



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 16, 2018 – 07:08 am GMT

PDB ID : 1B3B  
Title : THERMOTOGA MARITIMA GLUTAMATE DEHYDROGENASE MUTANT N97D, G376K  
Authors : Knapp, S.; Lebbink, J.H.G.; Van Der Oost, J.; Devos, W.M.; Rice, D.; Ladenstein, R.  
Deposited on : 1998-12-07  
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

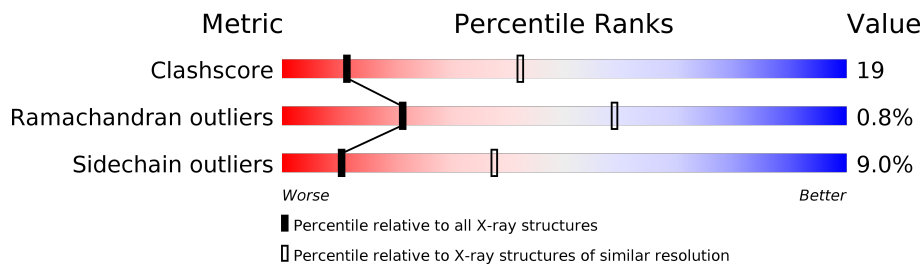
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	122078	1042 (3.10-3.10)
Ramachandran outliers	120005	1010 (3.10-3.10)
Sidechain outliers	119972	1010 (3.10-3.10)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	415	
1	B	415	
1	C	415	
1	D	415	
1	E	415	
1	F	415	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 19008 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 PROTEIN (GLUTAMATE DEHYDROGENASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	B	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	C	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	D	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	E	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	F	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			

There are 12 discrepancies between the modelled and reference sequences:

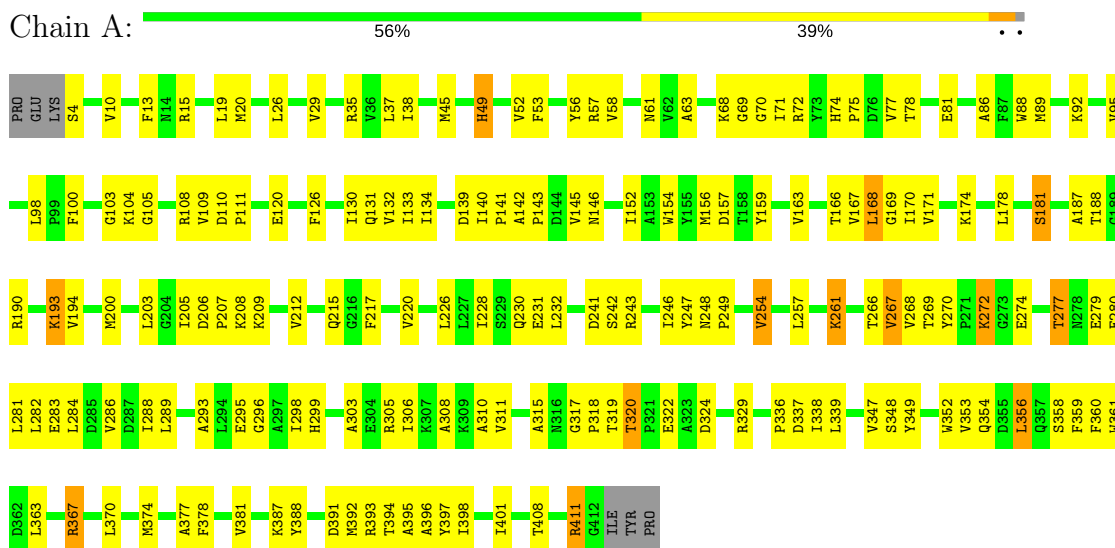
Chain	Residue	Modelled	Actual	Comment	Reference
A	97	ASP	ASN	ENGINEERED	UNP P96110
A	376	LYS	GLY	ENGINEERED	UNP P96110
B	97	ASP	ASN	ENGINEERED	UNP P96110
B	376	LYS	GLY	ENGINEERED	UNP P96110
C	97	ASP	ASN	ENGINEERED	UNP P96110
C	376	LYS	GLY	ENGINEERED	UNP P96110
D	97	ASP	ASN	ENGINEERED	UNP P96110
D	376	LYS	GLY	ENGINEERED	UNP P96110
E	97	ASP	ASN	ENGINEERED	UNP P96110
E	376	LYS	GLY	ENGINEERED	UNP P96110
F	97	ASP	ASN	ENGINEERED	UNP P96110
F	376	LYS	GLY	ENGINEERED	UNP P96110

### 3 Residue-property plots [i](#)

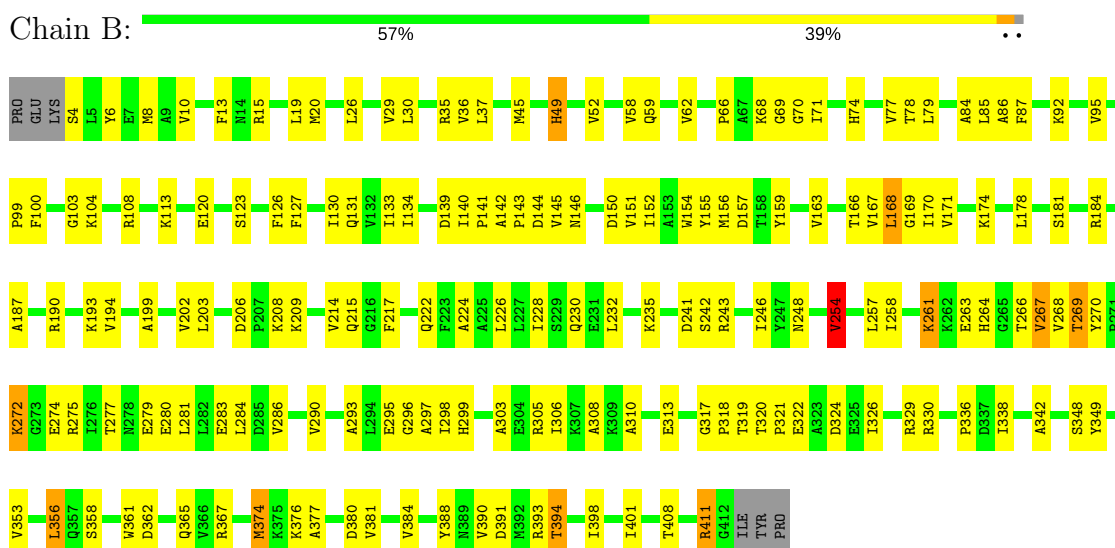
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

Note EDS was not executed.

#### • Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)



#### • Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)



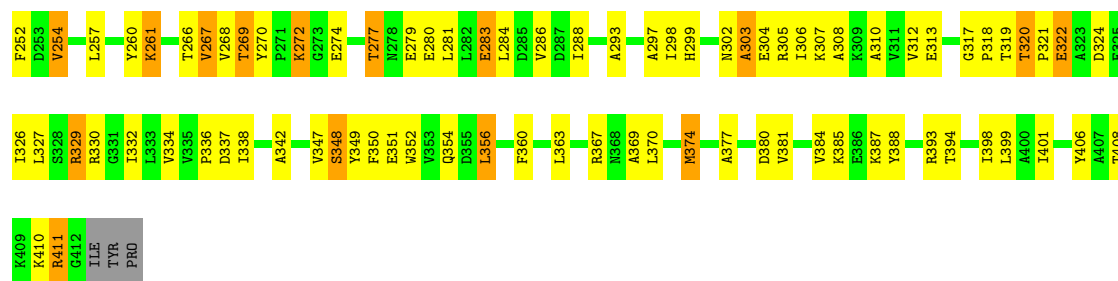
Chain C: 55% ●● 40%

Row	Col 1	Col 2	Col 3	Col 4	Col 5	Col 6	Col 7	Col 8	Col 9	Col 10	Col 11
1	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
2	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
3	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
4	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
5	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
6	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
7	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
8	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
9	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY
10	PRO	GLU	LYS	SER	GLN	GLY	ASP	GLY	GLY	GLY	GLY

Chain D: 57%  39%

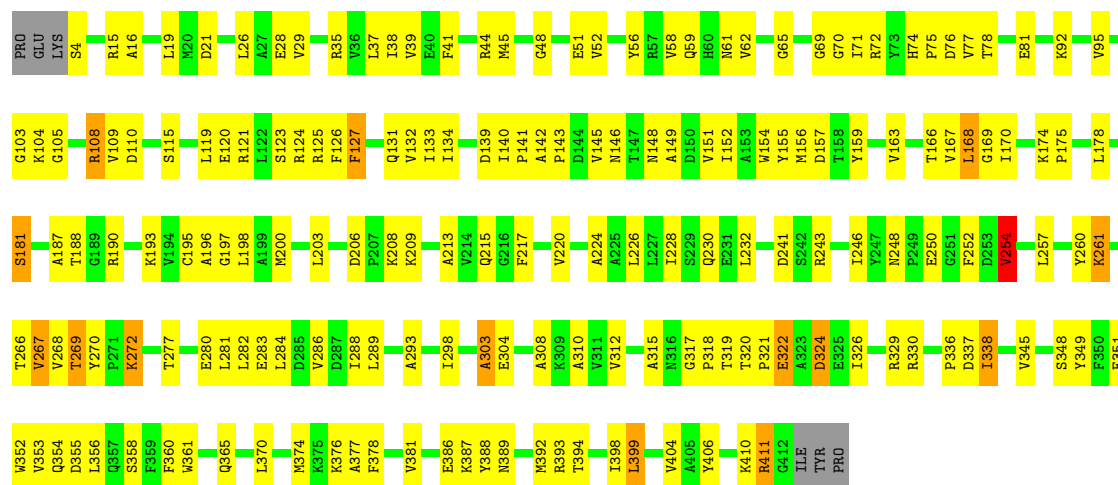
D337	Y260	K174	V95	PRO
I338	K261	L178	G103	GLU
A342	T266	S181	K104	LYS
S348	V268	R184	G105	S4
Q354	T269	A187	R108	Y6
D355	P271	I188	D110	E7
L356	K272	G189	P111	M8
Q357	G273	R190	L114	A9
S358	E274	K193	S115	V10
F359	T277	V194	E118	R15
W361	E280	A196	L119	L19
D362	L281	G197	E120	D21
Q365	T282	M200	L122	L22
V366	E283	D201	R121	L26
R367	L284	V202	F126	A27
M373	T285	L203	F127	E28
K387	D287	D206	I130	V29
Y388	L293	K208	Q131	L30
R393	E294	K209	I133	R31
Y397	E295	Q215	I134	R32
Y406	L298	G216	D139	R35
A407	H299	P217	I140	V36
T408	A303	V220	P141	L37
K409	E304	L226	A142	R44
K410	R305	L227	D144	F53
R411	L306	I228	N146	V58
G412	K307	S229	T147	Q59
ILE	A308	Q230	D150	H60
TYR	V312	E231	V151	N61
PRO	E313	L232	I154	V62
	N316	S240	M155	A63
	G317	D241	D157	K68
	P318	R243	I158	G69
	T320	I246	Y159	G70
	P321	Y247	V163	I71
	E322	N248	T166	R72
	A323	E250	L168	Y73
	D324	G251	G169	H74
	E325	P252	I170	P75
	L326	V254	V171	D76
	L327	L257		V77
	R330			T78
	G331			A86
	L332			F87
	P336			W88
				Y90

[illegible]



• Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)

Chain F: 55% 40%



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	145.10 Å   145.10 Å   272.50 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	8.00 – 3.10	Depositor
% Data completeness (in resolution range)	94.0 (8.00-3.10)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, $R_{free}$	0.225 , 0.298	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	19008	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	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	0.34	0/3227	0.53	0/4367
1	B	0.33	0/3227	0.52	0/4367
1	C	0.33	0/3227	0.51	0/4367
1	D	0.31	0/3227	0.51	0/4367
1	E	0.35	0/3227	0.53	0/4367
1	F	0.33	0/3227	0.51	1/4367 (0.0%)
All	All	0.33	0/19362	0.52	1/26202 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	168	LEU	CA-CB-CG	5.21	127.29	115.30

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	3168	0	3192	118	18
1	B	3168	0	3192	117	20
1	C	3168	0	3192	114	2
1	D	3168	0	3192	124	2
1	E	3168	0	3192	139	18
1	F	3168	0	3192	123	20

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	19008	0	19152	722	40

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 19.

All (722) 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:E:248:ASN:HD21	1:E:272:LYS:HE2	1.22	1.03
1:F:248:ASN:HD21	1:F:272:LYS:HE2	1.32	0.95
1:A:248:ASN:HD21	1:A:272:LYS:HE2	1.38	0.88
1:E:224:ALA:O	1:E:228:ILE:HG13	1.74	0.88
1:C:354:GLN:HG2	1:C:360:PHE:HA	1.55	0.87
1:C:261:LYS:HG3	1:C:267:VAL:HG13	1.62	0.82
1:D:387:LYS:HE2	1:D:388:TYR:HE2	1.43	0.82
1:E:69:GLY:HA3	1:E:103:GLY:O	1.80	0.81
1:C:134:ILE:HG22	1:C:139:ASP:HB3	1.63	0.81
1:B:26:LEU:O	1:B:29:VAL:HG22	1.81	0.80
1:B:35:ARG:HH11	1:B:133:ILE:HG23	1.46	0.80
1:C:248:ASN:HD21	1:C:272:LYS:HE2	1.45	0.80
1:A:298:ILE:HB	1:A:319:THR:HG22	1.65	0.79
1:B:35:ARG:NH1	1:B:133:ILE:HG23	1.98	0.78
1:A:354:GLN:HG2	1:A:360:PHE:HA	1.64	0.78
1:A:69:GLY:HA3	1:A:103:GLY:O	1.83	0.78
1:F:69:GLY:HA3	1:F:103:GLY:O	1.84	0.78
1:E:35:ARG:HH11	1:E:133:ILE:HG23	1.47	0.78
1:B:15:ARG:O	1:B:19:LEU:HD23	1.85	0.77
1:E:200:MET:HG3	1:E:288:ILE:HD11	1.68	0.76
1:D:200:MET:HG3	1:D:288:ILE:HD11	1.68	0.76
1:F:200:MET:HG3	1:F:288:ILE:HD11	1.68	0.76
1:A:188:THR:HG21	1:A:220:VAL:HG22	1.68	0.76
1:D:134:ILE:HG22	1:D:139:ASP:HB3	1.68	0.75
1:A:71:ILE:HD13	1:A:126:PHE:HE2	1.51	0.75
1:B:411:ARG:HH11	1:B:411:ARG:HG2	1.51	0.75
1:A:397:TYR:O	1:A:401:ILE:HG13	1.86	0.75
1:D:298:ILE:HB	1:D:319:THR:HG22	1.68	0.74
1:D:354:GLN:HG2	1:D:360:PHE:HA	1.68	0.74
1:E:26:LEU:O	1:E:29:VAL:HG22	1.87	0.74
1:F:298:ILE:HB	1:F:319:THR:HG22	1.69	0.74
1:E:354:GLN:HG2	1:E:360:PHE:HA	1.68	0.74
1:A:159:TYR:O	1:A:163:VAL:HG23	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ASN:HD21	1:B:272:LYS:HE2	1.52	0.73
1:B:261:LYS:HG3	1:B:267:VAL:HG13	1.68	0.73
1:D:69:GLY:HA3	1:D:103:GLY:O	1.89	0.72
1:D:68:LYS:HZ3	1:D:140:ILE:HG22	1.54	0.72
1:C:74:HIS:HB3	1:C:77:VAL:HG23	1.71	0.72
1:C:240:SER:HB3	1:C:281:LEU:HD13	1.72	0.71
1:C:69:GLY:HA3	1:C:103:GLY:O	1.89	0.71
1:E:246:ILE:HD11	1:E:257:LEU:HD21	1.72	0.71
1:F:399:LEU:HD12	1:F:399:LEU:O	1.90	0.71
1:C:59:GLN:NE2	1:C:133:ILE:HG22	2.05	0.70
1:B:159:TYR:O	1:B:163:VAL:HG23	1.92	0.70
1:D:71:ILE:HD13	1:D:126:PHE:HE2	1.55	0.70
1:F:143:PRO:HD3	1:F:152:ILE:HG13	1.73	0.70
1:E:74:HIS:HB3	1:E:77:VAL:HG23	1.74	0.70
1:F:261:LYS:HG3	1:F:267:VAL:HG13	1.72	0.70
1:D:184:ARG:HG2	1:D:184:ARG:HH11	1.56	0.69
1:A:277:THR:HG22	1:A:280:GLU:OE1	1.92	0.69
1:A:37:LEU:HD22	1:A:133:ILE:HD12	1.72	0.69
1:B:37:LEU:HD13	1:B:133:ILE:HD11	1.75	0.69
1:E:215:GLN:HE22	1:E:297:ALA:HB1	1.57	0.69
1:B:69:GLY:HA3	1:B:103:GLY:O	1.92	0.69
1:B:214:VAL:HG22	1:B:290:VAL:HB	1.73	0.69
1:E:92:LYS:O	1:E:95:VAL:HG12	1.93	0.69
1:A:142:ALA:HB1	1:A:143:PRO:HD2	1.74	0.68
1:E:134:ILE:HG22	1:E:139:ASP:HB3	1.73	0.68
1:B:74:HIS:HB3	1:B:77:VAL:HG23	1.73	0.68
1:E:377:ALA:O	1:E:381:VAL:HG23	1.93	0.68
1:C:190:ARG:O	1:C:194:VAL:HG23	1.94	0.67
1:C:224:ALA:O	1:C:228:ILE:HG13	1.93	0.67
1:F:142:ALA:HB1	1:F:143:PRO:HD2	1.77	0.67
1:B:298:ILE:HB	1:B:319:THR:HG22	1.76	0.67
1:C:159:TYR:O	1:C:163:VAL:HG23	1.93	0.67
1:A:134:ILE:HG22	1:A:139:ASP:HB3	1.77	0.67
1:C:59:GLN:HE22	1:C:133:ILE:HG22	1.60	0.66
1:E:170:ILE:HG23	1:E:171:VAL:HG13	1.76	0.66
1:A:68:LYS:NZ	1:A:140:ILE:HG22	2.10	0.66
1:F:215:GLN:OE1	1:F:293:ALA:HB3	1.95	0.66
1:B:141:PRO:HD2	1:B:170:ILE:O	1.96	0.66
1:F:377:ALA:O	1:F:381:VAL:HG23	1.94	0.66
1:E:215:GLN:OE1	1:E:293:ALA:HB3	1.96	0.65
1:D:159:TYR:O	1:D:163:VAL:HG23	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:248:ASN:ND2	1:E:272:LYS:HE2	2.04	0.65
1:B:215:GLN:OE1	1:B:293:ALA:HB3	1.96	0.65
1:B:134:ILE:HG22	1:B:139:ASP:HB3	1.78	0.65
1:B:246:ILE:HD11	1:B:257:LEU:HD21	1.79	0.65
1:E:203:LEU:HD11	1:E:310:ALA:HB2	1.80	0.64
1:E:200:MET:CG	1:E:288:ILE:HD11	2.28	0.64
1:B:349:TYR:O	1:B:353:VAL:HG23	1.98	0.64
1:B:190:ARG:O	1:B:194:VAL:HG23	1.98	0.64
1:D:248:ASN:HD21	1:D:272:LYS:HE2	1.62	0.64
1:F:246:ILE:HD11	1:F:257:LEU:HD21	1.78	0.64
1:F:159:TYR:O	1:F:163:VAL:HG23	1.98	0.64
1:D:174:LYS:HB2	1:D:174:LYS:HZ3	1.63	0.64
1:A:86:ALA:HB2	1:A:104:LYS:HB2	1.80	0.63
1:A:377:ALA:O	1:A:381:VAL:HG23	1.98	0.63
1:C:71:ILE:HD13	1:C:126:PHE:HE2	1.63	0.63
1:B:71:ILE:HD13	1:B:126:PHE:HE2	1.63	0.63
1:E:277:THR:HG22	1:E:280:GLU:OE1	1.97	0.63
1:C:215:GLN:OE1	1:C:293:ALA:HB3	1.98	0.63
1:D:15:ARG:O	1:D:19:LEU:HD23	1.98	0.63
1:A:317:GLY:N	1:A:318:PRO:HD3	2.13	0.63
1:B:203:LEU:HD11	1:B:310:ALA:HB2	1.81	0.62
1:F:148:ASN:OD1	1:F:151:VAL:HG23	2.00	0.62
1:B:313:GLU:OE1	1:B:318:PRO:HD2	2.00	0.62
1:F:349:TYR:O	1:F:353:VAL:HG23	2.00	0.62
1:C:248:ASN:OD1	1:C:250:GLU:HB2	2.00	0.62
1:C:141:PRO:HD2	1:C:170:ILE:O	2.00	0.62
1:D:59:GLN:NE2	1:D:133:ILE:HG22	2.13	0.62
1:B:59:GLN:NE2	1:B:133:ILE:HG22	2.14	0.61
1:E:261:LYS:HG3	1:E:267:VAL:HG13	1.82	0.61
1:D:246:ILE:HD11	1:D:257:LEU:HD21	1.82	0.61
1:E:196:ALA:HA	1:E:312:VAL:HG21	1.81	0.61
1:F:200:MET:HG3	1:F:288:ILE:CD1	2.30	0.61
1:C:247:TYR:CE2	1:C:249:PRO:HD3	2.34	0.61
1:E:37:LEU:HD22	1:E:133:ILE:HD12	1.82	0.61
1:A:157:ASP:OD1	1:B:411:ARG:NH1	2.34	0.61
1:D:36:VAL:HG13	1:D:58:VAL:HG22	1.81	0.61
1:F:354:GLN:HG2	1:F:360:PHE:HA	1.82	0.61
1:B:13:PHE:HE1	1:B:401:ILE:HG12	1.65	0.61
1:C:200:MET:HG3	1:C:288:ILE:HD11	1.82	0.61
1:C:35:ARG:HH11	1:C:133:ILE:HG23	1.66	0.60
1:D:281:LEU:HA	1:D:284:LEU:HG	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:246:ILE:HD11	1:C:257:LEU:HD21	1.84	0.60
1:E:243:ARG:HD3	1:E:266:THR:HG21	1.84	0.60
1:E:281:LEU:HA	1:E:284:LEU:HG	1.83	0.60
1:C:228:ILE:O	1:C:232:LEU:HB2	2.00	0.60
1:D:387:LYS:HE2	1:D:388:TYR:CE2	2.32	0.60
1:B:377:ALA:O	1:B:381:VAL:HG23	2.02	0.60
1:D:184:ARG:NH1	1:D:184:ARG:HG2	2.17	0.60
1:E:71:ILE:HD13	1:E:126:PHE:HE2	1.65	0.59
1:E:199:ALA:O	1:E:203:LEU:HG	2.02	0.59
1:C:203:LEU:HD11	1:C:310:ALA:HB2	1.84	0.59
1:E:142:ALA:HB1	1:E:143:PRO:HD2	1.84	0.59
1:A:167:VAL:HG12	1:A:169:GLY:H	1.68	0.59
1:B:127:PHE:CZ	1:B:141:PRO:HG2	2.38	0.59
1:B:86:ALA:HB2	1:B:104:LYS:HB2	1.85	0.59
1:E:317:GLY:N	1:E:318:PRO:HD3	2.18	0.59
1:E:62:VAL:O	1:E:62:VAL:HG12	2.03	0.59
1:D:228:ILE:O	1:D:232:LEU:HB2	2.02	0.59
1:E:35:ARG:NH1	1:E:133:ILE:HG23	2.16	0.59
1:A:74:HIS:HB3	1:A:77:VAL:HG23	1.85	0.59
1:B:13:PHE:CE1	1:B:401:ILE:HG12	2.38	0.59
1:B:156:MET:CG	1:B:168:LEU:HA	2.33	0.58
1:B:326:ILE:O	1:B:330:ARG:HG3	2.03	0.58
1:D:167:VAL:HG12	1:D:169:GLY:H	1.67	0.58
1:C:142:ALA:HB1	1:C:143:PRO:HD2	1.86	0.58
1:F:317:GLY:N	1:F:318:PRO:HD3	2.19	0.58
1:D:241:ASP:C	1:D:243:ARG:H	2.08	0.58
1:B:336:PRO:HB3	1:B:393:ARG:HA	1.86	0.57
1:B:411:ARG:NH1	1:B:411:ARG:HG2	2.14	0.57
1:F:15:ARG:O	1:F:19:LEU:HD23	2.03	0.57
1:D:326:ILE:O	1:D:330:ARG:HG3	2.04	0.57
1:E:313:GLU:OE1	1:E:318:PRO:HD2	2.05	0.57
1:B:127:PHE:CE1	1:B:141:PRO:HG2	2.39	0.57
1:D:74:HIS:HB3	1:D:77:VAL:HG23	1.86	0.57
1:E:120:GLU:HG3	1:E:154:TRP:CD2	2.40	0.57
1:E:141:PRO:HD2	1:E:170:ILE:O	2.05	0.57
1:E:399:LEU:HD12	1:E:399:LEU:O	2.04	0.57
1:A:53:PHE:HE2	1:A:109:VAL:HG23	1.69	0.57
1:B:277:THR:HG22	1:B:280:GLU:OE1	2.03	0.57
1:F:226:LEU:N	1:F:254:VAL:HG11	2.19	0.57
1:B:92:LYS:O	1:B:95:VAL:HG12	2.05	0.57
1:D:215:GLN:OE1	1:D:293:ALA:HB3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:336:PRO:HB3	1:D:393:ARG:HA	1.85	0.57
1:F:241:ASP:C	1:F:243:ARG:H	2.08	0.57
1:B:4:SER:O	1:B:8:MET:HG3	2.05	0.57
1:D:200:MET:HE2	1:D:288:ILE:HD13	1.86	0.57
1:E:127:PHE:CE1	1:E:141:PRO:HG2	2.40	0.57
1:F:361:TRP:HB3	1:F:365:GLN:CD	2.25	0.57
1:C:226:LEU:O	1:C:230:GLN:HG3	2.05	0.56
1:F:131:GLN:HA	1:F:134:ILE:CG1	2.35	0.56
1:C:326:ILE:O	1:C:330:ARG:HG3	2.04	0.56
1:C:45:MET:HG3	1:C:49:HIS:CE1	2.41	0.56
1:E:71:ILE:HA	1:E:105:GLY:O	2.06	0.56
1:B:131:GLN:NE2	1:B:159:TYR:HD2	2.03	0.56
1:C:145:VAL:O	1:C:146:ASN:HB2	2.05	0.56
1:C:354:GLN:HG2	1:C:359:PHE:O	2.06	0.56
1:F:74:HIS:HB3	1:F:77:VAL:HG23	1.87	0.56
1:A:228:ILE:O	1:A:232:LEU:HB2	2.05	0.56
1:C:391:ASP:HB3	1:C:394:THR:OG1	2.05	0.56
1:D:142:ALA:HB1	1:D:143:PRO:HD2	1.86	0.56
1:D:226:LEU:N	1:D:254:VAL:HG11	2.21	0.56
1:E:131:GLN:HA	1:E:134:ILE:CG1	2.36	0.56
1:F:74:HIS:HB3	1:F:77:VAL:CG2	2.35	0.56
1:B:131:GLN:HA	1:B:134:ILE:CG1	2.36	0.56
1:C:298:ILE:HB	1:C:319:THR:HG22	1.87	0.56
1:D:226:LEU:O	1:D:230:GLN:HG3	2.05	0.56
1:C:127:PHE:CD1	1:C:130:ILE:HD11	2.41	0.56
1:F:196:ALA:HA	1:F:312:VAL:HG21	1.87	0.56
1:A:26:LEU:O	1:A:29:VAL:HG22	2.06	0.56
1:F:277:THR:HG22	1:F:280:GLU:OE1	2.06	0.56
1:B:120:GLU:HG3	1:B:154:TRP:CE2	2.41	0.56
1:B:74:HIS:HB3	1:B:77:VAL:CG2	2.35	0.56
1:A:15:ARG:O	1:A:19:LEU:HD23	2.06	0.55
1:A:241:ASP:C	1:A:243:ARG:H	2.09	0.55
1:D:406:TYR:OH	1:D:410:LYS:HE2	2.06	0.55
1:A:298:ILE:CB	1:A:319:THR:HG22	2.36	0.55
1:D:92:LYS:O	1:D:95:VAL:HG12	2.06	0.55
1:F:174:LYS:NZ	1:F:355:ASP:OD2	2.39	0.55
1:A:352:TRP:O	1:A:356:LEU:HD22	2.06	0.55
1:C:37:LEU:HD22	1:C:133:ILE:CD1	2.37	0.55
1:E:194:VAL:HG11	1:E:374:MET:HB3	1.88	0.55
1:D:411:ARG:NH1	1:F:157:ASP:OD1	2.39	0.55
1:F:282:LEU:HD23	1:F:289:LEU:HD11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:ILE:HA	1:A:139:ASP:HB3	1.89	0.55
1:C:15:ARG:O	1:C:19:LEU:HD23	2.06	0.55
1:E:336:PRO:HB3	1:E:393:ARG:HA	1.88	0.55
1:C:148:ASN:OD1	1:C:150:ASP:HB2	2.07	0.55
1:F:71:ILE:HA	1:F:105:GLY:O	2.06	0.55
1:A:336:PRO:HB3	1:A:393:ARG:HA	1.89	0.55
1:A:212:VAL:HG22	1:A:288:ILE:HB	1.88	0.55
1:C:86:ALA:HB2	1:C:104:LYS:HB2	1.88	0.55
1:F:336:PRO:HB3	1:F:393:ARG:HA	1.88	0.55
1:B:243:ARG:HD3	1:B:266:THR:HG21	1.88	0.54
1:C:260:TYR:OH	1:C:269:THR:HB	2.07	0.54
1:D:188:THR:HG21	1:D:220:VAL:HG22	1.88	0.54
1:D:226:LEU:CA	1:D:254:VAL:HG11	2.37	0.54
1:A:246:ILE:HD11	1:A:257:LEU:HD21	1.88	0.54
1:C:26:LEU:O	1:C:29:VAL:HG22	2.07	0.54
1:D:68:LYS:NZ	1:D:140:ILE:O	2.36	0.54
1:D:145:VAL:O	1:D:146:ASN:HB2	2.07	0.54
1:F:167:VAL:HG12	1:F:169:GLY:H	1.72	0.54
1:A:248:ASN:ND2	1:A:272:LYS:HE2	2.16	0.54
1:A:347:VAL:HG23	1:A:370:LEU:HD13	1.88	0.54
1:B:241:ASP:C	1:B:243:ARG:H	2.11	0.54
1:B:269:THR:HA	1:B:275:ARG:NH2	2.23	0.54
1:C:336:PRO:HB3	1:C:393:ARG:HA	1.89	0.54
1:D:261:LYS:HG3	1:D:267:VAL:HG13	1.88	0.54
1:F:387:LYS:HE2	1:F:388:TYR:HE2	1.72	0.54
1:A:132:VAL:HG12	1:F:132:VAL:HG12	1.87	0.54
1:A:20:MET:SD	1:A:398:ILE:HG23	2.47	0.54
1:A:248:ASN:HD21	1:A:272:LYS:CE	2.17	0.54
1:C:317:GLY:N	1:C:318:PRO:HD3	2.23	0.54
1:A:152:ILE:HG22	1:A:174:LYS:HG2	1.89	0.54
1:A:92:LYS:O	1:A:95:VAL:HG12	2.08	0.54
1:D:209:LYS:O	1:D:209:LYS:HG2	2.08	0.54
1:F:226:LEU:HA	1:F:254:VAL:HG11	1.90	0.54
1:C:127:PHE:CE1	1:C:141:PRO:HG2	2.43	0.54
1:C:45:MET:HE3	1:C:51:GLU:HB3	1.90	0.54
1:D:20:MET:CE	1:D:22:LEU:HD13	2.38	0.54
1:E:15:ARG:O	1:E:19:LEU:HD23	2.08	0.54
1:E:159:TYR:O	1:E:163:VAL:HG23	2.07	0.54
1:F:224:ALA:O	1:F:228:ILE:HG13	2.08	0.54
1:F:248:ASN:ND2	1:F:272:LYS:HE2	2.14	0.54
1:B:145:VAL:O	1:B:146:ASN:HB2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:399:LEU:HD12	1:C:399:LEU:O	2.07	0.53
1:F:246:ILE:HD12	1:F:252:PHE:CE2	2.43	0.53
1:F:315:ALA:HB3	1:F:318:PRO:HG3	1.89	0.53
1:C:159:TYR:CE1	1:C:170:ILE:HD13	2.44	0.53
1:C:241:ASP:C	1:C:243:ARG:H	2.10	0.53
1:E:87:PHE:CE2	1:E:91:TRP:NE1	2.70	0.53
1:F:209:LYS:HG2	1:F:209:LYS:O	2.08	0.53
1:D:240:SER:HB3	1:D:281:LEU:HD13	1.90	0.53
1:D:196:ALA:HA	1:D:312:VAL:HG21	1.89	0.53
1:D:141:PRO:HD2	1:D:170:ILE:O	2.09	0.53
1:A:141:PRO:HD2	1:A:170:ILE:O	2.08	0.53
1:D:68:LYS:NZ	1:D:140:ILE:HG22	2.21	0.53
1:D:127:PHE:CE1	1:D:141:PRO:HG2	2.42	0.53
1:B:317:GLY:N	1:B:318:PRO:HD3	2.24	0.53
1:B:194:VAL:HG11	1:B:374:MET:HB3	1.91	0.53
1:E:380:ASP:O	1:E:384:VAL:HG23	2.09	0.53
1:D:130:ILE:O	1:D:134:ILE:HG12	2.09	0.53
1:F:45:MET:HE3	1:F:51:GLU:HB3	1.91	0.53
1:F:74:HIS:CE1	1:F:76:ASP:HB2	2.44	0.53
1:D:4:SER:O	1:D:8:MET:HG3	2.08	0.53
1:F:197:GLY:O	1:F:200:MET:HB2	2.09	0.53
1:F:226:LEU:CA	1:F:254:VAL:HG11	2.39	0.53
1:C:35:ARG:NH1	1:C:133:ILE:HG23	2.24	0.53
1:D:317:GLY:N	1:D:318:PRO:HD3	2.23	0.53
1:F:228:ILE:O	1:F:232:LEU:HB2	2.09	0.53
1:A:281:LEU:HA	1:A:284:LEU:HG	1.90	0.53
1:E:209:LYS:HG2	1:E:209:LYS:O	2.09	0.53
1:F:92:LYS:HD3	1:F:345:VAL:HG21	1.91	0.53
1:F:72:ARG:NH1	1:F:81:GLU:OE2	2.41	0.53
1:F:92:LYS:O	1:F:95:VAL:HG12	2.09	0.53
1:C:92:LYS:O	1:C:95:VAL:HG12	2.08	0.52
1:D:200:MET:CG	1:D:288:ILE:HD11	2.39	0.52
1:E:66:PRO:HD2	1:E:99:PRO:O	2.08	0.52
1:A:241:ASP:OD2	1:A:266:THR:HA	2.08	0.52
1:A:215:GLN:OE1	1:A:293:ALA:HB3	2.09	0.52
1:B:142:ALA:HB1	1:B:143:PRO:HD2	1.92	0.52
1:C:281:LEU:HA	1:C:284:LEU:HG	1.90	0.52
1:E:321:PRO:HG2	1:E:322:GLU:OE2	2.08	0.52
1:E:241:ASP:C	1:E:243:ARG:H	2.11	0.52
1:E:247:TYR:CE2	1:E:249:PRO:HD3	2.43	0.52
1:F:134:ILE:HG22	1:F:139:ASP:HB3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:PHE:HE1	1:B:349:TYR:HB2	1.75	0.52
1:B:222:GLN:OE1	1:B:258:ILE:HG12	2.10	0.52
1:B:29:VAL:HG23	1:B:30:LEU:HD23	1.91	0.52
1:C:10:VAL:O	1:C:13:PHE:HB3	2.10	0.52
1:E:326:ILE:O	1:E:330:ARG:HG3	2.09	0.52
1:A:354:GLN:HG2	1:A:359:PHE:O	2.09	0.52
1:C:100:PHE:HE1	1:C:349:TYR:HB2	1.74	0.52
1:C:277:THR:HG22	1:C:280:GLU:OE1	2.09	0.52
1:D:127:PHE:CZ	1:D:141:PRO:HG2	2.45	0.52
1:E:61:ASN:HD21	1:E:63:ALA:HB3	1.75	0.52
1:F:71:ILE:HD13	1:F:126:PHE:HE2	1.74	0.52
1:C:37:LEU:HD22	1:C:133:ILE:HG13	1.91	0.52
1:C:240:SER:HB3	1:C:281:LEU:CD1	2.39	0.52
1:E:120:GLU:HG3	1:E:154:TRP:CE2	2.45	0.52
1:B:20:MET:SD	1:B:398:ILE:HG23	2.50	0.52
1:D:226:LEU:HA	1:D:254:VAL:HG11	1.92	0.52
1:A:156:MET:CG	1:A:168:LEU:HA	2.40	0.52
1:B:298:ILE:HG23	1:B:306:ILE:HD11	1.92	0.52
1:B:52:VAL:HG22	1:E:29:VAL:HG12	1.92	0.52
1:A:57:ARG:HD2	1:A:104:LYS:O	2.10	0.51
1:E:241:ASP:OD2	1:E:266:THR:HA	2.10	0.51
1:E:44:ARG:NH1	1:E:48:GLY:O	2.42	0.51
1:E:79:LEU:HG	1:E:83:LYS:HE3	1.91	0.51
1:A:71:ILE:HA	1:A:105:GLY:O	2.10	0.51
1:C:13:PHE:CE1	1:C:401:ILE:HG12	2.45	0.51
1:E:72:ARG:NH1	1:E:81:GLU:OE2	2.44	0.51
1:F:281:LEU:HA	1:F:284:LEU:CD1	2.40	0.51
1:B:184:ARG:HH11	1:B:184:ARG:HG2	1.75	0.51
1:B:224:ALA:O	1:B:228:ILE:HG13	2.11	0.51
1:C:131:GLN:HA	1:C:134:ILE:CG1	2.41	0.51
1:D:131:GLN:HA	1:D:134:ILE:HD11	1.92	0.51
1:E:190:ARG:O	1:E:194:VAL:HG23	2.11	0.51
1:D:168:LEU:O	1:D:174:LYS:HE3	2.10	0.51
1:A:61:ASN:HD21	1:A:63:ALA:HB3	1.75	0.51
1:B:37:LEU:HB2	1:B:133:ILE:CD1	2.41	0.51
1:B:228:ILE:O	1:B:232:LEU:HB2	2.11	0.51
1:D:131:GLN:HA	1:D:134:ILE:CG1	2.41	0.51
1:F:260:TYR:OH	1:F:269:THR:HB	2.11	0.51
1:F:281:LEU:HA	1:F:284:LEU:HD12	1.93	0.51
1:F:326:ILE:O	1:F:330:ARG:HG3	2.10	0.51
1:A:286:VAL:O	1:A:308:ALA:HA	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:GLY:HA2	1:C:142:ALA:O	2.10	0.50
1:F:134:ILE:HA	1:F:139:ASP:HB3	1.93	0.50
1:F:59:GLN:NE2	1:F:139:ASP:HB2	2.26	0.50
1:A:143:PRO:HD3	1:A:152:ILE:HG13	1.92	0.50
1:A:71:ILE:HD13	1:A:126:PHE:CE2	2.40	0.50
1:C:167:VAL:O	1:C:168:LEU:HG	2.11	0.50
1:D:88:TRP:HZ3	1:D:397:TYR:CE1	2.29	0.50
1:E:131:GLN:HA	1:E:134:ILE:HD11	1.92	0.50
1:F:59:GLN:HE21	1:F:139:ASP:HB2	1.75	0.50
1:C:71:ILE:HA	1:C:105:GLY:O	2.10	0.50
1:C:109:VAL:HG21	1:C:114:LEU:HD11	1.92	0.50
1:D:247:TYR:CE2	1:D:249:PRO:HD3	2.47	0.50
1:B:100:PHE:CE1	1:B:349:TYR:HB2	2.47	0.50
1:C:321:PRO:O	1:C:324:ASP:HB2	2.12	0.50
1:F:141:PRO:HD2	1:F:170:ILE:O	2.11	0.50
1:E:298:ILE:HG12	1:E:306:ILE:HD11	1.92	0.50
1:A:131:GLN:HA	1:A:134:ILE:CG1	2.41	0.50
1:D:190:ARG:O	1:D:194:VAL:HG23	2.10	0.50
1:E:226:LEU:O	1:E:230:GLN:HG3	2.11	0.50
1:F:58:VAL:O	1:F:103:GLY:HA2	2.12	0.50
1:B:66:PRO:HD2	1:B:99:PRO:O	2.12	0.50
1:E:298:ILE:HG12	1:E:306:ILE:CD1	2.42	0.50
1:F:336:PRO:CD	1:F:392:MET:HG2	2.42	0.50
1:C:241:ASP:OD2	1:C:266:THR:HA	2.11	0.49
1:D:134:ILE:HA	1:D:139:ASP:HB3	1.94	0.49
1:F:406:TYR:OH	1:F:410:LYS:HE2	2.12	0.49
1:A:387:LYS:HE2	1:A:388:TYR:HE2	1.77	0.49
1:C:199:ALA:O	1:C:203:LEU:HG	2.11	0.49
1:B:152:ILE:HG22	1:B:174:LYS:HG2	1.95	0.49
1:D:241:ASP:OD2	1:D:266:THR:HA	2.11	0.49
1:D:35:ARG:HH11	1:D:133:ILE:HG23	1.75	0.49
1:E:13:PHE:CE1	1:E:401:ILE:HG12	2.46	0.49
1:B:68:LYS:NZ	1:B:140:ILE:HG22	2.27	0.49
1:E:13:PHE:HE1	1:E:401:ILE:HG12	1.78	0.49
1:F:35:ARG:NH1	1:F:59:GLN:OE1	2.45	0.49
1:A:145:VAL:O	1:A:146:ASN:HB2	2.12	0.49
1:B:131:GLN:HE21	1:B:159:TYR:HD2	1.60	0.49
1:F:44:ARG:NH1	1:F:48:GLY:O	2.45	0.49
1:C:209:LYS:HG2	1:C:209:LYS:O	2.13	0.49
1:D:313:GLU:OE1	1:D:318:PRO:HD2	2.12	0.49
1:D:44:ARG:NH1	1:D:48:GLY:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:HIS:CG	1:A:75:PRO:HD2	2.48	0.49
1:E:228:ILE:O	1:E:232:LEU:HB2	2.12	0.49
1:B:70:GLY:HA2	1:B:142:ALA:O	2.12	0.49
1:E:338:ILE:O	1:E:342:ALA:HB2	2.12	0.49
1:E:387:LYS:HE2	1:E:388:TYR:HE2	1.77	0.49
1:F:203:LEU:HD11	1:F:310:ALA:HB2	1.95	0.49
1:B:58:VAL:O	1:B:103:GLY:HA2	2.12	0.48
1:C:269:THR:HA	1:C:275:ARG:NH2	2.27	0.48
1:C:13:PHE:HE1	1:C:401:ILE:HG12	1.78	0.48
1:E:321:PRO:O	1:E:324:ASP:HB2	2.12	0.48
1:E:140:ILE:HD13	1:E:352:TRP:CD1	2.48	0.48
1:D:174:LYS:HB2	1:D:174:LYS:NZ	2.25	0.48
1:E:53:PHE:HE2	1:E:109:VAL:HG23	1.79	0.48
1:D:26:LEU:O	1:D:29:VAL:HG22	2.14	0.48
1:A:100:PHE:HE1	1:A:349:TYR:HB2	1.79	0.48
1:A:130:ILE:O	1:A:134:ILE:HG12	2.13	0.48
1:C:194:VAL:HG11	1:C:374:MET:HB3	1.95	0.48
1:E:37:LEU:HD22	1:E:133:ILE:CD1	2.43	0.48
1:C:214:VAL:HG22	1:C:290:VAL:HB	1.95	0.48
1:F:190:ARG:HD2	1:F:370:LEU:HD23	1.96	0.48
1:B:37:LEU:HD22	1:B:133:ILE:HD12	1.95	0.48
1:A:37:LEU:CD2	1:A:133:ILE:HD12	2.40	0.48
1:A:167:VAL:O	1:A:168:LEU:HD12	2.13	0.48
1:E:74:HIS:HB3	1:E:77:VAL:CG2	2.43	0.48
1:A:200:MET:CE	1:A:232:LEU:HD13	2.44	0.48
1:A:37:LEU:HD22	1:A:133:ILE:CD1	2.43	0.48
1:B:226:LEU:N	1:B:254:VAL:HG11	2.29	0.48
1:B:266:THR:HB	1:B:268:VAL:HG23	1.96	0.48
1:C:88:TRP:HZ3	1:C:397:TYR:CE1	2.32	0.48
1:E:170:ILE:O	1:E:170:ILE:HG13	2.13	0.48
1:F:108:ARG:HH11	1:F:108:ARG:CB	2.26	0.48
1:A:168:LEU:O	1:A:174:LYS:HE3	2.14	0.48
1:E:145:VAL:O	1:E:146:ASN:HB2	2.13	0.48
1:F:277:THR:HG23	1:F:280:GLU:H	1.79	0.48
1:A:299:HIS:HA	1:A:320:THR:OG1	2.14	0.48
1:A:226:LEU:N	1:A:254:VAL:HG11	2.29	0.47
1:A:282:LEU:CD2	1:A:289:LEU:HD21	2.43	0.47
1:D:200:MET:HG3	1:D:288:ILE:CD1	2.42	0.47
1:E:156:MET:CG	1:E:168:LEU:HA	2.44	0.47
1:A:52:VAL:CG2	1:F:29:VAL:HG12	2.44	0.47
1:F:140:ILE:HD13	1:F:352:TRP:CD1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:MET:CG	1:C:168:LEU:HA	2.44	0.47
1:E:172:THR:HG21	1:E:348:SER:O	2.15	0.47
1:A:188:THR:CG2	1:A:220:VAL:HG22	2.41	0.47
1:F:70:GLY:HA2	1:F:142:ALA:O	2.14	0.47
1:B:199:ALA:O	1:B:203:LEU:HG	2.14	0.47
1:B:29:VAL:HG23	1:B:30:LEU:N	2.28	0.47
1:D:151:VAL:HA	1:D:154:TRP:CE3	2.49	0.47
1:A:226:LEU:O	1:A:230:GLN:HG3	2.14	0.47
1:D:298:ILE:CB	1:D:319:THR:HG22	2.42	0.47
1:E:406:TYR:OH	1:E:410:LYS:HE2	2.15	0.47
1:A:393:ARG:HH11	1:A:393:ARG:HG3	1.79	0.47
1:B:338:ILE:O	1:B:342:ALA:HB2	2.15	0.47
1:D:74:HIS:HB3	1:D:77:VAL:CG2	2.45	0.47
1:F:226:LEU:O	1:F:230:GLN:HG3	2.14	0.47
1:A:282:LEU:HD22	1:A:289:LEU:HD21	1.96	0.47
1:D:411:ARG:HG2	1:D:411:ARG:HH11	1.78	0.47
1:E:62:VAL:HG13	1:E:65:GLY:O	2.15	0.47
1:F:26:LEU:O	1:F:29:VAL:HG22	2.15	0.47
1:C:120:GLU:HA	1:C:154:TRP:CZ3	2.50	0.47
1:C:303:ALA:O	1:C:330:ARG:NH1	2.47	0.47
1:C:286:VAL:O	1:C:308:ALA:HA	2.15	0.47
1:D:58:VAL:O	1:D:103:GLY:HA2	2.15	0.47
1:F:241:ASP:OD2	1:F:266:THR:HA	2.15	0.47
1:C:74:HIS:HB3	1:C:77:VAL:CG2	2.44	0.47
1:D:114:LEU:HD22	1:D:118:GLU:HB3	1.96	0.47
1:D:360:PHE:CD1	1:D:360:PHE:N	2.83	0.47
1:D:362:ASP:OD1	1:D:365:GLN:HG3	2.15	0.47
1:D:61:ASN:HD21	1:D:63:ALA:HB3	1.80	0.47
1:E:213:ALA:HB1	1:E:281:LEU:HD21	1.97	0.47
1:E:4:SER:O	1:E:8:MET:HG3	2.15	0.47
1:C:338:ILE:O	1:C:342:ALA:HB2	2.14	0.47
1:D:35:ARG:NH1	1:D:59:GLN:OE1	2.47	0.47
1:E:104:LYS:HE3	1:E:144:ASP:OD1	2.15	0.47
1:E:172:THR:HA	1:E:351:GLU:OE1	2.15	0.47
1:F:149:ALA:HB1	1:F:175:PRO:HG3	1.97	0.46
1:D:286:VAL:O	1:D:308:ALA:HA	2.15	0.46
1:B:215:GLN:HE22	1:B:297:ALA:HB1	1.80	0.46
1:C:268:VAL:C	1:C:270:TYR:H	2.19	0.46
1:C:323:ALA:O	1:C:327:LEU:HG	2.15	0.46
1:E:157:ASP:OD1	1:F:411:ARG:HG2	2.15	0.46
1:F:109:VAL:HG22	1:F:110:ASP:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:35:ARG:HH11	1:F:133:ILE:HG23	1.80	0.46
1:F:281:LEU:HG	1:F:284:LEU:HD12	1.98	0.46
1:D:86:ALA:HB2	1:D:104:LYS:HB2	1.97	0.46
1:D:243:ARG:HD3	1:D:266:THR:HG21	1.98	0.46
1:D:411:ARG:HG2	1:D:411:ARG:NH1	2.31	0.46
1:E:134:ILE:HA	1:E:139:ASP:HB3	1.97	0.46
1:A:10:VAL:O	1:A:13:PHE:HB3	2.16	0.46
1:A:170:ILE:HG23	1:A:171:VAL:HG13	1.98	0.46
1:A:203:LEU:HB2	1:A:205:ILE:HD12	1.98	0.46
1:B:68:LYS:HZ3	1:B:140:ILE:HG22	1.80	0.46
1:A:45:MET:HG3	1:A:49:HIS:CE1	2.51	0.46
1:B:361:TRP:HB3	1:B:365:GLN:CD	2.36	0.46
1:C:130:ILE:O	1:C:134:ILE:HG12	2.16	0.46
1:E:159:TYR:CE1	1:E:163:VAL:HG21	2.51	0.46
1:A:247:TYR:CE2	1:A:249:PRO:HD3	2.51	0.46
1:E:406:TYR:CZ	1:E:410:LYS:HE2	2.51	0.46
1:B:199:ALA:O	1:B:202:VAL:HG22	2.15	0.46
1:D:68:LYS:HZ3	1:D:140:ILE:CG2	2.26	0.46
1:D:73:TYR:CD1	1:D:147:THR:HG22	2.51	0.46
1:F:44:ARG:O	1:F:121:ARG:NH1	2.49	0.46
1:F:248:ASN:OD1	1:F:250:GLU:HB2	2.15	0.46
1:A:209:LYS:HG2	1:A:209:LYS:O	2.15	0.46
1:A:298:ILE:HD12	1:A:319:THR:CG2	2.46	0.46
1:B:36:VAL:CG1	1:B:79:LEU:HD11	2.46	0.45
1:F:145:VAL:O	1:F:146:ASN:HB2	2.15	0.45
1:D:277:THR:HG23	1:D:280:GLU:H	1.80	0.45
1:E:58:VAL:O	1:E:103:GLY:HA2	2.15	0.45
1:F:188:THR:HG21	1:F:220:VAL:HG22	1.98	0.45
1:F:206:ASP:OD2	1:F:208:LYS:HB3	2.15	0.45
1:A:338:ILE:HD11	1:A:396:ALA:HB3	1.99	0.45
1:A:411:ARG:NH1	1:A:411:ARG:HG2	2.31	0.45
1:A:70:GLY:HA2	1:A:142:ALA:O	2.16	0.45
1:C:58:VAL:O	1:C:103:GLY:HA2	2.16	0.45
1:E:130:ILE:O	1:E:134:ILE:HG12	2.16	0.45
1:F:156:MET:CG	1:F:168:LEU:HA	2.46	0.45
1:F:321:PRO:O	1:F:324:ASP:HB2	2.16	0.45
1:F:336:PRO:HB2	1:F:338:ILE:HG13	1.98	0.45
1:A:58:VAL:O	1:A:103:GLY:HA2	2.16	0.45
1:C:192:VAL:HG13	1:C:312:VAL:CG1	2.46	0.45
1:B:45:MET:HG3	1:B:49:HIS:CE1	2.52	0.45
1:D:338:ILE:O	1:D:342:ALA:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:268:VAL:C	1:E:270:TYR:H	2.20	0.45
1:F:286:VAL:O	1:F:308:ALA:HA	2.16	0.45
1:F:399:LEU:HD12	1:F:399:LEU:C	2.37	0.45
1:A:38:ILE:HG23	1:A:56:TYR:CE2	2.52	0.45
1:B:184:ARG:NH1	1:B:184:ARG:HG2	2.32	0.45
1:B:209:LYS:O	1:B:209:LYS:HG2	2.16	0.45
1:D:88:TRP:HZ3	1:D:397:TYR:HE1	1.63	0.45
1:F:198:LEU:HD13	1:F:378:PHE:CD1	2.52	0.45
1:B:286:VAL:O	1:B:308:ALA:HA	2.16	0.45
1:C:266:THR:HB	1:C:268:VAL:HG23	1.99	0.45
1:A:157:ASP:OD1	1:B:411:ARG:HG2	2.16	0.45
1:D:228:ILE:HG23	1:D:232:LEU:HD12	1.98	0.45
1:D:35:ARG:NH1	1:D:133:ILE:HG23	2.32	0.45
1:B:52:VAL:CG2	1:E:29:VAL:HG12	2.47	0.45
1:E:286:VAL:O	1:E:308:ALA:HA	2.16	0.45
1:A:68:LYS:HZ3	1:A:140:ILE:CG2	2.30	0.44
1:A:68:LYS:HZ2	1:A:140:ILE:HG22	1.81	0.44
1:A:317:GLY:N	1:A:318:PRO:CD	2.81	0.44
1:A:72:ARG:HG2	1:A:145:VAL:HB	1.99	0.44
1:B:157:ASP:OD1	1:C:411:ARG:NH1	2.49	0.44
1:E:70:GLY:HA2	1:E:142:ALA:O	2.17	0.44
1:E:100:PHE:HE1	1:E:349:TYR:HB2	1.82	0.44
1:A:203:LEU:HD11	1:A:310:ALA:HB2	1.98	0.44
1:B:130:ILE:O	1:B:134:ILE:HG12	2.17	0.44
1:E:260:TYR:OH	1:E:269:THR:HB	2.17	0.44
1:E:246:ILE:HD12	1:E:252:PHE:CE2	2.52	0.44
1:A:120:GLU:HA	1:A:154:TRP:CZ3	2.53	0.44
1:A:68:LYS:HZ3	1:A:140:ILE:HG22	1.79	0.44
1:F:127:PHE:CD1	1:F:155:TYR:CD2	3.06	0.44
1:F:41:PHE:CD2	1:F:41:PHE:N	2.85	0.44
1:A:29:VAL:HG12	1:F:52:VAL:HG22	1.99	0.44
1:A:363:LEU:HG	1:A:367:ARG:HD2	1.99	0.44
1:C:363:LEU:HG	1:C:367:ARG:HD2	1.99	0.44
1:D:103:GLY:O	1:D:104:LYS:HG2	2.17	0.44
1:E:298:ILE:CG2	1:E:319:THR:HG22	2.47	0.44
1:F:61:ASN:ND2	1:F:404:VAL:HG13	2.33	0.44
1:C:52:VAL:HG12	1:D:32:ARG:HH11	1.83	0.44
1:E:184:ARG:HA	1:E:347:VAL:HG11	2.00	0.44
1:E:320:THR:HB	1:E:321:PRO:HD2	1.99	0.44
1:B:131:GLN:HA	1:B:134:ILE:HD11	2.00	0.44
1:B:298:ILE:CB	1:B:319:THR:HG22	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:199:ALA:O	1:C:202:VAL:HG22	2.18	0.44
1:E:86:ALA:HB2	1:E:104:LYS:HB2	1.98	0.44
1:C:61:ASN:HD21	1:C:63:ALA:HB3	1.83	0.44
1:D:134:ILE:CG2	1:D:139:ASP:HB3	2.43	0.44
1:D:354:GLN:HG2	1:D:359:PHE:O	2.18	0.44
1:E:167:VAL:O	1:E:168:LEU:HG	2.18	0.44
1:B:277:THR:HG23	1:B:280:GLU:H	1.81	0.44
1:E:45:MET:HE3	1:E:51:GLU:HB3	2.00	0.44
1:F:156:MET:SD	1:F:156:MET:C	2.96	0.44
1:F:321:PRO:HG2	1:F:322:GLU:OE2	2.18	0.44
1:A:206:ASP:OD2	1:A:208:LYS:HB3	2.18	0.43
1:A:289:LEU:HB3	1:A:311:VAL:HG22	1.99	0.43
1:A:140:ILE:HD13	1:A:352:TRP:CD1	2.53	0.43
1:B:321:PRO:O	1:B:324:ASP:HB2	2.18	0.43
1:C:190:ARG:NH1	1:C:190:ARG:HG3	2.33	0.43
1:D:248:ASN:OD1	1:D:250:GLU:HB2	2.17	0.43
1:E:143:PRO:HD3	1:E:152:ILE:HG13	2.00	0.43
1:E:74:HIS:CG	1:E:75:PRO:HD2	2.53	0.43
1:F:181:SER:HB2	1:F:351:GLU:HB2	2.00	0.43
1:F:38:ILE:HG23	1:F:56:TYR:CE2	2.52	0.43
1:B:127:PHE:HB2	1:B:155:TYR:CD2	2.53	0.43
1:B:298:ILE:HD12	1:B:319:THR:CG2	2.49	0.43
1:D:327:LEU:HD23	1:D:332:ILE:HD12	2.00	0.43
1:E:46:ASP:OD2	1:E:118:GLU:HG3	2.18	0.43
1:E:29:VAL:HG23	1:E:30:LEU:N	2.32	0.43
1:B:151:VAL:HA	1:B:154:TRP:CE3	2.53	0.43
1:C:156:MET:HG3	1:C:168:LEU:HA	2.01	0.43
1:C:190:ARG:HG3	1:C:190:ARG:HH11	1.83	0.43
1:D:406:TYR:CZ	1:D:410:LYS:HE2	2.53	0.43
1:E:120:GLU:HA	1:E:154:TRP:CZ3	2.54	0.43
1:F:62:VAL:HG12	1:F:65:GLY:O	2.18	0.43
1:A:392:MET:O	1:A:395:ALA:HB3	2.19	0.43
1:B:167:VAL:HG12	1:B:169:GLY:H	1.83	0.43
1:E:131:GLN:HA	1:E:134:ILE:HG13	2.01	0.43
1:F:156:MET:HG3	1:F:168:LEU:HA	2.00	0.43
1:A:315:ALA:HB3	1:A:318:PRO:HG3	2.01	0.43
1:B:388:TYR:HB3	1:B:390:VAL:HG13	2.00	0.43
1:C:387:LYS:HE2	1:C:388:TYR:HE2	1.83	0.43
1:D:20:MET:HE2	1:D:22:LEU:HD13	2.01	0.43
1:D:303:ALA:O	1:D:330:ARG:NH1	2.51	0.43
1:E:226:LEU:N	1:E:254:VAL:HG11	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:356:LEU:HA	1:E:356:LEU:HD12	1.83	0.43
1:F:282:LEU:HD22	1:F:289:LEU:HD21	2.01	0.43
1:B:170:ILE:HG23	1:B:171:VAL:HG13	2.01	0.43
1:D:120:GLU:HB2	1:D:154:TRP:CZ2	2.54	0.43
1:C:124:ARG:HH11	1:C:124:ARG:HG2	1.84	0.43
1:D:37:LEU:HB2	1:D:133:ILE:CD1	2.49	0.43
1:D:74:HIS:CG	1:D:75:PRO:HD2	2.54	0.43
1:B:281:LEU:HA	1:B:284:LEU:HG	2.00	0.43
1:C:127:PHE:CZ	1:C:141:PRO:HG2	2.54	0.43
1:C:406:TYR:OH	1:C:410:LYS:HE2	2.18	0.43
1:E:206:ASP:OD2	1:E:208:LYS:HB3	2.18	0.43
1:E:347:VAL:HG23	1:E:370:LEU:HD13	2.00	0.43
1:A:200:MET:HE1	1:A:232:LEU:HD13	2.01	0.42
1:B:356:LEU:HA	1:B:356:LEU:HD12	1.89	0.42
1:C:37:LEU:HB2	1:C:133:ILE:HD12	2.01	0.42
1:E:139:ASP:O	1:E:141:PRO:HD3	2.19	0.42
1:F:119:LEU:HD23	1:F:154:TRP:HZ3	1.84	0.42
1:F:268:VAL:C	1:F:270:TYR:H	2.22	0.42
1:A:194:VAL:HG11	1:A:374:MET:HB3	2.01	0.42
1:C:313:GLU:OE1	1:C:318:PRO:HD2	2.18	0.42
1:D:283:GLU:HG2	1:D:305:ARG:HB3	2.01	0.42
1:F:406:TYR:CZ	1:F:410:LYS:HE2	2.54	0.42
1:B:156:MET:HG3	1:B:168:LEU:HA	2.01	0.42
1:D:131:GLN:HA	1:D:134:ILE:HG13	2.01	0.42
1:D:246:ILE:HD12	1:D:252:PHE:CE2	2.54	0.42
1:F:16:ALA:HB1	1:F:398:ILE:HG13	2.01	0.42
1:F:281:LEU:O	1:F:284:LEU:HB2	2.19	0.42
1:A:159:TYR:CE1	1:A:163:VAL:HG21	2.54	0.42
1:D:133:ILE:HG22	1:D:133:ILE:O	2.19	0.42
1:E:127:PHE:CZ	1:E:141:PRO:HG2	2.54	0.42
1:E:248:ASN:OD1	1:E:250:GLU:HB2	2.19	0.42
1:A:268:VAL:C	1:A:270:TYR:H	2.22	0.42
1:B:298:ILE:HD12	1:B:319:THR:HG22	2.02	0.42
1:C:226:LEU:N	1:C:254:VAL:HG11	2.34	0.42
1:C:253:ASP:OD2	1:C:256:GLU:HB2	2.19	0.42
1:C:44:ARG:NH1	1:C:48:GLY:O	2.51	0.42
1:D:268:VAL:C	1:D:270:TYR:H	2.22	0.42
1:D:299:HIS:HA	1:D:320:THR:OG1	2.19	0.42
1:E:124:ARG:HH11	1:E:124:ARG:HG2	1.84	0.42
1:A:156:MET:HG3	1:A:168:LEU:HA	2.00	0.42
1:A:349:TYR:O	1:A:353:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:VAL:HG12	1:B:62:VAL:O	2.20	0.42
1:D:156:MET:CG	1:D:168:LEU:HA	2.50	0.42
1:D:295:GLU:HG2	1:D:316:ASN:O	2.19	0.42
1:E:203:LEU:HB2	1:E:205:ILE:HD12	2.01	0.42
1:F:131:GLN:NE2	1:F:159:TYR:HD2	2.16	0.42
1:A:352:TRP:CE2	1:A:356:LEU:HD21	2.54	0.42
1:B:263:GLU:HB3	1:B:264:HIS:CE1	2.55	0.42
1:C:85:LEU:HB3	1:C:104:LYS:HG3	2.01	0.42
1:C:74:HIS:CE1	1:C:76:ASP:HB2	2.55	0.42
1:D:197:GLY:O	1:D:200:MET:HB2	2.19	0.42
1:E:283:GLU:HG2	1:E:305:ARG:HB3	2.00	0.42
1:F:120:GLU:O	1:F:124:ARG:HG3	2.19	0.42
1:A:354:GLN:OE1	1:A:361:TRP:N	2.48	0.42
1:A:88:TRP:HZ3	1:A:397:TYR:CE1	2.38	0.42
1:D:170:ILE:HG23	1:D:171:VAL:HG13	2.02	0.42
1:D:298:ILE:HG23	1:D:306:ILE:HD11	2.00	0.42
1:E:152:ILE:HG22	1:E:174:LYS:HG2	2.02	0.42
1:C:110:ASP:HA	1:C:111:PRO:HD2	1.84	0.42
1:C:289:LEU:HG	1:C:291:PRO:HD3	2.01	0.42
1:D:260:TYR:OH	1:D:269:THR:HB	2.20	0.42
1:E:299:HIS:HA	1:E:320:THR:OG1	2.20	0.42
1:E:363:LEU:HG	1:E:367:ARG:HD2	2.01	0.42
1:F:152:ILE:HG22	1:F:174:LYS:HG2	2.01	0.42
1:B:134:ILE:HA	1:B:139:ASP:HB3	2.02	0.42
1:B:68:LYS:HZ3	1:B:140:ILE:CG2	2.33	0.42
1:D:277:THR:HG22	1:D:280:GLU:OE1	2.20	0.42
1:E:327:LEU:HD23	1:E:332:ILE:HD12	2.02	0.42
1:F:74:HIS:CG	1:F:75:PRO:HD2	2.54	0.42
1:C:206:ASP:OD2	1:C:208:LYS:HB3	2.19	0.41
1:D:6:TYR:O	1:D:10:VAL:HG23	2.20	0.41
1:E:152:ILE:O	1:E:155:TYR:HB2	2.20	0.41
1:F:303:ALA:O	1:F:330:ARG:NH1	2.53	0.41
1:A:261:LYS:HG3	1:A:267:VAL:HG13	2.02	0.41
1:A:72:ARG:NH1	1:A:81:GLU:OE2	2.52	0.41
1:B:376:LYS:HE3	1:B:376:LYS:HB3	1.73	0.41
1:C:109:VAL:HG22	1:C:110:ASP:N	2.35	0.41
1:C:16:ALA:HB1	1:C:398:ILE:HG13	2.02	0.41
1:D:29:VAL:CG2	1:D:30:LEU:N	2.83	0.41
1:C:52:VAL:HG11	1:D:32:ARG:HD3	2.02	0.41
1:A:339:LEU:HD21	1:A:378:PHE:HA	2.02	0.41
1:A:391:ASP:HB3	1:A:394:THR:OG1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:GLU:HG3	1:C:295:GLU:H	1.61	0.41
1:C:4:SER:O	1:C:8:MET:HG3	2.20	0.41
1:C:72:ARG:NH1	1:C:81:GLU:OE2	2.53	0.41
1:D:71:ILE:HA	1:D:105:GLY:O	2.19	0.41
1:E:302:ASN:O	1:E:303:ALA:C	2.58	0.41
1:E:41:PHE:CZ	1:E:126:PHE:HB2	2.56	0.41
1:F:103:GLY:O	1:F:104:LYS:HG2	2.20	0.41
1:A:338:ILE:HD11	1:A:396:ALA:CB	2.50	0.41
1:C:37:LEU:HD22	1:C:133:ILE:CG1	2.51	0.41
1:C:68:LYS:HZ3	1:C:140:ILE:HG22	1.86	0.41
1:D:131:GLN:HA	1:D:134:ILE:CD1	2.50	0.41
1:D:157:ASP:OD1	1:E:411:ARG:HG2	2.20	0.41
1:E:131:GLN:HA	1:E:134:ILE:CD1	2.50	0.41
1:F:41:PHE:CD1	1:F:125:ARG:HG3	2.56	0.41
1:A:200:MET:SD	1:A:207:PRO:HA	2.61	0.41
1:B:266:THR:CB	1:B:268:VAL:HG23	2.50	0.41
1:C:376:LYS:HB3	1:C:376:LYS:HE3	1.86	0.41
1:D:226:LEU:HD11	1:D:230:GLN:NE2	2.36	0.41
1:E:124:ARG:NH1	1:E:124:ARG:HG2	2.35	0.41
1:F:213:ALA:HB1	1:F:281:LEU:HD21	2.03	0.41
1:F:376:LYS:HB3	1:F:376:LYS:HE3	1.80	0.41
1:A:266:THR:HB	1:A:268:VAL:HG23	2.03	0.41
1:A:181:SER:OG	1:A:354:GLN:NE2	2.54	0.41
1:B:380:ASP:O	1:B:384:VAL:HG23	2.20	0.41
1:B:391:ASP:HB3	1:B:394:THR:OG1	2.21	0.41
1:F:195:CYS:SG	1:F:374:MET:CE	3.08	0.41
1:F:200:MET:CG	1:F:288:ILE:HD11	2.45	0.41
1:F:387:LYS:HE2	1:F:388:TYR:CE2	2.55	0.41
1:A:110:ASP:HA	1:A:111:PRO:HD2	1.90	0.41
1:B:206:ASP:OD2	1:B:208:LYS:HB3	2.21	0.41
1:B:226:LEU:O	1:B:230:GLN:HG3	2.21	0.41
1:F:268:VAL:HG12	1:F:269:THR:N	2.36	0.41
1:F:37:LEU:HD22	1:F:133:ILE:CD1	2.50	0.41
1:D:202:VAL:HG23	1:D:203:LEU:HD23	2.03	0.41
1:D:206:ASP:OD2	1:D:208:LYS:HB3	2.21	0.41
1:E:387:LYS:HE2	1:E:388:TYR:CE2	2.56	0.41
1:B:268:VAL:C	1:B:270:TYR:H	2.23	0.41
1:C:197:GLY:O	1:C:200:MET:HB2	2.20	0.41
1:E:327:LEU:HD13	1:E:334:VAL:HG21	2.03	0.41
1:A:35:ARG:O	1:A:58:VAL:HG13	2.20	0.41
1:B:71:ILE:O	1:B:144:ASP:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:377:ALA:O	1:C:381:VAL:HG23	2.21	0.40
1:C:85:LEU:HA	1:C:85:LEU:HD23	1.84	0.40
1:D:321:PRO:O	1:D:324:ASP:HB2	2.21	0.40
1:E:227:LEU:HD22	1:E:231:GLU:OE2	2.22	0.40
1:F:152:ILE:HD13	1:F:155:TYR:HD1	1.86	0.40
1:A:193:LYS:NZ	1:A:231:GLU:OE1	2.46	0.40
1:A:411:ARG:HG2	1:A:411:ARG:HH11	1.85	0.40
1:B:85:LEU:HB3	1:B:104:LYS:HG3	2.04	0.40
1:D:53:PHE:HE2	1:D:109:VAL:HG23	1.86	0.40
1:D:110:ASP:HA	1:D:111:PRO:HD2	1.89	0.40
1:D:241:ASP:C	1:D:243:ARG:N	2.75	0.40
1:E:16:ALA:HB1	1:E:398:ILE:HG13	2.04	0.40
1:E:168:LEU:O	1:E:174:LYS:HE3	2.22	0.40
1:E:197:GLY:O	1:E:200:MET:HB2	2.21	0.40
1:E:73:TYR:CD1	1:E:147:THR:HG22	2.56	0.40
1:E:85:LEU:HA	1:E:85:LEU:HD23	1.90	0.40
1:B:6:TYR:O	1:B:10:VAL:HG23	2.21	0.40
1:B:362:ASP:O	1:B:365:GLN:HB2	2.21	0.40
1:B:84:ALA:O	1:B:87:PHE:HB3	2.21	0.40
1:E:127:PHE:HE1	1:E:141:PRO:HG2	1.84	0.40
1:E:281:LEU:HD23	1:E:281:LEU:O	2.21	0.40
1:A:190:ARG:HD2	1:A:370:LEU:HD23	2.03	0.40
1:A:86:ALA:O	1:A:89:MET:HB2	2.21	0.40
1:B:295:GLU:H	1:B:295:GLU:HG3	1.71	0.40
1:B:29:VAL:CG2	1:B:30:LEU:N	2.84	0.40
1:B:35:ARG:O	1:B:58:VAL:HG13	2.21	0.40
1:C:184:ARG:HG2	1:C:184:ARG:HH11	1.85	0.40
1:E:148:ASN:OD1	1:E:151:VAL:HG23	2.22	0.40
1:E:213:ALA:HB1	1:E:281:LEU:CD2	2.51	0.40
1:E:350:PHE:CZ	1:E:369:ALA:HB1	2.56	0.40
1:F:119:LEU:HD23	1:F:154:TRP:CZ3	2.56	0.40
1:F:268:VAL:HG12	1:F:269:THR:H	1.87	0.40
1:F:71:ILE:HD13	1:F:126:PHE:CE2	2.56	0.40

All (40) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:HIS:CG	1:E:304:GLU:OE1[6_655]	0.79	1.41
1:B:279:GLU:CG	1:F:330:ARG:O[6_665]	1.00	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:GLU:OE1	1:E:330:ARG:NE[6_655]	1.11	1.09
1:B:296:GLY:O	1:F:329:ARG:NH2[6_665]	1.20	1.00
1:A:299:HIS:ND1	1:E:304:GLU:OE1[6_655]	1.28	0.92
1:B:279:GLU:CD	1:F:330:ARG:O[6_665]	1.41	0.79
1:B:279:GLU:OE1	1:F:330:ARG:CB[6_665]	1.54	0.66
1:C:205:ILE:CG1	1:D:243:ARG:NH2[4_455]	1.57	0.63
1:B:296:GLY:O	1:F:329:ARG:CZ[6_665]	1.61	0.59
1:A:296:GLY:O	1:E:329:ARG:NH2[6_655]	1.63	0.57
1:A:279:GLU:OE1	1:E:330:ARG:CZ[6_655]	1.69	0.51
1:B:113:LYS:NZ	1:F:21:ASP:OD2[6_665]	1.72	0.48
1:A:299:HIS:CD2	1:E:304:GLU:OE1[6_655]	1.72	0.48
1:A:299:HIS:CB	1:E:304:GLU:OE1[6_655]	1.76	0.44
1:B:295:GLU:O	1:F:329:ARG:CD[6_665]	1.84	0.36
1:A:305:ARG:NH2	1:E:307:LYS:NZ[6_655]	1.90	0.30
1:B:296:GLY:C	1:F:329:ARG:NE[6_665]	1.93	0.27
1:B:296:GLY:O	1:F:329:ARG:NE[6_665]	1.94	0.26
1:B:299:HIS:CE1	1:F:330:ARG:CG[6_665]	1.94	0.26
1:A:279:GLU:OE1	1:E:330:ARG:NH2[6_655]	1.94	0.26
1:A:299:HIS:NE2	1:E:304:GLU:O[6_655]	1.95	0.25
1:A:299:HIS:CG	1:E:304:GLU:CD[6_655]	1.95	0.25
1:B:299:HIS:ND1	1:F:329:ARG:NH2[6_665]	1.97	0.23
1:B:279:GLU:CD	1:F:330:ARG:C[6_665]	1.97	0.23
1:B:299:HIS:CB	1:F:304:GLU:OE1[6_665]	2.02	0.18
1:A:296:GLY:C	1:E:329:ARG:NH2[6_655]	2.05	0.15
1:A:279:GLU:CD	1:E:330:ARG:NE[6_655]	2.05	0.15
1:B:279:GLU:OE1	1:F:330:ARG:CA[6_665]	2.08	0.12
1:A:295:GLU:O	1:E:329:ARG:CD[6_655]	2.10	0.10
1:B:299:HIS:NE2	1:F:330:ARG:CD[6_665]	2.11	0.09
1:A:329:ARG:O	1:E:279:GLU:OE1[3_564]	2.12	0.08
1:C:205:ILE:CD1	1:D:243:ARG:NH2[4_455]	2.12	0.08
1:B:279:GLU:OE1	1:F:330:ARG:O[6_665]	2.12	0.08
1:A:299:HIS:CE1	1:E:304:GLU:OE1[6_655]	2.13	0.07
1:B:243:ARG:NH2	1:F:386:GLU:OE1[6_665]	2.15	0.05
1:B:242:SER:O	1:F:389:ASN:OD1[6_665]	2.15	0.05
1:B:279:GLU:CD	1:F:330:ARG:CA[6_665]	2.17	0.03
1:A:295:GLU:O	1:E:329:ARG:NE[6_655]	2.18	0.02
1:B:299:HIS:CE1	1:F:330:ARG:CD[6_665]	2.18	0.02
1:A:299:HIS:CB	1:E:304:GLU:CD[6_655]	2.19	0.01

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	407/415 (98%)	365 (90%)	39 (10%)	3 (1%)	24	61
1	B	407/415 (98%)	366 (90%)	37 (9%)	4 (1%)	17	53
1	C	407/415 (98%)	369 (91%)	35 (9%)	3 (1%)	24	61
1	D	407/415 (98%)	370 (91%)	33 (8%)	4 (1%)	17	53
1	E	407/415 (98%)	373 (92%)	32 (8%)	2 (0%)	31	68
1	F	407/415 (98%)	366 (90%)	37 (9%)	4 (1%)	17	53
All	All	2442/2490 (98%)	2209 (90%)	213 (9%)	20 (1%)	21	59

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	178	LEU
1	A	178	LEU
1	A	303	ALA
1	B	178	LEU
1	B	303	ALA
1	C	178	LEU
1	D	303	ALA
1	E	178	LEU
1	E	303	ALA
1	F	178	LEU
1	F	303	ALA
1	B	187	ALA
1	C	187	ALA
1	C	303	ALA
1	D	187	ALA
1	A	187	ALA
1	F	187	ALA
1	B	254	VAL
1	F	254	VAL
1	D	254	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	333/339 (98%)	303 (91%)	30 (9%)	10	37
1	B	333/339 (98%)	303 (91%)	30 (9%)	10	37
1	C	333/339 (98%)	301 (90%)	32 (10%)	9	34
1	D	333/339 (98%)	303 (91%)	30 (9%)	10	37
1	E	333/339 (98%)	305 (92%)	28 (8%)	12	41
1	F	333/339 (98%)	304 (91%)	29 (9%)	11	40
All	All	1998/2034 (98%)	1819 (91%)	179 (9%)	10	37

All (179) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	49	HIS
1	A	78	THR
1	A	98	LEU
1	A	108	ARG
1	A	166	THR
1	A	168	LEU
1	A	181	SER
1	A	193	LYS
1	A	217	PHE
1	A	242	SER
1	A	254	VAL
1	A	261	LYS
1	A	267	VAL
1	A	269	THR
1	A	272	LYS
1	A	274	GLU
1	A	277	THR
1	A	283	GLU
1	A	306	ILE
1	A	320	THR
1	A	322	GLU

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Mol	Chain	Res	Type
1	A	324	ASP
1	A	337	ASP
1	A	348	SER
1	A	356	LEU
1	A	358	SER
1	A	367	ARG
1	A	408	THR
1	A	411	ARG
1	B	49	HIS
1	B	78	THR
1	B	108	ARG
1	B	123	SER
1	B	150	ASP
1	B	166	THR
1	B	168	LEU
1	B	181	SER
1	B	193	LYS
1	B	217	PHE
1	B	235	LYS
1	B	254	VAL
1	B	261	LYS
1	B	267	VAL
1	B	269	THR
1	B	272	LYS
1	B	274	GLU
1	B	283	GLU
1	B	305	ARG
1	B	320	THR
1	B	322	GLU
1	B	329	ARG
1	B	348	SER
1	B	356	LEU
1	B	358	SER
1	B	367	ARG
1	B	374	MET
1	B	394	THR
1	B	408	THR
1	B	411	ARG
1	C	28	GLU
1	C	57	ARG
1	C	78	THR
1	C	98	LEU

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Mol	Chain	Res	Type
1	C	108	ARG
1	C	115	SER
1	C	127	PHE
1	C	130	ILE
1	C	150	ASP
1	C	166	THR
1	C	181	SER
1	C	193	LYS
1	C	217	PHE
1	C	242	SER
1	C	254	VAL
1	C	259	ARG
1	C	261	LYS
1	C	269	THR
1	C	272	LYS
1	C	274	GLU
1	C	283	GLU
1	C	324	ASP
1	C	337	ASP
1	C	348	SER
1	C	354	GLN
1	C	356	LEU
1	C	358	SER
1	C	362	ASP
1	C	367	ARG
1	C	394	THR
1	C	408	THR
1	C	411	ARG
1	D	28	GLU
1	D	78	THR
1	D	108	ARG
1	D	115	SER
1	D	122	LEU
1	D	123	SER
1	D	127	PHE
1	D	150	ASP
1	D	166	THR
1	D	181	SER
1	D	193	LYS
1	D	217	PHE
1	D	242	SER
1	D	261	LYS

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Mol	Chain	Res	Type
1	D	267	VAL
1	D	269	THR
1	D	272	LYS
1	D	274	GLU
1	D	283	GLU
1	D	320	THR
1	D	322	GLU
1	D	324	ASP
1	D	337	ASP
1	D	348	SER
1	D	356	LEU
1	D	358	SER
1	D	367	ARG
1	D	373	MET
1	D	408	THR
1	D	411	ARG
1	E	57	ARG
1	E	78	THR
1	E	108	ARG
1	E	150	ASP
1	E	166	THR
1	E	181	SER
1	E	193	LYS
1	E	209	LYS
1	E	217	PHE
1	E	254	VAL
1	E	261	LYS
1	E	267	VAL
1	E	269	THR
1	E	272	LYS
1	E	274	GLU
1	E	277	THR
1	E	283	GLU
1	E	320	THR
1	E	322	GLU
1	E	329	ARG
1	E	337	ASP
1	E	348	SER
1	E	356	LEU
1	E	374	MET
1	E	385	LYS
1	E	394	THR

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Mol	Chain	Res	Type
1	E	408	THR
1	E	411	ARG
1	F	4	SER
1	F	28	GLU
1	F	39	VAL
1	F	78	THR
1	F	108	ARG
1	F	115	SER
1	F	123	SER
1	F	127	PHE
1	F	166	THR
1	F	181	SER
1	F	193	LYS
1	F	217	PHE
1	F	254	VAL
1	F	261	LYS
1	F	267	VAL
1	F	269	THR
1	F	272	LYS
1	F	283	GLU
1	F	320	THR
1	F	322	GLU
1	F	324	ASP
1	F	337	ASP
1	F	338	ILE
1	F	348	SER
1	F	356	LEU
1	F	358	SER
1	F	394	THR
1	F	399	LEU
1	F	411	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	B	59	GLN
1	B	61	ASN
1	B	165	HIS
1	C	61	ASN
1	C	131	GLN
1	C	357	GLN

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Mol	Chain	Res	Type
1	C	365	GLN
1	D	61	ASN
1	D	230	GLN
1	D	357	GLN
1	E	61	ASN
1	E	162	ASN
1	E	215	GLN
1	E	357	GLN
1	F	61	ASN
1	F	357	GLN

### 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.