



# Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 07:14 pm BST

PDB ID : 1IOK  
Title : CRYSTAL STRUCTURE OF CHAPERONIN-60 FROM PARACOCCUS DENITRIFICANS  
Authors : Fukami, T.A.; Yohda, M.; Taguchi, H.; Yoshida, M.; Miki, K.  
Deposited on : 2001-03-16  
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

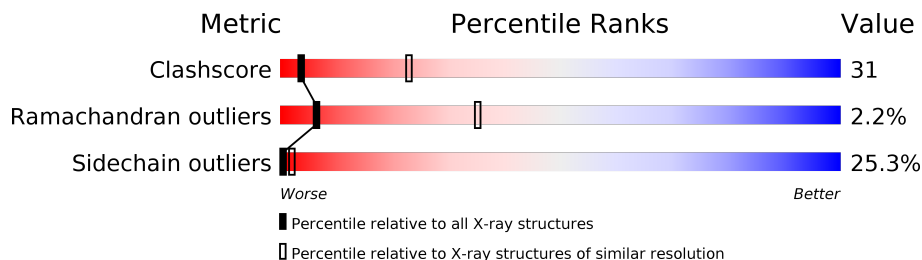
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	545	36% 42% 10% 12%
1	B	545	37% 42% 10% 12%
1	C	545	37% 41% 10% 12%
1	D	545	37% 42% 10% 12%
1	E	545	37% 41% 10% 12%
1	F	545	37% 41% 10% 12%
1	G	545	37% 41% 10% 12%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25095 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 CHAPERONIN 60.

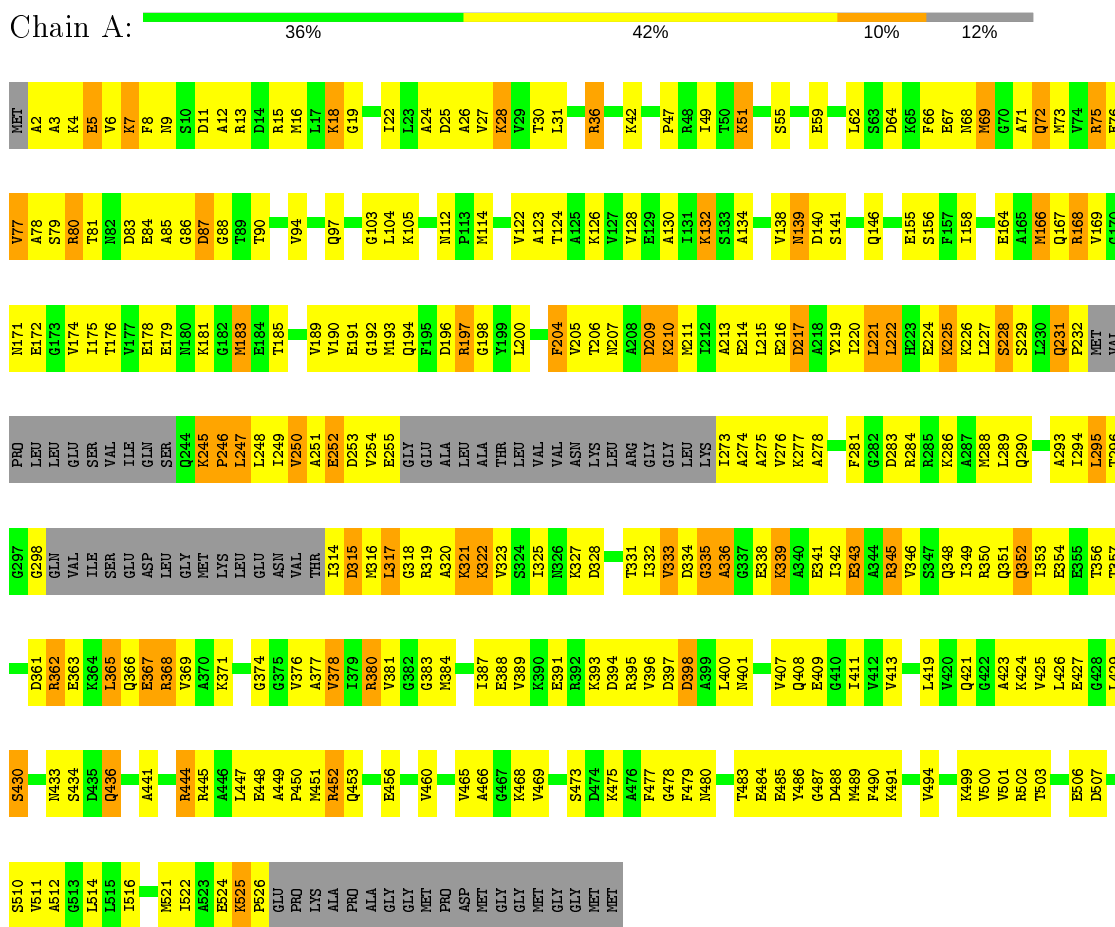
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	482	3585	2218	635	717	15	0	0	0
1	B	482	3585	2218	635	717	15	0	0	0
1	C	482	3585	2218	635	717	15	0	0	0
1	D	482	3585	2218	635	717	15	0	0	0
1	E	482	3585	2218	635	717	15	0	0	0
1	F	482	3585	2218	635	717	15	0	0	0
1	G	482	3585	2218	635	717	15	0	0	0

### 3 Residue-property plots

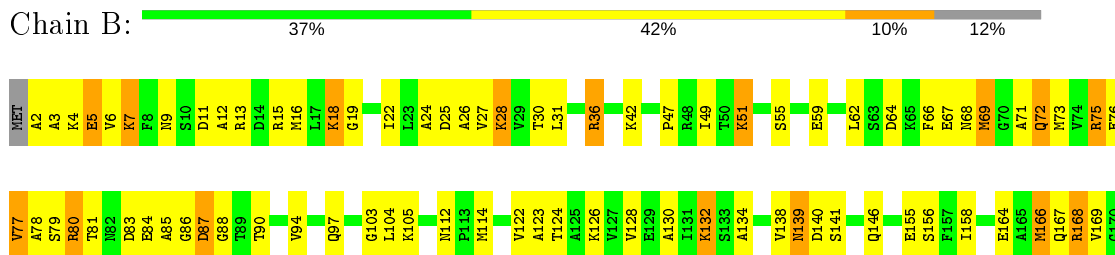
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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: CHAPERONIN 60

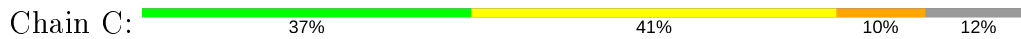


- Molecule 1: CHAPERONIN 60



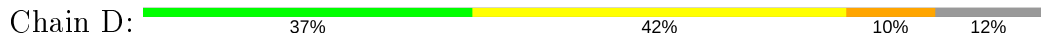
M171	MET	V111	VAL	T286	T357	M433	V511
E172	PRO	A512	PRO	G297	D361	M434	A512
G173	LEU	G513	LEU	G298	R362	S434	A512
V174	LEU	D435	LEU	GLN	R362	D435	G513
I175	GLU	L514	GLU	VAL	E363	Q436	L514
T176	SER	L516	SER	ILE	K364	A441	L516
V177	VAL	M521	VAL	ILE	L365	R444	M521
E178	ILE	I522	ILE	GLU	Q366	R444	I522
E179	GLN	A523	GLN	GLU	E367	R444	A523
K180	SER	K524	SER	ASP	R368	A446	K524
M181	SER	E524	SER	LEU	V369	L447	E524
G182	GLY	K525	GLY	LEU	A370	A448	K525
M183	MET	P526	MET	MET	K371	E448	P526
E184	K245	GLU	K245	LEU	V376	P450	GLU
T185	L247	PRO	L247	LEU	A377	M451	PRO
T185	L248	ALA	L248	LEU	V378	M451	ALA
V189	V250	PRO	V250	VAL	I379	R452	PRO
V190	E251	ALA	E251	THR	R380	Q453	ALA
E191	E252	ALA	E252	I314	V381	E456	ALA
G192	D253	GLY	D253	D815	G382	V460	GLY
M193	V254	GLY	M193	M316	M384	V465	M193
Q194	E255	GLY	Q194	L317	M384	G468	Q194
F195	GLY	PRO	F195	G318	M384	V469	PRO
D196	GLU	ASP	D196	R319	V465	S473	ASP
R197	ALA	MET	R197	A320	V466	M474	MET
G198	ALA	GLY	G198	K321	G467	K475	GLY
Y199	LEU	GLY	Y199	K322	R468	A476	GLY
S201	THR	GLY	S201	V323	K390	F477	THR
F204	VAL	MET	F204	I325	E391	G478	MET
V205	ASN	MET	V205	K327	R392	F479	MET
T206	LYS	GLY	T206	D828	D394	M480	LYS
M207	LEU	LEU	M207	T331	R394	T483	LEU
A208	ARG	ARG	A208	I332	R395	E484	ARG
D209	GLY	ARG	D209	V333	D396	E485	GLY
K210	GLY	GLY	K210	I332	D397	Y486	GLY
M211	LEU	LEU	M211	V333	D398	G487	LEU
L212	LYS	LEU	L212	D334	A399	D488	LYS
A213	LYS	LEU	A213	G335	L400	M489	LYS
E214	LEU	LEU	E214	A336	M401	F490	LEU
L215	LEU	LEU	L215	G337	V407	K491	LEU
E216	LEU	LEU	E216	E338	Q408	V494	LEU
D217	LEU	LEU	D217	V346	Y486	K489	LEU
A218	LEU	LEU	A218	S347	G487	V500	LEU
Y219	LEU	LEU	Y219	Q348	E409	R502	LEU
L220	LEU	LEU	L220	E342	E411	T503	LEU
L221	LEU	LEU	L221	I342	V412	E506	LEU
L222	LEU	LEU	L222	E344	V413	D507	LEU
R223	LEU	LEU	R223	R345	L419	S510	LEU
E224	LEU	LEU	E224	V346	Q421		LEU
K225	LEU	LEU	K225	S347	Q422		LEU
K226	LEU	LEU	K226	Q348	G422		LEU
L227	LEU	LEU	L227	I349	A423		LEU
S228	LEU	LEU	S228	R350	K424		LEU
S229	LEU	LEU	S229	Q351	V425		LEU
Q230	LEU	LEU	Q230	Q352	Q426		LEU
L230	LEU	LEU	L230	I353	E427		LEU
Q231	LEU	LEU	Q231	E354	G428		LEU
M232	LEU	LEU	M232	E354	E429		LEU
P232	LEU	LEU	P232	E355	L429		LEU
MET	LEU	LEU	MET	T356	S430		LEU
					M433		

• Molecule 1: CHAPERONIN 60

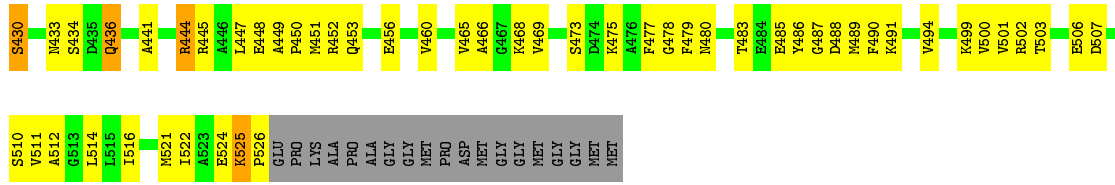


MET	V77	M171	PRO	G297	D361	S434	G513
A2	A78	E172	LEU	G298	D361	D435	L514
A3	S79	G173	LEU	GLN	R362	Q436	L516
K4	R80	V174	GLU	VAL	E363	A441	M521
E5	T81	I175	SER	ILE	K364	R444	I522
V6	N82	T176	SER	SER	L365	R444	A523
K7	D83	V177	VAL	GLU	Q366	R444	K524
F8	E84	E178	GLN	ASP	E367	R444	E524
N9	A85	E179	SER	LEU	R368	R446	P526
S10	G86	M180	SER	GLY	V369	L447	GLU
D11	D87	K181	MET	MET	A370	A448	PRO
A12	G88	G182	LEU	LEU	K371	E448	LYS
R13	T89	M183	LEU	LEU	V376	P450	ALA
R14	T90	E184	L247	GLU	A377	M451	ALA
D14	V94	T185	L248	ASN	V378	M451	ALA
R15	V94	V189	L249	VAL	I379	R452	ALA
M16	R17	V190	E250	THR	R380	Q453	ALA
R17	K18	E191	E251	I314	V381	E456	ALA
G19	G19	E191	E252	D815	G382	V460	GLY
T22	T22	G192	D253	M316	M384	V465	MET
L23	L23	M193	V254	G318	M384	V466	ASP
A24	L104	F195	E255	R319	M384	A466	MET
D25	K105	F195	GLY	R319	M384	K468	GLY
A26	G103	D196	ALA	R320	M384	V469	GLY
V27	L104	R197	ALA	A320	M384	V469	MET
R28	M12	G198	ALA	K321	M384	V469	MET
V29	M12	G198	ALA	K322	M384	V469	MET
R29	V122	G198	ALA	V323	M384	V469	MET
V29	A123	G198	ALA	I325	M384	V469	MET
L30	T124	G198	ALA	K327	M384	V469	MET
L31	A126	G198	ALA	D328	M384	V469	MET
R36	V127	G198	ALA	T331	M384	V469	MET
K42	E128	G198	ALA	I332	M384	V469	MET
P47	A130	G198	ALA	V333	M384	V469	MET
R48	I131	G198	ALA	D334	M384	V469	MET
I49	K132	G198	ALA	G335	M384	V469	MET
T50	S133	G198	ALA	A336	M384	V469	MET
K51	A134	G198	ALA	G337	M384	V469	MET
S55	V138	G198	ALA	E338	M384	V469	MET
E59	M139	G198	ALA	V339	M384	V469	MET
E59	D140	G198	ALA	A340	M384	V469	MET
E59	S141	G198	ALA	E341	M384	V469	MET
L62	I412	G198	ALA	I342	M384	V469	MET
S63	Q146	G198	ALA	E343	M384	V469	MET
D64	E155	G198	ALA	R344	M384	V469	MET
K65	E156	G198	ALA	R345	M384	V469	MET
F66	F157	G198	ALA	S347	M384	V469	MET
E57	I158	G198	ALA	Q348	M384	V469	MET
M68	E164	G198	ALA	I349	M384	V469	MET
M69	E164	G198	ALA	R350	M384	V469	MET
G70	E165	G198	ALA	Q351	M384	V469	MET
A71	A165	G198	ALA	Q352	M384	V469	MET
M66	Q167	G198	ALA	I353	M384	V469	MET
M73	Q167	G198	ALA	E354	M384	V469	MET
V74	R168	G198	ALA	E355	M384	V469	MET
R75	R168	G198	ALA	T357	M384	V469	MET
V75	G170	G198	ALA		M384	V469	MET
E76	G170	G198	ALA		M384	V469	MET

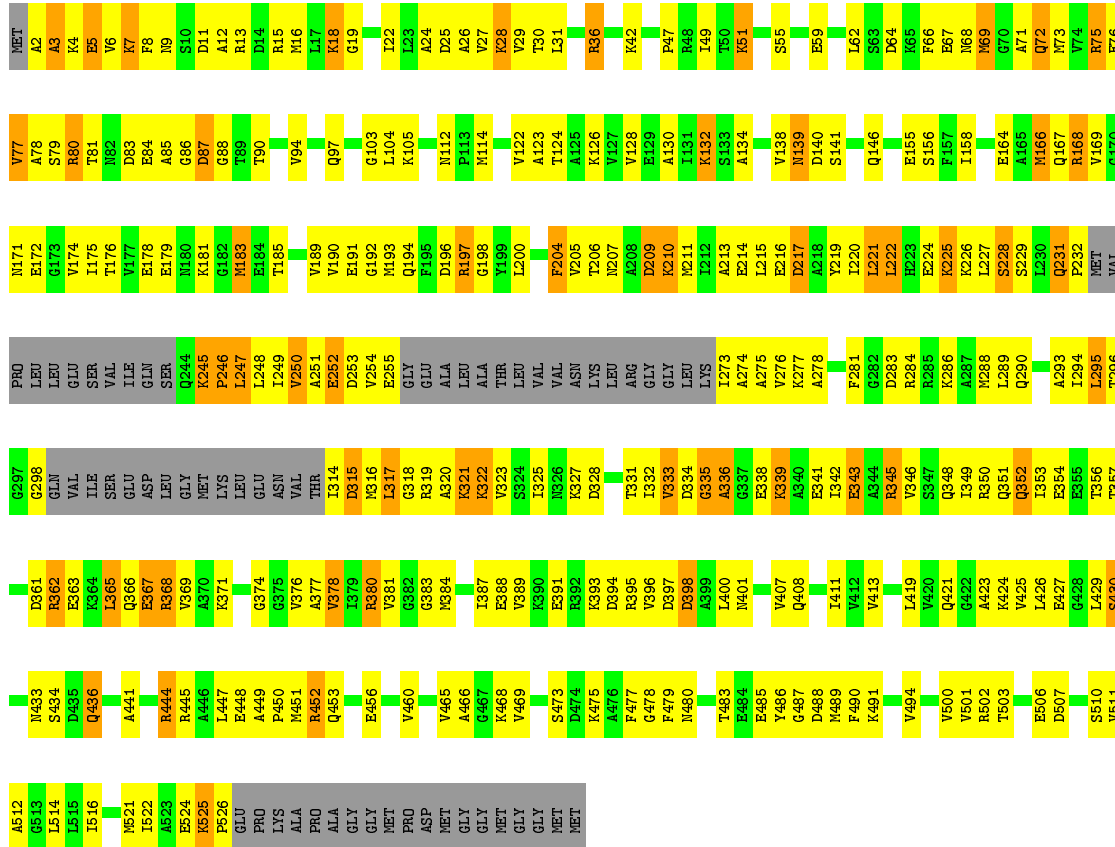
• Molecule 1: CHAPERONIN 60



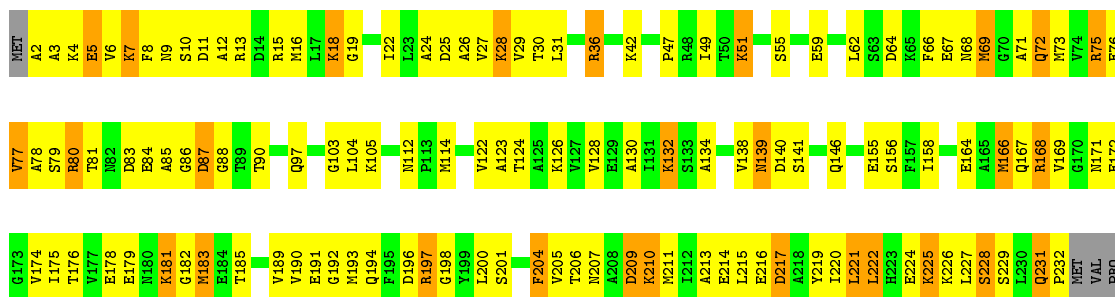
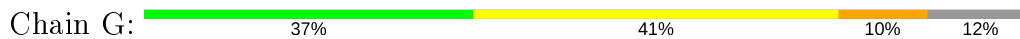
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• Molecule 1: CHAPERONIN 60



• Molecule 1: CHAPERONIN 60







## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	286.36Å 286.36Å 153.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 3.20	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-3.20)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.204 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	25095	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	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	0.32	0/3609	0.48	0/4855
1	B	0.33	0/3609	0.48	0/4855
1	C	0.32	0/3609	0.49	0/4855
1	D	0.34	0/3609	0.48	0/4855
1	E	0.33	0/3609	0.48	0/4855
1	F	0.32	0/3609	0.49	0/4855
1	G	0.33	0/3609	0.48	0/4855
All	All	0.33	0/25263	0.48	0/33985

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3585	0	3657	233	0
1	B	3585	0	3657	231	0
1	C	3585	0	3657	229	0
1	D	3585	0	3657	228	0
1	E	3585	0	3657	231	0
1	F	3585	0	3657	235	0
1	G	3585	0	3657	231	0
All	All	25095	0	25599	1574	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 31.

All (1574) 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:D:139:ASN:HD22	1:D:140:ASP:H	1.17	0.93
1:C:139:ASN:HD22	1:C:140:ASP:H	1.17	0.92
1:C:36:ARG:HG2	1:C:36:ARG:HH11	1.35	0.92
1:G:139:ASN:HD22	1:G:140:ASP:H	1.16	0.92
1:A:36:ARG:HH11	1:A:36:ARG:HG2	1.35	0.91
1:F:139:ASN:HD22	1:F:140:ASP:H	1.17	0.91
1:E:139:ASN:HD22	1:E:140:ASP:H	1.17	0.91
1:F:36:ARG:HH11	1:F:36:ARG:HG2	1.34	0.91
1:A:139:ASN:HD22	1:A:140:ASP:H	1.18	0.90
1:B:36:ARG:HH11	1:B:36:ARG:HG2	1.35	0.90
1:E:36:ARG:HG2	1:E:36:ARG:HH11	1.36	0.90
1:C:227:LEU:HB2	1:C:254:VAL:HA	1.54	0.89
1:F:227:LEU:HB2	1:F:254:VAL:HA	1.54	0.89
1:A:227:LEU:HB2	1:A:254:VAL:HA	1.55	0.89
1:G:227:LEU:HB2	1:G:254:VAL:HA	1.55	0.89
1:B:227:LEU:HB2	1:B:254:VAL:HA	1.55	0.89
1:B:139:ASN:HD22	1:B:140:ASP:H	1.18	0.88
1:D:227:LEU:HB2	1:D:254:VAL:HA	1.55	0.88
1:D:36:ARG:HH11	1:D:36:ARG:HG2	1.36	0.88
1:E:227:LEU:HB2	1:E:254:VAL:HA	1.55	0.88
1:G:36:ARG:HH11	1:G:36:ARG:HG2	1.40	0.86
1:A:228:SER:HA	1:A:255:GLU:HB2	1.58	0.85
1:G:228:SER:HA	1:G:255:GLU:HB2	1.59	0.85
1:B:228:SER:HA	1:B:255:GLU:HB2	1.59	0.84
1:C:228:SER:HA	1:C:255:GLU:HB2	1.59	0.83
1:A:449:ALA:HB3	1:A:450:PRO:HD3	1.60	0.83
1:E:228:SER:HA	1:E:255:GLU:HB2	1.59	0.83
1:F:514:LEU:HD13	1:G:49:ILE:HD12	1.61	0.82
1:D:228:SER:HA	1:D:255:GLU:HB2	1.59	0.82
1:F:228:SER:HA	1:F:255:GLU:HB2	1.59	0.82
1:G:449:ALA:HB3	1:G:450:PRO:HD3	1.62	0.82
1:B:514:LEU:HD13	1:C:49:ILE:HD12	1.63	0.81
1:F:449:ALA:HB3	1:F:450:PRO:HD3	1.62	0.81
1:A:322:LYS:HB3	1:A:333:VAL:HG23	1.63	0.81
1:B:449:ALA:HB3	1:B:450:PRO:HD3	1.62	0.81
1:D:322:LYS:HB3	1:D:333:VAL:HG23	1.63	0.81
1:F:322:LYS:HB3	1:F:333:VAL:HG23	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:449:ALA:HB3	1:D:450:PRO:HD3	1.61	0.80
1:E:322:LYS:HB3	1:E:333:VAL:HG23	1.63	0.80
1:A:49:ILE:HD12	1:G:514:LEU:HD13	1.63	0.80
1:G:322:LYS:HB3	1:G:333:VAL:HG23	1.64	0.80
1:C:514:LEU:HD13	1:D:49:ILE:HD12	1.63	0.80
1:B:322:LYS:HB3	1:B:333:VAL:HG23	1.64	0.80
1:C:322:LYS:HB3	1:C:333:VAL:HG23	1.64	0.80
1:C:449:ALA:HB3	1:C:450:PRO:HD3	1.61	0.79
1:F:250:VAL:HG13	1:F:276:VAL:HG23	1.65	0.78
1:A:197:ARG:HH11	1:A:277:LYS:HG2	1.49	0.78
1:E:449:ALA:HB3	1:E:450:PRO:HD3	1.64	0.78
1:G:250:VAL:HG13	1:G:276:VAL:HG23	1.66	0.78
1:D:197:ARG:HH11	1:D:277:LYS:HG2	1.49	0.77
1:A:250:VAL:HG13	1:A:276:VAL:HG23	1.66	0.77
1:E:197:ARG:HH11	1:E:277:LYS:HG2	1.50	0.77
1:B:380:ARG:HB2	1:B:380:ARG:HH11	1.50	0.77
1:B:197:ARG:HH11	1:B:277:LYS:HG2	1.50	0.77
1:D:250:VAL:HG13	1:D:276:VAL:HG23	1.66	0.77
1:F:197:ARG:HH11	1:F:277:LYS:HG2	1.50	0.77
1:G:197:ARG:HH11	1:G:277:LYS:HG2	1.50	0.77
1:E:250:VAL:HG13	1:E:276:VAL:HG23	1.67	0.77
1:E:380:ARG:HB2	1:E:380:ARG:HH11	1.50	0.77
1:C:250:VAL:HG13	1:C:276:VAL:HG23	1.66	0.77
1:A:380:ARG:HH11	1:A:380:ARG:HB2	1.50	0.76
1:G:380:ARG:HH11	1:G:380:ARG:HB2	1.50	0.76
1:C:197:ARG:HH11	1:C:277:LYS:HG2	1.50	0.76
1:C:380:ARG:HH11	1:C:380:ARG:HB2	1.50	0.76
1:F:380:ARG:HH11	1:F:380:ARG:HB2	1.50	0.76
1:C:413:VAL:HG12	1:C:489:MET:HB3	1.68	0.76
1:B:250:VAL:HG13	1:B:276:VAL:HG23	1.66	0.76
1:D:380:ARG:HH11	1:D:380:ARG:HB2	1.50	0.75
1:B:413:VAL:HG12	1:B:489:MET:HB3	1.69	0.75
1:G:413:VAL:HG12	1:G:489:MET:HB3	1.68	0.74
1:E:413:VAL:HG12	1:E:489:MET:HB3	1.68	0.74
1:A:413:VAL:HG12	1:A:489:MET:HB3	1.69	0.74
1:E:514:LEU:HD13	1:F:49:ILE:HD12	1.70	0.73
1:D:413:VAL:HG12	1:D:489:MET:HB3	1.70	0.73
1:F:413:VAL:HG12	1:F:489:MET:HB3	1.69	0.73
1:A:514:LEU:HD13	1:B:49:ILE:HD12	1.70	0.73
1:E:411:ILE:HD12	1:E:490:PHE:HE1	1.54	0.72
1:D:514:LEU:HD13	1:E:49:ILE:HD12	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:411:ILE:HD12	1:C:490:PHE:HE1	1.54	0.72
1:B:128:VAL:HG13	1:B:502:ARG:HG3	1.70	0.72
1:F:411:ILE:HD12	1:F:490:PHE:HE1	1.53	0.72
1:E:226:LYS:HG2	1:E:252:GLU:HB2	1.72	0.71
1:D:128:VAL:HG13	1:D:502:ARG:HG3	1.72	0.71
1:B:411:ILE:HD12	1:B:490:PHE:HE1	1.56	0.71
1:A:411:ILE:HD12	1:A:490:PHE:HE1	1.55	0.71
1:D:411:ILE:HD12	1:D:490:PHE:HE1	1.55	0.71
1:C:7:LYS:HD2	1:C:66:PHE:CZ	2.25	0.71
1:D:226:LYS:HG2	1:D:252:GLU:HB2	1.72	0.71
1:E:128:VAL:HG13	1:E:502:ARG:HG3	1.73	0.71
1:F:346:VAL:HG12	1:F:350:ARG:HE	1.56	0.71
1:C:128:VAL:HG13	1:C:502:ARG:HG3	1.72	0.71
1:A:346:VAL:HG12	1:A:350:ARG:HE	1.56	0.70
1:C:226:LYS:HG2	1:C:252:GLU:HB2	1.73	0.70
1:G:128:VAL:HG13	1:G:502:ARG:HG3	1.72	0.70
1:D:139:ASN:HD22	1:D:140:ASP:N	1.90	0.70
1:G:346:VAL:HG12	1:G:350:ARG:HE	1.56	0.70
1:F:7:LYS:HD2	1:F:66:PHE:CZ	2.26	0.70
1:G:7:LYS:HD2	1:G:66:PHE:CZ	2.26	0.70
1:B:346:VAL:HG12	1:B:350:ARG:HE	1.56	0.70
1:B:36:ARG:NH1	1:B:36:ARG:HG2	2.07	0.70
1:F:128:VAL:HG13	1:F:502:ARG:HG3	1.73	0.70
1:G:226:LYS:HG2	1:G:252:GLU:HB2	1.72	0.70
1:D:36:ARG:NH1	1:D:36:ARG:HG2	2.07	0.70
1:A:448:GLU:O	1:A:452:ARG:HD2	1.91	0.70
1:C:346:VAL:HG12	1:C:350:ARG:HE	1.56	0.70
1:F:226:LYS:HG2	1:F:252:GLU:HB2	1.72	0.70
1:A:226:LYS:HG2	1:A:252:GLU:HB2	1.73	0.69
1:D:7:LYS:HD2	1:D:66:PHE:CZ	2.26	0.69
1:F:130:ALA:CB	1:F:425:VAL:HG21	2.22	0.69
1:G:411:ILE:HD12	1:G:490:PHE:HE1	1.57	0.69
1:B:226:LYS:HG2	1:B:252:GLU:HB2	1.72	0.69
1:E:7:LYS:HD2	1:E:66:PHE:CZ	2.26	0.69
1:E:130:ALA:CB	1:E:425:VAL:HG21	2.22	0.69
1:D:346:VAL:HG12	1:D:350:ARG:HE	1.56	0.69
1:A:130:ALA:CB	1:A:425:VAL:HG21	2.23	0.69
1:G:139:ASN:HD22	1:G:140:ASP:N	1.90	0.69
1:G:130:ALA:CB	1:G:425:VAL:HG21	2.23	0.69
1:C:130:ALA:CB	1:C:425:VAL:HG21	2.23	0.69
1:G:227:LEU:HD22	1:G:254:VAL:HG22	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:166:MET:HG2	1:G:171:ASN:HA	1.74	0.68
1:E:346:VAL:HG12	1:E:350:ARG:HE	1.57	0.68
1:A:73:MET:CE	1:B:49:ILE:HD11	2.23	0.68
1:C:448:GLU:O	1:C:452:ARG:HD2	1.92	0.68
1:A:128:VAL:HG13	1:A:502:ARG:HG3	1.74	0.68
1:A:366:GLN:O	1:A:369:VAL:HG12	1.94	0.68
1:B:139:ASN:HD22	1:B:140:ASP:N	1.91	0.68
1:B:7:LYS:HD2	1:B:66:PHE:CZ	2.29	0.68
1:F:166:MET:HG2	1:F:171:ASN:HA	1.76	0.68
1:B:130:ALA:CB	1:B:425:VAL:HG21	2.23	0.68
1:C:366:GLN:O	1:C:369:VAL:HG12	1.94	0.68
1:D:166:MET:HG2	1:D:171:ASN:HA	1.75	0.68
1:F:448:GLU:O	1:F:452:ARG:HD2	1.94	0.68
1:B:227:LEU:HD22	1:B:254:VAL:HG22	1.76	0.68
1:E:139:ASN:HD22	1:E:140:ASP:N	1.90	0.68
1:E:166:MET:HG2	1:E:171:ASN:HA	1.76	0.68
1:A:227:LEU:HD22	1:A:254:VAL:HG22	1.76	0.67
1:C:321:LYS:HB3	1:C:334:ASP:HB3	1.76	0.67
1:D:130:ALA:CB	1:D:425:VAL:HG21	2.23	0.67
1:C:227:LEU:HD22	1:C:254:VAL:HG22	1.77	0.67
1:C:139:ASN:HD22	1:C:140:ASP:N	1.91	0.67
1:F:227:LEU:HD22	1:F:254:VAL:HG22	1.76	0.67
1:G:448:GLU:O	1:G:452:ARG:HD2	1.93	0.67
1:E:227:LEU:HD22	1:E:254:VAL:HG22	1.76	0.67
1:D:321:LYS:HB3	1:D:334:ASP:HB3	1.77	0.67
1:D:366:GLN:O	1:D:369:VAL:HG12	1.94	0.67
1:F:366:GLN:O	1:F:369:VAL:HG12	1.93	0.67
1:A:132:LYS:HD3	1:A:502:ARG:HD3	1.76	0.67
1:D:227:LEU:HD22	1:D:254:VAL:HG22	1.77	0.67
1:E:130:ALA:HB2	1:E:425:VAL:HG21	1.77	0.67
1:G:366:GLN:O	1:G:369:VAL:HG12	1.93	0.66
1:A:7:LYS:HD2	1:A:66:PHE:CZ	2.29	0.66
1:B:166:MET:HG2	1:B:171:ASN:HA	1.76	0.66
1:G:132:LYS:HD3	1:G:502:ARG:HD3	1.77	0.66
1:A:166:MET:HG2	1:A:171:ASN:HA	1.76	0.66
1:C:166:MET:HG2	1:C:171:ASN:HA	1.75	0.66
1:C:183:MET:HG2	1:C:384:MET:SD	2.35	0.66
1:E:366:GLN:O	1:E:369:VAL:HG12	1.94	0.66
1:A:183:MET:HG2	1:A:384:MET:SD	2.36	0.66
1:B:366:GLN:O	1:B:369:VAL:HG12	1.95	0.66
1:F:231:GLN:NE2	1:F:231:GLN:H	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:321:LYS:HB3	1:G:334:ASP:HB3	1.76	0.66
1:B:321:LYS:HB3	1:B:334:ASP:HB3	1.78	0.66
1:F:130:ALA:HB2	1:F:425:VAL:HG21	1.77	0.66
1:B:448:GLU:O	1:B:452:ARG:HD2	1.96	0.66
1:D:183:MET:HG2	1:D:384:MET:SD	2.36	0.66
1:A:321:LYS:HB3	1:A:334:ASP:HB3	1.76	0.65
1:E:226:LYS:NZ	1:E:252:GLU:HB3	2.11	0.65
1:E:321:LYS:HB3	1:E:334:ASP:HB3	1.77	0.65
1:F:321:LYS:HB3	1:F:334:ASP:HB3	1.77	0.65
1:B:183:MET:HG2	1:B:384:MET:SD	2.37	0.65
1:D:226:LYS:NZ	1:D:252:GLU:HB3	2.12	0.65
1:F:219:TYR:HB2	1:F:247:LEU:HA	1.79	0.65
1:A:219:TYR:HB2	1:A:247:LEU:HA	1.78	0.65
1:D:130:ALA:HB2	1:D:425:VAL:HG21	1.79	0.65
1:D:231:GLN:H	1:D:231:GLN:NE2	1.94	0.65
1:B:130:ALA:HB2	1:B:425:VAL:HG21	1.78	0.65
1:B:231:GLN:NE2	1:B:231:GLN:H	1.95	0.65
1:G:231:GLN:H	1:G:231:GLN:NE2	1.94	0.65
1:C:226:LYS:NZ	1:C:252:GLU:HB3	2.12	0.65
1:E:448:GLU:O	1:E:452:ARG:HD2	1.97	0.65
1:C:130:ALA:HB2	1:C:425:VAL:HG21	1.78	0.65
1:E:231:GLN:H	1:E:231:GLN:NE2	1.95	0.65
1:F:132:LYS:HD3	1:F:502:ARG:HD3	1.78	0.65
1:C:231:GLN:H	1:C:231:GLN:NE2	1.95	0.65
1:G:36:ARG:HG2	1:G:36:ARG:NH1	2.10	0.65
1:A:231:GLN:H	1:A:231:GLN:NE2	1.95	0.64
1:B:128:VAL:HG13	1:B:502:ARG:CG	2.27	0.64
1:E:209:ASP:HB3	1:E:210:LYS:NZ	2.12	0.64
1:B:72:GLN:HE22	1:B:75:ARG:NH1	1.95	0.64
1:A:226:LYS:NZ	1:A:252:GLU:HB3	2.12	0.64
1:C:209:ASP:HB3	1:C:210:LYS:NZ	2.12	0.64
1:C:36:ARG:HG2	1:C:36:ARG:NH1	2.07	0.64
1:D:448:GLU:O	1:D:452:ARG:HD2	1.97	0.64
1:D:73:MET:CE	1:E:49:ILE:HD11	2.27	0.64
1:F:429:LEU:HD12	1:F:430:SER:H	1.62	0.64
1:G:77:VAL:HA	1:G:80:ARG:HD3	1.79	0.64
1:D:429:LEU:HD12	1:D:430:SER:H	1.63	0.64
1:E:183:MET:HG2	1:E:384:MET:SD	2.37	0.64
1:F:226:LYS:NZ	1:F:252:GLU:HB3	2.12	0.64
1:G:183:MET:HG2	1:G:384:MET:SD	2.36	0.64
1:A:77:VAL:HA	1:A:80:ARG:HD3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:ASP:HB3	1:B:210:LYS:NZ	2.13	0.64
1:A:130:ALA:HB2	1:A:425:VAL:HG21	1.78	0.64
1:E:219:TYR:HB2	1:E:247:LEU:HA	1.78	0.64
1:B:226:LYS:NZ	1:B:252:GLU:HB3	2.12	0.64
1:D:132:LYS:HD3	1:D:502:ARG:HD3	1.78	0.64
1:G:130:ALA:HB2	1:G:425:VAL:HG21	1.79	0.64
1:G:209:ASP:HB3	1:G:210:LYS:NZ	2.13	0.64
1:A:36:ARG:HG2	1:A:36:ARG:NH1	2.05	0.64
1:B:219:TYR:HB2	1:B:247:LEU:HA	1.78	0.64
1:D:209:ASP:HB3	1:D:210:LYS:NZ	2.13	0.64
1:F:183:MET:HG2	1:F:384:MET:SD	2.38	0.64
1:G:250:VAL:HA	1:G:276:VAL:O	1.98	0.64
1:C:132:LYS:HD3	1:C:502:ARG:HD3	1.79	0.64
1:D:190:VAL:HG12	1:D:191:GLU:H	1.62	0.64
1:D:77:VAL:HA	1:D:80:ARG:HD3	1.78	0.64
1:G:219:TYR:HB2	1:G:247:LEU:HA	1.78	0.64
1:G:226:LYS:NZ	1:G:252:GLU:HB3	2.13	0.64
1:A:429:LEU:HD12	1:A:430:SER:H	1.64	0.63
1:D:219:TYR:HB2	1:D:247:LEU:HA	1.79	0.63
1:F:250:VAL:HA	1:F:276:VAL:O	1.98	0.63
1:F:77:VAL:HA	1:F:80:ARG:HD3	1.80	0.63
1:A:209:ASP:HB3	1:A:210:LYS:NZ	2.13	0.63
1:F:209:ASP:HB3	1:F:210:LYS:NZ	2.13	0.63
1:F:72:GLN:HE22	1:F:75:ARG:NH1	1.96	0.63
1:C:219:TYR:HB2	1:C:247:LEU:HA	1.79	0.63
1:E:77:VAL:HA	1:E:80:ARG:HD3	1.80	0.63
1:F:139:ASN:HD22	1:F:140:ASP:N	1.91	0.63
1:E:84:GLU:HG3	1:E:500:VAL:HG22	1.81	0.63
1:E:72:GLN:HE22	1:E:75:ARG:NH1	1.96	0.63
1:G:72:GLN:HE22	1:G:75:ARG:NH1	1.97	0.63
1:C:250:VAL:HA	1:C:276:VAL:O	1.98	0.63
1:G:128:VAL:HG13	1:G:502:ARG:CG	2.28	0.63
1:E:248:LEU:HA	1:E:274:ALA:HB3	1.81	0.63
1:A:250:VAL:HA	1:A:276:VAL:O	1.99	0.62
1:B:250:VAL:HA	1:B:276:VAL:O	1.98	0.62
1:D:250:VAL:HA	1:D:276:VAL:O	1.99	0.62
1:B:77:VAL:HA	1:B:80:ARG:HD3	1.79	0.62
1:C:429:LEU:HD12	1:C:430:SER:H	1.63	0.62
1:E:250:VAL:HA	1:E:276:VAL:O	1.98	0.62
1:F:138:VAL:HG12	1:F:407:VAL:HG12	1.81	0.62
1:C:72:GLN:HE22	1:C:75:ARG:NH1	1.97	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:128:VAL:HG13	1:E:502:ARG:CG	2.29	0.62
1:E:73:MET:CE	1:F:49:ILE:HD11	2.30	0.62
1:A:176:THR:O	1:A:378:VAL:HG23	2.00	0.62
1:A:138:VAL:HG12	1:A:407:VAL:HG12	1.82	0.62
1:B:174:VAL:HG22	1:B:376:VAL:HG13	1.81	0.62
1:B:429:LEU:HD12	1:B:430:SER:H	1.64	0.62
1:B:176:THR:O	1:B:378:VAL:HG23	1.99	0.62
1:C:190:VAL:HG12	1:C:191:GLU:H	1.63	0.62
1:E:429:LEU:HD12	1:E:430:SER:H	1.65	0.62
1:F:248:LEU:HA	1:F:274:ALA:HB3	1.82	0.62
1:B:84:GLU:HG3	1:B:500:VAL:HG22	1.81	0.62
1:C:128:VAL:HG13	1:C:502:ARG:CG	2.28	0.62
1:C:176:THR:O	1:C:378:VAL:HG23	1.99	0.62
1:C:193:MET:HB2	1:C:295:LEU:HD22	1.82	0.62
1:E:174:VAL:HG22	1:E:376:VAL:HG13	1.82	0.62
1:F:36:ARG:NH1	1:F:36:ARG:HG2	2.07	0.62
1:D:174:VAL:HG22	1:D:376:VAL:HG13	1.82	0.62
1:E:132:LYS:HD3	1:E:502:ARG:HD3	1.79	0.62
1:C:73:MET:CE	1:D:49:ILE:HD11	2.30	0.62
1:F:84:GLU:HG3	1:F:500:VAL:HG22	1.82	0.62
1:F:176:THR:O	1:F:378:VAL:HG23	2.00	0.62
1:G:429:LEU:HD12	1:G:430:SER:H	1.63	0.62
1:A:525:LYS:HD2	1:A:526:PRO:HD2	1.82	0.61
1:D:248:LEU:HA	1:D:274:ALA:HB3	1.82	0.61
1:G:190:VAL:HG12	1:G:191:GLU:H	1.65	0.61
1:A:128:VAL:HG13	1:A:502:ARG:CG	2.29	0.61
1:B:477:PHE:HA	1:B:487:GLY:O	1.99	0.61
1:D:128:VAL:HG13	1:D:502:ARG:CG	2.29	0.61
1:A:174:VAL:HG22	1:A:376:VAL:HG13	1.82	0.61
1:B:138:VAL:HG12	1:B:407:VAL:HG12	1.83	0.61
1:B:248:LEU:HA	1:B:274:ALA:HB3	1.82	0.61
1:B:132:LYS:HD3	1:B:502:ARG:HD3	1.80	0.61
1:C:174:VAL:HG22	1:C:376:VAL:HG13	1.83	0.61
1:A:139:ASN:HD22	1:A:140:ASP:N	1.92	0.61
1:A:49:ILE:HD11	1:G:73:MET:CE	2.31	0.61
1:C:221:LEU:HD11	1:C:249:ILE:HG23	1.82	0.61
1:C:248:LEU:HA	1:C:274:ALA:HB3	1.82	0.61
1:C:77:VAL:HA	1:C:80:ARG:HD3	1.81	0.61
1:E:409:GLU:OE2	1:E:499:LYS:HG3	1.99	0.61
1:A:193:MET:HB2	1:A:295:LEU:HD22	1.82	0.61
1:B:221:LEU:HD11	1:B:249:ILE:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:525:LYS:HD2	1:F:526:PRO:HD2	1.82	0.61
1:F:73:MET:CE	1:G:49:ILE:HD11	2.30	0.61
1:G:248:LEU:HA	1:G:274:ALA:HB3	1.82	0.61
1:A:248:LEU:HA	1:A:274:ALA:HB3	1.82	0.61
1:E:367:GLU:HG3	1:E:368:ARG:N	2.16	0.61
1:G:221:LEU:HD11	1:G:249:ILE:HG23	1.82	0.61
1:B:193:MET:HB2	1:B:295:LEU:HD22	1.82	0.61
1:E:525:LYS:HD2	1:E:526:PRO:HD2	1.82	0.61
1:F:73:MET:HE3	1:G:49:ILE:HD11	1.82	0.61
1:F:75:ARG:HG2	1:F:75:ARG:NH1	2.16	0.61
1:A:72:GLN:HE22	1:A:75:ARG:NH1	1.99	0.61
1:B:73:MET:HE3	1:C:49:ILE:HD11	1.82	0.61
1:D:525:LYS:HD2	1:D:526:PRO:HD2	1.82	0.61
1:A:49:ILE:HD11	1:G:73:MET:HE3	1.82	0.61
1:G:193:MET:HB2	1:G:295:LEU:HD22	1.82	0.61
1:F:174:VAL:HG22	1:F:376:VAL:HG13	1.84	0.60
1:G:525:LYS:HD2	1:G:526:PRO:HD2	1.83	0.60
1:D:176:THR:O	1:D:378:VAL:HG23	2.01	0.60
1:D:193:MET:HB2	1:D:295:LEU:HD22	1.83	0.60
1:F:221:LEU:HD11	1:F:249:ILE:HG23	1.82	0.60
1:D:84:GLU:HG3	1:D:500:VAL:HG22	1.83	0.60
1:G:174:VAL:HG22	1:G:376:VAL:HG13	1.84	0.60
1:G:477:PHE:HA	1:G:487:GLY:O	2.01	0.60
1:E:221:LEU:HD11	1:E:249:ILE:HG23	1.82	0.60
1:E:75:ARG:HG2	1:E:75:ARG:NH1	2.17	0.60
1:B:367:GLU:HG3	1:B:368:ARG:N	2.16	0.60
1:B:525:LYS:HD2	1:B:526:PRO:HD2	1.83	0.60
1:C:73:MET:HE3	1:D:49:ILE:HD11	1.81	0.60
1:F:128:VAL:HG13	1:F:502:ARG:CG	2.30	0.60
1:F:367:GLU:HG3	1:F:368:ARG:N	2.16	0.60
1:C:22:ILE:HG21	1:C:62:LEU:HD21	1.84	0.60
1:C:296:THR:O	1:C:336:ALA:HB3	2.02	0.60
1:G:367:GLU:HG3	1:G:368:ARG:N	2.16	0.60
1:C:367:GLU:HG3	1:C:368:ARG:N	2.16	0.60
1:C:138:VAL:HG12	1:C:407:VAL:HG12	1.83	0.60
1:E:176:THR:O	1:E:378:VAL:HG23	2.01	0.60
1:A:221:LEU:HD11	1:A:249:ILE:HG23	1.84	0.60
1:C:477:PHE:HA	1:C:487:GLY:O	2.02	0.60
1:C:525:LYS:HD2	1:C:526:PRO:HD2	1.83	0.60
1:C:84:GLU:HG3	1:C:500:VAL:HG22	1.83	0.60
1:D:73:MET:HE3	1:E:49:ILE:HD11	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:72:GLN:HE22	1:D:75:ARG:NH1	2.00	0.60
1:E:193:MET:HB2	1:E:295:LEU:HD22	1.82	0.60
1:F:477:PHE:HA	1:F:487:GLY:O	2.02	0.60
1:G:84:GLU:HG3	1:G:500:VAL:HG22	1.83	0.59
1:C:27:VAL:CG1	1:C:90:THR:HG23	2.32	0.59
1:B:73:MET:CE	1:C:49:ILE:HD11	2.32	0.59
1:F:296:THR:O	1:F:336:ALA:HB3	2.02	0.59
1:G:219:TYR:H	1:G:247:LEU:HA	1.66	0.59
1:A:477:PHE:HA	1:A:487:GLY:O	2.02	0.59
1:C:352:GLN:O	1:C:356:THR:HG23	2.02	0.59
1:D:352:GLN:O	1:D:356:THR:HG23	2.02	0.59
1:F:193:MET:HB2	1:F:295:LEU:HD22	1.82	0.59
1:A:84:GLU:HG3	1:A:500:VAL:HG22	1.82	0.59
1:D:296:THR:O	1:D:336:ALA:HB3	2.02	0.59
1:D:367:GLU:HG3	1:D:368:ARG:N	2.16	0.59
1:A:73:MET:HE3	1:B:49:ILE:HD11	1.83	0.59
1:C:219:TYR:H	1:C:247:LEU:HA	1.66	0.59
1:D:219:TYR:H	1:D:247:LEU:HA	1.67	0.59
1:E:73:MET:HE3	1:F:49:ILE:HD11	1.84	0.59
1:G:138:VAL:HG12	1:G:407:VAL:HG12	1.85	0.59
1:A:296:THR:O	1:A:336:ALA:HB3	2.02	0.59
1:A:367:GLU:HG3	1:A:368:ARG:N	2.16	0.59
1:D:27:VAL:CG1	1:D:90:THR:HG23	2.33	0.59
1:F:219:TYR:H	1:F:247:LEU:HA	1.67	0.59
1:A:219:TYR:H	1:A:247:LEU:HA	1.67	0.59
1:B:71:ALA:O	1:B:75:ARG:HB3	2.02	0.59
1:C:158:ILE:HG23	1:C:396:VAL:HG22	1.84	0.59
1:F:352:GLN:O	1:F:356:THR:HG23	2.03	0.59
1:G:296:THR:O	1:G:336:ALA:HB3	2.03	0.59
1:B:77:VAL:HG12	1:B:78:ALA:N	2.18	0.59
1:E:352:GLN:O	1:E:356:THR:HG23	2.03	0.59
1:A:394:ASP:O	1:A:398:ASP:HB2	2.03	0.59
1:B:296:THR:O	1:B:336:ALA:HB3	2.03	0.59
1:D:221:LEU:HD11	1:D:249:ILE:HG23	1.83	0.59
1:E:27:VAL:CG1	1:E:90:THR:HG23	2.33	0.59
1:F:483:THR:OG1	1:F:485:GLU:HG2	2.03	0.59
1:E:219:TYR:H	1:E:247:LEU:HA	1.66	0.59
1:E:477:PHE:HA	1:E:487:GLY:O	2.03	0.59
1:D:158:ILE:HG23	1:D:396:VAL:HG22	1.85	0.58
1:F:411:ILE:CD1	1:F:490:PHE:HE1	2.16	0.58
1:B:219:TYR:H	1:B:247:LEU:HA	1.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:190:VAL:HG12	1:E:191:GLU:H	1.67	0.58
1:G:353:ILE:HG12	1:G:365:LEU:HB3	1.85	0.58
1:A:168:ARG:HG2	1:A:189:VAL:HG21	1.86	0.58
1:D:77:VAL:HG12	1:D:78:ALA:N	2.17	0.58
1:G:394:ASP:O	1:G:398:ASP:HB2	2.03	0.58
1:D:394:ASP:O	1:D:398:ASP:HB2	2.03	0.58
1:G:352:GLN:O	1:G:356:THR:HG23	2.03	0.58
1:C:483:THR:OG1	1:C:485:GLU:HG2	2.03	0.58
1:C:394:ASP:O	1:C:398:ASP:HB2	2.03	0.58
1:E:296:THR:O	1:E:336:ALA:HB3	2.03	0.58
1:G:483:THR:OG1	1:G:485:GLU:HG2	2.04	0.58
1:A:353:ILE:HG12	1:A:365:LEU:HB3	1.86	0.58
1:F:168:ARG:HG2	1:F:189:VAL:HG21	1.86	0.58
1:F:353:ILE:HG12	1:F:365:LEU:HB3	1.85	0.58
1:G:27:VAL:CG1	1:G:90:THR:HG23	2.32	0.58
1:B:25:ASP:HA	1:B:28:LYS:HD2	1.86	0.58
1:D:22:ILE:HG21	1:D:62:LEU:HD21	1.86	0.58
1:G:71:ALA:O	1:G:75:ARG:HB3	2.04	0.58
1:D:477:PHE:HA	1:D:487:GLY:O	2.04	0.58
1:A:483:THR:OG1	1:A:485:GLU:HG2	2.04	0.58
1:A:19:GLY:HA3	1:A:67:GLU:O	2.04	0.58
1:C:77:VAL:HG12	1:C:78:ALA:N	2.18	0.58
1:E:138:VAL:HG12	1:E:407:VAL:HG12	1.85	0.58
1:G:365:LEU:O	1:G:368:ARG:HG3	2.04	0.58
1:G:176:THR:O	1:G:378:VAL:HG23	2.04	0.58
1:A:488:ASP:OD1	1:A:490:PHE:HB2	2.04	0.57
1:B:158:ILE:HG23	1:B:396:VAL:HG22	1.84	0.57
1:B:27:VAL:CG1	1:B:90:THR:HG23	2.33	0.57
1:A:352:GLN:O	1:A:356:THR:HG23	2.03	0.57
1:B:394:ASP:O	1:B:398:ASP:HB2	2.04	0.57
1:B:468:LYS:HD3	1:B:486:TYR:CZ	2.39	0.57
1:B:168:ARG:HG2	1:B:189:VAL:HG21	1.87	0.57
1:B:352:GLN:O	1:B:356:THR:HG23	2.03	0.57
1:B:353:ILE:HG12	1:B:365:LEU:HB3	1.85	0.57
1:B:75:ARG:HG2	1:B:75:ARG:NH1	2.19	0.57
1:D:138:VAL:HG12	1:D:407:VAL:HG12	1.86	0.57
1:F:77:VAL:HG12	1:F:78:ALA:N	2.19	0.57
1:G:158:ILE:HG23	1:G:396:VAL:HG22	1.85	0.57
1:G:25:ASP:HA	1:G:28:LYS:HD2	1.86	0.57
1:E:36:ARG:HG2	1:E:36:ARG:NH1	2.08	0.57
1:F:158:ILE:HG23	1:F:396:VAL:HG22	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:488:ASP:OD1	1:F:490:PHE:HB2	2.04	0.57
1:G:75:ARG:NH1	1:G:75:ARG:HG2	2.18	0.57
1:C:168:ARG:HG2	1:C:189:VAL:HG21	1.86	0.57
1:C:411:ILE:CD1	1:C:490:PHE:HE1	2.16	0.57
1:D:502:ARG:O	1:D:506:GLU:HG3	2.04	0.57
1:F:75:ARG:HH11	1:F:75:ARG:HG2	1.68	0.57
1:A:365:LEU:O	1:A:368:ARG:HG3	2.05	0.57
1:E:353:ILE:HG12	1:E:365:LEU:HB3	1.86	0.57
1:F:468:LYS:HD3	1:F:486:TYR:CZ	2.40	0.57
1:B:409:GLU:OE2	1:B:499:LYS:HG3	2.05	0.57
1:C:226:LYS:HZ1	1:C:252:GLU:HB3	1.69	0.57
1:A:75:ARG:HG2	1:A:75:ARG:NH1	2.20	0.57
1:B:483:THR:OG1	1:B:485:GLU:HG2	2.05	0.57
1:F:71:ALA:O	1:F:75:ARG:HB3	2.05	0.57
1:A:59:GLU:O	1:G:4:LYS:HD2	2.05	0.57
1:C:245:LYS:NZ	1:C:319:ARG:HH21	2.03	0.57
1:E:168:ARG:HG2	1:E:189:VAL:HG21	1.87	0.57
1:E:365:LEU:O	1:E:368:ARG:HG3	2.05	0.57
1:E:75:ARG:HG2	1:E:75:ARG:HH11	1.67	0.57
1:G:168:ARG:HG2	1:G:189:VAL:HG21	1.87	0.57
1:B:190:VAL:HG12	1:B:191:GLU:H	1.68	0.57
1:B:451:MET:HE1	1:B:466:ALA:HA	1.87	0.57
1:G:77:VAL:HG12	1:G:78:ALA:N	2.18	0.57
1:A:31:LEU:HD13	1:A:90:THR:CG2	2.35	0.56
1:F:365:LEU:O	1:F:368:ARG:HG3	2.05	0.56
1:F:394:ASP:O	1:F:398:ASP:HB2	2.05	0.56
1:A:27:VAL:CG1	1:A:90:THR:HG23	2.35	0.56
1:A:71:ALA:O	1:A:75:ARG:HB3	2.05	0.56
1:C:353:ILE:HG12	1:C:365:LEU:HB3	1.85	0.56
1:D:168:ARG:HG2	1:D:189:VAL:HG21	1.87	0.56
1:D:483:THR:OG1	1:D:485:GLU:HG2	2.04	0.56
1:E:22:ILE:HG21	1:E:62:LEU:HD21	1.87	0.56
1:E:394:ASP:O	1:E:398:ASP:HB2	2.05	0.56
1:E:71:ALA:O	1:E:75:ARG:HB3	2.05	0.56
1:G:468:LYS:HD3	1:G:486:TYR:CZ	2.41	0.56
1:G:502:ARG:O	1:G:506:GLU:HG3	2.05	0.56
1:A:158:ILE:HG23	1:A:396:VAL:HG22	1.85	0.56
1:B:365:LEU:O	1:B:368:ARG:HG3	2.05	0.56
1:B:479:PHE:N	1:B:489:MET:HE1	2.20	0.56
1:B:81:THR:HG23	1:B:503:THR:HG22	1.87	0.56
1:C:468:LYS:HD3	1:C:486:TYR:CZ	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:353:ILE:HG12	1:D:365:LEU:HB3	1.85	0.56
1:E:245:LYS:NZ	1:E:319:ARG:HH21	2.04	0.56
1:A:22:ILE:HG21	1:A:62:LEU:HD21	1.87	0.56
1:C:31:LEU:HD13	1:C:90:THR:CG2	2.36	0.56
1:D:468:LYS:HD3	1:D:486:TYR:CZ	2.40	0.56
1:F:245:LYS:NZ	1:F:319:ARG:HH21	2.03	0.56
1:G:19:GLY:HA3	1:G:67:GLU:O	2.06	0.56
1:A:77:VAL:HG12	1:A:78:ALA:N	2.19	0.56
1:C:75:ARG:HG2	1:C:75:ARG:NH1	2.20	0.56
1:D:81:THR:HG23	1:D:503:THR:HG22	1.88	0.56
1:E:411:ILE:CD1	1:E:490:PHE:HE1	2.19	0.56
1:G:13:ARG:HD3	1:G:104:LEU:HD22	1.88	0.56
1:A:209:ASP:HB3	1:A:210:LYS:HZ1	1.71	0.56
1:B:226:LYS:HZ1	1:B:252:GLU:HB3	1.69	0.56
1:B:393:LYS:O	1:B:397:ASP:HB2	2.05	0.56
1:D:411:ILE:CD1	1:D:490:PHE:HE1	2.19	0.56
1:D:4:LYS:HD2	1:E:59:GLU:O	2.06	0.56
1:F:25:ASP:HA	1:F:28:LYS:HD2	1.88	0.56
1:A:245:LYS:NZ	1:A:319:ARG:HH21	2.04	0.56
1:A:411:ILE:CD1	1:A:490:PHE:HE1	2.19	0.56
1:D:488:ASP:OD1	1:D:490:PHE:HB2	2.06	0.56
1:F:28:LYS:HG3	1:F:453:GLN:OE1	2.06	0.56
1:G:400:LEU:HG	1:G:400:LEU:O	2.06	0.56
1:A:393:LYS:O	1:A:397:ASP:HB2	2.06	0.56
1:A:81:THR:HG23	1:A:503:THR:HG22	1.88	0.56
1:D:25:ASP:HA	1:D:28:LYS:HD2	1.88	0.56
1:E:483:THR:OG1	1:E:485:GLU:HG2	2.05	0.56
1:G:245:LYS:NZ	1:G:319:ARG:HH21	2.04	0.56
1:A:468:LYS:HD3	1:A:486:TYR:CZ	2.40	0.56
1:B:245:LYS:NZ	1:B:319:ARG:HH21	2.04	0.56
1:C:200:LEU:HD23	1:C:275:ALA:O	2.06	0.56
1:C:71:ALA:O	1:C:75:ARG:HB3	2.06	0.56
1:E:209:ASP:HB3	1:E:210:LYS:HZ1	1.70	0.56
1:G:75:ARG:HH11	1:G:75:ARG:HG2	1.69	0.56
1:B:488:ASP:OD1	1:B:490:PHE:HB2	2.05	0.56
1:C:393:LYS:O	1:C:397:ASP:HB2	2.06	0.56
1:D:71:ALA:O	1:D:75:ARG:HB3	2.06	0.56
1:E:158:ILE:HG23	1:E:396:VAL:HG22	1.87	0.56
1:F:27:VAL:CG1	1:F:90:THR:HG23	2.35	0.56
1:D:13:ARG:HD3	1:D:104:LEU:HD22	1.88	0.55
1:E:13:ARG:HD3	1:E:104:LEU:HD22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:19:GLY:HA3	1:F:67:GLU:O	2.06	0.55
1:B:75:ARG:HG2	1:B:75:ARG:HH11	1.71	0.55
1:C:25:ASP:HA	1:C:28:LYS:HD2	1.88	0.55
1:C:19:GLY:HA3	1:C:67:GLU:O	2.06	0.55
1:E:25:ASP:HA	1:E:28:LYS:HD2	1.89	0.55
1:A:25:ASP:HA	1:A:28:LYS:HD2	1.88	0.55
1:A:69:MET:HG2	1:B:47:PRO:HB3	1.88	0.55
1:D:365:LEU:O	1:D:368:ARG:HG3	2.05	0.55
1:E:488:ASP:OD1	1:E:490:PHE:HB2	2.05	0.55
1:E:77:VAL:HG12	1:E:78:ALA:N	2.19	0.55
1:F:393:LYS:O	1:F:397:ASP:HB2	2.06	0.55
1:F:31:LEU:HD13	1:F:90:THR:CG2	2.36	0.55
1:G:393:LYS:O	1:G:397:ASP:HB2	2.06	0.55
1:B:19:GLY:HA3	1:B:67:GLU:O	2.06	0.55
1:C:488:ASP:OD1	1:C:490:PHE:HB2	2.05	0.55
1:D:245:LYS:NZ	1:D:319:ARG:HH21	2.04	0.55
1:D:393:LYS:O	1:D:397:ASP:HB2	2.07	0.55
1:F:502:ARG:O	1:F:506:GLU:HG3	2.06	0.55
1:G:488:ASP:OD1	1:G:490:PHE:HB2	2.07	0.55
1:A:200:LEU:HD23	1:A:275:ALA:O	2.07	0.55
1:B:342:ILE:O	1:B:346:VAL:HG23	2.06	0.55
1:B:22:ILE:HG21	1:B:62:LEU:HD21	1.89	0.55
1:C:349:ILE:HG21	1:C:369:VAL:HB	1.89	0.55
1:E:226:LYS:HG2	1:E:252:GLU:CB	2.37	0.55
1:E:342:ILE:O	1:E:346:VAL:HG23	2.07	0.55
1:F:227:LEU:HB3	1:F:254:VAL:HG13	1.89	0.55
1:F:400:LEU:HG	1:F:400:LEU:O	2.07	0.55
1:G:200:LEU:HD23	1:G:275:ALA:O	2.07	0.55
1:G:411:ILE:CD1	1:G:490:PHE:HE1	2.20	0.55
1:B:200:LEU:HD23	1:B:275:ALA:O	2.07	0.55
1:B:502:ARG:O	1:B:506:GLU:HG3	2.06	0.55
1:E:393:LYS:O	1:E:397:ASP:HB2	2.06	0.55
1:A:227:LEU:HB3	1:A:254:VAL:HG13	1.88	0.55
1:B:411:ILE:CD1	1:B:490:PHE:HE1	2.20	0.55
1:F:342:ILE:O	1:F:346:VAL:HG23	2.07	0.55
1:A:13:ARG:HD3	1:A:104:LEU:HD22	1.89	0.55
1:C:5:GLU:HG3	1:C:525:LYS:HD3	1.88	0.55
1:C:75:ARG:HG2	1:C:75:ARG:HH11	1.72	0.55
1:E:468:LYS:HD3	1:E:486:TYR:CZ	2.42	0.55
1:F:30:THR:HB	1:F:51:LYS:O	2.06	0.55
1:G:2:ALA:O	1:G:4:LYS:HG2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:LYS:HG3	1:A:453:GLN:OE1	2.06	0.55
1:A:342:ILE:O	1:A:346:VAL:HG23	2.06	0.55
1:D:342:ILE:O	1:D:346:VAL:HG23	2.07	0.55
1:F:413:VAL:CG1	1:F:489:MET:HB3	2.37	0.55
1:G:227:LEU:HB3	1:G:254:VAL:HG13	1.89	0.55
1:A:502:ARG:O	1:A:506:GLU:HG3	2.06	0.54
1:A:31:LEU:HD13	1:A:90:THR:HG21	1.88	0.54
1:B:31:LEU:HD13	1:B:90:THR:CG2	2.37	0.54
1:B:441:ALA:O	1:B:445:ARG:HD3	2.07	0.54
1:D:349:ILE:HG21	1:D:369:VAL:HB	1.89	0.54
1:E:413:VAL:CG1	1:E:489:MET:HB3	2.37	0.54
1:E:81:THR:HG23	1:E:503:THR:HG22	1.90	0.54
1:E:4:LYS:HD2	1:F:59:GLU:O	2.07	0.54
1:G:31:LEU:HD13	1:G:90:THR:HG21	1.89	0.54
1:G:460:VAL:HG21	1:G:479:PHE:HZ	1.73	0.54
1:A:5:GLU:HG3	1:A:525:LYS:HD3	1.88	0.54
1:A:24:ALA:HB3	1:A:97:GLN:NE2	2.23	0.54
1:C:365:LEU:O	1:C:368:ARG:HG3	2.06	0.54
1:C:179:GLU:HA	1:C:381:VAL:HG23	1.90	0.54
1:G:342:ILE:O	1:G:346:VAL:HG23	2.07	0.54
1:E:200:LEU:HD23	1:E:275:ALA:O	2.07	0.54
1:F:22:ILE:HG21	1:F:62:LEU:HD21	1.89	0.54
1:G:31:LEU:HD13	1:G:90:THR:CG2	2.37	0.54
1:D:179:GLU:HA	1:D:381:VAL:HG23	1.90	0.54
1:F:31:LEU:HD13	1:F:90:THR:HG21	1.89	0.54
1:G:192:GLY:HA2	1:G:295:LEU:HD21	1.90	0.54
1:A:226:LYS:HG2	1:A:252:GLU:CB	2.38	0.54
1:B:349:ILE:HG21	1:B:369:VAL:HB	1.90	0.54
1:C:502:ARG:O	1:C:506:GLU:HG3	2.06	0.54
1:D:200:LEU:HD23	1:D:275:ALA:O	2.08	0.54
1:B:5:GLU:HG3	1:B:525:LYS:HD3	1.88	0.54
1:C:226:LYS:HG2	1:C:252:GLU:CB	2.38	0.54
1:C:451:MET:HE1	1:C:466:ALA:HA	1.90	0.54
1:C:460:VAL:HG21	1:C:479:PHE:HZ	1.72	0.54
1:C:31:LEU:HD13	1:C:90:THR:HG21	1.89	0.54
1:D:5:GLU:HG3	1:D:525:LYS:HD3	1.89	0.54
1:E:5:GLU:HG3	1:E:525:LYS:HD3	1.88	0.54
1:F:179:GLU:HA	1:F:381:VAL:HG23	1.90	0.54
1:F:452:ARG:O	1:F:456:GLU:HG2	2.08	0.54
1:G:413:VAL:CG1	1:G:489:MET:HB3	2.38	0.54
1:B:383:GLY:N	1:B:389:VAL:HG22	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:28:LYS:HG3	1:C:453:GLN:OE1	2.07	0.54
1:E:227:LEU:HB3	1:E:254:VAL:HG13	1.89	0.54
1:F:226:LYS:HG2	1:F:252:GLU:CB	2.38	0.54
1:F:2:ALA:O	1:F:4:LYS:HG2	2.08	0.54
1:A:383:GLY:N	1:A:389:VAL:HG22	2.23	0.54
1:C:342:ILE:O	1:C:346:VAL:HG23	2.07	0.54
1:E:349:ILE:HG21	1:E:369:VAL:HB	1.90	0.54
1:F:200:LEU:HD23	1:F:275:ALA:O	2.08	0.54
1:G:349:ILE:HG21	1:G:369:VAL:HB	1.90	0.54
1:E:2:ALA:O	1:E:4:LYS:HG2	2.07	0.54
1:E:400:LEU:O	1:E:400:LEU:HG	2.07	0.54
1:F:383:GLY:N	1:F:389:VAL:HG22	2.23	0.54
1:F:81:THR:HG23	1:F:503:THR:HG22	1.90	0.54
1:G:5:GLU:HG3	1:G:525:LYS:HD3	1.89	0.54
1:D:31:LEU:HD13	1:D:90:THR:CG2	2.38	0.54
1:B:13:ARG:HD3	1:B:104:LEU:HD22	1.90	0.53
1:B:179:GLU:HA	1:B:381:VAL:HG23	1.90	0.53
1:C:250:VAL:HG12	1:C:278:ALA:HA	1.90	0.53
1:D:75:ARG:HG2	1:D:75:ARG:NH1	2.23	0.53
1:E:460:VAL:HG21	1:E:479:PHE:HZ	1.73	0.53
1:G:179:GLU:HA	1:G:381:VAL:HG23	1.90	0.53
1:G:441:ALA:O	1:G:445:ARG:HD3	2.07	0.53
1:G:479:PHE:N	1:G:489:MET:HE1	2.23	0.53
1:D:250:VAL:HG12	1:D:278:ALA:HA	1.90	0.53
1:F:349:ILE:HG21	1:F:369:VAL:HB	1.90	0.53
1:F:5:GLU:HG3	1:F:525:LYS:HD3	1.89	0.53
1:C:178:GLU:O	1:C:381:VAL:HG22	2.08	0.53
1:C:383:GLY:N	1:C:389:VAL:HG22	2.23	0.53
1:C:400:LEU:HG	1:C:400:LEU:O	2.07	0.53
1:C:81:THR:HG23	1:C:503:THR:HG22	1.90	0.53
1:E:179:GLU:HA	1:E:381:VAL:HG23	1.90	0.53
1:F:190:VAL:HG12	1:F:191:GLU:H	1.72	0.53
1:A:349:ILE:HG21	1:A:369:VAL:HB	1.89	0.53
1:A:413:VAL:CG1	1:A:489:MET:HB3	2.38	0.53
1:B:250:VAL:HG12	1:B:278:ALA:HA	1.90	0.53
1:A:75:ARG:HH11	1:A:75:ARG:HG2	1.73	0.53
1:B:226:LYS:HG2	1:B:252:GLU:CB	2.38	0.53
1:G:183:MET:HB3	1:G:384:MET:HE1	1.90	0.53
1:A:192:GLY:HA2	1:A:295:LEU:HD21	1.91	0.53
1:B:227:LEU:HB3	1:B:254:VAL:HG13	1.89	0.53
1:C:192:GLY:HA2	1:C:295:LEU:HD21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:222:LEU:HB2	1:C:289:LEU:HD22	1.91	0.53
1:C:66:PHE:HA	1:C:69:MET:HE2	1.91	0.53
1:D:226:LYS:HG2	1:D:252:GLU:CB	2.38	0.53
1:E:24:ALA:HB3	1:E:97:GLN:NE2	2.23	0.53
1:E:451:MET:HE1	1:E:466:ALA:HA	1.90	0.53
1:G:81:THR:HG23	1:G:503:THR:HG22	1.91	0.53
1:A:197:ARG:NH1	1:A:277:LYS:HG2	2.23	0.53
1:B:222:LEU:HB2	1:B:289:LEU:HD22	1.91	0.53
1:C:413:VAL:CG1	1:C:489:MET:HB3	2.37	0.53
1:F:192:GLY:HA2	1:F:295:LEU:HD21	1.90	0.53
1:A:2:ALA:O	1:A:4:LYS:HG2	2.09	0.53
1:B:139:ASN:ND2	1:B:139:ASN:H	2.07	0.53
1:B:400:LEU:O	1:B:400:LEU:HG	2.07	0.53
1:C:227:LEU:HB3	1:C:254:VAL:HG13	1.89	0.53
1:D:400:LEU:O	1:D:400:LEU:HG	2.07	0.53
1:F:209:ASP:HB3	1:F:210:LYS:HZ1	1.73	0.53
1:A:66:PHE:HA	1:A:69:MET:HE2	1.91	0.53
1:D:178:GLU:O	1:D:381:VAL:HG22	2.09	0.53
1:D:227:LEU:HB3	1:D:254:VAL:HG13	1.89	0.53
1:E:502:ARG:O	1:E:506:GLU:HG3	2.09	0.53
1:F:24:ALA:HB3	1:F:97:GLN:NE2	2.24	0.53
1:F:103:GLY:HA3	1:F:516:ILE:HD11	1.91	0.53
1:G:178:GLU:O	1:G:381:VAL:HG22	2.09	0.53
1:G:24:ALA:HB3	1:G:97:GLN:NE2	2.24	0.53
1:A:179:GLU:HA	1:A:381:VAL:HG23	1.91	0.53
1:B:178:GLU:O	1:B:381:VAL:HG22	2.09	0.53
1:B:460:VAL:HG21	1:B:479:PHE:HZ	1.74	0.53
1:D:441:ALA:O	1:D:445:ARG:HD3	2.09	0.53
1:D:452:ARG:O	1:D:456:GLU:HG2	2.09	0.53
1:F:178:GLU:O	1:F:381:VAL:HG22	2.09	0.53
1:G:30:THR:HB	1:G:51:LYS:O	2.09	0.53
1:A:190:VAL:HG12	1:A:191:GLU:H	1.73	0.52
1:A:479:PHE:N	1:A:489:MET:HE1	2.24	0.52
1:C:139:ASN:H	1:C:139:ASN:ND2	2.08	0.52
1:C:452:ARG:O	1:C:456:GLU:HG2	2.09	0.52
1:E:479:PHE:N	1:E:489:MET:HE1	2.24	0.52
1:A:250:VAL:HG12	1:A:278:ALA:HA	1.90	0.52
1:B:192:GLY:HA2	1:B:295:LEU:HD21	1.91	0.52
1:C:460:VAL:HG21	1:C:479:PHE:CZ	2.45	0.52
1:D:2:ALA:O	1:D:4:LYS:HG2	2.08	0.52
1:E:383:GLY:N	1:E:389:VAL:HG22	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:317:LEU:HG	1:F:318:GLY:N	2.24	0.52
1:G:139:ASN:ND2	1:G:139:ASN:H	2.06	0.52
1:G:383:GLY:N	1:G:389:VAL:HG22	2.25	0.52
1:E:250:VAL:HG12	1:E:278:ALA:HA	1.89	0.52
1:A:421:GLN:O	1:A:424:LYS:HB2	2.09	0.52
1:A:460:VAL:HG21	1:A:479:PHE:HZ	1.73	0.52
1:B:66:PHE:HA	1:B:69:MET:HE2	1.92	0.52
1:E:19:GLY:HA3	1:E:67:GLU:O	2.09	0.52
1:F:13:ARG:HD3	1:F:104:LEU:HD22	1.91	0.52
1:F:426:LEU:HB2	1:F:444:ARG:HD2	1.91	0.52
1:A:18:LYS:HB3	1:A:67:GLU:HG2	1.92	0.52
1:C:426:LEU:HB2	1:C:444:ARG:HD2	1.91	0.52
1:D:31:LEU:HD13	1:D:90:THR:HG21	1.91	0.52
1:D:413:VAL:CG1	1:D:489:MET:HB3	2.38	0.52
1:D:30:THR:HB	1:D:51:LYS:O	2.09	0.52
1:D:86:GLY:C	1:D:88:GLY:H	2.13	0.52
1:E:139:ASN:H	1:E:139:ASN:ND2	2.07	0.52
1:E:317:LEU:HG	1:E:318:GLY:N	2.25	0.52
1:F:460:VAL:HG21	1:F:479:PHE:HZ	1.73	0.52
1:A:47:PRO:HB3	1:G:69:MET:HG2	1.91	0.52
1:A:222:LEU:HB2	1:A:289:LEU:HD22	1.91	0.52
1:A:441:ALA:O	1:A:445:ARG:HD3	2.09	0.52
1:A:30:THR:HB	1:A:51:LYS:O	2.10	0.52
1:B:317:LEU:HG	1:B:318:GLY:N	2.25	0.52
1:B:413:VAL:CG1	1:B:489:MET:HB3	2.38	0.52
1:D:139:ASN:H	1:D:139:ASN:ND2	2.08	0.52
1:C:4:LYS:HD2	1:D:59:GLU:O	2.08	0.52
1:D:7:LYS:HD2	1:D:66:PHE:CE1	2.45	0.52
1:E:197:ARG:NH1	1:E:277:LYS:HG2	2.24	0.52
1:E:365:LEU:HD11	1:E:368:ARG:HH21	1.75	0.52
1:F:222:LEU:HB2	1:F:289:LEU:HD22	1.91	0.52
1:G:365:LEU:HD11	1:G:368:ARG:HH21	1.75	0.52
1:G:66:PHE:HA	1:G:69:MET:CE	2.40	0.52
1:B:2:ALA:O	1:B:4:LYS:HG2	2.09	0.52
1:D:185:THR:HA	1:D:380:ARG:O	2.10	0.52
1:D:192:GLY:HA2	1:D:295:LEU:HD21	1.91	0.52
1:D:383:GLY:N	1:D:389:VAL:HG22	2.24	0.52
1:E:433:ASN:N	1:E:433:ASN:OD1	2.42	0.52
1:E:31:LEU:HD13	1:E:90:THR:CG2	2.40	0.52
1:G:250:VAL:HG12	1:G:278:ALA:HA	1.90	0.52
1:B:30:THR:HB	1:B:51:LYS:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:441:ALA:O	1:C:445:ARG:HD3	2.10	0.52
1:D:460:VAL:HG21	1:D:479:PHE:HZ	1.74	0.52
1:D:69:MET:HG2	1:E:47:PRO:HB3	1.91	0.52
1:E:192:GLY:HA2	1:E:295:LEU:HD21	1.91	0.52
1:E:421:GLN:O	1:E:424:LYS:HB2	2.10	0.52
1:F:477:PHE:CE1	1:F:486:TYR:HB3	2.45	0.52
1:G:86:GLY:C	1:G:88:GLY:H	2.14	0.52
1:A:66:PHE:HA	1:A:69:MET:CE	2.40	0.52
1:B:86:GLY:C	1:B:88:GLY:H	2.13	0.52
1:D:66:PHE:HA	1:D:69:MET:HE2	1.92	0.52
1:E:452:ARG:O	1:E:456:GLU:HG2	2.10	0.52
1:G:7:LYS:HD2	1:G:66:PHE:CE1	2.44	0.52
1:B:365:LEU:HD11	1:B:368:ARG:HH21	1.75	0.52
1:D:222:LEU:HB2	1:D:289:LEU:HD22	1.91	0.52
1:E:185:THR:HA	1:E:380:ARG:O	2.10	0.52
1:E:365:LEU:HG	1:E:368:ARG:HE	1.75	0.52
1:E:31:LEU:HD13	1:E:90:THR:HG21	1.91	0.52
1:B:103:GLY:HA3	1:B:516:ILE:HD11	1.91	0.51
1:B:31:LEU:HD13	1:B:90:THR:HG21	1.90	0.51
1:C:30:THR:HB	1:C:51:LYS:O	2.09	0.51
1:E:138:VAL:O	1:E:138:VAL:HG12	2.09	0.51
1:E:169:VAL:CG2	1:E:377:ALA:HB2	2.41	0.51
1:F:185:THR:HA	1:F:380:ARG:O	2.10	0.51
1:F:365:LEU:HG	1:F:368:ARG:HE	1.76	0.51
1:G:452:ARG:O	1:G:456:GLU:HG2	2.10	0.51
1:F:4:LYS:HD2	1:G:59:GLU:O	2.10	0.51
1:G:22:ILE:HG21	1:G:62:LEU:HD21	1.91	0.51
1:A:365:LEU:HG	1:A:368:ARG:HE	1.76	0.51
1:C:13:ARG:HD3	1:C:104:LEU:HD22	1.93	0.51
1:C:421:GLN:O	1:C:424:LYS:HB2	2.10	0.51
1:E:460:VAL:HG21	1:E:479:PHE:CZ	2.45	0.51
1:G:220:ILE:HG23	1:G:248:LEU:HD22	1.92	0.51
1:G:197:ARG:NH1	1:G:277:LYS:HG2	2.24	0.51
1:G:322:LYS:HB3	1:G:333:VAL:CG2	2.39	0.51
1:A:185:THR:HA	1:A:380:ARG:O	2.10	0.51
1:A:460:VAL:HG21	1:A:479:PHE:CZ	2.45	0.51
1:C:317:LEU:HG	1:C:318:GLY:N	2.25	0.51
1:C:7:LYS:HD2	1:C:66:PHE:CE1	2.45	0.51
1:D:220:ILE:HG23	1:D:248:LEU:HD22	1.93	0.51
1:E:220:ILE:HG23	1:E:248:LEU:HD22	1.93	0.51
1:E:222:LEU:HB2	1:E:289:LEU:HD22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:28:LYS:HG3	1:E:453:GLN:OE1	2.11	0.51
1:E:66:PHE:HA	1:E:69:MET:CE	2.41	0.51
1:F:197:ARG:NH1	1:F:277:LYS:HG2	2.24	0.51
1:G:226:LYS:HG2	1:G:252:GLU:CB	2.38	0.51
1:G:222:LEU:HB2	1:G:289:LEU:HD22	1.91	0.51
1:G:317:LEU:HG	1:G:318:GLY:N	2.25	0.51
1:B:24:ALA:HB3	1:B:97:GLN:NE2	2.26	0.51
1:C:86:GLY:C	1:C:88:GLY:H	2.14	0.51
1:D:28:LYS:HG3	1:D:453:GLN:OE1	2.11	0.51
1:F:322:LYS:HB3	1:F:333:VAL:CG2	2.38	0.51
1:F:479:PHE:N	1:F:489:MET:HE1	2.25	0.51
1:B:452:ARG:O	1:B:456:GLU:HG2	2.11	0.51
1:B:468:LYS:HD3	1:B:486:TYR:CE1	2.46	0.51
1:C:6:VAL:HG22	1:C:522:ILE:HG12	1.92	0.51
1:D:451:MET:HE1	1:D:466:ALA:HA	1.92	0.51
1:D:468:LYS:HD3	1:D:486:TYR:CE1	2.45	0.51
1:D:479:PHE:N	1:D:489:MET:HE1	2.26	0.51
1:F:460:VAL:HG21	1:F:479:PHE:CZ	2.45	0.51
1:F:7:LYS:HD2	1:F:66:PHE:CE1	2.44	0.51
1:A:26:ALA:HA	1:G:8:PHE:HE1	1.76	0.51
1:C:185:THR:HA	1:C:380:ARG:O	2.10	0.51
1:A:317:LEU:HG	1:A:318:GLY:N	2.25	0.51
1:A:400:LEU:HG	1:A:400:LEU:O	2.10	0.51
1:D:365:LEU:HD11	1:D:368:ARG:HH21	1.76	0.51
1:E:178:GLU:O	1:E:381:VAL:HG22	2.10	0.51
1:F:284:ARG:HA	1:F:284:ARG:HH11	1.76	0.51
1:G:365:LEU:HG	1:G:368:ARG:HE	1.76	0.51
1:G:421:GLN:O	1:G:424:LYS:HB2	2.11	0.51
1:G:426:LEU:HB2	1:G:444:ARG:HD2	1.92	0.51
1:A:139:ASN:H	1:A:139:ASN:ND2	2.07	0.51
1:A:452:ARG:O	1:A:456:GLU:HG2	2.11	0.51
1:C:66:PHE:HA	1:C:69:MET:CE	2.41	0.51
1:D:433:ASN:OD1	1:D:433:ASN:N	2.44	0.51
1:F:220:ILE:HG23	1:F:248:LEU:HD22	1.93	0.51
1:F:250:VAL:HG12	1:F:278:ALA:HA	1.91	0.51
1:G:185:THR:HA	1:G:380:ARG:O	2.10	0.51
1:G:460:VAL:HG21	1:G:479:PHE:CZ	2.45	0.51
1:A:284:ARG:HA	1:A:284:ARG:HH11	1.76	0.51
1:A:489:MET:HG3	1:A:494:VAL:HB	1.93	0.51
1:B:185:THR:HA	1:B:380:ARG:O	2.10	0.51
1:B:64:ASP:OD1	1:B:64:ASP:C	2.50	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:ALA:HB3	1:C:97:GLN:NE2	2.26	0.51
1:E:7:LYS:HD2	1:E:66:PHE:CE1	2.45	0.51
1:F:421:GLN:O	1:F:424:LYS:HB2	2.10	0.51
1:A:178:GLU:O	1:A:381:VAL:HG22	2.11	0.51
1:C:103:GLY:HA3	1:C:516:ILE:HD11	1.92	0.51
1:D:421:GLN:O	1:D:424:LYS:HB2	2.11	0.51
1:D:19:GLY:HA3	1:D:67:GLU:O	2.10	0.51
1:E:24:ALA:O	1:E:28:LYS:HD2	2.11	0.51
1:E:441:ALA:O	1:E:445:ARG:HD3	2.11	0.51
1:G:103:GLY:HA3	1:G:516:ILE:HD11	1.93	0.51
1:G:18:LYS:HB3	1:G:67:GLU:HG2	1.93	0.51
1:B:314:ILE:HD12	1:B:315:ASP:N	2.26	0.50
1:C:314:ILE:HD12	1:C:315:ASP:N	2.26	0.50
1:D:460:VAL:HG21	1:D:479:PHE:CZ	2.46	0.50
1:E:226:LYS:HZ1	1:E:252:GLU:HB3	1.76	0.50
1:F:139:ASN:H	1:F:139:ASN:ND2	2.07	0.50
1:A:314:ILE:HD12	1:A:315:ASP:N	2.26	0.50
1:A:86:GLY:C	1:A:88:GLY:H	2.14	0.50
1:B:433:ASN:OD1	1:B:433:ASN:N	2.42	0.50
1:C:365:LEU:HG	1:C:368:ARG:HE	1.76	0.50
1:C:479:PHE:N	1:C:489:MET:HE1	2.26	0.50
1:D:66:PHE:HA	1:D:69:MET:CE	2.41	0.50
1:E:426:LEU:HB2	1:E:444:ARG:HD2	1.93	0.50
1:E:6:VAL:HG22	1:E:522:ILE:HG12	1.94	0.50
1:F:433:ASN:OD1	1:F:433:ASN:N	2.43	0.50
1:F:86:GLY:C	1:F:88:GLY:H	2.14	0.50
1:G:433:ASN:OD1	1:G:436:GLN:HB2	2.12	0.50
1:G:477:PHE:CE1	1:G:486:TYR:HB3	2.46	0.50
1:B:362:ARG:HE	1:B:363:GLU:N	2.09	0.50
1:B:460:VAL:HG21	1:B:479:PHE:CZ	2.47	0.50
1:A:4:LYS:HD2	1:B:59:GLU:O	2.10	0.50
1:C:18:LYS:HB3	1:C:67:GLU:HG2	1.93	0.50
1:C:220:ILE:HG23	1:C:248:LEU:HD22	1.93	0.50
1:D:231:GLN:N	1:D:232:PRO:HD2	2.27	0.50
1:D:365:LEU:HG	1:D:368:ARG:HE	1.76	0.50
1:E:231:GLN:N	1:E:232:PRO:HD2	2.26	0.50
1:G:433:ASN:OD1	1:G:433:ASN:N	2.44	0.50
1:G:28:LYS:HG3	1:G:453:GLN:OE1	2.12	0.50
1:A:220:ILE:HG23	1:A:248:LEU:HD22	1.93	0.50
1:B:66:PHE:HA	1:B:69:MET:CE	2.42	0.50
1:C:231:GLN:N	1:C:232:PRO:HD2	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:317:LEU:HG	1:D:318:GLY:N	2.25	0.50
1:D:169:VAL:CG2	1:D:377:ALA:HB2	2.42	0.50
1:D:426:LEU:HB2	1:D:444:ARG:HD2	1.92	0.50
1:F:362:ARG:HE	1:F:363:GLU:N	2.09	0.50
1:G:362:ARG:HE	1:G:363:GLU:N	2.09	0.50
1:A:169:VAL:CG2	1:A:377:ALA:HB2	2.41	0.50
1:B:231:GLN:N	1:B:232:PRO:HD2	2.27	0.50
1:C:365:LEU:HD11	1:C:368:ARG:HH21	1.76	0.50
1:D:477:PHE:CE1	1:D:486:TYR:HB3	2.46	0.50
1:E:103:GLY:HA3	1:E:516:ILE:HD11	1.93	0.50
1:E:18:LYS:HB3	1:E:67:GLU:HG2	1.93	0.50
1:E:284:ARG:HA	1:E:284:ARG:HH11	1.76	0.50
1:G:451:MET:HE1	1:G:466:ALA:HA	1.94	0.50
1:A:426:LEU:HB2	1:A:444:ARG:HD2	1.92	0.50
1:A:409:GLU:OE2	1:A:499:LYS:HG3	2.11	0.50
1:C:362:ARG:HE	1:C:363:GLU:N	2.10	0.50
1:C:433:ASN:OD1	1:C:433:ASN:N	2.45	0.50
1:C:433:ASN:OD1	1:C:436:GLN:HB2	2.12	0.50
1:D:284:ARG:HA	1:D:284:ARG:HH11	1.76	0.50
1:D:64:ASP:OD1	1:D:64:ASP:C	2.50	0.50
1:E:30:THR:HB	1:E:51:LYS:O	2.11	0.50
1:F:169:VAL:CG2	1:F:377:ALA:HB2	2.42	0.50
1:F:441:ALA:O	1:F:445:ARG:HD3	2.11	0.50
1:F:66:PHE:HA	1:F:69:MET:CE	2.41	0.50
1:B:284:ARG:HA	1:B:284:ARG:HH11	1.76	0.50
1:B:224:GLU:HG3	1:B:286:LYS:NZ	2.27	0.50
1:B:4:LYS:HD2	1:C:59:GLU:O	2.11	0.50
1:C:24:ALA:O	1:C:28:LYS:HD2	2.12	0.50
1:D:221:LEU:HD21	1:D:249:ILE:HG12	1.94	0.50
1:D:222:LEU:HD13	1:D:289:LEU:HB3	1.94	0.50
1:F:138:VAL:HG12	1:F:138:VAL:O	2.11	0.50
1:G:314:ILE:HD12	1:G:315:ASP:N	2.26	0.50
1:G:339:LYS:HB3	1:G:343:GLU:OE2	2.12	0.50
1:A:433:ASN:OD1	1:A:433:ASN:N	2.43	0.50
1:B:365:LEU:HG	1:B:368:ARG:HE	1.76	0.50
1:B:28:LYS:HG3	1:B:453:GLN:OE1	2.12	0.50
1:C:138:VAL:O	1:C:138:VAL:HG12	2.10	0.50
1:C:468:LYS:HD3	1:C:486:TYR:CE1	2.47	0.50
1:D:226:LYS:HZ3	1:D:252:GLU:HB3	1.77	0.50
1:D:314:ILE:HD12	1:D:315:ASP:N	2.26	0.50
1:A:477:PHE:CE1	1:A:486:TYR:HB3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:86:GLY:C	1:E:88:GLY:H	2.14	0.50
1:F:314:ILE:HD12	1:F:315:ASP:N	2.26	0.50
1:G:169:VAL:CG2	1:G:377:ALA:HB2	2.42	0.50
1:A:138:VAL:O	1:A:138:VAL:HG12	2.11	0.49
1:B:169:VAL:CG2	1:B:377:ALA:HB2	2.41	0.49
1:D:224:GLU:HG3	1:D:286:LYS:NZ	2.27	0.49
1:D:322:LYS:HB3	1:D:333:VAL:CG2	2.39	0.49
1:D:75:ARG:HH11	1:D:75:ARG:HG2	1.76	0.49
1:E:224:GLU:HG3	1:E:286:LYS:NZ	2.27	0.49
1:F:365:LEU:HD11	1:F:368:ARG:HH21	1.76	0.49
1:A:362:ARG:HE	1:A:363:GLU:N	2.10	0.49
1:B:220:ILE:HG23	1:B:248:LEU:HD22	1.93	0.49
1:B:222:LEU:HD13	1:B:289:LEU:HB3	1.94	0.49
1:B:322:LYS:HB3	1:B:333:VAL:CG2	2.39	0.49
1:C:222:LEU:HD13	1:C:289:LEU:HB3	1.94	0.49
1:F:224:GLU:HG3	1:F:286:LYS:NZ	2.27	0.49
1:A:248:LEU:HD13	1:A:323:VAL:HG11	1.95	0.49
1:A:365:LEU:HD11	1:A:368:ARG:HH21	1.76	0.49
1:C:2:ALA:O	1:C:4:LYS:HG2	2.11	0.49
1:C:169:VAL:CG2	1:C:377:ALA:HB2	2.42	0.49
1:A:231:GLN:N	1:A:232:PRO:HD2	2.27	0.49
1:A:322:LYS:HB3	1:A:333:VAL:CG2	2.38	0.49
1:A:361:ASP:OD1	1:A:365:LEU:HD13	2.13	0.49
1:B:248:LEU:HD13	1:B:323:VAL:HG11	1.95	0.49
1:B:339:LYS:HB3	1:B:343:GLU:OE2	2.13	0.49
1:C:224:GLU:HG3	1:C:286:LYS:NZ	2.28	0.49
1:C:361:ASP:OD1	1:C:365:LEU:HD13	2.13	0.49
1:E:314:ILE:HD12	1:E:315:ASP:N	2.26	0.49
1:F:11:ASP:CG	1:F:15:ARG:HH12	2.16	0.49
1:F:451:MET:CE	1:F:465:VAL:HG12	2.42	0.49
1:F:451:MET:HE1	1:F:466:ALA:HA	1.94	0.49
1:A:339:LYS:HB3	1:A:343:GLU:OE2	2.13	0.49
1:B:433:ASN:OD1	1:B:436:GLN:HB2	2.13	0.49
1:C:227:LEU:HD13	1:C:254:VAL:HG22	1.95	0.49
1:A:224:GLU:HG3	1:A:286:LYS:NZ	2.27	0.49
1:A:221:LEU:HD21	1:A:249:ILE:HG12	1.94	0.49
1:B:138:VAL:HG12	1:B:138:VAL:O	2.11	0.49
1:B:361:ASP:OD1	1:B:365:LEU:HD13	2.13	0.49
1:D:362:ARG:HE	1:D:363:GLU:N	2.09	0.49
1:E:248:LEU:HD13	1:E:323:VAL:HG11	1.95	0.49
1:E:169:VAL:HG21	1:E:377:ALA:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:231:GLN:N	1:F:232:PRO:HD2	2.27	0.49
1:F:64:ASP:C	1:F:64:ASP:OD1	2.51	0.49
1:G:284:ARG:HA	1:G:284:ARG:HH11	1.76	0.49
1:G:66:PHE:HA	1:G:69:MET:HE2	1.94	0.49
1:D:248:LEU:HD13	1:D:323:VAL:HG11	1.95	0.49
1:G:248:LEU:HD13	1:G:323:VAL:HG11	1.95	0.49
1:B:122:VAL:HG12	1:B:123:ALA:N	2.28	0.49
1:C:284:ARG:HA	1:C:284:ARG:HH11	1.76	0.49
1:D:18:LYS:HB3	1:D:67:GLU:HG2	1.93	0.49
1:D:227:LEU:HD13	1:D:254:VAL:HG22	1.95	0.49
1:E:339:LYS:HB3	1:E:343:GLU:OE2	2.12	0.49
1:E:477:PHE:CE1	1:E:486:TYR:HB3	2.47	0.49
1:G:231:GLN:N	1:G:232:PRO:HD2	2.27	0.49
1:G:227:LEU:HD13	1:G:254:VAL:HG22	1.94	0.49
1:G:469:VAL:HG22	1:G:478:GLY:HA2	1.94	0.49
1:G:501:VAL:HG12	1:G:501:VAL:O	2.13	0.49
1:A:222:LEU:HD13	1:A:289:LEU:HB3	1.94	0.49
1:A:69:MET:HG2	1:B:47:PRO:HG3	1.95	0.49
1:C:339:LYS:HB3	1:C:343:GLU:OE2	2.13	0.49
1:E:213:ALA:HB3	1:E:325:ILE:HB	1.95	0.49
1:F:489:MET:HG3	1:F:494:VAL:HB	1.95	0.49
1:F:6:VAL:HG22	1:F:522:ILE:HG12	1.95	0.49
1:G:138:VAL:HG12	1:G:138:VAL:O	2.13	0.49
1:B:227:LEU:HD13	1:B:254:VAL:HG22	1.95	0.49
1:B:469:VAL:HG22	1:B:478:GLY:HA2	1.95	0.49
1:C:477:PHE:CE1	1:C:486:TYR:HB3	2.47	0.49
1:E:362:ARG:HE	1:E:363:GLU:N	2.09	0.49
1:G:222:LEU:HD13	1:G:289:LEU:HB3	1.94	0.49
1:G:468:LYS:HD3	1:G:486:TYR:CE1	2.47	0.49
1:G:64:ASP:OD1	1:G:64:ASP:C	2.51	0.49
1:A:64:ASP:OD1	1:A:64:ASP:C	2.51	0.48
1:B:421:GLN:O	1:B:424:LYS:HB2	2.12	0.48
1:B:477:PHE:CE1	1:B:486:TYR:HB3	2.47	0.48
1:D:339:LYS:HB3	1:D:343:GLU:OE2	2.13	0.48
1:D:469:VAL:HG22	1:D:478:GLY:HA2	1.95	0.48
1:E:221:LEU:HD21	1:E:249:ILE:HG12	1.95	0.48
1:E:361:ASP:OD1	1:E:365:LEU:HD13	2.13	0.48
1:E:433:ASN:OD1	1:E:436:GLN:HB2	2.13	0.48
1:F:122:VAL:HG12	1:F:123:ALA:N	2.27	0.48
1:A:341:GLU:O	1:A:345:ARG:HG2	2.13	0.48
1:D:24:ALA:HB3	1:D:97:GLN:NE2	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:222:LEU:HD13	1:E:289:LEU:HB3	1.94	0.48
1:E:468:LYS:HD3	1:E:486:TYR:CE1	2.48	0.48
1:F:248:LEU:HD13	1:F:323:VAL:HG11	1.95	0.48
1:G:221:LEU:HD21	1:G:249:ILE:HG12	1.94	0.48
1:G:341:GLU:O	1:G:345:ARG:HG2	2.14	0.48
1:A:451:MET:HE1	1:A:466:ALA:HA	1.95	0.48
1:B:18:LYS:HB3	1:B:67:GLU:HG2	1.95	0.48
1:C:248:LEU:HD13	1:C:323:VAL:HG11	1.95	0.48
1:C:322:LYS:HB3	1:C:333:VAL:CG2	2.39	0.48
1:E:227:LEU:HD13	1:E:254:VAL:HG22	1.95	0.48
1:C:341:GLU:O	1:C:345:ARG:HG2	2.13	0.48
1:F:222:LEU:HD13	1:F:289:LEU:HB3	1.94	0.48
1:F:213:ALA:HB3	1:F:325:ILE:HB	1.96	0.48
1:F:361:ASP:OD1	1:F:365:LEU:HD13	2.13	0.48
1:F:468:LYS:HD3	1:F:486:TYR:CE1	2.47	0.48
1:F:69:MET:HG2	1:G:47:PRO:HB3	1.95	0.48
1:G:451:MET:CE	1:G:465:VAL:HG12	2.44	0.48
1:B:7:LYS:HD2	1:B:66:PHE:CE1	2.48	0.48
1:D:501:VAL:O	1:D:501:VAL:HG12	2.13	0.48
1:F:24:ALA:O	1:F:28:LYS:HD2	2.14	0.48
1:F:433:ASN:OD1	1:F:436:GLN:HB2	2.14	0.48
1:G:213:ALA:HB3	1:G:325:ILE:HB	1.95	0.48
1:G:224:GLU:HG3	1:G:286:LYS:NZ	2.28	0.48
1:B:426:LEU:HB2	1:B:444:ARG:HD2	1.94	0.48
1:B:501:VAL:O	1:B:501:VAL:HG12	2.14	0.48
1:C:221:LEU:HD21	1:C:249:ILE:HG12	1.95	0.48
1:A:433:ASN:OD1	1:A:436:GLN:HB2	2.14	0.48
1:A:469:VAL:HG22	1:A:478:GLY:HA2	1.95	0.48
1:C:122:VAL:HG12	1:C:123:ALA:N	2.29	0.48
1:C:469:VAL:HG22	1:C:478:GLY:HA2	1.94	0.48
1:D:433:ASN:OD1	1:D:436:GLN:HB2	2.14	0.48
1:F:501:VAL:HG12	1:F:501:VAL:O	2.13	0.48
1:A:468:LYS:HD3	1:A:486:TYR:CE1	2.48	0.48
1:C:64:ASP:C	1:C:64:ASP:OD1	2.52	0.48
1:D:11:ASP:CG	1:D:15:ARG:HH12	2.17	0.48
1:D:8:PHE:HE1	1:E:26:ALA:HA	1.78	0.48
1:E:12:ALA:HB1	1:E:521:MET:HG3	1.96	0.48
1:G:122:VAL:HG12	1:G:123:ALA:N	2.27	0.48
1:G:190:VAL:HG11	1:G:334:ASP:CG	2.34	0.48
1:C:489:MET:HG3	1:C:494:VAL:HB	1.95	0.48
1:D:361:ASP:OD1	1:D:365:LEU:HD13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:190:VAL:HG11	1:F:334:ASP:CB	2.43	0.48
1:F:339:LYS:HB3	1:F:343:GLU:OE2	2.13	0.48
1:F:183:MET:HB3	1:F:384:MET:HE1	1.95	0.48
1:B:169:VAL:HG21	1:B:377:ALA:HB2	1.95	0.48
1:D:122:VAL:HG12	1:D:123:ALA:N	2.29	0.48
1:F:341:GLU:O	1:F:345:ARG:HG2	2.14	0.48
1:G:6:VAL:HG22	1:G:522:ILE:HG12	1.95	0.48
1:B:227:LEU:CB	1:B:254:VAL:HG13	2.44	0.47
1:B:341:GLU:O	1:B:345:ARG:HG2	2.14	0.47
1:D:220:ILE:HD12	1:D:248:LEU:HD22	1.96	0.47
1:E:322:LYS:HB3	1:E:333:VAL:CG2	2.39	0.47
1:E:469:VAL:HG22	1:E:478:GLY:HA2	1.96	0.47
1:G:124:THR:O	1:G:128:VAL:HG23	2.14	0.47
1:A:501:VAL:HG12	1:A:501:VAL:O	2.14	0.47
1:B:205:VAL:HG12	1:B:207:ASN:H	1.79	0.47
1:C:227:LEU:CB	1:C:254:VAL:HG13	2.44	0.47
1:C:501:VAL:O	1:C:501:VAL:HG12	2.13	0.47
1:D:138:VAL:HG12	1:D:138:VAL:O	2.12	0.47
1:E:341:GLU:O	1:E:345:ARG:HG2	2.14	0.47
1:F:221:LEU:HD21	1:F:249:ILE:HG12	1.94	0.47
1:A:213:ALA:HB3	1:A:325:ILE:HB	1.96	0.47
1:B:205:VAL:HG12	1:B:207:ASN:N	2.30	0.47
1:B:221:LEU:HD21	1:B:249:ILE:HG12	1.95	0.47
1:C:183:MET:HB3	1:C:384:MET:HE1	1.96	0.47
1:D:489:MET:HG3	1:D:494:VAL:HB	1.96	0.47
1:E:64:ASP:C	1:E:64:ASP:OD1	2.52	0.47
1:F:227:LEU:HD13	1:F:254:VAL:HG22	1.95	0.47
1:A:227:LEU:HD13	1:A:254:VAL:HG22	1.96	0.47
1:D:169:VAL:HG21	1:D:377:ALA:HB2	1.96	0.47
1:F:226:LYS:HZ3	1:F:252:GLU:HB3	1.79	0.47
1:F:469:VAL:HG22	1:F:478:GLY:HA2	1.95	0.47
1:A:362:ARG:HE	1:A:363:GLU:HB2	1.79	0.47
1:A:7:LYS:HD2	1:A:66:PHE:CE1	2.49	0.47
1:D:219:TYR:CD1	1:D:247:LEU:HD12	2.50	0.47
1:D:341:GLU:O	1:D:345:ARG:HG2	2.14	0.47
1:F:220:ILE:HD12	1:F:248:LEU:HD22	1.95	0.47
1:B:220:ILE:HD12	1:B:248:LEU:HD22	1.96	0.47
1:C:220:ILE:HD12	1:C:248:LEU:HD22	1.96	0.47
1:A:220:ILE:HD12	1:A:248:LEU:HD22	1.95	0.47
1:F:169:VAL:HG21	1:F:377:ALA:HB2	1.96	0.47
1:G:362:ARG:HE	1:G:363:GLU:HB2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:361:ASP:OD1	1:G:365:LEU:HD13	2.13	0.47
1:A:221:LEU:HD21	1:A:249:ILE:CG1	2.45	0.47
1:B:174:VAL:O	1:B:174:VAL:HG22	2.14	0.47
1:D:227:LEU:CB	1:D:254:VAL:HG13	2.44	0.47
1:D:197:ARG:NH1	1:D:277:LYS:HG2	2.23	0.47
1:D:321:LYS:CB	1:D:334:ASP:HB3	2.45	0.47
1:F:77:VAL:HG21	1:F:511:VAL:HG13	1.97	0.47
1:G:227:LEU:CB	1:G:254:VAL:HG13	2.44	0.47
1:A:226:LYS:HZ1	1:A:252:GLU:HB3	1.78	0.47
1:A:289:LEU:O	1:A:293:ALA:HB2	2.15	0.47
1:B:219:TYR:CD1	1:B:247:LEU:HD12	2.50	0.47
1:B:183:MET:HB3	1:B:384:MET:HE1	1.97	0.47
1:E:227:LEU:CB	1:E:254:VAL:HG13	2.45	0.47
1:F:18:LYS:HB3	1:F:67:GLU:HG2	1.96	0.47
1:G:220:ILE:HD12	1:G:248:LEU:HD22	1.96	0.47
1:G:429:LEU:HD12	1:G:430:SER:N	2.30	0.47
1:B:362:ARG:HE	1:B:363:GLU:HB2	1.79	0.47
1:B:158:ILE:CG2	1:B:396:VAL:HG22	2.45	0.47
1:C:11:ASP:CG	1:C:15:ARG:HH12	2.18	0.47
1:C:213:ALA:HB3	1:C:325:ILE:HB	1.96	0.47
1:C:362:ARG:HE	1:C:363:GLU:HB2	1.80	0.47
1:C:511:VAL:HG23	1:C:512:ALA:N	2.29	0.47
1:D:124:THR:O	1:D:128:VAL:HG23	2.15	0.47
1:E:220:ILE:HD12	1:E:248:LEU:HD22	1.96	0.47
1:A:169:VAL:HG21	1:A:377:ALA:HB2	1.96	0.47
1:A:174:VAL:O	1:A:174:VAL:HG22	2.14	0.47
1:A:227:LEU:CB	1:A:254:VAL:HG13	2.44	0.47
1:B:213:ALA:HB3	1:B:325:ILE:HB	1.96	0.47
1:C:197:ARG:NH1	1:C:277:LYS:HG2	2.24	0.47
1:C:158:ILE:CG2	1:C:396:VAL:HG22	2.45	0.47
1:C:451:MET:CE	1:C:465:VAL:HG12	2.45	0.47
1:D:174:VAL:O	1:D:174:VAL:HG22	2.14	0.47
1:D:213:ALA:HB3	1:D:325:ILE:HB	1.96	0.47
1:F:227:LEU:CB	1:F:254:VAL:HG13	2.44	0.47
1:G:11:ASP:CG	1:G:15:ARG:HH12	2.18	0.47
1:G:219:TYR:CD1	1:G:247:LEU:HD12	2.50	0.47
1:A:69:MET:HG2	1:B:47:PRO:CB	2.45	0.46
1:C:112:ASN:OD1	1:C:114:MET:N	2.49	0.46
1:C:321:LYS:CB	1:C:334:ASP:HB3	2.45	0.46
1:F:221:LEU:HD21	1:F:249:ILE:CG1	2.45	0.46
1:G:24:ALA:O	1:G:28:LYS:HD2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:GLY:HA2	1:A:62:LEU:CD1	2.45	0.46
1:A:205:VAL:HG12	1:A:207:ASN:N	2.30	0.46
1:A:24:ALA:O	1:A:28:LYS:HD2	2.15	0.46
1:C:429:LEU:HD12	1:C:430:SER:N	2.30	0.46
1:D:198:GLY:O	1:D:276:VAL:HG12	2.15	0.46
1:D:362:ARG:HE	1:D:363:GLU:HB2	1.79	0.46
1:E:205:VAL:HG12	1:E:207:ASN:H	1.79	0.46
1:E:489:MET:HG3	1:E:494:VAL:HB	1.97	0.46
1:G:221:LEU:HD21	1:G:249:ILE:CG1	2.46	0.46
1:G:226:LYS:HZ1	1:G:252:GLU:HB3	1.79	0.46
1:G:169:VAL:HG21	1:G:377:ALA:HB2	1.97	0.46
1:A:205:VAL:HG12	1:A:207:ASN:H	1.80	0.46
1:A:219:TYR:CD1	1:A:247:LEU:HD12	2.50	0.46
1:B:36:ARG:NH1	1:B:36:ARG:CG	2.76	0.46
1:B:489:MET:HG3	1:B:494:VAL:HB	1.97	0.46
1:D:158:ILE:CG2	1:D:396:VAL:HG22	2.46	0.46
1:E:511:VAL:HG23	1:E:512:ALA:N	2.30	0.46
1:F:219:TYR:CD1	1:F:247:LEU:HD12	2.50	0.46
1:G:209:ASP:HB3	1:G:210:LYS:HZ2	1.80	0.46
1:A:11:ASP:CG	1:A:15:ARG:HH12	2.19	0.46
1:B:24:ALA:O	1:B:28:LYS:HD2	2.16	0.46
1:C:205:VAL:HG12	1:C:207:ASN:N	2.31	0.46
1:C:77:VAL:HG21	1:C:511:VAL:HG13	1.98	0.46
1:E:221:LEU:O	1:E:250:VAL:HG23	2.16	0.46
1:F:383:GLY:H	1:F:389:VAL:HG22	1.81	0.46
1:F:158:ILE:CG2	1:F:396:VAL:HG22	2.46	0.46
1:C:205:VAL:HG12	1:C:207:ASN:H	1.80	0.46
1:D:289:LEU:O	1:D:293:ALA:HB2	2.16	0.46
1:E:66:PHE:HA	1:E:69:MET:HE2	1.96	0.46
1:G:489:MET:HG3	1:G:494:VAL:HB	1.98	0.46
1:A:122:VAL:HG12	1:A:123:ALA:N	2.31	0.46
1:A:158:ILE:CG2	1:A:396:VAL:HG22	2.46	0.46
1:B:429:LEU:HD12	1:B:430:SER:N	2.31	0.46
1:C:219:TYR:CD1	1:C:247:LEU:HD12	2.51	0.46
1:C:169:VAL:HG21	1:C:377:ALA:HB2	1.96	0.46
1:D:429:LEU:HD12	1:D:430:SER:N	2.29	0.46
1:E:11:ASP:CG	1:E:15:ARG:HH12	2.18	0.46
1:E:219:TYR:CD1	1:E:247:LEU:HD12	2.51	0.46
1:F:227:LEU:HB2	1:F:254:VAL:CA	2.37	0.46
1:D:103:GLY:HA3	1:D:516:ILE:HD11	1.96	0.46
1:D:205:VAL:HG12	1:D:207:ASN:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:122:VAL:HG12	1:E:123:ALA:N	2.29	0.46
1:E:205:VAL:HG12	1:E:207:ASN:N	2.30	0.46
1:G:205:VAL:HG12	1:G:207:ASN:H	1.80	0.46
1:G:351:GLN:HA	1:G:354:GLU:HB2	1.98	0.46
1:B:197:ARG:NH1	1:B:277:LYS:HG2	2.23	0.46
1:D:205:VAL:HG12	1:D:207:ASN:N	2.31	0.46
1:D:351:GLN:HA	1:D:354:GLU:HB2	1.98	0.46
1:C:69:MET:HG2	1:D:47:PRO:HB3	1.98	0.46
1:E:174:VAL:HG22	1:E:174:VAL:O	2.15	0.46
1:E:198:GLY:O	1:E:276:VAL:HG12	2.16	0.46
1:E:383:GLY:H	1:E:389:VAL:HG22	1.81	0.46
1:F:351:GLN:HA	1:F:354:GLU:HB2	1.98	0.46
1:F:362:ARG:HE	1:F:363:GLU:HB2	1.79	0.46
1:F:80:ARG:HB2	1:F:80:ARG:HH11	1.81	0.46
1:G:69:MET:HB2	1:G:69:MET:HE3	1.53	0.46
1:A:217:ASP:O	1:A:246:PRO:HD2	2.16	0.46
1:A:90:THR:O	1:A:94:VAL:HG23	2.16	0.46
1:B:221:LEU:HD21	1:B:249:ILE:CG1	2.46	0.46
1:C:289:LEU:O	1:C:293:ALA:HB2	2.16	0.46
1:D:221:LEU:HD21	1:D:249:ILE:CG1	2.45	0.46
1:D:62:LEU:H	1:D:68:ASN:HD22	1.64	0.46
1:E:289:LEU:O	1:E:293:ALA:HB2	2.15	0.46
1:E:77:VAL:HG21	1:E:511:VAL:HG13	1.98	0.46
1:A:128:VAL:HG11	1:A:506:GLU:OE2	2.16	0.46
1:A:6:VAL:HG22	1:A:522:ILE:HG12	1.98	0.46
1:B:451:MET:CE	1:B:465:VAL:HG12	2.46	0.46
1:C:294:ILE:HD11	1:C:345:ARG:NH1	2.31	0.46
1:D:217:ASP:O	1:D:246:PRO:HD2	2.16	0.46
1:E:194:GLN:HG3	1:E:331:THR:OG1	2.16	0.46
1:G:62:LEU:H	1:G:68:ASN:HD22	1.63	0.46
1:C:217:ASP:O	1:C:246:PRO:HD2	2.16	0.45
1:G:80:ARG:HB2	1:G:80:ARG:HH11	1.81	0.45
1:A:175:ILE:HG22	1:A:176:THR:N	2.31	0.45
1:A:451:MET:CE	1:A:465:VAL:HG12	2.47	0.45
1:B:19:GLY:HA2	1:B:62:LEU:CD1	2.46	0.45
1:D:36:ARG:NH1	1:D:36:ARG:CG	2.75	0.45
1:D:69:MET:HE3	1:D:69:MET:HB2	1.53	0.45
1:E:221:LEU:HD21	1:E:249:ILE:CG1	2.46	0.45
1:E:351:GLN:HA	1:E:354:GLU:HB2	1.99	0.45
1:F:217:ASP:O	1:F:246:PRO:HD2	2.17	0.45
1:F:194:GLN:HG3	1:F:331:THR:OG1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:198:GLY:O	1:G:276:VAL:HG12	2.16	0.45
1:G:217:ASP:O	1:G:246:PRO:HD2	2.16	0.45
1:A:351:GLN:HA	1:A:354:GLU:HB2	1.99	0.45
1:A:103:GLY:HA3	1:A:516:ILE:HD11	1.97	0.45
1:B:12:ALA:HB1	1:B:521:MET:SD	2.57	0.45
1:B:11:ASP:CG	1:B:15:ARG:HH12	2.19	0.45
1:B:289:LEU:O	1:B:293:ALA:HB2	2.15	0.45
1:C:19:GLY:HA2	1:C:62:LEU:CD1	2.46	0.45
1:C:351:GLN:HA	1:C:354:GLU:HB2	1.98	0.45
1:C:478:GLY:HA3	1:C:489:MET:HE3	1.97	0.45
1:D:112:ASN:OD1	1:D:114:MET:N	2.49	0.45
1:E:225:LYS:HB2	1:E:226:LYS:H	1.62	0.45
1:E:362:ARG:HE	1:E:363:GLU:HB2	1.80	0.45
1:G:112:ASN:OD1	1:G:114:MET:N	2.49	0.45
1:G:378:VAL:HG22	1:G:378:VAL:O	2.16	0.45
1:G:19:GLY:HA2	1:G:62:LEU:CD1	2.47	0.45
1:B:321:LYS:CB	1:B:334:ASP:HB3	2.46	0.45
1:D:320:ALA:HA	1:D:335:GLY:O	2.17	0.45
1:D:348:GLN:O	1:D:352:GLN:HB2	2.17	0.45
1:D:378:VAL:O	1:D:378:VAL:HG22	2.17	0.45
1:F:112:ASN:OD1	1:F:114:MET:N	2.49	0.45
1:F:507:ASP:O	1:F:510:SER:HB3	2.17	0.45
1:B:348:GLN:O	1:B:352:GLN:HB2	2.17	0.45
1:B:80:ARG:HB2	1:B:80:ARG:HH11	1.82	0.45
1:C:383:GLY:H	1:C:389:VAL:HG22	1.82	0.45
1:E:112:ASN:OD1	1:E:114:MET:N	2.50	0.45
1:F:221:LEU:O	1:F:250:VAL:HG23	2.16	0.45
1:F:289:LEU:O	1:F:293:ALA:HB2	2.15	0.45
1:G:289:LEU:O	1:G:293:ALA:HB2	2.16	0.45
1:A:247:LEU:HB3	1:A:273:ILE:HD12	1.99	0.45
1:A:69:MET:HB2	1:A:69:MET:HE3	1.55	0.45
1:A:77:VAL:HG21	1:A:511:VAL:HG13	1.99	0.45
1:B:351:GLN:HA	1:B:354:GLU:HB2	1.98	0.45
1:C:221:LEU:O	1:C:250:VAL:HG23	2.16	0.45
1:F:128:VAL:HG11	1:F:506:GLU:OE2	2.17	0.45
1:F:66:PHE:HA	1:F:69:MET:HE2	1.97	0.45
1:G:194:GLN:HG3	1:G:331:THR:OG1	2.17	0.45
1:G:221:LEU:O	1:G:250:VAL:HG23	2.16	0.45
1:B:247:LEU:HB3	1:B:273:ILE:HD12	1.99	0.45
1:C:124:THR:O	1:C:128:VAL:HG23	2.16	0.45
1:C:198:GLY:O	1:C:276:VAL:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:320:ALA:HA	1:C:335:GLY:O	2.17	0.45
1:E:501:VAL:O	1:E:501:VAL:HG12	2.16	0.45
1:E:69:MET:HG2	1:F:47:PRO:HB3	1.99	0.45
1:F:19:GLY:HA2	1:F:62:LEU:CD1	2.46	0.45
1:F:478:GLY:HA3	1:F:489:MET:HE3	1.99	0.45
1:G:204:PHE:CE1	1:G:273:ILE:HG23	2.52	0.45
1:G:205:VAL:HG12	1:G:207:ASN:N	2.30	0.45
1:A:12:ALA:HB1	1:A:521:MET:HG3	1.99	0.45
1:A:221:LEU:O	1:A:250:VAL:HG23	2.16	0.45
1:C:348:GLN:O	1:C:352:GLN:HB2	2.17	0.45
1:E:348:GLN:O	1:E:352:GLN:HB2	2.17	0.45
1:E:69:MET:HE3	1:E:69:MET:HB2	1.50	0.45
1:E:80:ARG:HB2	1:E:80:ARG:HH11	1.82	0.45
1:B:217:ASP:O	1:B:246:PRO:HD2	2.17	0.45
1:D:221:LEU:O	1:D:250:VAL:HG23	2.16	0.45
1:E:217:ASP:O	1:E:246:PRO:HD2	2.17	0.45
1:F:204:PHE:CE1	1:F:273:ILE:HG23	2.52	0.45
1:F:511:VAL:HG23	1:F:512:ALA:N	2.32	0.45
1:A:124:THR:O	1:A:128:VAL:HG23	2.17	0.45
1:A:383:GLY:H	1:A:389:VAL:HG22	1.81	0.45
1:A:429:LEU:HD12	1:A:430:SER:N	2.29	0.45
1:B:112:ASN:OD1	1:B:114:MET:N	2.50	0.45
1:B:194:GLN:HG3	1:B:331:THR:OG1	2.17	0.45
1:C:480:ASN:O	1:C:484:GLU:N	2.45	0.45
1:C:62:LEU:H	1:C:68:ASN:HD22	1.64	0.45
1:C:72:GLN:HE22	1:C:75:ARG:CZ	2.30	0.45
1:D:175:ILE:HG22	1:D:176:THR:N	2.32	0.45
1:G:478:GLY:HA3	1:G:489:MET:HE3	1.99	0.45
1:B:225:LYS:HB2	1:B:226:LYS:H	1.62	0.44
1:B:383:GLY:H	1:B:389:VAL:HG22	1.81	0.44
1:C:174:VAL:O	1:C:174:VAL:HG22	2.16	0.44
1:C:221:LEU:HD21	1:C:249:ILE:CG1	2.47	0.44
1:C:80:ARG:HH11	1:C:80:ARG:HB2	1.82	0.44
1:D:19:GLY:HA2	1:D:62:LEU:CD1	2.47	0.44
1:D:383:GLY:H	1:D:389:VAL:HG22	1.82	0.44
1:D:511:VAL:HG23	1:D:512:ALA:N	2.33	0.44
1:D:6:VAL:HG22	1:D:522:ILE:HG12	1.98	0.44
1:G:158:ILE:CG2	1:G:396:VAL:HG22	2.46	0.44
1:A:194:GLN:HG3	1:A:331:THR:OG1	2.17	0.44
1:B:198:GLY:O	1:B:276:VAL:HG12	2.18	0.44
1:C:204:PHE:CE1	1:C:273:ILE:HG23	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:90:THR:O	1:D:94:VAL:HG23	2.17	0.44
1:E:320:ALA:HA	1:E:335:GLY:O	2.18	0.44
1:E:294:ILE:HD11	1:E:345:ARG:NH1	2.32	0.44
1:E:423:ALA:HB2	1:E:447:LEU:HD13	1.98	0.44
1:F:294:ILE:HD11	1:F:345:ARG:NH1	2.33	0.44
1:A:198:GLY:O	1:A:276:VAL:HG12	2.17	0.44
1:B:12:ALA:HB1	1:B:521:MET:HG3	1.98	0.44
1:B:221:LEU:O	1:B:250:VAL:HG23	2.16	0.44
1:B:6:VAL:HG22	1:B:522:ILE:HG12	1.99	0.44
1:C:247:LEU:HB3	1:C:273:ILE:HD12	1.99	0.44
1:D:507:ASP:O	1:D:510:SER:HB3	2.17	0.44
1:E:451:MET:CE	1:E:466:ALA:HA	2.48	0.44
1:F:247:LEU:HB3	1:F:273:ILE:HD12	1.99	0.44
1:G:174:VAL:HG22	1:G:174:VAL:O	2.16	0.44
1:G:294:ILE:HD11	1:G:345:ARG:NH1	2.32	0.44
1:G:348:GLN:O	1:G:352:GLN:HB2	2.17	0.44
1:B:69:MET:HB2	1:B:69:MET:HE3	1.55	0.44
1:C:128:VAL:HG11	1:C:506:GLU:OE2	2.18	0.44
1:E:158:ILE:CG2	1:E:396:VAL:HG22	2.48	0.44
1:F:320:ALA:HA	1:F:335:GLY:O	2.18	0.44
1:G:320:ALA:HA	1:G:335:GLY:O	2.17	0.44
1:A:80:ARG:HB2	1:A:80:ARG:HH11	1.82	0.44
1:C:90:THR:O	1:C:94:VAL:HG23	2.17	0.44
1:D:13:ARG:CD	1:D:104:LEU:HD22	2.47	0.44
1:D:423:ALA:HB2	1:D:447:LEU:HD13	1.99	0.44
1:E:204:PHE:CE1	1:E:273:ILE:HG23	2.53	0.44
1:F:245:LYS:HZ1	1:F:319:ARG:HH21	1.64	0.44
1:F:429:LEU:HD12	1:F:430:SER:N	2.29	0.44
1:G:219:TYR:N	1:G:246:PRO:O	2.51	0.44
1:A:183:MET:HB3	1:A:384:MET:HE1	1.99	0.44
1:A:480:ASN:HD21	1:A:483:THR:HG23	1.83	0.44
1:C:245:LYS:HZ1	1:C:319:ARG:HH21	1.65	0.44
1:D:183:MET:HB3	1:D:384:MET:HE1	2.00	0.44
1:D:231:GLN:N	1:D:231:GLN:NE2	2.65	0.44
1:D:80:ARG:HH11	1:D:80:ARG:HB2	1.82	0.44
1:E:429:LEU:HD12	1:E:430:SER:N	2.31	0.44
1:E:62:LEU:H	1:E:68:ASN:HD22	1.66	0.44
1:F:205:VAL:HG12	1:F:207:ASN:N	2.31	0.44
1:F:205:VAL:HG12	1:F:207:ASN:H	1.81	0.44
1:F:231:GLN:NE2	1:F:231:GLN:N	2.65	0.44
1:F:219:TYR:N	1:F:246:PRO:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:13:ARG:CD	1:G:104:LEU:HD22	2.48	0.44
1:G:488:ASP:HB3	1:G:491:LYS:HG3	1.99	0.44
1:G:511:VAL:HG23	1:G:512:ALA:N	2.33	0.44
1:A:511:VAL:HG23	1:A:512:ALA:N	2.32	0.44
1:B:72:GLN:HE22	1:B:75:ARG:CZ	2.31	0.44
1:C:126:LYS:HG3	1:C:429:LEU:CD2	2.48	0.44
1:D:194:GLN:HG3	1:D:331:THR:OG1	2.18	0.44
1:E:75:ARG:HH11	1:E:75:ARG:CG	2.30	0.44
1:F:175:ILE:HG22	1:F:176:THR:N	2.32	0.44
1:F:348:GLN:O	1:F:352:GLN:HB2	2.17	0.44
1:G:72:GLN:HE22	1:G:75:ARG:CZ	2.31	0.44
1:B:77:VAL:HG21	1:B:511:VAL:HG13	2.00	0.44
1:C:190:VAL:HG12	1:C:191:GLU:N	2.32	0.44
1:C:225:LYS:HG3	1:C:225:LYS:H	1.61	0.44
1:C:69:MET:HE3	1:C:69:MET:HB2	1.59	0.44
1:D:423:ALA:HB2	1:D:447:LEU:CD1	2.47	0.44
1:E:175:ILE:HG22	1:E:176:THR:N	2.33	0.44
1:F:174:VAL:HG22	1:F:174:VAL:O	2.17	0.44
1:G:507:ASP:O	1:G:510:SER:HB3	2.18	0.44
1:G:77:VAL:HG21	1:G:511:VAL:HG13	2.00	0.44
1:A:13:ARG:CD	1:A:104:LEU:HD22	2.48	0.44
1:A:320:ALA:HA	1:A:335:GLY:O	2.17	0.44
1:A:348:GLN:O	1:A:352:GLN:HB2	2.18	0.44
1:B:320:ALA:HA	1:B:335:GLY:O	2.17	0.44
1:D:24:ALA:O	1:D:28:LYS:HD2	2.17	0.44
1:E:219:TYR:N	1:E:246:PRO:O	2.51	0.44
1:E:247:LEU:HB3	1:E:273:ILE:HD12	1.99	0.44
1:F:198:GLY:O	1:F:276:VAL:HG12	2.17	0.44
1:A:219:TYR:N	1:A:246:PRO:O	2.51	0.43
1:B:451:MET:CE	1:B:466:ALA:HA	2.48	0.43
1:C:175:ILE:HG22	1:C:176:THR:N	2.33	0.43
1:C:349:ILE:HG22	1:C:353:ILE:HD11	2.00	0.43
1:E:72:GLN:HE22	1:E:75:ARG:CZ	2.30	0.43
1:F:126:LYS:HG3	1:F:429:LEU:CD2	2.48	0.43
1:A:204:PHE:CE1	1:A:273:ILE:HG23	2.54	0.43
1:A:8:PHE:HE1	1:B:26:ALA:HA	1.83	0.43
1:B:294:ILE:HD11	1:B:345:ARG:NH1	2.33	0.43
1:C:227:LEU:CD1	1:C:251:ALA:HB3	2.48	0.43
1:C:12:ALA:HB1	1:C:521:MET:HG3	1.99	0.43
1:D:139:ASN:N	1:D:139:ASN:ND2	2.66	0.43
1:D:349:ILE:HG22	1:D:353:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:72:GLN:HE22	1:D:75:ARG:CZ	2.31	0.43
1:E:365:LEU:HA	1:E:368:ARG:HG2	2.00	0.43
1:F:480:ASN:HD21	1:F:483:THR:HG23	1.84	0.43
1:A:112:ASN:OD1	1:A:114:MET:N	2.51	0.43
1:A:488:ASP:HB3	1:A:491:LYS:HG3	2.00	0.43
1:E:19:GLY:HA2	1:E:62:LEU:CD1	2.48	0.43
1:G:128:VAL:HG11	1:G:506:GLU:OE2	2.19	0.43
1:G:225:LYS:HG3	1:G:225:LYS:H	1.62	0.43
1:G:174:VAL:HG13	1:G:376:VAL:HA	2.00	0.43
1:B:488:ASP:HB3	1:B:491:LYS:HG3	1.99	0.43
1:D:247:LEU:HB3	1:D:273:ILE:HD12	1.99	0.43
1:E:423:ALA:HB2	1:E:447:LEU:CD1	2.48	0.43
1:F:488:ASP:HB3	1:F:491:LYS:HG3	1.99	0.43
1:F:62:LEU:H	1:F:68:ASN:HD22	1.66	0.43
1:B:103:GLY:HA3	1:B:516:ILE:CD1	2.49	0.43
1:C:139:ASN:N	1:C:139:ASN:ND2	2.67	0.43
1:D:227:LEU:CD1	1:D:251:ALA:HB3	2.48	0.43
1:C:8:PHE:HE1	1:D:26:ALA:HA	1.84	0.43
1:D:294:ILE:HD11	1:D:345:ARG:NH1	2.32	0.43
1:E:13:ARG:CD	1:E:104:LEU:HD22	2.48	0.43
1:F:225:LYS:HB2	1:F:226:LYS:H	1.62	0.43
1:F:227:LEU:CD1	1:F:251:ALA:HB3	2.48	0.43
1:G:12:ALA:HB1	1:G:521:MET:SD	2.58	0.43
1:G:175:ILE:HG22	1:G:176:THR:N	2.33	0.43
1:G:247:LEU:HB3	1:G:273:ILE:HD12	2.00	0.43
1:B:204:PHE:CE1	1:B:273:ILE:HG23	2.53	0.43
1:B:511:VAL:HG23	1:B:512:ALA:N	2.34	0.43
1:B:69:MET:HG2	1:C:47:PRO:HB3	2.01	0.43
1:D:204:PHE:CE1	1:D:273:ILE:HG23	2.53	0.43
1:D:480:ASN:HD21	1:D:483:THR:HG23	1.84	0.43
1:E:12:ALA:HB1	1:E:521:MET:SD	2.59	0.43
1:E:451:MET:CE	1:E:465:VAL:HG12	2.49	0.43
1:F:365:LEU:HA	1:F:368:ARG:HG2	2.00	0.43
1:G:75:ARG:HH11	1:G:75:ARG:CG	2.31	0.43
1:A:478:GLY:HA3	1:A:489:MET:HE3	1.99	0.43
1:B:349:ILE:HG22	1:B:353:ILE:HD11	2.00	0.43
1:D:365:LEU:HA	1:D:368:ARG:HG2	2.00	0.43
1:D:451:MET:CE	1:D:465:VAL:HG12	2.49	0.43
1:E:224:GLU:HG3	1:E:286:LYS:CE	2.49	0.43
1:F:103:GLY:HA3	1:F:516:ILE:CD1	2.49	0.43
1:F:124:THR:O	1:F:128:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ILE:HD11	1:A:345:ARG:NH1	2.33	0.43
1:A:480:ASN:O	1:A:484:GLU:N	2.47	0.43
1:B:227:LEU:CD1	1:B:251:ALA:HB3	2.49	0.43
1:B:365:LEU:HA	1:B:368:ARG:HG2	2.00	0.43
1:C:488:ASP:HB3	1:C:491:LYS:HG3	1.99	0.43
1:C:103:GLY:HA3	1:C:516:ILE:CD1	2.49	0.43
1:D:224:GLU:HG3	1:D:286:LYS:CE	2.49	0.43
1:D:478:GLY:HA3	1:D:489:MET:HE3	2.00	0.43
1:F:349:ILE:HG22	1:F:353:ILE:HD11	2.00	0.43
1:F:451:MET:CE	1:F:466:ALA:HA	2.49	0.43
1:A:321:LYS:CB	1:A:334:ASP:HB3	2.45	0.43
1:B:175:ILE:HG22	1:B:176:THR:N	2.33	0.43
1:B:224:GLU:HG3	1:B:286:LYS:CE	2.49	0.43
1:B:507:ASP:O	1:B:510:SER:HB3	2.18	0.43
1:C:224:GLU:HG3	1:C:286:LYS:CE	2.49	0.43
1:C:194:GLN:HG3	1:C:331:THR:OG1	2.17	0.43
1:C:365:LEU:HA	1:C:368:ARG:HG2	2.01	0.43
1:C:507:ASP:O	1:C:510:SER:HB3	2.19	0.43
1:D:12:ALA:HB1	1:D:521:MET:HG3	2.00	0.43
1:E:128:VAL:HG11	1:E:506:GLU:OE2	2.18	0.43
1:G:227:LEU:CD1	1:G:251:ALA:HB3	2.49	0.43
1:G:365:LEU:HA	1:G:368:ARG:HG2	2.00	0.43
1:A:225:LYS:HB2	1:A:226:LYS:H	1.62	0.43
1:A:227:LEU:CD1	1:A:251:ALA:HB3	2.48	0.43
1:B:126:LYS:HG3	1:B:429:LEU:CD2	2.49	0.43
1:B:62:LEU:H	1:B:68:ASN:HD22	1.65	0.43
1:D:488:ASP:HB3	1:D:491:LYS:HG3	2.00	0.43
1:E:124:THR:O	1:E:128:VAL:HG23	2.19	0.43
1:E:478:GLY:HA3	1:E:489:MET:HE3	2.01	0.43
1:G:383:GLY:H	1:G:389:VAL:HG22	1.83	0.43
1:A:24:ALA:O	1:A:28:LYS:HB3	2.18	0.42
1:A:451:MET:HE1	1:A:465:VAL:HG12	2.01	0.42
1:D:480:ASN:O	1:D:484:GLU:N	2.48	0.42
1:E:227:LEU:CD1	1:E:251:ALA:HB3	2.48	0.42
1:E:248:LEU:CA	1:E:274:ALA:HB3	2.49	0.42
1:D:69:MET:HG2	1:E:47:PRO:HG3	2.00	0.42
1:F:13:ARG:CD	1:F:104:LEU:HD22	2.49	0.42
1:F:75:ARG:HH11	1:F:75:ARG:CG	2.30	0.42
1:A:365:LEU:HA	1:A:368:ARG:HG2	2.00	0.42
1:B:231:GLN:N	1:B:231:GLN:NE2	2.65	0.42
1:B:449:ALA:CB	1:B:450:PRO:HD3	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:217:ASP:HA	1:C:320:ALA:O	2.19	0.42
1:D:128:VAL:O	1:D:128:VAL:HG12	2.18	0.42
1:F:226:LYS:HZ1	1:F:252:GLU:HB3	1.84	0.42
1:F:26:ALA:O	1:F:29:VAL:HG22	2.18	0.42
1:F:321:LYS:CB	1:F:334:ASP:HB3	2.45	0.42
1:A:507:ASP:O	1:A:510:SER:HB3	2.19	0.42
1:B:378:VAL:HG22	1:B:378:VAL:O	2.19	0.42
1:A:126:LYS:HG3	1:A:429:LEU:CD2	2.49	0.42
1:A:62:LEU:H	1:A:68:ASN:HD22	1.65	0.42
1:C:227:LEU:HD11	1:C:251:ALA:HB3	2.02	0.42
1:C:451:MET:CE	1:C:466:ALA:HA	2.48	0.42
1:D:219:TYR:N	1:D:246:PRO:O	2.52	0.42
1:E:378:VAL:O	1:E:378:VAL:HG22	2.19	0.42
1:D:69:MET:HG2	1:E:47:PRO:CB	2.49	0.42
1:E:488:ASP:HB3	1:E:491:LYS:HG3	2.00	0.42
1:F:220:ILE:CD1	1:F:248:LEU:HD22	2.49	0.42
1:G:248:LEU:CA	1:G:274:ALA:HB3	2.49	0.42
1:A:224:GLU:HG3	1:A:286:LYS:CE	2.49	0.42
1:A:349:ILE:HG22	1:A:353:ILE:HD11	2.01	0.42
1:A:423:ALA:HB2	1:A:447:LEU:HD13	2.01	0.42
1:B:124:THR:O	1:B:128:VAL:HG23	2.19	0.42
1:B:174:VAL:HG13	1:B:376:VAL:HA	2.02	0.42
1:B:90:THR:O	1:B:94:VAL:HG23	2.20	0.42
1:C:174:VAL:HG13	1:C:376:VAL:HA	2.01	0.42
1:C:19:GLY:O	1:C:71:ALA:HB2	2.20	0.42
1:F:126:LYS:HG3	1:F:429:LEU:HD22	2.00	0.42
1:G:321:LYS:CB	1:G:334:ASP:HB3	2.45	0.42
1:G:480:ASN:HD21	1:G:483:THR:HG23	1.84	0.42
1:A:174:VAL:HG13	1:A:376:VAL:HA	2.02	0.42
1:A:220:ILE:CD1	1:A:248:LEU:HD22	2.50	0.42
1:E:126:LYS:HG3	1:E:429:LEU:CD2	2.49	0.42
1:F:12:ALA:HB1	1:F:521:MET:HG3	2.01	0.42
1:F:36:ARG:CG	1:F:36:ARG:NH1	2.75	0.42
1:G:380:ARG:HH11	1:G:380:ARG:CB	2.28	0.42
1:C:112:ASN:OD1	1:C:112:ASN:C	2.58	0.42
1:D:112:ASN:C	1:D:112:ASN:OD1	2.58	0.42
1:E:221:LEU:HG	1:E:249:ILE:HA	2.02	0.42
1:F:72:GLN:HE22	1:F:75:ARG:CZ	2.31	0.42
1:A:112:ASN:OD1	1:A:112:ASN:C	2.58	0.42
1:A:2:ALA:O	1:A:3:ALA:C	2.57	0.42
1:C:220:ILE:CD1	1:C:248:LEU:HD22	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:126:LYS:HG3	1:D:429:LEU:CD2	2.49	0.42
1:D:227:LEU:HD11	1:D:251:ALA:HB3	2.02	0.42
1:D:298:GLY:HA2	1:D:317:LEU:C	2.40	0.42
1:D:174:VAL:HG13	1:D:376:VAL:HA	2.01	0.42
1:E:139:ASN:ND2	1:E:139:ASN:N	2.66	0.42
1:E:321:LYS:CB	1:E:334:ASP:HB3	2.45	0.42
1:E:507:ASP:O	1:E:510:SER:HB3	2.20	0.42
1:F:2:ALA:O	1:F:3:ALA:C	2.57	0.42
1:B:13:ARG:CD	1:B:104:LEU:HD22	2.49	0.42
1:B:112:ASN:C	1:B:112:ASN:OD1	2.59	0.42
1:B:128:VAL:HG11	1:B:506:GLU:OE2	2.20	0.42
1:B:227:LEU:HD11	1:B:251:ALA:HB3	2.02	0.42
1:B:423:ALA:HB2	1:B:447:LEU:HD13	2.01	0.42
1:D:128:VAL:HG11	1:D:506:GLU:OE2	2.19	0.42
1:D:451:MET:CE	1:D:466:ALA:HA	2.49	0.42
1:E:220:ILE:CD1	1:E:248:LEU:HD22	2.50	0.42
1:F:123:ALA:HB1	1:F:426:LEU:HD22	2.02	0.42
1:G:224:GLU:HG3	1:G:286:LYS:CE	2.50	0.42
1:A:139:ASN:ND2	1:A:139:ASN:N	2.66	0.42
1:A:217:ASP:HA	1:A:320:ALA:O	2.20	0.42
1:B:219:TYR:N	1:B:246:PRO:O	2.52	0.42
1:B:221:LEU:HG	1:B:249:ILE:HA	2.02	0.42
1:D:215:LEU:HD22	1:D:274:ALA:HB2	2.02	0.42
1:D:220:ILE:CD1	1:D:248:LEU:HD22	2.50	0.42
1:D:77:VAL:HG21	1:D:511:VAL:HG13	2.02	0.42
1:F:215:LEU:HD22	1:F:274:ALA:HB2	2.02	0.42
1:G:225:LYS:HB2	1:G:226:LYS:H	1.62	0.42
1:G:215:LEU:HD22	1:G:274:ALA:HB2	2.02	0.42
1:G:349:ILE:HG22	1:G:353:ILE:HD11	2.01	0.42
1:G:126:LYS:HG3	1:G:429:LEU:CD2	2.50	0.42
1:A:378:VAL:O	1:A:378:VAL:HG22	2.20	0.41
1:C:219:TYR:N	1:C:246:PRO:O	2.52	0.41
1:C:298:GLY:HA2	1:C:317:LEU:C	2.40	0.41
1:E:90:THR:O	1:E:94:VAL:HG23	2.20	0.41
1:F:224:GLU:HG3	1:F:286:LYS:CE	2.49	0.41
1:A:215:LEU:HD22	1:A:274:ALA:HB2	2.02	0.41
1:A:423:ALA:HB2	1:A:447:LEU:CD1	2.50	0.41
1:B:139:ASN:N	1:B:139:ASN:ND2	2.66	0.41
1:E:7:LYS:HB3	1:E:12:ALA:HB2	2.03	0.41
1:E:298:GLY:HA2	1:E:317:LEU:C	2.41	0.41
1:F:323:VAL:HG13	1:F:332:ILE:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:LYS:HB3	1:A:12:ALA:HB2	2.03	0.41
1:B:75:ARG:HH11	1:B:75:ARG:CG	2.32	0.41
1:C:221:LEU:HG	1:C:249:ILE:HA	2.03	0.41
1:C:480:ASN:HD21	1:C:483:THR:HG23	1.85	0.41
1:D:220:ILE:HG23	1:D:248:LEU:CD2	2.50	0.41
1:F:423:ALA:HB2	1:F:447:LEU:HD13	2.01	0.41
1:F:69:MET:HE3	1:F:69:MET:HB2	1.53	0.41
1:G:112:ASN:C	1:G:112:ASN:OD1	2.58	0.41
1:A:227:LEU:HD11	1:A:251:ALA:HB3	2.02	0.41
1:C:126:LYS:HG3	1:C:429:LEU:HD22	2.02	0.41
1:C:220:ILE:HG23	1:C:248:LEU:CD2	2.51	0.41
1:C:423:ALA:HB2	1:C:447:LEU:CD1	2.50	0.41
1:E:227:LEU:HB2	1:E:254:VAL:CA	2.38	0.41
1:E:217:ASP:HA	1:E:320:ALA:O	2.21	0.41
1:F:217:ASP:HA	1:F:320:ALA:O	2.21	0.41
1:F:221:LEU:HG	1:F:249:ILE:HA	2.03	0.41
1:G:220:ILE:CD1	1:G:248:LEU:HD22	2.50	0.41
1:G:12:ALA:HB1	1:G:521:MET:HG3	2.03	0.41
1:A:451:MET:CE	1:A:466:ALA:HA	2.50	0.41
1:A:12:ALA:HB1	1:A:521:MET:SD	2.60	0.41
1:B:215:LEU:HD22	1:B:274:ALA:HB2	2.02	0.41
1:B:220:ILE:CD1	1:B:248:LEU:HD22	2.50	0.41
1:B:80:ARG:HB2	1:B:80:ARG:NH1	2.36	0.41
1:E:349:ILE:HG22	1:E:353:ILE:HD11	2.01	0.41
1:E:36:ARG:CG	1:E:36:ARG:NH1	2.76	0.41
1:E:2:ALA:O	1:E:3:ALA:C	2.58	0.41
1:B:2:ALA:O	1:B:3:ALA:C	2.59	0.41
1:B:423:ALA:HB2	1:B:447:LEU:CD1	2.51	0.41
1:C:215:LEU:HD22	1:C:274:ALA:HB2	2.03	0.41
1:D:221:LEU:HG	1:D:249:ILE:HA	2.03	0.41
1:E:174:VAL:HG13	1:E:376:VAL:HA	2.01	0.41
1:F:220:ILE:HG23	1:F:248:LEU:CD2	2.50	0.41
1:F:298:GLY:HA2	1:F:317:LEU:C	2.41	0.41
1:F:174:VAL:HG13	1:F:376:VAL:HA	2.02	0.41
1:F:8:PHE:HE1	1:G:26:ALA:HA	1.86	0.41
1:G:24:ALA:O	1:G:28:LYS:HB3	2.20	0.41
1:G:298:GLY:HA2	1:G:317:LEU:C	2.41	0.41
1:C:24:ALA:O	1:C:28:LYS:HB3	2.21	0.41
1:E:245:LYS:HZ1	1:E:319:ARG:HH21	1.66	0.41
1:E:480:ASN:HD21	1:E:483:THR:HG23	1.85	0.41
1:E:103:GLY:HA3	1:E:516:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:227:LEU:HD11	1:F:251:ALA:HB3	2.02	0.41
1:G:231:GLN:N	1:G:231:GLN:NE2	2.65	0.41
1:A:248:LEU:CB	1:A:274:ALA:HB3	2.51	0.41
1:B:220:ILE:HG23	1:B:248:LEU:CD2	2.51	0.41
1:B:248:LEU:CB	1:B:274:ALA:HB3	2.51	0.41
1:C:26:ALA:O	1:C:29:VAL:HG22	2.21	0.41
1:C:378:VAL:HG22	1:C:378:VAL:O	2.21	0.41
1:D:227:LEU:HB2	1:D:254:VAL:CA	2.38	0.41
1:D:248:LEU:CA	1:D:274:ALA:HB3	2.49	0.41
1:D:2:ALA:O	1:D:3:ALA:C	2.59	0.41
1:D:126:LYS:HG3	1:D:429:LEU:HD22	2.02	0.41
1:D:482:GLN:HA	1:D:482:GLN:NE2	2.36	0.41
1:G:181:LYS:HB2	1:G:182:GLY:H	1.78	0.41
1:A:298:GLY:HA2	1:A:317:LEU:C	2.41	0.41
1:C:482:GLN:HA	1:C:482:GLN:NE2	2.36	0.41
1:F:423:ALA:HB2	1:F:447:LEU:CD1	2.51	0.41
1:G:2:ALA:O	1:G:3:ALA:C	2.58	0.41
1:G:36:ARG:CG	1:G:36:ARG:NH1	2.79	0.41
1:A:220:ILE:HG23	1:A:248:LEU:CD2	2.51	0.41
1:A:231:GLN:N	1:A:231:GLN:NE2	2.65	0.41
1:A:190:VAL:HG11	1:A:334:ASP:CB	2.51	0.41
1:C:13:ARG:CD	1:C:104:LEU:HD22	2.50	0.41
1:C:423:ALA:HB2	1:C:447:LEU:HD13	2.02	0.41
1:E:220:ILE:HG23	1:E:248:LEU:CD2	2.50	0.41
1:E:227:LEU:HD11	1:E:251:ALA:HB3	2.02	0.41
1:E:215:LEU:HD22	1:E:274:ALA:HB2	2.03	0.41
1:F:451:MET:HE1	1:F:465:VAL:HG12	2.02	0.41
1:F:90:THR:O	1:F:94:VAL:HG23	2.21	0.41
1:A:221:LEU:HG	1:A:249:ILE:HA	2.03	0.41
1:A:72:GLN:HE22	1:A:75:ARG:CZ	2.34	0.41
1:B:298:GLY:HA2	1:B:317:LEU:C	2.41	0.41
1:C:55:SER:O	1:C:59:GLU:HG2	2.20	0.41
1:F:380:ARG:HH11	1:F:380:ARG:CB	2.29	0.41
1:F:7:LYS:HB3	1:F:12:ALA:HB2	2.03	0.40
1:F:489:MET:HG3	1:F:494:VAL:O	2.21	0.40
1:G:220:ILE:HG23	1:G:248:LEU:CD2	2.50	0.40
1:G:248:LEU:CB	1:G:274:ALA:HB3	2.51	0.40
1:G:26:ALA:O	1:G:29:VAL:HG22	2.21	0.40
1:G:323:VAL:HG13	1:G:332:ILE:HG12	2.03	0.40
1:B:201:SER:O	1:B:204:PHE:HB2	2.21	0.40
1:B:480:ASN:HD21	1:B:483:THR:HG23	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:ARG:HB2	1:C:80:ARG:NH1	2.36	0.40
1:D:19:GLY:HA2	1:D:62:LEU:HD11	2.03	0.40
1:E:112:ASN:C	1:E:112:ASN:OD1	2.58	0.40
1:G:103:GLY:HA3	1:G:516:ILE:CD1	2.50	0.40
1:G:227:LEU:HD11	1:G:251:ALA:HB3	2.03	0.40
1:A:323:VAL:HG13	1:A:332:ILE:HG12	2.03	0.40
1:B:7:LYS:HB3	1:B:12:ALA:HB2	2.04	0.40
1:E:126:LYS:HG3	1:E:429:LEU:HD22	2.02	0.40
1:F:190:VAL:HG12	1:F:191:GLU:N	2.36	0.40
1:F:80:ARG:HB2	1:F:80:ARG:NH1	2.35	0.40
1:G:217:ASP:HA	1:G:320:ALA:O	2.22	0.40
1:G:480:ASN:O	1:G:484:GLU:N	2.48	0.40
1:B:217:ASP:HA	1:B:320:ALA:O	2.22	0.40
1:B:323:VAL:HG13	1:B:332:ILE:HG12	2.03	0.40
1:F:378:VAL:HG22	1:F:378:VAL:O	2.21	0.40
1:A:80:ARG:NH1	1:A:80:ARG:HB2	2.36	0.40
1:C:2:ALA:O	1:C:3:ALA:C	2.60	0.40
1:E:144:VAL:O	1:E:144:VAL:CG1	2.70	0.40
1:G:201:SER:O	1:G:204:PHE:HB2	2.21	0.40
1:G:482:GLN:NE2	1:G:482:GLN:HA	2.37	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	474/545 (87%)	404 (85%)	59 (12%)	11 (2%)	6	34
1	B	474/545 (87%)	405 (85%)	59 (12%)	10 (2%)	7	37
1	C	474/545 (87%)	404 (85%)	60 (13%)	10 (2%)	7	37
1	D	474/545 (87%)	404 (85%)	60 (13%)	10 (2%)	7	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	474/545 (87%)	404 (85%)	60 (13%)	10 (2%)	7	37
1	F	474/545 (87%)	404 (85%)	58 (12%)	12 (2%)	5	32
1	G	474/545 (87%)	405 (85%)	59 (12%)	10 (2%)	7	37
All	All	3318/3815 (87%)	2830 (85%)	415 (12%)	73 (2%)	6	35

All (73) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	85	ALA
1	A	228	SER
1	A	378	VAL
1	B	9	ASN
1	B	85	ALA
1	B	134	ALA
1	B	228	SER
1	B	378	VAL
1	C	9	ASN
1	C	85	ALA
1	C	134	ALA
1	C	228	SER
1	C	378	VAL
1	D	9	ASN
1	D	85	ALA
1	D	228	SER
1	D	378	VAL
1	E	9	ASN
1	E	85	ALA
1	E	134	ALA
1	E	228	SER
1	E	378	VAL
1	F	9	ASN
1	F	85	ALA
1	F	228	SER
1	F	378	VAL
1	G	9	ASN
1	G	85	ALA
1	G	228	SER
1	G	378	VAL
1	A	134	ALA
1	A	335	GLY

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	335	GLY
1	C	335	GLY
1	D	134	ALA
1	D	335	GLY
1	E	335	GLY
1	F	134	ALA
1	F	335	GLY
1	G	134	ALA
1	G	335	GLY
1	A	87	ASP
1	A	336	ALA
1	A	475	LYS
1	B	87	ASP
1	B	336	ALA
1	B	475	LYS
1	C	87	ASP
1	C	336	ALA
1	C	475	LYS
1	D	87	ASP
1	D	336	ALA
1	D	475	LYS
1	E	87	ASP
1	E	336	ALA
1	E	475	LYS
1	F	87	ASP
1	F	336	ALA
1	F	475	LYS
1	G	87	ASP
1	G	336	ALA
1	G	475	LYS
1	F	3	ALA
1	A	246	PRO
1	B	246	PRO
1	C	246	PRO
1	D	246	PRO
1	F	246	PRO
1	E	246	PRO
1	G	246	PRO
1	F	374	GLY
1	A	374	GLY

### 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	372/421 (88%)	278 (75%)	94 (25%)	0	2
1	B	372/421 (88%)	279 (75%)	93 (25%)	0	2
1	C	372/421 (88%)	277 (74%)	95 (26%)	0	2
1	D	372/421 (88%)	279 (75%)	93 (25%)	0	2
1	E	372/421 (88%)	278 (75%)	94 (25%)	0	2
1	F	372/421 (88%)	278 (75%)	94 (25%)	0	2
1	G	372/421 (88%)	277 (74%)	95 (26%)	0	2
All	All	2604/2947 (88%)	1946 (75%)	658 (25%)	0	2

All (658) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU
1	A	7	LYS
1	A	16	MET
1	A	18	LYS
1	A	28	LYS
1	A	36	ARG
1	A	42	LYS
1	A	51	LYS
1	A	55	SER
1	A	69	MET
1	A	72	GLN
1	A	75	ARG
1	A	76	GLU
1	A	77	VAL
1	A	79	SER
1	A	80	ARG
1	A	83	ASP
1	A	87	ASP
1	A	105	LYS
1	A	132	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	139	ASN
1	A	141	SER
1	A	146	GLN
1	A	155	GLU
1	A	156	SER
1	A	164	GLU
1	A	166	MET
1	A	167	GLN
1	A	168	ARG
1	A	172	GLU
1	A	181	LYS
1	A	183	MET
1	A	196	ASP
1	A	197	ARG
1	A	204	PHE
1	A	206	THR
1	A	209	ASP
1	A	210	LYS
1	A	211	MET
1	A	214	GLU
1	A	216	GLU
1	A	217	ASP
1	A	221	LEU
1	A	222	LEU
1	A	225	LYS
1	A	229	SER
1	A	231	GLN
1	A	245	LYS
1	A	247	LEU
1	A	250	VAL
1	A	252	GLU
1	A	253	ASP
1	A	281	PHE
1	A	283	ASP
1	A	288	MET
1	A	290	GLN
1	A	295	LEU
1	A	315	ASP
1	A	316	MET
1	A	317	LEU
1	A	321	LYS
1	A	322	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	327	LYS
1	A	328	ASP
1	A	333	VAL
1	A	338	GLU
1	A	339	LYS
1	A	343	GLU
1	A	345	ARG
1	A	352	GLN
1	A	357	THR
1	A	362	ARG
1	A	365	LEU
1	A	367	GLU
1	A	368	ARG
1	A	371	LYS
1	A	380	ARG
1	A	387	ILE
1	A	388	GLU
1	A	391	GLU
1	A	395	ARG
1	A	398	ASP
1	A	401	ASN
1	A	408	GLN
1	A	419	LEU
1	A	427	GLU
1	A	430	SER
1	A	434	SER
1	A	436	GLN
1	A	444	ARG
1	A	452	ARG
1	A	473	SER
1	A	524	GLU
1	A	525	LYS
1	B	5	GLU
1	B	7	LYS
1	B	16	MET
1	B	18	LYS
1	B	28	LYS
1	B	36	ARG
1	B	42	LYS
1	B	51	LYS
1	B	55	SER
1	B	69	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	72	GLN
1	B	75	ARG
1	B	76	GLU
1	B	77	VAL
1	B	79	SER
1	B	80	ARG
1	B	83	ASP
1	B	87	ASP
1	B	105	LYS
1	B	132	LYS
1	B	139	ASN
1	B	141	SER
1	B	146	GLN
1	B	155	GLU
1	B	156	SER
1	B	164	GLU
1	B	166	MET
1	B	167	GLN
1	B	168	ARG
1	B	172	GLU
1	B	181	LYS
1	B	183	MET
1	B	196	ASP
1	B	197	ARG
1	B	204	PHE
1	B	206	THR
1	B	209	ASP
1	B	210	LYS
1	B	211	MET
1	B	214	GLU
1	B	216	GLU
1	B	217	ASP
1	B	221	LEU
1	B	222	LEU
1	B	225	LYS
1	B	229	SER
1	B	231	GLN
1	B	245	LYS
1	B	247	LEU
1	B	250	VAL
1	B	252	GLU
1	B	253	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	281	PHE
1	B	283	ASP
1	B	288	MET
1	B	290	GLN
1	B	295	LEU
1	B	315	ASP
1	B	316	MET
1	B	317	LEU
1	B	321	LYS
1	B	322	LYS
1	B	327	LYS
1	B	328	ASP
1	B	333	VAL
1	B	338	GLU
1	B	339	LYS
1	B	343	GLU
1	B	345	ARG
1	B	352	GLN
1	B	357	THR
1	B	362	ARG
1	B	365	LEU
1	B	367	GLU
1	B	368	ARG
1	B	371	LYS
1	B	380	ARG
1	B	387	ILE
1	B	388	GLU
1	B	391	GLU
1	B	395	ARG
1	B	398	ASP
1	B	401	ASN
1	B	408	GLN
1	B	419	LEU
1	B	427	GLU
1	B	430	SER
1	B	434	SER
1	B	436	GLN
1	B	444	ARG
1	B	473	SER
1	B	524	GLU
1	B	525	LYS
1	C	5	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	7	LYS
1	C	16	MET
1	C	18	LYS
1	C	28	LYS
1	C	36	ARG
1	C	42	LYS
1	C	51	LYS
1	C	55	SER
1	C	69	MET
1	C	72	GLN
1	C	75	ARG
1	C	76	GLU
1	C	77	VAL
1	C	79	SER
1	C	80	ARG
1	C	83	ASP
1	C	87	ASP
1	C	105	LYS
1	C	132	LYS
1	C	139	ASN
1	C	141	SER
1	C	146	GLN
1	C	155	GLU
1	C	156	SER
1	C	164	GLU
1	C	166	MET
1	C	167	GLN
1	C	168	ARG
1	C	172	GLU
1	C	181	LYS
1	C	183	MET
1	C	196	ASP
1	C	197	ARG
1	C	204	PHE
1	C	206	THR
1	C	209	ASP
1	C	210	LYS
1	C	211	MET
1	C	214	GLU
1	C	216	GLU
1	C	217	ASP
1	C	221	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	222	LEU
1	C	225	LYS
1	C	229	SER
1	C	231	GLN
1	C	245	LYS
1	C	247	LEU
1	C	250	VAL
1	C	252	GLU
1	C	253	ASP
1	C	281	PHE
1	C	283	ASP
1	C	288	MET
1	C	290	GLN
1	C	295	LEU
1	C	315	ASP
1	C	316	MET
1	C	317	LEU
1	C	321	LYS
1	C	322	LYS
1	C	327	LYS
1	C	328	ASP
1	C	333	VAL
1	C	338	GLU
1	C	339	LYS
1	C	343	GLU
1	C	345	ARG
1	C	352	GLN
1	C	357	THR
1	C	362	ARG
1	C	365	LEU
1	C	367	GLU
1	C	368	ARG
1	C	371	LYS
1	C	380	ARG
1	C	387	ILE
1	C	388	GLU
1	C	391	GLU
1	C	392	ARG
1	C	395	ARG
1	C	398	ASP
1	C	401	ASN
1	C	408	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	419	LEU
1	C	427	GLU
1	C	430	SER
1	C	434	SER
1	C	436	GLN
1	C	444	ARG
1	C	452	ARG
1	C	473	SER
1	C	524	GLU
1	C	525	LYS
1	D	5	GLU
1	D	7	LYS
1	D	16	MET
1	D	18	LYS
1	D	28	LYS
1	D	36	ARG
1	D	42	LYS
1	D	51	LYS
1	D	55	SER
1	D	69	MET
1	D	72	GLN
1	D	75	ARG
1	D	76	GLU
1	D	77	VAL
1	D	79	SER
1	D	80	ARG
1	D	83	ASP
1	D	87	ASP
1	D	105	LYS
1	D	132	LYS
1	D	139	ASN
1	D	141	SER
1	D	146	GLN
1	D	155	GLU
1	D	156	SER
1	D	164	GLU
1	D	166	MET
1	D	167	GLN
1	D	168	ARG
1	D	172	GLU
1	D	181	LYS
1	D	183	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	196	ASP
1	D	197	ARG
1	D	204	PHE
1	D	206	THR
1	D	209	ASP
1	D	210	LYS
1	D	211	MET
1	D	214	GLU
1	D	216	GLU
1	D	217	ASP
1	D	221	LEU
1	D	222	LEU
1	D	225	LYS
1	D	229	SER
1	D	231	GLN
1	D	245	LYS
1	D	247	LEU
1	D	250	VAL
1	D	252	GLU
1	D	253	ASP
1	D	281	PHE
1	D	283	ASP
1	D	288	MET
1	D	290	GLN
1	D	295	LEU
1	D	315	ASP
1	D	316	MET
1	D	317	LEU
1	D	321	LYS
1	D	322	LYS
1	D	327	LYS
1	D	328	ASP
1	D	333	VAL
1	D	338	GLU
1	D	339	LYS
1	D	343	GLU
1	D	345	ARG
1	D	352	GLN
1	D	357	THR
1	D	362	ARG
1	D	365	LEU
1	D	367	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	368	ARG
1	D	371	LYS
1	D	380	ARG
1	D	387	ILE
1	D	388	GLU
1	D	391	GLU
1	D	395	ARG
1	D	398	ASP
1	D	401	ASN
1	D	408	GLN
1	D	419	LEU
1	D	427	GLU
1	D	430	SER
1	D	434	SER
1	D	436	GLN
1	D	444	ARG
1	D	473	SER
1	D	524	GLU
1	D	525	LYS
1	E	5	GLU
1	E	7	LYS
1	E	16	MET
1	E	18	LYS
1	E	28	LYS
1	E	36	ARG
1	E	42	LYS
1	E	51	LYS
1	E	55	SER
1	E	64	ASP
1	E	69	MET
1	E	72	GLN
1	E	75	ARG
1	E	76	GLU
1	E	77	VAL
1	E	79	SER
1	E	80	ARG
1	E	83	ASP
1	E	87	ASP
1	E	105	LYS
1	E	132	LYS
1	E	139	ASN
1	E	141	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	146	GLN
1	E	155	GLU
1	E	156	SER
1	E	164	GLU
1	E	166	MET
1	E	167	GLN
1	E	168	ARG
1	E	172	GLU
1	E	181	LYS
1	E	183	MET
1	E	196	ASP
1	E	197	ARG
1	E	204	PHE
1	E	206	THR
1	E	209	ASP
1	E	210	LYS
1	E	211	MET
1	E	214	GLU
1	E	216	GLU
1	E	217	ASP
1	E	221	LEU
1	E	222	LEU
1	E	225	LYS
1	E	229	SER
1	E	231	GLN
1	E	245	LYS
1	E	247	LEU
1	E	250	VAL
1	E	252	GLU
1	E	253	ASP
1	E	281	PHE
1	E	283	ASP
1	E	288	MET
1	E	290	GLN
1	E	295	LEU
1	E	315	ASP
1	E	316	MET
1	E	317	LEU
1	E	321	LYS
1	E	322	LYS
1	E	327	LYS
1	E	328	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	333	VAL
1	E	338	GLU
1	E	339	LYS
1	E	343	GLU
1	E	345	ARG
1	E	352	GLN
1	E	357	THR
1	E	362	ARG
1	E	365	LEU
1	E	367	GLU
1	E	368	ARG
1	E	371	LYS
1	E	380	ARG
1	E	387	ILE
1	E	388	GLU
1	E	391	GLU
1	E	395	ARG
1	E	398	ASP
1	E	401	ASN
1	E	408	GLN
1	E	419	LEU
1	E	427	GLU
1	E	430	SER
1	E	434	SER
1	E	436	GLN
1	E	444	ARG
1	E	473	SER
1	E	524	GLU
1	E	525	LYS
1	F	5	GLU
1	F	7	LYS
1	F	16	MET
1	F	18	LYS
1	F	28	LYS
1	F	36	ARG
1	F	42	LYS
1	F	51	LYS
1	F	55	SER
1	F	69	MET
1	F	72	GLN
1	F	75	ARG
1	F	76	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	F	77	VAL
1	F	79	SER
1	F	80	ARG
1	F	83	ASP
1	F	87	ASP
1	F	105	LYS
1	F	132	LYS
1	F	139	ASN
1	F	141	SER
1	F	146	GLN
1	F	155	GLU
1	F	156	SER
1	F	164	GLU
1	F	166	MET
1	F	167	GLN
1	F	168	ARG
1	F	172	GLU
1	F	181	LYS
1	F	183	MET
1	F	196	ASP
1	F	197	ARG
1	F	204	PHE
1	F	206	THR
1	F	209	ASP
1	F	210	LYS
1	F	211	MET
1	F	214	GLU
1	F	216	GLU
1	F	217	ASP
1	F	221	LEU
1	F	222	LEU
1	F	225	LYS
1	F	229	SER
1	F	231	GLN
1	F	245	LYS
1	F	247	LEU
1	F	250	VAL
1	F	252	GLU
1	F	253	ASP
1	F	281	PHE
1	F	283	ASP
1	F	288	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	F	290	GLN
1	F	295	LEU
1	F	315	ASP
1	F	316	MET
1	F	317	LEU
1	F	321	LYS
1	F	322	LYS
1	F	327	LYS
1	F	328	ASP
1	F	333	VAL
1	F	338	GLU
1	F	339	LYS
1	F	343	GLU
1	F	345	ARG
1	F	352	GLN
1	F	357	THR
1	F	362	ARG
1	F	365	LEU
1	F	367	GLU
1	F	368	ARG
1	F	371	LYS
1	F	380	ARG
1	F	387	ILE
1	F	388	GLU
1	F	391	GLU
1	F	395	ARG
1	F	398	ASP
1	F	401	ASN
1	F	408	GLN
1	F	419	LEU
1	F	427	GLU
1	F	430	SER
1	F	434	SER
1	F	436	GLN
1	F	444	ARG
1	F	452	ARG
1	F	473	SER
1	F	524	GLU
1	F	525	LYS
1	G	5	GLU
1	G	7	LYS
1	G	10	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	16	MET
1	G	18	LYS
1	G	28	LYS
1	G	36	ARG
1	G	42	LYS
1	G	51	LYS
1	G	55	SER
1	G	69	MET
1	G	72	GLN
1	G	75	ARG
1	G	76	GLU
1	G	77	VAL
1	G	79	SER
1	G	80	ARG
1	G	83	ASP
1	G	87	ASP
1	G	105	LYS
1	G	132	LYS
1	G	139	ASN
1	G	141	SER
1	G	146	GLN
1	G	155	GLU
1	G	156	SER
1	G	164	GLU
1	G	166	MET
1	G	167	GLN
1	G	168	ARG
1	G	172	GLU
1	G	181	LYS
1	G	183	MET
1	G	196	ASP
1	G	197	ARG
1	G	204	PHE
1	G	206	THR
1	G	209	ASP
1	G	210	LYS
1	G	211	MET
1	G	214	GLU
1	G	216	GLU
1	G	217	ASP
1	G	221	LEU
1	G	222	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	225	LYS
1	G	229	SER
1	G	231	GLN
1	G	245	LYS
1	G	247	LEU
1	G	250	VAL
1	G	252	GLU
1	G	253	ASP
1	G	281	PHE
1	G	283	ASP
1	G	288	MET
1	G	290	GLN
1	G	295	LEU
1	G	315	ASP
1	G	316	MET
1	G	317	LEU
1	G	321	LYS
1	G	322	LYS
1	G	327	LYS
1	G	328	ASP
1	G	333	VAL
1	G	338	GLU
1	G	339	LYS
1	G	343	GLU
1	G	345	ARG
1	G	352	GLN
1	G	357	THR
1	G	362	ARG
1	G	365	LEU
1	G	367	GLU
1	G	368	ARG
1	G	371	LYS
1	G	380	ARG
1	G	387	ILE
1	G	388	GLU
1	G	391	GLU
1	G	395	ARG
1	G	398	ASP
1	G	401	ASN
1	G	408	GLN
1	G	419	LEU
1	G	427	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	430	SER
1	G	434	SER
1	G	436	GLN
1	G	444	ARG
1	G	452	ARG
1	G	473	SER
1	G	524	GLU
1	G	525	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	68	ASN
1	A	72	GLN
1	A	97	GLN
1	A	139	ASN
1	A	153	ASN
1	A	194	GLN
1	A	231	GLN
1	A	348	GLN
1	A	352	GLN
1	A	480	ASN
1	B	68	ASN
1	B	72	GLN
1	B	97	GLN
1	B	139	ASN
1	B	153	ASN
1	B	194	GLN
1	B	231	GLN
1	B	348	GLN
1	B	352	GLN
1	B	480	ASN
1	C	37	ASN
1	C	68	ASN
1	C	72	GLN
1	C	97	GLN
1	C	139	ASN
1	C	153	ASN
1	C	194	GLN
1	C	231	GLN
1	C	348	GLN
1	C	352	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	480	ASN
1	D	68	ASN
1	D	72	GLN
1	D	139	ASN
1	D	153	ASN
1	D	194	GLN
1	D	231	GLN
1	D	348	GLN
1	D	352	GLN
1	D	480	ASN
1	E	68	ASN
1	E	72	GLN
1	E	97	GLN
1	E	139	ASN
1	E	153	ASN
1	E	231	GLN
1	E	348	GLN
1	E	352	GLN
1	E	480	ASN
1	F	68	ASN
1	F	72	GLN
1	F	97	GLN
1	F	139	ASN
1	F	153	ASN
1	F	194	GLN
1	F	231	GLN
1	F	348	GLN
1	F	352	GLN
1	F	480	ASN
1	G	68	ASN
1	G	72	GLN
1	G	97	GLN
1	G	139	ASN
1	G	153	ASN
1	G	194	GLN
1	G	231	GLN
1	G	348	GLN
1	G	352	GLN
1	G	480	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

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.