



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:37 PM GMT

PDB ID : 1L1F
Title : Structure of human glutamate dehydrogenase-apo form
Authors : Smith, T.J.; Schmidt, T.; Fang, J.; Wu, J.; Siuzdak, G.; Stanley, C.A.
Deposited on : 2002-02-15
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

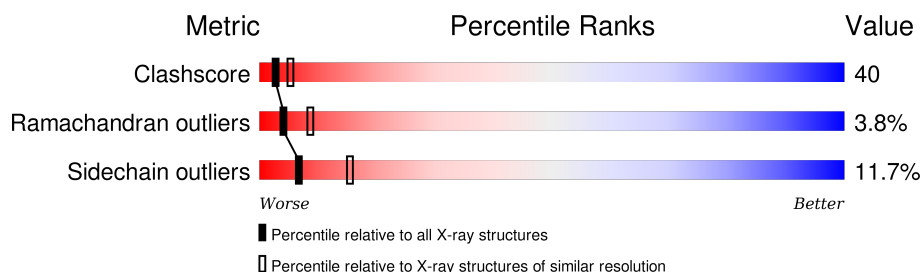
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	505	
1	B	505	
1	C	505	
1	D	505	
1	E	505	
1	F	505	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 23244 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 Glutamate Dehydrogenase 1.

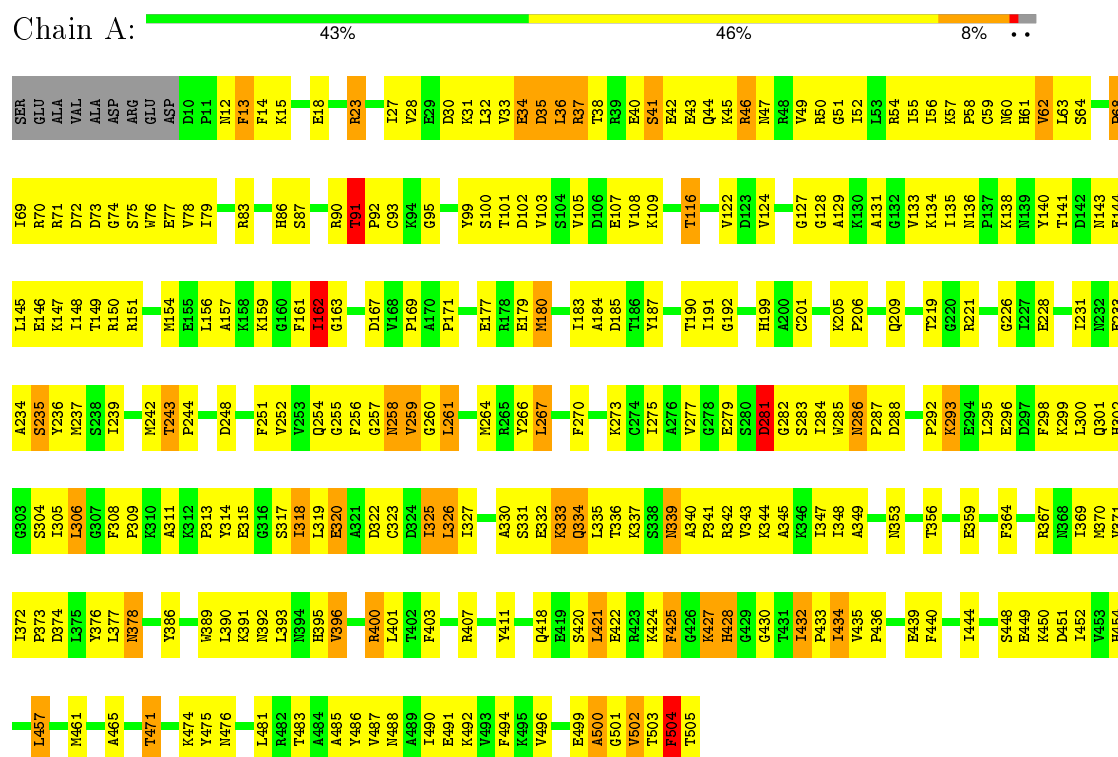
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total	C	N	O	S	0	0	0
			3874	2450	679	726	19			
1	B	496	Total	C	N	O	S	0	0	0
			3874	2450	679	726	19			
1	C	496	Total	C	N	O	S	0	0	0
			3874	2450	679	726	19			
1	D	496	Total	C	N	O	S	0	0	0
			3874	2450	679	726	19			
1	E	496	Total	C	N	O	S	0	0	0
			3874	2450	679	726	19			
1	F	496	Total	C	N	O	S	0	0	0
			3874	2450	679	726	19			

3 Residue-property plots

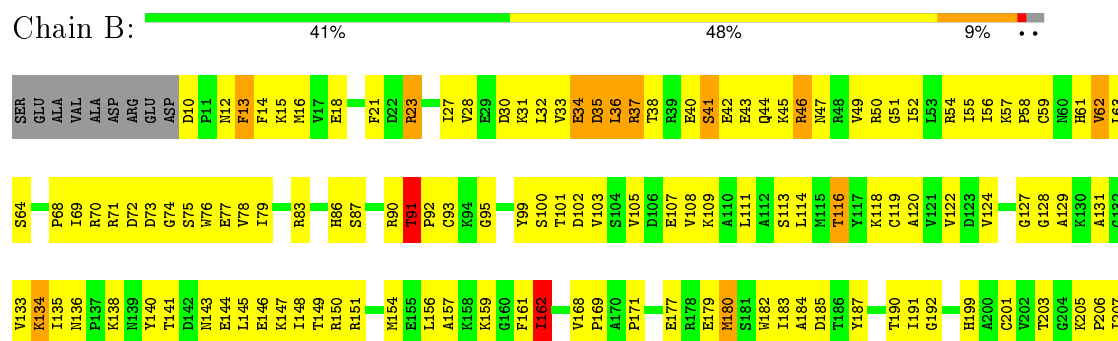
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

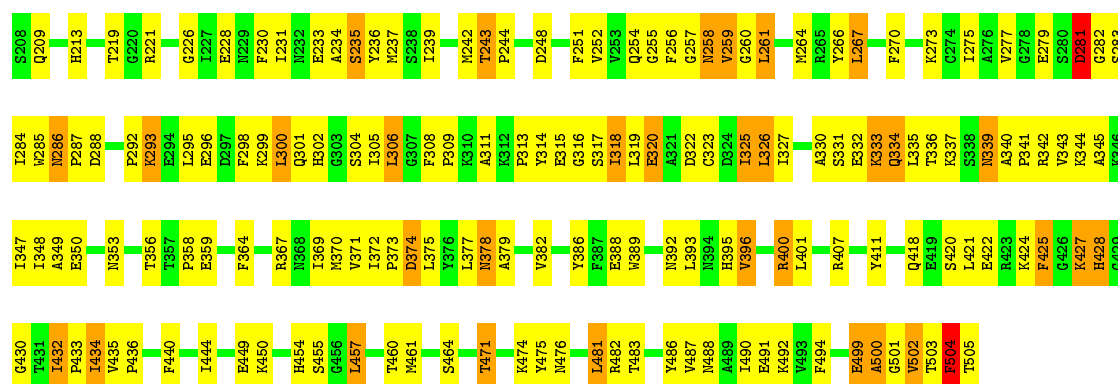
Note EDS was not executed.

• Molecule 1: Glutamate Dehydrogenase 1



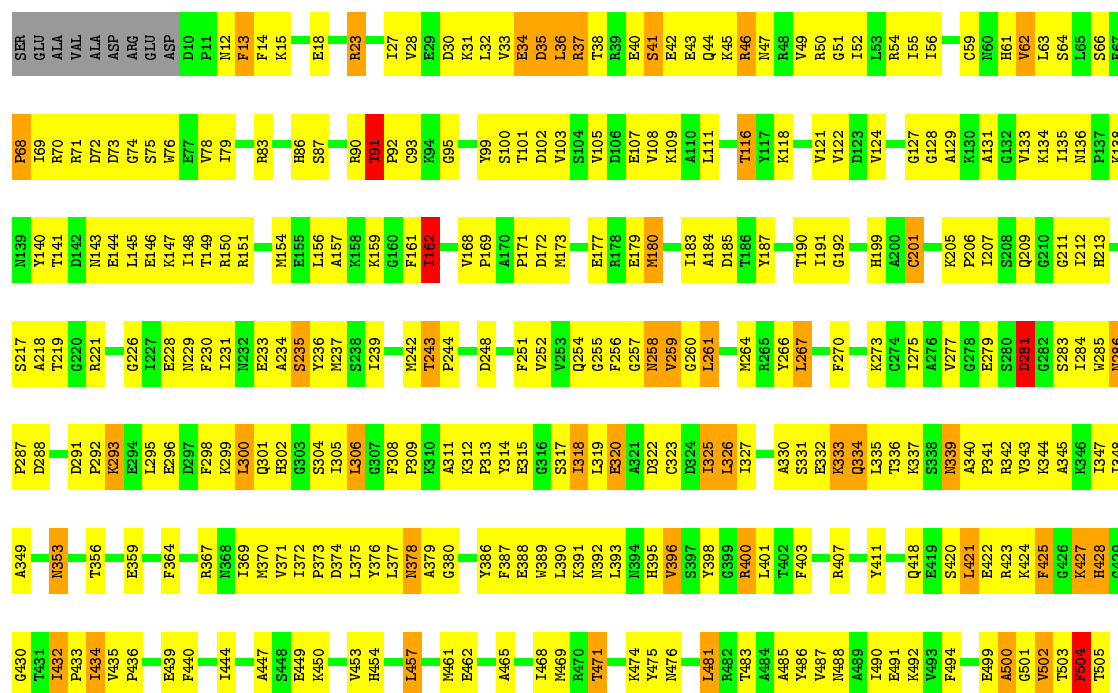
• Molecule 1: Glutamate Dehydrogenase 1





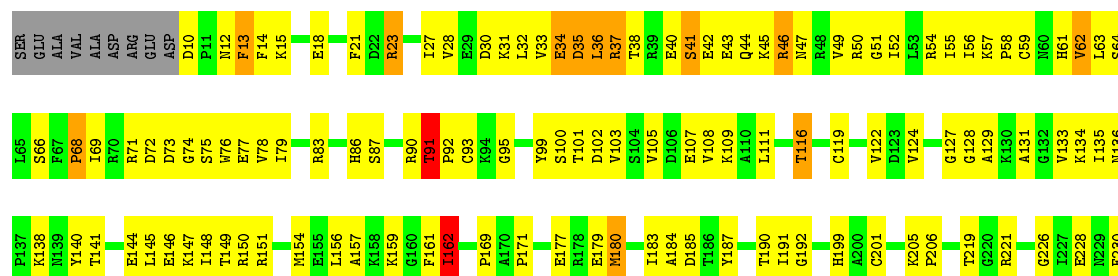
• Molecule 1: Glutamate Dehydrogenase 1

Chain C: 40% 49% 9% ..



• Molecule 1: Glutamate Dehydrogenase 1

Chain D: 43% 46% 9% ..





A234	G303	V371	H454
S235	S304	I372	
Y236	I305	P373	L457
M237	I306	D374	
	G307	L375	E462
S238	F308	Y376	R463
I239	P309	L377	S464
	K310	K378	A465
M242	A311	A379	
T243	K312		T471
P244	P313	Y386	
	Y314		K474
	E315	K389	Y475
	G316	L390	M476
P251	S317	K391	
V252	I318	K392	L481
V253	I319	L393	R482
Q254	E320	K394	T483
Q255	A321	K395	A484
P256	D322	V396	A485
Q257	C323		Y486
M258	D324	R400	V487
V259	I325	L401	M488
G260	L326	T402	A489
L261	I327	F403	I490
	P328		E491
M264	A329	R407	
R265	A330	Y411	V493
Y266	S331		F494
L267	E332		
		Q418	E499
F270	K333	E419	A500
	Q334	S420	G501
K273	L335	L421	V502
C274	T336	E422	T503
I275	K337	R423	F504
	S338	K424	T505
A276	M339	F425	
V277	A340	G426	
G278	P341	K427	
E279	R342	H428	
S280	V343	G429	
D281	K344	Q430	
S283	A345	T431	
I284	K346	I432	
M285	I347	P433	
I286	I348	T434	
P287	A349	V435	
D288		P436	
	M353		
		E439	
P292	T356	F440	
K293			
E294	E359	I444	
L295			
E296	F364	A447	
D297		S448	
F298	R367	E449	
K299	M368	K450	
L300	I369		
Q301	M370		
H302			

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	97.80 Å 98.80 Å 124.20 Å 86.26° 70.28° 60.34°	Depositor
Resolution (Å)	8.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	O	Depositor
R, R_{free}	0.262 , 0.302	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	23244	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.62	1/3958 (0.0%)	0.82	3/5340 (0.1%)
1	B	0.63	1/3958 (0.0%)	0.82	5/5340 (0.1%)
1	C	0.65	2/3958 (0.1%)	0.82	4/5340 (0.1%)
1	D	0.62	1/3958 (0.0%)	0.82	5/5340 (0.1%)
1	E	0.62	1/3958 (0.0%)	0.82	4/5340 (0.1%)
1	F	0.62	2/3958 (0.1%)	0.82	5/5340 (0.1%)
All	All	0.63	8/23748 (0.0%)	0.82	26/32040 (0.1%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	59	CYS	CB-SG	8.91	1.97	1.82
1	C	59	CYS	CB-SG	8.33	1.96	1.82
1	A	59	CYS	CB-SG	7.79	1.95	1.82
1	B	59	CYS	CB-SG	7.48	1.95	1.82
1	F	201	CYS	CB-SG	-7.10	1.70	1.82
1	E	59	CYS	CB-SG	6.18	1.92	1.82
1	C	201	CYS	CB-SG	-6.09	1.71	1.82
1	F	59	CYS	CB-SG	5.80	1.92	1.82

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	504	PHE	N-CA-C	-7.28	91.34	111.00
1	C	504	PHE	N-CA-C	-7.28	91.35	111.00
1	B	504	PHE	N-CA-C	-7.27	91.38	111.00
1	F	504	PHE	N-CA-C	-7.25	91.43	111.00
1	D	504	PHE	N-CA-C	-7.19	91.60	111.00
1	A	504	PHE	N-CA-C	-7.17	91.64	111.00
1	D	326	LEU	CA-CB-CG	6.70	130.71	115.30
1	C	326	LEU	CA-CB-CG	6.64	130.58	115.30
1	E	326	LEU	CA-CB-CG	6.63	130.55	115.30
1	F	326	LEU	CA-CB-CG	6.63	130.54	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	LEU	CA-CB-CG	6.60	130.47	115.30
1	B	326	LEU	CA-CB-CG	6.58	130.43	115.30
1	B	91	THR	N-CA-C	6.03	127.29	111.00
1	C	91	THR	N-CA-C	6.02	127.25	111.00
1	F	91	THR	N-CA-C	5.93	127.03	111.00
1	A	91	THR	N-CA-C	5.87	126.85	111.00
1	E	91	THR	N-CA-C	5.86	126.83	111.00
1	D	91	THR	N-CA-C	5.84	126.77	111.00
1	F	66	SER	N-CA-C	-5.11	97.21	111.00
1	B	316	GLY	N-CA-C	-5.09	100.38	113.10
1	E	66	SER	N-CA-C	-5.08	97.27	111.00
1	D	66	SER	N-CA-C	-5.06	97.35	111.00
1	F	316	GLY	N-CA-C	-5.05	100.47	113.10
1	B	374	ASP	CB-CG-OD2	5.04	122.84	118.30
1	D	316	GLY	N-CA-C	-5.03	100.53	113.10
1	C	66	SER	N-CA-C	-5.01	97.48	111.00

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	3874	0	3841	316	0
1	B	3874	0	3841	333	0
1	C	3874	0	3841	366	0
1	D	3874	0	3841	326	0
1	E	3874	0	3841	341	0
1	F	3874	0	3841	324	0
All	All	23244	0	23046	1865	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 40.

All (1865) 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:C:285:TRP:HB2	1:C:314:TYR:HB2	1.31	1.13
1:E:285:TRP:HB2	1:E:314:TYR:HB2	1.30	1.12
1:F:285:TRP:HB2	1:F:314:TYR:HB2	1.29	1.09
1:A:285:TRP:HB2	1:A:314:TYR:HB2	1.30	1.08
1:B:285:TRP:HB2	1:B:314:TYR:HB2	1.29	1.08
1:D:285:TRP:HB2	1:D:314:TYR:HB2	1.29	1.06
1:C:427:LYS:HD3	1:C:430:GLY:HA3	1.45	0.99
1:E:427:LYS:HD3	1:E:430:GLY:HA3	1.45	0.98
1:A:99:TYR:OH	1:A:149:THR:HG22	1.63	0.98
1:F:427:LYS:HD3	1:F:430:GLY:HA3	1.46	0.98
1:A:427:LYS:HD3	1:A:430:GLY:HA3	1.46	0.97
1:D:427:LYS:HD3	1:D:430:GLY:HA3	1.47	0.96
1:C:99:TYR:OH	1:C:149:THR:HG22	1.65	0.95
1:B:427:LYS:HD3	1:B:430:GLY:HA3	1.46	0.94
1:E:99:TYR:OH	1:E:149:THR:HG22	1.69	0.93
1:B:99:TYR:OH	1:B:149:THR:HG22	1.68	0.93
1:F:99:TYR:OH	1:F:149:THR:HG22	1.68	0.93
1:C:61:HIS:HD2	1:F:159:LYS:HE3	1.33	0.93
1:E:41:SER:HA	1:E:46:ARG:HD2	1.50	0.93
1:F:41:SER:HA	1:F:46:ARG:HD2	1.50	0.92
1:A:40:GLU:HG3	1:A:46:ARG:HH12	1.35	0.92
1:D:41:SER:HA	1:D:46:ARG:HD2	1.50	0.92
1:C:159:LYS:HE3	1:F:61:HIS:HD2	1.35	0.92
1:B:41:SER:HA	1:B:46:ARG:HD2	1.51	0.92
1:F:40:GLU:HG3	1:F:46:ARG:HH12	1.35	0.92
1:E:327:ILE:HG22	1:E:349:ALA:HB3	1.53	0.91
1:C:40:GLU:HG3	1:C:46:ARG:HH12	1.35	0.91
1:C:41:SER:HA	1:C:46:ARG:HD2	1.50	0.91
1:A:327:ILE:HG22	1:A:349:ALA:HB3	1.53	0.91
1:B:327:ILE:HG22	1:B:349:ALA:HB3	1.53	0.91
1:A:41:SER:HA	1:A:46:ARG:HD2	1.51	0.90
1:D:99:TYR:OH	1:D:149:THR:HG22	1.67	0.90
1:E:40:GLU:HG3	1:E:46:ARG:HH12	1.36	0.90
1:E:83:ARG:HD2	1:E:131:ALA:HB2	1.54	0.90
1:A:83:ARG:HD2	1:A:131:ALA:HB2	1.53	0.89
1:B:40:GLU:HG3	1:B:46:ARG:HH12	1.36	0.89
1:F:83:ARG:HD2	1:F:131:ALA:HB2	1.53	0.89
1:F:327:ILE:HG22	1:F:349:ALA:HB3	1.53	0.89
1:C:83:ARG:HD2	1:C:131:ALA:HB2	1.55	0.89
1:D:327:ILE:HG22	1:D:349:ALA:HB3	1.53	0.89
1:D:40:GLU:HG3	1:D:46:ARG:HH12	1.35	0.89
1:E:427:LYS:HA	1:E:427:LYS:HE2	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:427:LYS:HE2	1:F:427:LYS:HA	1.55	0.88
1:D:83:ARG:HD2	1:D:131:ALA:HB2	1.54	0.88
1:C:427:LYS:HE2	1:C:427:LYS:HA	1.54	0.88
1:D:427:LYS:HE2	1:D:427:LYS:HA	1.54	0.87
1:B:83:ARG:HD2	1:B:131:ALA:HB2	1.54	0.87
1:D:325:ILE:HG22	1:D:347:ILE:HB	1.56	0.87
1:B:427:LYS:HA	1:B:427:LYS:HE2	1.55	0.87
1:F:325:ILE:HG22	1:F:347:ILE:HB	1.56	0.87
1:B:61:HIS:HD2	1:D:159:LYS:HE3	1.39	0.87
1:C:325:ILE:HG22	1:C:347:ILE:HB	1.57	0.86
1:A:325:ILE:HG22	1:A:347:ILE:HB	1.56	0.86
1:C:159:LYS:HE3	1:F:61:HIS:CD2	2.11	0.86
1:C:327:ILE:HG22	1:C:349:ALA:HB3	1.54	0.86
1:A:427:LYS:HA	1:A:427:LYS:HE2	1.55	0.86
1:A:159:LYS:HE3	1:E:61:HIS:HD2	1.41	0.85
1:E:325:ILE:HG22	1:E:347:ILE:HB	1.56	0.85
1:D:145:LEU:O	1:D:149:THR:HG23	1.76	0.85
1:C:145:LEU:O	1:C:149:THR:HG23	1.77	0.85
1:B:418:GLN:HB2	1:B:433:PRO:HD2	1.60	0.84
1:C:61:HIS:CD2	1:F:159:LYS:HE3	2.11	0.84
1:F:145:LEU:O	1:F:149:THR:HG23	1.76	0.84
1:B:159:LYS:HE3	1:D:61:HIS:HD2	1.40	0.84
1:D:146:GLU:O	1:D:150:ARG:HG3	1.77	0.84
1:C:376:TYR:OH	1:C:465:ALA:HB2	1.77	0.83
1:E:486:TYR:O	1:E:490:ILE:HG12	1.79	0.82
1:C:13:PHE:HD1	1:C:14:PHE:N	1.77	0.82
1:E:146:GLU:O	1:E:150:ARG:HG3	1.79	0.82
1:D:147:LYS:HD2	1:D:151:ARG:HH21	1.44	0.82
1:E:418:GLN:HB2	1:E:433:PRO:HD2	1.61	0.82
1:F:13:PHE:HD1	1:F:14:PHE:N	1.77	0.82
1:A:418:GLN:HB2	1:A:433:PRO:HD2	1.62	0.82
1:E:147:LYS:HD2	1:E:151:ARG:HH21	1.45	0.82
1:B:13:PHE:HD1	1:B:14:PHE:N	1.78	0.82
1:A:145:LEU:O	1:A:149:THR:HG23	1.80	0.82
1:B:147:LYS:HD2	1:B:151:ARG:HH21	1.45	0.82
1:B:325:ILE:HG22	1:B:347:ILE:HB	1.58	0.82
1:D:13:PHE:HD1	1:D:14:PHE:N	1.77	0.82
1:B:86:HIS:CD2	1:B:116:THR:HG21	2.14	0.82
1:C:229:ASN:OD1	1:C:462:GLU:HG3	1.78	0.82
1:D:486:TYR:O	1:D:490:ILE:HG12	1.79	0.82
1:E:13:PHE:HD1	1:E:14:PHE:N	1.78	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:86:HIS:CD2	1:E:116:THR:HG21	2.14	0.82
1:F:147:LYS:HD2	1:F:151:ARG:HH21	1.45	0.81
1:F:486:TYR:O	1:F:490:ILE:HG12	1.80	0.81
1:E:145:LEU:O	1:E:149:THR:HG23	1.79	0.81
1:B:145:LEU:O	1:B:149:THR:HG23	1.79	0.81
1:C:38:THR:HG23	1:C:41:SER:HB3	1.62	0.81
1:E:38:THR:HG23	1:E:41:SER:HB3	1.62	0.81
1:A:13:PHE:HD1	1:A:14:PHE:N	1.77	0.81
1:F:146:GLU:O	1:F:150:ARG:HG3	1.79	0.81
1:A:38:THR:HG23	1:A:41:SER:HB3	1.63	0.81
1:A:146:GLU:O	1:A:150:ARG:HG3	1.81	0.81
1:D:418:GLN:HB2	1:D:433:PRO:HD2	1.61	0.81
1:F:38:THR:HG23	1:F:41:SER:HB3	1.63	0.81
1:A:86:HIS:CD2	1:A:116:THR:HG21	2.16	0.81
1:A:486:TYR:O	1:A:490:ILE:HG12	1.80	0.81
1:C:116:THR:HG22	1:C:128:GLY:HA3	1.63	0.81
1:C:486:TYR:O	1:C:490:ILE:HG12	1.81	0.80
1:A:61:HIS:HD2	1:E:159:LYS:HE3	1.47	0.80
1:D:38:THR:HG23	1:D:41:SER:HB3	1.63	0.80
1:B:486:TYR:O	1:B:490:ILE:HG12	1.81	0.80
1:C:147:LYS:HD2	1:C:151:ARG:HH21	1.45	0.80
1:F:63:LEU:HD22	1:F:161:PHE:CD2	2.16	0.80
1:D:86:HIS:CD2	1:D:116:THR:HG21	2.17	0.80
1:F:418:GLN:HB2	1:F:433:PRO:HD2	1.63	0.80
1:F:86:HIS:CD2	1:F:116:THR:HG21	2.16	0.80
1:A:147:LYS:HD2	1:A:151:ARG:HH21	1.45	0.80
1:A:116:THR:HG22	1:A:128:GLY:HA3	1.64	0.80
1:B:146:GLU:O	1:B:150:ARG:HG3	1.82	0.80
1:C:146:GLU:O	1:C:150:ARG:HG3	1.82	0.80
1:C:63:LEU:HD22	1:C:161:PHE:CD2	2.17	0.80
1:B:285:TRP:CB	1:B:314:TYR:HB2	2.11	0.79
1:D:285:TRP:CB	1:D:314:TYR:HB2	2.12	0.79
1:B:38:THR:HG23	1:B:41:SER:HB3	1.63	0.79
1:E:63:LEU:HD22	1:E:161:PHE:CD2	2.17	0.79
1:B:77:GLU:HA	1:D:54:ARG:NH1	1.97	0.79
1:D:505:THR:HG23	1:E:185:ASP:OD1	1.82	0.79
1:F:221:ARG:HD2	1:F:454:HIS:NE2	1.97	0.79
1:E:285:TRP:CB	1:E:314:TYR:HB2	2.12	0.79
1:C:86:HIS:CD2	1:C:116:THR:HG21	2.16	0.79
1:C:281:ASP:HB2	1:C:306:LEU:HD11	1.63	0.79
1:D:281:ASP:HB2	1:D:306:LEU:HD11	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:ASP:HB2	1:A:306:LEU:HD11	1.64	0.79
1:B:281:ASP:HB2	1:B:306:LEU:HD11	1.64	0.78
1:D:63:LEU:HD22	1:D:161:PHE:CD2	2.19	0.78
1:A:13:PHE:HD1	1:A:14:PHE:H	1.32	0.78
1:F:116:THR:HG22	1:F:128:GLY:HA3	1.66	0.78
1:F:281:ASP:HB2	1:F:306:LEU:HD11	1.65	0.78
1:B:63:LEU:HD22	1:B:161:PHE:CD2	2.18	0.78
1:C:418:GLN:HB2	1:C:433:PRO:HD2	1.64	0.78
1:B:61:HIS:CD2	1:D:159:LYS:HE3	2.19	0.77
1:D:116:THR:HG22	1:D:128:GLY:HA3	1.66	0.77
1:C:221:ARG:HD2	1:C:454:HIS:CD2	2.20	0.77
1:A:71:ARG:HH11	1:A:71:ARG:HB3	1.50	0.77
1:D:13:PHE:HD1	1:D:14:PHE:H	1.32	0.77
1:B:13:PHE:HD1	1:B:14:PHE:H	1.32	0.77
1:A:285:TRP:CB	1:A:314:TYR:HB2	2.13	0.77
1:E:116:THR:HG22	1:E:128:GLY:HA3	1.67	0.76
1:A:63:LEU:HD22	1:A:161:PHE:CD2	2.21	0.76
1:D:71:ARG:HH11	1:D:71:ARG:HB3	1.51	0.76
1:E:71:ARG:HB3	1:E:71:ARG:HH11	1.50	0.76
1:E:340:ALA:HB3	1:E:341:PRO:HD3	1.67	0.76
1:C:504:PHE:CZ	1:F:151:ARG:NH2	2.52	0.76
1:B:116:THR:HG22	1:B:128:GLY:HA3	1.65	0.76
1:E:281:ASP:HB2	1:E:306:LEU:HD11	1.64	0.76
1:B:340:ALA:HB3	1:B:341:PRO:HD3	1.66	0.76
1:F:13:PHE:HD1	1:F:14:PHE:H	1.31	0.76
1:C:285:TRP:CB	1:C:314:TYR:HB2	2.13	0.75
1:A:159:LYS:HE3	1:E:61:HIS:CD2	2.20	0.75
1:E:13:PHE:HD1	1:E:14:PHE:H	1.32	0.75
1:B:71:ARG:HH11	1:B:71:ARG:HB3	1.51	0.75
1:C:71:ARG:HB3	1:C:71:ARG:HH11	1.51	0.75
1:B:159:LYS:HE3	1:D:61:HIS:CD2	2.22	0.75
1:D:340:ALA:HB3	1:D:341:PRO:HD3	1.68	0.75
1:E:221:ARG:HD2	1:E:454:HIS:NE2	2.01	0.75
1:F:434:ILE:O	1:F:436:PRO:HD3	1.87	0.74
1:F:285:TRP:CB	1:F:314:TYR:HB2	2.12	0.74
1:A:340:ALA:HB3	1:A:341:PRO:HD3	1.69	0.74
1:C:13:PHE:HD1	1:C:14:PHE:H	1.32	0.74
1:F:71:ARG:HB3	1:F:71:ARG:HH11	1.52	0.74
1:C:434:ILE:O	1:C:436:PRO:HD3	1.88	0.74
1:A:434:ILE:O	1:A:436:PRO:HD3	1.87	0.74
1:F:340:ALA:HB3	1:F:341:PRO:HD3	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:VAL:HG11	1:E:76:TRP:CD1	2.23	0.74
1:C:340:ALA:HB3	1:C:341:PRO:HD3	1.69	0.73
1:E:243:THR:N	1:E:244:PRO:HD3	2.03	0.73
1:A:251:PHE:HB3	1:A:325:ILE:HG13	1.69	0.73
1:B:284:ILE:HG23	1:B:311:ALA:HB1	1.71	0.73
1:B:434:ILE:O	1:B:436:PRO:HD3	1.89	0.73
1:B:251:PHE:HB3	1:B:325:ILE:HG13	1.69	0.73
1:E:251:PHE:HB3	1:E:325:ILE:HG13	1.70	0.73
1:C:420:SER:CB	1:E:433:PRO:HA	2.19	0.73
1:E:434:ILE:O	1:E:436:PRO:HD3	1.88	0.73
1:D:434:ILE:O	1:D:436:PRO:HD3	1.89	0.73
1:D:23:ARG:HE	1:D:27:ILE:HD11	1.54	0.73
1:D:318:ILE:H	1:D:318:ILE:HD13	1.54	0.73
1:C:23:ARG:HE	1:C:27:ILE:HD11	1.54	0.72
1:E:318:ILE:HD13	1:E:318:ILE:H	1.54	0.72
1:D:190:THR:HG23	1:F:190:THR:HG23	1.71	0.72
1:D:284:ILE:HG23	1:D:311:ALA:HB1	1.70	0.72
1:D:251:PHE:HB3	1:D:325:ILE:HG13	1.70	0.72
1:A:190:THR:HG23	1:C:190:THR:HG23	1.69	0.72
1:C:284:ILE:HG23	1:C:311:ALA:HB1	1.71	0.72
1:A:318:ILE:H	1:A:318:ILE:HD13	1.55	0.72
1:F:43:GLU:HB3	1:F:45:LYS:HG3	1.72	0.72
1:F:318:ILE:H	1:F:318:ILE:HD13	1.55	0.72
1:E:284:ILE:HG23	1:E:311:ALA:HB1	1.71	0.72
1:B:318:ILE:HD13	1:B:318:ILE:H	1.53	0.72
1:D:243:THR:N	1:D:244:PRO:HD3	2.05	0.71
1:F:251:PHE:HB3	1:F:325:ILE:HG13	1.70	0.71
1:B:502:VAL:HG23	1:B:503:THR:H	1.56	0.71
1:E:502:VAL:HG23	1:E:503:THR:H	1.56	0.71
1:F:243:THR:N	1:F:244:PRO:HD3	2.05	0.71
1:B:505:THR:HG23	1:F:185:ASP:OD1	1.90	0.71
1:E:69:ILE:HA	1:E:151:ARG:NH1	2.06	0.71
1:A:279:GLU:HG3	1:A:305:ILE:HG13	1.73	0.71
1:B:27:ILE:HG22	1:B:475:TYR:CD1	2.24	0.71
1:B:23:ARG:HE	1:B:27:ILE:HD11	1.56	0.71
1:E:43:GLU:HB3	1:E:45:LYS:HG3	1.72	0.71
1:F:502:VAL:HG23	1:F:503:THR:H	1.55	0.71
1:A:23:ARG:HE	1:A:27:ILE:HD11	1.56	0.71
1:D:502:VAL:HG23	1:D:503:THR:H	1.55	0.71
1:C:118:LYS:NZ	1:C:353:ASN:HD21	1.89	0.71
1:B:190:THR:HG23	1:E:190:THR:HG23	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:THR:N	1:B:244:PRO:HD3	2.04	0.71
1:C:243:THR:N	1:C:244:PRO:HD3	2.05	0.71
1:A:502:VAL:HG23	1:A:503:THR:H	1.55	0.71
1:A:43:GLU:HB3	1:A:45:LYS:HG3	1.73	0.70
1:C:43:GLU:HB3	1:C:45:LYS:HG3	1.73	0.70
1:A:243:THR:N	1:A:244:PRO:HD3	2.05	0.70
1:F:69:ILE:HA	1:F:151:ARG:NH1	2.07	0.70
1:C:251:PHE:HB3	1:C:325:ILE:HG13	1.73	0.70
1:C:221:ARG:HD2	1:C:454:HIS:NE2	2.06	0.70
1:D:279:GLU:HG3	1:D:305:ILE:HG13	1.72	0.70
1:A:284:ILE:HG23	1:A:311:ALA:HB1	1.72	0.70
1:F:23:ARG:HE	1:F:27:ILE:HD11	1.56	0.70
1:F:284:ILE:HG23	1:F:311:ALA:HB1	1.73	0.69
1:C:502:VAL:HG23	1:C:503:THR:H	1.56	0.69
1:B:279:GLU:HG3	1:B:305:ILE:HG13	1.74	0.69
1:B:43:GLU:HB3	1:B:45:LYS:HG3	1.73	0.69
1:E:23:ARG:HE	1:E:27:ILE:HD11	1.56	0.69
1:F:425:PHE:HD1	1:F:427:LYS:HB2	1.57	0.69
1:B:69:ILE:HA	1:B:151:ARG:NH1	2.07	0.69
1:A:61:HIS:CD2	1:E:159:LYS:HE3	2.28	0.69
1:F:285:TRP:HB2	1:F:314:TYR:CB	2.17	0.69
1:B:78:VAL:N	1:D:54:ARG:HH12	1.91	0.69
1:D:69:ILE:HA	1:D:151:ARG:NH1	2.08	0.69
1:A:179:GLU:O	1:A:183:ILE:HG13	1.92	0.69
1:C:318:ILE:HD13	1:C:318:ILE:H	1.58	0.69
1:D:43:GLU:HB3	1:D:45:LYS:HG3	1.73	0.69
1:C:279:GLU:HG3	1:C:305:ILE:HG13	1.73	0.69
1:F:229:ASN:OD1	1:F:462:GLU:HG3	1.93	0.69
1:B:343:VAL:HG21	1:B:364:PHE:HE1	1.58	0.69
1:E:279:GLU:HG3	1:E:305:ILE:HG13	1.73	0.69
1:D:28:VAL:CG2	1:D:487:VAL:HG13	2.23	0.69
1:C:116:THR:HG22	1:C:128:GLY:CA	2.22	0.68
1:D:336:THR:H	1:D:339:ASN:HD21	1.41	0.68
1:D:179:GLU:O	1:D:183:ILE:HG13	1.94	0.68
1:A:69:ILE:HA	1:A:151:ARG:NH1	2.07	0.68
1:C:400:ARG:HH11	1:C:400:ARG:HG3	1.58	0.68
1:C:69:ILE:HA	1:C:151:ARG:NH1	2.07	0.68
1:F:279:GLU:HG3	1:F:305:ILE:HG13	1.73	0.68
1:C:425:PHE:HD1	1:C:427:LYS:HB2	1.59	0.68
1:C:231:ILE:HD12	1:C:237:MET:SD	2.33	0.68
1:C:205:LYS:NZ	1:C:392:ASN:HD21	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:400:ARG:HH11	1:E:400:ARG:HG3	1.59	0.68
1:F:336:THR:H	1:F:339:ASN:HD21	1.41	0.68
1:F:343:VAL:HG21	1:F:364:PHE:HE1	1.59	0.68
1:C:336:THR:H	1:C:339:ASN:HD21	1.41	0.68
1:D:231:ILE:HD12	1:D:237:MET:SD	2.33	0.68
1:D:343:VAL:HG21	1:D:364:PHE:HE1	1.58	0.68
1:A:336:THR:H	1:A:339:ASN:HD21	1.42	0.68
1:F:400:ARG:HG3	1:F:400:ARG:HH11	1.60	0.67
1:E:147:LYS:O	1:E:151:ARG:HG3	1.94	0.67
1:A:116:THR:HG22	1:A:128:GLY:CA	2.25	0.67
1:C:375:LEU:HD23	1:C:485:ALA:HB1	1.77	0.67
1:D:147:LYS:O	1:D:151:ARG:HG3	1.93	0.67
1:A:343:VAL:HG21	1:A:364:PHE:HE1	1.59	0.67
1:B:179:GLU:O	1:B:183:ILE:HG13	1.94	0.67
1:C:147:LYS:O	1:C:151:ARG:HG3	1.95	0.67
1:A:231:ILE:HD12	1:A:237:MET:SD	2.35	0.67
1:F:407:ARG:O	1:F:411:TYR:HD2	1.78	0.67
1:C:343:VAL:HG21	1:C:364:PHE:HE1	1.60	0.67
1:E:62:VAL:HG21	1:E:105:VAL:HG13	1.77	0.67
1:C:373:PRO:CG	1:C:481:LEU:HB3	2.25	0.67
1:A:71:ARG:NH1	1:A:71:ARG:HB3	2.11	0.67
1:B:231:ILE:HD12	1:B:237:MET:SD	2.35	0.67
1:E:179:GLU:O	1:E:183:ILE:HG13	1.94	0.66
1:D:298:PHE:CZ	1:D:302:HIS:HE1	2.13	0.66
1:F:298:PHE:CZ	1:F:302:HIS:HE1	2.14	0.66
1:F:221:ARG:HD2	1:F:454:HIS:CD2	2.31	0.66
1:C:122:VAL:HG11	1:C:379:ALA:CB	2.24	0.66
1:D:285:TRP:HB2	1:D:314:TYR:CB	2.17	0.66
1:E:336:THR:H	1:E:339:ASN:HD21	1.43	0.66
1:A:407:ARG:O	1:A:411:TYR:HD2	1.79	0.66
1:C:298:PHE:CZ	1:C:302:HIS:HE1	2.14	0.66
1:B:407:ARG:O	1:B:411:TYR:HD2	1.79	0.66
1:F:147:LYS:O	1:F:151:ARG:HG3	1.95	0.66
1:E:298:PHE:CZ	1:E:302:HIS:HE1	2.13	0.66
1:E:425:PHE:HD1	1:E:427:LYS:HB2	1.60	0.66
1:B:147:LYS:O	1:B:151:ARG:HG3	1.95	0.66
1:A:147:LYS:O	1:A:151:ARG:HG3	1.95	0.66
1:E:27:ILE:HG22	1:E:475:TYR:CD1	2.31	0.66
1:C:285:TRP:HB2	1:C:314:TYR:CB	2.18	0.66
1:E:285:TRP:HB2	1:E:314:TYR:CB	2.18	0.66
1:A:298:PHE:CZ	1:A:302:HIS:HE1	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:343:VAL:HG21	1:E:364:PHE:HE1	1.59	0.66
1:F:433:PRO:O	1:F:435:VAL:N	2.29	0.65
1:B:298:PHE:CZ	1:B:302:HIS:HE1	2.13	0.65
1:B:336:THR:H	1:B:339:ASN:HD21	1.42	0.65
1:F:231:ILE:HD12	1:F:237:MET:SD	2.36	0.65
1:D:425:PHE:HD1	1:D:427:LYS:HB2	1.60	0.65
1:B:264:MET:CE	1:B:292:PRO:HA	2.26	0.65
1:B:116:THR:HG22	1:B:128:GLY:CA	2.26	0.65
1:D:433:PRO:HA	1:E:420:SER:CB	2.25	0.65
1:C:277:VAL:HG21	1:C:295:LEU:CD2	2.26	0.65
1:D:264:MET:CE	1:D:292:PRO:HA	2.26	0.65
1:C:122:VAL:HG11	1:C:379:ALA:HB3	1.77	0.65
1:D:277:VAL:HG21	1:D:295:LEU:CD2	2.27	0.65
1:F:179:GLU:O	1:F:183:ILE:HG13	1.96	0.65
1:A:425:PHE:HD1	1:A:427:LYS:HB2	1.60	0.65
1:E:264:MET:CE	1:E:292:PRO:HA	2.25	0.65
1:E:71:ARG:HB3	1:E:71:ARG:NH1	2.11	0.65
1:A:277:VAL:HG21	1:A:295:LEU:CD2	2.27	0.65
1:B:71:ARG:HB3	1:B:71:ARG:NH1	2.12	0.65
1:C:54:ARG:HH12	1:F:78:VAL:N	1.95	0.65
1:C:54:ARG:HH12	1:F:78:VAL:H	1.42	0.65
1:B:425:PHE:HD1	1:B:427:LYS:HB2	1.60	0.65
1:D:407:ARG:O	1:D:411:TYR:HD2	1.78	0.65
1:C:62:VAL:HG21	1:C:105:VAL:HG13	1.78	0.65
1:A:264:MET:CE	1:A:292:PRO:HA	2.27	0.65
1:F:277:VAL:HG21	1:F:295:LEU:CD2	2.27	0.65
1:B:400:ARG:HG3	1:B:400:ARG:HH11	1.61	0.65
1:C:427:LYS:CD	1:C:430:GLY:HA3	2.25	0.65
1:F:264:MET:CE	1:F:292:PRO:HA	2.27	0.65
1:B:62:VAL:HG21	1:B:105:VAL:HG13	1.78	0.65
1:B:285:TRP:HB2	1:B:314:TYR:CB	2.17	0.64
1:E:37:ARG:HB2	1:E:37:ARG:HH11	1.62	0.64
1:D:71:ARG:NH1	1:D:71:ARG:HB3	2.12	0.64
1:B:162:ILE:O	1:B:162:ILE:HD13	1.97	0.64
1:A:37:ARG:HB2	1:A:37:ARG:HH11	1.63	0.64
1:D:62:VAL:HG21	1:D:105:VAL:HG13	1.79	0.64
1:F:62:VAL:HG21	1:F:105:VAL:HG13	1.79	0.64
1:E:231:ILE:HD12	1:E:237:MET:SD	2.36	0.64
1:C:393:LEU:O	1:C:395:HIS:CD2	2.50	0.64
1:D:116:THR:HG22	1:D:128:GLY:CA	2.27	0.64
1:F:71:ARG:HB3	1:F:71:ARG:NH1	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:171:PRO:HG3	1:D:180:MET:SD	2.38	0.64
1:A:62:VAL:HG21	1:A:105:VAL:HG13	1.79	0.64
1:B:37:ARG:HB2	1:B:37:ARG:HH11	1.63	0.64
1:A:285:TRP:HB2	1:A:314:TYR:CB	2.18	0.64
1:A:275:ILE:HG13	1:A:287:PRO:HA	1.80	0.64
1:B:33:VAL:HG12	1:B:38:THR:OG1	1.98	0.64
1:C:33:VAL:HG12	1:C:38:THR:OG1	1.98	0.64
1:E:433:PRO:O	1:E:435:VAL:N	2.31	0.64
1:F:116:THR:HG22	1:F:128:GLY:CA	2.27	0.64
1:E:162:ILE:O	1:E:162:ILE:HD13	1.98	0.64
1:C:407:ARG:O	1:C:411:TYR:HD2	1.80	0.64
1:B:77:GLU:HA	1:D:54:ARG:HH12	1.59	0.64
1:C:71:ARG:HB3	1:C:71:ARG:NH1	2.11	0.64
1:E:407:ARG:O	1:E:411:TYR:HD2	1.80	0.64
1:B:277:VAL:HG21	1:B:295:LEU:CD2	2.28	0.64
1:A:400:ARG:HG3	1:A:400:ARG:HH11	1.61	0.64
1:B:28:VAL:CG2	1:B:487:VAL:HG13	2.27	0.64
1:A:427:LYS:CD	1:A:430:GLY:HA3	2.26	0.64
1:D:325:ILE:HG22	1:D:347:ILE:CB	2.28	0.64
1:C:423:ARG:HH21	1:E:435:VAL:HG13	1.63	0.64
1:E:33:VAL:HG12	1:E:38:THR:OG1	1.98	0.63
1:D:46:ARG:O	1:D:49:VAL:HG12	1.99	0.63
1:C:32:LEU:HD11	1:C:494:PHE:CE2	2.33	0.63
1:B:52:ILE:O	1:B:56:ILE:HG13	1.98	0.63
1:D:275:ILE:HG13	1:D:287:PRO:HA	1.80	0.63
1:F:33:VAL:HG12	1:F:38:THR:OG1	1.98	0.63
1:A:33:VAL:HG12	1:A:38:THR:OG1	1.98	0.63
1:C:37:ARG:HH11	1:C:37:ARG:HB2	1.63	0.63
1:D:400:ARG:HG3	1:D:400:ARG:HH11	1.63	0.63
1:B:275:ILE:HG13	1:B:287:PRO:HA	1.80	0.63
1:C:179:GLU:O	1:C:183:ILE:HG13	1.99	0.63
1:E:275:ILE:HG13	1:E:287:PRO:HA	1.81	0.63
1:C:264:MET:CE	1:C:292:PRO:HA	2.28	0.63
1:C:335:LEU:HD13	1:C:348:ILE:HD13	1.81	0.63
1:D:33:VAL:HG12	1:D:38:THR:OG1	1.99	0.63
1:D:37:ARG:HH11	1:D:37:ARG:HB2	1.63	0.63
1:A:76:TRP:CD1	1:E:502:VAL:HG11	2.33	0.63
1:E:277:VAL:HG21	1:E:295:LEU:CD2	2.28	0.63
1:E:116:THR:HG22	1:E:128:GLY:CA	2.28	0.63
1:B:427:LYS:CD	1:B:430:GLY:HA3	2.25	0.63
1:E:325:ILE:HG22	1:E:347:ILE:CB	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:32:LEU:HD11	1:E:494:PHE:CE2	2.34	0.63
1:D:393:LEU:O	1:D:395:HIS:CD2	2.52	0.63
1:F:427:LYS:CD	1:F:430:GLY:HA3	2.25	0.62
1:D:433:PRO:O	1:D:435:VAL:N	2.32	0.62
1:C:46:ARG:O	1:C:49:VAL:HG12	1.99	0.62
1:A:335:LEU:HD13	1:A:348:ILE:HD13	1.81	0.62
1:E:427:LYS:CD	1:E:430:GLY:HA3	2.25	0.62
1:F:376:TYR:OH	1:F:465:ALA:HB2	1.99	0.62
1:F:37:ARG:HH11	1:F:37:ARG:HB2	1.64	0.62
1:B:49:VAL:O	1:B:52:ILE:HG12	2.00	0.62
1:C:72:ASP:OD1	1:C:144:GLU:HG3	1.99	0.62
1:B:32:LEU:HD11	1:B:494:PHE:CE2	2.35	0.62
1:F:49:VAL:O	1:F:52:ILE:HG12	1.99	0.62
1:B:46:ARG:O	1:B:49:VAL:HG12	2.00	0.62
1:C:52:ILE:O	1:C:56:ILE:HG13	2.00	0.62
1:A:171:PRO:HG3	1:A:180:MET:SD	2.40	0.62
1:D:427:LYS:CD	1:D:430:GLY:HA3	2.27	0.62
1:C:433:PRO:O	1:C:435:VAL:N	2.33	0.62
1:F:335:LEU:HD13	1:F:348:ILE:HD13	1.81	0.61
1:C:206:PRO:HB2	1:C:209:GLN:HG2	1.81	0.61
1:E:205:LYS:NZ	1:E:388:GLU:OE1	2.33	0.61
1:F:32:LEU:HD11	1:F:494:PHE:CE2	2.35	0.61
1:A:28:VAL:CG2	1:A:487:VAL:HG13	2.30	0.61
1:F:135:ILE:HG13	1:F:140:TYR:CE2	2.35	0.61
1:E:49:VAL:O	1:E:52:ILE:HG12	2.00	0.61
1:A:505:THR:HG23	1:B:185:ASP:OD1	2.00	0.61
1:B:433:PRO:O	1:B:435:VAL:N	2.33	0.61
1:F:205:LYS:NZ	1:F:392:ASN:HD21	1.98	0.61
1:D:335:LEU:HD13	1:D:348:ILE:HD13	1.82	0.61
1:B:221:ARG:HD2	1:B:454:HIS:NE2	2.15	0.61
1:D:162:ILE:HD13	1:D:162:ILE:O	2.00	0.61
1:E:37:ARG:HH21	1:E:49:VAL:HG11	1.65	0.61
1:B:345:ALA:O	1:B:369:ILE:HD12	2.00	0.61
1:A:162:ILE:O	1:A:162:ILE:HD13	2.00	0.61
1:F:275:ILE:HG13	1:F:287:PRO:HA	1.81	0.61
1:E:46:ARG:O	1:E:49:VAL:HG12	2.00	0.61
1:F:46:ARG:O	1:F:49:VAL:HG12	2.00	0.61
1:F:325:ILE:HG22	1:F:347:ILE:CB	2.29	0.61
1:C:256:PHE:HE2	1:C:264:MET:HE2	1.65	0.61
1:F:345:ALA:O	1:F:369:ILE:HD12	2.00	0.61
1:B:95:GLY:O	1:B:169:PRO:HA	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:ARG:O	1:A:49:VAL:HG12	1.99	0.61
1:C:14:PHE:O	1:C:18:GLU:HB2	2.00	0.61
1:A:433:PRO:O	1:A:435:VAL:N	2.33	0.61
1:C:162:ILE:O	1:C:162:ILE:HD13	2.00	0.61
1:D:49:VAL:O	1:D:52:ILE:HG12	2.00	0.61
1:C:135:ILE:HG13	1:C:140:TYR:CE2	2.36	0.61
1:D:32:LEU:HD11	1:D:494:PHE:CE2	2.36	0.61
1:F:72:ASP:OD1	1:F:144:GLU:HG3	2.00	0.61
1:A:325:ILE:HG22	1:A:347:ILE:CB	2.29	0.61
1:B:13:PHE:CD1	1:B:14:PHE:N	2.66	0.61
1:A:95:GLY:O	1:A:169:PRO:HA	2.01	0.61
1:A:32:LEU:HD11	1:A:494:PHE:CE2	2.35	0.61
1:C:151:ARG:NH2	1:F:504:PHE:CZ	2.69	0.61
1:B:393:LEU:O	1:B:395:HIS:CD2	2.54	0.61
1:A:49:VAL:O	1:A:52:ILE:HG12	2.00	0.60
1:B:72:ASP:OD1	1:B:144:GLU:HG3	2.01	0.60
1:D:505:THR:N	1:E:150:ARG:HH12	1.99	0.60
1:D:345:ALA:O	1:D:369:ILE:HD12	2.01	0.60
1:F:393:LEU:O	1:F:395:HIS:CD2	2.54	0.60
1:B:37:ARG:HH21	1:B:49:VAL:HG11	1.66	0.60
1:E:256:PHE:HE2	1:E:264:MET:HE2	1.66	0.60
1:D:14:PHE:O	1:D:18:GLU:HB2	2.01	0.60
1:D:343:VAL:HG22	1:D:367:ARG:NH2	2.16	0.60
1:D:483:THR:O	1:D:487:VAL:HG23	2.01	0.60
1:C:95:GLY:O	1:C:169:PRO:HA	2.02	0.60
1:E:335:LEU:HD13	1:E:348:ILE:HD13	1.83	0.60
1:F:37:ARG:HH21	1:F:49:VAL:HG11	1.65	0.60
1:C:49:VAL:O	1:C:52:ILE:HG12	2.00	0.60
1:A:185:ASP:OD1	1:F:505:THR:HG23	2.01	0.60
1:C:185:ASP:OD1	1:E:505:THR:HG23	2.02	0.60
1:B:335:LEU:HD13	1:B:348:ILE:HD13	1.81	0.60
1:A:37:ARG:HH21	1:A:49:VAL:HG11	1.66	0.60
1:B:325:ILE:HG22	1:B:347:ILE:CB	2.30	0.60
1:E:345:ALA:O	1:E:369:ILE:HD12	2.01	0.60
1:D:13:PHE:CD1	1:D:14:PHE:N	2.65	0.60
1:D:95:GLY:O	1:D:169:PRO:HA	2.02	0.60
1:E:95:GLY:O	1:E:169:PRO:HA	2.02	0.60
1:C:275:ILE:HG13	1:C:287:PRO:HA	1.83	0.60
1:E:52:ILE:O	1:E:56:ILE:HG13	2.01	0.60
1:A:502:VAL:HG11	1:E:76:TRP:HD1	1.64	0.60
1:F:14:PHE:O	1:F:18:GLU:HB2	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:PHE:O	1:B:18:GLU:HB2	2.02	0.60
1:E:13:PHE:CD1	1:E:14:PHE:N	2.66	0.60
1:F:162:ILE:O	1:F:162:ILE:HD13	2.00	0.60
1:B:10:ASP:HB2	1:B:333:LYS:CD	2.31	0.60
1:A:393:LEU:O	1:A:395:HIS:CD2	2.54	0.60
1:D:52:ILE:O	1:D:56:ILE:HG13	2.02	0.60
1:E:14:PHE:O	1:E:18:GLU:HB2	2.01	0.60
1:A:14:PHE:O	1:A:18:GLU:HB2	2.01	0.60
1:D:343:VAL:HG21	1:D:364:PHE:CE1	2.36	0.60
1:F:52:ILE:O	1:F:56:ILE:HG13	2.02	0.60
1:C:69:ILE:HG22	1:C:151:ARG:HD2	1.84	0.60
1:C:217:SER:OG	1:C:454:HIS:NE2	2.35	0.60
1:C:335:LEU:HB2	1:C:356:THR:HG22	1.84	0.60
1:E:135:ILE:HG13	1:E:140:TYR:CE2	2.37	0.60
1:F:256:PHE:HE2	1:F:264:MET:HE2	1.66	0.60
1:B:418:GLN:CB	1:B:433:PRO:HD2	2.31	0.60
1:E:418:GLN:CB	1:E:433:PRO:HD2	2.32	0.60
1:B:78:VAL:H	1:D:54:ARG:HH12	1.49	0.59
1:E:343:VAL:HG21	1:E:364:PHE:CE1	2.37	0.59
1:A:343:VAL:HG21	1:A:364:PHE:CE1	2.36	0.59
1:B:343:VAL:HG22	1:B:367:ARG:NH2	2.18	0.59
1:D:72:ASP:OD1	1:D:144:GLU:HG3	2.02	0.59
1:C:343:VAL:HG22	1:C:367:ARG:NH2	2.17	0.59
1:A:143:ASN:HD21	1:C:70:ARG:HH12	1.51	0.59
1:C:308:PHE:HD2	1:C:311:ALA:HB2	1.67	0.59
1:F:12:ASN:OD1	1:F:15:LYS:HG2	2.02	0.59
1:D:335:LEU:HB2	1:D:356:THR:HG22	1.84	0.59
1:E:343:VAL:HG22	1:E:367:ARG:NH2	2.17	0.59
1:F:483:THR:O	1:F:487:VAL:HG23	2.03	0.59
1:A:54:ARG:NH1	1:E:77:GLU:HA	2.17	0.59
1:C:37:ARG:HH21	1:C:49:VAL:HG11	1.66	0.59
1:A:72:ASP:OD1	1:A:144:GLU:HG3	2.03	0.59
1:B:335:LEU:HB2	1:B:356:THR:HG22	1.85	0.59
1:E:474:LYS:HD3	1:E:475:TYR:CE2	2.38	0.59
1:E:69:ILE:HG22	1:E:151:ARG:HD2	1.84	0.59
1:C:325:ILE:HG22	1:C:347:ILE:CB	2.30	0.59
1:B:256:PHE:HE2	1:B:264:MET:HE2	1.67	0.59
1:F:146:GLU:HG2	1:F:150:ARG:HD2	1.85	0.59
1:D:279:GLU:HG3	1:D:305:ILE:CG1	2.32	0.59
1:D:135:ILE:HG13	1:D:140:TYR:CE2	2.38	0.59
1:D:69:ILE:HG22	1:D:151:ARG:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:ASN:OD1	1:C:15:LYS:HG2	2.03	0.59
1:F:343:VAL:HG22	1:F:367:ARG:NH2	2.18	0.59
1:F:335:LEU:HB2	1:F:356:THR:HG22	1.84	0.59
1:F:13:PHE:CD1	1:F:14:PHE:N	2.65	0.59
1:B:244:PRO:HB2	1:B:248:ASP:H	1.68	0.59
1:E:335:LEU:HB2	1:E:356:THR:HG22	1.85	0.59
1:E:146:GLU:HG2	1:E:150:ARG:HD2	1.85	0.59
1:F:23:ARG:O	1:F:27:ILE:HG13	2.02	0.59
1:E:28:VAL:CG2	1:E:487:VAL:HG13	2.33	0.59
1:A:504:PHE:CE1	1:E:70:ARG:HB3	2.38	0.59
1:A:264:MET:HE3	1:A:292:PRO:HA	1.84	0.59
1:B:12:ASN:OD1	1:B:15:LYS:HG2	2.03	0.59
1:E:12:ASN:OD1	1:E:15:LYS:HG2	2.03	0.59
1:B:343:VAL:HG21	1:B:364:PHE:CE1	2.36	0.59
1:F:244:PRO:HB2	1:F:248:ASP:H	1.68	0.59
1:D:37:ARG:HH21	1:D:49:VAL:HG11	1.66	0.58
1:D:256:PHE:HE2	1:D:264:MET:HE2	1.68	0.58
1:F:91:THR:OG1	1:F:92:PRO:HD3	2.03	0.58
1:B:69:ILE:HG22	1:B:151:ARG:HD2	1.84	0.58
1:D:146:GLU:HG2	1:D:150:ARG:HD2	1.84	0.58
1:D:264:MET:HE3	1:D:292:PRO:HA	1.85	0.58
1:D:12:ASN:OD1	1:D:15:LYS:HG2	2.03	0.58
1:A:69:ILE:HG22	1:A:151:ARG:HD2	1.85	0.58
1:B:190:THR:HG22	1:B:191:ILE:N	2.18	0.58
1:D:93:CYS:HB3	1:D:129:ALA:HB2	1.85	0.58
1:D:418:GLN:CB	1:D:433:PRO:HD2	2.32	0.58
1:F:343:VAL:HG21	1:F:364:PHE:CE1	2.37	0.58
1:A:483:THR:O	1:A:487:VAL:HG23	2.02	0.58
1:B:54:ARG:HH12	1:D:78:VAL:N	2.02	0.58
1:A:308:PHE:HD2	1:A:311:ALA:HB2	1.68	0.58
1:C:502:VAL:HG11	1:F:76:TRP:CD1	2.39	0.58
1:A:70:ARG:HH12	1:C:143:ASN:HD21	1.51	0.58
1:C:345:ALA:O	1:C:369:ILE:HD12	2.03	0.58
1:E:91:THR:OG1	1:E:92:PRO:HD3	2.04	0.58
1:D:435:VAL:HG13	1:E:423:ARG:HH21	1.68	0.58
1:C:279:GLU:HG3	1:C:305:ILE:CG1	2.34	0.58
1:B:135:ILE:HG13	1:B:140:TYR:CE2	2.38	0.58
1:A:386:TYR:OH	1:B:396:VAL:HG13	2.04	0.58
1:A:91:THR:OG1	1:A:92:PRO:HD3	2.04	0.58
1:C:13:PHE:CD1	1:C:14:PHE:N	2.65	0.58
1:A:345:ALA:O	1:A:369:ILE:HD12	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:VAL:HG22	1:A:367:ARG:NH2	2.18	0.58
1:F:91:THR:CB	1:F:92:PRO:HD3	2.34	0.58
1:D:308:PHE:HD2	1:D:311:ALA:HB2	1.68	0.58
1:D:427:LYS:HZ3	1:D:428:HIS:H	1.52	0.58
1:F:69:ILE:HG22	1:F:151:ARG:HD2	1.85	0.58
1:F:279:GLU:HG3	1:F:305:ILE:CG1	2.34	0.58
1:B:54:ARG:NH1	1:D:77:GLU:HA	2.18	0.58
1:E:427:LYS:CE	1:E:427:LYS:HA	2.32	0.58
1:C:190:THR:HG22	1:C:191:ILE:N	2.19	0.58
1:C:93:CYS:HB3	1:C:129:ALA:HB2	1.86	0.58
1:C:91:THR:OG1	1:C:92:PRO:HD3	2.04	0.58
1:F:308:PHE:HD2	1:F:311:ALA:HB2	1.68	0.58
1:A:432:ILE:HG22	1:A:434:ILE:HG12	1.86	0.58
1:B:264:MET:HE3	1:B:292:PRO:HA	1.86	0.58
1:A:146:GLU:HG2	1:A:150:ARG:HD2	1.86	0.58
1:E:190:THR:HG22	1:E:191:ILE:N	2.19	0.58
1:B:433:PRO:HA	1:F:420:SER:CB	2.34	0.57
1:A:418:GLN:CB	1:A:433:PRO:HD2	2.32	0.57
1:E:244:PRO:HB2	1:E:248:ASP:H	1.69	0.57
1:C:343:VAL:HG21	1:C:364:PHE:CE1	2.37	0.57
1:C:207:ILE:C	1:C:209:GLN:H	2.06	0.57
1:A:157:ALA:HA	1:A:162:ILE:HG22	1.86	0.57
1:E:72:ASP:OD1	1:E:144:GLU:HG3	2.02	0.57
1:C:293:LYS:O	1:C:296:GLU:HB3	2.04	0.57
1:F:418:GLN:CB	1:F:433:PRO:HD2	2.33	0.57
1:C:146:GLU:HG2	1:C:150:ARG:HD2	1.85	0.57
1:B:252:VAL:HG11	1:B:318:ILE:HB	1.86	0.57
1:A:335:LEU:HB2	1:A:356:THR:HG22	1.86	0.57
1:B:93:CYS:HB3	1:B:129:ALA:HB2	1.85	0.57
1:B:10:ASP:HB2	1:B:333:LYS:HD3	1.86	0.57
1:C:213:HIS:O	1:C:453:VAL:HG21	2.04	0.57
1:A:293:LYS:O	1:A:296:GLU:HB3	2.04	0.57
1:E:171:PRO:HG3	1:E:180:MET:SD	2.43	0.57
1:C:171:PRO:HG3	1:C:180:MET:SD	2.44	0.57
1:C:230:PHE:CD2	1:C:469:MET:HE2	2.39	0.57
1:B:76:TRP:CZ3	1:D:49:VAL:HA	2.40	0.57
1:A:12:ASN:OD1	1:A:15:LYS:HG2	2.03	0.57
1:B:154:MET:SD	1:B:190:THR:HG21	2.45	0.57
1:E:154:MET:SD	1:E:190:THR:HG21	2.44	0.57
1:C:252:VAL:HG11	1:C:318:ILE:HB	1.87	0.57
1:E:157:ALA:HA	1:E:162:ILE:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:THR:OG1	1:D:92:PRO:HD3	2.04	0.57
1:E:69:ILE:HA	1:E:151:ARG:CZ	2.35	0.57
1:A:504:PHE:CZ	1:E:151:ARG:NH2	2.73	0.57
1:D:105:VAL:O	1:D:109:LYS:HG3	2.04	0.57
1:B:28:VAL:HG23	1:B:487:VAL:HG13	1.85	0.57
1:A:52:ILE:O	1:A:56:ILE:HG13	2.04	0.57
1:A:244:PRO:HB2	1:A:248:ASP:H	1.70	0.57
1:F:171:PRO:HG3	1:F:180:MET:SD	2.45	0.57
1:C:320:GLU:O	1:C:344:LYS:HG2	2.05	0.57
1:C:244:PRO:HB2	1:C:248:ASP:H	1.69	0.57
1:A:54:ARG:HH12	1:E:78:VAL:H	1.52	0.57
1:A:190:THR:HG22	1:A:191:ILE:N	2.20	0.57
1:A:252:VAL:HG11	1:A:318:ILE:HB	1.87	0.57
1:F:252:VAL:HG11	1:F:318:ILE:HB	1.86	0.57
1:F:105:VAL:O	1:F:109:LYS:HG3	2.04	0.57
1:F:157:ALA:HA	1:F:162:ILE:HG22	1.87	0.57
1:C:396:VAL:HG13	1:E:386:TYR:OH	2.05	0.57
1:A:221:ARG:HD2	1:A:454:HIS:NE2	2.19	0.57
1:B:308:PHE:HD2	1:B:311:ALA:HB2	1.69	0.57
1:B:279:GLU:HG3	1:B:305:ILE:CG1	2.34	0.57
1:E:279:GLU:HG3	1:E:305:ILE:CG1	2.34	0.57
1:C:205:LYS:HZ3	1:C:392:ASN:ND2	2.03	0.57
1:F:95:GLY:O	1:F:169:PRO:HA	2.04	0.57
1:A:427:LYS:HA	1:A:427:LYS:CE	2.33	0.57
1:F:264:MET:HE3	1:F:292:PRO:HA	1.87	0.57
1:D:244:PRO:HB2	1:D:248:ASP:H	1.68	0.57
1:D:157:ALA:HA	1:D:162:ILE:HG22	1.86	0.57
1:C:91:THR:CB	1:C:92:PRO:HD3	2.35	0.57
1:B:293:LYS:O	1:B:296:GLU:HB3	2.05	0.57
1:C:23:ARG:O	1:C:27:ILE:HG13	2.05	0.56
1:D:190:THR:HG22	1:D:191:ILE:N	2.20	0.56
1:B:95:GLY:HA3	1:B:129:ALA:O	2.05	0.56
1:E:91:THR:CB	1:E:92:PRO:HD3	2.35	0.56
1:B:91:THR:CB	1:B:92:PRO:HD3	2.35	0.56
1:D:320:GLU:O	1:D:344:LYS:HG2	2.05	0.56
1:E:320:GLU:O	1:E:344:LYS:HG2	2.05	0.56
1:C:427:LYS:CE	1:C:427:LYS:HA	2.33	0.56
1:A:256:PHE:HE2	1:A:264:MET:HE2	1.70	0.56
1:F:320:GLU:O	1:F:344:LYS:HG2	2.04	0.56
1:E:432:ILE:HG22	1:E:434:ILE:HG12	1.88	0.56
1:D:304:SER:OG	1:D:306:LEU:HD13	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:ARG:O	1:B:27:ILE:HG13	2.05	0.56
1:C:157:ALA:HA	1:C:162:ILE:HG22	1.87	0.56
1:F:93:CYS:HB3	1:F:129:ALA:HB2	1.87	0.56
1:E:393:LEU:O	1:E:395:HIS:CD2	2.58	0.56
1:B:254:GLN:OE1	1:B:334:GLN:HG2	2.05	0.56
1:A:135:ILE:HG13	1:A:140:TYR:CE2	2.39	0.56
1:B:320:GLU:O	1:B:344:LYS:HG2	2.05	0.56
1:F:375:LEU:HD23	1:F:485:ALA:HB1	1.87	0.56
1:A:320:GLU:O	1:A:344:LYS:HG2	2.04	0.56
1:F:500:ALA:C	1:F:505:THR:HA	2.26	0.56
1:F:293:LYS:O	1:F:296:GLU:HB3	2.05	0.56
1:B:205:LYS:NZ	1:B:388:GLU:OE1	2.35	0.56
1:E:254:GLN:OE1	1:E:334:GLN:HG2	2.05	0.56
1:B:76:TRP:CD1	1:D:502:VAL:HG11	2.41	0.56
1:E:252:VAL:HG11	1:E:318:ILE:HB	1.87	0.56
1:A:91:THR:CB	1:A:92:PRO:HD3	2.36	0.56
1:E:293:LYS:O	1:E:296:GLU:HB3	2.06	0.56
1:A:99:TYR:HH	1:A:149:THR:HG22	1.66	0.56
1:D:500:ALA:C	1:D:505:THR:HA	2.26	0.56
1:C:503:THR:HG21	1:F:151:ARG:CD	2.35	0.56
1:A:69:ILE:HA	1:A:151:ARG:CZ	2.36	0.56
1:D:154:MET:SD	1:D:190:THR:HG21	2.45	0.56
1:B:91:THR:OG1	1:B:92:PRO:HD3	2.06	0.56
1:F:40:GLU:HG3	1:F:46:ARG:NH1	2.15	0.56
1:F:69:ILE:HA	1:F:151:ARG:CZ	2.35	0.56
1:D:27:ILE:HG22	1:D:475:TYR:CD1	2.41	0.56
1:A:279:GLU:HG3	1:A:305:ILE:CG1	2.33	0.56
1:D:496:VAL:O	1:E:209:GLN:NE2	2.39	0.56
1:F:206:PRO:HD2	1:F:209:GLN:HB2	1.88	0.56
1:A:13:PHE:CD1	1:A:14:PHE:N	2.65	0.56
1:E:500:ALA:C	1:E:505:THR:HA	2.26	0.56
1:C:304:SER:OG	1:C:306:LEU:HD13	2.06	0.56
1:D:252:VAL:HG11	1:D:318:ILE:HB	1.88	0.56
1:B:62:VAL:HG11	1:B:109:LYS:NZ	2.21	0.56
1:F:221:ARG:CD	1:F:454:HIS:CD2	2.90	0.55
1:E:23:ARG:O	1:E:27:ILE:HG13	2.06	0.55
1:B:171:PRO:HG3	1:B:180:MET:SD	2.45	0.55
1:F:41:SER:CA	1:F:46:ARG:HD2	2.31	0.55
1:B:146:GLU:HG2	1:B:150:ARG:HD2	1.87	0.55
1:E:304:SER:OG	1:E:306:LEU:HD13	2.06	0.55
1:D:28:VAL:HG23	1:D:487:VAL:HG13	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:ALA:HA	1:B:162:ILE:HG22	1.87	0.55
1:B:483:THR:O	1:B:487:VAL:HG23	2.06	0.55
1:D:91:THR:CB	1:D:92:PRO:HD3	2.35	0.55
1:A:500:ALA:C	1:A:505:THR:HA	2.27	0.55
1:D:432:ILE:HG22	1:D:434:ILE:HG12	1.88	0.55
1:F:243:THR:N	1:F:244:PRO:CD	2.69	0.55
1:B:243:THR:N	1:B:244:PRO:CD	2.68	0.55
1:E:308:PHE:HD2	1:E:311:ALA:HB2	1.71	0.55
1:C:500:ALA:C	1:C:505:THR:HA	2.26	0.55
1:B:77:GLU:CA	1:D:54:ARG:NH1	2.68	0.55
1:F:304:SER:OG	1:F:306:LEU:HD13	2.06	0.55
1:F:190:THR:HG22	1:F:191:ILE:N	2.20	0.55
1:A:254:GLN:OE1	1:A:334:GLN:HG2	2.06	0.55
1:C:483:THR:O	1:C:487:VAL:HG23	2.06	0.55
1:D:254:GLN:OE1	1:D:334:GLN:HG2	2.07	0.55
1:A:503:THR:HG21	1:E:151:ARG:NE	2.22	0.55
1:D:293:LYS:O	1:D:296:GLU:HB3	2.06	0.55
1:B:37:ARG:NH1	1:B:37:ARG:HB2	2.22	0.55
1:C:33:VAL:HG13	1:C:46:ARG:HB2	1.89	0.55
1:C:69:ILE:HA	1:C:151:ARG:CZ	2.36	0.55
1:B:304:SER:OG	1:B:306:LEU:HD13	2.06	0.55
1:D:386:TYR:OH	1:E:396:VAL:HG13	2.07	0.55
1:B:488:ASN:HD21	1:B:492:LYS:HZ2	1.53	0.55
1:A:251:PHE:CB	1:A:325:ILE:HG13	2.37	0.55
1:C:116:THR:HG22	1:C:128:GLY:N	2.21	0.55
1:A:304:SER:OG	1:A:306:LEU:HD13	2.06	0.55
1:C:221:ARG:CD	1:C:454:HIS:CD2	2.89	0.55
1:F:154:MET:SD	1:F:190:THR:HG21	2.47	0.55
1:A:93:CYS:HB3	1:A:129:ALA:HB2	1.89	0.55
1:F:273:LYS:HE2	1:F:288:ASP:O	2.07	0.55
1:F:33:VAL:HG13	1:F:46:ARG:HB2	1.89	0.55
1:D:505:THR:HG23	1:E:150:ARG:NH2	2.22	0.55
1:B:500:ALA:C	1:B:505:THR:HA	2.27	0.55
1:B:77:GLU:CA	1:D:54:ARG:HH12	2.19	0.55
1:A:154:MET:SD	1:A:190:THR:HG21	2.47	0.55
1:E:483:THR:O	1:E:487:VAL:HG23	2.07	0.55
1:D:10:ASP:HB2	1:D:333:LYS:CD	2.36	0.55
1:B:16:MET:HG2	1:B:358:PRO:CG	2.37	0.55
1:A:37:ARG:HB2	1:A:37:ARG:NH1	2.21	0.55
1:B:69:ILE:HA	1:B:151:ARG:CZ	2.36	0.55
1:E:95:GLY:HA3	1:E:129:ALA:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ARG:HH12	1:E:78:VAL:N	2.05	0.55
1:C:273:LYS:HE2	1:C:288:ASP:O	2.07	0.55
1:C:41:SER:CA	1:C:46:ARG:HD2	2.32	0.54
1:A:337:LYS:NZ	1:A:359:GLU:HG3	2.22	0.54
1:D:337:LYS:NZ	1:D:359:GLU:HG3	2.22	0.54
1:D:273:LYS:HE2	1:D:288:ASP:O	2.07	0.54
1:F:337:LYS:NZ	1:F:359:GLU:HG3	2.22	0.54
1:D:37:ARG:HB2	1:D:37:ARG:NH1	2.22	0.54
1:A:13:PHE:CZ	1:A:107:GLU:HA	2.42	0.54
1:A:87:SER:O	1:A:127:GLY:HA3	2.07	0.54
1:B:105:VAL:O	1:B:109:LYS:HG3	2.07	0.54
1:F:254:GLN:OE1	1:F:334:GLN:HG2	2.07	0.54
1:C:254:GLN:OE1	1:C:334:GLN:HG2	2.07	0.54
1:E:37:ARG:HB2	1:E:37:ARG:NH1	2.21	0.54
1:C:37:ARG:HB2	1:C:37:ARG:NH1	2.21	0.54
1:B:432:ILE:HG22	1:B:434:ILE:HG12	1.89	0.54
1:D:23:ARG:O	1:D:27:ILE:HG13	2.06	0.54
1:B:499:GLU:HB2	1:F:209:GLN:NE2	2.23	0.54
1:E:273:LYS:HE2	1:E:288:ASP:O	2.08	0.54
1:C:432:ILE:HG22	1:C:434:ILE:HG12	1.88	0.54
1:A:62:VAL:HG11	1:A:109:LYS:NZ	2.23	0.54
1:A:95:GLY:HA3	1:A:129:ALA:O	2.08	0.54
1:E:93:CYS:HB3	1:E:129:ALA:HB2	1.89	0.54
1:C:388:GLU:O	1:C:391:LYS:N	2.40	0.54
1:D:427:LYS:NZ	1:D:428:HIS:H	2.05	0.54
1:E:62:VAL:HG11	1:E:109:LYS:NZ	2.23	0.54
1:A:273:LYS:HE2	1:A:288:ASP:O	2.08	0.54
1:E:337:LYS:NZ	1:E:359:GLU:HG3	2.23	0.54
1:A:427:LYS:NZ	1:A:428:HIS:H	2.05	0.54
1:C:418:GLN:CB	1:C:433:PRO:HD2	2.34	0.54
1:F:37:ARG:HB2	1:F:37:ARG:NH1	2.22	0.54
1:D:33:VAL:HG13	1:D:46:ARG:HB2	1.90	0.54
1:C:503:THR:HG21	1:F:151:ARG:NE	2.23	0.54
1:D:69:ILE:HA	1:D:151:ARG:CZ	2.37	0.54
1:E:221:ARG:HD2	1:E:454:HIS:CD2	2.43	0.54
1:C:403:PHE:CD2	1:C:447:ALA:HB1	2.43	0.54
1:B:251:PHE:CB	1:B:325:ILE:HG13	2.38	0.54
1:C:154:MET:SD	1:C:190:THR:HG21	2.47	0.54
1:B:499:GLU:HB2	1:F:209:GLN:HE21	1.73	0.54
1:A:308:PHE:O	1:A:311:ALA:HB3	2.08	0.54
1:C:427:LYS:NZ	1:C:428:HIS:H	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:VAL:HG13	1:A:46:ARG:HB2	1.89	0.54
1:A:440:PHE:O	1:A:444:ILE:HG13	2.08	0.54
1:D:13:PHE:CZ	1:D:107:GLU:HA	2.43	0.54
1:C:105:VAL:O	1:C:109:LYS:HG3	2.08	0.54
1:D:255:GLY:HA3	1:D:330:ALA:HB2	1.90	0.54
1:C:28:VAL:CG2	1:C:487:VAL:HG13	2.38	0.53
1:C:337:LYS:NZ	1:C:359:GLU:HG3	2.22	0.53
1:B:33:VAL:HG13	1:B:46:ARG:HB2	1.89	0.53
1:C:264:MET:HE3	1:C:292:PRO:HA	1.91	0.53
1:B:474:LYS:HD3	1:B:475:TYR:CE2	2.43	0.53
1:B:13:PHE:CZ	1:B:107:GLU:HA	2.43	0.53
1:A:23:ARG:O	1:A:27:ILE:HG13	2.08	0.53
1:B:337:LYS:NZ	1:B:359:GLU:HG3	2.23	0.53
1:B:427:LYS:NZ	1:B:428:HIS:H	2.07	0.53
1:C:13:PHE:CZ	1:C:107:GLU:HA	2.44	0.53
1:F:432:ILE:HG22	1:F:434:ILE:HG12	1.89	0.53
1:B:205:LYS:NZ	1:B:392:ASN:HD21	2.07	0.53
1:A:503:THR:HG21	1:E:151:ARG:CZ	2.39	0.53
1:C:423:ARG:HH21	1:E:435:VAL:CG1	2.20	0.53
1:B:21:PHE:CE1	1:B:490:ILE:HD12	2.43	0.53
1:E:105:VAL:O	1:E:109:LYS:HG3	2.09	0.53
1:B:386:TYR:OH	1:F:396:VAL:HG13	2.08	0.53
1:E:427:LYS:HZ3	1:E:428:HIS:H	1.57	0.53
1:E:427:LYS:NZ	1:E:428:HIS:H	2.06	0.53
1:E:41:SER:CA	1:E:46:ARG:HD2	2.32	0.53
1:F:251:PHE:CB	1:F:325:ILE:HG13	2.38	0.53
1:E:440:PHE:O	1:E:444:ILE:HG13	2.08	0.53
1:B:502:VAL:HG11	1:D:76:TRP:CD1	2.43	0.53
1:B:335:LEU:HD12	1:B:356:THR:HG22	1.91	0.53
1:C:118:LYS:HZ1	1:C:353:ASN:HD21	1.55	0.53
1:C:243:THR:N	1:C:244:PRO:CD	2.69	0.53
1:C:207:ILE:C	1:C:209:GLN:N	2.61	0.53
1:F:308:PHE:O	1:F:311:ALA:HB3	2.07	0.53
1:D:318:ILE:HG12	1:D:319:LEU:HD12	1.91	0.53
1:B:243:THR:H	1:B:244:PRO:HD3	1.74	0.53
1:E:33:VAL:HG13	1:E:46:ARG:HB2	1.89	0.53
1:A:252:VAL:CG1	1:A:318:ILE:HB	2.39	0.53
1:E:205:LYS:NZ	1:E:392:ASN:HD21	2.06	0.53
1:B:255:GLY:HA3	1:B:330:ALA:HB2	1.90	0.53
1:B:427:LYS:HA	1:B:427:LYS:CE	2.33	0.53
1:E:264:MET:HE3	1:E:292:PRO:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:LYS:HD2	1:C:151:ARG:NH2	2.21	0.53
1:A:243:THR:N	1:A:244:PRO:CD	2.69	0.53
1:C:205:LYS:NZ	1:C:392:ASN:ND2	2.55	0.53
1:F:373:PRO:CG	1:F:481:LEU:HB3	2.39	0.53
1:F:147:LYS:HD2	1:F:151:ARG:NH2	2.21	0.52
1:D:251:PHE:CB	1:D:325:ILE:HG13	2.38	0.52
1:F:427:LYS:NZ	1:F:428:HIS:H	2.06	0.52
1:B:347:ILE:HA	1:B:370:MET:O	2.09	0.52
1:C:205:LYS:HZ3	1:C:392:ASN:HD21	1.53	0.52
1:C:122:VAL:CG1	1:C:379:ALA:CB	2.87	0.52
1:F:255:GLY:HA3	1:F:330:ALA:HB2	1.91	0.52
1:C:78:VAL:H	1:F:54:ARG:HH12	1.57	0.52
1:F:285:TRP:O	1:F:286:ASN:HB2	2.10	0.52
1:C:116:THR:HG22	1:C:128:GLY:H	1.72	0.52
1:A:105:VAL:O	1:A:109:LYS:HG3	2.08	0.52
1:C:95:GLY:HA3	1:C:129:ALA:O	2.10	0.52
1:B:273:LYS:HE2	1:B:288:ASP:O	2.09	0.52
1:C:308:PHE:O	1:C:311:ALA:HB3	2.09	0.52
1:B:285:TRP:O	1:B:286:ASN:HB2	2.10	0.52
1:D:87:SER:O	1:D:127:GLY:HA3	2.08	0.52
1:D:336:THR:H	1:D:339:ASN:ND2	2.07	0.52
1:A:116:THR:HG22	1:A:128:GLY:N	2.25	0.52
1:C:62:VAL:HG11	1:C:109:LYS:NZ	2.24	0.52
1:E:41:SER:HA	1:E:46:ARG:CD	2.34	0.52
1:D:79:ILE:N	1:D:79:ILE:HD12	2.25	0.52
1:C:336:THR:H	1:C:339:ASN:ND2	2.07	0.52
1:F:62:VAL:HG11	1:F:109:LYS:NZ	2.24	0.52
1:E:255:GLY:HA3	1:E:330:ALA:HB2	1.91	0.52
1:A:73:ASP:O	1:A:75:SER:N	2.43	0.52
1:C:428:HIS:N	1:C:428:HIS:CD2	2.78	0.52
1:D:41:SER:HA	1:D:46:ARG:CD	2.34	0.52
1:E:205:LYS:HZ3	1:E:392:ASN:HD21	1.57	0.52
1:E:335:LEU:HD12	1:E:356:THR:HG22	1.91	0.52
1:B:332:GLU:HG2	1:B:333:LYS:HG2	1.91	0.52
1:D:73:ASP:O	1:D:75:SER:N	2.43	0.52
1:E:87:SER:O	1:E:127:GLY:HA3	2.09	0.52
1:B:30:ASP:O	1:B:34:GLU:HG2	2.10	0.52
1:B:73:ASP:O	1:B:75:SER:N	2.43	0.52
1:B:147:LYS:HD2	1:B:151:ARG:NH2	2.21	0.52
1:F:440:PHE:O	1:F:444:ILE:HG13	2.09	0.52
1:A:79:ILE:HD12	1:A:79:ILE:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:PRO:HG2	1:B:389:TRP:CZ2	2.45	0.52
1:E:425:PHE:CD1	1:E:427:LYS:HB2	2.44	0.52
1:B:41:SER:CA	1:B:46:ARG:HD2	2.32	0.52
1:E:327:ILE:CG2	1:E:349:ALA:HB3	2.35	0.52
1:E:13:PHE:CZ	1:E:107:GLU:HA	2.44	0.52
1:A:255:GLY:HA3	1:A:330:ALA:HB2	1.91	0.52
1:C:255:GLY:HA3	1:C:330:ALA:HB2	1.92	0.52
1:F:243:THR:O	1:F:243:THR:HG23	2.10	0.52
1:F:92:PRO:HG2	1:F:389:TRP:CZ2	2.45	0.52
1:B:79:ILE:N	1:B:79:ILE:HD12	2.25	0.51
1:F:13:PHE:CZ	1:F:107:GLU:HA	2.44	0.51
1:E:243:THR:H	1:E:244:PRO:HD3	1.74	0.51
1:F:252:VAL:CG1	1:F:318:ILE:HB	2.39	0.51
1:F:428:HIS:CD2	1:F:428:HIS:N	2.78	0.51
1:C:376:TYR:HB2	1:C:468:ILE:CD1	2.40	0.51
1:D:433:PRO:HA	1:E:420:SER:HB3	1.93	0.51
1:E:252:VAL:CG1	1:E:318:ILE:HB	2.41	0.51
1:B:252:VAL:CG1	1:B:318:ILE:HB	2.40	0.51
1:D:95:GLY:HA3	1:D:129:ALA:O	2.09	0.51
1:B:322:ASP:HA	1:B:344:LYS:HB2	1.92	0.51
1:A:322:ASP:HA	1:A:344:LYS:HB2	1.93	0.51
1:A:122:VAL:HG23	1:A:124:VAL:HG23	1.92	0.51
1:F:427:LYS:HZ3	1:F:428:HIS:H	1.58	0.51
1:D:40:GLU:HG3	1:D:46:ARG:NH1	2.16	0.51
1:D:504:PHE:HB3	1:E:146:GLU:OE1	2.09	0.51
1:B:226:GLY:HA3	1:B:377:LEU:CD1	2.40	0.51
1:B:318:ILE:HG12	1:B:319:LEU:HD12	1.92	0.51
1:D:62:VAL:HG11	1:D:109:LYS:NZ	2.25	0.51
1:A:78:VAL:HG23	1:A:78:VAL:O	2.11	0.51
1:E:308:PHE:O	1:E:311:ALA:HB3	2.10	0.51
1:C:471:THR:HA	1:C:474:LYS:HB3	1.92	0.51
1:C:243:THR:HG23	1:C:243:THR:O	2.09	0.51
1:C:318:ILE:HG12	1:C:319:LEU:HD12	1.92	0.51
1:A:428:HIS:N	1:A:428:HIS:CD2	2.78	0.51
1:D:474:LYS:HD3	1:D:475:TYR:CE2	2.45	0.51
1:D:487:VAL:O	1:D:491:GLU:HG3	2.11	0.51
1:A:348:ILE:HB	1:A:371:VAL:HG22	1.92	0.51
1:A:471:THR:HA	1:A:474:LYS:HB3	1.93	0.51
1:E:147:LYS:HD2	1:E:151:ARG:NH2	2.20	0.51
1:E:79:ILE:HD12	1:E:79:ILE:N	2.25	0.51
1:D:99:TYR:HH	1:D:149:THR:HG22	1.72	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:348:ILE:HB	1:D:371:VAL:HG22	1.92	0.51
1:F:318:ILE:N	1:F:318:ILE:HD13	2.25	0.51
1:F:28:VAL:CG2	1:F:487:VAL:HG13	2.39	0.51
1:F:226:GLY:HA3	1:F:377:LEU:CD1	2.40	0.51
1:A:285:TRP:O	1:A:286:ASN:HB2	2.11	0.51
1:D:308:PHE:O	1:D:311:ALA:HB3	2.09	0.51
1:D:41:SER:CA	1:D:46:ARG:HD2	2.31	0.51
1:C:251:PHE:CB	1:C:325:ILE:HG13	2.41	0.51
1:C:221:ARG:HD2	1:C:454:HIS:CE1	2.45	0.51
1:E:243:THR:HG23	1:E:243:THR:O	2.11	0.51
1:B:308:PHE:O	1:B:311:ALA:HB3	2.09	0.51
1:B:40:GLU:HG3	1:B:46:ARG:NH1	2.17	0.51
1:C:252:VAL:CG1	1:C:318:ILE:HB	2.40	0.51
1:F:471:THR:HA	1:F:474:LYS:HB3	1.93	0.51
1:A:92:PRO:HG2	1:A:389:TRP:CZ2	2.46	0.51
1:B:266:TYR:O	1:B:270:PHE:HD2	1.94	0.51
1:F:40:GLU:O	1:F:42:GLU:N	2.44	0.51
1:C:41:SER:HA	1:C:46:ARG:CD	2.34	0.51
1:B:440:PHE:O	1:B:444:ILE:HG13	2.10	0.51
1:A:116:THR:HG22	1:A:128:GLY:H	1.76	0.51
1:D:335:LEU:HD12	1:D:356:THR:HG22	1.92	0.51
1:C:78:VAL:N	1:F:54:ARG:HH12	2.08	0.51
1:B:87:SER:O	1:B:127:GLY:HA3	2.11	0.51
1:E:285:TRP:O	1:E:286:ASN:HB2	2.10	0.51
1:C:425:PHE:CD1	1:C:427:LYS:HB2	2.43	0.51
1:A:425:PHE:CD1	1:A:427:LYS:HB2	2.44	0.51
1:C:226:GLY:HA3	1:C:377:LEU:CD1	2.41	0.51
1:D:62:VAL:HG11	1:D:109:LYS:HZ3	1.76	0.51
1:B:54:ARG:HH12	1:D:77:GLU:HA	1.75	0.51
1:F:95:GLY:HA3	1:F:129:ALA:O	2.11	0.51
1:F:266:TYR:O	1:F:270:PHE:HD2	1.94	0.51
1:E:73:ASP:O	1:E:75:SER:N	2.42	0.51
1:A:298:PHE:HE1	1:A:309:PRO:HD3	1.76	0.50
1:F:30:ASP:O	1:F:34:GLU:HG2	2.11	0.50
1:C:30:ASP:O	1:C:34:GLU:HG2	2.11	0.50
1:B:505:THR:N	1:F:150:ARG:HH12	2.08	0.50
1:D:40:GLU:O	1:D:42:GLU:N	2.44	0.50
1:E:251:PHE:CB	1:E:325:ILE:HG13	2.39	0.50
1:D:252:VAL:CG1	1:D:318:ILE:HB	2.41	0.50
1:B:348:ILE:HB	1:B:371:VAL:HG22	1.93	0.50
1:D:243:THR:O	1:D:243:THR:HG23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:ASP:O	1:C:75:SER:N	2.45	0.50
1:F:73:ASP:O	1:F:75:SER:N	2.44	0.50
1:B:425:PHE:CD1	1:B:427:LYS:HB2	2.44	0.50
1:E:38:THR:CG2	1:E:41:SER:HB3	2.40	0.50
1:B:40:GLU:O	1:B:42:GLU:N	2.44	0.50
1:C:40:GLU:O	1:C:42:GLU:N	2.44	0.50
1:B:116:THR:HG22	1:B:128:GLY:H	1.77	0.50
1:B:116:THR:HG22	1:B:128:GLY:N	2.25	0.50
1:A:243:THR:O	1:A:243:THR:HG23	2.12	0.50
1:D:488:ASN:HD21	1:D:492:LYS:HZ2	1.59	0.50
1:A:298:PHE:CE1	1:A:309:PRO:HD3	2.47	0.50
1:D:285:TRP:O	1:D:286:ASN:HB2	2.10	0.50
1:C:502:VAL:HG11	1:F:76:TRP:HD1	1.77	0.50
1:C:376:TYR:HB2	1:C:468:ILE:HD11	1.92	0.50
1:E:243:THR:N	1:E:244:PRO:CD	2.67	0.50
1:D:471:THR:HA	1:D:474:LYS:HB3	1.93	0.50
1:C:243:THR:H	1:C:244:PRO:HD3	1.74	0.50
1:C:372:ILE:HA	1:C:481:LEU:HD23	1.93	0.50
1:A:474:LYS:HD3	1:A:475:TYR:CE2	2.46	0.50
1:A:332:GLU:HG2	1:A:333:LYS:HG2	1.92	0.50
1:C:332:GLU:HG2	1:C:333:LYS:HG2	1.93	0.50
1:E:266:TYR:O	1:E:270:PHE:HD2	1.95	0.50
1:E:428:HIS:CD2	1:E:428:HIS:N	2.78	0.50
1:D:440:PHE:O	1:D:444:ILE:HG13	2.11	0.50
1:E:318:ILE:HG12	1:E:319:LEU:HD12	1.92	0.50
1:F:335:LEU:HD12	1:F:356:THR:HG22	1.94	0.50
1:C:335:LEU:HD12	1:C:356:THR:HG22	1.94	0.50
1:A:78:VAL:N	1:E:54:ARG:HH12	2.10	0.50
1:D:30:ASP:O	1:D:34:GLU:HG2	2.11	0.50
1:D:428:HIS:CD2	1:D:428:HIS:N	2.79	0.50
1:A:318:ILE:HG12	1:A:319:LEU:HD12	1.92	0.50
1:C:285:TRP:O	1:C:286:ASN:HB2	2.12	0.50
1:C:420:SER:HB3	1:E:432:ILE:O	2.12	0.50
1:F:318:ILE:HG12	1:F:319:LEU:HD12	1.93	0.50
1:B:105:VAL:HG12	1:B:109:LYS:HE2	1.94	0.50
1:C:390:LEU:HD13	1:D:396:VAL:HG21	1.93	0.50
1:D:122:VAL:HG23	1:D:124:VAL:HG23	1.94	0.50
1:B:428:HIS:CD2	1:B:428:HIS:N	2.79	0.50
1:D:347:ILE:HA	1:D:370:MET:O	2.12	0.50
1:C:440:PHE:O	1:C:444:ILE:HG13	2.11	0.50
1:A:343:VAL:CG2	1:A:364:PHE:HE1	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:348:ILE:HB	1:F:371:VAL:HG22	1.93	0.50
1:E:28:VAL:HG23	1:E:487:VAL:HG13	1.94	0.50
1:D:425:PHE:CD1	1:D:427:LYS:HB2	2.44	0.50
1:E:226:GLY:HA3	1:E:377:LEU:CD1	2.42	0.50
1:E:347:ILE:HA	1:E:370:MET:O	2.12	0.50
1:B:435:VAL:HG13	1:F:423:ARG:HH21	1.75	0.50
1:C:348:ILE:HB	1:C:371:VAL:HG22	1.93	0.50
1:A:335:LEU:HD12	1:A:356:THR:HG22	1.93	0.50
1:E:488:ASN:HD21	1:E:492:LYS:HZ2	1.60	0.50
1:C:504:PHE:CE1	1:F:70:ARG:HB3	2.47	0.49
1:D:327:ILE:CG2	1:D:349:ALA:HB3	2.34	0.49
1:F:116:THR:HG22	1:F:128:GLY:N	2.27	0.49
1:D:319:LEU:HD12	1:D:319:LEU:N	2.27	0.49
1:C:213:HIS:HB2	1:C:449:GLU:HB3	1.93	0.49
1:E:322:ASP:HA	1:E:344:LYS:HB2	1.93	0.49
1:F:322:ASP:HA	1:F:344:LYS:HB2	1.93	0.49
1:C:421:LEU:HD21	1:E:421:LEU:HD21	1.93	0.49
1:E:40:GLU:O	1:E:42:GLU:N	2.45	0.49
1:A:40:GLU:HG3	1:A:46:ARG:NH1	2.15	0.49
1:F:79:ILE:HD12	1:F:79:ILE:N	2.27	0.49
1:D:318:ILE:N	1:D:318:ILE:HD13	2.25	0.49
1:B:471:THR:HA	1:B:474:LYS:HB3	1.93	0.49
1:E:471:THR:HA	1:E:474:LYS:HB3	1.93	0.49
1:D:391:LYS:NZ	1:D:449:GLU:OE1	2.43	0.49
1:F:332:GLU:HG2	1:F:333:LYS:HG2	1.93	0.49
1:E:30:ASP:O	1:E:34:GLU:HG2	2.12	0.49
1:B:243:THR:HG23	1:B:243:THR:O	2.11	0.49
1:C:206:PRO:HB2	1:C:209:GLN:CG	2.43	0.49
1:C:78:VAL:O	1:C:78:VAL:HG23	2.13	0.49
1:D:266:TYR:O	1:D:270:PHE:HD2	1.95	0.49
1:C:298:PHE:HE1	1:C:309:PRO:HD3	1.78	0.49
1:F:298:PHE:CE1	1:F:309:PRO:HD3	2.48	0.49
1:C:79:ILE:N	1:C:79:ILE:HD12	2.27	0.49
1:F:336:THR:H	1:F:339:ASN:ND2	2.08	0.49
1:A:336:THR:H	1:A:339:ASN:ND2	2.08	0.49
1:F:474:LYS:HD3	1:F:475:TYR:CE2	2.47	0.49
1:F:337:LYS:HZ2	1:F:359:GLU:HG3	1.77	0.49
1:D:221:ARG:HD2	1:D:454:HIS:NE2	2.27	0.49
1:A:40:GLU:O	1:A:42:GLU:N	2.45	0.49
1:B:76:TRP:HB2	1:D:51:GLY:HA3	1.95	0.49
1:F:347:ILE:HA	1:F:370:MET:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:VAL:N	1:B:505:THR:HB	2.28	0.49
1:C:242:MET:O	1:C:243:THR:HG22	2.13	0.49
1:C:122:VAL:CG1	1:C:379:ALA:HB3	2.41	0.49
1:D:332:GLU:HG2	1:D:333:LYS:HG2	1.92	0.49
1:F:87:SER:O	1:F:127:GLY:HA3	2.12	0.49
1:E:332:GLU:HG2	1:E:333:LYS:HG2	1.93	0.49
1:E:37:ARG:NH2	1:E:49:VAL:HG11	2.28	0.49
1:D:505:THR:HG23	1:E:150:ARG:HH22	1.77	0.49
1:A:226:GLY:HA3	1:A:377:LEU:CD1	2.42	0.49
1:A:347:ILE:HA	1:A:370:MET:O	2.13	0.49
1:B:375:LEU:HD22	1:B:486:TYR:CE2	2.47	0.49
1:A:147:LYS:HD2	1:A:151:ARG:NH2	2.20	0.49
1:B:336:THR:H	1:B:339:ASN:ND2	2.09	0.49
1:F:105:VAL:HG12	1:F:109:LYS:HE2	1.95	0.49
1:F:487:VAL:O	1:F:491:GLU:HG3	2.12	0.49
1:E:136:ASN:OD1	1:E:138:LYS:HB2	2.13	0.49
1:D:502:VAL:N	1:D:505:THR:HB	2.28	0.49
1:C:376:TYR:CZ	1:C:465:ALA:HB2	2.47	0.49
1:E:116:THR:HG22	1:E:128:GLY:N	2.27	0.49
1:D:116:THR:HG22	1:D:128:GLY:N	2.27	0.49
1:C:105:VAL:HG12	1:C:109:LYS:HE2	1.95	0.49
1:E:348:ILE:HB	1:E:371:VAL:HG22	1.94	0.49
1:B:16:MET:SD	1:B:358:PRO:HD3	2.52	0.49
1:A:30:ASP:O	1:A:34:GLU:HG2	2.13	0.49
1:C:505:THR:C	1:D:150:ARG:HH22	2.15	0.49
1:E:13:PHE:CE2	1:E:107:GLU:HG3	2.48	0.49
1:C:69:ILE:HG12	1:C:79:ILE:CD1	2.43	0.49
1:D:243:THR:H	1:D:244:PRO:HD3	1.75	0.49
1:C:228:GLU:O	1:C:231:ILE:HG22	2.13	0.49
1:C:488:ASN:HD21	1:C:492:LYS:NZ	2.11	0.49
1:D:322:ASP:HA	1:D:344:LYS:HB2	1.93	0.49
1:A:199:HIS:O	1:A:205:LYS:HE2	2.13	0.49
1:A:69:ILE:HG12	1:A:79:ILE:CD1	2.43	0.49
1:F:242:MET:O	1:F:243:THR:HG22	2.12	0.49
1:C:122:VAL:HG23	1:C:124:VAL:HG23	1.94	0.49
1:C:28:VAL:HG22	1:C:487:VAL:HG13	1.94	0.49
1:F:285:TRP:CD1	1:F:287:PRO:HD3	2.48	0.49
1:D:13:PHE:CE2	1:D:107:GLU:HG3	2.48	0.49
1:C:76:TRP:CD1	1:F:502:VAL:HG11	2.46	0.49
1:C:400:ARG:NH1	1:C:400:ARG:HG3	2.28	0.49
1:C:122:VAL:HG11	1:C:379:ALA:HB1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:THR:HB	1:B:92:PRO:HD3	1.95	0.49
1:A:266:TYR:O	1:A:270:PHE:HD2	1.95	0.49
1:F:425:PHE:CD1	1:F:427:LYS:HB2	2.42	0.48
1:D:505:THR:N	1:E:150:ARG:NH1	2.60	0.48
1:B:13:PHE:CE2	1:B:107:GLU:HG3	2.48	0.48
1:F:252:VAL:HG23	1:F:323:CYS:SG	2.53	0.48
1:B:343:VAL:CG2	1:B:364:PHE:HE1	2.25	0.48
1:B:487:VAL:O	1:B:491:GLU:HG3	2.13	0.48
1:A:233:GLU:HG2	1:A:236:TYR:HD1	1.78	0.48
1:F:427:LYS:HA	1:F:427:LYS:CE	2.33	0.48
1:C:420:SER:HB2	1:E:433:PRO:HA	1.94	0.48
1:D:116:THR:HG22	1:D:128:GLY:H	1.78	0.48
1:F:343:VAL:CG2	1:F:364:PHE:HE1	2.25	0.48
1:F:91:THR:HB	1:F:92:PRO:HD3	1.95	0.48
1:F:235:SER:O	1:F:239:ILE:HG12	2.13	0.48
1:C:425:PHE:HD1	1:C:427:LYS:CB	2.26	0.48
1:F:13:PHE:CE2	1:F:107:GLU:HG3	2.49	0.48
1:A:243:THR:H	1:A:244:PRO:HD3	1.74	0.48
1:D:78:VAL:O	1:D:78:VAL:HG23	2.12	0.48
1:C:78:VAL:HG13	1:F:54:ARG:NH1	2.28	0.48
1:C:136:ASN:OD1	1:C:138:LYS:HB2	2.13	0.48
1:C:266:TYR:O	1:C:270:PHE:HD2	1.96	0.48
1:D:298:PHE:HE1	1:D:309:PRO:HD3	1.77	0.48
1:F:425:PHE:HD1	1:F:427:LYS:CB	2.25	0.48
1:B:427:LYS:HZ3	1:B:428:HIS:H	1.59	0.48
1:A:13:PHE:CE2	1:A:107:GLU:HG3	2.48	0.48
1:E:319:LEU:N	1:E:319:LEU:HD12	2.28	0.48
1:C:252:VAL:HG23	1:C:323:CYS:SG	2.53	0.48
1:C:322:ASP:HA	1:C:344:LYS:HB2	1.93	0.48
1:A:488:ASN:HD21	1:A:492:LYS:NZ	2.12	0.48
1:E:221:ARG:CD	1:E:454:HIS:CD2	2.96	0.48
1:E:242:MET:O	1:E:243:THR:HG22	2.14	0.48
1:A:187:TYR:CE2	1:A:192:GLY:HA3	2.48	0.48
1:F:122:VAL:HG23	1:F:124:VAL:HG23	1.95	0.48
1:D:298:PHE:CE1	1:D:309:PRO:HD3	2.48	0.48
1:A:427:LYS:HZ3	1:A:428:HIS:H	1.60	0.48
1:A:49:VAL:HA	1:E:76:TRP:CZ3	2.48	0.48
1:C:40:GLU:HG3	1:C:46:ARG:NH1	2.15	0.48
1:C:13:PHE:CE2	1:C:107:GLU:HG3	2.48	0.48
1:F:502:VAL:N	1:F:505:THR:HB	2.28	0.48
1:E:343:VAL:CG2	1:E:364:PHE:HE1	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:78:VAL:O	1:E:78:VAL:HG23	2.12	0.48
1:E:487:VAL:O	1:E:491:GLU:HG3	2.14	0.48
1:A:78:VAL:H	1:E:54:ARG:HH12	1.61	0.48
1:C:87:SER:O	1:C:127:GLY:HA3	2.14	0.48
1:C:187:TYR:CE2	1:C:192:GLY:HA3	2.49	0.48
1:E:233:GLU:HG2	1:E:236:TYR:HD1	1.79	0.48
1:C:298:PHE:CE1	1:C:309:PRO:HD3	2.48	0.48
1:A:283:SER:HB2	1:A:314:TYR:O	2.13	0.48
1:D:37:ARG:NH2	1:D:49:VAL:HG11	2.29	0.48
1:C:502:VAL:N	1:C:505:THR:HB	2.28	0.48
1:B:319:LEU:HD12	1:B:319:LEU:N	2.29	0.48
1:C:283:SER:HB2	1:C:314:TYR:O	2.14	0.48
1:F:298:PHE:HE1	1:F:309:PRO:HD3	1.77	0.48
1:A:41:SER:CA	1:A:46:ARG:HD2	2.32	0.48
1:A:327:ILE:CG2	1:A:349:ALA:HB3	2.34	0.48
1:B:78:VAL:HG23	1:B:78:VAL:O	2.14	0.48
1:A:154:MET:CE	1:A:190:THR:HG21	2.44	0.48
1:F:118:LYS:NZ	1:F:353:ASN:HD21	2.12	0.48
1:F:38:THR:CG2	1:F:41:SER:HB3	2.41	0.48
1:B:33:VAL:O	1:B:38:THR:N	2.47	0.48
1:A:76:TRP:HD1	1:E:502:VAL:HG11	1.76	0.48
1:A:319:LEU:N	1:A:319:LEU:HD12	2.29	0.48
1:A:242:MET:O	1:A:243:THR:HG22	2.13	0.48
1:E:91:THR:HB	1:E:92:PRO:HD3	1.96	0.48
1:E:235:SER:O	1:E:239:ILE:HG12	2.14	0.48
1:F:283:SER:HB2	1:F:314:TYR:O	2.13	0.48
1:A:502:VAL:N	1:A:505:THR:HB	2.28	0.48
1:C:150:ARG:HH12	1:E:505:THR:C	2.17	0.48
1:E:502:VAL:N	1:E:505:THR:HB	2.28	0.48
1:B:242:MET:O	1:B:243:THR:HG22	2.13	0.48
1:F:488:ASN:HD21	1:F:492:LYS:NZ	2.12	0.48
1:D:100:SER:O	1:D:103:VAL:HG22	2.14	0.48
1:C:37:ARG:NH2	1:C:49:VAL:HG11	2.29	0.47
1:E:336:THR:H	1:E:339:ASN:ND2	2.09	0.47
1:B:54:ARG:HH12	1:D:78:VAL:H	1.60	0.47
1:A:235:SER:O	1:A:239:ILE:HG12	2.14	0.47
1:A:391:LYS:NZ	1:A:449:GLU:OE1	2.41	0.47
1:B:230:PHE:CE2	1:B:481:LEU:HD21	2.49	0.47
1:D:205:LYS:NZ	1:D:388:GLU:OE1	2.43	0.47
1:A:251:PHE:HB3	1:A:325:ILE:CG1	2.41	0.47
1:C:217:SER:OG	1:C:454:HIS:CE1	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:343:VAL:CG2	1:D:364:PHE:HE1	2.25	0.47
1:A:318:ILE:HD13	1:A:318:ILE:N	2.26	0.47
1:C:211:GLY:O	1:C:391:LYS:NZ	2.42	0.47
1:C:100:SER:O	1:C:103:VAL:HG22	2.15	0.47
1:C:427:LYS:HZ3	1:C:428:HIS:H	1.60	0.47
1:E:116:THR:HG22	1:E:128:GLY:H	1.79	0.47
1:F:116:THR:HG22	1:F:128:GLY:H	1.79	0.47
1:F:372:ILE:HA	1:F:373:PRO:HD3	1.64	0.47
1:D:488:ASN:HD21	1:D:492:LYS:NZ	2.12	0.47
1:A:257:GLY:O	1:A:260:GLY:N	2.48	0.47
1:D:136:ASN:OD1	1:D:138:LYS:HB2	2.14	0.47
1:E:122:VAL:HG23	1:E:124:VAL:HG23	1.96	0.47
1:A:285:TRP:CD1	1:A:287:PRO:HD3	2.49	0.47
1:B:283:SER:HB2	1:B:314:TYR:O	2.14	0.47
1:B:285:TRP:CD1	1:B:287:PRO:HD3	2.50	0.47
1:F:41:SER:HA	1:F:46:ARG:CD	2.33	0.47
1:E:69:ILE:HG12	1:E:79:ILE:CD1	2.44	0.47
1:C:503:THR:HG21	1:F:151:ARG:HD3	1.96	0.47
1:F:69:ILE:HG12	1:F:79:ILE:CD1	2.44	0.47
1:D:226:GLY:HA3	1:D:377:LEU:CD1	2.44	0.47
1:F:319:LEU:HD12	1:F:319:LEU:N	2.29	0.47
1:C:343:VAL:CG2	1:C:364:PHE:HE1	2.26	0.47
1:B:235:SER:O	1:B:239:ILE:HG12	2.14	0.47
1:B:187:TYR:CE2	1:B:192:GLY:HA3	2.49	0.47
1:E:298:PHE:HE1	1:E:309:PRO:HD3	1.78	0.47
1:A:251:PHE:CE2	1:A:264:MET:HA	2.50	0.47
1:A:432:ILE:HG22	1:A:434:ILE:CG1	2.43	0.47
1:F:418:GLN:OE1	1:F:434:ILE:HG23	2.15	0.47
1:F:221:ARG:HD2	1:F:454:HIS:CE1	2.48	0.47
1:C:319:LEU:HD12	1:C:319:LEU:N	2.30	0.47
1:C:373:PRO:HD3	1:C:481:LEU:HB3	1.96	0.47
1:D:105:VAL:HG12	1:D:109:LYS:HE2	1.96	0.47
1:A:487:VAL:O	1:A:491:GLU:HG3	2.14	0.47
1:E:233:GLU:CG	1:E:236:TYR:HD1	2.27	0.47
1:C:257:GLY:O	1:C:258:ASN:C	2.53	0.47
1:D:184:ALA:HA	1:D:201:CYS:SG	2.54	0.47
1:B:298:PHE:CE1	1:B:309:PRO:HD3	2.49	0.47
1:B:298:PHE:CE1	1:B:302:HIS:HE1	2.33	0.47
1:B:298:PHE:HE1	1:B:309:PRO:HD3	1.78	0.47
1:A:37:ARG:NH2	1:A:49:VAL:HG11	2.30	0.47
1:A:33:VAL:O	1:A:38:THR:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:154:MET:CE	1:D:190:THR:HG21	2.45	0.47
1:D:91:THR:HB	1:D:92:PRO:HD3	1.97	0.47
1:C:235:SER:O	1:C:239:ILE:HG12	2.14	0.47
1:A:100:SER:O	1:A:103:VAL:HG22	2.15	0.47
1:B:122:VAL:HG23	1:B:124:VAL:HG23	1.97	0.47
1:C:285:TRP:CD1	1:C:287:PRO:HD3	2.50	0.47
1:E:298:PHE:CE1	1:E:302:HIS:HE1	2.33	0.47
1:F:327:ILE:CG2	1:F:349:ALA:HB3	2.33	0.47
1:F:251:PHE:HB3	1:F:325:ILE:CG1	2.41	0.47
1:C:347:ILE:HA	1:C:370:MET:O	2.14	0.47
1:C:327:ILE:CG2	1:C:349:ALA:HB3	2.36	0.47
1:E:21:PHE:CE1	1:E:490:ILE:HD12	2.49	0.47
1:E:432:ILE:HG22	1:E:434:ILE:CG1	2.45	0.47
1:D:13:PHE:CE1	1:D:107:GLU:HA	2.50	0.47
1:D:92:PRO:HG2	1:D:389:TRP:CZ2	2.50	0.47
1:A:233:GLU:CG	1:A:236:TYR:HD1	2.27	0.47
1:B:136:ASN:OD1	1:B:138:LYS:HB2	2.14	0.47
1:E:177:GLU:HB2	1:E:206:PRO:HG3	1.97	0.47
1:C:33:VAL:O	1:C:38:THR:N	2.47	0.47
1:D:242:MET:O	1:D:243:THR:HG22	2.14	0.47
1:A:228:GLU:O	1:A:231:ILE:HG22	2.15	0.47
1:A:54:ARG:HH12	1:E:77:GLU:HA	1.80	0.47
1:E:187:TYR:CE2	1:E:192:GLY:HA3	2.50	0.47
1:D:257:GLY:O	1:D:260:GLY:N	2.48	0.47
1:D:432:ILE:HG22	1:D:434:ILE:CG1	2.45	0.47
1:B:374:ASP:O	1:B:378:ASN:ND2	2.48	0.47
1:F:243:THR:H	1:F:244:PRO:HD3	1.75	0.47
1:E:105:VAL:HG12	1:E:109:LYS:HE2	1.97	0.47
1:B:339:ASN:N	1:B:339:ASN:HD22	2.13	0.47
1:C:91:THR:HB	1:C:92:PRO:HD3	1.97	0.47
1:F:298:PHE:CE1	1:F:302:HIS:HE1	2.33	0.47
1:D:283:SER:HB2	1:D:314:TYR:O	2.14	0.47
1:D:33:VAL:O	1:D:38:THR:N	2.48	0.47
1:C:421:LEU:HA	1:C:421:LEU:HD12	1.74	0.47
1:D:187:TYR:CE2	1:D:192:GLY:HA3	2.50	0.47
1:D:425:PHE:HD1	1:D:427:LYS:CB	2.27	0.46
1:A:41:SER:HA	1:A:46:ARG:CD	2.35	0.46
1:C:38:THR:CG2	1:C:41:SER:HB3	2.40	0.46
1:C:154:MET:CE	1:C:190:THR:HG21	2.45	0.46
1:C:373:PRO:CD	1:C:481:LEU:HB3	2.46	0.46
1:C:54:ARG:NH1	1:F:77:GLU:HA	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:GLU:HG2	1:C:236:TYR:HD1	1.80	0.46
1:B:69:ILE:HG12	1:B:79:ILE:CD1	2.46	0.46
1:C:423:ARG:NH2	1:E:435:VAL:HG13	2.27	0.46
1:D:418:GLN:OE1	1:D:434:ILE:HG23	2.16	0.46
1:E:154:MET:CE	1:E:190:THR:HG21	2.45	0.46
1:D:339:ASN:H	1:D:339:ASN:ND2	2.13	0.46
1:E:320:GLU:HG3	1:E:342:ARG:HG2	1.98	0.46
1:B:233:GLU:HG2	1:B:236:TYR:HD1	1.80	0.46
1:F:233:GLU:HG2	1:F:236:TYR:HD1	1.80	0.46
1:A:184:ALA:HA	1:A:201:CYS:SG	2.55	0.46
1:C:298:PHE:CE1	1:C:302:HIS:HE1	2.33	0.46
1:E:283:SER:HB2	1:E:314:TYR:O	2.15	0.46
1:B:41:SER:HA	1:B:46:ARG:CD	2.34	0.46
1:F:251:PHE:CE2	1:F:264:MET:HA	2.50	0.46
1:A:13:PHE:CE1	1:A:107:GLU:HA	2.50	0.46
1:F:78:VAL:O	1:F:78:VAL:HG23	2.14	0.46
1:C:334:GLN:HA	1:C:334:GLN:HE21	1.80	0.46
1:C:388:GLU:O	1:C:391:LYS:HB3	2.15	0.46
1:E:488:ASN:HD21	1:E:492:LYS:NZ	2.13	0.46
1:F:257:GLY:O	1:F:260:GLY:N	2.48	0.46
1:C:374:ASP:O	1:C:378:ASN:ND2	2.48	0.46
1:A:177:GLU:HB2	1:A:206:PRO:HG3	1.97	0.46
1:A:425:PHE:HD1	1:A:427:LYS:CB	2.28	0.46
1:E:33:VAL:O	1:E:38:THR:N	2.47	0.46
1:C:505:THR:C	1:D:150:ARG:HH12	2.19	0.46
1:E:13:PHE:CE1	1:E:107:GLU:HA	2.51	0.46
1:D:252:VAL:HG23	1:D:323:CYS:SG	2.56	0.46
1:F:133:VAL:HG12	1:F:135:ILE:HB	1.98	0.46
1:C:184:ALA:HA	1:C:201:CYS:SG	2.56	0.46
1:E:298:PHE:CE1	1:E:309:PRO:HD3	2.49	0.46
1:A:298:PHE:CE1	1:A:302:HIS:HE1	2.34	0.46
1:D:427:LYS:CE	1:D:427:LYS:HA	2.32	0.46
1:C:13:PHE:CE1	1:C:107:GLU:HA	2.51	0.46
1:B:502:VAL:HG23	1:B:503:THR:N	2.28	0.46
1:B:505:THR:HG23	1:F:150:ARG:NH2	2.31	0.46
1:A:150:ARG:HH12	1:F:505:THR:C	2.19	0.46
1:B:190:THR:HG22	1:B:191:ILE:HG12	1.98	0.46
1:C:487:VAL:O	1:C:491:GLU:HG3	2.15	0.46
1:F:334:GLN:HE21	1:F:334:GLN:HA	1.81	0.46
1:D:257:GLY:O	1:D:258:ASN:C	2.54	0.46
1:D:285:TRP:CD1	1:D:287:PRO:HD3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:427:LYS:HG3	1:B:430:GLY:H	1.81	0.46
1:B:327:ILE:CG2	1:B:349:ALA:HB3	2.34	0.46
1:B:418:GLN:OE1	1:B:434:ILE:HG23	2.16	0.46
1:D:435:VAL:HG13	1:E:423:ARG:NH2	2.31	0.46
1:F:432:ILE:HG22	1:F:434:ILE:CG1	2.46	0.46
1:E:120:ALA:O	1:E:492:LYS:NZ	2.48	0.46
1:D:421:LEU:HD23	1:E:421:LEU:HD11	1.96	0.46
1:C:233:GLU:CG	1:C:236:TYR:HD1	2.28	0.46
1:B:257:GLY:O	1:B:260:GLY:N	2.48	0.46
1:C:51:GLY:O	1:C:55:ILE:HG13	2.15	0.46
1:E:285:TRP:CD1	1:E:287:PRO:HD3	2.50	0.46
1:F:37:ARG:NH2	1:F:49:VAL:HG11	2.29	0.46
1:B:432:ILE:HG22	1:B:434:ILE:CG1	2.45	0.46
1:D:435:VAL:CG1	1:E:423:ARG:HH21	2.28	0.46
1:C:150:ARG:HH12	1:E:505:THR:N	2.13	0.46
1:C:418:GLN:OE1	1:C:434:ILE:HG23	2.15	0.46
1:B:154:MET:CE	1:B:190:THR:HG21	2.45	0.46
1:B:322:ASP:OD1	1:B:344:LYS:HB3	2.16	0.46
1:C:257:GLY:O	1:C:260:GLY:N	2.49	0.46
1:F:100:SER:O	1:F:103:VAL:HG22	2.15	0.46
1:C:427:LYS:HG3	1:C:430:GLY:H	1.81	0.46
1:B:13:PHE:CE1	1:B:107:GLU:HA	2.51	0.46
1:F:339:ASN:H	1:F:339:ASN:ND2	2.14	0.46
1:E:339:ASN:ND2	1:E:339:ASN:H	2.14	0.46
1:C:133:VAL:HG12	1:C:135:ILE:HB	1.98	0.46
1:B:91:THR:CB	1:B:92:PRO:CD	2.94	0.46
1:A:206:PRO:HD2	1:A:209:GLN:HB2	1.98	0.46
1:B:257:GLY:O	1:B:258:ASN:C	2.54	0.46
1:F:187:TYR:CE2	1:F:192:GLY:HA3	2.51	0.46
1:D:233:GLU:HG2	1:D:236:TYR:HD1	1.80	0.46
1:F:136:ASN:OD1	1:F:138:LYS:HB2	2.15	0.46
1:A:421:LEU:HA	1:A:421:LEU:HD12	1.73	0.46
1:C:49:VAL:HA	1:F:76:TRP:CZ3	2.50	0.46
1:C:12:ASN:ND2	1:C:14:PHE:HB3	2.30	0.46
1:A:70:ARG:HB3	1:E:504:PHE:CE1	2.50	0.46
1:C:432:ILE:HG22	1:C:434:ILE:CG1	2.45	0.46
1:E:339:ASN:N	1:E:339:ASN:HD22	2.13	0.46
1:D:277:VAL:HG21	1:D:295:LEU:HD22	1.98	0.46
1:A:91:THR:HB	1:A:92:PRO:HD3	1.97	0.46
1:B:320:GLU:HG3	1:B:342:ARG:HG2	1.98	0.46
1:B:184:ALA:HA	1:B:201:CYS:SG	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:308:PHE:CD2	1:C:311:ALA:HB2	2.49	0.46
1:E:12:ASN:ND2	1:E:14:PHE:HB3	2.31	0.46
1:A:252:VAL:HG23	1:A:323:CYS:SG	2.56	0.46
1:B:339:ASN:HD22	1:B:339:ASN:H	1.64	0.46
1:F:228:GLU:O	1:F:231:ILE:HG22	2.15	0.46
1:F:91:THR:CB	1:F:92:PRO:CD	2.93	0.46
1:C:320:GLU:HG3	1:C:342:ARG:HG2	1.98	0.46
1:C:273:LYS:HE2	1:C:288:ASP:C	2.36	0.46
1:C:421:LEU:HD11	1:E:421:LEU:HD23	1.97	0.46
1:E:374:ASP:O	1:E:378:ASN:ND2	2.49	0.46
1:A:374:ASP:O	1:A:378:ASN:ND2	2.48	0.46
1:A:136:ASN:OD1	1:A:138:LYS:HB2	2.15	0.46
1:E:298:PHE:CE1	1:E:308:PHE:HA	2.52	0.45
1:D:298:PHE:CE1	1:D:302:HIS:HE1	2.33	0.45
1:D:69:ILE:HG12	1:D:79:ILE:CD1	2.46	0.45
1:F:12:ASN:ND2	1:F:14:PHE:HB3	2.31	0.45
1:A:339:ASN:HD22	1:A:339:ASN:N	2.14	0.45
1:C:373:PRO:HG3	1:C:481:LEU:HB3	1.96	0.45
1:B:133:VAL:HG12	1:B:135:ILE:HB	1.98	0.45
1:F:122:VAL:HG11	1:F:379:ALA:HB3	1.98	0.45
1:F:233:GLU:CG	1:F:236:TYR:HD1	2.28	0.45
1:F:51:GLY:O	1:F:55:ILE:HG13	2.16	0.45
1:A:372:ILE:HA	1:A:373:PRO:HD3	1.63	0.45
1:B:100:SER:O	1:B:103:VAL:HG22	2.17	0.45
1:E:149:THR:HG1	1:E:182:TRP:HE3	1.64	0.45
1:D:502:VAL:HG23	1:D:503:THR:N	2.28	0.45
1:C:251:PHE:CE2	1:C:264:MET:HA	2.51	0.45
1:C:420:SER:HB3	1:E:433:PRO:HA	1.95	0.45
1:B:118:LYS:NZ	1:B:378:ASN:ND2	2.64	0.45
1:B:339:ASN:ND2	1:B:339:ASN:H	2.13	0.45
1:D:233:GLU:CG	1:D:236:TYR:HD1	2.29	0.45
1:B:177:GLU:HB2	1:B:206:PRO:HG3	1.99	0.45
1:B:372:ILE:HA	1:B:373:PRO:HD3	1.62	0.45
1:E:427:LYS:HG3	1:E:430:GLY:H	1.81	0.45
1:A:38:THR:CG2	1:A:41:SER:HB3	2.41	0.45
1:A:504:PHE:CE1	1:E:70:ARG:CB	2.99	0.45
1:F:13:PHE:CE1	1:F:107:GLU:HA	2.51	0.45
1:E:252:VAL:HG23	1:E:323:CYS:SG	2.57	0.45
1:C:118:LYS:HZ3	1:C:353:ASN:HD21	1.64	0.45
1:D:235:SER:O	1:D:239:ILE:HG12	2.15	0.45
1:E:257:GLY:O	1:E:260:GLY:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:ARG:HH12	1:E:143:ASN:HD21	1.65	0.45
1:B:12:ASN:ND2	1:B:14:PHE:HB3	2.32	0.45
1:F:36:LEU:HD11	1:F:474:LYS:HZ1	1.81	0.45
1:A:28:VAL:HG23	1:A:487:VAL:HG13	1.98	0.45
1:D:133:VAL:HG12	1:D:135:ILE:HB	1.98	0.45
1:F:320:GLU:HG3	1:F:342:ARG:HG2	1.99	0.45
1:D:496:VAL:HA	1:E:209:GLN:NE2	2.31	0.45
1:B:120:ALA:O	1:B:492:LYS:NZ	2.49	0.45
1:D:273:LYS:HE2	1:D:288:ASP:C	2.37	0.45
1:C:386:TYR:OH	1:D:396:VAL:HG13	2.16	0.45
1:E:251:PHE:HB3	1:E:325:ILE:CG1	2.42	0.45
1:A:12:ASN:ND2	1:A:14:PHE:HB3	2.31	0.45
1:A:180:MET:HE3	1:A:183:ILE:HD12	1.99	0.45
1:A:339:ASN:H	1:A:339:ASN:ND2	2.14	0.45
1:F:277:VAL:HG21	1:F:295:LEU:HD22	1.99	0.45
1:F:322:ASP:OD1	1:F:344:LYS:HB3	2.16	0.45
1:A:334:GLN:HA	1:A:334:GLN:HE21	1.82	0.45
1:A:273:LYS:HE2	1:A:288:ASP:C	2.37	0.45
1:C:298:PHE:CE1	1:C:308:PHE:HA	2.52	0.45
1:F:427:LYS:HG3	1:F:430:GLY:H	1.81	0.45
1:E:40:GLU:HG3	1:E:46:ARG:NH1	2.16	0.45
1:C:474:LYS:HD3	1:C:475:TYR:CE2	2.51	0.45
1:D:251:PHE:HA	1:D:325:ILE:O	2.17	0.45
1:D:375:LEU:HD22	1:D:486:TYR:CE2	2.52	0.45
1:B:318:ILE:N	1:B:318:ILE:HD13	2.24	0.45
1:C:318:ILE:HD13	1:C:318:ILE:N	2.29	0.45
1:B:334:GLN:HE21	1:B:334:GLN:HA	1.80	0.45
1:A:320:GLU:HG3	1:A:342:ARG:HG2	1.99	0.45
1:F:308:PHE:CD2	1:F:311:ALA:HB2	2.50	0.45
1:E:425:PHE:HD1	1:E:427:LYS:CB	2.27	0.45
1:A:133:VAL:HG12	1:A:135:ILE:HB	1.98	0.45
1:E:334:GLN:HE21	1:E:334:GLN:HA	1.81	0.45
1:D:350:GLU:OE1	1:D:482:ARG:NH2	2.50	0.45
1:F:374:ASP:O	1:F:378:ASN:ND2	2.50	0.45
1:E:418:GLN:OE1	1:E:434:ILE:HG23	2.16	0.45
1:B:251:PHE:CE2	1:B:264:MET:HA	2.52	0.45
1:D:12:ASN:ND2	1:D:14:PHE:HB3	2.31	0.45
1:F:501:GLY:N	1:F:505:THR:HA	2.32	0.45
1:F:281:ASP:HB2	1:F:282:GLY:H	1.56	0.45
1:D:243:THR:N	1:D:244:PRO:CD	2.69	0.45
1:C:209:GLN:NE2	1:E:499:GLU:HB2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:226:GLY:HA3	1:F:377:LEU:HD12	1.98	0.45
1:D:372:ILE:HA	1:D:373:PRO:HD3	1.62	0.45
1:C:226:GLY:HA3	1:C:377:LEU:HD12	1.99	0.45
1:E:91:THR:CB	1:E:92:PRO:CD	2.94	0.45
1:B:488:ASN:HD21	1:B:492:LYS:NZ	2.15	0.45
1:D:374:ASP:O	1:D:378:ASN:ND2	2.50	0.45
1:F:298:PHE:CE1	1:F:308:PHE:HA	2.52	0.45
1:F:425:PHE:CD1	1:F:427:LYS:HD2	2.51	0.45
1:D:425:PHE:CD1	1:D:427:LYS:HD2	2.52	0.45
1:D:427:LYS:HG3	1:D:430:GLY:H	1.82	0.45
1:C:502:VAL:HG23	1:C:503:THR:N	2.28	0.45
1:D:325:ILE:HG22	1:D:347:ILE:CG2	2.47	0.45
1:C:150:ARG:NH2	1:E:505:THR:HG23	2.32	0.45
1:D:339:ASN:H	1:D:339:ASN:HD22	1.65	0.45
1:D:228:GLU:O	1:D:231:ILE:HG22	2.17	0.45
1:F:400:ARG:HG3	1:F:400:ARG:NH1	2.29	0.45
1:E:228:GLU:O	1:E:231:ILE:HG22	2.17	0.45
1:F:205:LYS:HZ3	1:F:392:ASN:HD21	1.64	0.45
1:A:91:THR:CB	1:A:92:PRO:CD	2.95	0.45
1:A:322:ASP:OD1	1:A:344:LYS:HB3	2.17	0.45
1:F:177:GLU:HB2	1:F:206:PRO:HG3	1.99	0.45
1:F:273:LYS:HE2	1:F:288:ASP:C	2.37	0.45
1:D:199:HIS:O	1:D:205:LYS:HE2	2.16	0.45
1:B:233:GLU:CG	1:B:236:TYR:HD1	2.29	0.45
1:A:136:ASN:OD1	1:A:138:LYS:N	2.50	0.45
1:B:350:GLU:OE1	1:B:482:ARG:NH2	2.50	0.45
1:A:298:PHE:CE1	1:A:308:PHE:HA	2.51	0.44
1:F:33:VAL:O	1:F:38:THR:N	2.48	0.44
1:B:251:PHE:HA	1:B:325:ILE:O	2.17	0.44
1:F:154:MET:CE	1:F:190:THR:HG21	2.47	0.44
1:E:400:ARG:HG3	1:E:400:ARG:NH1	2.28	0.44
1:F:339:ASN:N	1:F:339:ASN:HD22	2.14	0.44
1:C:339:ASN:ND2	1:C:339:ASN:H	2.15	0.44
1:D:322:ASP:OD1	1:D:344:LYS:HB3	2.16	0.44
1:E:257:GLY:O	1:E:258:ASN:C	2.55	0.44
1:A:396:VAL:HG13	1:F:386:TYR:OH	2.17	0.44
1:D:299:LYS:O	1:D:299:LYS:HG3	2.17	0.44
1:B:425:PHE:CD1	1:B:427:LYS:HD2	2.52	0.44
1:A:433:PRO:HA	1:B:420:SER:CB	2.47	0.44
1:E:86:HIS:HD2	1:E:116:THR:HG21	1.78	0.44
1:F:502:VAL:C	1:F:505:THR:HB	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:LYS:HZ1	1:B:378:ASN:HD21	1.65	0.44
1:A:151:ARG:CZ	1:E:503:THR:HG21	2.48	0.44
1:F:364:PHE:HB3	1:F:369:ILE:HB	1.98	0.44
1:D:28:VAL:HG22	1:D:487:VAL:HG13	1.99	0.44
1:C:277:VAL:HG21	1:C:295:LEU:HD22	1.98	0.44
1:A:257:GLY:O	1:A:258:ASN:C	2.55	0.44
1:B:136:ASN:OD1	1:B:138:LYS:N	2.50	0.44
1:A:51:GLY:O	1:A:55:ILE:HG13	2.17	0.44
1:D:501:GLY:N	1:D:505:THR:HA	2.32	0.44
1:D:502:VAL:C	1:D:505:THR:HB	2.38	0.44
1:C:501:GLY:N	1:C:505:THR:HA	2.32	0.44
1:F:251:PHE:CE1	1:F:267:LEU:HB3	2.52	0.44
1:A:251:PHE:HA	1:A:325:ILE:O	2.17	0.44
1:C:440:PHE:CG	1:D:412:HIS:HB3	2.52	0.44
1:E:318:ILE:N	1:E:318:ILE:HD13	2.25	0.44
1:D:339:ASN:HD22	1:D:339:ASN:N	2.14	0.44
1:C:339:ASN:N	1:C:339:ASN:HD22	2.15	0.44
1:A:339:ASN:H	1:A:339:ASN:HD22	1.65	0.44
1:E:133:VAL:HG12	1:E:135:ILE:HB	1.99	0.44
1:C:322:ASP:OD1	1:C:344:LYS:HB3	2.17	0.44
1:D:320:GLU:HG3	1:D:342:ARG:HG2	1.98	0.44
1:E:322:ASP:OD1	1:E:344:LYS:HB3	2.18	0.44
1:A:337:LYS:HZ2	1:A:359:GLU:HG3	1.83	0.44
1:E:16:MET:SD	1:E:358:PRO:HD3	2.57	0.44
1:E:425:PHE:CD1	1:E:427:LYS:HD2	2.52	0.44
1:A:427:LYS:HG3	1:A:430:GLY:H	1.81	0.44
1:B:37:ARG:NH2	1:B:49:VAL:HG11	2.29	0.44
1:D:251:PHE:CE2	1:D:264:MET:HA	2.52	0.44
1:B:251:PHE:HB3	1:B:325:ILE:CG1	2.41	0.44
1:B:325:ILE:HG22	1:B:347:ILE:CG2	2.48	0.44
1:C:91:THR:CB	1:C:92:PRO:CD	2.94	0.44
1:D:337:LYS:HZ2	1:D:359:GLU:HG3	1.83	0.44
1:D:308:PHE:CD2	1:D:311:ALA:HB2	2.50	0.44
1:C:425:PHE:CD1	1:C:427:LYS:HD2	2.53	0.44
1:C:505:THR:HG23	1:D:185:ASP:OD1	2.17	0.44
1:A:277:VAL:HG21	1:A:295:LEU:HD22	1.98	0.44
1:C:180:MET:HE3	1:C:183:ILE:HD12	2.00	0.44
1:F:199:HIS:O	1:F:205:LYS:HE2	2.18	0.44
1:B:205:LYS:HG3	1:B:388:GLU:OE1	2.18	0.44
1:E:136:ASN:OD1	1:E:138:LYS:N	2.50	0.44
1:D:147:LYS:HD2	1:D:151:ARG:NH2	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:VAL:C	1:B:505:THR:HB	2.37	0.44
1:C:69:ILE:HD13	1:C:148:ILE:CG1	2.47	0.44
1:B:252:VAL:HG23	1:B:323:CYS:SG	2.58	0.44
1:A:105:VAL:HG12	1:A:109:LYS:HE2	1.98	0.44
1:D:421:LEU:HD12	1:D:421:LEU:HA	1.73	0.44
1:D:111:LEU:HA	1:D:111:LEU:HD23	1.81	0.44
1:C:31:LYS:HA	1:C:34:GLU:HG2	2.00	0.44
1:E:501:GLY:N	1:E:505:THR:HA	2.32	0.44
1:E:502:VAL:C	1:E:505:THR:HB	2.38	0.44
1:D:400:ARG:NH1	1:D:400:ARG:HG3	2.31	0.44
1:B:273:LYS:HE2	1:B:288:ASP:C	2.38	0.44
1:A:390:LEU:O	1:A:391:LYS:C	2.56	0.44
1:F:257:GLY:O	1:F:258:ASN:C	2.55	0.44
1:E:100:SER:O	1:E:103:VAL:HG22	2.17	0.44
1:F:47:ASN:HD21	1:F:50:ARG:NH1	2.16	0.44
1:C:284:ILE:CG2	1:C:285:TRP:N	2.81	0.44
1:B:298:PHE:CE1	1:B:308:PHE:HA	2.53	0.44
1:E:184:ALA:HA	1:E:201:CYS:SG	2.58	0.44
1:D:251:PHE:HB3	1:D:325:ILE:CG1	2.42	0.44
1:B:27:ILE:CG2	1:B:475:TYR:CD1	2.99	0.44
1:D:177:GLU:HB2	1:D:206:PRO:HG3	2.00	0.44
1:F:205:LYS:NZ	1:F:392:ASN:ND2	2.63	0.44
1:A:254:GLN:HE21	1:A:330:ALA:HB3	1.82	0.44
1:E:273:LYS:HE2	1:E:288:ASP:C	2.38	0.44
1:A:47:ASN:HD21	1:A:50:ARG:NH1	2.16	0.44
1:A:60:ASN:HA	1:E:66:SER:OG	2.18	0.44
1:A:502:VAL:C	1:A:505:THR:HB	2.38	0.44
1:B:226:GLY:HA3	1:B:377:LEU:HD12	1.99	0.44
1:E:251:PHE:CE2	1:E:264:MET:HA	2.53	0.44
1:A:418:GLN:OE1	1:A:434:ILE:HG23	2.17	0.44
1:C:372:ILE:HA	1:C:373:PRO:HD3	1.64	0.44
1:F:284:ILE:HD13	1:F:308:PHE:HB3	2.00	0.43
1:F:69:ILE:HD13	1:F:148:ILE:CG1	2.48	0.43
1:A:226:GLY:HA3	1:A:377:LEU:HD12	1.98	0.43
1:D:251:PHE:CE1	1:D:267:LEU:HB3	2.53	0.43
1:A:190:THR:HG22	1:A:191:ILE:HG12	2.00	0.43
1:B:323:CYS:O	1:B:345:ALA:HA	2.18	0.43
1:F:488:ASN:HD21	1:F:492:LYS:HZ1	1.66	0.43
1:B:16:MET:HG2	1:B:358:PRO:HG2	2.00	0.43
1:B:31:LYS:HD3	1:B:35:ASP:OD2	2.18	0.43
1:A:457:LEU:CD2	1:A:461:MET:HG2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:301:GLN:O	1:C:301:GLN:HG2	2.18	0.43
1:F:301:GLN:O	1:F:301:GLN:HG2	2.18	0.43
1:D:298:PHE:CE1	1:D:308:PHE:HA	2.52	0.43
1:B:151:ARG:NH2	1:D:504:PHE:CZ	2.86	0.43
1:D:51:GLY:O	1:D:55:ILE:HG13	2.18	0.43
1:C:291:ASP:HA	1:C:292:PRO:HD3	1.88	0.43
1:B:436:PRO:HB3	1:B:440:PHE:CD1	2.54	0.43
1:F:502:VAL:HG23	1:F:503:THR:N	2.28	0.43
1:C:199:HIS:O	1:C:205:LYS:HE2	2.18	0.43
1:D:334:GLN:HE21	1:D:334:GLN:HA	1.82	0.43
1:C:300:LEU:HD22	1:C:300:LEU:HA	1.87	0.43
1:E:299:LYS:O	1:E:299:LYS:HG3	2.17	0.43
1:C:284:ILE:HD13	1:C:308:PHE:HB3	2.01	0.43
1:E:69:ILE:HD13	1:E:148:ILE:CG1	2.49	0.43
1:C:503:THR:HG21	1:F:151:ARG:CZ	2.48	0.43
1:D:21:PHE:CE1	1:D:490:ILE:HD12	2.54	0.43
1:F:433:PRO:C	1:F:435:VAL:N	2.70	0.43
1:D:364:PHE:HB3	1:D:369:ILE:HB	2.00	0.43
1:B:228:GLU:O	1:B:231:ILE:HG22	2.18	0.43
1:E:339:ASN:H	1:E:339:ASN:HD22	1.65	0.43
1:D:254:GLN:HE21	1:D:330:ALA:HB3	1.83	0.43
1:F:184:ALA:HA	1:F:201:CYS:SG	2.58	0.43
1:F:403:PHE:CD2	1:F:447:ALA:HB1	2.53	0.43
1:B:301:GLN:O	1:B:301:GLN:HG2	2.18	0.43
1:D:47:ASN:HD21	1:D:50:ARG:NH1	2.16	0.43
1:A:425:PHE:CD1	1:A:427:LYS:HD2	2.54	0.43
1:E:180:MET:HE3	1:E:183:ILE:HD12	2.00	0.43
1:E:226:GLY:HA3	1:E:377:LEU:HD12	1.99	0.43
1:D:323:CYS:O	1:D:345:ALA:HA	2.18	0.43
1:E:190:THR:HG22	1:E:191:ILE:HG12	2.00	0.43
1:B:400:ARG:HG3	1:B:400:ARG:NH1	2.30	0.43
1:B:31:LYS:HA	1:B:34:GLU:HG2	2.00	0.43
1:A:205:LYS:NZ	1:A:392:ASN:HD21	2.17	0.43
1:A:284:ILE:CG2	1:A:285:TRP:N	2.82	0.43
1:D:284:ILE:HD13	1:D:308:PHE:HB3	2.01	0.43
1:E:422:GLU:HB3	1:E:427:LYS:HB3	2.00	0.43
1:A:501:GLY:N	1:A:505:THR:HA	2.33	0.43
1:A:69:ILE:HD13	1:A:148:ILE:CG1	2.49	0.43
1:E:364:PHE:HB3	1:E:369:ILE:HB	2.00	0.43
1:D:228:GLU:HA	1:D:231:ILE:HG22	2.01	0.43
1:C:54:ARG:NH1	1:F:78:VAL:HG13	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:68:PRO:HA	1:F:78:VAL:HA	2.01	0.43
1:E:199:HIS:O	1:E:205:LYS:HE2	2.18	0.43
1:F:28:VAL:HG22	1:F:487:VAL:HG13	2.00	0.43
1:E:47:ASN:HD21	1:E:50:ARG:NH1	2.17	0.43
1:D:403:PHE:CE2	1:D:452:ILE:HD11	2.53	0.43
1:E:308:PHE:CD2	1:E:311:ALA:HB2	2.53	0.43
1:F:284:ILE:CG2	1:F:285:TRP:N	2.82	0.43
1:B:284:ILE:HD13	1:B:308:PHE:HB3	2.00	0.43
1:B:69:ILE:HD13	1:B:148:ILE:CG1	2.48	0.43
1:C:502:VAL:HG23	1:C:504:PHE:CD1	2.54	0.43
1:C:502:VAL:C	1:C:505:THR:HB	2.38	0.43
1:F:251:PHE:HA	1:F:325:ILE:O	2.19	0.43
1:A:228:GLU:HA	1:A:231:ILE:HG22	2.00	0.43
1:C:62:VAL:HG11	1:C:109:LYS:HZ3	1.83	0.43
1:A:28:VAL:HG22	1:A:487:VAL:HG13	1.99	0.43
1:D:350:GLU:CD	1:D:482:ARG:HH22	2.21	0.43
1:C:47:ASN:HD21	1:C:50:ARG:NH1	2.17	0.43
1:B:425:PHE:HD1	1:B:427:LYS:CB	2.27	0.43
1:B:143:ASN:HD21	1:E:70:ARG:HH12	1.67	0.43
1:F:325:ILE:HG22	1:F:347:ILE:CG2	2.49	0.43
1:A:325:ILE:HG22	1:A:347:ILE:CG2	2.48	0.43
1:E:325:ILE:HG22	1:E:347:ILE:CG2	2.48	0.43
1:A:436:PRO:HB3	1:A:440:PHE:CD1	2.53	0.43
1:F:180:MET:HE3	1:F:183:ILE:HD12	1.99	0.43
1:A:376:TYR:OH	1:A:465:ALA:HB2	2.18	0.43
1:B:51:GLY:O	1:B:55:ILE:HG13	2.19	0.43
1:A:496:VAL:O	1:B:209:GLN:NE2	2.47	0.43
1:B:299:LYS:HG3	1:B:299:LYS:O	2.17	0.43
1:A:284:ILE:HD13	1:A:308:PHE:HB3	2.00	0.43
1:B:422:GLU:HB3	1:B:427:LYS:HB3	2.01	0.43
1:C:31:LYS:HD2	1:C:474:LYS:HZ1	1.84	0.43
1:C:504:PHE:HZ	1:F:151:ARG:NH2	2.10	0.43
1:E:291:ASP:HA	1:E:292:PRO:HD3	1.89	0.43
1:D:69:ILE:HD13	1:D:148:ILE:CG1	2.49	0.43
1:E:433:PRO:C	1:E:435:VAL:N	2.71	0.43
1:A:151:ARG:NH2	1:E:504:PHE:CZ	2.86	0.43
1:E:261:LEU:HD12	1:E:261:LEU:C	2.39	0.43
1:A:299:LYS:HG3	1:A:299:LYS:O	2.17	0.43
1:D:422:GLU:HB3	1:D:427:LYS:HB3	2.01	0.43
1:A:502:VAL:HG23	1:A:503:THR:N	2.28	0.43
1:A:503:THR:HG21	1:E:151:ARG:CD	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:504:PHE:HE1	1:E:70:ARG:CB	2.32	0.43
1:C:40:GLU:O	1:C:42:GLU:HG3	2.19	0.43
1:F:305:ILE:H	1:F:305:ILE:HG13	1.67	0.43
1:C:32:LEU:HD21	1:C:494:PHE:CD1	2.54	0.43
1:D:421:LEU:HD21	1:E:421:LEU:HD21	2.00	0.43
1:D:136:ASN:OD1	1:D:138:LYS:N	2.51	0.43
1:D:57:LYS:HB3	1:D:58:PRO:HD3	2.01	0.43
1:F:31:LYS:HA	1:F:34:GLU:HG2	2.01	0.43
1:C:325:ILE:HG22	1:C:347:ILE:CG2	2.49	0.43
1:E:375:LEU:HD22	1:E:486:TYR:CE2	2.54	0.43
1:B:501:GLY:N	1:B:505:THR:HA	2.33	0.43
1:C:177:GLU:HB2	1:C:206:PRO:HG3	2.01	0.43
1:B:180:MET:HE3	1:B:183:ILE:HD12	2.00	0.43
1:B:203:THR:HA	1:B:388:GLU:OE1	2.19	0.43
1:C:387:PHE:CD1	1:D:401:LEU:HD21	2.54	0.43
1:B:111:LEU:HA	1:B:111:LEU:HD23	1.83	0.43
1:A:439:GLU:H	1:A:439:GLU:CD	2.22	0.43
1:A:261:LEU:HD12	1:A:261:LEU:C	2.39	0.43
1:E:284:ILE:CG2	1:E:285:TRP:N	2.81	0.42
1:E:251:PHE:HA	1:E:325:ILE:O	2.18	0.42
1:D:144:GLU:O	1:D:148:ILE:HG13	2.19	0.42
1:F:435:VAL:O	1:F:435:VAL:HG13	2.19	0.42
1:B:305:ILE:H	1:B:305:ILE:HG13	1.68	0.42
1:C:364:PHE:HB3	1:C:369:ILE:HB	2.00	0.42
1:C:206:PRO:HD2	1:C:209:GLN:HB2	1.99	0.42
1:D:390:LEU:O	1:D:391:LYS:C	2.57	0.42
1:A:233:GLU:HG2	1:A:236:TYR:CD1	2.54	0.42
1:B:122:VAL:HA	1:B:464:SER:OG	2.19	0.42
1:D:47:ASN:O	1:D:50:ARG:HG2	2.19	0.42
1:B:308:PHE:CD2	1:B:311:ALA:HB2	2.51	0.42
1:B:502:VAL:HG23	1:B:504:PHE:CD1	2.54	0.42
1:E:502:VAL:HG23	1:E:504:PHE:CD1	2.54	0.42
1:C:436:PRO:HA	1:D:416:SER:OG	2.19	0.42
1:D:190:THR:HG22	1:D:191:ILE:HG12	2.01	0.42
1:E:105:VAL:HA	1:E:108:VAL:HG22	2.01	0.42
1:D:105:VAL:HA	1:D:108:VAL:HG22	2.01	0.42
1:B:199:HIS:O	1:B:205:LYS:HE2	2.19	0.42
1:F:373:PRO:HD3	1:F:481:LEU:HB3	2.01	0.42
1:A:68:PRO:HA	1:A:78:VAL:HA	2.00	0.42
1:A:77:GLU:HA	1:E:54:ARG:NH1	2.33	0.42
1:D:391:LYS:HD2	1:D:449:GLU:OE2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:300:LEU:HD22	1:D:300:LEU:HA	1.88	0.42
1:E:300:LEU:HD22	1:E:300:LEU:HA	1.88	0.42
1:F:31:LYS:HD3	1:F:35:ASP:OD2	2.19	0.42
1:B:144:GLU:O	1:B:148:ILE:HG13	2.19	0.42
1:E:349:ALA:HB1	1:E:377:LEU:CD2	2.49	0.42
1:A:251:PHE:CE1	1:A:267:LEU:HB3	2.55	0.42
1:C:69:ILE:HG23	1:C:79:ILE:HD13	2.00	0.42
1:D:435:VAL:HG13	1:D:435:VAL:O	2.20	0.42
1:A:323:CYS:O	1:A:345:ALA:HA	2.19	0.42
1:F:323:CYS:O	1:F:345:ALA:HA	2.18	0.42
1:D:91:THR:CB	1:D:92:PRO:CD	2.94	0.42
1:B:205:LYS:HZ3	1:B:392:ASN:HD21	1.67	0.42
1:A:31:LYS:HA	1:A:34:GLU:HG2	2.01	0.42
1:A:209:GLN:NE2	1:F:499:GLU:HB2	2.35	0.42
1:F:136:ASN:OD1	1:F:138:LYS:N	2.52	0.42
1:F:449:GLU:O	1:F:450:LYS:C	2.58	0.42
1:A:57:LYS:HB3	1:A:58:PRO:HD3	2.00	0.42
1:C:299:LYS:O	1:C:299:LYS:HG3	2.18	0.42
1:C:111:LEU:HD23	1:C:111:LEU:HA	1.82	0.42
1:A:403:PHE:CE2	1:A:452:ILE:HD11	2.53	0.42
1:E:284:ILE:HD13	1:E:308:PHE:HB3	2.01	0.42
1:F:40:GLU:O	1:F:42:GLU:HG3	2.20	0.42
1:D:502:VAL:HG23	1:D:504:PHE:CD1	2.54	0.42
1:D:349:ALA:HB1	1:D:377:LEU:CD2	2.50	0.42
1:C:251:PHE:HA	1:C:325:ILE:O	2.20	0.42
1:B:86:HIS:CG	1:B:116:THR:HG21	2.53	0.42
1:C:436:PRO:HB3	1:C:440:PHE:CD1	2.54	0.42
1:A:105:VAL:HA	1:A:108:VAL:HG22	2.01	0.42
1:C:32:LEU:HA	1:C:36:LEU:HD13	2.02	0.42
1:F:485:ALA:O	1:F:488:ASN:HB3	2.20	0.42
1:E:254:GLN:HE21	1:E:330:ALA:HB3	1.84	0.42
1:C:254:GLN:HE21	1:C:330:ALA:HB3	1.84	0.42
1:D:31:LYS:HA	1:D:34:GLU:HG2	2.02	0.42
1:E:233:GLU:HG2	1:E:236:TYR:CD1	2.54	0.42
1:A:448:SER:O	1:A:451:ASP:HB2	2.19	0.42
1:D:261:LEU:HD12	1:D:261:LEU:C	2.40	0.42
1:F:424:LYS:HE3	1:F:424:LYS:HB3	1.87	0.42
1:F:261:LEU:C	1:F:261:LEU:HD12	2.40	0.42
1:F:299:LYS:HG3	1:F:299:LYS:O	2.19	0.42
1:E:449:GLU:O	1:E:450:LYS:C	2.57	0.42
1:C:251:PHE:CE1	1:C:267:LEU:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:502:VAL:HG23	1:F:504:PHE:CD1	2.54	0.42
1:D:436:PRO:HB3	1:D:440:PHE:CD1	2.55	0.42
1:F:50:ARG:O	1:F:50:ARG:HG3	2.20	0.42
1:E:457:LEU:CD2	1:E:461:MET:HG2	2.50	0.42
1:C:380:GLY:HA2	1:C:457:LEU:HD21	2.00	0.42
1:C:457:LEU:CD2	1:C:461:MET:HG2	2.50	0.42
1:B:62:VAL:HG11	1:B:109:LYS:HZ2	1.84	0.42
1:B:277:VAL:HG21	1:B:295:LEU:HD22	1.99	0.42
1:B:457:LEU:CD2	1:B:461:MET:HG2	2.49	0.42
1:B:47:ASN:O	1:B:50:ARG:HG2	2.20	0.42
1:A:424:LYS:HB3	1:A:424:LYS:HE3	1.88	0.42
1:B:284:ILE:CG2	1:B:285:TRP:N	2.82	0.42
1:B:99:TYR:HH	1:B:149:THR:HG22	1.81	0.42
1:A:502:VAL:HG23	1:A:504:PHE:CD1	2.54	0.42
1:C:144:GLU:O	1:C:148:ILE:HG13	2.20	0.42
1:B:364:PHE:HB3	1:B:369:ILE:HB	2.01	0.42
1:C:121:VAL:HG21	1:C:375:LEU:HG	2.02	0.42
1:E:277:VAL:HG21	1:E:295:LEU:HD22	1.99	0.42
1:F:254:GLN:HE21	1:F:330:ALA:HB3	1.85	0.42
1:C:68:PRO:HA	1:C:78:VAL:HA	2.01	0.42
1:E:421:LEU:HA	1:E:421:LEU:HD12	1.76	0.42
1:D:205:LYS:NZ	1:D:392:ASN:HD21	2.18	0.42
1:E:33:VAL:O	1:E:34:GLU:O	2.38	0.42
1:B:38:THR:CG2	1:B:41:SER:HB3	2.40	0.42
1:F:144:GLU:O	1:F:148:ILE:HG13	2.20	0.42
1:E:436:PRO:HB3	1:E:440:PHE:CD1	2.55	0.42
1:C:433:PRO:C	1:C:435:VAL:N	2.73	0.42
1:E:323:CYS:O	1:E:345:ALA:HA	2.19	0.42
1:B:228:GLU:HA	1:B:231:ILE:HG22	2.01	0.42
1:C:105:VAL:HA	1:C:108:VAL:HG22	2.02	0.42
1:B:32:LEU:HA	1:B:36:LEU:HD13	2.02	0.42
1:A:78:VAL:CG2	1:A:78:VAL:O	2.68	0.42
1:F:390:LEU:O	1:F:391:LYS:C	2.57	0.42
1:E:111:LEU:HA	1:E:111:LEU:HD23	1.82	0.42
1:B:261:LEU:HD12	1:B:261:LEU:C	2.40	0.42
1:B:424:LYS:HE3	1:B:424:LYS:HB3	1.87	0.42
1:D:319:LEU:HD23	1:D:335:LEU:HD23	2.02	0.42
1:A:364:PHE:HB3	1:A:369:ILE:HB	2.00	0.42
1:C:323:CYS:O	1:C:345:ALA:HA	2.19	0.42
1:F:105:VAL:HA	1:F:108:VAL:HG22	2.02	0.42
1:E:205:LYS:HZ3	1:E:392:ASN:ND2	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:GLN:HE21	1:B:330:ALA:HB3	1.83	0.42
1:D:31:LYS:HD3	1:D:35:ASP:OD2	2.19	0.42
1:C:380:GLY:CA	1:C:457:LEU:HD21	2.50	0.42
1:C:31:LYS:HD3	1:C:35:ASP:OD2	2.19	0.42
1:B:433:PRO:HA	1:F:420:SER:HB3	2.02	0.42
1:B:505:THR:C	1:F:150:ARG:HH12	2.24	0.42
1:B:504:PHE:HB3	1:F:146:GLU:OE1	2.19	0.42
1:B:505:THR:N	1:F:150:ARG:NH1	2.68	0.42
1:B:118:LYS:HD3	1:B:379:ALA:HA	2.02	0.42
1:A:420:SER:CB	1:F:433:PRO:HA	2.50	0.42
1:F:436:PRO:HB3	1:F:440:PHE:CD1	2.55	0.42
1:D:318:ILE:H	1:D:318:ILE:CD1	2.29	0.42
1:B:317:SER:C	1:B:319:LEU:N	2.73	0.42
1:B:122:VAL:HB	1:B:460:THR:CG2	2.50	0.42
1:C:251:PHE:HB3	1:C:325:ILE:CG1	2.44	0.41
1:F:150:ARG:NH2	1:F:185:ASP:OD1	2.53	0.41
1:D:86:HIS:HD2	1:D:87:SER:HB2	1.85	0.41
1:B:281:ASP:HB2	1:B:282:GLY:H	1.56	0.41
1:D:317:SER:C	1:D:319:LEU:N	2.73	0.41
1:C:190:THR:HG22	1:C:191:ILE:HG12	2.00	0.41
1:C:339:ASN:H	1:C:339:ASN:HD22	1.67	0.41
1:C:92:PRO:HG2	1:C:389:TRP:CZ2	2.55	0.41
1:E:31:LYS:HA	1:E:34:GLU:HG2	2.01	0.41
1:D:40:GLU:O	1:D:42:GLU:HG3	2.20	0.41
1:B:118:LYS:HG3	1:B:375:LEU:O	2.20	0.41
1:E:502:VAL:HG23	1:E:503:THR:N	2.28	0.41
1:F:32:LEU:HA	1:F:36:LEU:HD13	2.02	0.41
1:B:54:ARG:NH1	1:D:78:VAL:HG13	2.35	0.41
1:E:92:PRO:HG2	1:E:389:TRP:CZ2	2.55	0.41
1:A:31:LYS:HD3	1:A:35:ASP:OD2	2.19	0.41
1:B:47:ASN:HD21	1:B:50:ARG:NH1	2.17	0.41
1:D:301:GLN:HG2	1:D:301:GLN:O	2.19	0.41
1:C:312:LYS:O	1:C:314:TYR:N	2.53	0.41
1:A:284:ILE:CG2	1:A:311:ALA:HB1	2.48	0.41
1:E:31:LYS:HD3	1:E:35:ASP:OD2	2.19	0.41
1:E:251:PHE:CE1	1:E:267:LEU:HB3	2.55	0.41
1:E:318:ILE:CD1	1:E:318:ILE:H	2.29	0.41
1:B:319:LEU:HD23	1:B:335:LEU:HD23	2.03	0.41
1:B:105:VAL:HA	1:B:108:VAL:HG22	2.02	0.41
1:E:68:PRO:HA	1:E:78:VAL:HA	2.02	0.41
1:E:337:LYS:HZ2	1:E:359:GLU:HG3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:257:GLY:O	1:C:259:VAL:N	2.53	0.41
1:A:47:ASN:O	1:A:50:ARG:HG2	2.20	0.41
1:C:218:ALA:O	1:C:457:LEU:HD11	2.20	0.41
1:E:51:GLY:O	1:E:55:ILE:HG13	2.19	0.41
1:B:57:LYS:HB3	1:B:58:PRO:HD3	2.01	0.41
1:C:261:LEU:HD12	1:C:261:LEU:C	2.40	0.41
1:E:149:THR:HG21	1:E:179:GLU:HG3	2.02	0.41
1:C:228:GLU:HA	1:C:231:ILE:HG22	2.02	0.41
1:E:32:LEU:HA	1:E:36:LEU:HD13	2.02	0.41
1:E:301:GLN:HG2	1:E:301:GLN:O	2.20	0.41
1:C:439:GLU:CD	1:C:439:GLU:H	2.24	0.41
1:F:33:VAL:O	1:F:34:GLU:O	2.39	0.41
1:B:40:GLU:O	1:B:42:GLU:HG3	2.21	0.41
1:A:86:HIS:HD2	1:A:87:SER:HB2	1.84	0.41
1:B:118:LYS:HG3	1:B:379:ALA:HB2	2.02	0.41
1:A:32:LEU:HA	1:A:36:LEU:HD13	2.02	0.41
1:B:134:LYS:HB2	1:B:134:LYS:HE3	1.94	0.41
1:C:422:GLU:HB3	1:C:427:LYS:HB3	2.02	0.41
1:C:349:ALA:HB1	1:C:377:LEU:CD2	2.51	0.41
1:E:118:LYS:HG3	1:E:375:LEU:O	2.21	0.41
1:A:435:VAL:O	1:A:435:VAL:HG13	2.20	0.41
1:D:12:ASN:HD21	1:D:14:PHE:HB3	1.86	0.41
1:E:281:ASP:HB2	1:E:282:GLY:H	1.56	0.41
1:F:319:LEU:HD23	1:F:335:LEU:HD23	2.03	0.41
1:E:474:LYS:HD3	1:E:475:TYR:HE2	1.83	0.41
1:F:228:GLU:HA	1:F:231:ILE:HG22	2.01	0.41
1:A:400:ARG:NH1	1:A:400:ARG:HG3	2.30	0.41
1:F:254:GLN:HB3	1:F:328:PRO:HA	2.03	0.41
1:C:47:ASN:O	1:C:50:ARG:HG2	2.21	0.41
1:E:57:LYS:HB3	1:E:58:PRO:HD3	2.02	0.41
1:B:207:ILE:HG21	1:B:213:HIS:NE2	2.36	0.41
1:C:33:VAL:O	1:C:34:GLU:O	2.38	0.41
1:B:349:ALA:HB1	1:B:377:LEU:CD2	2.51	0.41
1:A:12:ASN:HD21	1:A:14:PHE:HB3	1.86	0.41
1:D:86:HIS:CG	1:D:116:THR:HG21	2.55	0.41
1:F:339:ASN:H	1:F:339:ASN:HD22	1.66	0.41
1:E:62:VAL:HG11	1:E:109:LYS:HZ3	1.85	0.41
1:D:32:LEU:HA	1:D:36:LEU:HD13	2.03	0.41
1:D:78:VAL:O	1:D:78:VAL:CG2	2.69	0.41
1:B:350:GLU:CD	1:B:482:ARG:HH22	2.24	0.41
1:F:439:GLU:H	1:F:439:GLU:CD	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:CYS:SG	1:B:382:VAL:HG11	2.60	0.41
1:A:308:PHE:CD2	1:A:311:ALA:HB2	2.50	0.41
1:E:183:ILE:O	1:E:184:ALA:C	2.59	0.41
1:A:349:ALA:HB1	1:A:377:LEU:CD2	2.51	0.41
1:D:291:ASP:HA	1:D:292:PRO:HD3	1.89	0.41
1:C:377:LEU:HD12	1:C:377:LEU:HA	1.93	0.41
1:A:69:ILE:HG23	1:A:79:ILE:HD13	2.02	0.41
1:C:435:VAL:HG13	1:C:435:VAL:O	2.21	0.41
1:C:168:VAL:HA	1:C:201:CYS:O	2.21	0.41
1:F:47:ASN:O	1:F:50:ARG:HG2	2.21	0.41
1:C:212:ILE:HD11	1:C:398:TYR:CE1	2.56	0.41
1:B:300:LEU:HD22	1:B:300:LEU:HA	1.88	0.41
1:D:457:LEU:CD2	1:D:461:MET:HG2	2.51	0.41
1:D:284:ILE:CG2	1:D:285:TRP:N	2.83	0.41
1:B:424:LYS:O	1:B:425:PHE:HB2	2.21	0.41
1:B:149:THR:HG1	1:B:182:TRP:HE3	1.67	0.41
1:E:40:GLU:O	1:E:42:GLU:HG3	2.20	0.41
1:F:69:ILE:HG23	1:F:79:ILE:HD13	2.03	0.41
1:A:433:PRO:C	1:A:435:VAL:N	2.73	0.41
1:A:144:GLU:O	1:A:148:ILE:HG13	2.21	0.41
1:C:221:ARG:CD	1:C:454:HIS:CG	3.04	0.41
1:B:318:ILE:CD1	1:B:318:ILE:H	2.28	0.41
1:C:485:ALA:O	1:C:488:ASN:HB3	2.21	0.41
1:E:156:LEU:HB3	1:E:162:ILE:HB	2.03	0.41
1:C:449:GLU:O	1:C:450:LYS:C	2.57	0.41
1:D:485:ALA:O	1:D:488:ASN:HB3	2.21	0.41
1:B:233:GLU:HG2	1:B:236:TYR:CD1	2.56	0.41
1:E:50:ARG:HG3	1:E:50:ARG:O	2.21	0.41
1:C:424:LYS:HB3	1:C:424:LYS:HE3	1.87	0.41
1:B:449:GLU:O	1:B:450:LYS:C	2.60	0.41
1:F:285:TRP:NE1	1:F:287:PRO:HG3	2.36	0.41
1:D:38:THR:CG2	1:D:41:SER:HB3	2.40	0.41
1:E:150:ARG:NH2	1:E:185:ASP:OD1	2.54	0.41
1:C:31:LYS:HB2	1:C:475:TYR:HE1	1.86	0.41
1:A:150:ARG:HH12	1:F:505:THR:N	2.19	0.41
1:A:281:ASP:HB2	1:A:282:GLY:H	1.56	0.41
1:B:319:LEU:CD1	1:B:319:LEU:H	2.34	0.41
1:E:228:GLU:HA	1:E:231:ILE:HG22	2.02	0.41
1:D:177:GLU:HA	1:D:180:MET:HB2	2.03	0.41
1:A:105:VAL:HG12	1:A:109:LYS:HG3	2.03	0.41
1:C:136:ASN:OD1	1:C:138:LYS:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:VAL:HA	1:B:201:CYS:O	2.21	0.41
1:E:472:ALA:O	1:E:476:ASN:N	2.54	0.41
1:D:230:PHE:CE2	1:D:481:LEU:HD21	2.55	0.41
1:A:301:GLN:HG2	1:A:301:GLN:O	2.20	0.41
1:F:463:ARG:HB3	1:F:463:ARG:HE	1.72	0.41
1:F:69:ILE:HG21	1:F:148:ILE:HG12	2.03	0.40
1:D:433:PRO:C	1:D:435:VAL:N	2.72	0.40
1:A:70:ARG:CB	1:E:504:PHE:CE1	3.04	0.40
1:D:23:ARG:NE	1:D:27:ILE:HD11	2.30	0.40
1:D:319:LEU:H	1:D:319:LEU:CD1	2.33	0.40
1:C:23:ARG:NE	1:C:27:ILE:HD11	2.30	0.40
1:F:190:THR:HG22	1:F:191:ILE:HG12	2.03	0.40
1:A:317:SER:C	1:A:319:LEU:N	2.74	0.40
1:A:319:LEU:H	1:A:319:LEU:CD1	2.34	0.40
1:C:243:THR:CG2	1:C:243:THR:O	2.69	0.40
1:C:317:SER:C	1:C:319:LEU:N	2.75	0.40
1:F:91:THR:HB	1:F:92:PRO:CD	2.51	0.40
1:D:119:CYS:SG	1:D:382:VAL:HG11	2.61	0.40
1:E:372:ILE:HA	1:E:373:PRO:HD3	1.64	0.40
1:E:285:TRP:NE1	1:E:287:PRO:HG3	2.37	0.40
1:B:150:ARG:NH2	1:B:185:ASP:OD1	2.54	0.40
1:C:504:PHE:CE1	1:F:70:ARG:CB	3.05	0.40
1:D:226:GLY:HA3	1:D:377:LEU:HD12	2.01	0.40
1:F:12:ASN:HD21	1:F:14:PHE:HB3	1.86	0.40
1:B:251:PHE:CE1	1:B:267:LEU:HB3	2.56	0.40
1:D:105:VAL:HG12	1:D:109:LYS:HG3	2.03	0.40
1:B:337:LYS:HZ2	1:B:359:GLU:HG3	1.84	0.40
1:A:449:GLU:O	1:A:450:LYS:C	2.59	0.40
1:C:233:GLU:HG2	1:C:236:TYR:CD1	2.55	0.40
1:E:309:PRO:O	1:E:310:LYS:HB2	2.22	0.40
1:B:284:ILE:CG2	1:B:311:ALA:HB1	2.47	0.40
1:A:40:GLU:O	1:A:42:GLU:HG3	2.20	0.40
1:D:500:ALA:HB1	1:D:505:THR:OXT	2.21	0.40
1:B:433:PRO:C	1:B:435:VAL:N	2.73	0.40
1:C:69:ILE:HG12	1:C:79:ILE:HD11	2.03	0.40
1:F:63:LEU:HD22	1:F:161:PHE:CE2	2.55	0.40
1:E:319:LEU:H	1:E:319:LEU:CD1	2.34	0.40
1:C:205:LYS:HD2	1:C:209:GLN:O	2.21	0.40
1:D:68:PRO:HA	1:D:78:VAL:HA	2.03	0.40
1:A:163:GLY:O	1:A:167:ASP:O	2.39	0.40
1:C:172:ASP:O	1:C:173:MET:C	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:TRP:NE1	1:A:287:PRO:HG3	2.36	0.40
1:A:422:GLU:HB3	1:A:427:LYS:HB3	2.03	0.40
1:C:12:ASN:HD21	1:C:14:PHE:HB3	1.86	0.40
1:C:433:PRO:HA	1:D:420:SER:CB	2.51	0.40
1:E:279:GLU:HB3	1:E:280:SER:H	1.73	0.40
1:A:485:ALA:O	1:A:488:ASN:HB3	2.21	0.40
1:F:233:GLU:HG2	1:F:236:TYR:CD1	2.56	0.40
1:F:391:LYS:NZ	1:F:449:GLU:OE1	2.50	0.40
1:B:113:SER:O	1:B:114:LEU:C	2.58	0.40
1:E:284:ILE:CG2	1:E:311:ALA:HB1	2.47	0.40
1:F:312:LYS:O	1:F:314:TYR:N	2.54	0.40
1:A:284:ILE:CD1	1:A:308:PHE:HB3	2.51	0.40
1:A:69:ILE:HG12	1:A:79:ILE:HD11	2.04	0.40
1:B:243:THR:CG2	1:B:243:THR:O	2.70	0.40
1:D:279:GLU:HB3	1:D:280:SER:H	1.74	0.40
1:F:105:VAL:HG12	1:F:109:LYS:HG3	2.03	0.40
1:A:257:GLY:O	1:A:259:VAL:N	2.54	0.40
1:B:257:GLY:O	1:B:259:VAL:N	2.55	0.40
1:A:50:ARG:O	1:A:50:ARG:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	494/505 (98%)	428 (87%)	47 (10%)	19 (4%)	4	9
1	B	494/505 (98%)	428 (87%)	47 (10%)	19 (4%)	4	9
1	C	494/505 (98%)	428 (87%)	47 (10%)	19 (4%)	4	9
1	D	494/505 (98%)	426 (86%)	49 (10%)	19 (4%)	4	9
1	E	494/505 (98%)	425 (86%)	50 (10%)	19 (4%)	4	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	494/505 (98%)	428 (87%)	47 (10%)	19 (4%)	4	9
All	All	2964/3030 (98%)	2563 (86%)	287 (10%)	114 (4%)	4	9

All (114) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	GLU
1	A	41	SER
1	A	91	THR
1	A	102	ASP
1	A	258	ASN
1	A	331	SER
1	B	34	GLU
1	B	41	SER
1	B	91	THR
1	B	102	ASP
1	B	258	ASN
1	B	331	SER
1	C	34	GLU
1	C	41	SER
1	C	91	THR
1	C	102	ASP
1	C	258	ASN
1	C	331	SER
1	D	34	GLU
1	D	41	SER
1	D	91	THR
1	D	102	ASP
1	D	258	ASN
1	D	331	SER
1	E	34	GLU
1	E	41	SER
1	E	91	THR
1	E	102	ASP
1	E	258	ASN
1	E	331	SER
1	F	34	GLU
1	F	41	SER
1	F	91	THR
1	F	102	ASP
1	F	258	ASN
1	F	331	SER

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Mol	Chain	Res	Type
1	A	74	GLY
1	A	333	LYS
1	A	434	ILE
1	B	74	GLY
1	B	333	LYS
1	B	434	ILE
1	C	74	GLY
1	C	333	LYS
1	C	434	ILE
1	D	74	GLY
1	D	333	LYS
1	D	434	ILE
1	E	74	GLY
1	E	333	LYS
1	E	434	ILE
1	F	74	GLY
1	F	333	LYS
1	F	434	ILE
1	A	425	PHE
1	A	500	ALA
1	B	425	PHE
1	B	500	ALA
1	C	425	PHE
1	C	500	ALA
1	D	425	PHE
1	D	500	ALA
1	E	425	PHE
1	E	500	ALA
1	F	425	PHE
1	F	500	ALA
1	A	35	ASP
1	A	134	LYS
1	A	234	ALA
1	B	35	ASP
1	B	134	LYS
1	B	234	ALA
1	C	35	ASP
1	C	134	LYS
1	C	234	ALA
1	D	35	ASP
1	D	234	ALA
1	E	35	ASP

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Mol	Chain	Res	Type
1	E	134	LYS
1	E	234	ALA
1	F	35	ASP
1	F	234	ALA
1	A	281	ASP
1	A	286	ASN
1	A	313	PRO
1	B	162	ILE
1	B	281	ASP
1	B	286	ASN
1	B	313	PRO
1	C	162	ILE
1	C	281	ASP
1	C	286	ASN
1	C	313	PRO
1	D	134	LYS
1	D	281	ASP
1	D	286	ASN
1	D	313	PRO
1	E	162	ILE
1	E	281	ASP
1	E	286	ASN
1	E	313	PRO
1	F	134	LYS
1	F	281	ASP
1	F	286	ASN
1	F	313	PRO
1	A	162	ILE
1	A	502	VAL
1	B	502	VAL
1	C	502	VAL
1	D	162	ILE
1	D	502	VAL
1	F	162	ILE
1	F	502	VAL
1	E	502	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	413/420 (98%)	365 (88%)	48 (12%)	7	16
1	B	413/420 (98%)	364 (88%)	49 (12%)	6	15
1	C	413/420 (98%)	365 (88%)	48 (12%)	7	16
1	D	413/420 (98%)	364 (88%)	49 (12%)	6	15
1	E	413/420 (98%)	365 (88%)	48 (12%)	7	16
1	F	413/420 (98%)	365 (88%)	48 (12%)	7	16
All	All	2478/2520 (98%)	2188 (88%)	290 (12%)	7	15

All (290) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	PHE
1	A	23	ARG
1	A	36	LEU
1	A	37	ARG
1	A	44	GLN
1	A	46	ARG
1	A	62	VAL
1	A	64	SER
1	A	68	PRO
1	A	90	ARG
1	A	101	THR
1	A	116	THR
1	A	141	THR
1	A	156	LEU
1	A	162	ILE
1	A	180	MET
1	A	219	THR
1	A	235	SER
1	A	243	THR
1	A	259	VAL
1	A	261	LEU
1	A	267	LEU
1	A	281	ASP
1	A	293	LYS
1	A	300	LEU
1	A	306	LEU
1	A	315	GLU

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Mol	Chain	Res	Type
1	A	318	ILE
1	A	320	GLU
1	A	325	ILE
1	A	326	LEU
1	A	334	GLN
1	A	339	ASN
1	A	353	ASN
1	A	378	ASN
1	A	396	VAL
1	A	400	ARG
1	A	401	LEU
1	A	421	LEU
1	A	427	LYS
1	A	428	HIS
1	A	432	ILE
1	A	457	LEU
1	A	471	THR
1	A	476	ASN
1	A	481	LEU
1	A	499	GLU
1	A	504	PHE
1	B	13	PHE
1	B	23	ARG
1	B	36	LEU
1	B	37	ARG
1	B	44	GLN
1	B	46	ARG
1	B	62	VAL
1	B	64	SER
1	B	68	PRO
1	B	90	ARG
1	B	101	THR
1	B	116	THR
1	B	141	THR
1	B	156	LEU
1	B	162	ILE
1	B	180	MET
1	B	219	THR
1	B	235	SER
1	B	243	THR
1	B	259	VAL
1	B	261	LEU

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Mol	Chain	Res	Type
1	B	267	LEU
1	B	281	ASP
1	B	293	LYS
1	B	300	LEU
1	B	306	LEU
1	B	315	GLU
1	B	318	ILE
1	B	320	GLU
1	B	325	ILE
1	B	326	LEU
1	B	334	GLN
1	B	339	ASN
1	B	353	ASN
1	B	378	ASN
1	B	396	VAL
1	B	400	ARG
1	B	401	LEU
1	B	421	LEU
1	B	427	LYS
1	B	428	HIS
1	B	432	ILE
1	B	455	SER
1	B	457	LEU
1	B	471	THR
1	B	476	ASN
1	B	481	LEU
1	B	499	GLU
1	B	504	PHE
1	C	13	PHE
1	C	23	ARG
1	C	36	LEU
1	C	37	ARG
1	C	44	GLN
1	C	46	ARG
1	C	62	VAL
1	C	64	SER
1	C	68	PRO
1	C	90	ARG
1	C	101	THR
1	C	116	THR
1	C	141	THR
1	C	156	LEU

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Mol	Chain	Res	Type
1	C	162	ILE
1	C	180	MET
1	C	219	THR
1	C	235	SER
1	C	243	THR
1	C	259	VAL
1	C	261	LEU
1	C	267	LEU
1	C	281	ASP
1	C	293	LYS
1	C	300	LEU
1	C	306	LEU
1	C	315	GLU
1	C	318	ILE
1	C	320	GLU
1	C	325	ILE
1	C	326	LEU
1	C	334	GLN
1	C	339	ASN
1	C	353	ASN
1	C	378	ASN
1	C	396	VAL
1	C	400	ARG
1	C	401	LEU
1	C	421	LEU
1	C	427	LYS
1	C	428	HIS
1	C	432	ILE
1	C	457	LEU
1	C	471	THR
1	C	476	ASN
1	C	481	LEU
1	C	499	GLU
1	C	504	PHE
1	D	13	PHE
1	D	23	ARG
1	D	36	LEU
1	D	37	ARG
1	D	44	GLN
1	D	46	ARG
1	D	62	VAL
1	D	64	SER

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Mol	Chain	Res	Type
1	D	68	PRO
1	D	90	ARG
1	D	101	THR
1	D	116	THR
1	D	141	THR
1	D	156	LEU
1	D	162	ILE
1	D	180	MET
1	D	219	THR
1	D	235	SER
1	D	243	THR
1	D	259	VAL
1	D	261	LEU
1	D	267	LEU
1	D	281	ASP
1	D	293	LYS
1	D	300	LEU
1	D	306	LEU
1	D	315	GLU
1	D	318	ILE
1	D	320	GLU
1	D	325	ILE
1	D	326	LEU
1	D	334	GLN
1	D	339	ASN
1	D	353	ASN
1	D	378	ASN
1	D	396	VAL
1	D	400	ARG
1	D	401	LEU
1	D	421	LEU
1	D	427	LYS
1	D	428	HIS
1	D	432	ILE
1	D	455	SER
1	D	457	LEU
1	D	471	THR
1	D	476	ASN
1	D	481	LEU
1	D	499	GLU
1	D	504	PHE
1	E	13	PHE

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Mol	Chain	Res	Type
1	E	23	ARG
1	E	36	LEU
1	E	37	ARG
1	E	44	GLN
1	E	46	ARG
1	E	62	VAL
1	E	64	SER
1	E	68	PRO
1	E	90	ARG
1	E	101	THR
1	E	116	THR
1	E	141	THR
1	E	156	LEU
1	E	162	ILE
1	E	180	MET
1	E	219	THR
1	E	235	SER
1	E	243	THR
1	E	259	VAL
1	E	261	LEU
1	E	267	LEU
1	E	281	ASP
1	E	293	LYS
1	E	300	LEU
1	E	306	LEU
1	E	315	GLU
1	E	318	ILE
1	E	320	GLU
1	E	325	ILE
1	E	326	LEU
1	E	334	GLN
1	E	339	ASN
1	E	353	ASN
1	E	378	ASN
1	E	396	VAL
1	E	400	ARG
1	E	401	LEU
1	E	421	LEU
1	E	427	LYS
1	E	428	HIS
1	E	432	ILE
1	E	457	LEU

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Mol	Chain	Res	Type
1	E	471	THR
1	E	476	ASN
1	E	481	LEU
1	E	499	GLU
1	E	504	PHE
1	F	13	PHE
1	F	23	ARG
1	F	36	LEU
1	F	37	ARG
1	F	44	GLN
1	F	46	ARG
1	F	62	VAL
1	F	64	SER
1	F	68	PRO
1	F	90	ARG
1	F	101	THR
1	F	116	THR
1	F	141	THR
1	F	156	LEU
1	F	162	ILE
1	F	180	MET
1	F	219	THR
1	F	235	SER
1	F	243	THR
1	F	259	VAL
1	F	261	LEU
1	F	267	LEU
1	F	281	ASP
1	F	293	LYS
1	F	300	LEU
1	F	306	LEU
1	F	315	GLU
1	F	318	ILE
1	F	320	GLU
1	F	325	ILE
1	F	326	LEU
1	F	334	GLN
1	F	339	ASN
1	F	353	ASN
1	F	378	ASN
1	F	396	VAL
1	F	400	ARG

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Mol	Chain	Res	Type
1	F	401	LEU
1	F	421	LEU
1	F	427	LYS
1	F	428	HIS
1	F	432	ILE
1	F	457	LEU
1	F	471	THR
1	F	476	ASN
1	F	481	LEU
1	F	499	GLU
1	F	504	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	86	HIS
1	A	143	ASN
1	A	302	HIS
1	A	339	ASN
1	A	353	ASN
1	A	378	ASN
1	A	392	ASN
1	A	395	HIS
1	A	410	ASN
1	A	428	HIS
1	A	488	ASN
1	A	498	ASN
1	B	47	ASN
1	B	61	HIS
1	B	86	HIS
1	B	143	ASN
1	B	302	HIS
1	B	339	ASN
1	B	353	ASN
1	B	378	ASN
1	B	392	ASN
1	B	395	HIS
1	B	410	ASN
1	B	428	HIS
1	B	488	ASN
1	B	498	ASN

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Mol	Chain	Res	Type
1	C	47	ASN
1	C	86	HIS
1	C	143	ASN
1	C	209	GLN
1	C	302	HIS
1	C	339	ASN
1	C	353	ASN
1	C	378	ASN
1	C	392	ASN
1	C	395	HIS
1	C	410	ASN
1	C	428	HIS
1	C	488	ASN
1	C	498	ASN
1	D	47	ASN
1	D	86	HIS
1	D	143	ASN
1	D	302	HIS
1	D	339	ASN
1	D	353	ASN
1	D	378	ASN
1	D	392	ASN
1	D	395	HIS
1	D	410	ASN
1	D	428	HIS
1	D	488	ASN
1	D	498	ASN
1	E	47	ASN
1	E	61	HIS
1	E	86	HIS
1	E	143	ASN
1	E	209	GLN
1	E	302	HIS
1	E	339	ASN
1	E	353	ASN
1	E	378	ASN
1	E	392	ASN
1	E	395	HIS
1	E	410	ASN
1	E	428	HIS
1	E	488	ASN
1	E	498	ASN

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Mol	Chain	Res	Type
1	F	47	ASN
1	F	61	HIS
1	F	86	HIS
1	F	143	ASN
1	F	209	GLN
1	F	302	HIS
1	F	339	ASN
1	F	353	ASN
1	F	378	ASN
1	F	392	ASN
1	F	395	HIS
1	F	410	ASN
1	F	428	HIS
1	F	488	ASN
1	F	498	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.