYS:O	1:A:431:THR:CG2	2.30	0.74
1:B:670:ALA:O	1:B:671:ILE:HG22	1.87	0.74
2:E:93:LEU:HD23	2:E:128:ILE:HG12	1.68	0.74
1:A:32:VAL:HG12	1:A:390:ILE:O	1.86	0.74
1:C:267:LYS:C	1:C:268:ILE:HD13	2.08	0.74
1:A:242:SER:HB2	1:A:244:GLU:HG2	1.70	0.74
1:B:990:VAL:HG12	1:B:991:ILE:N	2.00	0.74
1:A:942:ALA:O	1:A:946:VAL:HG12	1.87	0.74
1:C:671:ILE:CG1	1:C:671:ILE:O	2.29	0.74
1:A:721:LEU:HD12	1:A:814:PRO:HG2	1.67	0.74
1:C:247:GLY:O	1:C:263:ARG:CG	2.36	0.74
1:C:910:ILE:CG2	1:C:1013:THR:HG21	2.17	0.74
1:A:897:ILE:N	1:A:898:PRO:CD	2.51	0.73
2:E:100:LEU:HD21	2:E:106:VAL:CG1	2.17	0.73
1:C:327:TYR:CD1	1:C:628:PHE:HB3	2.23	0.73
1:C:512:PHE:C	1:C:512:PHE:CD1	2.57	0.73
1:B:705:GLU:HB3	1:B:847:LEU:HD22	1.70	0.73
1:A:580:ALA:HA	1:A:623:ASN:ND2	2.03	0.73
1:B:365:THR:HG23	1:B:366:LEU:HD23	1.70	0.73
1:A:721:LEU:CD1	1:A:814:PRO:HG2	2.13	0.73
1:C:11:PHE:C	1:C:11:PHE:CD1	2.57	0.73
1:B:169:THR:HG22	1:B:172:VAL:CG1	2.17	0.73
1:C:203:VAL:O	1:C:207:ILE:HG13	1.88	0.73
1:B:224:PRO:HA	1:C:781:MET:CE	2.18	0.73
1:C:247:GLY:O	1:C:263:ARG:HG3	1.88	0.73
1:B:59:ASP:O	1:B:63:GLN:HB2	1.89	0.73
1:A:478:MET:O	1:A:482:VAL:CG2	2.30	0.73
1:A:488:LEU:O	1:A:488:LEU:CD1	2.30	0.73
1:C:876:LEU:O	1:C:876:LEU:HD23	1.88	0.73
1:B:254:ASN:HB2	1:B:258:SER:O	1.88	0.73
1:A:808:ARG:NH1	1:A:808:ARG:CB	2.30	0.73
1:C:671:ILE:CD1	1:C:674:LEU:CD2	2.67	0.73
1:A:621:GLY:HA3	1:A:624:THR:HG22	1.71	0.73
1:C:149:MET:SD	1:C:321:LEU:HD13	2.29	0.73
1:A:754:TRP:CZ3	1:C:219:LEU:HD23	2.22	0.73
1:C:669:PRO:HD3	1:C:676:THR:O	1.89	0.73
1:A:956:GLU:HA	1:A:956:GLU:OE2	1.87	0.73
1:C:156:ASP:CG	1:C:182:TYR:CD2	2.62	0.73
1:C:754:TRP:CZ2	1:C:786:ILE:HG12	2.24	0.72
1:B:254:ASN:HD22	1:B:258:SER:CB	1.97	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:161:ASN:N	1:B:161:ASN:HD22	1.87	0.72
1:A:376:LEU:O	1:A:380:PHE:CD1	2.42	0.72
1:B:986:VAL:O	1:B:986:VAL:HG12	1.89	0.72
1:B:948:PHE:CE2	1:B:971:ARG:NE	2.53	0.72
1:C:259:ARG:HH12	2:E:155:ASP:CG	1.93	0.72
1:B:183:ALA:N	1:B:271:GLY:O	2.22	0.72
1:B:771:VAL:O	1:B:771:VAL:HG12	1.88	0.72
1:A:427:PRO:HD3	1:A:499:PRO:HB3	1.72	0.72
1:A:407:ASP:OD1	1:A:978:THR:HG21	1.90	0.72
1:A:535:LEU:HD22	1:A:1027:VAL:HG21	1.71	0.72
1:B:874:PRO:HB3	1:B:877:TYR:HD2	1.51	0.72
1:C:534:ILE:HG13	1:C:541:TYR:CE2	2.25	0.72
1:A:463:THR:O	1:A:467:TYR:HD2	1.73	0.72
1:C:896:SER:HG	1:C:897:ILE:CD1	2.03	0.72
1:C:926:TYR:HD2	1:C:1003:VAL:HG22	1.55	0.72
1:A:151:GLN:HB3	1:A:285:PRO:HB3	1.71	0.72
1:C:757:SER:O	1:C:772:TYR:HD1	1.70	0.72
1:A:498:LYS:C	1:A:498:LYS:HE3	2.08	0.72
1:A:383:LEU:HD11	1:A:473:THR:HG22	1.70	0.72
1:B:36:PRO:HG3	1:B:391:ASN:ND2	2.05	0.72
1:B:394:THR:HG22	1:B:473:THR:OG1	1.90	0.72
1:C:314:GLU:O	1:C:317:PHE:CD1	2.35	0.72
1:B:254:ASN:C	1:B:257:GLY:H	1.93	0.72
1:B:671:ILE:O	1:B:672:VAL:HG12	1.89	0.72
1:B:69:MET:CE	1:B:72:ILE:CD1	2.67	0.72
1:B:254:ASN:HB2	1:B:258:SER:N	2.05	0.72
1:A:519:MET:CG	1:A:520:PHE:N	2.52	0.72
1:B:102:ILE:HG23	1:B:103:ALA:N	2.02	0.72
1:C:810:GLU:C	1:C:811:TYR:CD2	2.63	0.72
1:C:457:ALA:HB1	1:C:468:ARG:HG2	1.72	0.72
1:C:793:ALA:O	1:C:794:ALA:C	2.28	0.72
1:C:513:PHE:O	1:C:516:PHE:N	2.23	0.72
1:B:670:ALA:O	1:B:671:ILE:CB	2.33	0.71
1:B:557:VAL:CG2	1:B:557:VAL:O	2.38	0.71
2:E:125:HIS:ND1	2:E:128:ILE:HG13	2.06	0.71
1:C:204:ILE:HG23	1:C:759:VAL:CG2	2.20	0.71
1:C:891:LEU:HD12	1:C:892:TYR:CE1	2.25	0.71
1:C:582:ALA:HB3	1:C:623:ASN:HB2	1.72	0.71
1:A:520:PHE:CD2	1:A:520:PHE:C	2.60	0.71
1:C:230:LEU:HG	1:C:230:LEU:O	1.89	0.71
1:B:182:TYR:CD1	1:B:270:LEU:HD13	2.26	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:GLN:CD	1:B:229:GLN:N	2.32	0.71
1:A:423:GLU:C	1:A:502:LYS:HG3	2.11	0.71
1:B:605:ASN:HD21	1:B:642:ASN:HB3	1.54	0.71
1:A:1016:VAL:HG23	1:A:1017:LEU:HD12	1.71	0.71
1:C:405:LEU:O	1:C:405:LEU:HD12	1.91	0.71
1:A:489:THR:CB	1:A:490:PRO:CD	2.69	0.71
1:B:702:LEU:HB2	1:B:851:LEU:HD21	1.73	0.71
1:A:527:TYR:CD1	1:A:972:LEU:HD23	2.25	0.71
1:C:739:LEU:H	1:C:739:LEU:HD22	1.55	0.71
1:A:6:ILE:HD13	1:A:431:THR:HG21	1.72	0.71
1:B:150:THR:OG1	1:B:152:GLU:HB2	1.91	0.71
1:A:829:GLY:C	1:A:830:GLN:OE1	2.29	0.71
1:A:234:ILE:CA	1:A:235:ILE:HD13	2.18	0.70
1:A:901:VAL:O	1:A:901:VAL:CG1	2.39	0.70
1:A:73:ASP:C	1:A:74:ASN:OD1	2.30	0.70
1:B:513:PHE:C	1:B:515:TRP:H	1.94	0.70
1:A:504:ASP:C	1:A:504:ASP:OD1	2.30	0.70
1:C:937:LEU:O	1:C:940:LYS:CG	2.39	0.70
1:B:512:PHE:O	1:B:513:PHE:CB	2.36	0.70
1:C:673:GLU:N	1:C:673:GLU:CD	2.38	0.70
1:C:795:ASP:OD1	1:C:795:ASP:C	2.30	0.70
1:B:229:GLN:OE1	1:B:229:GLN:C	2.30	0.70
1:A:527:TYR:CD1	1:A:972:LEU:CD2	2.75	0.70
1:C:1032:ARG:O	1:C:1033:PHE:CB	2.37	0.70
1:C:429:GLU:OE1	1:C:429:GLU:C	2.29	0.70
1:A:489:THR:HB	1:A:490:PRO:CD	2.22	0.70
2:D:129:VAL:O	2:D:133:LEU:CD1	2.30	0.70
1:C:910:ILE:HG23	1:C:1013:THR:HG21	1.74	0.70
1:A:317:PHE:HB3	1:A:321:LEU:HB3	1.71	0.70
2:D:61:GLU:O	2:D:65:VAL:CG2	2.34	0.70
1:A:504:ASP:CG	1:A:504:ASP:O	2.30	0.70
1:C:724:THR:HB	1:C:725:PRO:HD2	1.73	0.70
1:C:435:MET:CE	1:C:435:MET:CA	2.55	0.70
1:A:182:TYR:CD2	1:A:270:LEU:CD2	2.74	0.70
1:B:534:ILE:HA	1:B:541:TYR:OH	1.90	0.70
1:C:993:THR:O	1:C:993:THR:CG2	2.35	0.70
1:C:325:TYR:HD1	1:C:325:TYR:H	1.39	0.70
2:D:73:VAL:HG13	2:D:74:ASN:OD1	1.92	0.70
1:A:58:GLN:NE2	1:A:818:ARG:HH11	1.88	0.70
1:B:818:ARG:NH1	1:B:821:GLY:O	2.25	0.70
1:B:905:VAL:HB	1:B:906:PRO:HD3	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:GLN:C	1:B:213:GLN:OE1	2.30	0.70
1:C:891:LEU:CD1	1:C:892:TYR:CE1	2.74	0.70
1:B:672:VAL:O	1:B:672:VAL:CG2	2.30	0.70
1:A:989:LEU:HD22	1:A:1000:GLN:HB3	1.72	0.70
1:B:62:THR:OG1	1:B:88:VAL:HG21	1.92	0.70
2:D:152:ILE:O	2:D:156:ASN:HB2	1.91	0.70
1:C:531:VAL:HA	1:C:534:ILE:HG22	1.74	0.70
1:B:758:TYR:HB2	1:B:772:TYR:CD1	2.26	0.69
1:C:504:ASP:OD1	1:C:507:GLU:HA	1.92	0.69
1:B:901:VAL:O	1:B:904:VAL:HG22	1.92	0.69
1:C:82:SER:O	1:C:815:ARG:HA	1.90	0.69
1:B:459:PHE:O	1:B:464:GLY:HA3	1.92	0.69
1:C:1:FME:N	1:C:2:PRO:HD2	2.06	0.69
2:D:56:TYR:CD1	2:D:90:ARG:CG	2.75	0.69
2:E:145:PHE:O	2:E:145:PHE:HD1	1.74	0.69
1:B:712:MET:HE1	1:B:839:GLU:OE2	1.92	0.69
1:B:713:LEU:HD22	1:B:843:LEU:HD23	1.73	0.69
1:C:672:VAL:HG23	1:C:673:GLU:OE1	1.90	0.69
2:D:13:ASP:C	2:D:13:ASP:OD1	2.30	0.69
1:B:1:FME:HE1	1:B:487:ILE:CD1	2.22	0.69
1:B:780:ARG:O	1:B:780:ARG:HD2	1.92	0.69
1:B:765:ARG:HB3	1:B:765:ARG:NH1	2.07	0.69
1:C:327:TYR:CD1	1:C:628:PHE:HD1	2.11	0.69
1:B:182:TYR:CD1	1:B:270:LEU:HD11	2.27	0.69
1:B:5:PHE:CE1	1:B:487:ILE:HG12	2.27	0.69
1:C:816:LEU:HD12	1:C:816:LEU:N	2.07	0.69
1:C:65:ILE:O	1:C:69:MET:HG2	1.92	0.69
1:B:450:SER:O	1:B:454:VAL:HG12	1.92	0.69
1:B:183:ALA:HB3	1:B:271:GLY:O	1.92	0.69
1:C:190:PRO:HG3	1:C:789:TRP:CH2	2.27	0.69
1:B:274:ASN:OD1	1:B:276:ASP:N	2.22	0.69
1:C:732:ASP:C	1:C:732:ASP:OD1	2.30	0.69
1:A:360:GLN:CG	1:A:513:PHE:CZ	2.69	0.69
1:C:412:VAL:O	1:C:416:VAL:HG23	1.92	0.69
1:A:537:SER:OG	1:A:540:ARG:CB	2.41	0.69
1:B:184:MET:HB3	1:B:771:VAL:HG22	1.73	0.69
1:A:580:ALA:HA	1:A:623:ASN:HD22	1.56	0.69
1:C:429:GLU:HA	1:C:432:ARG:HG3	1.75	0.69
1:A:781:MET:SD	1:C:220:GLY:HA2	2.33	0.69
1:B:99:ASP:OD1	1:B:99:ASP:C	2.30	0.69
1:A:414:GLU:CD	1:A:974:PRO:HG3	2.14	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:PHE:HD2	1:C:4:PHE:C	1.95	0.69
1:A:463:THR:CG2	1:A:467:TYR:CE2	2.76	0.69
1:C:940:LYS:HG3	1:C:941:ASN:N	2.08	0.69
1:B:143:ILE:HG22	1:B:286:ALA:HB2	1.74	0.69
1:B:671:ILE:C	1:B:672:VAL:HG12	2.13	0.68
1:A:780:ARG:O	1:A:780:ARG:CG	2.41	0.68
1:C:924:ASP:O	1:C:927:PHE:HB3	1.92	0.68
2:D:77:ASP:C	2:D:77:ASP:OD1	2.30	0.68
1:A:483:LEU:O	1:A:486:LEU:HD23	1.93	0.68
1:C:94:PHE:O	1:C:95:GLU:C	2.30	0.68
1:C:211:ASN:HD22	1:C:760:ASN:HD21	1.41	0.68
1:B:274:ASN:OD1	1:B:274:ASN:C	2.30	0.68
1:A:966:ASP:HA	1:A:969:ARG:HD3	1.74	0.68
1:B:764:ASP:OD1	1:B:765:ARG:CG	2.40	0.68
1:A:423:GLU:C	1:A:502:LYS:HE3	2.12	0.68
1:C:237:GLN:O	1:C:238:THR:CG2	2.41	0.68
1:A:544:LEU:O	1:A:548:ILE:HG13	1.93	0.68
1:A:860:THR:O	1:A:861:GLY:C	2.29	0.68
1:C:689:GLY:O	1:C:690:LEU:CD2	2.37	0.68
1:A:423:GLU:O	1:A:502:LYS:CE	2.42	0.68
1:A:491:ALA:O	1:A:495:THR:CG2	2.41	0.68
1:A:194:ASN:ND2	1:A:798:MET:HG3	2.08	0.68
1:B:795:ASP:OD2	1:B:797:GLN:HB2	1.94	0.68
1:B:222:THR:CG2	1:C:275:TYR:HB3	2.24	0.68
1:B:231:ASN:HD22	1:B:232:ALA:N	1.92	0.68
1:B:670:ALA:O	1:B:671:ILE:CG2	2.42	0.68
2:D:14:LEU:N	2:D:14:LEU:HD12	2.08	0.68
1:B:871:ASN:CB	1:B:872:GLN:HG2	2.19	0.68
1:B:169:THR:CG2	1:B:172:VAL:CG1	2.72	0.68
1:B:166:ILE:O	1:B:172:VAL:HG21	1.93	0.68
2:D:76:ASP:O	2:D:77:ASP:HB3	1.94	0.68
1:C:707:ALA:O	1:C:710:PRO:HD3	1.94	0.68
1:C:980:LEU:HD22	1:C:980:LEU:H	1.56	0.68
1:B:403:GLY:HA3	1:B:982:PHE:CE1	2.28	0.68
2:D:92:HIS:O	2:D:96:VAL:HG23	1.93	0.68
1:A:218:GLN:HA	1:A:234:ILE:HG13	1.76	0.67
1:B:815:ARG:HG2	1:B:815:ARG:NH1	2.09	0.67
1:B:140:VAL:O	1:B:288:GLY:HA2	1.94	0.67
1:B:764:ASP:OD1	1:B:765:ARG:HG3	1.93	0.67
2:D:77:ASP:OD1	2:D:79:LEU:N	2.26	0.67
1:B:13:TRP:O	1:B:17:ILE:HG13	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:336:SER:O	1:C:340:VAL:HG23	1.95	0.67
1:B:800:PRO:O	1:B:800:PRO:HD2	1.94	0.67
1:C:879:ILE:O	1:C:879:ILE:CD1	2.30	0.67
1:C:733:GLN:CD	1:C:743:ILE:HD13	2.15	0.67
1:B:670:ALA:O	1:B:671:ILE:HB	1.94	0.67
1:C:760:ASN:O	1:C:771:VAL:HB	1.95	0.67
1:B:732:ASP:OD1	1:B:732:ASP:C	2.30	0.67
1:A:586:ARG:O	1:A:590:VAL:HG23	1.95	0.67
1:A:945:ILE:HG22	1:A:946:VAL:N	2.10	0.67
1:C:742:SER:O	1:C:746:ILE:HD13	1.93	0.67
1:C:629:VAL:CG2	1:C:629:VAL:O	2.43	0.67
1:A:298:ASN:HD22	1:A:301:ASP:CB	2.07	0.67
1:B:939:ALA:O	1:B:943:ILE:HG13	1.95	0.67
1:C:53:ASP:OD1	1:C:53:ASP:C	2.30	0.67
1:C:876:LEU:HD22	1:C:876:LEU:C	2.13	0.67
1:C:200:PRO:CG	1:C:749:THR:HG23	2.23	0.67
1:A:39:ALA:HB1	1:A:40:PRO:HD2	1.76	0.67
1:B:281:PHE:HD1	1:B:610:PHE:CD1	2.11	0.67
1:B:10:ILE:CB	1:C:893:GLU:OE2	2.43	0.67
1:A:137:LEU:HD13	1:A:293:LEU:HD12	1.77	0.67
1:A:721:LEU:HD13	1:A:814:PRO:HG3	1.71	0.67
2:E:152:ILE:CD1	2:E:153:SER:N	2.58	0.67
1:A:358:PHE:CD1	1:A:977:MET:HE3	2.29	0.67
1:A:488:LEU:C	1:A:488:LEU:CD1	2.62	0.67
1:B:61:VAL:O	1:B:65:ILE:CG1	2.42	0.67
1:B:1022:VAL:HA	1:B:1025:PHE:HD1	1.60	0.67
1:A:423:GLU:O	1:A:502:LYS:CD	2.43	0.66
1:B:874:PRO:HB3	1:B:877:TYR:CD2	2.28	0.66
1:C:896:SER:HG	1:C:897:ILE:HD13	1.60	0.66
1:B:512:PHE:O	1:B:513:PHE:HB2	1.94	0.66
2:D:79:LEU:HD22	2:D:111:HIS:CE1	2.29	0.66
1:B:512:PHE:O	1:B:513:PHE:C	2.32	0.66
1:C:689:GLY:N	1:C:690:LEU:HD23	2.09	0.66
1:A:445:ILE:HD11	1:A:943:ILE:HG21	1.77	0.66
1:A:534:ILE:HG13	1:A:535:LEU:N	2.10	0.66
1:C:757:SER:O	1:C:772:TYR:CD1	2.47	0.66
1:C:563:PHE:CE2	1:C:564:LEU:HD12	2.30	0.66
1:B:561:SER:HA	1:B:923:ASN:HB3	1.78	0.66
1:A:74:ASN:N	1:A:74:ASN:OD1	2.28	0.66
1:C:972:LEU:HD13	1:C:976:LEU:HD23	1.78	0.66
1:B:853:THR:HG22	1:B:853:THR:O	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:ILE:HG12	1:C:893:GLU:OE2	1.94	0.66
1:C:463:THR:HG22	1:C:467:TYR:CE1	2.30	0.66
1:A:652:THR:HA	1:A:655:PHE:HD2	1.59	0.66
1:C:575:MET:O	1:C:575:MET:CG	2.30	0.66
1:B:38:ILE:HD11	1:B:671:ILE:HD11	1.78	0.66
1:A:373:PRO:O	1:A:377:LEU:HG	1.95	0.66
1:A:520:PHE:C	1:A:520:PHE:HD2	1.99	0.66
1:B:762:PHE:CD2	1:B:771:VAL:HG23	2.31	0.66
1:B:361:ASN:N	1:B:361:ASN:ND2	2.32	0.66
1:B:583:THR:O	1:B:587:THR:HG22	1.96	0.66
1:B:563:PHE:CB	1:B:564:LEU:CD1	2.73	0.66
1:A:360:GLN:CG	1:A:513:PHE:HZ	2.00	0.66
1:B:69:MET:HE1	1:B:72:ILE:HD11	1.78	0.66
2:D:57:PHE:H	2:D:58:GLY:HA2	1.60	0.66
1:C:671:ILE:CG1	1:C:674:LEU:CD2	2.62	0.66
2:D:46:VAL:O	2:D:46:VAL:HG23	1.94	0.66
1:C:559:LEU:HD12	1:C:560:PRO:HD2	1.77	0.66
1:B:727:PHE:CE1	1:B:783:PRO:HB3	2.30	0.66
1:C:497:LEU:HD22	1:C:498:LYS:N	2.09	0.66
1:B:1:FME:CE	1:B:487:ILE:CD1	2.73	0.66
1:B:116:PRO:C	1:B:117:LEU:CD1	2.64	0.66
1:B:63:GLN:O	1:B:67:GLN:HG3	1.96	0.66
1:C:345:VAL:O	1:C:349:ILE:HG13	1.95	0.66
1:B:196:PHE:CA	1:B:197:GLN:NE2	2.59	0.66
1:A:242:SER:OG	1:A:245:GLU:HG3	1.94	0.66
1:C:429:GLU:OE1	1:C:430:ALA:N	2.29	0.66
1:C:573:MET:HE3	1:C:626:ILE:HD11	1.77	0.66
1:C:187:TRP:NE1	1:C:269:GLU:OE2	2.28	0.66
1:B:541:TYR:O	1:B:544:LEU:HB2	1.96	0.65
1:C:919:ARG:NH1	1:C:990:VAL:HG12	2.03	0.65
1:A:463:THR:HG22	1:A:467:TYR:CD2	2.30	0.65
1:A:568:ASP:OD2	1:A:643:LYS:HG3	1.96	0.65
1:A:483:LEU:C	1:A:486:LEU:CD2	2.64	0.65
1:A:483:LEU:O	1:A:486:LEU:HD22	1.96	0.65
1:A:463:THR:HG22	1:A:467:TYR:CE2	2.31	0.65
1:C:937:LEU:O	1:C:940:LYS:HG3	1.96	0.65
1:C:546:LEU:O	1:C:550:VAL:HG23	1.95	0.65
1:B:254:ASN:O	1:B:257:GLY:N	2.30	0.65
1:A:754:TRP:N	1:A:754:TRP:CD1	2.62	0.65
1:C:563:PHE:HE2	1:C:862:MET:HE1	1.61	0.65
1:B:229:GLN:OE1	1:B:229:GLN:N	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:848:ALA:CA	1:B:851:LEU:HD13	2.26	0.65
1:B:365:THR:O	1:B:368:PRO:HD2	1.96	0.65
1:C:332:PHE:CE2	1:C:569:GLN:NE2	2.64	0.65
1:C:640:GLU:OE1	1:C:640:GLU:N	2.29	0.65
2:E:143:ASP:N	2:E:146:GLY:O	2.30	0.65
1:C:1:FME:N	1:C:2:PRO:HD3	2.09	0.65
1:C:982:PHE:CD2	1:C:1011:MET:HG3	2.30	0.65
1:B:274:ASN:OD1	1:B:275:TYR:N	2.30	0.65
1:C:361:ASN:OD1	1:C:362:PHE:N	2.30	0.65
1:C:724:THR:CB	1:C:725:PRO:HD2	2.26	0.65
1:C:145:THR:OG1	1:C:146:ASP:N	2.29	0.65
1:B:527:TYR:CE2	1:B:968:VAL:HG13	2.31	0.65
1:A:726:GLN:CG	1:A:812:GLY:HA3	2.26	0.65
1:A:489:THR:CB	1:A:490:PRO:HD3	2.27	0.65
1:B:213:GLN:OE1	1:B:214:VAL:N	2.30	0.65
1:C:616:GLY:O	1:C:619:GLY:N	2.30	0.65
1:B:1018:ALA:O	1:B:1022:VAL:HG22	1.96	0.65
1:C:55:LYS:O	1:C:56:THR:C	2.32	0.65
1:B:712:MET:HB3	1:B:713:LEU:HD13	1.79	0.65
1:B:407:ASP:OD2	1:B:978:THR:HB	1.97	0.65
1:C:225:VAL:HG12	1:C:226:LYS:O	1.97	0.65
1:C:671:ILE:O	1:C:674:LEU:HD23	1.96	0.65
1:A:489:THR:HB	1:A:490:PRO:HD3	1.78	0.65
1:C:83:ASP:O	1:C:84:SER:HB3	1.95	0.65
1:A:55:LYS:NZ	1:A:59:ASP:OD1	2.30	0.65
1:B:628:PHE:CD2	1:B:628:PHE:N	2.64	0.65
1:C:161:ASN:OD1	1:C:161:ASN:N	2.29	0.64
1:B:99:ASP:OD1	1:B:101:ASP:N	2.29	0.64
1:B:633:ASP:OD1	1:B:634:TRP:N	2.29	0.64
2:E:95:VAL:O	2:E:99:LEU:HG	1.98	0.64
1:C:743:ILE:O	1:C:747:ASN:ND2	2.30	0.64
1:B:174:ASP:OD2	1:B:175:VAL:N	2.30	0.64
1:A:956:GLU:N	1:A:956:GLU:OE2	2.29	0.64
1:A:445:ILE:HD11	1:A:943:ILE:CG2	2.27	0.64
1:B:715:SER:O	1:B:717:ARG:NH1	2.30	0.64
1:C:893:GLU:O	1:C:894:SER:HB2	1.96	0.64
2:E:156:ASN:C	2:E:156:ASN:HD22	2.01	0.64
1:A:463:THR:CG2	1:A:467:TYR:HE2	2.10	0.64
1:C:761:ASP:HB3	1:C:768:VAL:CG1	2.28	0.64
1:B:705:GLU:CG	1:B:847:LEU:HD21	2.18	0.64
2:D:126:LEU:C	2:D:129:VAL:HG23	2.17	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:LEU:H	1:A:240:LEU:CD1	2.10	0.64
1:C:230:LEU:H	1:C:230:LEU:HD23	1.62	0.64
1:A:370:ILE:O	1:A:374:VAL:HG23	1.97	0.64
1:B:456:MET:HG2	1:B:467:TYR:HB3	1.80	0.64
1:B:210:GLN:OE1	1:B:249:ILE:HG23	1.97	0.64
1:C:736:ALA:HB1	1:C:741:VAL:HG11	1.80	0.64
1:B:234:ILE:C	1:B:235:ILE:CD1	2.62	0.64
1:B:988:PRO:O	1:B:991:ILE:HG23	1.98	0.64
1:A:894:SER:HB2	1:A:897:ILE:HD12	1.79	0.64
1:B:197:GLN:N	1:B:197:GLN:OE1	2.30	0.64
1:B:188:MET:HE1	1:B:773:VAL:HG21	1.79	0.64
2:D:77:ASP:OD1	2:D:78:SER:N	2.30	0.64
1:B:435:MET:O	1:B:437:GLN:N	2.31	0.64
1:B:746:ILE:HD13	1:B:804:PHE:CE2	2.32	0.64
1:A:488:LEU:HD11	1:A:492:LEU:CD1	2.28	0.64
1:A:379:THR:HG22	1:A:383:LEU:HD21	1.80	0.64
1:B:717:ARG:NH1	1:B:717:ARG:CG	2.43	0.64
1:A:754:TRP:HZ3	1:C:219:LEU:CD2	2.09	0.64
1:A:298:ASN:HD22	1:A:301:ASP:H	1.44	0.64
2:E:61:GLU:O	2:E:65:VAL:HG23	1.98	0.64
1:A:236:ALA:HB2	1:B:729:ILE:CG2	2.28	0.64
1:A:696:THR:O	1:A:700:ASN:ND2	2.31	0.64
1:B:254:ASN:O	1:B:257:GLY:HA2	1.98	0.64
1:A:527:TYR:O	1:A:531:VAL:CG2	2.43	0.64
1:B:800:PRO:CD	1:B:800:PRO:O	2.44	0.64
1:B:848:ALA:O	1:B:851:LEU:HD13	1.97	0.64
2:E:112:ASN:HA	2:E:144:LYS:CE	2.22	0.64
1:B:871:ASN:HB3	1:B:872:GLN:CG	2.22	0.64
1:B:459:PHE:HB2	1:B:464:GLY:CA	2.26	0.64
1:B:355:MET:HG2	1:B:365:THR:HA	1.80	0.64
1:C:583:THR:O	1:C:587:THR:HG22	1.98	0.64
1:A:463:THR:HG23	1:A:467:TYR:HE2	1.61	0.64
1:B:54:ALA:HB1	1:B:82:SER:O	1.98	0.64
1:B:144:ASN:OD1	1:B:149:MET:HG2	1.98	0.64
1:B:225:VAL:CG2	1:B:225:VAL:O	2.46	0.64
1:B:225:VAL:HG23	1:B:225:VAL:O	1.96	0.64
1:C:733:GLN:OE1	1:C:743:ILE:CD1	2.46	0.63
2:D:93:LEU:HD23	2:D:128:ILE:HG12	1.80	0.63
1:C:163:LYS:HD2	1:C:177:LEU:HB2	1.79	0.63
1:A:190:PRO:HG3	1:A:789:TRP:CZ2	2.33	0.63
1:A:181:GLN:HE21	1:A:769:LYS:CE	2.10	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ASN:O	1:A:112:GLN:HG3	1.99	0.63
1:A:218:GLN:HB2	1:A:232:ALA:O	1.98	0.63
1:C:568:ASP:OD2	1:C:644:VAL:CG2	2.46	0.63
1:B:60:THR:OG1	1:B:61:VAL:N	2.29	0.63
1:B:153:ASP:N	1:B:153:ASP:OD2	2.30	0.63
1:C:989:LEU:HD22	1:C:1000:GLN:CB	2.23	0.63
1:C:98:THR:CG2	1:C:99:ASP:N	2.61	0.63
1:B:919:ARG:CB	1:B:919:ARG:NH1	2.30	0.63
1:B:669:PRO:HG2	1:B:669:PRO:O	1.97	0.63
1:C:88:VAL:HG23	1:C:89:GLN:H	1.63	0.63
1:B:150:THR:OG1	1:B:152:GLU:N	2.30	0.63
1:B:501:ALA:HB3	1:B:504:ASP:OD2	1.98	0.63
1:C:435:MET:O	1:C:439:GLN:HB2	1.98	0.63
1:B:871:ASN:N	1:B:871:ASN:OD1	2.30	0.63
1:B:669:PRO:CG	1:B:669:PRO:O	2.45	0.63
1:A:531:VAL:O	1:A:534:ILE:HG12	1.99	0.63
1:A:897:ILE:O	1:A:897:ILE:HG22	1.97	0.63
1:C:919:ARG:HH12	1:C:990:VAL:CG1	2.04	0.63
1:C:531:VAL:HA	1:C:534:ILE:CG2	2.29	0.63
1:C:681:ASP:HB3	1:C:860:THR:HG23	1.81	0.63
1:C:730:ASP:N	1:C:730:ASP:OD1	2.30	0.63
1:A:899:PHE:O	1:A:900:SER:C	2.36	0.63
1:C:629:VAL:HG23	1:C:629:VAL:O	1.96	0.63
1:A:527:TYR:CE1	1:A:972:LEU:HD21	2.31	0.63
1:B:150:THR:CG2	1:B:153:ASP:OD2	2.46	0.63
1:B:278:ILE:CG1	1:B:278:ILE:O	2.47	0.63
1:B:501:ALA:HB3	1:B:504:ASP:HB2	1.80	0.63
1:A:498:LYS:NZ	1:A:500:ILE:HD11	2.14	0.63
1:C:739:LEU:HB2	1:C:741:VAL:HG23	1.81	0.63
1:B:561:SER:CA	1:B:923:ASN:HB3	2.29	0.63
2:D:76:ASP:O	2:D:77:ASP:CB	2.44	0.63
1:A:489:THR:CG2	1:A:490:PRO:HD3	2.29	0.62
1:C:884:VAL:O	1:C:888:LEU:HG	1.98	0.62
1:B:851:LEU:HB3	1:B:852:PRO:HD2	1.79	0.62
1:A:379:THR:HG22	1:A:383:LEU:CD2	2.29	0.62
1:C:721:LEU:N	1:C:721:LEU:CD2	2.52	0.62
1:A:758:TYR:HE1	1:A:760:ASN:O	1.82	0.62
1:C:259:ARG:NH1	2:E:155:ASP:OD2	2.32	0.62
1:C:143:ILE:HG22	1:C:286:ALA:HB2	1.80	0.62
1:A:971:ARG:O	1:A:974:PRO:CD	2.37	0.62
1:B:83:ASP:HA	1:B:815:ARG:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:LYS:HG3	1:A:164:ASP:N	2.14	0.62
1:C:1030:ARG:O	1:C:1034:SER:HB2	1.99	0.62
1:B:765:ARG:CB	1:B:765:ARG:HH11	2.09	0.62
1:C:237:GLN:C	1:C:238:THR:HG23	2.19	0.62
1:C:926:TYR:CD2	1:C:1003:VAL:HG22	2.33	0.62
1:C:36:PRO:HG3	1:C:391:ASN:HD21	1.64	0.62
1:B:270:LEU:HD23	1:B:271:GLY:CA	2.27	0.62
1:C:724:THR:CG2	1:C:814:PRO:HG3	2.29	0.62
2:D:14:LEU:H	2:D:14:LEU:CD1	2.09	0.62
1:B:678:THR:CG2	1:B:678:THR:O	2.39	0.62
1:C:937:LEU:HD13	1:C:1011:MET:HG2	1.81	0.62
1:A:455:PRO:HG2	1:A:880:SER:OG	2.00	0.62
1:B:668:LEU:HB2	1:B:669:PRO:HD2	1.81	0.62
1:B:1:FME:H	1:B:2:PRO:HD3	1.64	0.62
1:C:925:VAL:O	1:C:926:TYR:C	2.35	0.62
1:B:412:VAL:HG13	1:B:435:MET:SD	2.40	0.62
1:C:638:PRO:O	1:C:642:ASN:ND2	2.30	0.62
1:C:53:ASP:CG	1:C:56:THR:OG1	2.38	0.62
1:C:382:VAL:HG11	1:C:476:SER:OG	2.00	0.62
1:B:990:VAL:HG22	1:B:1005:THR:HG22	1.82	0.62
2:E:121:ALA:HB1	2:E:152:ILE:HG12	1.82	0.62
1:B:534:ILE:HA	1:B:541:TYR:CE1	2.35	0.62
1:B:1:FME:N	1:B:2:PRO:HD3	2.15	0.62
1:B:575:MET:HG3	1:B:576:VAL:H	1.65	0.62
1:C:1008:MET:O	1:C:1012:VAL:HG23	2.00	0.62
1:A:392:THR:O	1:A:396:PHE:HD1	1.82	0.62
1:A:782:LEU:HB2	1:A:785:ASP:OD1	1.99	0.62
1:C:268:ILE:CD1	1:C:268:ILE:N	2.58	0.62
1:A:764:ASP:HB3	1:A:769:LYS:HD2	1.81	0.62
1:B:732:ASP:OD1	1:B:734:GLU:N	2.33	0.62
2:E:84:LEU:HD22	2:E:116:PRO:HB3	1.82	0.62
1:C:379:THR:O	1:C:383:LEU:HB2	2.00	0.62
1:A:394:THR:HG23	1:A:473:THR:HG21	1.81	0.62
1:B:176:GLN:O	1:B:289:LEU:HD23	1.99	0.62
1:C:566:ASP:OD2	1:C:678:THR:CG2	2.48	0.62
1:B:903:LEU:O	1:B:906:PRO:HD2	1.99	0.62
1:C:815:ARG:C	1:C:816:LEU:HD12	2.20	0.62
1:B:844:MET:HE3	1:B:844:MET:HA	1.81	0.62
2:E:67:LEU:CD2	2:E:73:VAL:HG22	2.30	0.62
1:C:983:ILE:HG23	1:C:1008:MET:HG3	1.81	0.62
1:C:314:GLU:C	1:C:317:PHE:HD1	2.02	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:GLY:O	1:A:382:VAL:HG23	1.99	0.61
1:B:197:GLN:C	1:B:798:MET:HE2	2.16	0.61
1:A:410:ILE:HD12	1:A:978:THR:HG22	1.80	0.61
1:A:1024:VAL:O	1:A:1028:VAL:HG23	1.99	0.61
1:B:61:VAL:CG2	1:B:122:VAL:HG21	2.29	0.61
1:C:911:GLY:HA3	1:C:1013:THR:OG1	1.99	0.61
1:B:324:VAL:HG22	1:B:325:TYR:N	2.15	0.61
1:A:115:MET:HB2	1:A:116:PRO:HD3	1.81	0.61
1:A:498:LYS:HD3	1:A:498:LYS:N	1.98	0.61
1:C:671:ILE:CD1	1:C:674:LEU:CG	2.74	0.61
1:C:324:VAL:HG22	1:C:325:TYR:N	2.14	0.61
1:C:952:LEU:N	1:C:952:LEU:CD1	2.61	0.61
1:B:534:ILE:CG1	1:B:541:TYR:CZ	2.78	0.61
1:C:910:ILE:HG23	1:C:911:GLY:N	2.15	0.61
1:C:527:TYR:CZ	1:C:968:VAL:HG13	2.35	0.61
1:B:402:ILE:O	1:B:406:VAL:HG23	2.00	0.61
1:B:333:VAL:O	1:B:337:ILE:HG13	1.99	0.61
1:A:459:PHE:HB2	1:A:464:GLY:HA2	1.83	0.61
1:C:200:PRO:CG	1:C:749:THR:HG22	2.24	0.61
1:B:461:GLY:HA3	1:B:868:LEU:HD22	1.82	0.61
1:C:318:PRO:O	1:C:319:SER:OG	2.16	0.61
2:E:145:PHE:O	2:E:145:PHE:CD1	2.53	0.61
1:B:775:SER:HG	1:B:780:ARG:HG2	1.64	0.61
1:A:187:TRP:HH2	1:A:275:TYR:HE1	1.49	0.61
1:C:876:LEU:C	1:C:876:LEU:HD23	2.20	0.61
2:D:53:LEU:H	2:D:53:LEU:HD22	1.50	0.61
1:C:44:THR:HB	1:C:132:SER:HG	1.60	0.61
1:C:496:MET:O	1:C:496:MET:HG2	1.99	0.61
1:C:225:VAL:O	1:C:225:VAL:HG12	1.93	0.61
1:A:955:LYS:C	1:A:956:GLU:OE2	2.38	0.61
1:C:36:PRO:HG3	1:C:391:ASN:ND2	2.14	0.61
1:C:567:GLU:OE2	1:C:998:GLY:N	2.20	0.61
1:C:682:PHE:HE2	1:C:684:LEU:HD23	1.65	0.61
1:B:988:PRO:O	1:B:991:ILE:HG22	1.98	0.61
1:C:502:LYS:HG2	1:C:503:GLY:H	1.65	0.61
1:B:492:LEU:HB3	1:B:496:MET:CE	2.31	0.60
1:B:495:THR:HG22	1:B:496:MET:HG3	1.82	0.60
1:B:966:ASP:O	1:B:970:MET:CG	2.48	0.60
1:C:937:LEU:HA	1:C:940:LYS:HG2	1.83	0.60
1:C:937:LEU:O	1:C:940:LYS:HG2	2.01	0.60
1:A:236:ALA:CB	1:B:729:ILE:O	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:723:ASP:OD1	1:C:723:ASP:N	2.31	0.60
1:C:689:GLY:N	1:C:690:LEU:CD2	2.64	0.60
1:C:736:ALA:HB1	1:C:741:VAL:CG1	2.31	0.60
1:C:372:VAL:O	1:C:376:LEU:HB2	2.02	0.60
1:B:553:ALA:O	1:B:557:VAL:HG12	2.02	0.60
1:B:730:ASP:OD2	1:B:730:ASP:N	2.30	0.60
1:B:632:LYS:O	1:B:637:ARG:NH2	2.33	0.60
1:C:482:VAL:O	1:C:486:LEU:HD12	2.02	0.60
1:A:684:LEU:O	1:A:824:SER:HA	2.00	0.60
1:C:960:LEU:CD1	1:C:1027:VAL:HG22	2.26	0.60
1:B:160:ALA:C	1:B:161:ASN:ND2	2.52	0.60
2:E:151:ASP:O	2:E:154:ILE:HG12	2.00	0.60
1:B:859:TRP:CE3	1:B:859:TRP:HA	2.36	0.60
1:A:997:SER:O	1:A:999:ALA:N	2.34	0.60
1:A:202:ASP:OD2	1:A:792:ARG:NH2	2.34	0.60
1:B:563:PHE:C	1:B:564:LEU:CG	2.68	0.60
1:C:150:THR:OG1	1:C:151:GLN:N	2.30	0.60
1:A:527:TYR:HE1	1:A:972:LEU:HD23	1.62	0.60
1:B:513:PHE:C	1:B:515:TRP:N	2.53	0.60
2:D:49:THR:HB	2:D:50:PRO:CD	2.31	0.60
1:B:348:ILE:CG2	1:B:369:THR:HG23	2.30	0.60
1:A:489:THR:HG22	1:A:490:PRO:HD3	1.82	0.60
1:C:155:SER:HB3	1:C:287:SER:CB	2.32	0.60
1:B:72:ILE:CG2	1:B:73:ASP:N	2.65	0.60
1:C:596:HIS:NE2	1:C:600:THR:HG21	2.17	0.60
2:D:49:THR:HB	2:D:50:PRO:HD2	1.82	0.60
1:B:715:SER:HB2	1:B:830:GLN:HG2	1.83	0.60
1:C:464:GLY:HA2	1:C:467:TYR:HD1	1.66	0.60
1:B:534:ILE:HG13	1:B:541:TYR:CD2	2.33	0.60
2:D:44:ASP:OD1	2:D:45:HIS:N	2.35	0.60
1:B:347:ALA:O	1:B:351:VAL:HG23	2.00	0.60
1:C:640:GLU:H	1:C:640:GLU:CD	2.04	0.60
2:E:84:LEU:O	2:E:84:LEU:HD23	2.01	0.60
1:B:421:ALA:HA	1:B:500:ILE:HG21	1.83	0.60
1:A:905:VAL:HB	1:A:906:PRO:HD3	1.83	0.60
1:A:70:ASN:C	1:A:70:ASN:OD1	2.40	0.60
2:E:92:HIS:O	2:E:96:VAL:CG2	2.41	0.60
1:A:964:THR:O	1:A:968:VAL:HG23	2.02	0.60
1:C:71:GLY:C	1:C:72:ILE:HG13	2.22	0.60
1:C:211:ASN:ND2	1:C:760:ASN:ND2	2.49	0.60
1:B:842:GLU:O	1:B:846:GLN:HG3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:ASN:CB	1:B:258:SER:O	2.49	0.59
1:A:685:ILE:HD13	1:A:685:ILE:N	2.16	0.59
1:A:777:ALA:O	1:A:781:MET:HG2	2.03	0.59
1:A:694:LYS:HA	1:A:697:GLN:OE1	2.01	0.59
1:A:457:ALA:HB2	1:A:471:SER:CB	2.32	0.59
1:C:454:VAL:HB	1:C:455:PRO:HD3	1.83	0.59
1:C:259:ARG:NH2	2:E:155:ASP:OD2	2.35	0.59
1:B:726:GLN:NE2	1:B:812:GLY:CA	2.63	0.59
1:A:69:MET:O	1:C:168:ARG:HD3	2.02	0.59
1:B:372:VAL:HB	1:B:373:PRO:HD3	1.85	0.59
1:B:382:VAL:CG2	1:B:382:VAL:O	2.48	0.59
1:B:739:LEU:HD13	1:B:799:VAL:CG2	2.31	0.59
2:E:145:PHE:C	2:E:145:PHE:CD1	2.75	0.59
2:E:93:LEU:HD21	2:E:128:ILE:HG13	1.83	0.59
1:C:490:PRO:O	1:C:493:CYS:HB2	2.02	0.59
1:A:444:GLY:O	1:A:448:VAL:HG12	2.03	0.59
1:A:899:PHE:C	1:A:901:VAL:N	2.52	0.59
1:C:496:MET:HG3	1:C:496:MET:O	2.03	0.59
1:C:541:TYR:HA	1:C:544:LEU:HD23	1.85	0.59
2:D:110:ASP:C	2:D:112:ASN:N	2.53	0.59
2:D:133:LEU:HA	2:D:137:ALA:HB2	1.84	0.59
1:B:848:ALA:C	1:B:851:LEU:CD1	2.71	0.59
1:B:685:ILE:HG23	1:B:686:ASP:N	2.16	0.59
1:C:506:GLY:C	1:C:507:GLU:CG	2.65	0.59
1:B:117:LEU:HD12	1:B:117:LEU:N	2.16	0.59
1:C:204:ILE:HG23	1:C:759:VAL:HG22	1.83	0.59
1:B:714:THR:CG2	1:B:832:ALA:HA	2.31	0.59
1:A:795:ASP:OD1	1:A:795:ASP:N	2.30	0.59
1:A:308:ALA:O	1:A:312:LYS:HG3	2.02	0.59
1:B:254:ASN:O	1:B:257:GLY:CA	2.50	0.59
1:A:983:ILE:HG23	1:A:1008:MET:HG3	1.85	0.59
1:C:651:ALA:O	1:C:655:PHE:CD2	2.56	0.59
1:A:78:MET:CG	1:A:78:MET:O	2.50	0.59
1:B:241:THR:HA	1:B:763:ILE:O	2.03	0.59
1:A:412:VAL:HG11	1:A:489:THR:HG21	1.85	0.59
1:A:485:ALA:O	1:A:490:PRO:HD2	2.00	0.59
1:C:570:GLY:C	1:C:571:VAL:HG13	2.22	0.59
1:B:60:THR:O	1:B:64:VAL:HG23	2.03	0.59
1:B:116:PRO:C	1:B:117:LEU:HD12	2.23	0.59
1:C:793:ALA:O	1:C:795:ASP:N	2.35	0.59
1:C:225:VAL:CG1	1:C:226:LYS:O	2.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:667:ASN:OD1	1:C:668:LEU:N	2.30	0.59
1:B:202:ASP:OD2	1:B:792:ARG:NH2	2.35	0.59
1:B:250:LEU:HD23	1:B:251:LEU:H	1.55	0.59
1:A:485:ALA:O	1:A:490:PRO:CG	2.51	0.59
1:B:715:SER:O	1:B:829:GLY:HA2	2.03	0.59
1:B:759:VAL:HG23	1:B:771:VAL:HG12	1.84	0.59
1:B:765:ARG:CB	1:B:765:ARG:NH1	2.65	0.59
1:B:352:PHE:HD2	1:B:353:LEU:HD12	1.68	0.59
1:B:293:LEU:HD11	1:B:299:ALA:HB2	1.84	0.59
1:A:971:ARG:CG	1:A:971:ARG:NH1	2.38	0.58
1:B:83:ASP:N	1:B:83:ASP:OD2	2.34	0.58
1:C:927:PHE:CE2	1:C:931:LEU:HD12	2.38	0.58
1:C:435:MET:O	1:C:439:GLN:CB	2.51	0.58
1:B:712:MET:CE	1:B:839:GLU:OE2	2.51	0.58
1:C:1:FME:CN	1:C:2:PRO:CD	2.79	0.58
1:B:422:GLU:O	1:B:423:GLU:HG2	2.03	0.58
1:C:259:ARG:NH1	2:E:155:ASP:CG	2.55	0.58
1:A:894:SER:CB	1:A:897:ILE:HD12	2.34	0.58
1:C:876:LEU:HD22	1:C:876:LEU:O	2.02	0.58
1:C:731:ILE:CD1	1:C:746:ILE:HG21	2.33	0.58
1:C:154:ILE:CD1	1:C:154:ILE:O	2.31	0.58
1:B:420:MET:HE3	1:B:425:LEU:O	2.03	0.58
1:B:116:PRO:C	1:B:117:LEU:HD13	2.22	0.58
1:A:14:VAL:HG11	1:B:886:LEU:O	2.03	0.58
1:B:435:MET:O	1:B:438:ILE:N	2.27	0.58
1:C:773:VAL:O	1:C:773:VAL:HG13	2.04	0.58
1:A:758:TYR:CE1	1:A:760:ASN:O	2.57	0.58
1:C:115:MET:N	1:C:116:PRO:HD2	2.18	0.58
1:A:183:ALA:O	1:A:271:GLY:O	2.22	0.58
1:B:452:VAL:CG1	1:B:932:LEU:HD22	2.33	0.58
1:B:991:ILE:HD12	1:B:991:ILE:C	2.11	0.58
2:D:49:THR:CB	2:D:50:PRO:CD	2.82	0.58
1:A:411:VAL:CG2	1:A:971:ARG:NH2	2.58	0.58
1:B:685:ILE:CG2	1:B:686:ASP:H	2.16	0.58
1:C:563:PHE:CE2	1:C:862:MET:HE1	2.39	0.58
1:A:366:LEU:O	1:A:370:ILE:HG13	2.03	0.58
1:A:146:ASP:HB3	1:A:148:THR:HG23	1.85	0.58
2:D:44:ASP:OD1	2:D:45:HIS:CG	2.56	0.58
2:D:63:VAL:O	2:D:67:LEU:HG	2.03	0.58
1:B:724:THR:HB	1:B:725:PRO:CD	2.33	0.58
1:C:1016:VAL:HG23	1:C:1017:LEU:HD12	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:972:LEU:O	1:A:975:ILE:HG22	2.04	0.58
1:B:878:ALA:O	1:B:882:ILE:HG13	2.04	0.58
1:C:688:ALA:HB2	1:C:854:GLY:CA	2.33	0.58
1:C:447:MET:SD	1:C:891:LEU:HD23	2.44	0.58
1:B:671:ILE:O	1:B:672:VAL:HG13	2.03	0.58
1:C:71:GLY:C	1:C:72:ILE:CG1	2.71	0.58
1:C:72:ILE:CG2	1:C:94:PHE:HE2	2.16	0.58
1:B:414:GLU:OE2	1:B:974:PRO:HG3	2.04	0.58
1:C:98:THR:HG23	1:C:99:ASP:N	2.19	0.58
1:A:997:SER:C	1:A:999:ALA:N	2.54	0.58
1:C:733:GLN:NE2	1:C:743:ILE:HD13	2.18	0.58
1:B:668:LEU:HD13	1:B:669:PRO:HD2	1.86	0.58
1:B:713:LEU:CD2	1:B:843:LEU:HD23	2.33	0.58
1:B:69:MET:HE1	1:B:107:VAL:HG13	1.85	0.58
1:C:980:LEU:CD2	1:C:980:LEU:H	2.16	0.58
1:A:359:LEU:HD11	1:A:413:VAL:HG11	1.86	0.58
1:C:735:LYS:O	1:C:739:LEU:CD2	2.49	0.58
1:B:10:ILE:HG23	1:C:895:TRP:CZ2	2.39	0.58
1:A:704:ALA:O	1:A:708:LYS:HG3	2.03	0.58
1:A:423:GLU:O	1:A:502:LYS:HD2	2.03	0.57
1:B:848:ALA:C	1:B:851:LEU:HD12	2.24	0.57
1:B:531:VAL:O	1:B:534:ILE:HG22	2.04	0.57
1:C:324:VAL:C	1:C:325:TYR:CD1	2.76	0.57
1:B:365:THR:HG23	1:B:366:LEU:N	2.19	0.57
1:A:188:MET:HE1	1:A:203:VAL:HG11	1.84	0.57
1:C:527:TYR:CE2	1:C:968:VAL:HG13	2.38	0.57
1:C:531:VAL:HG21	1:C:968:VAL:HG11	1.84	0.57
2:D:110:ASP:C	2:D:112:ASN:H	2.03	0.57
1:C:453:PHE:CE1	1:C:474:ILE:HG21	2.38	0.57
1:B:449:LEU:O	1:B:453:PHE:CD1	2.53	0.57
1:C:837:THR:O	1:C:841:MET:HG3	2.04	0.57
1:A:230:LEU:HD12	1:A:231:ASN:H	1.69	0.57
1:C:30:LEU:HD13	1:C:390:ILE:HG13	1.86	0.57
1:A:815:ARG:O	1:A:815:ARG:HG3	2.05	0.57
1:C:879:ILE:HG23	1:C:880:SER:H	1.69	0.57
1:B:534:ILE:HG13	1:B:541:TYR:CE1	2.36	0.57
1:B:685:ILE:HG23	1:B:686:ASP:H	1.68	0.57
1:B:578:LEU:HD12	1:B:579:PRO:HD3	1.87	0.57
1:A:774:MET:HG2	1:A:775:SER:H	1.69	0.57
1:C:58:GLN:OE1	1:C:818:ARG:HD2	2.04	0.57
1:A:14:VAL:HG12	1:A:14:VAL:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:LEU:HD23	1:C:230:LEU:N	2.19	0.57
1:A:949:ALA:O	1:A:953:MET:HG2	2.04	0.57
1:B:853:THR:CA	1:B:857:TYR:N	2.67	0.57
1:A:534:ILE:HG22	1:A:541:TYR:CE1	2.40	0.57
1:A:223:PRO:HD2	1:B:780:ARG:NH2	2.19	0.57
2:D:46:VAL:HG22	2:D:46:VAL:O	2.03	0.57
1:A:315:PRO:HB2	1:A:316:PHE:CE1	2.39	0.57
1:C:841:MET:HE3	1:C:859:TRP:CE2	2.40	0.57
1:A:728:LYS:NZ	1:C:236:ALA:O	2.21	0.57
1:A:449:LEU:O	1:A:452:VAL:HG22	2.05	0.57
1:A:423:GLU:CA	1:A:502:LYS:HG3	2.35	0.57
1:C:572:PHE:CZ	1:C:629:VAL:HG21	2.39	0.57
1:C:927:PHE:CZ	1:C:931:LEU:HD11	2.40	0.57
1:B:501:ALA:CB	1:B:504:ASP:HB2	2.33	0.57
1:B:47:ALA:HB2	1:B:127:VAL:HG13	1.85	0.57
1:B:452:VAL:HG12	1:B:932:LEU:HD22	1.87	0.57
1:A:878:ALA:O	1:A:882:ILE:HG12	2.04	0.57
1:A:591:LEU:HD12	1:A:613:ASN:ND2	2.20	0.57
1:C:714:THR:HG22	1:C:715:SER:N	2.19	0.57
1:A:36:PRO:HD3	1:A:391:ASN:ND2	2.19	0.57
1:B:420:MET:HE1	1:B:499:PRO:HA	1.87	0.57
1:A:558:ARG:C	1:A:558:ARG:HD2	2.23	0.57
1:B:403:GLY:HA3	1:B:982:PHE:HE1	1.69	0.57
1:B:1022:VAL:HA	1:B:1025:PHE:CD1	2.39	0.57
1:C:332:PHE:CD2	1:C:569:GLN:NE2	2.73	0.57
1:B:493:CYS:O	1:B:497:LEU:HB2	2.04	0.57
1:C:746:ILE:HG22	1:C:747:ASN:N	2.20	0.57
1:B:726:GLN:HE22	1:B:812:GLY:CA	2.11	0.57
1:C:156:ASP:OD1	1:C:182:TYR:CB	2.52	0.57
1:A:243:THR:OG1	1:A:244:GLU:N	2.38	0.57
1:C:190:PRO:HG3	1:C:789:TRP:CZ3	2.39	0.57
1:B:11:PHE:HE1	1:B:15:ILE:HD11	1.70	0.57
1:B:686:ASP:HB2	1:B:695:LEU:HD12	1.87	0.56
1:B:775:SER:OG	1:B:780:ARG:CG	2.50	0.56
1:C:153:ASP:OD1	1:C:182:TYR:OH	2.23	0.56
1:C:448:VAL:HG11	1:C:939:ALA:HB3	1.85	0.56
1:A:892:TYR:OH	1:A:946:VAL:HG13	2.04	0.56
1:B:56:THR:O	1:B:60:THR:HG23	2.05	0.56
1:A:194:ASN:HD22	1:A:798:MET:HG3	1.68	0.56
1:C:34:GLN:HG2	1:C:35:TYR:CD1	2.40	0.56
1:A:621:GLY:HA3	1:A:624:THR:CG2	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:156:ASN:C	2:E:156:ASN:ND2	2.59	0.56
1:C:482:VAL:HG12	1:C:486:LEU:CD1	2.35	0.56
2:D:87:ALA:O	2:D:91:GLY:N	2.37	0.56
1:A:668:LEU:N	1:A:668:LEU:HD23	2.18	0.56
1:C:671:ILE:HD11	1:C:674:LEU:HG	1.84	0.56
1:A:943:ILE:O	1:A:946:VAL:HG13	2.06	0.56
1:A:892:TYR:HE2	1:A:947:GLU:HA	1.70	0.56
1:A:686:ASP:HB3	1:A:823:PRO:HB2	1.87	0.56
1:B:958:LYS:NZ	1:B:966:ASP:OD2	2.38	0.56
1:C:247:GLY:O	1:C:263:ARG:HG2	2.04	0.56
1:B:62:THR:HG22	1:B:62:THR:O	2.05	0.56
1:C:978:THR:OG1	1:C:979:SER:N	2.39	0.56
1:C:448:VAL:HG21	1:C:943:ILE:HD11	1.86	0.56
1:B:596:HIS:CD2	1:B:600:THR:OG1	2.57	0.56
1:A:742:SER:OG	1:A:744:ASN:HB2	2.05	0.56
2:D:34:MET:CE	2:D:34:MET:HA	2.35	0.56
1:B:189:ASN:OD1	1:B:189:ASN:N	2.38	0.56
2:D:27:ASP:N	2:D:27:ASP:OD2	2.39	0.56
2:E:105:ASP:OD1	2:E:106:VAL:N	2.38	0.56
1:C:164:ASP:OD2	1:C:767:ARG:NH2	2.31	0.56
1:B:987:MET:HG2	1:B:988:PRO:CD	2.35	0.56
1:A:488:LEU:HD11	1:A:492:LEU:HD13	1.88	0.56
1:C:879:ILE:HG23	1:C:880:SER:N	2.20	0.56
1:A:236:ALA:HB2	1:B:729:ILE:HG23	1.87	0.56
1:C:240:LEU:HD22	1:C:245:GLU:HB3	1.87	0.56
1:B:987:MET:HG2	1:B:988:PRO:N	2.21	0.56
1:A:897:ILE:N	1:A:898:PRO:HD2	2.21	0.56
1:B:712:MET:CB	1:B:713:LEU:HD13	2.36	0.56
1:C:672:VAL:HG22	1:C:673:GLU:OE1	2.04	0.56
1:A:469:GLN:HA	1:A:469:GLN:OE1	2.05	0.56
1:B:893:GLU:O	1:B:893:GLU:HG3	2.05	0.56
1:B:540:ARG:O	1:B:544:LEU:HD13	2.05	0.56
1:B:10:ILE:CG1	1:C:893:GLU:OE2	2.54	0.56
1:C:567:GLU:CD	1:C:998:GLY:HA3	2.26	0.56
1:B:987:MET:HG2	1:B:988:PRO:HD3	1.88	0.56
1:A:248:LYS:O	1:A:261:LEU:CD2	2.49	0.56
2:E:56:TYR:O	2:E:56:TYR:CG	2.58	0.56
1:C:34:GLN:NE2	1:C:333:VAL:HG22	2.20	0.56
1:C:903:LEU:O	1:C:906:PRO:HD2	2.06	0.56
1:C:324:VAL:CG2	1:C:325:TYR:N	2.69	0.56
1:C:146:ASP:CB	1:C:148:THR:HG21	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:902:MET:HE2	1:C:902:MET:HA	1.88	0.56
1:A:694:LYS:C	1:A:697:GLN:OE1	2.44	0.56
1:B:979:SER:O	1:B:983:ILE:HG13	2.07	0.56
1:A:205:THR:HG22	1:A:206:ALA:N	2.19	0.56
1:B:988:PRO:C	1:B:991:ILE:HG22	2.27	0.55
1:C:572:PHE:CE2	1:C:629:VAL:HG21	2.40	0.55
2:D:44:ASP:OD1	2:D:45:HIS:CD2	2.60	0.55
2:E:100:LEU:O	2:E:103:GLY:HA2	2.06	0.55
2:D:73:VAL:HG12	2:D:74:ASN:H	1.68	0.55
1:A:277:ILE:C	1:A:278:ILE:HG12	2.27	0.55
1:B:764:ASP:OD1	1:B:765:ARG:HG2	2.05	0.55
1:A:456:MET:HG3	1:A:467:TYR:HB3	1.88	0.55
2:E:57:PHE:H	2:E:58:GLY:HA2	1.70	0.55
1:A:23:GLY:O	1:A:26:ALA:HB3	2.05	0.55
1:B:1:FME:HE1	1:B:487:ILE:CG1	2.36	0.55
1:C:810:GLU:O	1:C:811:TYR:CD2	2.59	0.55
1:C:637:ARG:N	1:C:638:PRO:HD3	2.21	0.55
1:A:583:THR:H	1:A:586:ARG:HG3	1.72	0.55
1:A:655:PHE:O	1:A:658:ILE:HG13	2.07	0.55
1:A:949:ALA:O	1:A:953:MET:CG	2.54	0.55
1:B:328:ASP:OD1	1:B:329:THR:N	2.40	0.55
1:A:542:LEU:O	1:A:545:TYR:CB	2.55	0.55
1:B:169:THR:CG2	1:B:172:VAL:HG11	2.36	0.55
1:B:72:ILE:HG22	1:B:73:ASP:H	1.70	0.55
1:C:933:THR:O	1:C:937:LEU:HG	2.07	0.55
1:C:816:LEU:CD1	1:C:816:LEU:N	2.70	0.55
1:A:1026:PHE:O	1:A:1026:PHE:CD2	2.59	0.55
1:B:197:GLN:HA	1:B:798:MET:HE2	1.61	0.55
1:B:162:MET:O	1:B:166:ILE:HG12	2.07	0.55
1:C:327:TYR:CD1	1:C:628:PHE:CD1	2.94	0.55
1:C:894:SER:O	1:C:898:PRO:CD	2.54	0.55
1:B:336:SER:OG	1:B:395:MET:CE	2.55	0.55
1:C:482:VAL:HG12	1:C:486:LEU:HD11	1.88	0.55
1:A:391:ASN:O	1:A:395:MET:HG2	2.07	0.55
1:A:555:LEU:CD1	1:A:914:LEU:HD23	2.37	0.55
1:C:674:LEU:CD2	1:C:674:LEU:N	2.30	0.55
1:C:327:TYR:C	1:C:327:TYR:CD2	2.80	0.55
1:A:139:VAL:O	1:A:326:PRO:HD2	2.07	0.55
1:A:184:MET:HG2	1:A:246:PHE:CE1	2.42	0.55
2:D:132:LEU:O	2:D:136:GLY:O	2.25	0.55
2:E:77:ASP:HB3	2:E:81:VAL:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:367:ILE:HB	1:C:368:PRO:HD3	1.87	0.55
1:A:16:ALA:HB2	1:A:488:LEU:HD23	1.89	0.55
1:B:184:MET:CE	1:B:268:ILE:CG2	2.85	0.55
1:A:749:THR:HG21	1:A:791:VAL:CG1	2.33	0.55
1:A:792:ARG:HG3	1:A:793:ALA:N	2.21	0.55
1:B:952:LEU:O	1:B:956:GLU:HB2	2.07	0.55
1:B:108:GLN:HG3	1:C:112:GLN:HG3	1.87	0.55
2:D:100:LEU:HD21	2:D:106:VAL:HG13	1.88	0.55
1:C:688:ALA:HB2	1:C:854:GLY:HA3	1.87	0.55
1:C:876:LEU:O	1:C:880:SER:HB2	2.06	0.55
1:B:668:LEU:HB2	1:B:669:PRO:CD	2.36	0.55
2:E:46:VAL:HG22	2:E:78:SER:HB3	1.89	0.55
1:C:940:LYS:HG3	1:C:941:ASN:H	1.72	0.55
1:A:471:SER:O	1:A:475:VAL:HG23	2.06	0.55
1:B:671:ILE:C	1:B:672:VAL:CG1	2.74	0.55
1:B:673:GLU:C	1:B:675:GLY:N	2.59	0.55
1:C:184:MET:HB3	1:C:771:VAL:HG22	1.89	0.55
2:E:154:ILE:CG1	2:E:155:ASP:N	2.70	0.55
1:C:948:PHE:HD1	1:C:967:ALA:HA	1.71	0.55
1:B:705:GLU:HB3	1:B:847:LEU:CD2	2.37	0.54
1:B:987:MET:O	1:B:991:ILE:HG22	2.08	0.54
1:A:528:THR:OG1	1:A:529:ASP:N	2.39	0.54
1:A:219:LEU:CD1	1:B:783:PRO:HG3	2.37	0.54
1:B:634:TRP:O	1:B:637:ARG:O	2.25	0.54
1:C:480:LEU:O	1:C:484:VAL:HG23	2.06	0.54
2:E:49:THR:O	2:E:52:HIS:HB2	2.08	0.54
1:A:572:PHE:CZ	1:A:629:VAL:HG11	2.43	0.54
1:B:194:ASN:ND2	1:B:790:TYR:CB	2.70	0.54
1:A:899:PHE:O	1:A:902:MET:N	2.30	0.54
1:A:380:PHE:CD1	1:A:380:PHE:N	2.75	0.54
1:A:898:PRO:O	1:A:901:VAL:HB	2.08	0.54
1:C:343:THR:HG21	1:C:989:LEU:HD23	1.90	0.54
1:C:158:VAL:HA	1:C:162:MET:CE	2.33	0.54
1:C:789:TRP:O	1:C:801:PHE:HB2	2.06	0.54
1:C:626:ILE:CG2	1:C:626:ILE:O	2.50	0.54
2:E:66:LEU:O	2:E:71:ALA:HB2	2.07	0.54
1:A:598:TYR:HA	1:A:602:GLU:CB	2.37	0.54
1:C:811:TYR:CD2	1:C:811:TYR:N	2.76	0.54
1:A:685:ILE:HG12	1:A:687:GLN:HE22	1.73	0.54
1:B:557:VAL:HG23	1:B:557:VAL:O	2.06	0.54
1:B:435:MET:C	1:B:437:GLN:N	2.58	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:352:PHE:CD2	1:B:353:LEU:HD12	2.43	0.54
1:B:776:GLU:O	1:B:777:ALA:C	2.45	0.54
1:C:429:GLU:CA	1:C:429:GLU:OE1	2.55	0.54
1:B:859:TRP:HE3	1:B:859:TRP:HA	1.69	0.54
1:B:330:THR:N	1:B:331:PRO:CD	2.71	0.54
1:C:169:THR:HG22	1:C:170:SER:N	2.21	0.54
1:C:607:GLU:O	1:C:607:GLU:HG3	2.08	0.54
1:C:327:TYR:HB2	1:C:628:PHE:HB3	1.89	0.54
1:C:72:ILE:HG22	1:C:94:PHE:HE2	1.73	0.54
1:C:793:ALA:N	1:C:797:GLN:O	2.41	0.54
1:A:236:ALA:HB1	1:B:729:ILE:O	2.07	0.54
2:E:115:THR:OG1	2:E:118:HIS:CD2	2.60	0.54
1:A:489:THR:O	1:A:493:CYS:N	2.37	0.54
2:D:50:PRO:HA	2:D:53:LEU:CD2	2.37	0.54
2:E:152:ILE:HD12	2:E:153:SER:N	2.17	0.54
1:A:423:GLU:C	1:A:502:LYS:CG	2.75	0.54
1:A:527:TYR:CD1	1:A:972:LEU:HD21	2.42	0.54
1:B:367:ILE:N	1:B:368:PRO:CD	2.71	0.54
1:C:894:SER:O	1:C:898:PRO:HG2	2.08	0.54
1:A:598:TYR:HA	1:A:602:GLU:HB3	1.89	0.54
1:A:527:TYR:HE1	1:A:968:VAL:HG12	1.72	0.54
1:B:143:ILE:HG22	1:B:286:ALA:CB	2.37	0.54
1:C:361:ASN:C	1:C:361:ASN:OD1	2.46	0.54
1:C:687:GLN:HA	1:C:822:LEU:HD23	1.89	0.54
2:D:49:THR:C	2:D:53:LEU:HD21	2.28	0.54
1:C:910:ILE:CG2	1:C:911:GLY:N	2.70	0.54
1:C:754:TRP:CZ2	1:C:786:ILE:CG1	2.91	0.54
1:C:36:PRO:HD2	1:C:393:LEU:HD12	1.90	0.54
1:B:668:LEU:CD1	1:B:669:PRO:HD2	2.38	0.54
1:A:594:VAL:HG22	1:A:655:PHE:CE1	2.43	0.54
1:A:6:ILE:HG23	1:A:494:ALA:CB	2.38	0.53
1:B:242:SER:HB3	1:B:245:GLU:HG3	1.89	0.53
1:B:853:THR:HA	1:B:857:TYR:N	2.23	0.53
1:C:261:LEU:HD12	1:C:263:ARG:HD2	1.89	0.53
1:C:815:ARG:HG2	1:C:815:ARG:O	2.09	0.53
1:C:681:ASP:HB3	1:C:860:THR:CG2	2.38	0.53
2:D:110:ASP:HB3	2:D:112:ASN:H	1.73	0.53
1:A:24:GLY:O	1:A:28:LEU:HG	2.08	0.53
1:B:250:LEU:C	1:B:250:LEU:HD22	2.24	0.53
1:C:302:THR:O	1:C:306:ILE:HG13	2.08	0.53
1:A:1:FME:CN	1:A:2:PRO:HD2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:926:TYR:HD2	1:C:1003:VAL:CG2	2.20	0.53
1:C:375:VAL:HB	1:C:405:LEU:HD13	1.88	0.53
1:C:753:ALA:O	1:C:775:SER:HB3	2.08	0.53
1:A:466:ILE:HD13	1:A:466:ILE:N	2.22	0.53
2:D:13:ASP:O	2:D:14:LEU:C	2.44	0.53
2:D:13:ASP:OD1	2:D:14:LEU:N	2.42	0.53
1:B:419:VAL:O	1:B:423:GLU:HG3	2.08	0.53
1:C:71:GLY:O	1:C:72:ILE:HG13	2.07	0.53
1:C:754:TRP:HZ2	1:C:786:ILE:HG12	1.73	0.53
1:B:557:VAL:O	1:B:557:VAL:HG22	2.08	0.53
2:D:57:PHE:N	2:D:58:GLY:HA2	2.20	0.53
1:B:988:PRO:HA	1:B:991:ILE:CG2	2.38	0.53
1:A:445:ILE:CG2	1:A:940:LYS:HE2	2.35	0.53
1:C:720:GLY:C	1:C:721:LEU:HD23	2.27	0.53
1:C:1:FME:HB2	1:C:2:PRO:HD3	1.90	0.53
1:C:712:MET:SD	1:C:835:LYS:HG3	2.49	0.53
1:A:815:ARG:CG	1:A:815:ARG:O	2.56	0.53
1:C:750:LEU:O	1:C:750:LEU:CD2	2.30	0.53
1:B:69:MET:HE3	1:B:72:ILE:CD1	2.33	0.53
1:C:361:ASN:O	1:C:365:THR:HG22	2.08	0.53
1:A:694:LYS:CA	1:A:697:GLN:OE1	2.56	0.53
1:B:781:MET:HE2	1:B:781:MET:HA	1.89	0.53
1:B:196:PHE:CA	1:B:197:GLN:HE22	2.13	0.53
1:C:741:VAL:CG1	1:C:746:ILE:HD13	2.36	0.53
1:A:539:GLY:O	1:A:543:VAL:CG2	2.57	0.53
1:B:777:ALA:HA	1:B:780:ARG:NH2	2.23	0.53
1:C:923:ASN:OD1	1:C:927:PHE:HD2	1.90	0.53
1:C:880:SER:O	1:C:884:VAL:HG23	2.07	0.53
1:A:424:GLY:CA	1:A:502:LYS:HB2	2.39	0.53
2:E:133:LEU:HA	2:E:136:GLY:O	2.09	0.53
1:A:298:ASN:ND2	1:A:301:ASP:N	2.50	0.53
1:C:926:TYR:CD2	1:C:1003:VAL:CG2	2.92	0.53
1:A:314:GLU:N	1:A:315:PRO:CD	2.72	0.53
1:C:323:ILE:HG22	1:C:324:VAL:N	2.24	0.53
1:C:673:GLU:OE2	1:C:673:GLU:N	2.30	0.53
1:C:204:ILE:HG23	1:C:759:VAL:HG21	1.88	0.53
1:C:901:VAL:HG12	1:C:946:VAL:HG21	1.91	0.53
1:C:101:ASP:O	1:C:105:VAL:HG23	2.08	0.53
2:D:126:LEU:CA	2:D:129:VAL:CG2	2.86	0.53
1:C:623:ASN:O	1:C:623:ASN:ND2	2.29	0.53
1:B:1:FME:CE	1:B:487:ILE:CG1	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:811:TYR:N	1:C:811:TYR:HD2	2.07	0.53
1:B:596:HIS:CD2	1:B:600:THR:HG1	2.27	0.53
1:C:687:GLN:HA	1:C:822:LEU:CD2	2.39	0.53
1:B:764:ASP:CG	1:B:765:ARG:HG3	2.30	0.53
1:B:217:GLY:O	1:B:234:ILE:HG13	2.09	0.53
1:C:207:ILE:HG22	1:C:760:ASN:HD21	1.72	0.53
1:B:714:THR:HG21	1:B:832:ALA:HA	1.90	0.53
2:D:100:LEU:HD21	2:D:106:VAL:CG1	2.39	0.53
1:A:743:ILE:HD12	1:A:743:ILE:N	2.23	0.53
1:C:724:THR:HG21	1:C:814:PRO:HG3	1.91	0.52
1:B:207:ILE:O	1:B:207:ILE:CG2	2.50	0.52
2:E:93:LEU:CD2	2:E:128:ILE:CG1	2.70	0.52
1:C:74:ASN:OD1	1:C:74:ASN:N	2.41	0.52
1:B:879:ILE:O	1:B:883:VAL:HG23	2.07	0.52
1:B:443:VAL:O	1:B:446:ALA:HB3	2.09	0.52
1:C:695:LEU:O	1:C:695:LEU:HD23	2.09	0.52
1:C:567:GLU:CD	1:C:998:GLY:H	2.10	0.52
1:C:506:GLY:O	1:C:507:GLU:CG	2.58	0.52
1:A:189:ASN:HD22	1:A:192:GLU:CD	2.12	0.52
1:B:501:ALA:O	1:B:504:ASP:CB	2.56	0.52
1:C:157:TYR:CD2	1:C:157:TYR:O	2.62	0.52
1:B:62:THR:O	1:B:66:GLU:HG3	2.09	0.52
2:D:51:LEU:HD22	2:D:83:PRO:CG	2.39	0.52
1:C:724:THR:HB	1:C:725:PRO:HD3	1.91	0.52
1:B:1:FME:HE3	1:B:487:ILE:HD11	1.88	0.52
1:A:207:ILE:HG22	1:A:760:ASN:HD22	1.75	0.52
1:A:1:FME:N	1:A:2:PRO:HD3	2.21	0.52
1:C:793:ALA:C	1:C:795:ASP:N	2.59	0.52
2:D:63:VAL:HG12	2:D:64:GLU:N	2.23	0.52
1:B:173:GLY:CA	1:B:294:ALA:HB2	2.40	0.52
1:A:445:ILE:O	1:A:449:LEU:HB2	2.09	0.52
1:B:166:ILE:O	1:B:169:THR:HB	2.09	0.52
1:C:924:ASP:N	1:C:924:ASP:OD2	2.35	0.52
1:C:736:ALA:O	1:C:741:VAL:CB	2.49	0.52
1:A:935:ILE:CG1	1:A:935:ILE:O	2.56	0.52
1:A:558:ARG:O	1:A:558:ARG:HD3	2.08	0.52
1:C:667:ASN:CG	1:C:668:LEU:H	2.11	0.52
1:C:347:ALA:O	1:C:351:VAL:HG23	2.09	0.52
1:B:926:TYR:HB3	1:B:1003:VAL:HG13	1.90	0.52
2:E:100:LEU:O	2:E:103:GLY:N	2.42	0.52
1:C:512:PHE:O	1:C:512:PHE:HD1	1.88	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:687:GLN:NE2	1:B:859:TRP:HB2	2.24	0.52
1:C:681:ASP:O	1:C:859:TRP:HE3	1.93	0.52
1:A:481:SER:OG	1:A:482:VAL:N	2.39	0.52
1:B:61:VAL:HG13	1:B:65:ILE:HD11	1.91	0.52
1:C:378:GLY:O	1:C:382:VAL:HG23	2.10	0.52
1:B:898:PRO:O	1:B:902:MET:HE2	2.09	0.52
1:C:631:LEU:HD11	1:C:644:VAL:HG12	1.91	0.52
1:A:531:VAL:HA	1:A:534:ILE:HG12	1.92	0.52
1:B:659:LYS:O	1:B:660:ASP:HB2	2.09	0.52
2:D:73:VAL:HG13	2:D:74:ASN:N	2.16	0.52
1:C:952:LEU:O	1:C:956:GLU:HB3	2.09	0.52
2:E:117:LEU:HD12	2:E:132:LEU:HD12	1.92	0.52
1:B:564:LEU:N	1:B:564:LEU:CD1	2.63	0.52
1:A:519:MET:HG3	1:A:520:PHE:N	2.25	0.52
1:C:44:THR:HB	1:C:132:SER:CB	2.39	0.52
1:A:269:GLU:O	1:A:270:LEU:C	2.41	0.52
1:C:669:PRO:O	1:C:669:PRO:CD	2.53	0.52
1:A:236:ALA:HB2	1:B:729:ILE:HG22	1.92	0.52
1:B:729:ILE:HG13	1:B:806:SER:O	2.10	0.52
1:B:126:GLY:HA2	1:C:116:PRO:HB3	1.91	0.52
1:C:330:THR:N	1:C:331:PRO:CD	2.73	0.52
1:C:278:ILE:HD13	1:C:278:ILE:H	1.75	0.52
1:C:505:HIS:ND1	1:C:505:HIS:O	2.39	0.52
1:A:1021:PHE:HB3	1:A:1025:PHE:CZ	2.45	0.52
1:B:184:MET:CB	1:B:771:VAL:HG22	2.38	0.52
1:C:156:ASP:OD1	1:C:182:TYR:CD2	2.62	0.52
1:A:139:VAL:HG13	1:A:178:PHE:HE2	1.75	0.52
1:B:108:GLN:HG3	1:C:112:GLN:CG	2.40	0.52
1:C:169:THR:CG2	1:C:170:SER:N	2.72	0.52
1:A:288:GLY:O	1:A:289:LEU:HD23	2.10	0.52
1:B:489:THR:N	1:B:490:PRO:CD	2.74	0.51
1:A:92:LEU:HD12	1:A:92:LEU:N	2.25	0.51
1:A:488:LEU:HD11	1:A:492:LEU:HD11	1.91	0.51
1:B:905:VAL:O	1:B:909:VAL:HG23	2.10	0.51
2:E:57:PHE:HB2	2:E:58:GLY:HA2	1.92	0.51
1:C:957:GLY:O	1:C:958:LYS:HG2	2.11	0.51
1:B:447:MET:HA	1:B:447:MET:CE	2.40	0.51
1:B:846:GLN:O	1:B:849:SER:OG	2.23	0.51
1:A:489:THR:HG22	1:A:490:PRO:CD	2.40	0.51
1:C:74:ASN:HB3	1:C:95:GLU:CB	2.34	0.51
1:A:504:ASP:OD1	1:A:506:GLY:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:785:ASP:O	1:C:788:ASP:HB2	2.09	0.51
2:D:93:LEU:CD2	2:D:128:ILE:HG12	2.39	0.51
1:C:71:GLY:H	1:C:110:LYS:NZ	2.09	0.51
1:C:160:ALA:CB	1:C:161:ASN:OD1	2.59	0.51
1:A:609:VAL:HG22	1:A:629:VAL:HG22	1.92	0.51
1:A:213:GLN:HA	1:A:237:GLN:O	2.10	0.51
1:B:26:ALA:O	1:B:30:LEU:HD22	2.10	0.51
1:C:889:ALA:O	1:C:892:TYR:O	2.29	0.51
1:A:685:ILE:HG12	1:A:687:GLN:NE2	2.26	0.51
1:A:450:SER:O	1:A:454:VAL:HG23	2.10	0.51
1:B:482:VAL:HG12	1:B:486:LEU:HD13	1.91	0.51
1:B:1007:VAL:O	1:B:1011:MET:HB2	2.11	0.51
1:B:516:PHE:C	1:B:516:PHE:CD1	2.83	0.51
1:B:336:SER:OG	1:B:395:MET:HE1	2.10	0.51
1:C:974:PRO:O	1:C:978:THR:HG23	2.11	0.51
1:C:724:THR:HG23	1:C:814:PRO:HG3	1.92	0.51
1:B:762:PHE:CE1	1:B:764:ASP:HB2	2.32	0.51
1:B:776:GLU:HB3	1:B:779:TYR:HD1	1.76	0.51
1:A:767:ARG:HG3	1:A:768:VAL:N	2.26	0.51
1:A:683:GLU:OE2	1:A:860:THR:HG21	2.11	0.51
1:A:975:ILE:HD13	1:A:1019:ILE:CD1	2.41	0.51
1:B:184:MET:HB2	1:B:762:PHE:CE2	2.46	0.51
1:C:729:ILE:C	1:C:730:ASP:OD1	2.49	0.51
1:C:686:ASP:O	1:C:686:ASP:OD1	2.29	0.51
1:B:960:LEU:HD21	1:B:1027:VAL:HG22	1.92	0.51
1:B:188:MET:C	1:B:189:ASN:OD1	2.49	0.51
1:C:616:GLY:O	1:C:619:GLY:O	2.29	0.51
1:B:310:LEU:HD13	1:B:323:ILE:CD1	2.41	0.51
1:C:692:HIS:O	1:C:696:THR:HG22	2.11	0.51
1:A:180:SER:HB3	1:A:274:ASN:ND2	2.26	0.51
1:A:588:GLN:O	1:A:589:LYS:C	2.49	0.51
1:A:807:SER:O	1:A:808:ARG:HG3	2.11	0.51
1:B:790:TYR:CD1	1:B:800:PRO:HA	2.46	0.51
1:A:997:SER:O	1:A:998:GLY:C	2.48	0.51
1:C:196:PHE:O	1:C:197:GLN:CG	2.59	0.50
1:C:94:PHE:C	1:C:95:GLU:O	2.44	0.50
1:C:69:MET:HE2	1:C:92:LEU:HD21	1.93	0.50
1:C:53:ASP:OD2	1:C:56:THR:OG1	2.29	0.50
1:A:183:ALA:N	1:A:271:GLY:O	2.39	0.50
1:C:278:ILE:HD11	1:C:613:ASN:HB3	1.91	0.50
1:B:146:ASP:HB2	1:B:320:GLY:HA3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:ASP:OD1	1:C:329:THR:N	2.43	0.50
1:A:498:LYS:HZ2	1:A:500:ILE:HD11	1.76	0.50
1:C:741:VAL:HG12	1:C:746:ILE:CD1	2.38	0.50
1:B:61:VAL:CG1	1:B:65:ILE:HD11	2.42	0.50
1:C:504:ASP:OD1	1:C:504:ASP:O	2.29	0.50
1:A:830:GLN:OE1	1:A:830:GLN:N	2.44	0.50
1:A:70:ASN:OD1	1:A:70:ASN:O	2.29	0.50
1:C:451:ALA:O	1:C:455:PRO:HD2	2.10	0.50
1:A:33:ALA:O	1:A:391:ASN:HA	2.11	0.50
1:C:686:ASP:C	1:C:686:ASP:OD1	2.48	0.50
1:A:84:SER:OG	1:A:814:PRO:HA	2.12	0.50
1:A:972:LEU:CD1	1:A:972:LEU:C	2.80	0.50
1:B:175:VAL:CG1	1:B:289:LEU:CD2	2.89	0.50
1:B:420:MET:CE	1:B:499:PRO:HA	2.42	0.50
1:A:355:MET:CE	1:A:368:PRO:HG2	2.41	0.50
1:A:150:THR:HG23	1:A:153:ASP:H	1.76	0.50
1:B:199:THR:HG21	1:B:792:ARG:H	1.77	0.50
1:B:595:THR:HG23	1:B:609:VAL:HB	1.93	0.50
1:B:799:VAL:HG12	1:B:800:PRO:O	2.11	0.50
1:A:448:VAL:HG21	1:A:888:LEU:HD21	1.94	0.50
1:A:394:THR:HG23	1:A:473:THR:CG2	2.41	0.50
1:B:158:VAL:CA	1:B:162:MET:HG3	2.27	0.50
1:A:248:LYS:C	1:A:261:LEU:HD23	2.31	0.50
1:C:23:GLY:O	1:C:27:ILE:HG13	2.11	0.50
1:B:982:PHE:O	1:B:986:VAL:HG23	2.12	0.50
1:A:58:GLN:NE2	1:A:818:ARG:NH1	2.57	0.50
1:B:778:LYS:O	1:B:778:LYS:HG3	2.12	0.50
1:B:623:ASN:HD22	1:B:623:ASN:C	2.14	0.50
1:B:988:PRO:HA	1:B:991:ILE:HG21	1.93	0.50
1:A:354:VAL:O	1:A:358:PHE:HD1	1.93	0.50
1:B:605:ASN:ND2	1:B:642:ASN:HB3	2.23	0.50
1:B:774:MET:CE	1:B:780:ARG:NH1	2.75	0.50
1:B:414:GLU:HG3	1:B:977:MET:HE2	1.94	0.50
1:C:801:PHE:O	1:C:805:SER:OG	2.30	0.50
1:B:324:VAL:HG22	1:B:325:TYR:H	1.75	0.50
2:E:49:THR:HG22	2:E:52:HIS:CE1	2.47	0.50
1:B:682:PHE:N	1:B:827:ILE:O	2.38	0.50
1:B:925:VAL:O	1:B:929:VAL:HG23	2.12	0.50
1:B:194:ASN:O	1:B:194:ASN:OD1	2.30	0.50
1:A:431:THR:HG22	1:A:432:ARG:N	2.23	0.50
1:A:528:THR:OG1	1:A:529:ASP:OD2	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:761:ASP:HB3	1:C:768:VAL:HG13	1.92	0.50
1:C:592:ASN:O	1:C:596:HIS:HB2	2.11	0.50
1:A:899:PHE:C	1:A:902:MET:H	2.13	0.50
2:D:44:ASP:CG	2:D:45:HIS:CA	2.80	0.50
1:B:235:ILE:N	1:B:235:ILE:HD13	2.26	0.50
1:C:157:TYR:HD2	1:C:157:TYR:C	2.13	0.50
1:C:780:ARG:HG3	1:C:780:ARG:HH11	1.77	0.50
1:C:559:LEU:HD12	1:C:560:PRO:CD	2.41	0.50
1:C:664:PHE:HD1	1:C:715:SER:HG	1.60	0.50
1:A:589:LYS:NZ	1:A:593:GLU:OE2	2.45	0.50
1:B:397:GLY:O	1:B:474:ILE:HG12	2.12	0.50
2:D:143:ASP:HB2	2:D:147:LYS:O	2.10	0.50
1:A:721:LEU:HD11	1:A:814:PRO:CB	2.42	0.50
1:A:829:GLY:O	1:A:830:GLN:OE1	2.30	0.50
1:A:1:FME:CN	1:A:2:PRO:CD	2.90	0.50
1:C:927:PHE:O	1:C:930:GLY:N	2.41	0.50
1:B:58:GLN:HA	1:B:62:THR:HB	1.94	0.50
1:C:53:ASP:OD1	1:C:56:THR:OG1	2.30	0.50
1:B:324:VAL:O	1:B:326:PRO:HD3	2.11	0.50
1:A:36:PRO:HD3	1:A:391:ASN:HD22	1.77	0.50
1:A:13:TRP:O	1:A:17:ILE:HG12	2.12	0.50
1:C:497:LEU:O	1:C:499:PRO:HD3	2.12	0.50
1:B:53:ASP:OD2	1:B:56:THR:OG1	2.30	0.50
1:B:218:GLN:HE22	1:B:231:ASN:HD21	1.58	0.50
1:B:231:ASN:HD22	1:B:231:ASN:C	2.14	0.50
1:B:291:ILE:HD12	1:B:306:ILE:HD12	1.94	0.50
1:C:531:VAL:CA	1:C:534:ILE:HG22	2.41	0.50
1:B:705:GLU:CB	1:B:847:LEU:CD2	2.78	0.49
1:A:488:LEU:CD1	1:A:492:LEU:CD1	2.81	0.49
1:C:732:ASP:OD1	1:C:734:GLU:N	2.45	0.49
1:B:6:ILE:HG12	1:B:490:PRO:O	2.11	0.49
1:A:647:ILE:HA	1:A:650:ARG:HD2	1.93	0.49
1:B:414:GLU:CD	1:B:974:PRO:HG3	2.32	0.49
1:B:224:PRO:HA	1:C:781:MET:HE3	1.94	0.49
1:C:186:ILE:HB	1:C:773:VAL:HG23	1.94	0.49
1:A:146:ASP:CB	1:A:148:THR:HG23	2.41	0.49
2:D:150:PHE:O	2:D:154:ILE:HG13	2.11	0.49
1:C:719:ASN:O	1:C:719:ASN:OD1	2.29	0.49
1:B:250:LEU:HD23	1:B:251:LEU:CA	2.37	0.49
1:A:412:VAL:CG1	1:A:489:THR:HG21	2.42	0.49
1:B:195:LYS:O	1:B:197:GLN:OE1	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:GLY:HA3	1:A:502:LYS:HB2	1.94	0.49
2:D:61:GLU:HG2	2:D:62:ILE:N	2.28	0.49
2:E:143:ASP:O	2:E:146:GLY:O	2.29	0.49
1:C:83:ASP:O	1:C:84:SER:OG	2.30	0.49
1:A:944:LEU:CD1	1:A:971:ARG:NH2	2.76	0.49
1:B:729:ILE:C	1:B:730:ASP:OD2	2.50	0.49
1:A:187:TRP:HD1	1:A:267:LYS:O	1.94	0.49
1:B:897:ILE:N	1:B:898:PRO:HD2	2.26	0.49
1:C:137:LEU:HD22	1:C:293:LEU:HD13	1.92	0.49
1:C:138:MET:HE2	1:C:140:VAL:HG23	1.93	0.49
1:B:211:ASN:O	1:B:211:ASN:OD1	2.29	0.49
1:A:498:LYS:HE3	1:A:498:LYS:CA	2.43	0.49
1:C:607:GLU:OE2	1:C:632:LYS:HE3	2.12	0.49
1:B:606:VAL:HA	1:B:631:LEU:HD23	1.93	0.49
1:B:973:ARG:HB3	1:B:974:PRO:HD3	1.94	0.49
1:C:373:PRO:O	1:C:377:LEU:HB2	2.12	0.49
1:B:81:ASN:OD1	1:B:81:ASN:O	2.30	0.49
1:C:312:LYS:HG2	1:C:313:MET:N	2.28	0.49
1:B:182:TYR:HD1	1:B:270:LEU:CD1	2.24	0.49
2:D:43:SER:O	2:D:43:SER:OG	2.30	0.49
2:D:19:LEU:CD2	2:D:50:PRO:HG3	2.41	0.49
1:B:8:ARG:N	1:B:9:PRO:HD3	2.27	0.49
1:C:261:LEU:CD1	1:C:263:ARG:HD2	2.42	0.49
1:C:780:ARG:HG3	1:C:780:ARG:O	2.12	0.49
1:B:340:VAL:HG21	1:B:395:MET:HB3	1.95	0.49
1:C:92:LEU:HD12	1:C:92:LEU:N	2.26	0.49
1:B:173:GLY:N	1:B:294:ALA:HB2	2.27	0.49
1:C:782:LEU:O	1:C:785:ASP:HB2	2.12	0.49
1:A:174:ASP:HB3	1:A:292:LYS:HB2	1.95	0.49
1:B:53:ASP:CG	1:B:56:THR:OG1	2.50	0.49
1:B:504:ASP:C	1:B:505:HIS:O	2.41	0.49
1:C:640:GLU:N	1:C:640:GLU:CD	2.66	0.49
1:C:391:ASN:H	1:C:394:THR:HG22	1.77	0.49
1:A:591:LEU:HD12	1:A:613:ASN:HD22	1.77	0.49
1:B:733:GLN:NE2	1:B:743:ILE:HD11	2.27	0.49
2:D:51:LEU:HD22	2:D:83:PRO:HG3	1.95	0.49
1:A:423:GLU:O	1:A:502:LYS:HE3	2.09	0.49
1:C:567:GLU:OE1	1:C:998:GLY:CA	2.47	0.49
1:B:281:PHE:CD1	1:B:610:PHE:HD1	2.17	0.49
1:B:160:ALA:HB3	1:B:161:ASN:ND2	2.28	0.49
1:C:561:SER:HA	1:C:923:ASN:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:808:ARG:HA	2:D:79:LEU:HD13	1.95	0.49
1:C:979:SER:O	1:C:983:ILE:HG13	2.12	0.49
1:B:329:THR:O	1:B:329:THR:OG1	2.30	0.49
1:C:887:CYS:O	1:C:891:LEU:HG	2.13	0.49
1:B:150:THR:HG1	1:B:152:GLU:HB2	1.78	0.49
1:B:180:SER:HB2	1:B:273:GLU:HG3	1.95	0.49
2:E:146:GLY:CA	2:E:147:LYS:CB	2.90	0.49
1:B:302:THR:O	1:B:306:ILE:CG2	2.58	0.49
1:B:682:PHE:HB3	1:B:827:ILE:HB	1.94	0.49
1:C:1036:LYS:O	1:C:1037:ASN:C	2.48	0.49
1:C:431:THR:O	1:C:435:MET:HG2	2.13	0.49
1:A:539:GLY:HA2	1:A:542:LEU:H	1.78	0.49
1:B:53:ASP:OD1	1:B:56:THR:OG1	2.29	0.49
1:C:94:PHE:O	1:C:95:GLU:O	2.31	0.49
1:C:53:ASP:OD1	1:C:56:THR:N	2.30	0.49
1:C:616:GLY:N	1:C:619:GLY:O	2.37	0.49
1:B:382:VAL:HG23	1:B:382:VAL:O	2.13	0.49
1:C:714:THR:CG2	1:C:715:SER:N	2.76	0.49
1:A:743:ILE:HD12	1:A:743:ILE:H	1.78	0.49
1:B:794:ALA:C	1:B:796:GLY:H	2.14	0.49
1:C:521:GLU:O	1:C:525:HIS:HD2	1.95	0.49
1:A:693:GLU:N	1:A:693:GLU:OE1	2.30	0.49
1:A:488:LEU:O	1:A:492:LEU:HD13	2.13	0.48
1:A:223:PRO:HD2	1:B:780:ARG:HH22	1.78	0.48
1:C:754:TRP:CE3	1:C:780:ARG:HB2	2.48	0.48
1:B:388:PHE:CE2	1:B:472:ILE:HG21	2.48	0.48
1:B:668:LEU:CB	1:B:669:PRO:CD	2.91	0.48
1:B:60:THR:O	1:B:61:VAL:C	2.49	0.48
1:A:754:TRP:HE3	1:C:218:GLN:O	1.96	0.48
1:B:218:GLN:CB	1:B:232:ALA:O	2.57	0.48
2:D:79:LEU:HD22	2:D:111:HIS:NE2	2.28	0.48
1:C:240:LEU:HB2	1:C:246:PHE:CE1	2.48	0.48
1:C:278:ILE:CD1	1:C:613:ASN:HB3	2.44	0.48
1:C:14:VAL:HG12	1:C:14:VAL:O	2.13	0.48
1:C:314:GLU:N	1:C:317:PHE:HE1	2.11	0.48
1:B:222:THR:HG23	1:C:275:TYR:CB	2.36	0.48
1:C:987:MET:HB3	1:C:988:PRO:HD3	1.95	0.48
1:A:382:VAL:HG11	1:A:476:SER:HB3	1.94	0.48
1:C:23:GLY:HA3	1:C:377:LEU:O	2.13	0.48
1:A:504:ASP:OD1	1:A:504:ASP:O	2.30	0.48
1:C:616:GLY:HA3	1:C:624:THR:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:448:VAL:HG11	1:C:939:ALA:CB	2.42	0.48
1:C:313:MET:O	1:C:317:PHE:CE1	2.67	0.48
1:B:534:ILE:HG23	1:B:535:LEU:HG	1.95	0.48
1:A:240:LEU:H	1:A:240:LEU:HD13	1.78	0.48
1:B:115:MET:N	1:B:116:PRO:CD	2.76	0.48
1:B:137:LEU:HD22	1:B:293:LEU:CD1	2.39	0.48
1:B:903:LEU:HD13	1:B:1025:PHE:CD2	2.48	0.48
1:B:808:ARG:HA	2:D:79:LEU:CD1	2.44	0.48
1:A:457:ALA:HB2	1:A:471:SER:HB3	1.95	0.48
1:A:445:ILE:HA	1:A:448:VAL:CG1	2.43	0.48
1:C:447:MET:SD	1:C:887:CYS:HB3	2.53	0.48
1:B:166:ILE:HD13	1:B:166:ILE:N	2.28	0.48
1:A:164:ASP:OD2	1:A:767:ARG:NH2	2.44	0.48
1:C:259:ARG:CZ	2:E:155:ASP:OD2	2.62	0.48
1:C:795:ASP:OD1	1:C:795:ASP:O	2.30	0.48
1:B:435:MET:O	1:B:436:GLY:C	2.47	0.48
1:A:139:VAL:CG1	1:A:178:PHE:HE2	2.26	0.48
1:B:910:ILE:HG23	1:B:1013:THR:HG21	1.95	0.48
1:C:406:VAL:O	1:C:410:ILE:HG13	2.14	0.48
1:B:183:ALA:CB	1:B:271:GLY:O	2.60	0.48
2:D:13:ASP:C	2:D:15:GLY:N	2.62	0.48
1:B:418:ARG:O	1:B:422:GLU:HG3	2.14	0.48
1:A:1013:THR:O	1:A:1017:LEU:HB2	2.13	0.48
1:B:727:PHE:HE1	1:B:783:PRO:HB3	1.76	0.48
1:B:324:VAL:CG2	1:B:325:TYR:N	2.76	0.48
1:C:598:TYR:HB3	1:C:606:VAL:HG21	1.95	0.48
1:B:222:THR:HG22	1:C:275:TYR:CB	2.24	0.48
1:A:410:ILE:CD1	1:A:978:THR:HG22	2.44	0.48
1:B:184:MET:CE	1:B:268:ILE:HG22	2.43	0.48
1:C:504:ASP:CG	1:C:504:ASP:O	2.52	0.48
1:A:236:ALA:HB2	1:B:729:ILE:O	2.13	0.48
2:E:84:LEU:CD2	2:E:116:PRO:HB3	2.44	0.48
1:A:459:PHE:CB	1:A:464:GLY:HA2	2.43	0.48
1:B:182:TYR:HB3	1:B:270:LEU:CG	2.44	0.48
1:B:198:LEU:N	1:B:798:MET:CE	2.76	0.48
1:C:199:THR:HB	1:C:200:PRO:HD2	1.96	0.48
1:A:380:PHE:H	1:A:380:PHE:HD1	1.61	0.48
1:A:534:ILE:CA	1:A:541:TYR:CE1	2.94	0.48
1:A:527:TYR:CE1	1:A:968:VAL:HG12	2.48	0.48
1:A:242:SER:HB2	1:A:244:GLU:CG	2.41	0.48
1:A:987:MET:N	1:A:988:PRO:CD	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:94:GLU:CD	2:D:94:GLU:H	2.18	0.48
1:A:497:LEU:HB3	1:A:498:LYS:HE2	1.95	0.48
1:B:660:ASP:OD1	2:D:16:LYS:NZ	2.41	0.48
1:B:351:VAL:O	1:B:355:MET:HB2	2.12	0.48
1:A:758:TYR:CG	1:A:758:TYR:O	2.61	0.48
1:A:190:PRO:HD2	1:A:779:TYR:CG	2.49	0.48
1:C:429:GLU:CA	1:C:432:ARG:HG3	2.43	0.48
2:D:77:ASP:CG	2:D:78:SER:N	2.67	0.48
1:C:391:ASN:O	1:C:395:MET:HG2	2.14	0.48
1:C:210:GLN:NE2	1:C:249:ILE:HG23	2.29	0.48
1:C:166:ILE:CG2	1:C:166:ILE:O	2.56	0.48
1:A:497:LEU:HA	1:A:497:LEU:HD22	1.58	0.48
2:D:56:TYR:O	2:D:56:TYR:CG	2.66	0.48
1:B:561:SER:O	1:B:562:SER:OG	2.30	0.48
1:B:668:LEU:CB	1:B:669:PRO:HD2	2.44	0.48
2:D:61:GLU:HG2	2:D:62:ILE:H	1.78	0.48
1:B:1:FME:HE2	1:B:487:ILE:HG13	1.94	0.48
1:A:751:GLY:O	1:A:754:TRP:O	2.32	0.48
1:B:729:ILE:O	1:B:729:ILE:HG23	2.14	0.48
2:D:110:ASP:HB3	2:D:112:ASN:HB2	1.96	0.48
2:D:130:GLU:HG3	2:D:131:VAL:N	2.29	0.48
1:B:790:TYR:CE1	1:B:800:PRO:HB3	2.49	0.47
1:A:448:VAL:HG21	1:A:888:LEU:CD2	2.44	0.47
1:B:197:GLN:C	1:B:798:MET:HE3	2.13	0.47
1:A:813:SER:HB2	1:A:814:PRO:HD2	1.95	0.47
2:E:143:ASP:H	2:E:146:GLY:C	2.16	0.47
2:E:93:LEU:HD11	2:E:127:GLU:CB	2.44	0.47
1:C:158:VAL:CG2	1:C:162:MET:HE3	2.35	0.47
1:B:324:VAL:CG2	1:B:325:TYR:H	2.27	0.47
1:A:910:ILE:CG2	1:A:911:GLY:N	2.77	0.47
1:A:489:THR:N	1:A:490:PRO:HD2	2.30	0.47
1:A:519:MET:CE	1:A:519:MET:CA	2.88	0.47
1:A:972:LEU:CD1	1:A:972:LEU:O	2.62	0.47
1:B:231:ASN:OD1	1:C:622:GLN:CG	2.62	0.47
1:B:328:ASP:C	1:B:328:ASP:OD1	2.51	0.47
1:C:948:PHE:HE1	1:C:970:MET:SD	2.37	0.47
1:C:278:ILE:HD12	1:C:584:GLN:OE1	2.14	0.47
2:D:145:PHE:C	2:D:147:LYS:H	2.16	0.47
1:B:767:ARG:HH22	1:C:67:GLN:HE22	1.62	0.47
1:B:716:VAL:HG13	1:B:716:VAL:O	2.13	0.47
1:B:196:PHE:O	1:B:197:GLN:C	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ASN:HB3	1:A:95:GLU:HG3	1.96	0.47
2:D:44:ASP:CG	2:D:45:HIS:HA	2.33	0.47
1:B:674:LEU:HD12	1:B:674:LEU:O	2.12	0.47
2:E:154:ILE:HG13	2:E:155:ASP:N	2.30	0.47
1:B:480:LEU:HA	1:B:483:LEU:HD23	1.95	0.47
1:C:960:LEU:HD12	1:C:960:LEU:C	2.31	0.47
1:B:686:ASP:HB2	1:B:695:LEU:CD1	2.44	0.47
1:A:650:ARG:CG	1:A:651:ALA:N	2.77	0.47
1:B:687:GLN:NE2	1:B:859:TRP:CB	2.77	0.47
1:A:648:THR:O	1:A:652:THR:HG22	2.14	0.47
1:C:1037:ASN:OD1	1:C:1039:ASP:O	2.32	0.47
1:C:842:GLU:O	1:C:846:GLN:HG3	2.14	0.47
1:C:733:GLN:NE2	1:C:743:ILE:CG2	2.72	0.47
1:B:2:PRO:O	1:B:6:ILE:HG13	2.14	0.47
1:B:576:VAL:HG22	1:B:663:VAL:HG22	1.96	0.47
1:B:47:ALA:HB3	1:B:88:VAL:CG1	2.44	0.47
1:A:1012:VAL:O	1:A:1016:VAL:HG22	2.14	0.47
1:C:1033:PHE:O	1:C:1034:SER:OG	2.30	0.47
1:A:697:GLN:HA	1:A:700:ASN:HD22	1.80	0.47
1:B:378:GLY:HA3	1:B:480:LEU:HD23	1.95	0.47
1:B:263:ARG:HG2	1:B:263:ARG:O	2.14	0.47
1:B:193:LEU:CD2	1:B:265:VAL:HB	2.44	0.47
1:A:971:ARG:HH11	1:A:971:ARG:HG2	1.69	0.47
1:A:181:GLN:NE2	1:A:769:LYS:HE3	2.25	0.47
1:A:454:VAL:N	1:A:455:PRO:CD	2.77	0.47
1:A:492:LEU:N	1:A:492:LEU:CD1	2.78	0.47
1:B:255:GLN:C	1:B:257:GLY:N	2.64	0.47
1:B:537:SER:O	1:B:541:TYR:HD1	1.97	0.47
1:A:534:ILE:HG22	1:A:541:TYR:CZ	2.50	0.47
1:B:293:LEU:HD11	1:B:299:ALA:CB	2.45	0.47
1:B:504:ASP:OD1	1:B:505:HIS:O	2.33	0.47
1:C:669:PRO:N	1:C:678:THR:HG22	2.29	0.47
1:A:987:MET:HB3	1:A:988:PRO:HD3	1.97	0.47
2:D:48:TRP:NE1	2:D:77:ASP:OD2	2.44	0.47
1:A:860:THR:O	1:A:860:THR:OG1	2.30	0.47
2:D:110:ASP:CB	2:D:112:ASN:HB2	2.45	0.47
1:A:78:MET:O	1:A:78:MET:HG3	2.14	0.47
1:C:488:LEU:O	1:C:492:LEU:HG	2.15	0.47
2:D:94:GLU:O	2:D:98:VAL:HG23	2.15	0.47
1:A:306:ILE:HG12	1:A:306:ILE:H	1.34	0.47
1:C:727:PHE:CE1	1:C:807:SER:HB3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:908:GLY:HA3	1:C:938:SER:OG	2.14	0.47
1:A:423:GLU:N	1:A:502:LYS:HG3	2.29	0.47
1:B:365:THR:HG23	1:B:366:LEU:H	1.79	0.47
1:A:182:TYR:HD2	1:A:270:LEU:CD2	2.26	0.47
1:C:332:PHE:HA	1:C:335:ILE:HG22	1.96	0.47
1:B:182:TYR:HD1	1:B:270:LEU:CD2	2.27	0.47
2:D:49:THR:O	2:D:53:LEU:HD23	2.10	0.47
2:D:49:THR:O	2:D:52:HIS:HB2	2.15	0.47
2:D:125:HIS:O	2:D:129:VAL:CG2	2.57	0.47
1:C:631:LEU:HD12	1:C:637:ARG:CZ	2.45	0.47
1:A:41:PRO:HD2	1:A:95:GLU:O	2.15	0.47
1:B:72:ILE:CG2	1:B:73:ASP:H	2.25	0.47
1:C:885:PHE:HE1	1:C:898:PRO:HB2	1.80	0.47
1:B:243:THR:HG23	1:B:244:GLU:N	2.30	0.47
1:A:423:GLU:C	1:A:502:LYS:CE	2.81	0.47
1:A:539:GLY:O	1:A:543:VAL:HG22	2.15	0.47
1:A:211:ASN:HA	1:A:240:LEU:HD13	1.97	0.47
1:A:621:GLY:CA	1:A:624:THR:HG22	2.44	0.47
1:A:314:GLU:N	1:A:315:PRO:HD2	2.30	0.47
2:E:57:PHE:N	2:E:58:GLY:HA2	2.30	0.47
1:C:598:TYR:HB3	1:C:606:VAL:HG11	1.97	0.47
1:A:241:THR:HG23	1:A:763:ILE:O	2.15	0.47
1:A:343:THR:HA	1:A:346:GLU:HB2	1.96	0.47
1:A:570:GLY:N	1:A:634:TRP:HH2	2.13	0.47
1:B:370:ILE:HG21	1:B:492:LEU:HD11	1.97	0.46
1:C:247:GLY:C	1:C:263:ARG:HG2	2.36	0.46
1:B:456:MET:O	1:B:456:MET:HG2	2.14	0.46
1:A:692:HIS:O	1:A:696:THR:OG1	2.33	0.46
2:D:89:ASP:C	2:D:91:GLY:N	2.65	0.46
1:C:958:LYS:HD3	1:C:962:GLU:CD	2.36	0.46
1:A:1026:PHE:CG	1:A:1026:PHE:O	2.68	0.46
1:A:815:ARG:HB2	1:A:815:ARG:HE	1.22	0.46
1:A:431:THR:O	1:A:432:ARG:C	2.53	0.46
2:D:65:VAL:O	2:D:69:ASN:ND2	2.40	0.46
1:C:87:THR:C	1:C:88:VAL:HG12	2.35	0.46
1:A:944:LEU:HD12	1:A:971:ARG:NH2	2.29	0.46
1:C:412:VAL:HG23	1:C:442:LEU:HD21	1.96	0.46
1:C:987:MET:O	1:C:990:VAL:N	2.45	0.46
1:C:76:MET:HG2	1:C:95:GLU:OE2	2.15	0.46
1:B:605:ASN:HD22	1:B:647:ILE:HD11	1.80	0.46
1:C:885:PHE:CE1	1:C:898:PRO:HB2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:782:LEU:HB2	1:A:785:ASP:CG	2.35	0.46
1:B:733:GLN:HE22	1:B:743:ILE:HD11	1.80	0.46
1:B:222:THR:HG23	1:C:275:TYR:HB3	1.95	0.46
1:B:669:PRO:CD	1:B:669:PRO:O	2.63	0.46
1:B:671:ILE:HG23	1:B:673:GLU:N	2.30	0.46
1:C:952:LEU:N	1:C:952:LEU:HD13	2.30	0.46
1:C:722:GLU:HG3	1:C:723:ASP:H	1.81	0.46
1:A:212:ALA:O	1:A:237:GLN:HG2	2.15	0.46
1:C:719:ASN:HB2	1:C:828:LEU:CD1	2.46	0.46
1:B:393:LEU:HD12	1:B:469:GLN:HG3	1.97	0.46
1:A:427:PRO:HD3	1:A:499:PRO:CB	2.44	0.46
1:C:436:GLY:O	1:C:439:GLN:HB3	2.15	0.46
1:A:754:TRP:N	1:A:754:TRP:HD1	2.12	0.46
2:E:67:LEU:HD22	2:E:73:VAL:HG22	1.97	0.46
1:A:219:LEU:HD13	1:B:783:PRO:HD3	1.96	0.46
1:C:63:GLN:O	1:C:67:GLN:HG2	2.15	0.46
1:A:435:MET:O	1:A:439:GLN:HB2	2.14	0.46
1:A:584:GLN:N	1:A:622:GLN:OE1	2.49	0.46
1:A:248:LYS:HA	1:A:261:LEU:HD23	1.98	0.46
1:B:733:GLN:O	1:B:736:ALA:HB3	2.15	0.46
1:B:341:VAL:O	1:B:345:VAL:HG23	2.15	0.46
2:D:43:SER:HA	2:D:49:THR:HA	1.97	0.46
1:B:605:ASN:HD21	1:B:642:ASN:CB	2.26	0.46
1:A:685:ILE:HA	1:A:823:PRO:O	2.16	0.46
1:B:774:MET:CE	1:B:780:ARG:HH11	2.28	0.46
1:B:881:LEU:HD22	1:B:881:LEU:O	2.16	0.46
1:B:758:TYR:HB2	1:B:772:TYR:HE1	1.70	0.46
1:C:925:VAL:C	1:C:927:PHE:N	2.65	0.46
1:B:291:ILE:CD1	1:B:306:ILE:HD12	2.46	0.46
1:C:466:ILE:HG12	1:C:466:ILE:H	1.40	0.46
1:A:229:GLN:OE1	1:B:586:ARG:HD2	2.15	0.46
1:C:713:LEU:HD21	1:C:843:LEU:HD23	1.96	0.46
1:B:183:ALA:CA	1:B:271:GLY:O	2.64	0.46
1:A:449:LEU:HD23	1:A:478:MET:SD	2.56	0.46
1:B:102:ILE:O	1:B:103:ALA:C	2.54	0.46
1:A:480:LEU:HD23	1:A:480:LEU:HA	1.69	0.46
1:C:907:LEU:O	1:C:910:ILE:HG22	2.14	0.46
1:B:88:VAL:HG22	1:B:89:GLN:N	2.30	0.46
2:D:76:ASP:HB3	2:D:80:GLY:HA2	1.97	0.46
1:B:717:ARG:HG3	1:B:828:LEU:HD12	1.98	0.46
1:B:445:ILE:HD13	1:B:940:LYS:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:925:VAL:O	1:C:928:GLN:N	2.49	0.46
1:A:159:ALA:HB1	1:A:181:GLN:HB2	1.97	0.46
1:A:17:ILE:O	1:A:21:LEU:HB2	2.16	0.46
2:E:143:ASP:O	2:E:146:GLY:N	2.39	0.46
1:B:235:ILE:HD12	1:B:235:ILE:HA	1.60	0.46
1:A:525:HIS:O	1:A:528:THR:OG1	2.30	0.46
1:B:350:LEU:O	1:B:354:VAL:HG13	2.16	0.46
1:A:182:TYR:CD2	1:A:270:LEU:HD21	2.51	0.46
1:C:1015:THR:O	1:C:1019:ILE:HB	2.15	0.46
1:A:693:GLU:H	1:A:693:GLU:CD	2.16	0.46
1:C:465:ALA:O	1:C:469:GLN:HG2	2.15	0.46
1:B:746:ILE:C	1:B:748:THR:H	2.20	0.45
1:A:813:SER:CB	1:A:814:PRO:HD2	2.45	0.45
1:A:519:MET:O	1:A:519:MET:SD	2.67	0.45
1:C:672:VAL:HG23	1:C:673:GLU:N	2.30	0.45
2:D:13:ASP:O	2:D:16:LYS:N	2.50	0.45
1:A:1:FME:N	1:A:2:PRO:HD2	2.30	0.45
1:A:182:TYR:HD2	1:A:270:LEU:HD21	1.81	0.45
1:B:733:GLN:HE22	1:B:743:ILE:CD1	2.28	0.45
2:E:97:GLU:OE1	2:E:97:GLU:CA	2.46	0.45
1:B:903:LEU:HD13	1:B:1025:PHE:HD2	1.81	0.45
1:A:781:MET:HE1	1:C:228:GLN:CB	2.46	0.45
2:D:80:GLY:O	2:D:82:THR:HG23	2.15	0.45
1:C:62:THR:O	1:C:66:GLU:HB2	2.15	0.45
1:A:470:PHE:O	1:A:474:ILE:HG13	2.16	0.45
2:D:56:TYR:HD1	2:D:90:ARG:CG	2.19	0.45
1:C:876:LEU:HD11	1:C:932:LEU:HD11	1.98	0.45
1:C:879:ILE:HD12	1:C:883:VAL:HG23	1.91	0.45
2:E:106:VAL:HG21	2:E:136:GLY:HA3	1.98	0.45
1:B:815:ARG:CG	1:B:815:ARG:NH1	2.73	0.45
1:A:351:VAL:HG23	1:A:981:ALA:HB1	1.98	0.45
1:B:44:THR:HG21	1:B:89:GLN:NE2	2.31	0.45
1:C:801:PHE:O	1:C:801:PHE:CD1	2.70	0.45
1:C:446:ALA:CB	1:C:482:VAL:HG22	2.46	0.45
1:B:733:GLN:HG2	1:B:733:GLN:H	1.53	0.45
1:B:908:GLY:HA2	1:B:1014:ALA:HB2	1.99	0.45
1:A:908:GLY:HA2	1:A:1014:ALA:HB2	1.98	0.45
1:A:650:ARG:HG2	1:A:651:ALA:N	2.32	0.45
1:C:894:SER:O	1:C:898:PRO:CG	2.64	0.45
1:C:514:GLY:O	1:C:518:ARG:HG3	2.17	0.45
1:B:214:VAL:CG1	1:B:215:ALA:N	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:57:PHE:N	2:D:58:GLY:CA	2.79	0.45
1:C:269:GLU:HG3	1:C:269:GLU:O	2.15	0.45
1:C:616:GLY:HA3	1:C:624:THR:CG2	2.47	0.45
1:A:55:LYS:O	1:A:56:THR:C	2.50	0.45
1:C:555:LEU:HA	1:C:555:LEU:HD23	1.84	0.45
2:E:82:THR:O	2:E:85:HIS:HB2	2.16	0.45
1:C:986:VAL:HG13	1:C:986:VAL:O	2.16	0.45
1:A:943:ILE:O	1:A:946:VAL:CG1	2.64	0.45
1:B:197:GLN:C	1:B:798:MET:HE1	2.31	0.45
1:C:154:ILE:HG13	1:C:155:SER:N	2.30	0.45
1:C:506:GLY:O	1:C:507:GLU:HG2	2.13	0.45
1:B:178:PHE:HE2	1:B:290:GLY:N	2.15	0.45
1:A:219:LEU:HD11	1:B:783:PRO:HG3	1.98	0.45
1:B:76:MET:HG2	1:B:95:GLU:OE2	2.17	0.45
1:A:888:LEU:HD13	1:A:901:VAL:HB	1.97	0.45
1:B:713:LEU:HD12	1:B:713:LEU:HA	1.64	0.45
1:A:378:GLY:HA3	1:A:480:LEU:CD1	2.47	0.45
1:A:189:ASN:HD22	1:A:192:GLU:CG	2.29	0.45
1:A:244:GLU:H	1:A:244:GLU:HG2	1.36	0.45
1:A:58:GLN:HE21	1:A:818:ARG:HH11	1.60	0.45
1:C:542:LEU:O	1:C:546:LEU:HD13	2.16	0.45
1:C:318:PRO:C	1:C:319:SER:HG	2.16	0.45
1:A:578:LEU:HD13	1:A:587:THR:HG23	1.99	0.45
1:C:444:GLY:O	1:C:448:VAL:HG23	2.16	0.45
1:C:695:LEU:CD2	1:C:695:LEU:C	2.85	0.45
1:C:586:ARG:O	1:C:590:VAL:HG23	2.17	0.45
1:B:522:LYS:O	1:B:525:HIS:HB2	2.15	0.45
1:B:21:LEU:HA	1:B:21:LEU:HD13	1.81	0.45
1:A:199:THR:O	1:A:199:THR:HG23	2.17	0.45
1:B:588:GLN:HB2	1:B:613:ASN:HD22	1.80	0.45
1:A:427:PRO:CG	1:A:497:LEU:O	2.65	0.45
2:E:112:ASN:HB2	2:E:114:PHE:HD2	1.82	0.45
1:A:972:LEU:O	1:A:972:LEU:HD13	2.16	0.45
1:A:40:PRO:HA	1:A:41:PRO:HD3	1.82	0.45
2:E:100:LEU:O	2:E:103:GLY:CA	2.65	0.45
1:A:264:ASP:N	1:A:264:ASP:OD2	2.48	0.45
1:C:937:LEU:CA	1:C:940:LYS:HG2	2.47	0.45
1:C:775:SER:HG	1:C:789:TRP:HZ2	1.64	0.45
1:B:892:TYR:OH	1:B:943:ILE:HA	2.17	0.45
1:C:335:ILE:HD12	1:C:338:HIS:HB3	1.98	0.45
1:C:750:LEU:CD2	1:C:751:GLY:N	2.77	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:725:PRO:CD	1:C:725:PRO:O	2.64	0.45
1:C:447:MET:HE3	1:C:891:LEU:CD2	2.40	0.45
1:C:567:GLU:OE2	1:C:997:SER:N	2.50	0.45
1:B:169:THR:CG2	1:B:172:VAL:HG13	2.34	0.45
1:A:753:ALA:HB3	1:A:754:TRP:HD1	1.82	0.45
1:A:1008:MET:O	1:A:1012:VAL:HG23	2.17	0.45
1:B:456:MET:O	1:B:467:TYR:HB3	2.17	0.45
1:C:98:THR:HG23	1:C:99:ASP:H	1.80	0.45
1:B:1013:THR:CG2	1:B:1017:LEU:HD12	2.47	0.45
1:A:144:ASN:OD1	1:A:149:MET:HG3	2.16	0.45
1:A:913:LEU:HD23	1:A:927:PHE:HZ	1.82	0.45
1:C:472:ILE:HG23	1:C:473:THR:N	2.31	0.45
2:D:50:PRO:HA	2:D:53:LEU:HD23	1.98	0.45
1:B:118:LEU:O	1:B:123:GLN:OE1	2.33	0.45
2:D:14:LEU:O	2:D:15:GLY:C	2.52	0.45
1:B:575:MET:O	1:B:576:VAL:HG23	2.16	0.45
1:B:435:MET:C	1:B:437:GLN:H	2.18	0.45
1:A:230:LEU:HD23	1:B:782:LEU:HD22	1.99	0.45
1:A:910:ILE:HG23	1:A:911:GLY:N	2.32	0.45
1:B:698:ALA:O	1:B:851:LEU:HD23	2.16	0.45
1:B:293:LEU:CD1	1:B:299:ALA:HB2	2.46	0.45
1:B:488:LEU:O	1:B:492:LEU:HG	2.17	0.45
1:B:501:ALA:HB3	1:B:504:ASP:CG	2.38	0.45
1:B:62:THR:CG2	1:B:62:THR:O	2.63	0.45
1:A:316:PHE:CD2	1:B:687:GLN:HB3	2.52	0.45
1:B:98:THR:HG22	1:B:99:ASP:N	2.32	0.45
1:A:694:LYS:O	1:A:697:GLN:HB2	2.17	0.45
1:C:719:ASN:HD22	1:C:828:LEU:HD11	1.82	0.45
1:A:908:GLY:CA	1:A:1014:ALA:HB2	2.47	0.45
1:B:813:SER:HB3	1:B:816:LEU:CD2	2.48	0.44
2:D:73:VAL:HG11	2:D:103:GLY:O	2.17	0.44
1:B:10:ILE:HD12	1:C:895:TRP:NE1	2.32	0.44
1:C:53:ASP:OD1	1:C:53:ASP:O	2.35	0.44
2:E:77:ASP:HB2	2:E:81:VAL:O	2.17	0.44
1:C:5:PHE:CE2	1:C:487:ILE:HG12	2.51	0.44
1:C:5:PHE:CE2	1:C:487:ILE:HG23	2.53	0.44
1:A:427:PRO:HG2	1:A:497:LEU:O	2.17	0.44
1:A:483:LEU:HA	1:A:486:LEU:HD23	1.99	0.44
1:B:340:VAL:O	1:B:344:LEU:HG	2.17	0.44
1:C:559:LEU:HA	1:C:560:PRO:HD3	1.87	0.44
1:B:416:VAL:HG22	1:B:434:SER:CB	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:9:PRO:HD2	1:C:10:ILE:H	1.81	0.44
1:A:899:PHE:O	1:A:903:LEU:HD12	2.17	0.44
1:C:568:ASP:HA	1:C:644:VAL:CG2	2.47	0.44
1:B:406:VAL:C	1:B:408:ASP:H	2.19	0.44
1:A:997:SER:C	1:A:999:ALA:H	2.20	0.44
1:C:367:ILE:CB	1:C:368:PRO:HD3	2.47	0.44
2:D:164:ILE:H	2:D:164:ILE:HG13	1.57	0.44
1:C:45:ILE:HD11	1:C:107:VAL:CG1	2.47	0.44
1:C:733:GLN:O	1:C:734:GLU:C	2.55	0.44
1:C:886:LEU:O	1:C:887:CYS:C	2.55	0.44
1:B:673:GLU:C	1:B:675:GLY:H	2.18	0.44
1:B:1020:PHE:O	1:B:1023:PRO:HD2	2.18	0.44
1:A:726:GLN:HB3	1:C:235:ILE:HG12	1.99	0.44
1:C:952:LEU:HA	1:C:952:LEU:HD12	1.40	0.44
1:B:416:VAL:HG22	1:B:434:SER:HB3	1.99	0.44
1:A:725:PRO:HA	1:A:810:GLU:O	2.17	0.44
1:B:911:GLY:C	1:B:1010:GLY:HA2	2.37	0.44
1:C:999:ALA:O	1:C:1000:GLN:C	2.55	0.44
1:C:342:LYS:O	1:C:343:THR:C	2.53	0.44
1:B:365:THR:C	1:B:368:PRO:HD2	2.37	0.44
1:B:853:THR:O	1:B:853:THR:HG23	2.14	0.44
1:B:754:TRP:CE3	1:B:780:ARG:HB2	2.52	0.44
1:B:62:THR:OG1	1:B:88:VAL:CG2	2.65	0.44
1:B:33:ALA:O	1:B:391:ASN:HA	2.18	0.44
1:A:987:MET:C	1:A:989:LEU:H	2.20	0.44
1:C:390:ILE:O	1:C:390:ILE:HG22	2.17	0.44
2:E:57:PHE:H	2:E:58:GLY:CA	2.31	0.44
2:E:44:ASP:HA	2:E:45:HIS:HA	1.50	0.44
1:B:508:GLY:C	1:B:510:LYS:N	2.63	0.44
2:E:126:LEU:HA	2:E:129:VAL:HG22	2.00	0.44
1:A:519:MET:HE2	1:A:519:MET:HB2	1.34	0.44
1:A:239:ARG:C	1:A:240:LEU:HD12	2.31	0.44
1:A:388:PHE:CE1	1:A:469:GLN:OE1	2.71	0.44
1:C:367:ILE:HG23	1:C:492:LEU:HD12	1.99	0.44
1:C:48:SER:HB3	1:C:125:GLN:HG2	1.99	0.44
1:A:401:ALA:O	1:A:405:LEU:HD13	2.18	0.44
2:D:18:LEU:C	2:D:18:LEU:HD22	2.36	0.44
1:B:702:LEU:HD11	1:B:844:MET:CE	2.48	0.44
1:A:753:ALA:HB3	1:A:754:TRP:CD1	2.52	0.44
1:C:172:VAL:HG13	1:C:291:ILE:HG23	2.00	0.44
1:A:190:PRO:HG3	1:A:789:TRP:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:ARG:HG3	1:A:264:ASP:N	2.32	0.44
1:C:527:TYR:CZ	1:C:1019:ILE:HG13	2.53	0.44
1:C:69:MET:HE3	1:C:69:MET:HA	2.00	0.44
1:C:952:LEU:N	1:C:952:LEU:HD12	2.27	0.44
1:B:724:THR:HB	1:B:725:PRO:HD2	1.99	0.44
1:A:721:LEU:HD11	1:A:814:PRO:HG2	1.85	0.44
1:B:534:ILE:HG23	1:B:535:LEU:N	2.32	0.44
1:A:531:VAL:O	1:A:534:ILE:CG1	2.66	0.44
1:B:166:ILE:CG2	1:B:175:VAL:HG21	2.38	0.44
1:A:462:SER:OG	1:A:463:THR:N	2.49	0.44
1:B:578:LEU:CD1	1:B:579:PRO:HD3	2.48	0.44
1:C:448:VAL:HG12	1:C:936:GLY:HA2	2.00	0.44
2:E:101:LYS:O	2:E:102:ASN:C	2.50	0.44
1:A:492:LEU:HD12	1:A:492:LEU:N	2.32	0.44
1:B:960:LEU:HD22	1:B:961:ILE:HD13	1.99	0.44
1:C:431:THR:HG22	1:C:435:MET:HG3	1.98	0.44
1:C:163:LYS:O	1:C:164:ASP:C	2.56	0.44
1:A:159:ALA:O	1:A:163:LYS:HE2	2.18	0.44
1:C:281:PHE:O	1:C:282:ASN:HB2	2.18	0.44
1:A:645:GLU:O	1:A:649:MET:HG3	2.18	0.44
1:A:72:ILE:HD13	1:A:107:VAL:HG22	1.99	0.44
1:C:471:SER:O	1:C:475:VAL:HG23	2.17	0.44
1:C:737:GLN:O	1:C:738:ALA:C	2.53	0.43
1:C:151:GLN:HA	1:C:154:ILE:HG23	2.00	0.43
1:C:144:ASN:ND2	1:C:149:MET:N	2.66	0.43
1:C:672:VAL:HG23	1:C:673:GLU:CD	2.37	0.43
1:A:1013:THR:C	1:A:1015:THR:H	2.21	0.43
1:A:897:ILE:O	1:A:897:ILE:CG2	2.64	0.43
1:C:741:VAL:HG11	1:C:746:ILE:HD11	1.84	0.43
1:B:561:SER:HA	1:B:923:ASN:CB	2.48	0.43
2:D:126:LEU:C	2:D:129:VAL:CG2	2.86	0.43
1:C:724:THR:HG23	1:C:814:PRO:CG	2.48	0.43
1:A:190:PRO:HD2	1:A:779:TYR:CD2	2.53	0.43
1:C:648:THR:HA	1:C:651:ALA:HB3	2.00	0.43
1:C:594:VAL:CG1	1:C:598:TYR:HE2	2.31	0.43
1:B:139:VAL:HG22	1:B:327:TYR:HB3	1.99	0.43
1:B:187:TRP:HD1	1:B:267:LYS:O	2.00	0.43
2:D:148:THR:H	2:D:151:ASP:HB2	1.83	0.43
1:C:358:PHE:CG	1:C:977:MET:HG2	2.54	0.43
1:A:98:THR:CG2	1:A:103:ALA:HB2	2.47	0.43
1:C:404:LEU:HD22	1:C:404:LEU:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:25:GLY:CA	2:E:59:HIS:CE1	3.01	0.43
1:B:531:VAL:HA	1:B:534:ILE:HG22	2.00	0.43
1:B:531:VAL:C	1:B:534:ILE:HG22	2.38	0.43
1:C:415:ASN:HD22	1:C:434:SER:HB3	1.84	0.43
1:A:534:ILE:HD12	1:A:1024:VAL:CG2	2.48	0.43
1:C:993:THR:HA	1:C:997:SER:CB	2.49	0.43
1:A:189:ASN:ND2	1:A:192:GLU:HG3	2.34	0.43
1:C:372:VAL:H	1:C:373:PRO:HD2	1.83	0.43
1:C:563:PHE:CE2	1:C:862:MET:CE	3.01	0.43
1:C:226:LYS:HD3	1:C:226:LYS:HA	1.83	0.43
1:A:184:MET:HG2	1:A:246:PHE:CD1	2.53	0.43
1:B:733:GLN:HA	1:B:736:ALA:HB3	2.00	0.43
1:C:521:GLU:O	1:C:525:HIS:CD2	2.71	0.43
1:B:699:ARG:HD3	1:B:825:MET:HG2	2.00	0.43
1:B:157:TYR:CD2	1:B:157:TYR:C	2.91	0.43
1:A:485:ALA:HB3	1:A:486:LEU:CD1	2.49	0.43
2:D:50:PRO:C	2:D:53:LEU:HD23	2.39	0.43
1:C:780:ARG:CG	1:C:780:ARG:O	2.66	0.43
1:C:391:ASN:H	1:C:394:THR:CG2	2.31	0.43
1:B:310:LEU:HD13	1:B:323:ILE:HD12	2.00	0.43
1:A:739:LEU:HD13	1:A:799:VAL:HG11	2.00	0.43
1:C:194:ASN:O	1:C:194:ASN:ND2	2.52	0.43
1:B:746:ILE:HG23	1:B:801:PHE:CE1	2.53	0.43
1:B:869:SER:C	1:B:871:ASN:N	2.66	0.43
1:C:177:LEU:HD13	1:C:179:GLY:N	2.34	0.43
1:C:207:ILE:HG22	1:C:760:ASN:ND2	2.33	0.43
1:B:223:PRO:HA	1:B:224:PRO:HD3	1.78	0.43
1:A:587:THR:HB	1:A:613:ASN:HD21	1.82	0.43
1:B:11:PHE:O	1:B:11:PHE:CD1	2.72	0.43
1:A:185:ARG:HA	1:A:185:ARG:HD2	1.86	0.43
1:C:741:VAL:HG12	1:C:746:ILE:HD13	1.97	0.43
2:D:50:PRO:CA	2:D:53:LEU:HD23	2.49	0.43
1:B:997:SER:O	1:B:1000:GLN:N	2.52	0.43
2:E:143:ASP:O	2:E:144:LYS:C	2.55	0.43
1:A:379:THR:CG2	1:A:383:LEU:HD21	2.47	0.43
1:C:577:GLN:HE22	1:C:623:ASN:HD21	1.65	0.43
1:B:353:LEU:C	1:B:355:MET:H	2.20	0.43
1:B:83:ASP:HA	1:B:815:ARG:N	2.30	0.43
1:B:495:THR:HG22	1:B:496:MET:CG	2.48	0.43
1:B:754:TRP:CH2	1:B:780:ARG:HA	2.54	0.43
1:C:263:ARG:HG3	1:C:263:ARG:H	1.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:696:THR:O	1:A:699:ARG:HB3	2.18	0.43
1:B:497:LEU:HA	1:B:497:LEU:HD12	1.73	0.43
1:C:614:GLY:HA2	1:C:621:GLY:O	2.19	0.43
1:A:140:VAL:O	1:A:140:VAL:HG22	2.17	0.43
2:E:28:ASP:O	2:E:32:ILE:HG13	2.19	0.43
1:A:431:THR:HG22	1:A:432:ARG:H	1.82	0.43
1:A:538:THR:C	1:A:540:ARG:N	2.69	0.43
2:E:100:LEU:HA	2:E:100:LEU:HD23	1.64	0.43
1:B:351:VAL:O	1:B:355:MET:CB	2.66	0.43
1:B:774:MET:SD	1:B:780:ARG:NH1	2.91	0.43
1:C:1019:ILE:HA	1:C:1019:ILE:HD12	1.84	0.43
1:B:391:ASN:O	1:B:395:MET:HG3	2.19	0.43
1:B:448:VAL:O	1:B:452:VAL:HG23	2.19	0.43
1:C:5:PHE:C	1:C:7:ASP:N	2.69	0.43
1:C:522:LYS:HG2	1:C:526:HIS:HE1	1.83	0.43
1:A:52:ALA:C	1:A:53:ASP:O	2.54	0.43
1:B:351:VAL:HG13	1:B:410:ILE:HD11	2.00	0.43
1:C:925:VAL:O	1:C:927:PHE:N	2.51	0.43
1:A:187:TRP:O	1:A:266:ALA:HA	2.18	0.43
1:C:822:LEU:N	1:C:822:LEU:HD12	2.33	0.43
1:A:961:ILE:HD13	1:A:961:ILE:O	2.19	0.43
1:B:566:ASP:OD1	1:B:566:ASP:N	2.52	0.43
1:A:497:LEU:CA	1:A:498:LYS:HE2	2.49	0.43
2:D:56:TYR:HD1	2:D:90:ARG:HE	1.61	0.43
1:A:973:ARG:O	1:A:977:MET:CG	2.53	0.43
1:B:753:ALA:HB1	1:B:789:TRP:CZ2	2.54	0.43
1:C:213:GLN:HG2	1:C:239:ARG:HD3	2.00	0.43
1:C:669:PRO:HG3	1:C:675:GLY:O	2.19	0.43
1:A:14:VAL:HG13	1:B:886:LEU:HD12	2.01	0.43
1:C:945:ILE:HD11	1:C:1019:ILE:HD12	2.00	0.43
1:A:314:GLU:C	1:A:316:PHE:H	2.22	0.43
1:C:318:PRO:C	1:C:319:SER:OG	2.55	0.43
1:C:578:LEU:HD12	1:C:578:LEU:N	2.33	0.43
1:C:604:ASN:HD22	1:C:604:ASN:HA	1.60	0.43
1:C:185:ARG:HG3	1:C:271:GLY:HA3	2.00	0.43
1:B:102:ILE:O	1:B:105:VAL:HG12	2.18	0.43
1:C:911:GLY:CA	1:C:1013:THR:OG1	2.64	0.43
1:B:909:VAL:O	1:B:912:ALA:HB3	2.18	0.43
1:A:996:GLY:O	1:A:999:ALA:HB3	2.19	0.43
1:A:886:LEU:HB3	1:C:14:VAL:HG13	2.00	0.43
1:B:702:LEU:HD11	1:B:844:MET:HE1	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:GLN:CD	1:A:513:PHE:CE1	2.93	0.42
1:B:353:LEU:HD12	1:B:353:LEU:N	2.34	0.42
1:B:674:LEU:CD1	1:B:674:LEU:C	2.85	0.42
1:A:158:VAL:CG1	1:A:289:LEU:HD21	2.49	0.42
1:A:45:ILE:HG12	1:A:111:LEU:HD12	2.00	0.42
1:B:871:ASN:HA	1:B:872:GLN:HA	1.35	0.42
2:D:44:ASP:CG	2:D:45:HIS:HB3	2.37	0.42
1:B:107:VAL:H	1:B:107:VAL:HG23	1.44	0.42
1:B:814:PRO:O	1:B:815:ARG:C	2.57	0.42
1:C:372:VAL:N	1:C:373:PRO:HD2	2.34	0.42
1:B:687:GLN:HE22	1:B:859:TRP:CB	2.32	0.42
1:B:1022:VAL:N	1:B:1023:PRO:CD	2.82	0.42
1:A:275:TYR:CD1	1:C:223:PRO:HD3	2.55	0.42
1:C:719:ASN:HB2	1:C:828:LEU:HD11	2.00	0.42
1:A:570:GLY:N	1:A:634:TRP:CH2	2.87	0.42
1:A:489:THR:CG2	1:A:490:PRO:CD	2.95	0.42
1:A:814:PRO:HG2	1:A:815:ARG:H	1.85	0.42
1:C:742:SER:HB3	1:C:745:ASP:HB2	2.00	0.42
1:B:5:PHE:CD1	1:B:487:ILE:HG12	2.55	0.42
1:B:371:ALA:HB2	1:B:489:THR:CG2	2.48	0.42
1:B:160:ALA:HB3	1:B:161:ASN:HD21	1.85	0.42
1:C:793:ALA:HB3	1:C:797:GLN:H	1.84	0.42
1:B:11:PHE:CE2	1:C:890:ALA:HB1	2.54	0.42
1:B:915:ALA:HB2	1:B:1009:GLY:HA3	2.00	0.42
1:C:231:ASN:CG	1:C:231:ASN:O	2.56	0.42
1:B:991:ILE:HG23	1:B:992:SER:N	2.33	0.42
1:B:799:VAL:HG12	1:B:800:PRO:HD2	1.84	0.42
2:D:27:ASP:HB3	2:D:62:ILE:CG1	2.49	0.42
1:B:199:THR:CG2	1:B:792:ARG:H	2.33	0.42
1:A:912:ALA:O	1:A:927:PHE:CE2	2.73	0.42
1:A:60:THR:HG22	1:A:61:VAL:HG23	2.01	0.42
1:C:597:TYR:C	1:C:597:TYR:CD2	2.93	0.42
1:C:431:THR:O	1:C:435:MET:CG	2.67	0.42
1:C:412:VAL:HA	1:C:438:ILE:CD1	2.50	0.42
1:A:539:GLY:O	1:A:540:ARG:C	2.58	0.42
1:A:975:ILE:O	1:A:979:SER:HB2	2.18	0.42
1:A:355:MET:HE2	1:A:368:PRO:HG2	2.01	0.42
1:A:990:VAL:HG11	1:A:1008:MET:HE2	2.02	0.42
1:C:943:ILE:O	1:C:947:GLU:HB3	2.19	0.42
1:A:302:THR:O	1:A:306:ILE:HG12	2.20	0.42
1:A:912:ALA:O	1:A:927:PHE:HE2	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:25:GLY:HA3	2:E:59:HIS:CE1	2.55	0.42
1:B:931:LEU:O	1:B:935:ILE:HG13	2.19	0.42
1:B:212:ALA:O	1:B:237:GLN:HG3	2.20	0.42
1:B:961:ILE:HG22	1:B:965:LEU:HD13	2.02	0.42
1:C:632:LYS:O	1:C:633:ASP:C	2.58	0.42
1:A:537:SER:HB3	1:A:541:TYR:CD1	2.55	0.42
1:C:162:MET:O	1:C:163:LYS:C	2.55	0.42
1:B:690:LEU:HD11	1:B:857:TYR:CB	2.50	0.42
1:A:66:GLU:O	1:C:168:ARG:NH1	2.53	0.42
1:C:65:ILE:O	1:C:69:MET:CG	2.65	0.42
1:C:453:PHE:O	1:C:456:MET:HG2	2.20	0.42
1:B:377:LEU:HD12	1:B:377:LEU:HA	1.63	0.42
1:B:182:TYR:HB3	1:B:270:LEU:HD21	2.02	0.42
2:D:53:LEU:HD23	2:D:53:LEU:N	2.03	0.42
1:B:828:LEU:O	1:B:828:LEU:HD12	2.20	0.42
1:B:184:MET:HE3	1:B:268:ILE:HG22	2.02	0.42
1:B:764:ASP:HB3	1:B:769:LYS:HD2	2.02	0.42
1:A:74:ASN:O	1:A:95:GLU:HG2	2.20	0.42
1:C:980:LEU:HD13	1:C:980:LEU:HA	1.73	0.42
1:A:570:GLY:HA3	1:A:634:TRP:CH2	2.54	0.42
1:C:254:ASN:C	1:C:256:ASP:H	2.23	0.42
1:B:156:ASP:CB	1:B:182:TYR:CD2	2.98	0.42
1:B:671:ILE:CG2	1:B:673:GLU:N	2.82	0.42
1:C:571:VAL:HB	1:C:629:VAL:O	2.19	0.42
1:C:507:GLU:HB2	1:C:508:GLY:H	1.58	0.42
1:B:777:ALA:HA	1:B:780:ARG:HH21	1.85	0.42
1:A:600:THR:O	1:A:603:LYS:HG2	2.20	0.42
1:C:142:VAL:HG13	1:C:322:LYS:O	2.20	0.42
1:B:519:MET:CG	1:B:520:PHE:N	2.78	0.42
1:A:841:MET:O	1:A:844:MET:HB2	2.20	0.42
1:C:277:ILE:HD12	1:C:277:ILE:N	2.34	0.42
1:C:567:GLU:OE2	1:C:996:GLY:CA	2.68	0.42
1:B:511:GLY:HA2	1:B:512:PHE:C	2.40	0.42
1:C:898:PRO:O	1:C:902:MET:HB2	2.20	0.42
1:C:222:THR:HA	1:C:224:PRO:HD3	2.02	0.42
1:A:973:ARG:HB3	1:A:974:PRO:HD3	2.01	0.42
1:C:342:LYS:O	1:C:344:LEU:N	2.53	0.42
1:C:988:PRO:O	1:C:992:SER:HB3	2.20	0.42
1:B:575:MET:CG	1:B:576:VAL:N	2.76	0.42
1:A:580:ALA:CA	1:A:623:ASN:ND2	2.81	0.42
1:C:761:ASP:HB3	1:C:768:VAL:HG12	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:454:VAL:HB	1:C:455:PRO:CD	2.48	0.42
1:B:623:ASN:O	1:B:623:ASN:ND2	2.50	0.42
1:A:470:PHE:CD1	1:A:929:VAL:HG11	2.55	0.42
1:B:864:TYR:O	1:B:865:GLN:C	2.58	0.42
1:C:528:THR:HG22	1:C:529:ASP:N	2.34	0.42
1:C:185:ARG:HH22	1:C:774:MET:HE1	1.86	0.41
1:C:154:ILE:HD12	1:C:155:SER:N	2.24	0.41
1:C:54:ALA:N	1:C:84:SER:HA	2.35	0.41
1:A:376:LEU:O	1:A:379:THR:HB	2.20	0.41
1:B:672:VAL:O	1:B:672:VAL:HG13	2.19	0.41
1:B:715:SER:CB	1:B:830:GLN:HE21	2.33	0.41
1:C:896:SER:OG	1:C:897:ILE:HD13	2.04	0.41
1:C:153:ASP:OD1	1:C:153:ASP:N	2.52	0.41
1:C:934:THR:HA	1:C:937:LEU:HD12	2.02	0.41
1:A:310:LEU:HD12	1:A:313:MET:HE3	2.01	0.41
1:A:900:SER:HA	1:A:1025:PHE:HB3	2.02	0.41
1:A:971:ARG:HD2	1:A:971:ARG:HA	1.49	0.41
1:C:987:MET:O	1:C:989:LEU:N	2.53	0.41
1:A:975:ILE:O	1:A:979:SER:CB	2.68	0.41
1:B:813:SER:HA	1:B:814:PRO:HD2	1.90	0.41
1:B:631:LEU:HA	1:B:631:LEU:HD23	1.77	0.41
1:C:795:ASP:OD1	1:C:797:GLN:HG2	2.20	0.41
1:A:1016:VAL:HG23	1:A:1017:LEU:CD1	2.45	0.41
1:C:555:LEU:HD11	1:C:914:LEU:CD2	2.49	0.41
1:A:111:LEU:HD23	1:A:111:LEU:O	2.20	0.41
1:B:74:ASN:OD1	1:B:74:ASN:N	2.52	0.41
1:B:254:ASN:ND2	1:B:258:SER:CB	2.69	0.41
1:C:199:THR:HB	1:C:200:PRO:CD	2.50	0.41
1:C:177:LEU:HD23	1:C:289:LEU:CD1	2.51	0.41
1:A:774:MET:CG	1:A:775:SER:H	2.33	0.41
2:D:106:VAL:O	2:D:116:PRO:HD2	2.20	0.41
1:B:938:SER:HB3	1:B:1014:ALA:HB1	2.02	0.41
1:A:405:LEU:HD11	1:A:477:ALA:HB1	2.02	0.41
1:B:25:LEU:O	1:B:25:LEU:HD12	2.19	0.41
1:B:352:PHE:HD2	1:B:353:LEU:CD1	2.31	0.41
1:C:72:ILE:HG21	1:C:94:PHE:HE2	1.85	0.41
1:A:189:ASN:OD1	1:A:779:TYR:CZ	2.73	0.41
1:C:564:LEU:HA	1:C:565:PRO:HD3	1.86	0.41
1:C:569:GLN:C	1:C:634:TRP:HZ2	2.24	0.41
1:B:456:MET:CG	1:B:467:TYR:HB3	2.49	0.41
1:A:487:ILE:HG22	1:A:488:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:535:LEU:HA	1:A:535:LEU:HD23	1.80	0.41
1:A:789:TRP:C	1:A:790:TYR:HD2	2.23	0.41
1:C:682:PHE:CE2	1:C:684:LEU:HD23	2.51	0.41
1:A:198:LEU:HA	1:A:198:LEU:HD23	1.86	0.41
1:C:572:PHE:CE2	1:C:631:LEU:HD21	2.56	0.41
1:B:184:MET:HE3	1:B:268:ILE:CG2	2.51	0.41
1:A:67:GLN:NE2	1:C:767:ARG:HH11	2.15	0.41
1:B:10:ILE:HD12	1:C:895:TRP:HE1	1.86	0.41
1:B:138:MET:HE3	1:B:325:TYR:CD2	2.56	0.41
1:C:454:VAL:O	1:C:455:PRO:C	2.58	0.41
1:B:876:LEU:H	1:B:876:LEU:HG	1.30	0.41
1:A:492:LEU:O	1:A:493:CYS:C	2.57	0.41
1:B:540:ARG:O	1:B:544:LEU:CD1	2.69	0.41
1:C:582:ALA:HB3	1:C:623:ASN:CB	2.48	0.41
1:B:971:ARG:O	1:B:975:ILE:HG13	2.21	0.41
1:A:949:ALA:O	1:A:953:MET:HG3	2.20	0.41
1:A:393:LEU:HD13	1:A:466:ILE:HG23	2.03	0.41
1:C:588:GLN:NE2	1:C:613:ASN:HD22	2.17	0.41
1:B:1013:THR:C	1:B:1015:THR:H	2.24	0.41
1:A:331:PRO:O	1:A:335:ILE:HG13	2.20	0.41
1:C:873:ALA:N	1:C:874:PRO:CD	2.83	0.41
1:A:731:ILE:HG12	1:A:731:ILE:H	1.67	0.41
2:D:27:ASP:OD1	2:D:61:GLU:HG3	2.21	0.41
1:A:505:HIS:CE1	1:A:973:ARG:HH12	2.39	0.41
1:B:870:GLY:C	1:B:871:ASN:OD1	2.59	0.41
1:B:498:LYS:HA	1:B:499:PRO:HD3	1.85	0.41
1:C:156:ASP:OD1	1:C:182:TYR:CG	2.74	0.41
1:A:652:THR:HA	1:A:655:PHE:CD2	2.48	0.41
1:C:36:PRO:CD	1:C:393:LEU:HD12	2.51	0.41
1:A:591:LEU:CD1	1:A:613:ASN:HD22	2.33	0.41
1:A:330:THR:N	1:A:331:PRO:CD	2.84	0.41
1:A:569:GLN:O	1:A:571:VAL:HG23	2.21	0.41
1:B:937:LEU:O	1:B:937:LEU:HD23	2.21	0.41
1:A:131:LYS:O	1:A:295:THR:OG1	2.36	0.41
1:B:303:ALA:O	1:B:307:ARG:HB2	2.21	0.41
1:B:846:GLN:O	1:B:847:LEU:C	2.58	0.41
1:A:946:VAL:HG23	1:A:1026:PHE:CD1	2.56	0.41
2:E:46:VAL:CG1	2:E:47:GLY:N	2.56	0.41
1:B:851:LEU:H	1:B:851:LEU:HD12	1.85	0.41
2:E:133:LEU:HD23	2:E:137:ALA:HA	2.02	0.41
1:B:420:MET:O	1:B:423:GLU:O	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:158:VAL:HG12	1:C:159:ALA:N	2.27	0.41
1:C:513:PHE:O	1:C:514:GLY:C	2.58	0.41
1:A:219:LEU:HD13	1:B:783:PRO:HG3	2.02	0.41
1:C:569:GLN:HE21	1:C:569:GLN:HB3	1.47	0.41
1:B:246:PHE:O	1:B:249:ILE:HG13	2.21	0.41
1:B:408:ASP:O	1:B:412:VAL:HG23	2.20	0.41
1:B:578:LEU:HD13	1:B:578:LEU:HA	1.96	0.41
1:A:913:LEU:HD23	1:A:913:LEU:HA	1.78	0.41
1:C:9:PRO:CD	1:C:10:ILE:H	2.34	0.41
1:B:693:GLU:HA	1:B:696:THR:HG22	2.03	0.41
1:A:108:GLN:HE22	1:B:113:LEU:HG	1.85	0.41
2:D:123:ILE:O	2:D:123:ILE:HG12	2.21	0.41
1:B:681:ASP:HB3	1:B:863:SER:O	2.20	0.41
1:C:180:SER:CB	1:C:274:ASN:H	2.33	0.41
2:E:121:ALA:CB	2:E:152:ILE:HG12	2.50	0.41
1:B:193:LEU:CD2	1:B:193:LEU:H	2.06	0.41
1:A:519:MET:HG3	1:A:520:PHE:H	1.84	0.41
1:B:58:GLN:CG	1:B:59:ASP:N	2.82	0.41
1:B:249:ILE:O	1:B:262:LEU:N	2.48	0.41
1:A:454:VAL:N	1:A:455:PRO:HD2	2.35	0.41
1:C:115:MET:N	1:C:116:PRO:CD	2.84	0.41
1:C:351:VAL:O	1:C:352:PHE:C	2.57	0.41
1:A:910:ILE:HD12	1:A:910:ILE:HA	1.88	0.41
1:B:187:TRP:O	1:B:266:ALA:HA	2.21	0.41
1:A:416:VAL:HG12	1:A:420:MET:HE2	2.03	0.41
1:A:991:ILE:HA	1:A:991:ILE:HD12	1.81	0.41
1:B:919:ARG:HD3	1:B:1005:THR:HG21	2.03	0.40
1:B:987:MET:N	1:B:988:PRO:CD	2.83	0.40
1:C:154:ILE:CG1	1:C:155:SER:N	2.81	0.40
1:C:632:LYS:O	1:C:633:ASP:O	2.38	0.40
1:B:537:SER:O	1:B:541:TYR:CD1	2.73	0.40
1:A:293:LEU:HD11	1:A:299:ALA:HA	2.03	0.40
2:D:112:ASN:HB3	2:D:114:PHE:CD2	2.56	0.40
1:B:582:ALA:HB3	1:B:623:ASN:HB3	2.02	0.40
1:C:80:SER:HB3	1:C:90:ILE:HG23	2.02	0.40
1:B:1021:PHE:O	1:B:1024:VAL:HB	2.20	0.40
1:C:314:GLU:C	1:C:317:PHE:CD1	2.85	0.40
1:B:869:SER:OG	1:B:870:GLY:N	2.54	0.40
1:C:571:VAL:HG23	1:C:572:PHE:N	2.37	0.40
1:A:542:LEU:O	1:A:545:TYR:N	2.48	0.40
1:B:414:GLU:HG3	1:B:977:MET:CE	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:781:MET:CE	1:B:781:MET:HA	2.51	0.40
1:A:637:ARG:N	1:A:638:PRO:HD3	2.36	0.40
1:B:543:VAL:O	1:B:547:ILE:HG13	2.21	0.40
1:A:489:THR:HB	1:A:490:PRO:HD2	1.99	0.40
1:C:568:ASP:HA	1:C:644:VAL:HG22	2.02	0.40
2:D:44:ASP:HA	2:D:45:HIS:HA	1.53	0.40
1:C:213:GLN:HE22	1:C:238:THR:HG22	1.86	0.40
1:A:150:THR:OG1	1:A:151:GLN:N	2.55	0.40
1:C:502:LYS:CG	1:C:503:GLY:N	2.77	0.40
1:A:158:VAL:HG12	1:A:289:LEU:HD21	2.03	0.40
1:A:306:ILE:HG23	1:A:306:ILE:HD13	1.71	0.40
1:C:483:LEU:O	1:C:487:ILE:HB	2.21	0.40
2:E:79:LEU:HD22	2:E:111:HIS:NE2	2.36	0.40
1:B:790:TYR:CD1	1:B:800:PRO:CA	3.04	0.40
1:C:733:GLN:HE22	1:C:743:ILE:HD13	1.85	0.40
2:D:52:HIS:NE2	2:D:83:PRO:HD3	2.37	0.40
1:A:228:GLN:C	1:B:583:THR:HG21	2.41	0.40
1:C:457:ALA:CB	1:C:468:ARG:HG2	2.49	0.40
1:B:734:GLU:O	1:B:735:LYS:C	2.58	0.40
1:A:109:ASN:O	1:A:113:LEU:HD12	2.21	0.40
1:A:306:ILE:O	1:A:307:ARG:C	2.60	0.40
1:B:104:GLN:NE2	1:B:129:VAL:O	2.54	0.40
1:B:142:VAL:HG13	1:B:321:LEU:HD11	2.03	0.40
1:B:799:VAL:CG1	1:B:804:PHE:HE1	2.35	0.40
1:B:851:LEU:HD12	1:B:851:LEU:N	2.36	0.40
1:A:531:VAL:O	1:A:532:GLY:C	2.59	0.40
1:A:390:ILE:H	1:A:390:ILE:HG12	1.73	0.40
1:A:314:GLU:HA	1:A:317:PHE:CE2	2.56	0.40
1:A:699:ARG:O	1:A:702:LEU:HB3	2.22	0.40
1:B:379:THR:O	1:B:383:LEU:HG	2.21	0.40
1:A:309:GLU:O	1:A:309:GLU:HG3	2.22	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	1004/1049 (96%)	919 (92%)	78 (8%)	7 (1%)	26	67
1	B	1022/1049 (97%)	941 (92%)	73 (7%)	8 (1%)	24	64
1	C	1038/1049 (99%)	954 (92%)	80 (8%)	4 (0%)	39	77
2	D	152/169 (90%)	141 (93%)	10 (7%)	1 (1%)	26	67
2	E	147/169 (87%)	136 (92%)	10 (7%)	1 (1%)	26	67
All	All	3363/3485 (96%)	3091 (92%)	251 (8%)	21 (1%)	30	69

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	638	PRO
1	B	671	ILE
1	C	224	PRO
1	B	1014	ALA
1	A	315	PRO
1	C	633	ASP
2	D	70	GLY
1	A	184	MET
1	B	200	PRO
1	B	747	ASN
1	B	864	TYR
1	C	36	PRO
1	B	448	VAL
2	E	50	PRO
1	A	746	ILE
1	A	852	PRO
1	A	998	GLY
1	A	560	PRO
1	B	436	GLY
1	A	988	PRO
1	C	771	VAL

5.3.2 Protein sidechains [i](#)

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	770/854 (90%)	685 (89%)	85 (11%)	8	31
1	B	772/854 (90%)	656 (85%)	116 (15%)	3	17
1	C	802/854 (94%)	695 (87%)	107 (13%)	5	21
2	D	103/133 (77%)	90 (87%)	13 (13%)	5	24
2	E	88/133 (66%)	81 (92%)	7 (8%)	15	49
All	All	2535/2828 (90%)	2207 (87%)	328 (13%)	5	23

All (328) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LEU
1	A	30	LEU
1	A	32	VAL
1	A	46	SER
1	A	48	SER
1	A	65	ILE
1	A	74	ASN
1	A	75	LEU
1	A	78	MET
1	A	79	SER
1	A	82	SER
1	A	127	VAL
1	A	140	VAL
1	A	144	ASN
1	A	180	SER
1	A	197	GLN
1	A	205	THR
1	A	235	ILE
1	A	237	GLN
1	A	241	THR
1	A	244	GLU
1	A	262	LEU
1	A	264	ASP
1	A	269	GLU
1	A	278	ILE
1	A	295	THR
1	A	306	ILE
1	A	312	LYS
1	A	321	LEU

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Mol	Chain	Res	Type
1	A	390	ILE
1	A	478	MET
1	A	486	LEU
1	A	488	LEU
1	A	489	THR
1	A	495	THR
1	A	497	LEU
1	A	498	LYS
1	A	519	MET
1	A	520	PHE
1	A	543	VAL
1	A	558	ARG
1	A	583	THR
1	A	586	ARG
1	A	587	THR
1	A	601	LYS
1	A	602	GLU
1	A	605	ASN
1	A	612	VAL
1	A	622	GLN
1	A	640	GLU
1	A	650	ARG
1	A	658	ILE
1	A	685	ILE
1	A	687	GLN
1	A	696	THR
1	A	717	ARG
1	A	723	ASP
1	A	754	TRP
1	A	757	SER
1	A	758	TYR
1	A	775	SER
1	A	780	ARG
1	A	795	ASP
1	A	807	SER
1	A	811	TYR
1	A	813	SER
1	A	815	ARG
1	A	822	LEU
1	A	823	PRO
1	A	830	GLN
1	A	847	LEU

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Mol	Chain	Res	Type
1	A	860	THR
1	A	893	GLU
1	A	894	SER
1	A	900	SER
1	A	917	THR
1	A	932	LEU
1	A	935	ILE
1	A	953	MET
1	A	956	GLU
1	A	961	ILE
1	A	971	ARG
1	A	972	LEU
1	A	976	LEU
1	A	978	THR
1	B	21	LEU
1	B	46	SER
1	B	49	TYR
1	B	53	ASP
1	B	58	GLN
1	B	60	THR
1	B	75	LEU
1	B	79	SER
1	B	80	SER
1	B	82	SER
1	B	87	THR
1	B	99	ASP
1	B	108	GLN
1	B	111	LEU
1	B	117	LEU
1	B	128	SER
1	B	143	ILE
1	B	150	THR
1	B	153	ASP
1	B	161	ASN
1	B	162	MET
1	B	163	LYS
1	B	166	ILE
1	B	170	SER
1	B	189	ASN
1	B	193	LEU
1	B	197	GLN
1	B	207	ILE

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Mol	Chain	Res	Type
1	B	218	GLN
1	B	229	GLN
1	B	230	LEU
1	B	231	ASN
1	B	233	SER
1	B	235	ILE
1	B	237	GLN
1	B	250	LEU
1	B	253	VAL
1	B	259	ARG
1	B	274	ASN
1	B	278	ILE
1	B	284	GLN
1	B	289	LEU
1	B	306	ILE
1	B	321	LEU
1	B	329	THR
1	B	361	ASN
1	B	365	THR
1	B	366	LEU
1	B	369	THR
1	B	377	LEU
1	B	382	VAL
1	B	399	VAL
1	B	405	LEU
1	B	408	ASP
1	B	423	GLU
1	B	425	LEU
1	B	462	SER
1	B	493	CYS
1	B	495	THR
1	B	497	LEU
1	B	507	GLU
1	B	513	PHE
1	B	519	MET
1	B	540	ARG
1	B	555	LEU
1	B	557	VAL
1	B	566	ASP
1	B	577	GLN
1	B	587	THR
1	B	623	ASN

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Mol	Chain	Res	Type
1	B	628	PHE
1	B	649	MET
1	B	658	ILE
1	B	669	PRO
1	B	671	ILE
1	B	674	LEU
1	B	687	GLN
1	B	695	LEU
1	B	705	GLU
1	B	712	MET
1	B	713	LEU
1	B	714	THR
1	B	717	ARG
1	B	723	ASP
1	B	731	ILE
1	B	733	GLN
1	B	757	SER
1	B	759	VAL
1	B	763	ILE
1	B	765	ARG
1	B	771	VAL
1	B	780	ARG
1	B	808	ARG
1	B	815	ARG
1	B	822	LEU
1	B	824	SER
1	B	825	MET
1	B	844	MET
1	B	853	THR
1	B	859	TRP
1	B	862	MET
1	B	867	ARG
1	B	871	ASN
1	B	874	PRO
1	B	876	LEU
1	B	888	LEU
1	B	894	SER
1	B	919	ARG
1	B	968	VAL
1	B	971	ARG
1	B	972	LEU
1	B	987	MET

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Mol	Chain	Res	Type
1	B	989	LEU
1	B	990	VAL
1	B	991	ILE
1	B	1028	VAL
1	C	4	PHE
1	C	11	PHE
1	C	49	TYR
1	C	56	THR
1	C	58	GLN
1	C	81	ASN
1	C	84	SER
1	C	85	THR
1	C	88	VAL
1	C	98	THR
1	C	127	VAL
1	C	133	SER
1	C	143	ILE
1	C	145	THR
1	C	148	THR
1	C	150	THR
1	C	154	ILE
1	C	157	TYR
1	C	161	ASN
1	C	167	SER
1	C	182	TYR
1	C	197	GLN
1	C	218	GLN
1	C	226	LYS
1	C	233	SER
1	C	241	THR
1	C	263	ARG
1	C	268	ILE
1	C	278	ILE
1	C	289	LEU
1	C	298	ASN
1	C	310	LEU
1	C	321	LEU
1	C	325	TYR
1	C	329	THR
1	C	372	VAL
1	C	404	LEU
1	C	429	GLU

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Mol	Chain	Res	Type
1	C	435	MET
1	C	437	GLN
1	C	452	VAL
1	C	466	ILE
1	C	473	THR
1	C	497	LEU
1	C	505	HIS
1	C	507	GLU
1	C	510	LYS
1	C	512	PHE
1	C	528	THR
1	C	542	LEU
1	C	561	SER
1	C	566	ASP
1	C	567	GLU
1	C	569	GLN
1	C	571	VAL
1	C	575	MET
1	C	587	THR
1	C	604	ASN
1	C	623	ASN
1	C	626	ILE
1	C	631	LEU
1	C	640	GLU
1	C	641	GLU
1	C	674	LEU
1	C	684	LEU
1	C	690	LEU
1	C	695	LEU
1	C	712	MET
1	C	715	SER
1	C	717	ARG
1	C	721	LEU
1	C	723	ASP
1	C	730	ASP
1	C	732	ASP
1	C	739	LEU
1	C	742	SER
1	C	743	ILE
1	C	744	ASN
1	C	749	THR
1	C	757	SER

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Mol	Chain	Res	Type
1	C	774	MET
1	C	782	LEU
1	C	805	SER
1	C	815	ARG
1	C	830	GLN
1	C	862	MET
1	C	869	SER
1	C	875	SER
1	C	876	LEU
1	C	879	ILE
1	C	880	SER
1	C	891	LEU
1	C	910	ILE
1	C	917	THR
1	C	922	THR
1	C	924	ASP
1	C	947	GLU
1	C	951	ASP
1	C	956	GLU
1	C	960	LEU
1	C	976	LEU
1	C	978	THR
1	C	979	SER
1	C	990	VAL
1	C	993	THR
1	C	1011	MET
1	C	1035	ARG
2	D	18	LEU
2	D	27	ASP
2	D	41	ASN
2	D	45	HIS
2	D	46	VAL
2	D	53	LEU
2	D	73	VAL
2	D	77	ASP
2	D	78	SER
2	D	83	PRO
2	D	84	LEU
2	D	111	HIS
2	D	129	VAL
2	E	99	LEU
2	E	102	ASN

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Mol	Chain	Res	Type
2	E	145	PHE
2	E	152	ILE
2	E	154	ILE
2	E	155	ASP
2	E	156	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (79) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	67	GLN
1	A	123	GLN
1	A	176	GLN
1	A	181	GLN
1	A	189	ASN
1	A	191	ASN
1	A	194	ASN
1	A	197	GLN
1	A	231	ASN
1	A	274	ASN
1	A	284	GLN
1	A	298	ASN
1	A	361	ASN
1	A	577	GLN
1	A	613	ASN
1	A	687	GLN
1	A	700	ASN
1	A	737	GLN
1	A	760	ASN
1	A	1000	GLN
1	A	1001	ASN
1	B	81	ASN
1	B	108	GLN
1	B	123	GLN
1	B	124	GLN
1	B	125	GLN
1	B	161	ASN
1	B	176	GLN
1	B	197	GLN
1	B	218	GLN
1	B	254	ASN
1	B	284	GLN

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Mol	Chain	Res	Type
1	B	361	ASN
1	B	569	GLN
1	B	577	GLN
1	B	592	ASN
1	B	596	HIS
1	B	605	ASN
1	B	623	ASN
1	B	687	GLN
1	B	701	GLN
1	B	726	GLN
1	B	733	GLN
1	B	747	ASN
1	B	760	ASN
1	B	830	GLN
1	B	923	ASN
1	B	941	ASN
1	C	34	GLN
1	C	67	GLN
1	C	68	ASN
1	C	104	GLN
1	C	125	GLN
1	C	144	ASN
1	C	181	GLN
1	C	194	ASN
1	C	197	GLN
1	C	213	GLN
1	C	298	ASN
1	C	415	ASN
1	C	525	HIS
1	C	569	GLN
1	C	588	GLN
1	C	604	ASN
1	C	623	ASN
1	C	701	GLN
1	C	719	ASN
1	C	747	ASN
1	C	760	ASN
1	C	830	GLN
1	C	865	GLN
2	D	45	HIS
2	D	52	HIS
2	D	111	HIS

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Mol	Chain	Res	Type
2	D	118	HIS
2	E	69	ASN
2	E	118	HIS
2	E	156	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	FME	A	1	1	8,9,10	0.26	0	6,9,11	0.94	0
1	FME	B	1	1	8,9,10	0.47	0	6,9,11	1.17	1 (16%)
1	FME	C	1	1	8,9,10	0.56	0	6,9,11	0.78	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	FME	A	1	1	-	1/6/9/11	0/0/0/0
1	FME	B	1	1	-	1/6/9/11	0/0/0/0
1	FME	C	1	1	-	0/6/9/11	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	1	FME	O-C-CA	-2.04	120.06	125.44

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	1	FME	O1-CN-N-CA
1	A	1	FME	O1-CN-N-CA

There are no ring outliers.

3 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	FME	5	0
1	B	1	FME	11	0
1	C	1	FME	6	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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 ²)	Q<0.9
1	A	1007/1049 (95%)	-0.32	8 (0%) 87 88	30, 72, 139, 274	1 (0%)
1	B	1027/1049 (97%)	-0.26	18 (1%) 71 70	26, 71, 142, 330	0
1	C	1037/1049 (98%)	-0.33	15 (1%) 78 79	26, 63, 126, 198	0
2	D	154/169 (91%)	0.16	10 (6%) 22 22	30, 85, 134, 207	1 (0%)
2	E	148/169 (87%)	1.31	41 (27%) 1 1	70, 147, 256, 372	1 (0%)
All	All	3373/3485 (96%)	-0.21	92 (2%) 58 57	26, 71, 152, 372	3 (0%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	32	ILE	5.4
1	B	134	SER	5.4
2	E	36	ASN	5.3
2	E	35	ALA	5.2
2	D	139	VAL	5.1
1	B	675	GLY	5.0
1	B	509	LYS	4.7
2	E	145	PHE	4.6
2	E	144	LYS	4.2
2	E	162	ALA	4.1
2	E	158	ASN	4.0
2	D	150	PHE	3.9
2	E	33	LEU	3.9
1	C	501	ALA	3.8
2	E	124	GLY	3.8
1	B	216	ALA	3.7
2	E	34	MET	3.6
2	E	38	ALA	3.6
2	E	82	THR	3.6
1	A	833	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	859	TRP	3.4
2	D	158	ASN	3.4
2	D	126	LEU	3.4
2	E	111	HIS	3.3
2	E	31	ARG	3.3
2	E	163	GLU	3.3
2	D	140	ASN	3.3
2	E	137	ALA	3.3
2	E	114	PHE	3.2
1	B	407	ASP	3.1
2	E	159	GLU	3.0
2	D	141	ALA	3.0
1	C	730	ASP	3.0
1	C	701	GLN	3.0
2	E	37	GLY	2.9
2	E	76	ASP	2.9
1	C	425	LEU	2.8
2	D	148	THR	2.8
2	E	117	LEU	2.8
2	E	166	GLN	2.8
1	B	361	ASN	2.7
1	A	254	ASN	2.7
1	B	674	LEU	2.7
2	E	66	LEU	2.7
1	C	424	GLY	2.7
1	B	628	PHE	2.6
1	A	860	THR	2.6
1	C	851	LEU	2.5
1	A	836	SER	2.5
1	A	872	GLN	2.5
1	A	678	THR	2.5
1	B	858	ASP	2.5
2	E	143	ASP	2.4
2	D	138	ASP	2.4
1	C	804	PHE	2.4
1	B	326	PRO	2.4
1	C	423	GLU	2.4
2	E	154	ILE	2.3
1	C	502	LYS	2.3
2	E	99	LEU	2.3
1	B	996	GLY	2.3
2	E	64	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	771	VAL	2.3
2	E	69	ASN	2.3
2	E	75	ALA	2.2
2	E	54	ALA	2.2
2	D	161	LEU	2.2
1	C	791	VAL	2.2
2	D	137	ALA	2.2
2	E	141	ALA	2.2
2	E	48	TRP	2.2
2	E	126	LEU	2.2
2	E	45	HIS	2.2
1	B	617	PHE	2.2
1	C	811	TYR	2.2
1	B	599	LEU	2.2
1	C	193	LEU	2.2
2	E	112	ASN	2.2
2	E	122	ASN	2.2
2	E	87	ALA	2.1
1	C	806	SER	2.1
1	B	501	ALA	2.1
1	B	848	ALA	2.1
1	A	959	GLY	2.1
1	C	506	GLY	2.1
1	C	513	PHE	2.1
2	E	30	VAL	2.1
1	A	859	TRP	2.0
1	B	511	GLY	2.0
2	E	119	LEU	2.0
2	E	84	LEU	2.0
2	E	155	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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, 95th 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(Å ²)	Q<0.9
1	FME	A	1	10/11	0.87	0.18	-	87,88,108,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	FME	B	1	10/11	0.85	0.24	-	68,71,78,80	0
1	FME	C	1	10/11	0.94	0.13	-	62,64,181,181	0

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.