



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:45 PM UTC

PDB ID : 5CDI / pdb\_00005cdi  
Title : Chloroplast chaperonin 60b1 of Chlamydomonas  
Authors : Zhang, S.; Zhou, H.; Yu, F.; Gao, F.; He, J.; Liu, C.  
Deposited on : 2015-07-04  
Resolution : 3.81 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

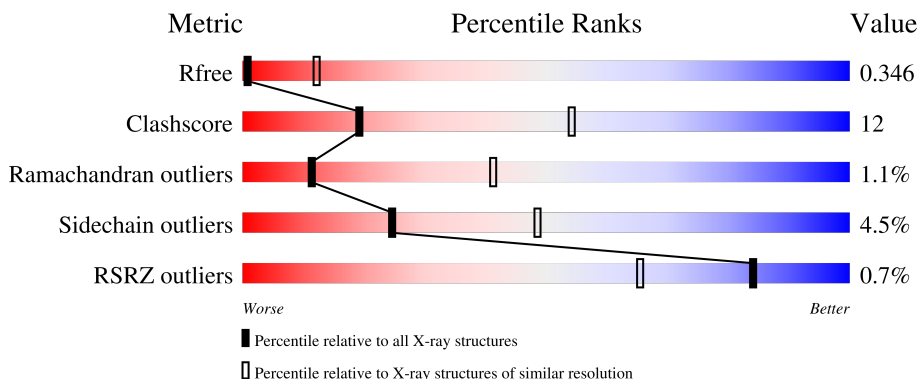
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.81 Å.

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









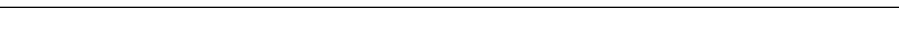
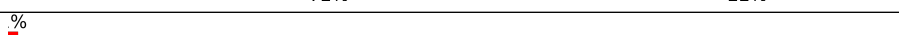
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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 of 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	552	67% 27% . .
1	B	552	73% 20% . .
1	C	552	71% 23% . .
1	D	552	71% 23% . .
1	E	552	64% 26% 5% . .

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Mol	Chain	Length	Quality of chain
1	F	552	 74% 21% . .
1	G	552	%  71% 23% . .
1	H	552	%  72% 22% . .
1	I	552	%  71% 23% . .
1	J	552	 71% 23% . .
1	K	552	%  74% 20% . .
1	L	552	 72% 22% . .
1	M	552	 72% 22% . .
1	N	552	%  75% 19% . .

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 55706 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 60B1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	528	3979	2471	696	788	24	0	0	0
1	N	528	3979	2471	696	788	24	0	0	0
1	B	528	3979	2471	696	788	24	0	0	0
1	C	528	3979	2471	696	788	24	0	0	0
1	D	528	3979	2471	696	788	24	0	0	0
1	E	528	3979	2471	696	788	24	0	0	0
1	F	528	3979	2471	696	788	24	0	0	0
1	G	528	3979	2471	696	788	24	0	0	0
1	H	528	3979	2471	696	788	24	0	0	0
1	I	528	3979	2471	696	788	24	0	0	0
1	J	528	3979	2471	696	788	24	0	0	0
1	K	528	3979	2471	696	788	24	0	0	0
1	L	528	3979	2471	696	788	24	0	0	0
1	M	528	3979	2471	696	788	24	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A8JE91

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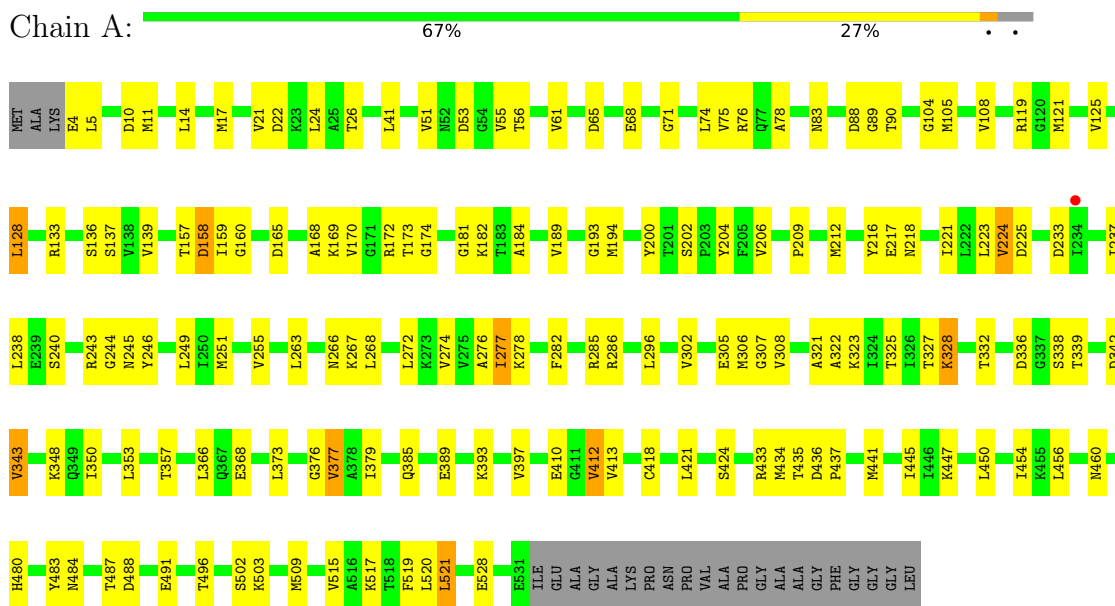
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Chain	Residue	Modelled	Actual	Comment	Reference
A	138	VAL	-	see sequence details	UNP A8JE91
N	1	MET	-	expression tag	UNP A8JE91
N	138	VAL	-	see sequence details	UNP A8JE91
B	1	MET	-	expression tag	UNP A8JE91
B	138	VAL	-	see sequence details	UNP A8JE91
C	1	MET	-	expression tag	UNP A8JE91
C	138	VAL	-	see sequence details	UNP A8JE91
D	1	MET	-	expression tag	UNP A8JE91
D	138	VAL	-	see sequence details	UNP A8JE91
E	1	MET	-	expression tag	UNP A8JE91
E	138	VAL	-	see sequence details	UNP A8JE91
F	1	MET	-	expression tag	UNP A8JE91
F	138	VAL	-	see sequence details	UNP A8JE91
G	1	MET	-	expression tag	UNP A8JE91
G	138	VAL	-	see sequence details	UNP A8JE91
H	1	MET	-	expression tag	UNP A8JE91
H	138	VAL	-	see sequence details	UNP A8JE91
I	1	MET	-	expression tag	UNP A8JE91
I	138	VAL	-	see sequence details	UNP A8JE91
J	1	MET	-	expression tag	UNP A8JE91
J	138	VAL	-	see sequence details	UNP A8JE91
K	1	MET	-	expression tag	UNP A8JE91
K	138	VAL	-	see sequence details	UNP A8JE91
L	1	MET	-	expression tag	UNP A8JE91
L	138	VAL	-	see sequence details	UNP A8JE91
M	1	MET	-	expression tag	UNP A8JE91
M	138	VAL	-	see sequence details	UNP A8JE91

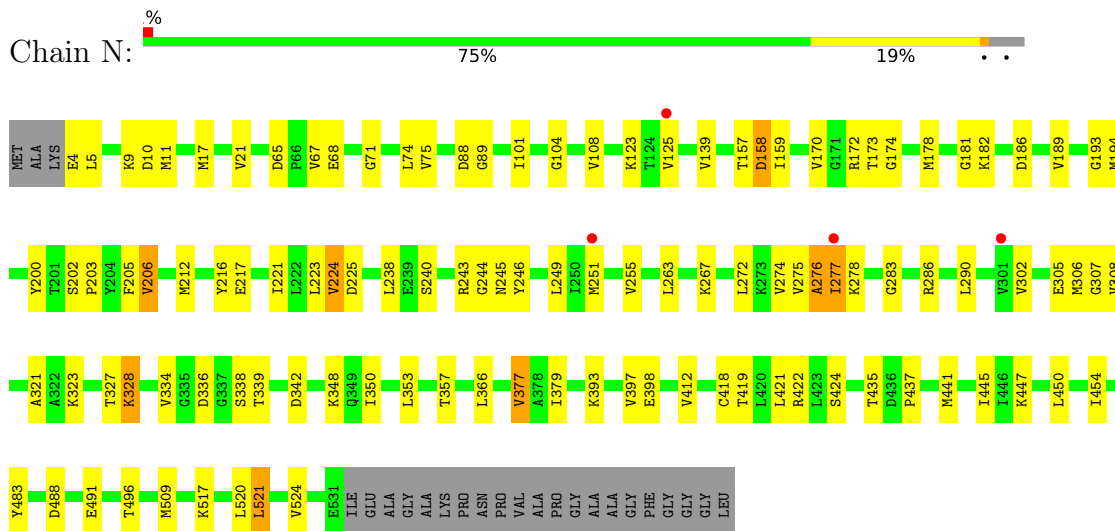
### 3 Residue-property plots i

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

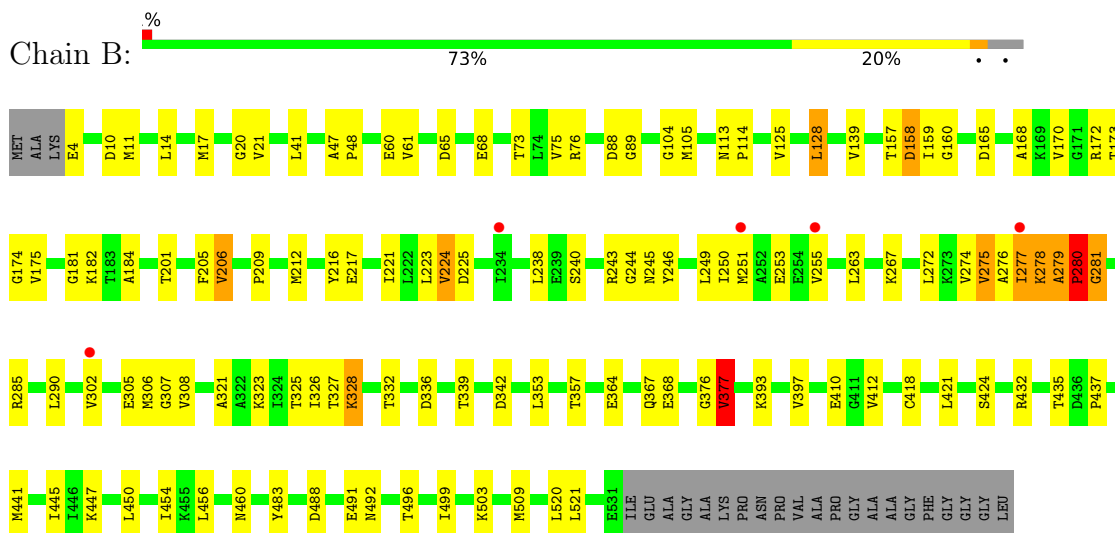
- Molecule 1: Chaperonin 60B1



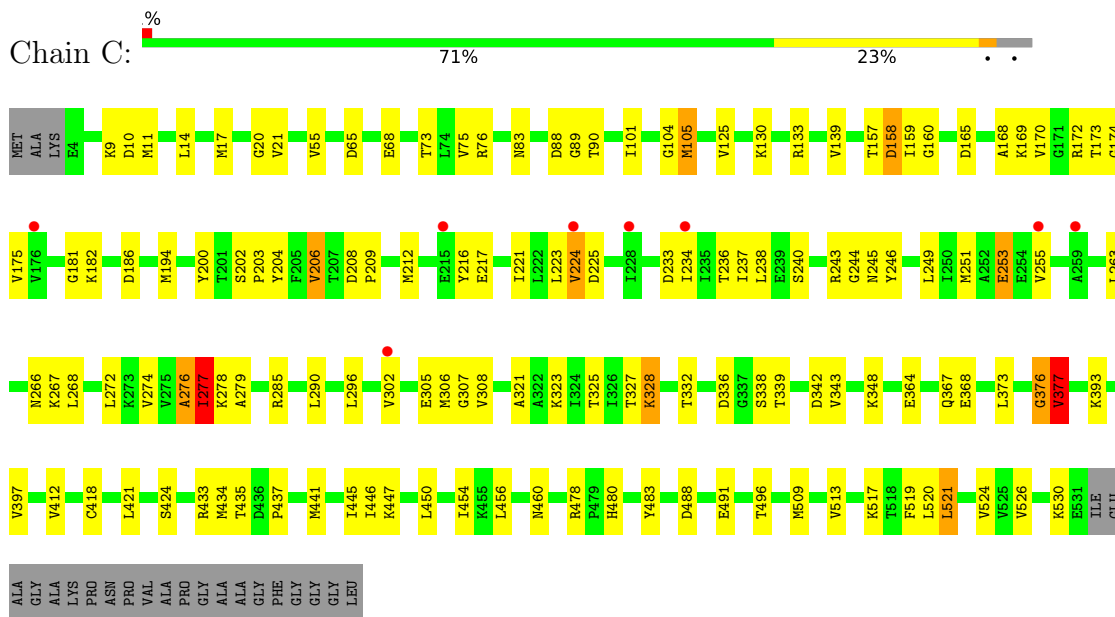
- Molecule 1: Chaperonin 60B1



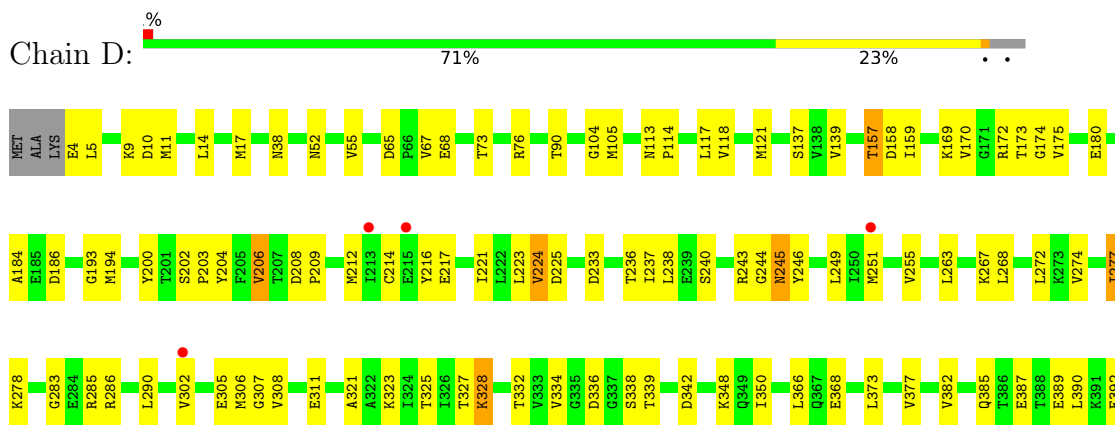
- Molecule 1: Chaperonin 60B1

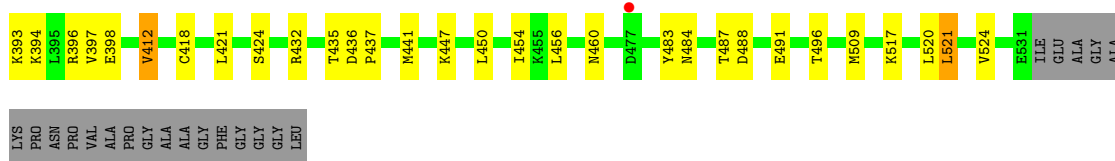


• Molecule 1: Chaperonin 60B1

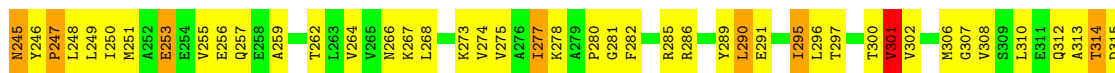
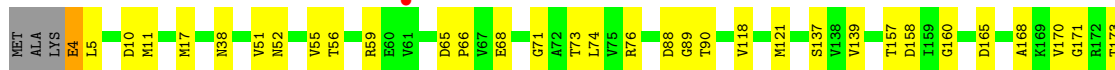


• Molecule 1: Chaperonin 60B1

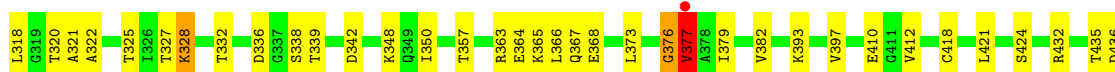




● Molecule 1: Chaperonin 60B1

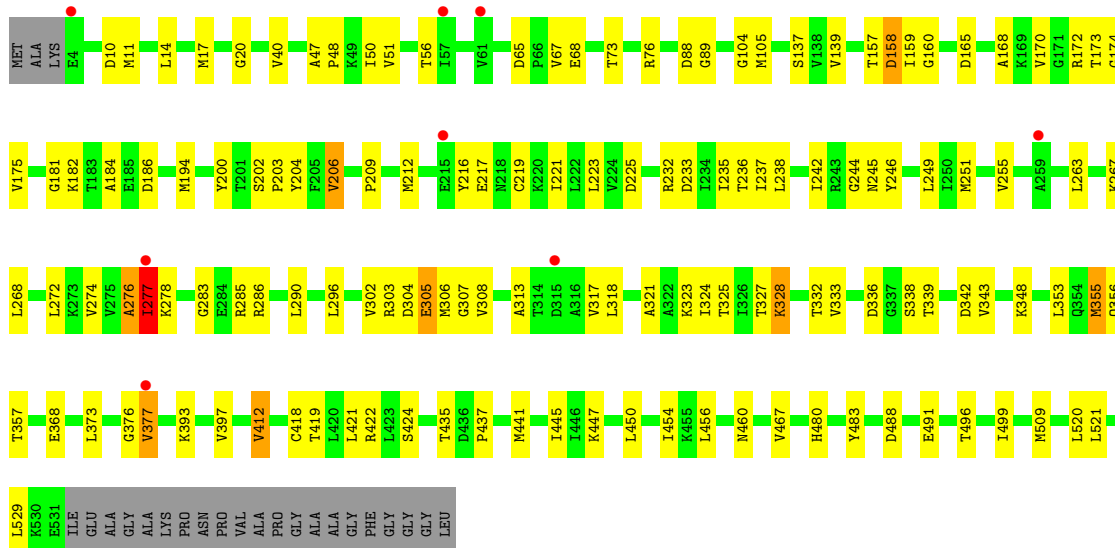


● Molecule 1: Chaperonin 60B1

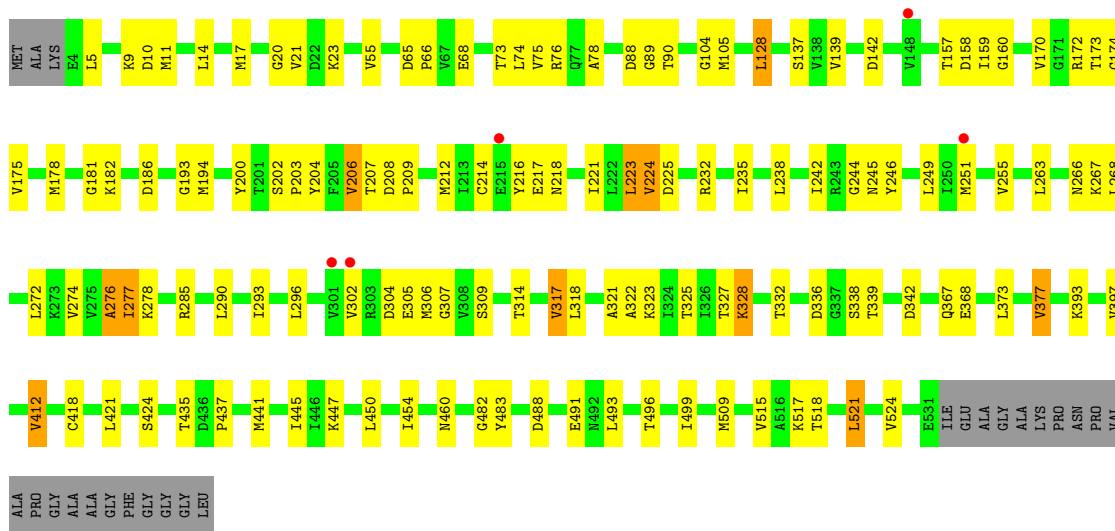


● Molecule 1: Chaperonin 60B1

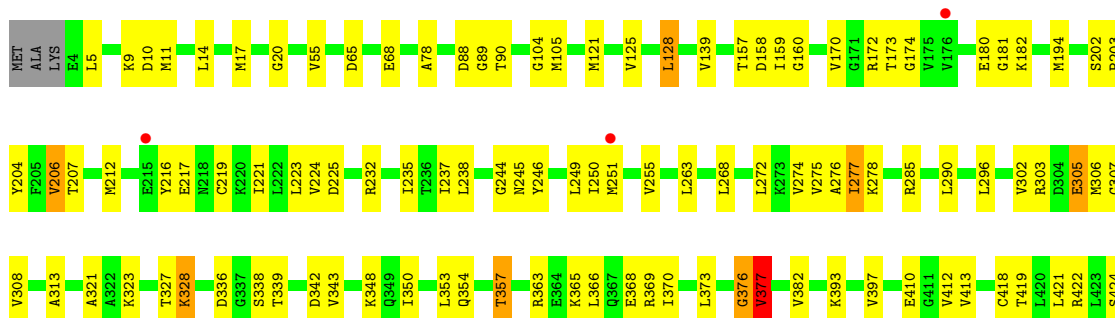




• Molecule 1: Chaperonin 60B1

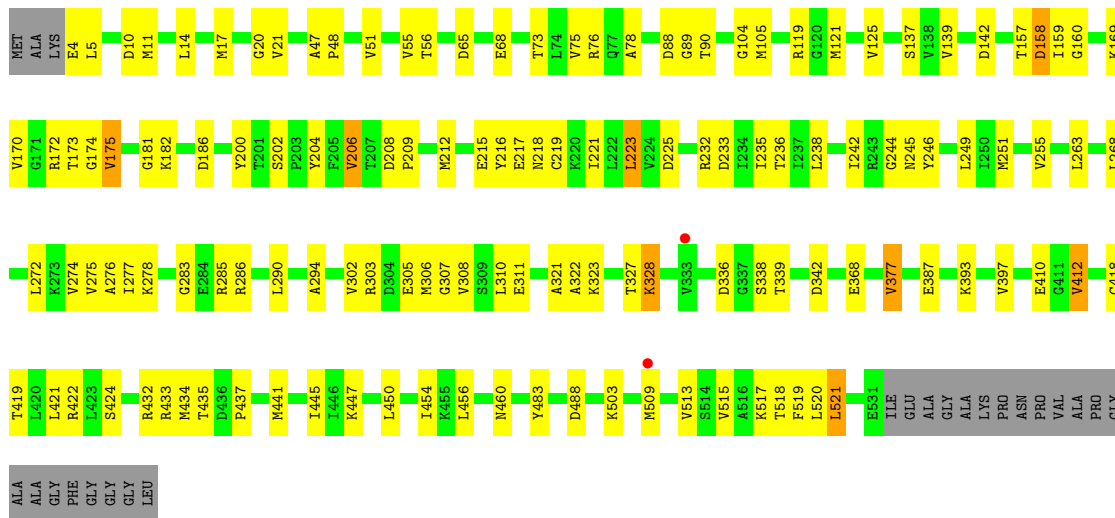


• Molecule 1: Chaperonin 60B1

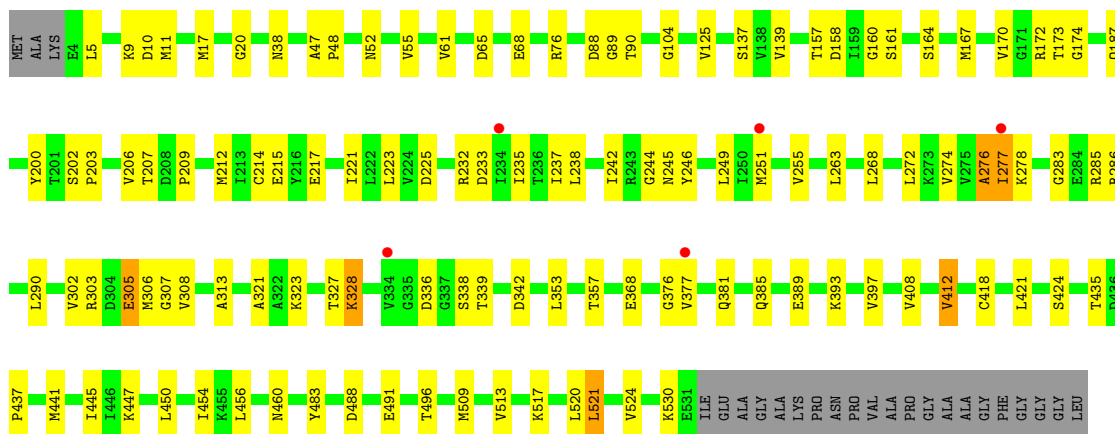
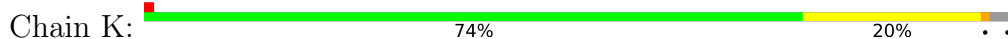




• Molecule 1: Chaperonin 60B1

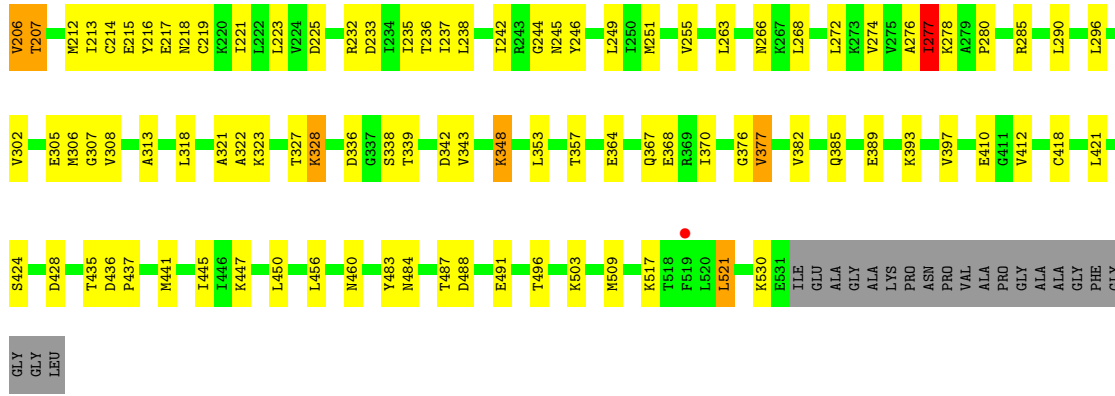


• Molecule 1: Chaperonin 60B1

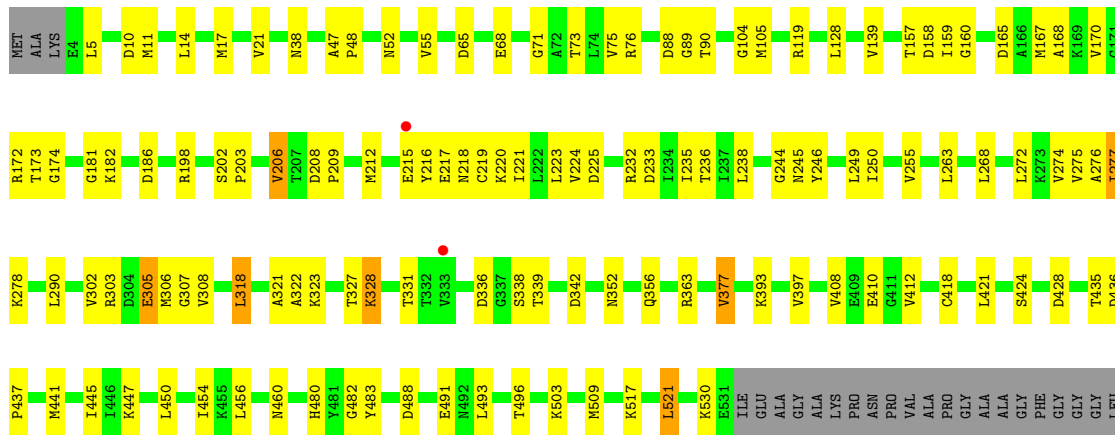


• Molecule 1: Chaperonin 60B1





• Molecule 1: Chaperonin 60B1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	143.34Å 174.39Å 213.68Å 90.00° 94.69° 90.00°	Depositor
Resolution (Å)	48.66 – 3.81 48.66 – 3.81	Depositor EDS
% Data completeness (in resolution range)	96.7 (48.66-3.81) 85.0 (48.66-3.81)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.77 (at 3.77Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.275 , 0.325 0.298 , 0.346	Depositor DCC
$R_{free}$ test set	2003 reflections (2.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	129.8	Xtrriage
Anisotropy	0.235	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 155.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	55706	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	186.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.30	0/4011	0.73	0/5417
1	B	0.37	4/4011 (0.1%)	0.78	3/5417 (0.1%)
1	C	0.37	4/4011 (0.1%)	0.77	4/5417 (0.1%)
1	D	0.34	2/4011 (0.0%)	0.74	0/5417
1	E	0.46	5/4011 (0.1%)	0.85	14/5417 (0.3%)
1	F	0.34	3/4011 (0.1%)	0.73	0/5417
1	G	0.37	3/4011 (0.1%)	0.74	0/5417
1	H	0.34	1/4011 (0.0%)	0.76	3/5417 (0.1%)
1	I	0.32	2/4011 (0.0%)	0.75	1/5417 (0.0%)
1	J	0.36	3/4011 (0.1%)	0.74	0/5417
1	K	0.31	1/4011 (0.0%)	0.76	4/5417 (0.1%)
1	L	0.32	0/4011	0.74	1/5417 (0.0%)
1	M	0.37	3/4011 (0.1%)	0.73	1/5417 (0.0%)
1	N	0.35	2/4011 (0.0%)	0.75	3/5417 (0.1%)
All	All	0.35	33/56154 (0.1%)	0.75	34/75838 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
1	E	0	1
1	L	0	1
All	All	0	4

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	377	VAL	C-N	17.61	1.57	1.33
1	N	276	ALA	C-N	-9.51	1.20	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	206	VAL	C-N	-9.12	1.21	1.33
1	M	215	GLU	C-N	8.25	1.45	1.33
1	H	276	ALA	C-N	-8.14	1.22	1.33
1	M	206	VAL	C-N	-8.13	1.23	1.33
1	B	206	VAL	C-N	-8.05	1.23	1.33
1	J	377	VAL	C-N	-7.98	1.22	1.33
1	J	215	GLU	C-N	7.73	1.44	1.33
1	C	377	VAL	C-N	-7.61	1.23	1.33
1	G	276	ALA	C-N	-7.42	1.23	1.33
1	C	276	ALA	C-N	-7.42	1.23	1.33
1	B	205	PHE	C-N	-7.35	1.24	1.33
1	M	377	VAL	C-N	-7.10	1.23	1.33
1	D	206	VAL	C-N	-6.53	1.25	1.33
1	B	377	VAL	C-N	-6.16	1.24	1.33
1	I	376	GLY	C-N	6.12	1.42	1.33
1	C	206	VAL	C-N	-6.11	1.25	1.33
1	D	214	CYS	C-N	6.01	1.41	1.33
1	K	276	ALA	C-N	-5.86	1.25	1.33
1	I	377	VAL	C-N	-5.78	1.25	1.33
1	E	376	GLY	C-N	-5.78	1.25	1.33
1	F	215	GLU	C-N	-5.76	1.25	1.33
1	C	376	GLY	C-N	5.73	1.41	1.33
1	F	376	GLY	C-N	5.67	1.41	1.33
1	E	209	PRO	N-CD	5.52	1.55	1.47
1	N	205	PHE	C-N	5.52	1.40	1.33
1	B	280	PRO	N-CD	5.47	1.55	1.47
1	E	203	PRO	N-CD	5.32	1.55	1.47
1	E	208	ASP	C-N	5.29	1.40	1.33
1	F	377	VAL	C-N	-5.23	1.25	1.33
1	G	277	ILE	C-N	5.05	1.40	1.33
1	J	206	VAL	C-N	-5.04	1.27	1.33

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	277	ILE	N-CA-C	13.70	127.65	107.37
1	C	276	ALA	O-C-N	-9.68	110.61	123.10
1	H	276	ALA	O-C-N	-8.84	111.69	123.10
1	E	202	SER	C-N-CD	8.81	139.97	120.60
1	E	246	TYR	CA-C-N	8.76	130.79	119.84
1	E	246	TYR	C-N-CA	8.76	130.79	119.84
1	B	275	VAL	N-CA-C	8.53	118.98	108.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	376	GLY	O-C-N	-8.12	113.61	122.62
1	E	376	GLY	O-C-N	-7.71	114.18	122.67
1	C	276	ALA	CA-C-N	7.42	135.32	121.97
1	C	276	ALA	C-N-CA	7.42	135.32	121.97
1	I	207	THR	N-CA-C	7.38	119.40	111.36
1	C	277	ILE	O-C-N	-7.21	113.55	122.57
1	E	208	ASP	CA-C-N	-7.17	113.31	120.98
1	E	208	ASP	C-N-CA	-7.17	113.31	120.98
1	H	276	ALA	CA-C-N	6.98	134.53	121.97
1	H	276	ALA	C-N-CA	6.98	134.53	121.97
1	E	377	VAL	O-C-N	-6.57	114.35	122.57
1	K	276	ALA	O-C-N	-6.15	115.17	123.10
1	E	301	VAL	CA-C-N	5.88	132.28	121.70
1	E	301	VAL	C-N-CA	5.88	132.28	121.70
1	E	205	PHE	N-CA-C	-5.77	99.49	108.90
1	L	207	THR	N-CA-C	5.65	117.52	111.36
1	B	277	ILE	N-CA-CB	-5.59	104.62	111.67
1	M	206	VAL	O-C-N	-5.35	117.21	122.67
1	E	202	SER	CA-C-N	-5.32	114.23	127.00
1	E	202	SER	C-N-CA	-5.32	114.23	127.00
1	K	276	ALA	CA-C-N	5.25	131.41	121.97
1	K	276	ALA	C-N-CA	5.25	131.41	121.97
1	E	200	TYR	N-CA-C	5.07	116.81	111.28
1	N	276	ALA	O-C-N	-5.05	116.59	123.10
1	E	199	GLY	N-CA-C	5.02	119.40	112.37
1	N	206	VAL	CA-C-N	5.02	127.26	120.44
1	N	206	VAL	C-N-CA	5.02	127.26	120.44

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	279	ALA	Peptide
1	C	277	ILE	Mainchain
1	E	202	SER	Peptide
1	L	277	ILE	Mainchain

## 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	3979	0	4104	98	0
1	B	3979	0	4104	97	0
1	C	3979	0	4104	91	0
1	D	3979	0	4104	95	0
1	E	3979	0	4104	219	0
1	F	3979	0	4104	92	0
1	G	3979	0	4104	87	0
1	H	3979	0	4104	82	0
1	I	3979	0	4104	80	0
1	J	3979	0	4104	86	0
1	K	3979	0	4104	75	0
1	L	3979	0	4104	77	0
1	M	3979	0	4104	74	0
1	N	3979	0	4104	81	0
All	All	55706	0	57456	1325	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 12.

All (1325) 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:205:PHE:CE2	1:E:267:LYS:CB	1.85	1.55
1:E:205:PHE:CE2	1:E:267:LYS:HB3	0.97	1.47
1:E:59:ARG:HH22	1:E:212:MET:CE	1.27	1.46
1:E:251:MET:HA	1:E:277:ILE:CG2	1.46	1.46
1:E:277:ILE:HD12	1:E:278:LYS:N	1.27	1.43
1:E:59:ARG:NH2	1:E:212:MET:HE1	1.27	1.43
1:F:277:ILE:HD12	1:F:278:LYS:N	1.33	1.41
1:E:205:PHE:HZ	1:E:267:LYS:C	1.25	1.41
1:E:205:PHE:CZ	1:E:267:LYS:C	2.03	1.36
1:N:193:GLY:HA3	1:N:377:VAL:CG2	1.67	1.24
1:L:276:ALA:O	1:L:277:ILE:HG23	1.31	1.24
1:I:250:ILE:O	1:I:277:ILE:HD12	1.07	1.23
1:N:193:GLY:C	1:N:377:VAL:CG2	2.11	1.23
1:I:250:ILE:O	1:I:277:ILE:CD1	1.86	1.20
1:N:193:GLY:CA	1:N:377:VAL:HG23	1.71	1.20
1:E:201:THR:O	1:E:203:PRO:N	1.71	1.19
1:N:193:GLY:C	1:N:377:VAL:HG23	1.66	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:205:PHE:CG	1:E:267:LYS:HE3	1.77	1.18
1:E:267:LYS:NZ	1:E:273:LYS:HG3	1.59	1.18
1:N:193:GLY:CA	1:N:377:VAL:CG2	2.22	1.17
1:N:276:ALA:O	1:N:277:ILE:HG23	1.40	1.16
1:E:205:PHE:CD2	1:E:267:LYS:HB3	1.80	1.16
1:B:251:MET:HB3	1:B:277:ILE:HG13	1.17	1.16
1:E:200:TYR:CE1	1:E:328:LYS:HE3	1.81	1.16
1:K:276:ALA:O	1:K:277:ILE:HG23	1.42	1.15
1:G:251:MET:CB	1:G:277:ILE:HD11	1.74	1.14
1:E:205:PHE:CZ	1:E:267:LYS:CB	2.31	1.14
1:E:251:MET:HG3	1:E:277:ILE:HG21	1.21	1.13
1:G:276:ALA:O	1:G:277:ILE:HG23	1.47	1.13
1:C:276:ALA:O	1:C:277:ILE:HG23	1.45	1.12
1:E:251:MET:CA	1:E:277:ILE:CG2	2.28	1.12
1:L:276:ALA:O	1:L:277:ILE:CG2	1.98	1.11
1:H:276:ALA:O	1:H:277:ILE:HG23	1.47	1.11
1:E:277:ILE:CD1	1:E:278:LYS:H	1.63	1.10
1:D:200:TYR:HA	1:D:277:ILE:HG12	1.11	1.09
1:F:277:ILE:HD11	1:F:278:LYS:O	1.52	1.09
1:D:334:VAL:HG23	1:D:377:VAL:HG11	1.10	1.09
1:E:205:PHE:CZ	1:E:267:LYS:HG2	1.88	1.08
1:F:277:ILE:CD1	1:F:278:LYS:O	2.03	1.06
1:F:253:GLU:C	1:F:278:LYS:NZ	2.13	1.06
1:E:205:PHE:CE1	1:E:267:LYS:HG2	1.90	1.05
1:E:205:PHE:CD1	1:E:267:LYS:HE3	1.92	1.05
1:K:200:TYR:HA	1:K:277:ILE:HG22	1.38	1.04
1:A:276:ALA:O	1:A:277:ILE:HG23	1.57	1.04
1:A:251:MET:CB	1:A:277:ILE:HD11	1.87	1.03
1:E:205:PHE:CZ	1:E:268:LEU:N	2.25	1.03
1:N:276:ALA:O	1:N:277:ILE:CG2	2.06	1.03
1:E:251:MET:CG	1:E:277:ILE:HG21	1.88	1.03
1:L:251:MET:HB3	1:L:277:ILE:HD11	1.41	1.02
1:E:205:PHE:CZ	1:E:267:LYS:HB3	1.90	1.02
1:G:251:MET:HB3	1:G:277:ILE:CD1	1.89	1.02
1:C:251:MET:CB	1:C:277:ILE:HD11	1.88	1.02
1:L:251:MET:CB	1:L:277:ILE:HD11	1.90	1.02
1:E:251:MET:CA	1:E:277:ILE:HG23	1.88	1.01
1:N:193:GLY:HA3	1:N:377:VAL:HG21	1.39	1.01
1:E:251:MET:HG3	1:E:277:ILE:CG2	1.91	1.01
1:E:251:MET:HA	1:E:277:ILE:HG23	1.04	1.00
1:E:301:VAL:HB	1:E:302:VAL:HA	1.42	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:277:ILE:CD1	1:E:278:LYS:N	2.20	1.00
1:K:251:MET:CB	1:K:277:ILE:HD11	1.91	1.00
1:E:267:LYS:HD2	1:E:274:VAL:H	1.26	1.00
1:G:251:MET:HB3	1:G:277:ILE:HD11	1.39	1.00
1:A:200:TYR:HA	1:A:277:ILE:HG22	1.44	1.00
1:E:205:PHE:CZ	1:E:267:LYS:CG	2.46	0.99
1:D:334:VAL:HG23	1:D:377:VAL:CG1	1.92	0.99
1:A:251:MET:HB3	1:A:277:ILE:HD11	1.42	0.99
1:G:251:MET:CB	1:G:277:ILE:CD1	2.40	0.99
1:K:276:ALA:O	1:K:277:ILE:CG2	2.11	0.98
1:H:200:TYR:HA	1:H:277:ILE:HG22	1.46	0.98
1:D:277:ILE:HD12	1:D:278:LYS:H	1.28	0.97
1:F:277:ILE:CD1	1:F:278:LYS:N	2.28	0.96
1:D:200:TYR:CA	1:D:277:ILE:HG12	1.95	0.96
1:G:276:ALA:O	1:G:277:ILE:CG2	2.12	0.96
1:D:334:VAL:HG21	1:D:377:VAL:HG21	1.42	0.96
1:D:334:VAL:CG2	1:D:377:VAL:HG21	1.95	0.96
1:E:201:THR:O	1:E:203:PRO:CD	2.13	0.96
1:N:251:MET:CB	1:N:277:ILE:HD11	1.96	0.95
1:E:267:LYS:HD2	1:E:274:VAL:N	1.81	0.95
1:K:251:MET:HB3	1:K:277:ILE:HD11	1.46	0.95
1:H:251:MET:HB3	1:H:277:ILE:HD11	1.46	0.95
1:B:253:GLU:O	1:B:278:LYS:NZ	1.99	0.94
1:C:276:ALA:O	1:C:277:ILE:CG2	2.15	0.94
1:N:200:TYR:HA	1:N:277:ILE:HG22	1.50	0.94
1:E:251:MET:HA	1:E:277:ILE:HG22	1.49	0.94
1:E:205:PHE:CD1	1:E:267:LYS:CE	2.51	0.93
1:C:251:MET:HB3	1:C:277:ILE:HD11	1.48	0.93
1:H:276:ALA:O	1:H:277:ILE:CG2	2.16	0.93
1:D:200:TYR:HA	1:D:277:ILE:CG1	1.99	0.93
1:G:200:TYR:HA	1:G:277:ILE:HG22	1.49	0.92
1:E:209:PRO:HA	1:E:212:MET:H	1.34	0.92
1:J:276:ALA:C	1:J:277:ILE:HD12	1.94	0.92
1:L:200:TYR:HA	1:L:277:ILE:HG22	1.52	0.92
1:F:253:GLU:O	1:F:278:LYS:CE	2.18	0.92
1:I:206:VAL:HG21	1:I:212:MET:HA	1.51	0.92
1:C:200:TYR:HA	1:C:277:ILE:HG22	1.50	0.91
1:E:200:TYR:CE2	1:E:202:SER:O	2.24	0.91
1:H:251:MET:CB	1:H:277:ILE:HD11	1.99	0.91
1:N:251:MET:HB3	1:N:277:ILE:HD11	1.52	0.90
1:F:277:ILE:HD12	1:F:278:LYS:H	1.09	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:267:LYS:HZ1	1:E:273:LYS:HG3	1.34	0.89
1:E:211:ARG:HH11	1:E:211:ARG:HG2	1.35	0.89
1:E:267:LYS:HZ3	1:E:273:LYS:HG3	1.32	0.89
1:H:207:THR:OG1	1:H:214:CYS:HA	1.72	0.88
1:E:200:TYR:CE1	1:E:328:LYS:CE	2.57	0.87
1:D:334:VAL:CG2	1:D:377:VAL:HG11	1.99	0.87
1:F:253:GLU:C	1:F:278:LYS:HZ1	1.77	0.87
1:E:59:ARG:CZ	1:E:212:MET:HE1	2.04	0.87
1:N:193:GLY:CA	1:N:377:VAL:HG21	1.97	0.86
1:E:205:PHE:HZ	1:E:267:LYS:O	1.59	0.86
1:E:205:PHE:CG	1:E:267:LYS:CE	2.58	0.85
1:E:205:PHE:CE2	1:E:267:LYS:CG	2.57	0.85
1:A:276:ALA:O	1:A:277:ILE:CG2	2.24	0.85
1:G:251:MET:HB3	1:G:277:ILE:CG1	2.06	0.84
1:E:205:PHE:CB	1:E:267:LYS:HE3	2.05	0.84
1:B:278:LYS:HA	1:B:278:LYS:CE	2.06	0.84
1:B:251:MET:HB3	1:B:277:ILE:CG1	2.03	0.84
1:E:205:PHE:HZ	1:E:268:LEU:N	1.67	0.83
1:C:251:MET:HB2	1:C:277:ILE:HD11	1.59	0.83
1:L:207:THR:OG1	1:L:214:CYS:HA	1.78	0.83
1:B:250:ILE:O	1:B:277:ILE:HG12	1.78	0.83
1:A:251:MET:HB3	1:A:277:ILE:CD1	2.08	0.82
1:M:275:VAL:HG12	1:M:277:ILE:HD11	1.59	0.82
1:E:59:ARG:HH22	1:E:212:MET:HE1	0.68	0.82
1:G:251:MET:HB2	1:G:277:ILE:CD1	2.09	0.81
1:E:251:MET:CB	1:E:277:ILE:HG21	2.09	0.81
1:E:205:PHE:HE2	1:E:267:LYS:HB3	1.00	0.81
1:E:251:MET:CG	1:E:277:ILE:CG2	2.55	0.81
1:K:200:TYR:CA	1:K:277:ILE:HG22	2.11	0.81
1:B:274:VAL:O	1:B:275:VAL:CG2	2.28	0.81
1:B:280:PRO:O	1:B:281:GLY:O	1.97	0.81
1:F:253:GLU:O	1:F:278:LYS:NZ	2.14	0.81
1:E:205:PHE:CE2	1:E:267:LYS:CA	2.64	0.80
1:G:251:MET:SD	1:G:277:ILE:HD11	2.21	0.80
1:K:251:MET:HB3	1:K:277:ILE:CD1	2.11	0.79
1:J:200:TYR:HA	1:J:277:ILE:HG13	1.63	0.79
1:L:276:ALA:C	1:L:277:ILE:HG23	2.08	0.79
1:L:251:MET:HB3	1:L:277:ILE:CD1	2.13	0.79
1:E:205:PHE:HB3	1:E:267:LYS:HE3	1.64	0.78
1:E:205:PHE:CZ	1:E:267:LYS:CA	2.65	0.78
1:E:200:TYR:HE1	1:E:328:LYS:HE3	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:334:VAL:HG21	1:D:377:VAL:CG2	2.14	0.78
1:G:251:MET:HB2	1:G:277:ILE:HD11	1.60	0.78
1:E:201:THR:O	1:E:202:SER:C	2.26	0.78
1:A:251:MET:CB	1:A:277:ILE:CD1	2.60	0.77
1:A:251:MET:HB2	1:A:277:ILE:HD11	1.66	0.77
1:E:201:THR:O	1:E:203:PRO:HD3	1.83	0.77
1:E:205:PHE:CE2	1:E:268:LEU:N	2.53	0.76
1:E:249:LEU:HD22	1:E:324:ILE:HD13	1.66	0.76
1:H:251:MET:HB3	1:H:277:ILE:CD1	2.15	0.76
1:F:278:LYS:HE3	1:F:278:LYS:HA	1.67	0.76
1:B:253:GLU:H	1:B:279:ALA:HB2	1.49	0.76
1:K:251:MET:CB	1:K:277:ILE:CD1	2.63	0.75
1:I:276:ALA:C	1:I:277:ILE:HG13	2.10	0.75
1:E:251:MET:CB	1:E:277:ILE:CG2	2.63	0.75
1:C:251:MET:CB	1:C:277:ILE:CD1	2.65	0.75
1:E:295:ILE:HD12	1:E:346:ARG:HH11	1.51	0.75
1:E:205:PHE:CD1	1:E:267:LYS:NZ	2.55	0.75
1:E:202:SER:OG	1:E:204:TYR:HB2	1.86	0.74
1:N:251:MET:HB3	1:N:277:ILE:CD1	2.17	0.74
1:L:251:MET:HB2	1:L:277:ILE:HD11	1.69	0.74
1:C:251:MET:HB3	1:C:277:ILE:CD1	2.18	0.74
1:B:251:MET:CB	1:B:277:ILE:HG13	2.09	0.74
1:D:390:LEU:HA	1:D:393:LYS:HB2	1.69	0.74
1:E:209:PRO:HB2	1:E:210:GLU:HA	1.69	0.73
1:L:251:MET:CB	1:L:277:ILE:CD1	2.66	0.73
1:I:206:VAL:CG2	1:I:212:MET:HA	2.18	0.73
1:D:193:GLY:HA3	1:D:377:VAL:CG1	2.18	0.73
1:J:275:VAL:HG12	1:J:277:ILE:CD1	2.18	0.72
1:D:277:ILE:CD1	1:D:278:LYS:H	2.01	0.72
1:G:221:ILE:HD11	1:G:251:MET:HE2	1.71	0.72
1:E:219:CYS:SG	1:E:220:LYS:N	2.60	0.72
1:E:211:ARG:HG2	1:E:211:ARG:NH1	2.03	0.72
1:F:254:GLU:HA	1:F:278:LYS:HZ2	1.55	0.72
1:J:274:VAL:O	1:J:275:VAL:CG2	2.38	0.72
1:J:274:VAL:O	1:J:275:VAL:HG23	1.90	0.72
1:N:251:MET:HB2	1:N:277:ILE:HD11	1.72	0.71
1:E:244:GLY:O	1:E:245:ASN:ND2	2.22	0.71
1:K:251:MET:HB2	1:K:277:ILE:HD11	1.70	0.71
1:N:251:MET:CB	1:N:277:ILE:CD1	2.68	0.71
1:M:277:ILE:N	1:M:277:ILE:HD12	2.05	0.71
1:E:200:TYR:HE2	1:E:202:SER:O	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:199:GLY:O	1:E:277:ILE:HD13	1.91	0.71
1:G:223:LEU:HD21	1:G:251:MET:HE3	1.73	0.71
1:M:250:ILE:O	1:M:277:ILE:CD1	2.38	0.71
1:F:253:GLU:C	1:F:278:LYS:HZ2	1.97	0.71
1:E:209:PRO:HB3	1:E:212:MET:HB3	1.73	0.71
1:K:206:VAL:HG11	1:K:212:MET:HB2	1.73	0.71
1:E:249:LEU:HG	1:E:275:VAL:HB	1.70	0.70
1:G:276:ALA:C	1:G:277:ILE:HG23	2.15	0.70
1:E:250:ILE:O	1:E:277:ILE:HG22	1.91	0.70
1:F:277:ILE:CD1	1:F:278:LYS:H	1.97	0.70
1:F:253:GLU:O	1:F:278:LYS:HE3	1.92	0.70
1:G:251:MET:HB3	1:G:277:ILE:HG13	1.71	0.70
1:E:59:ARG:NH2	1:E:212:MET:CE	2.08	0.70
1:C:17:MET:HA	1:C:68:GLU:HA	1.73	0.70
1:E:209:PRO:HA	1:E:212:MET:N	2.06	0.69
1:L:277:ILE:HD12	1:L:278:LYS:N	2.07	0.69
1:J:276:ALA:O	1:J:277:ILE:HD12	1.93	0.69
1:E:296:LEU:HD12	1:E:297:THR:HG23	1.73	0.69
1:E:203:PRO:HG2	1:E:205:PHE:O	1.92	0.69
1:F:253:GLU:C	1:F:278:LYS:CE	2.64	0.68
1:A:276:ALA:C	1:A:277:ILE:HG23	2.19	0.68
1:E:282:PHE:O	1:E:286:ARG:N	2.19	0.68
1:E:209:PRO:HB2	1:E:210:GLU:CA	2.23	0.68
1:B:253:GLU:HA	1:B:279:ALA:HB3	1.76	0.68
1:B:278:LYS:HA	1:B:278:LYS:HE2	1.75	0.67
1:M:250:ILE:O	1:M:277:ILE:HD13	1.94	0.67
1:F:277:ILE:HD12	1:F:278:LYS:CA	2.21	0.67
1:B:274:VAL:O	1:B:275:VAL:HG23	1.95	0.67
1:D:334:VAL:CG2	1:D:377:VAL:CG2	2.71	0.67
1:E:205:PHE:CE2	1:E:267:LYS:C	2.62	0.67
1:E:200:TYR:HE1	1:E:328:LYS:CE	2.04	0.67
1:N:334:VAL:HG23	1:N:377:VAL:HB	1.77	0.66
1:F:277:ILE:HD12	1:F:277:ILE:C	2.15	0.66
1:B:274:VAL:O	1:B:275:VAL:HG22	1.95	0.66
1:M:276:ALA:C	1:M:277:ILE:HD12	2.21	0.66
1:N:194:MET:N	1:N:377:VAL:CG2	2.59	0.66
1:N:276:ALA:C	1:N:277:ILE:HG23	2.18	0.66
1:F:456:LEU:O	1:F:460:ASN:ND2	2.23	0.66
1:N:441:MET:HE1	1:L:441:MET:HE1	1.78	0.66
1:N:193:GLY:C	1:N:377:VAL:HG21	2.10	0.66
1:D:277:ILE:CD1	1:D:278:LYS:HG2	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:17:MET:HA	1:N:68:GLU:HA	1.76	0.65
1:I:353:LEU:O	1:I:357:THR:OG1	2.14	0.65
1:A:17:MET:HA	1:A:68:GLU:HA	1.77	0.65
1:E:207:THR:CB	1:E:214:CYS:HA	2.27	0.65
1:D:17:MET:HA	1:D:68:GLU:HA	1.78	0.65
1:M:17:MET:HA	1:M:68:GLU:HA	1.77	0.65
1:N:193:GLY:O	1:N:377:VAL:HG23	1.95	0.65
1:K:276:ALA:C	1:K:277:ILE:HG23	2.22	0.65
1:E:277:ILE:HD12	1:E:278:LYS:H	0.73	0.64
1:E:321:ALA:HA	1:E:336:ASP:HB3	1.78	0.64
1:E:59:ARG:HH22	1:E:212:MET:HE2	1.52	0.64
1:B:274:VAL:C	1:B:275:VAL:HG23	2.23	0.64
1:B:278:LYS:NZ	1:B:278:LYS:HA	2.12	0.64
1:E:220:LYS:HG3	1:E:318:LEU:HD23	1.80	0.64
1:E:456:LEU:O	1:E:460:ASN:ND2	2.26	0.64
1:H:14:LEU:HB3	1:H:105:MET:HE1	1.78	0.64
1:I:251:MET:HB3	1:I:277:ILE:HD13	1.80	0.63
1:I:277:ILE:HG22	1:I:278:LYS:H	1.64	0.63
1:H:137:SER:HB3	1:H:412:VAL:HG12	1.78	0.63
1:A:251:MET:HB2	1:A:277:ILE:CD1	2.26	0.63
1:C:251:MET:HB2	1:C:277:ILE:CD1	2.25	0.63
1:I:418:CYS:HA	1:I:421:LEU:HD13	1.81	0.63
1:D:456:LEU:O	1:D:460:ASN:ND2	2.25	0.63
1:B:327:THR:OG1	1:B:328:LYS:N	2.32	0.63
1:F:254:GLU:CA	1:F:278:LYS:HZ2	2.12	0.63
1:G:137:SER:HB3	1:G:412:VAL:HG12	1.81	0.63
1:K:200:TYR:HA	1:K:277:ILE:CG2	2.24	0.62
1:E:267:LYS:HG3	1:E:273:LYS:HA	1.81	0.62
1:E:121:MET:HE2	1:E:445:ILE:HG21	1.81	0.62
1:B:253:GLU:C	1:B:278:LYS:HZ1	2.03	0.62
1:D:277:ILE:HD12	1:D:278:LYS:N	2.10	0.62
1:F:483:TYR:OH	1:F:488:ASP:OD1	2.17	0.62
1:B:17:MET:HA	1:B:68:GLU:HA	1.82	0.62
1:F:17:MET:HA	1:F:68:GLU:HA	1.82	0.62
1:G:17:MET:HA	1:G:68:GLU:HA	1.82	0.62
1:D:245:ASN:ND2	1:E:233:ASP:OD2	2.32	0.61
1:M:276:ALA:O	1:M:277:ILE:HG13	2.00	0.61
1:I:206:VAL:HG21	1:I:212:MET:CA	2.26	0.61
1:E:231:ALA:HB2	1:E:259:ALA:HA	1.83	0.61
1:C:277:ILE:HD12	1:C:278:LYS:N	2.15	0.61
1:E:201:THR:O	1:E:203:PRO:CA	2.49	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:17:MET:HA	1:J:68:GLU:HA	1.82	0.61
1:B:253:GLU:O	1:B:278:LYS:CE	2.48	0.61
1:D:157:THR:O	1:D:159:ILE:N	2.34	0.61
1:D:206:VAL:HG11	1:D:212:MET:HB2	1.83	0.61
1:E:216:TYR:HD2	1:E:247:PRO:HG2	1.65	0.61
1:L:483:TYR:OH	1:L:488:ASP:OD1	2.17	0.61
1:F:254:GLU:N	1:F:278:LYS:NZ	2.49	0.60
1:B:418:CYS:HA	1:B:421:LEU:HD13	1.82	0.60
1:D:193:GLY:HA3	1:D:377:VAL:HG11	1.83	0.60
1:H:17:MET:HA	1:H:68:GLU:HA	1.82	0.60
1:B:253:GLU:H	1:B:279:ALA:CB	2.12	0.60
1:D:418:CYS:HA	1:D:421:LEU:HD13	1.83	0.60
1:K:277:ILE:HD12	1:K:278:LYS:O	2.02	0.60
1:L:221:ILE:HA	1:L:249:LEU:HB2	1.84	0.60
1:L:353:LEU:O	1:L:357:THR:OG1	2.11	0.60
1:A:327:THR:OG1	1:A:328:LYS:N	2.33	0.60
1:C:14:LEU:HB3	1:C:105:MET:HE1	1.83	0.60
1:D:327:THR:OG1	1:D:328:LYS:N	2.32	0.60
1:K:277:ILE:HD12	1:K:278:LYS:N	2.17	0.60
1:I:14:LEU:HB3	1:I:105:MET:HE1	1.84	0.59
1:B:483:TYR:OH	1:B:488:ASP:OD1	2.19	0.59
1:N:251:MET:HB2	1:N:277:ILE:CD1	2.32	0.59
1:H:251:MET:CB	1:H:277:ILE:CD1	2.74	0.59
1:D:339:THR:HG22	1:D:342:ASP:H	1.67	0.59
1:E:267:LYS:CD	1:E:274:VAL:H	2.10	0.59
1:A:200:TYR:CA	1:A:277:ILE:HG22	2.28	0.59
1:B:278:LYS:HA	1:B:278:LYS:HZ3	1.67	0.59
1:J:321:ALA:HA	1:J:336:ASP:HB3	1.84	0.59
1:G:14:LEU:HB3	1:G:105:MET:HE1	1.84	0.59
1:A:456:LEU:O	1:A:460:ASN:ND2	2.27	0.59
1:B:280:PRO:O	1:B:281:GLY:C	2.45	0.59
1:K:251:MET:HB2	1:K:277:ILE:CD1	2.29	0.59
1:N:157:THR:O	1:N:159:ILE:N	2.35	0.58
1:E:267:LYS:NZ	1:E:273:LYS:CG	2.51	0.58
1:K:483:TYR:OH	1:K:488:ASP:OD1	2.20	0.58
1:L:157:THR:O	1:L:159:ILE:N	2.35	0.58
1:A:206:VAL:HG11	1:A:212:MET:HB2	1.86	0.58
1:G:483:TYR:OH	1:G:488:ASP:OD1	2.21	0.58
1:F:206:VAL:HG11	1:F:212:MET:HB2	1.86	0.58
1:K:65:ASP:HB3	1:K:68:GLU:HG2	1.85	0.58
1:M:321:ALA:HA	1:M:336:ASP:HB3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:327:THR:OG1	1:M:328:LYS:N	2.36	0.58
1:J:327:THR:OG1	1:J:328:LYS:N	2.36	0.58
1:A:277:ILE:HD12	1:A:278:LYS:O	2.04	0.58
1:K:321:ALA:HA	1:K:336:ASP:HB3	1.86	0.58
1:F:321:ALA:HA	1:F:336:ASP:HB3	1.84	0.58
1:K:17:MET:HA	1:K:68:GLU:HA	1.85	0.58
1:K:327:THR:OG1	1:K:328:LYS:N	2.35	0.58
1:N:321:ALA:HA	1:N:336:ASP:HB3	1.86	0.58
1:C:216:TYR:OH	1:C:267:LYS:NZ	2.36	0.58
1:E:205:PHE:CE2	1:E:264:VAL:O	2.57	0.58
1:A:483:TYR:OH	1:A:488:ASP:OD1	2.20	0.58
1:K:418:CYS:HA	1:K:421:LEU:HD13	1.86	0.58
1:A:216:TYR:OH	1:A:267:LYS:NZ	2.37	0.58
1:D:385:GLN:HB2	1:D:389:GLU:HG2	1.86	0.58
1:E:218:ASN:N	1:E:322:ALA:O	2.37	0.58
1:D:216:TYR:OH	1:D:267:LYS:NZ	2.37	0.58
1:L:321:ALA:HA	1:L:336:ASP:HB3	1.86	0.58
1:H:221:ILE:HD11	1:H:251:MET:HE2	1.86	0.57
1:I:17:MET:HA	1:I:68:GLU:HA	1.85	0.57
1:L:251:MET:HB2	1:L:277:ILE:CD1	2.33	0.57
1:C:441:MET:HE1	1:F:441:MET:HE1	1.85	0.57
1:F:253:GLU:HA	1:F:278:LYS:HE3	1.86	0.57
1:G:221:ILE:HA	1:G:249:LEU:HB2	1.86	0.57
1:C:456:LEU:O	1:C:460:ASN:ND2	2.26	0.57
1:G:237:ILE:HG12	1:G:313:ALA:HB3	1.86	0.57
1:I:20:GLY:HA3	1:I:68:GLU:HB2	1.85	0.57
1:K:20:GLY:HA3	1:K:68:GLU:HB2	1.87	0.57
1:L:277:ILE:HD12	1:L:278:LYS:O	2.05	0.57
1:E:231:ALA:O	1:E:233:ASP:N	2.38	0.57
1:N:483:TYR:OH	1:N:488:ASP:OD1	2.19	0.57
1:C:9:LYS:HG2	1:C:524:VAL:HG22	1.86	0.57
1:H:277:ILE:HD12	1:H:278:LYS:N	2.20	0.57
1:E:207:THR:HB	1:E:214:CYS:HA	1.87	0.57
1:I:327:THR:OG1	1:I:328:LYS:N	2.37	0.57
1:J:275:VAL:HG12	1:J:276:ALA:N	2.18	0.57
1:N:418:CYS:HA	1:N:421:LEU:HD13	1.86	0.57
1:E:205:PHE:CE1	1:E:267:LYS:CG	2.77	0.57
1:M:38:ASN:OD1	1:M:52:ASN:ND2	2.38	0.57
1:D:238:LEU:HD12	1:D:272:LEU:HD22	1.86	0.57
1:G:313:ALA:HB1	1:G:317:VAL:HG21	1.86	0.57
1:H:327:THR:OG1	1:H:328:LYS:N	2.31	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:354:GLN:O	1:I:363:ARG:NH1	2.38	0.57
1:A:441:MET:HE1	1:K:441:MET:HE1	1.87	0.57
1:B:157:THR:O	1:B:159:ILE:N	2.37	0.57
1:F:327:THR:OG1	1:F:328:LYS:N	2.37	0.57
1:M:250:ILE:O	1:M:277:ILE:HD12	2.05	0.57
1:D:421:LEU:HD11	1:D:454:ILE:HG21	1.87	0.56
1:F:253:GLU:C	1:F:278:LYS:HE3	2.30	0.56
1:E:17:MET:HA	1:E:68:GLU:HA	1.86	0.56
1:A:137:SER:HB3	1:A:412:VAL:HG12	1.86	0.56
1:A:282:PHE:HA	1:A:286:ARG:HE	1.70	0.56
1:F:253:GLU:O	1:F:278:LYS:CD	2.54	0.56
1:F:278:LYS:CE	1:F:278:LYS:HA	2.31	0.56
1:G:251:MET:CG	1:G:277:ILE:HD11	2.34	0.56
1:M:206:VAL:HG11	1:M:212:MET:HB2	1.86	0.56
1:B:277:ILE:HG22	1:B:326:ILE:HD13	1.87	0.56
1:C:206:VAL:HG11	1:C:212:MET:HB2	1.87	0.56
1:M:418:CYS:HA	1:M:421:LEU:HD13	1.87	0.56
1:L:277:ILE:HD12	1:L:278:LYS:H	1.69	0.56
1:A:251:MET:HB3	1:A:277:ILE:CG1	2.36	0.56
1:E:247:PRO:HG3	1:E:273:LYS:HB3	1.87	0.56
1:D:387:GLU:HA	1:E:282:PHE:CZ	2.40	0.56
1:D:441:MET:HE1	1:G:441:MET:HE1	1.87	0.56
1:E:286:ARG:O	1:E:290:LEU:HB2	2.06	0.56
1:G:327:THR:OG1	1:G:328:LYS:N	2.33	0.56
1:G:339:THR:HG22	1:G:342:ASP:H	1.70	0.56
1:N:221:ILE:HA	1:N:249:LEU:HB2	1.88	0.56
1:E:483:TYR:OH	1:E:488:ASP:OD1	2.24	0.56
1:I:65:ASP:HB3	1:I:68:GLU:HG2	1.88	0.55
1:I:221:ILE:HA	1:I:249:LEU:HB2	1.87	0.55
1:A:321:ALA:HA	1:A:336:ASP:HB3	1.87	0.55
1:B:321:ALA:HA	1:B:336:ASP:HB3	1.87	0.55
1:D:321:ALA:HA	1:D:336:ASP:HB3	1.88	0.55
1:G:491:GLU:HB3	1:G:496:THR:HG21	1.88	0.55
1:I:491:GLU:HB3	1:I:496:THR:HG21	1.87	0.55
1:C:277:ILE:HD12	1:C:278:LYS:O	2.06	0.55
1:D:221:ILE:HA	1:D:249:LEU:HB2	1.88	0.55
1:H:491:GLU:HB3	1:H:496:THR:HG21	1.88	0.55
1:M:221:ILE:HA	1:M:249:LEU:HB2	1.87	0.55
1:C:418:CYS:HA	1:C:421:LEU:HD13	1.88	0.55
1:B:216:TYR:OH	1:B:267:LYS:NZ	2.35	0.55
1:D:277:ILE:CD1	1:D:278:LYS:N	2.68	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:277:ILE:HD12	1:N:278:LYS:N	2.21	0.55
1:A:424:SER:HB2	1:A:447:LYS:HD2	1.88	0.55
1:G:88:ASP:OD1	1:G:89:GLY:N	2.39	0.55
1:L:17:MET:HA	1:L:68:GLU:HA	1.88	0.55
1:L:65:ASP:HB3	1:L:68:GLU:HG2	1.89	0.55
1:B:244:GLY:O	1:B:246:TYR:N	2.40	0.55
1:E:418:CYS:HA	1:E:421:LEU:HD13	1.89	0.55
1:G:216:TYR:OH	1:G:267:LYS:NZ	2.40	0.55
1:H:277:ILE:HD12	1:H:278:LYS:O	2.07	0.55
1:A:244:GLY:O	1:A:246:TYR:N	2.40	0.55
1:N:157:THR:OG1	1:N:158:ASP:N	2.39	0.55
1:N:339:THR:HG22	1:N:342:ASP:H	1.71	0.55
1:H:263:LEU:HG	1:H:274:VAL:HG21	1.89	0.55
1:I:441:MET:HE1	1:M:441:MET:HE1	1.89	0.55
1:N:244:GLY:O	1:N:246:TYR:N	2.40	0.54
1:I:157:THR:O	1:I:160:GLY:N	2.39	0.54
1:K:55:VAL:HG22	1:K:90:THR:HG21	1.89	0.54
1:B:277:ILE:HG13	1:B:277:ILE:O	2.06	0.54
1:F:254:GLU:N	1:F:278:LYS:HZ1	2.05	0.54
1:H:321:ALA:HA	1:H:336:ASP:HB3	1.89	0.54
1:J:275:VAL:HG12	1:J:277:ILE:HD12	1.88	0.54
1:D:244:GLY:O	1:D:246:TYR:N	2.41	0.54
1:F:221:ILE:HA	1:F:249:LEU:HB2	1.90	0.54
1:H:251:MET:HB2	1:H:277:ILE:HD11	1.83	0.54
1:H:276:ALA:C	1:H:277:ILE:HG23	2.26	0.54
1:A:125:VAL:HG23	1:A:509:MET:HE2	1.89	0.54
1:I:483:TYR:OH	1:I:488:ASP:OD1	2.20	0.54
1:E:88:ASP:OD1	1:E:89:GLY:N	2.41	0.54
1:F:14:LEU:HB3	1:F:105:MET:HE1	1.90	0.54
1:G:251:MET:HB2	1:G:277:ILE:HD12	1.88	0.54
1:I:339:THR:HG22	1:I:342:ASP:H	1.72	0.54
1:K:221:ILE:HA	1:K:249:LEU:HB2	1.89	0.54
1:B:424:SER:HB2	1:B:447:LYS:HD2	1.90	0.54
1:C:450:LEU:HD21	1:C:509:MET:HE3	1.90	0.54
1:E:267:LYS:CD	1:E:274:VAL:O	2.56	0.54
1:J:65:ASP:HB3	1:J:68:GLU:HG2	1.90	0.54
1:A:353:LEU:O	1:A:357:THR:OG1	2.21	0.54
1:B:250:ILE:O	1:B:277:ILE:CG1	2.53	0.54
1:D:193:GLY:N	1:D:377:VAL:HG12	2.23	0.54
1:D:263:LEU:HG	1:D:274:VAL:HG21	1.90	0.54
1:B:277:ILE:HG22	1:B:326:ILE:CD1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:483:TYR:OH	1:D:488:ASP:OD1	2.25	0.54
1:E:200:TYR:HB3	1:E:328:LYS:HA	1.90	0.54
1:E:202:SER:HB3	1:E:203:PRO:HA	1.89	0.54
1:K:251:MET:HB3	1:K:277:ILE:CG1	2.38	0.54
1:B:274:VAL:C	1:B:275:VAL:CG2	2.80	0.54
1:G:157:THR:O	1:G:159:ILE:N	2.40	0.53
1:H:159:ILE:HG12	1:H:397:VAL:HG12	1.89	0.53
1:H:450:LEU:HD21	1:H:509:MET:HE3	1.90	0.53
1:L:263:LEU:HG	1:L:274:VAL:HG21	1.90	0.53
1:H:418:CYS:HA	1:H:421:LEU:HD13	1.89	0.53
1:B:201:THR:HB	1:B:276:ALA:HB1	1.90	0.53
1:A:263:LEU:HG	1:A:274:VAL:HG21	1.91	0.53
1:B:353:LEU:O	1:B:357:THR:OG1	2.24	0.53
1:C:157:THR:O	1:C:160:GLY:N	2.38	0.53
1:E:281:GLY:HA3	1:E:285:ARG:HB2	1.90	0.53
1:D:73:THR:HA	1:D:76:ARG:HD3	1.90	0.53
1:J:339:THR:HG22	1:J:342:ASP:H	1.74	0.53
1:G:244:GLY:O	1:G:246:TYR:N	2.42	0.53
1:K:157:THR:O	1:K:160:GLY:N	2.42	0.53
1:K:421:LEU:HD11	1:K:454:ILE:HG21	1.91	0.53
1:K:424:SER:HB2	1:K:447:LYS:HD2	1.91	0.53
1:M:491:GLU:HB3	1:M:496:THR:HG21	1.90	0.53
1:G:202:SER:HB3	1:G:204:TYR:HD1	1.73	0.53
1:H:238:LEU:HD12	1:H:272:LEU:HD22	1.91	0.53
1:K:456:LEU:O	1:K:460:ASN:ND2	2.26	0.53
1:K:491:GLU:HB3	1:K:496:THR:HG21	1.91	0.53
1:G:233:ASP:O	1:G:236:THR:OG1	2.27	0.53
1:M:483:TYR:OH	1:M:488:ASP:OD1	2.27	0.53
1:D:137:SER:HB3	1:D:412:VAL:HG12	1.91	0.53
1:D:334:VAL:CG2	1:D:377:VAL:CG1	2.75	0.53
1:F:198:ARG:NH1	1:F:279:ALA:O	2.42	0.53
1:G:338:SER:OG	1:G:339:THR:N	2.42	0.53
1:A:88:ASP:OD1	1:A:89:GLY:N	2.41	0.53
1:B:238:LEU:HD12	1:B:272:LEU:HD22	1.92	0.53
1:C:276:ALA:C	1:C:277:ILE:HG23	2.26	0.53
1:E:202:SER:N	1:E:203:PRO:HA	2.24	0.53
1:F:253:GLU:HG2	1:F:278:LYS:HZ1	1.74	0.53
1:J:88:ASP:OD1	1:J:89:GLY:N	2.41	0.53
1:L:327:THR:OG1	1:L:328:LYS:N	2.31	0.53
1:C:244:GLY:O	1:C:246:TYR:N	2.42	0.52
1:C:277:ILE:HD12	1:C:278:LYS:H	1.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:491:GLU:HB3	1:E:496:THR:HG21	1.90	0.52
1:I:121:MET:HE2	1:I:445:ILE:HG21	1.89	0.52
1:I:321:ALA:HA	1:I:336:ASP:HB3	1.90	0.52
1:J:421:LEU:HD11	1:J:454:ILE:HG21	1.91	0.52
1:A:238:LEU:HD12	1:A:272:LEU:HD22	1.90	0.52
1:D:277:ILE:HD13	1:D:278:LYS:HG2	1.90	0.52
1:I:159:ILE:HG12	1:I:397:VAL:HG12	1.91	0.52
1:E:233:ASP:OD1	1:E:234:ILE:N	2.40	0.52
1:F:491:GLU:HB3	1:F:496:THR:HG21	1.91	0.52
1:I:456:LEU:O	1:I:460:ASN:ND2	2.28	0.52
1:L:456:LEU:O	1:L:460:ASN:ND2	2.25	0.52
1:M:244:GLY:O	1:M:246:TYR:N	2.43	0.52
1:B:206:VAL:HG11	1:B:212:MET:HB2	1.91	0.52
1:E:194:MET:HE1	1:E:372:ARG:HG3	1.91	0.52
1:H:424:SER:HB2	1:H:447:LYS:HD2	1.91	0.52
1:B:278:LYS:HZ3	1:B:278:LYS:CA	2.23	0.52
1:B:339:THR:HG22	1:B:342:ASP:H	1.73	0.52
1:E:211:ARG:NH1	1:E:211:ARG:CG	2.73	0.52
1:J:157:THR:O	1:J:159:ILE:N	2.43	0.52
1:K:221:ILE:HD11	1:K:251:MET:HE2	1.91	0.52
1:L:276:ALA:O	1:L:277:ILE:HG22	2.04	0.52
1:D:450:LEU:HD21	1:D:509:MET:HE3	1.92	0.52
1:E:291:GLU:O	1:E:295:ILE:HB	2.10	0.52
1:M:456:LEU:O	1:M:460:ASN:ND2	2.29	0.52
1:C:238:LEU:HD12	1:C:272:LEU:HD22	1.91	0.52
1:J:157:THR:O	1:J:160:GLY:N	2.40	0.52
1:J:285:ARG:NH2	1:J:368:GLU:OE2	2.43	0.52
1:J:450:LEU:HD21	1:J:509:MET:HE3	1.90	0.52
1:K:263:LEU:HG	1:K:274:VAL:HG21	1.91	0.52
1:N:238:LEU:HD12	1:N:272:LEU:HD22	1.91	0.52
1:G:238:LEU:HD12	1:G:272:LEU:HD22	1.92	0.52
1:B:221:ILE:HA	1:B:249:LEU:HB2	1.91	0.52
1:B:456:LEU:O	1:B:460:ASN:ND2	2.28	0.52
1:C:88:ASP:OD1	1:C:89:GLY:N	2.41	0.52
1:D:306:MET:HB2	1:D:307:GLY:HA2	1.92	0.52
1:E:205:PHE:CD2	1:E:267:LYS:CB	2.63	0.52
1:A:51:VAL:HG12	1:A:53:ASP:H	1.74	0.52
1:A:221:ILE:HD11	1:A:251:MET:HE2	1.92	0.52
1:G:456:LEU:O	1:G:460:ASN:ND2	2.27	0.52
1:H:88:ASP:OD1	1:H:89:GLY:N	2.42	0.52
1:J:483:TYR:OH	1:J:488:ASP:OD1	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:244:GLY:O	1:I:246:TYR:N	2.43	0.51
1:J:221:ILE:HA	1:J:249:LEU:HB2	1.91	0.51
1:K:88:ASP:OD1	1:K:89:GLY:N	2.38	0.51
1:L:339:THR:HG22	1:L:342:ASP:H	1.74	0.51
1:M:421:LEU:HD11	1:M:454:ILE:HG21	1.91	0.51
1:N:240:SER:OG	1:N:243:ARG:NH1	2.43	0.51
1:B:157:THR:OG1	1:B:158:ASP:N	2.42	0.51
1:B:278:LYS:NZ	1:B:278:LYS:CB	2.73	0.51
1:E:421:LEU:HD11	1:E:454:ILE:HG21	1.92	0.51
1:M:424:SER:HB2	1:M:447:LYS:HD2	1.92	0.51
1:N:277:ILE:HD12	1:N:278:LYS:O	2.10	0.51
1:B:201:THR:CB	1:B:276:ALA:HB1	2.41	0.51
1:C:73:THR:HA	1:C:76:ARG:HD3	1.92	0.51
1:G:206:VAL:HG11	1:G:212:MET:HB2	1.90	0.51
1:I:338:SER:OG	1:I:339:THR:N	2.43	0.51
1:J:137:SER:HB3	1:J:412:VAL:HG12	1.92	0.51
1:A:105:MET:HA	1:A:108:VAL:HB	1.91	0.51
1:B:285:ARG:NH2	1:B:368:GLU:OE2	2.43	0.51
1:E:306:MET:N	1:E:307:GLY:HA2	2.26	0.51
1:H:206:VAL:HG11	1:H:212:MET:HB2	1.92	0.51
1:J:274:VAL:C	1:J:275:VAL:HG23	2.35	0.51
1:A:240:SER:OG	1:A:243:ARG:NH1	2.43	0.51
1:E:241:ALA:O	1:E:245:ASN:N	2.39	0.51
1:F:194:MET:HE1	1:F:373:LEU:HA	1.91	0.51
1:F:244:GLY:O	1:F:246:TYR:N	2.44	0.51
1:J:104:GLY:HA2	1:J:445:ILE:HD13	1.93	0.51
1:L:238:LEU:HD12	1:L:272:LEU:HD22	1.92	0.51
1:L:244:GLY:O	1:L:246:TYR:N	2.44	0.51
1:M:55:VAL:HG22	1:M:90:THR:HG21	1.93	0.51
1:A:418:CYS:HA	1:A:421:LEU:HD13	1.91	0.51
1:B:278:LYS:NZ	1:B:278:LYS:CA	2.73	0.51
1:E:194:MET:HG3	1:E:296:LEU:HD22	1.93	0.51
1:G:20:GLY:HA3	1:G:68:GLU:HB2	1.92	0.51
1:A:157:THR:O	1:A:159:ILE:N	2.44	0.51
1:H:216:TYR:OH	1:H:267:LYS:NZ	2.43	0.51
1:L:285:ARG:NH2	1:L:368:GLU:OE2	2.44	0.51
1:N:221:ILE:HD11	1:N:251:MET:HE2	1.93	0.51
1:D:251:MET:HB3	1:D:277:ILE:HG22	1.92	0.51
1:E:450:LEU:HD21	1:E:509:MET:HE3	1.93	0.51
1:G:40:VAL:HG22	1:G:50:ILE:HG22	1.92	0.51
1:G:424:SER:HB2	1:G:447:LYS:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:20:GLY:HA3	1:H:68:GLU:HB2	1.92	0.51
1:H:483:TYR:OH	1:H:488:ASP:OD1	2.24	0.51
1:M:277:ILE:HG22	1:M:278:LYS:H	1.75	0.51
1:B:450:LEU:HD21	1:B:509:MET:HE3	1.91	0.51
1:C:240:SER:OG	1:C:243:ARG:NH1	2.44	0.51
1:D:217:GLU:HG2	1:D:323:LYS:HG2	1.93	0.51
1:F:253:GLU:O	1:F:278:LYS:HD2	2.10	0.51
1:F:263:LEU:HG	1:F:274:VAL:HG21	1.92	0.51
1:F:450:LEU:HD21	1:F:509:MET:HE3	1.93	0.51
1:G:450:LEU:HD21	1:G:509:MET:HE3	1.91	0.51
1:J:263:LEU:HG	1:J:274:VAL:HG21	1.92	0.51
1:J:387:GLU:OE2	1:M:198:ARG:NH2	2.44	0.51
1:N:88:ASP:OD1	1:N:89:GLY:N	2.43	0.51
1:D:424:SER:HB2	1:D:447:LYS:HD2	1.93	0.51
1:G:157:THR:O	1:G:160:GLY:N	2.41	0.51
1:G:232:ARG:H	1:G:232:ARG:HD2	1.76	0.51
1:G:277:ILE:HD12	1:G:278:LYS:O	2.10	0.51
1:K:244:GLY:O	1:K:246:TYR:N	2.44	0.51
1:C:65:ASP:HB3	1:C:68:GLU:HG2	1.92	0.50
1:F:278:LYS:HE3	1:F:278:LYS:CA	2.38	0.50
1:K:38:ASN:OD1	1:K:52:ASN:ND2	2.43	0.50
1:N:216:TYR:OH	1:N:267:LYS:NZ	2.36	0.50
1:N:491:GLU:HB3	1:N:496:THR:HG21	1.92	0.50
1:E:195:GLN:HB2	1:E:332:THR:HG22	1.93	0.50
1:E:202:SER:HB3	1:E:203:PRO:C	2.36	0.50
1:F:376:GLY:O	1:F:377:VAL:HG23	2.11	0.50
1:N:424:SER:HB2	1:N:447:LYS:HD2	1.93	0.50
1:C:83:ASN:HB2	1:C:90:THR:HG22	1.94	0.50
1:E:73:THR:HA	1:E:76:ARG:HD3	1.94	0.50
1:E:209:PRO:CA	1:E:212:MET:H	2.16	0.50
1:M:88:ASP:OD1	1:M:89:GLY:N	2.39	0.50
1:M:338:SER:OG	1:M:339:THR:N	2.43	0.50
1:B:217:GLU:HG2	1:B:323:LYS:HG2	1.93	0.50
1:C:421:LEU:HD11	1:C:454:ILE:HG21	1.92	0.50
1:E:205:PHE:CD2	1:E:267:LYS:HD3	2.46	0.50
1:F:218:ASN:N	1:F:322:ALA:O	2.33	0.50
1:M:104:GLY:HA2	1:M:445:ILE:HD13	1.92	0.50
1:E:202:SER:CB	1:E:203:PRO:C	2.85	0.50
1:M:238:LEU:HD12	1:M:272:LEU:HD22	1.93	0.50
1:E:202:SER:HB3	1:E:203:PRO:CA	2.42	0.50
1:E:209:PRO:HB2	1:E:210:GLU:C	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:73:THR:HA	1:J:76:ARG:HD3	1.94	0.50
1:A:10:ASP:CG	1:A:11:MET:H	2.20	0.50
1:E:137:SER:HB3	1:E:412:VAL:HG12	1.94	0.50
1:E:202:SER:OG	1:E:204:TYR:CB	2.58	0.50
1:F:61:VAL:O	1:F:76:ARG:NH1	2.44	0.50
1:I:263:LEU:HG	1:I:274:VAL:HG21	1.94	0.50
1:K:339:THR:HG22	1:K:342:ASP:H	1.77	0.50
1:L:207:THR:OG1	1:L:213:ILE:O	2.29	0.50
1:N:104:GLY:HA2	1:N:445:ILE:HD13	1.93	0.50
1:N:338:SER:OG	1:N:339:THR:N	2.44	0.50
1:J:275:VAL:CG1	1:J:276:ALA:N	2.74	0.50
1:J:456:LEU:O	1:J:460:ASN:ND2	2.29	0.50
1:M:277:ILE:HG21	1:M:331:THR:HG21	1.94	0.50
1:A:157:THR:O	1:A:160:GLY:N	2.41	0.50
1:N:217:GLU:HG2	1:N:323:LYS:HG2	1.93	0.50
1:B:14:LEU:HB3	1:B:105:MET:HE1	1.94	0.50
1:C:483:TYR:OH	1:C:488:ASP:OD1	2.25	0.50
1:E:205:PHE:CG	1:E:267:LYS:CD	2.94	0.50
1:E:424:SER:HB2	1:E:447:LYS:HD2	1.94	0.50
1:J:277:ILE:CG2	1:J:278:LYS:N	2.75	0.50
1:K:207:THR:OG1	1:K:214:CYS:HA	2.12	0.50
1:M:167:MET:HE1	1:M:408:VAL:HG11	1.94	0.50
1:M:276:ALA:C	1:M:277:ILE:CD1	2.85	0.50
1:A:450:LEU:HD21	1:A:509:MET:HE3	1.94	0.49
1:B:491:GLU:HB3	1:B:496:THR:HG21	1.94	0.49
1:G:353:LEU:O	1:G:357:THR:OG1	2.19	0.49
1:K:9:LYS:HG2	1:K:524:VAL:HG22	1.94	0.49
1:B:278:LYS:CE	1:B:278:LYS:CA	2.85	0.49
1:E:118:VAL:HG21	1:E:517:LYS:HG3	1.92	0.49
1:G:418:CYS:HA	1:G:421:LEU:HD13	1.94	0.49
1:E:209:PRO:CA	1:E:210:GLU:C	2.85	0.49
1:E:209:PRO:CB	1:E:210:GLU:C	2.85	0.49
1:E:350:ILE:HG21	1:E:370:ILE:HB	1.94	0.49
1:H:339:THR:HG22	1:H:342:ASP:H	1.76	0.49
1:J:104:GLY:HA3	1:J:520:LEU:HD21	1.94	0.49
1:L:233:ASP:O	1:L:236:THR:OG1	2.30	0.49
1:C:20:GLY:HA3	1:C:68:GLU:HB2	1.94	0.49
1:C:200:TYR:CA	1:C:277:ILE:HG22	2.34	0.49
1:C:217:GLU:HG2	1:C:323:LYS:HG2	1.94	0.49
1:E:216:TYR:CD2	1:E:247:PRO:HG2	2.44	0.49
1:H:327:THR:HG1	1:H:328:LYS:H	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:221:ILE:HD11	1:I:251:MET:HE2	1.94	0.49
1:K:217:GLU:HG2	1:K:323:LYS:HG2	1.93	0.49
1:L:157:THR:OG1	1:L:158:ASP:N	2.39	0.49
1:M:276:ALA:C	1:M:277:ILE:CG1	2.85	0.49
1:C:221:ILE:HA	1:C:249:LEU:HB2	1.94	0.49
1:G:263:LEU:HG	1:G:274:VAL:HG21	1.95	0.49
1:H:393:LYS:O	1:H:397:VAL:HG13	2.12	0.49
1:K:285:ARG:NH2	1:K:368:GLU:OE2	2.46	0.49
1:B:263:LEU:HG	1:B:274:VAL:HG21	1.94	0.49
1:E:205:PHE:HE2	1:E:264:VAL:O	1.95	0.49
1:I:424:SER:HB2	1:I:447:LYS:HD2	1.93	0.49
1:K:137:SER:HB3	1:K:412:VAL:HG12	1.93	0.49
1:L:338:SER:OG	1:L:339:THR:N	2.44	0.49
1:A:217:GLU:HG2	1:A:323:LYS:HG2	1.93	0.49
1:N:353:LEU:O	1:N:357:THR:OG1	2.24	0.49
1:B:253:GLU:O	1:B:278:LYS:HE3	2.13	0.49
1:E:205:PHE:CD2	1:E:267:LYS:CD	2.95	0.49
1:F:104:GLY:HA2	1:F:445:ILE:HD13	1.94	0.49
1:K:238:LEU:HD12	1:K:272:LEU:HD22	1.94	0.49
1:A:137:SER:N	1:A:412:VAL:O	2.38	0.49
1:N:194:MET:N	1:N:377:VAL:HG21	2.26	0.49
1:B:104:GLY:HA2	1:B:445:ILE:HD13	1.94	0.49
1:C:424:SER:HB2	1:C:447:LYS:HD2	1.94	0.49
1:E:180:GLU:HA	1:E:382:VAL:HG12	1.93	0.49
1:K:167:MET:HE1	1:K:408:VAL:HG11	1.95	0.49
1:F:285:ARG:NH2	1:F:368:GLU:OE2	2.46	0.49
1:G:65:ASP:HB3	1:G:68:GLU:HG2	1.95	0.49
1:H:306:MET:HB2	1:H:307:GLY:HA2	1.95	0.49
1:K:232:ARG:H	1:K:232:ARG:HD2	1.78	0.49
1:M:157:THR:O	1:M:160:GLY:N	2.45	0.49
1:N:421:LEU:HD11	1:N:454:ILE:HG21	1.94	0.48
1:B:157:THR:O	1:B:160:GLY:N	2.43	0.48
1:C:181:GLY:HA2	1:C:182:LYS:HA	1.64	0.48
1:E:175:VAL:CG1	1:E:377:VAL:HG22	2.42	0.48
1:G:321:ALA:HA	1:G:336:ASP:HB3	1.94	0.48
1:J:424:SER:HB2	1:J:447:LYS:HD2	1.95	0.48
1:K:206:VAL:HB	1:K:212:MET:HA	1.94	0.48
1:L:266:ASN:HB3	1:L:272:LEU:HB3	1.95	0.48
1:C:104:GLY:HA2	1:C:445:ILE:HD13	1.94	0.48
1:E:157:THR:O	1:E:160:GLY:N	2.46	0.48
1:E:209:PRO:HA	1:E:211:ARG:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:217:GLU:HG2	1:J:323:LYS:HG2	1.96	0.48
1:C:306:MET:HB2	1:C:307:GLY:HA2	1.94	0.48
1:D:221:ILE:HD11	1:D:251:MET:HE2	1.94	0.48
1:E:38:ASN:OD1	1:E:52:ASN:ND2	2.44	0.48
1:E:200:TYR:CD1	1:E:328:LYS:HD3	2.48	0.48
1:J:418:CYS:HA	1:J:421:LEU:HD13	1.95	0.48
1:L:73:THR:HA	1:L:76:ARG:HD3	1.94	0.48
1:N:65:ASP:HB3	1:N:68:GLU:HG2	1.95	0.48
1:C:21:VAL:HG11	1:C:101:ILE:HD12	1.94	0.48
1:D:377:VAL:O	1:D:377:VAL:HG13	2.12	0.48
1:E:10:ASP:CG	1:E:11:MET:H	2.21	0.48
1:E:205:PHE:C	1:E:206:VAL:CG2	2.85	0.48
1:G:355:MET:SD	1:G:356:GLN:HG2	2.53	0.48
1:J:306:MET:H	1:J:307:GLY:HA3	1.78	0.48
1:M:14:LEU:HB3	1:M:105:MET:HE1	1.94	0.48
1:D:325:THR:O	1:D:332:THR:OG1	2.28	0.48
1:E:212:MET:O	1:E:212:MET:HG2	2.13	0.48
1:F:338:SER:OG	1:F:339:THR:N	2.44	0.48
1:I:88:ASP:OD1	1:I:89:GLY:N	2.42	0.48
1:I:125:VAL:HG23	1:I:509:MET:HE2	1.95	0.48
1:I:421:LEU:HD11	1:I:454:ILE:HG21	1.95	0.48
1:L:424:SER:HB2	1:L:447:LYS:HD2	1.95	0.48
1:N:263:LEU:HG	1:N:274:VAL:HG21	1.95	0.48
1:B:437:PRO:O	1:B:441:MET:HG2	2.14	0.48
1:D:285:ARG:NH2	1:D:368:GLU:OE2	2.47	0.48
1:E:233:ASP:C	1:E:235:ILE:H	2.22	0.48
1:M:263:LEU:HG	1:M:274:VAL:HG21	1.93	0.48
1:N:251:MET:HB3	1:N:277:ILE:CG1	2.43	0.48
1:C:157:THR:O	1:C:159:ILE:N	2.47	0.48
1:H:338:SER:OG	1:H:339:THR:N	2.45	0.48
1:J:275:VAL:CG1	1:J:277:ILE:HD11	2.44	0.48
1:K:517:LYS:O	1:K:521:LEU:HB2	2.14	0.48
1:N:21:VAL:HG13	1:N:75:VAL:HG21	1.95	0.48
1:N:306:MET:HB2	1:N:307:GLY:HA2	1.96	0.48
1:C:221:ILE:HD11	1:C:251:MET:HE2	1.95	0.48
1:C:321:ALA:HA	1:C:336:ASP:HB3	1.96	0.48
1:I:393:LYS:O	1:I:397:VAL:HG13	2.14	0.48
1:L:418:CYS:HA	1:L:421:LEU:HD13	1.94	0.48
1:G:277:ILE:HD12	1:G:278:LYS:N	2.29	0.48
1:J:200:TYR:CA	1:J:277:ILE:HG13	2.40	0.48
1:C:327:THR:OG1	1:C:328:LYS:N	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:306:MET:HB2	1:G:307:GLY:HA2	1.96	0.47
1:G:325:THR:O	1:G:332:THR:OG1	2.29	0.47
1:H:437:PRO:O	1:H:441:MET:HG2	2.14	0.47
1:A:218:ASN:N	1:A:322:ALA:O	2.34	0.47
1:N:181:GLY:HA2	1:N:182:LYS:HA	1.68	0.47
1:N:327:THR:OG1	1:N:328:LYS:N	2.32	0.47
1:B:253:GLU:CA	1:B:279:ALA:HB3	2.43	0.47
1:E:208:ASP:OD1	1:E:209:PRO:HD2	2.13	0.47
1:F:339:THR:HG22	1:F:342:ASP:H	1.79	0.47
1:I:232:ARG:H	1:I:232:ARG:HD2	1.79	0.47
1:A:491:GLU:HB3	1:A:496:THR:HG21	1.95	0.47
1:E:189:VAL:HG12	1:E:191:VAL:HG13	1.95	0.47
1:G:47:ALA:HA	1:G:48:PRO:HD3	1.79	0.47
1:H:104:GLY:HA2	1:H:445:ILE:HD13	1.96	0.47
1:L:306:MET:HB2	1:L:307:GLY:HA2	1.95	0.47
1:C:251:MET:HB3	1:C:277:ILE:CG1	2.44	0.47
1:F:424:SER:HB2	1:F:447:LYS:HD2	1.95	0.47
1:G:437:PRO:O	1:G:441:MET:HG2	2.15	0.47
1:I:251:MET:HB3	1:I:277:ILE:HB	1.95	0.47
1:M:339:THR:HG22	1:M:342:ASP:H	1.79	0.47
1:B:41:LEU:HD21	1:B:60:GLU:HG3	1.96	0.47
1:B:278:LYS:HZ3	1:B:279:ALA:N	2.13	0.47
1:B:280:PRO:C	1:B:281:GLY:O	2.58	0.47
1:B:306:MET:HB2	1:B:307:GLY:HA2	1.95	0.47
1:C:263:LEU:HG	1:C:274:VAL:HG21	1.96	0.47
1:C:376:GLY:C	1:C:377:VAL:HG23	2.40	0.47
1:E:200:TYR:CZ	1:E:328:LYS:HE3	2.44	0.47
1:F:10:ASP:CG	1:F:11:MET:H	2.21	0.47
1:F:221:ILE:HD11	1:F:251:MET:HE2	1.96	0.47
1:F:437:PRO:O	1:F:441:MET:HG2	2.14	0.47
1:H:202:SER:HB3	1:H:204:TYR:HD1	1.79	0.47
1:I:128:LEU:HD23	1:I:509:MET:HE1	1.96	0.47
1:M:306:MET:HB2	1:M:307:GLY:HA2	1.95	0.47
1:D:193:GLY:CA	1:D:377:VAL:HG12	2.44	0.47
1:F:277:ILE:HD12	1:F:278:LYS:O	2.00	0.47
1:F:418:CYS:HA	1:F:421:LEU:HD13	1.96	0.47
1:G:104:GLY:HA2	1:G:445:ILE:HD13	1.96	0.47
1:K:450:LEU:HD21	1:K:509:MET:HE3	1.97	0.47
1:A:65:ASP:HB3	1:A:68:GLU:HG2	1.95	0.47
1:A:104:GLY:HA2	1:A:445:ILE:HD13	1.96	0.47
1:A:221:ILE:HA	1:A:249:LEU:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:GLU:HB2	1:A:503:LYS:HB2	1.97	0.47
1:N:9:LYS:HG2	1:N:524:VAL:HG22	1.97	0.47
1:N:193:GLY:C	1:N:377:VAL:HG22	2.27	0.47
1:B:88:ASP:OD1	1:B:89:GLY:N	2.44	0.47
1:E:66:PRO:HB2	1:E:527:THR:HG21	1.97	0.47
1:E:200:TYR:CD1	1:E:201:THR:N	2.83	0.47
1:E:255:VAL:HG23	1:E:259:ALA:HB3	1.97	0.47
1:E:310:LEU:H	1:E:310:LEU:HD22	1.79	0.47
1:F:421:LEU:HD11	1:F:454:ILE:HG21	1.97	0.47
1:H:172:ARG:O	1:H:174:GLY:N	2.48	0.47
1:J:20:GLY:HA3	1:J:68:GLU:HB2	1.95	0.47
1:J:517:LYS:O	1:J:521:LEU:HB2	2.14	0.47
1:N:125:VAL:HG23	1:N:509:MET:HE2	1.97	0.47
1:E:205:PHE:O	1:E:206:VAL:HG22	2.15	0.47
1:E:350:ILE:HG12	1:E:369:ARG:HH21	1.80	0.47
1:I:276:ALA:O	1:I:277:ILE:HG13	2.14	0.47
1:L:217:GLU:HG2	1:L:323:LYS:HG2	1.96	0.47
1:A:133:ARG:O	1:A:136:SER:OG	2.30	0.47
1:D:65:ASP:HB3	1:D:68:GLU:HG2	1.96	0.47
1:F:238:LEU:HD12	1:F:272:LEU:HD22	1.97	0.47
1:F:277:ILE:HD12	1:F:278:LYS:C	2.39	0.47
1:L:232:ARG:H	1:L:232:ARG:HD2	1.80	0.47
1:A:22:ASP:O	1:A:26:THR:OG1	2.24	0.47
1:D:437:PRO:O	1:D:441:MET:HG2	2.15	0.47
1:H:421:LEU:HD11	1:H:454:ILE:HG21	1.97	0.47
1:J:125:VAL:HG23	1:J:509:MET:HE2	1.97	0.47
1:L:21:VAL:HG13	1:L:75:VAL:HG21	1.98	0.47
1:A:121:MET:HE2	1:A:445:ILE:HG21	1.96	0.46
1:A:393:LYS:O	1:A:397:VAL:HG13	2.15	0.46
1:A:437:PRO:O	1:A:441:MET:HG2	2.16	0.46
1:E:198:ARG:HB3	1:E:277:ILE:HD11	1.97	0.46
1:I:306:MET:HB2	1:I:307:GLY:HA2	1.95	0.46
1:K:137:SER:N	1:K:412:VAL:O	2.41	0.46
1:L:491:GLU:HB3	1:L:496:THR:HG21	1.97	0.46
1:A:24:LEU:HD11	1:A:76:ARG:HG3	1.97	0.46
1:A:338:SER:OG	1:A:339:THR:N	2.46	0.46
1:B:201:THR:HB	1:B:276:ALA:CB	2.45	0.46
1:B:201:THR:OG1	1:B:276:ALA:HB1	2.15	0.46
1:G:172:ARG:O	1:G:174:GLY:N	2.48	0.46
1:H:244:GLY:O	1:H:246:TYR:N	2.48	0.46
1:M:232:ARG:H	1:M:232:ARG:HD2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:276:ALA:C	1:M:277:ILE:HG13	2.40	0.46
1:C:339:THR:HG22	1:C:342:ASP:H	1.81	0.46
1:E:437:PRO:O	1:E:441:MET:HG2	2.15	0.46
1:F:410:GLU:HB2	1:F:503:LYS:HB2	1.96	0.46
1:G:296:LEU:HG	1:G:343:VAL:HG22	1.97	0.46
1:G:303:ARG:HE	1:G:305:GLU:HB2	1.79	0.46
1:H:142:ASP:OD1	1:H:142:ASP:N	2.48	0.46
1:I:216:TYR:HB3	1:I:219:CYS:SG	2.55	0.46
1:K:306:MET:HB2	1:K:307:GLY:HA2	1.95	0.46
1:A:285:ARG:NH2	1:A:368:GLU:OE2	2.49	0.46
1:A:436:ASP:OD1	1:A:436:ASP:N	2.48	0.46
1:C:10:ASP:CG	1:C:11:MET:H	2.23	0.46
1:C:376:GLY:O	1:C:377:VAL:HG23	2.15	0.46
1:H:251:MET:HB2	1:H:277:ILE:CD1	2.45	0.46
1:I:275:VAL:HG12	1:I:277:ILE:HD11	1.97	0.46
1:B:172:ARG:O	1:B:174:GLY:N	2.48	0.46
1:B:221:ILE:HD11	1:B:251:MET:HE2	1.96	0.46
1:D:393:LYS:O	1:D:397:VAL:HG13	2.15	0.46
1:G:421:LEU:HD11	1:G:454:ILE:HG21	1.97	0.46
1:L:172:ARG:O	1:L:174:GLY:N	2.49	0.46
1:M:65:ASP:HB3	1:M:68:GLU:HG2	1.96	0.46
1:N:437:PRO:O	1:N:441:MET:HG2	2.16	0.46
1:B:251:MET:CB	1:B:277:ILE:O	2.64	0.46
1:D:338:SER:OG	1:D:339:THR:N	2.44	0.46
1:E:202:SER:CB	1:E:203:PRO:CA	2.93	0.46
1:K:209:PRO:HA	1:K:212:MET:H	1.80	0.46
1:M:159:ILE:HG12	1:M:397:VAL:HG12	1.98	0.46
1:M:181:GLY:HA2	1:M:182:LYS:HA	1.68	0.46
1:A:339:THR:HG22	1:A:342:ASP:H	1.81	0.46
1:E:205:PHE:CD2	1:E:267:LYS:CG	2.97	0.46
1:F:172:ARG:O	1:F:174:GLY:N	2.49	0.46
1:F:253:GLU:CA	1:F:278:LYS:HE3	2.45	0.46
1:H:65:ASP:HB3	1:H:68:GLU:HG2	1.97	0.46
1:H:78:ALA:HB2	1:H:515:VAL:HG11	1.98	0.46
1:J:410:GLU:HB2	1:J:503:LYS:HB2	1.97	0.46
1:K:104:GLY:HA2	1:K:445:ILE:HD13	1.96	0.46
1:L:207:THR:HG23	1:L:214:CYS:SG	2.56	0.46
1:N:172:ARG:O	1:N:174:GLY:N	2.48	0.46
1:D:104:GLY:HA3	1:D:520:LEU:HD21	1.96	0.46
1:D:334:VAL:HG23	1:D:377:VAL:HG21	1.91	0.46
1:H:206:VAL:HB	1:H:212:MET:HA	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:172:ARG:O	1:J:174:GLY:N	2.48	0.46
1:J:238:LEU:HD12	1:J:272:LEU:HD22	1.97	0.46
1:L:251:MET:HB3	1:L:277:ILE:CG1	2.45	0.46
1:C:437:PRO:O	1:C:441:MET:HG2	2.16	0.46
1:E:277:ILE:HG12	1:E:331:THR:HG21	1.97	0.46
1:F:393:LYS:O	1:F:397:VAL:HG13	2.16	0.46
1:I:172:ARG:O	1:I:174:GLY:N	2.49	0.46
1:J:119:ARG:O	1:J:119:ARG:NH1	2.48	0.46
1:J:121:MET:HE2	1:J:445:ILE:HG21	1.98	0.46
1:K:215:GLU:O	1:K:215:GLU:HG3	2.15	0.46
1:K:353:LEU:O	1:K:357:THR:OG1	2.25	0.46
1:A:325:THR:O	1:A:332:THR:OG1	2.30	0.46
1:C:172:ARG:O	1:C:174:GLY:N	2.49	0.46
1:E:205:PHE:CZ	1:E:267:LYS:O	2.45	0.46
1:F:65:ASP:HB3	1:F:68:GLU:HG2	1.97	0.46
1:F:325:THR:O	1:F:332:THR:OG1	2.31	0.46
1:K:437:PRO:O	1:K:441:MET:HG2	2.16	0.46
1:A:17:MET:HB2	1:A:71:GLY:HA3	1.98	0.45
1:A:306:MET:HB2	1:A:307:GLY:HA2	1.98	0.45
1:C:130:LYS:HG2	1:C:133:ARG:HH21	1.81	0.45
1:C:224:VAL:HG12	1:C:225:ASP:H	1.79	0.45
1:G:104:GLY:HA3	1:G:520:LEU:HD21	1.97	0.45
1:G:157:THR:OG1	1:G:158:ASP:N	2.47	0.45
1:I:9:LYS:HG2	1:I:524:VAL:HG22	1.97	0.45
1:I:55:VAL:HG22	1:I:90:THR:HG21	1.98	0.45
1:J:225:ASP:HB3	1:J:290:LEU:HD21	1.98	0.45
1:M:517:LYS:O	1:M:521:LEU:HB2	2.16	0.45
1:H:232:ARG:H	1:H:232:ARG:HD2	1.81	0.45
1:H:325:THR:O	1:H:332:THR:OG1	2.31	0.45
1:I:238:LEU:HD12	1:I:272:LEU:HD22	1.97	0.45
1:L:216:TYR:HB3	1:L:219:CYS:SG	2.56	0.45
1:M:73:THR:HA	1:M:76:ARG:HD3	1.99	0.45
1:A:348:LYS:HE2	1:A:348:LYS:HB3	1.87	0.45
1:A:517:LYS:O	1:A:521:LEU:HB2	2.17	0.45
1:H:304:ASP:OD1	1:H:309:SER:OG	2.30	0.45
1:I:157:THR:O	1:I:159:ILE:N	2.50	0.45
1:I:202:SER:HA	1:I:203:PRO:HD3	1.84	0.45
1:L:221:ILE:HD11	1:L:251:MET:HE2	1.98	0.45
1:N:10:ASP:CG	1:N:11:MET:H	2.25	0.45
1:B:21:VAL:HG13	1:B:75:VAL:HG21	1.98	0.45
1:D:225:ASP:HB3	1:D:290:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:393:LYS:O	1:G:397:VAL:HG13	2.16	0.45
1:J:437:PRO:O	1:J:441:MET:HG2	2.16	0.45
1:K:303:ARG:HE	1:K:305:GLU:HB2	1.81	0.45
1:L:437:PRO:O	1:L:441:MET:HG2	2.17	0.45
1:N:206:VAL:HG11	1:N:212:MET:HB2	1.97	0.45
1:C:233:ASP:O	1:C:236:THR:OG1	2.30	0.45
1:C:285:ARG:NH2	1:C:368:GLU:OE2	2.50	0.45
1:G:217:GLU:HG2	1:G:323:LYS:HG2	1.97	0.45
1:H:285:ARG:NH2	1:H:368:GLU:OE2	2.49	0.45
1:I:450:LEU:HD21	1:I:509:MET:HE3	1.99	0.45
1:L:436:ASP:N	1:L:436:ASP:OD1	2.49	0.45
1:M:216:TYR:HB3	1:M:219:CYS:SG	2.56	0.45
1:B:325:THR:O	1:B:332:THR:OG1	2.29	0.45
1:E:198:ARG:HD3	1:E:198:ARG:HA	1.68	0.45
1:F:376:GLY:O	1:F:377:VAL:CG2	2.65	0.45
1:I:10:ASP:CG	1:I:11:MET:H	2.25	0.45
1:K:385:GLN:HB2	1:K:389:GLU:HG2	1.99	0.45
1:L:202:SER:HA	1:L:203:PRO:HD3	1.85	0.45
1:M:233:ASP:O	1:M:236:THR:OG1	2.34	0.45
1:M:303:ARG:HE	1:M:305:GLU:HB2	1.81	0.45
1:N:200:TYR:CA	1:N:277:ILE:HG22	2.33	0.45
1:D:172:ARG:O	1:D:174:GLY:N	2.49	0.45
1:D:240:SER:OG	1:D:243:ARG:NH1	2.49	0.45
1:E:65:ASP:HB3	1:E:68:GLU:HG2	1.98	0.45
1:H:55:VAL:HG22	1:H:90:THR:HG21	1.97	0.45
1:H:202:SER:HA	1:H:203:PRO:HD3	1.86	0.45
1:I:250:ILE:C	1:I:277:ILE:CD1	2.79	0.45
1:J:14:LEU:HB3	1:J:105:MET:HE1	1.98	0.45
1:L:198:ARG:HE	1:L:280:PRO:HA	1.81	0.45
1:L:450:LEU:HD21	1:L:509:MET:HE3	1.99	0.45
1:M:437:PRO:O	1:M:441:MET:HG2	2.16	0.45
1:A:172:ARG:O	1:A:174:GLY:N	2.50	0.45
1:D:202:SER:HB3	1:D:204:TYR:HD1	1.82	0.45
1:F:348:LYS:HB3	1:F:348:LYS:HE2	1.85	0.45
1:H:200:TYR:CA	1:H:277:ILE:HG22	2.33	0.45
1:H:517:LYS:O	1:H:521:LEU:HB2	2.17	0.45
1:J:142:ASP:OD1	1:J:142:ASP:N	2.49	0.45
1:L:133:ARG:O	1:L:136:SER:OG	2.35	0.45
1:M:172:ARG:O	1:M:174:GLY:N	2.50	0.45
1:D:55:VAL:HG22	1:D:90:THR:HG21	1.99	0.45
1:J:275:VAL:CG1	1:J:277:ILE:CD1	2.92	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:165:ASP:HA	1:L:168:ALA:HB3	1.98	0.45
1:M:202:SER:HA	1:M:203:PRO:HD3	1.83	0.45
1:M:393:LYS:O	1:M:397:VAL:HG13	2.17	0.45
1:E:267:LYS:HZ1	1:E:273:LYS:CG	2.19	0.45
1:J:47:ALA:HA	1:J:48:PRO:HD3	1.86	0.45
1:J:221:ILE:HD11	1:J:251:MET:HE2	1.98	0.45
1:J:277:ILE:HG22	1:J:278:LYS:N	2.31	0.45
1:E:59:ARG:NH2	1:E:212:MET:SD	2.89	0.44
1:J:274:VAL:O	1:J:275:VAL:HG22	2.16	0.44
1:L:517:LYS:O	1:L:521:LEU:HB2	2.17	0.44
1:M:277:ILE:N	1:M:277:ILE:CD1	2.74	0.44
1:B:128:LEU:HD23	1:B:509:MET:HE1	1.99	0.44
1:D:233:ASP:O	1:D:236:THR:OG1	2.29	0.44
1:D:392:GLU:OE2	1:D:396:ARG:NH2	2.50	0.44
1:E:280:PRO:HG2	1:E:289:TYR:HD2	1.81	0.44
1:H:194:MET:HE1	1:H:373:LEU:HA	1.98	0.44
1:I:437:PRO:O	1:I:441:MET:HG2	2.16	0.44
1:K:61:VAL:O	1:K:76:ARG:NH1	2.50	0.44
1:M:10:ASP:OD1	1:M:11:MET:N	2.49	0.44
1:M:352:ASN:O	1:M:356:GLN:HG2	2.17	0.44
1:A:157:THR:OG1	1:A:158:ASP:N	2.50	0.44
1:A:202:SER:HB3	1:A:204:TYR:HD1	1.82	0.44
1:A:421:LEU:HD11	1:A:454:ILE:HG21	1.97	0.44
1:D:10:ASP:OD1	1:D:11:MET:N	2.50	0.44
1:E:17:MET:HB2	1:E:71:GLY:HA3	1.99	0.44
1:G:233:ASP:O	1:G:237:ILE:HG13	2.18	0.44
1:L:484:ASN:HB3	1:L:487:THR:HG22	1.99	0.44
1:N:450:LEU:HD21	1:N:509:MET:HE3	1.99	0.44
1:H:515:VAL:HA	1:H:518:THR:HG22	1.98	0.44
1:I:104:GLY:HA2	1:I:445:ILE:HD13	1.99	0.44
1:J:78:ALA:HB2	1:J:515:VAL:HG11	2.00	0.44
1:J:393:LYS:O	1:J:397:VAL:HG13	2.17	0.44
1:B:364:GLU:HA	1:B:367:GLN:HB2	1.99	0.44
1:E:186:ASP:OD1	1:E:186:ASP:N	2.51	0.44
1:E:251:MET:CG	1:E:277:ILE:HG23	2.44	0.44
1:G:216:TYR:HB3	1:G:219:CYS:SG	2.57	0.44
1:H:266:ASN:HB3	1:H:272:LEU:HB3	1.99	0.44
1:K:187:GLN:HB3	1:K:381:GLN:HB2	1.99	0.44
1:A:128:LEU:HD23	1:A:509:MET:HE1	1.99	0.44
1:A:181:GLY:HA2	1:A:182:LYS:HA	1.69	0.44
1:D:180:GLU:HA	1:D:382:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:254:GLU:CA	1:F:278:LYS:NZ	2.79	0.44
1:G:51:VAL:HG11	1:G:56:THR:HB	1.99	0.44
1:H:181:GLY:HA2	1:H:182:LYS:HA	1.64	0.44
1:H:314:THR:O	1:H:317:VAL:HG22	2.18	0.44
1:I:517:LYS:O	1:I:521:LEU:HB2	2.18	0.44
1:J:51:VAL:HG11	1:J:56:THR:HB	1.98	0.44
1:N:348:LYS:HE2	1:N:348:LYS:HB3	1.85	0.44
1:B:432:ARG:HD3	1:B:432:ARG:HA	1.87	0.44
1:G:209:PRO:HA	1:G:212:MET:H	1.83	0.44
1:H:217:GLU:HG2	1:H:323:LYS:HG2	2.00	0.44
1:H:221:ILE:HA	1:H:249:LEU:HB2	1.98	0.44
1:C:517:LYS:O	1:C:521:LEU:HB2	2.18	0.44
1:D:194:MET:HE1	1:D:373:LEU:HA	1.99	0.44
1:E:215:GLU:O	1:E:216:TYR:HD1	2.01	0.44
1:E:346:ARG:HD2	1:E:346:ARG:HA	1.77	0.44
1:E:420:LEU:HD22	1:E:450:LEU:HD22	1.99	0.44
1:G:159:ILE:HG12	1:G:397:VAL:HG12	1.99	0.44
1:G:276:ALA:O	1:G:277:ILE:HG22	2.13	0.44
1:G:376:GLY:O	1:G:377:VAL:HG23	2.18	0.44
1:K:172:ARG:O	1:K:174:GLY:N	2.51	0.44
1:M:21:VAL:HG13	1:M:75:VAL:HG21	2.00	0.44
1:A:159:ILE:HG12	1:A:397:VAL:HG12	1.99	0.44
1:N:393:LYS:O	1:N:397:VAL:HG13	2.18	0.44
1:B:65:ASP:HB3	1:B:68:GLU:HG2	2.00	0.44
1:B:376:GLY:O	1:B:377:VAL:HG23	2.18	0.44
1:C:104:GLY:HA3	1:C:520:LEU:HD21	2.00	0.44
1:E:225:ASP:HB2	1:E:290:LEU:HD22	2.00	0.44
1:F:20:GLY:HA3	1:F:68:GLU:HB2	2.00	0.44
1:J:216:TYR:HB3	1:J:219:CYS:SG	2.58	0.44
1:B:125:VAL:HG23	1:B:509:MET:HE2	2.00	0.43
1:C:202:SER:HA	1:C:203:PRO:HD3	1.86	0.43
1:C:376:GLY:O	1:C:377:VAL:CG2	2.66	0.43
1:D:113:ASN:HA	1:D:114:PRO:HD3	1.85	0.43
1:E:193:GLY:HA3	1:E:377:VAL:HB	1.99	0.43
1:E:205:PHE:CD1	1:E:267:LYS:HG2	2.49	0.43
1:G:324:ILE:HD12	1:G:333:VAL:HG12	1.99	0.43
1:J:186:ASP:OD1	1:J:186:ASP:N	2.51	0.43
1:J:283:GLY:H	1:J:286:ARG:NH1	2.16	0.43
1:L:410:GLU:HB2	1:L:503:LYS:HB2	1.99	0.43
1:B:10:ASP:CG	1:B:11:MET:H	2.25	0.43
1:C:21:VAL:HG13	1:C:75:VAL:HG21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:206:VAL:HG11	1:J:212:MET:HB2	1.98	0.43
1:M:220:LYS:HD2	1:M:318:LEU:HD13	1.99	0.43
1:N:189:VAL:HB	1:N:379:ILE:HG23	2.00	0.43
1:E:198:ARG:HG2	1:E:280:PRO:HB3	2.00	0.43
1:H:208:ASP:HA	1:H:209:PRO:HD2	1.90	0.43
1:J:433:ARG:HA	1:J:434:MET:HA	1.79	0.43
1:E:222:LEU:HD13	1:E:237:ILE:HD13	2.00	0.43
1:F:364:GLU:HA	1:F:367:GLN:HB2	2.00	0.43
1:F:376:GLY:C	1:F:377:VAL:HG23	2.44	0.43
1:H:277:ILE:HD12	1:H:278:LYS:H	1.83	0.43
1:I:413:VAL:HG13	1:I:502:SER:HB2	2.01	0.43
1:J:157:THR:OG1	1:J:158:ASP:N	2.50	0.43
1:K:104:GLY:HA3	1:K:520:LEU:HD21	2.01	0.43
1:N:186:ASP:OD1	1:N:186:ASP:N	2.51	0.43
1:B:393:LYS:O	1:B:397:VAL:HG13	2.17	0.43
1:C:393:LYS:O	1:C:397:VAL:HG13	2.18	0.43
1:E:51:VAL:HG11	1:E:56:THR:HB	2.01	0.43
1:F:365:LYS:HA	1:F:368:GLU:HG2	2.00	0.43
1:G:186:ASP:OD1	1:G:186:ASP:N	2.51	0.43
1:G:194:MET:HE1	1:G:373:LEU:HA	2.00	0.43
1:J:10:ASP:CG	1:J:11:MET:H	2.26	0.43
1:M:218:ASN:N	1:M:322:ALA:O	2.32	0.43
1:A:119:ARG:O	1:A:119:ARG:NH1	2.52	0.43
1:B:225:ASP:HB3	1:B:290:LEU:HD21	2.00	0.43
1:C:55:VAL:HG22	1:C:90:THR:HG21	2.00	0.43
1:D:348:LYS:HE2	1:D:348:LYS:HB3	1.87	0.43
1:E:205:PHE:CZ	1:E:268:LEU:CA	3.01	0.43
1:E:215:GLU:O	1:E:216:TYR:CD1	2.72	0.43
1:G:165:ASP:HA	1:G:168:ALA:HB3	2.00	0.43
1:G:181:GLY:HA2	1:G:182:LYS:HA	1.67	0.43
1:L:393:LYS:O	1:L:397:VAL:HG13	2.18	0.43
1:A:51:VAL:HG11	1:A:56:THR:HB	2.00	0.43
1:F:159:ILE:HG12	1:F:397:VAL:HG12	2.01	0.43
1:G:304:ASP:OD1	1:G:304:ASP:N	2.52	0.43
1:I:181:GLY:HA2	1:I:182:LYS:HA	1.66	0.43
1:K:283:GLY:H	1:K:286:ARG:NH1	2.16	0.43
1:M:217:GLU:HG2	1:M:323:LYS:HG2	2.00	0.43
1:N:17:MET:HB2	1:N:71:GLY:HA3	2.00	0.43
1:B:181:GLY:HA2	1:B:182:LYS:HA	1.70	0.43
1:C:491:GLU:HB3	1:C:496:THR:HG21	2.00	0.43
1:D:117:LEU:O	1:D:121:MET:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:181:GLY:HA2	1:E:182:LYS:HA	1.65	0.43
1:E:205:PHE:CE1	1:E:267:LYS:NZ	2.82	0.43
1:E:220:LYS:HG2	1:E:248:LEU:HD13	2.00	0.43
1:E:313:ALA:O	1:E:314:THR:OG1	2.31	0.43
1:G:10:ASP:OD1	1:G:11:MET:N	2.51	0.43
1:I:436:ASP:OD1	1:I:436:ASP:N	2.52	0.43
1:J:233:ASP:O	1:J:236:THR:OG1	2.35	0.43
1:L:88:ASP:OD1	1:L:89:GLY:N	2.41	0.43
1:L:186:ASP:OD1	1:L:186:ASP:N	2.52	0.43
1:M:186:ASP:OD1	1:M:186:ASP:N	2.52	0.43
1:A:41:LEU:HA	1:C:526:VAL:HG22	2.00	0.43
1:A:266:ASN:HB3	1:A:272:LEU:HB3	2.01	0.43
1:E:285:ARG:HE	1:E:365:LYS:HE2	1.84	0.43
1:E:339:THR:HG22	1:E:342:ASP:H	1.83	0.43
1:F:306:MET:N	1:F:307:GLY:HA2	2.32	0.43
1:F:432:ARG:HD3	1:F:432:ARG:HA	1.87	0.43
1:J:21:VAL:HG13	1:J:75:VAL:HG21	1.99	0.43
1:J:232:ARG:H	1:J:232:ARG:HD2	1.84	0.43
1:K:277:ILE:HD12	1:K:278:LYS:H	1.81	0.43
1:L:10:ASP:CG	1:L:11:MET:H	2.27	0.43
1:L:218:ASN:N	1:L:322:ALA:O	2.29	0.43
1:N:517:LYS:O	1:N:521:LEU:HB2	2.19	0.43
1:B:104:GLY:HA3	1:B:520:LEU:HD21	2.00	0.43
1:D:9:LYS:HG2	1:D:524:VAL:HG22	2.01	0.43
1:D:14:LEU:HB3	1:D:105:MET:HE1	2.01	0.43
1:E:212:MET:HB3	1:E:212:MET:HE3	1.83	0.43
1:H:193:GLY:C	1:H:377:VAL:HG23	2.44	0.43
1:I:202:SER:HB3	1:I:204:TYR:HD1	1.84	0.43
1:I:285:ARG:NH2	1:I:368:GLU:OE2	2.52	0.43
1:J:208:ASP:HA	1:J:209:PRO:HD2	1.88	0.43
1:M:428:ASP:OD1	1:M:428:ASP:N	2.52	0.43
1:A:61:VAL:O	1:A:76:ARG:NH1	2.52	0.42
1:D:517:LYS:O	1:D:521:LEU:HB2	2.19	0.42
1:E:201:THR:C	1:E:203:PRO:N	2.52	0.42
1:H:174:GLY:HA3	1:H:175:VAL:HA	1.85	0.42
1:I:348:LYS:HE2	1:I:348:LYS:HB3	1.88	0.42
1:K:47:ALA:HA	1:K:48:PRO:HD3	1.85	0.42
1:K:202:SER:HA	1:K:203:PRO:HD3	1.83	0.42
1:L:237:ILE:HG12	1:L:313:ALA:HB3	2.00	0.42
1:M:128:LEU:HD23	1:M:509:MET:HE1	2.01	0.42
1:N:225:ASP:HB3	1:N:290:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:ASP:HB3	1:C:290:LEU:HD21	2.02	0.42
1:E:204:TYR:HD1	1:E:204:TYR:HA	1.71	0.42
1:I:350:ILE:HG12	1:I:369:ARG:HH21	1.84	0.42
1:J:244:GLY:O	1:J:246:TYR:N	2.52	0.42
1:L:225:ASP:HB3	1:L:290:LEU:HD21	2.01	0.42
1:L:296:LEU:HG	1:L:343:VAL:HG22	2.01	0.42
1:N:104:GLY:HA3	1:N:520:LEU:HD21	2.01	0.42
1:E:203:PRO:CG	1:E:205:PHE:O	2.66	0.42
1:E:300:THR:O	1:E:302:VAL:HG23	2.19	0.42
1:I:180:GLU:HA	1:I:382:VAL:HG12	2.01	0.42
1:M:208:ASP:HA	1:M:209:PRO:HD2	1.89	0.42
1:A:193:GLY:C	1:A:377:VAL:HG23	2.44	0.42
1:B:159:ILE:HG12	1:B:397:VAL:HG12	2.01	0.42
1:B:376:GLY:C	1:B:377:VAL:HG23	2.45	0.42
1:C:169:LYS:HA	1:C:169:LYS:HD2	1.94	0.42
1:C:478:ARG:C	1:C:480:HIS:H	2.27	0.42
1:D:38:ASN:OD1	1:D:52:ASN:ND2	2.53	0.42
1:F:88:ASP:OD1	1:F:89:GLY:N	2.44	0.42
1:H:23:LYS:HD3	1:H:23:LYS:HA	1.89	0.42
1:H:193:GLY:HA3	1:H:377:VAL:HB	2.02	0.42
1:I:419:THR:HA	1:I:422:ARG:HD3	2.01	0.42
1:N:21:VAL:HG11	1:N:101:ILE:HD12	2.02	0.42
1:C:186:ASP:OD1	1:C:186:ASP:N	2.52	0.42
1:E:55:VAL:HG22	1:E:90:THR:HG21	2.01	0.42
1:E:201:THR:C	1:E:203:PRO:CA	2.91	0.42
1:F:186:ASP:OD1	1:F:186:ASP:N	2.52	0.42
1:H:21:VAL:HG13	1:H:75:VAL:HG21	2.01	0.42
1:A:515:VAL:O	1:A:519:PHE:HB2	2.18	0.42
1:B:61:VAL:O	1:B:76:ARG:NH1	2.52	0.42
1:B:224:VAL:HG12	1:B:225:ASP:H	1.83	0.42
1:B:421:LEU:HD11	1:B:454:ILE:HG21	2.01	0.42
1:C:157:THR:OG1	1:C:158:ASP:N	2.52	0.42
1:C:202:SER:HB3	1:C:204:TYR:HD1	1.85	0.42
1:D:169:LYS:HA	1:D:169:LYS:HD2	1.94	0.42
1:E:221:ILE:HG13	1:E:319:GLY:O	2.19	0.42
1:E:267:LYS:CE	1:E:273:LYS:HG3	2.45	0.42
1:E:295:ILE:HG23	1:E:342:ASP:OD1	2.20	0.42
1:F:350:ILE:HG23	1:F:366:LEU:HD22	2.02	0.42
1:A:4:GLU:O	1:A:528:GLU:HG3	2.20	0.42
1:B:277:ILE:CG2	1:B:326:ILE:HD13	2.48	0.42
1:E:251:MET:HG3	1:E:277:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:348:LYS:HE2	1:E:348:LYS:HB3	1.88	0.42
1:G:419:THR:HA	1:G:422:ARG:HD3	2.02	0.42
1:H:10:ASP:CG	1:H:11:MET:H	2.28	0.42
1:H:128:LEU:HD23	1:H:509:MET:HE1	2.01	0.42
1:I:433:ARG:HA	1:I:434:MET:HA	1.80	0.42
1:K:200:TYR:HA	1:K:277:ILE:HA	2.02	0.42
1:M:436:ASP:OD1	1:M:436:ASP:N	2.53	0.42
1:A:194:MET:HE1	1:A:373:LEU:HA	2.02	0.42
1:N:178:MET:HE1	1:N:398:GLU:HA	2.02	0.42
1:D:208:ASP:HA	1:D:209:PRO:HD2	1.88	0.42
1:E:267:LYS:HD3	1:E:274:VAL:O	2.20	0.42
1:G:73:THR:HA	1:G:76:ARG:HD3	2.00	0.42
1:J:55:VAL:HG22	1:J:90:THR:HG21	2.01	0.42
1:J:432:ARG:HD3	1:J:432:ARG:HA	1.90	0.42
1:C:194:MET:HE1	1:C:373:LEU:HA	2.01	0.42
1:D:350:ILE:HG23	1:D:366:LEU:HD22	2.02	0.42
1:H:223:LEU:HD23	1:H:290:LEU:HB2	2.02	0.42
1:J:181:GLY:HA2	1:J:182:LYS:HA	1.67	0.42
1:L:181:GLY:HA2	1:L:182:LYS:HA	1.73	0.42
1:A:169:LYS:HA	1:A:169:LYS:HD2	1.95	0.42
1:A:433:ARG:HA	1:A:434:MET:HA	1.75	0.42
1:E:301:VAL:CB	1:E:302:VAL:HA	2.31	0.42
1:I:350:ILE:HG23	1:I:366:LEU:HD22	2.01	0.42
1:J:515:VAL:HA	1:J:518:THR:HG22	2.02	0.42
1:L:233:ASP:O	1:L:237:ILE:HG13	2.19	0.42
1:L:385:GLN:HB2	1:L:389:GLU:HG2	2.02	0.42
1:M:225:ASP:HB3	1:M:290:LEU:HD21	2.00	0.42
1:A:55:VAL:HG22	1:A:90:THR:HG21	2.02	0.41
1:A:104:GLY:HA3	1:A:520:LEU:HD21	2.02	0.41
1:N:202:SER:HA	1:N:203:PRO:HD3	1.86	0.41
1:B:278:LYS:CB	1:B:278:LYS:HZ2	2.34	0.41
1:D:277:ILE:HD13	1:D:277:ILE:HA	1.84	0.41
1:D:484:ASN:HB3	1:D:487:THR:HG22	2.01	0.41
1:E:277:ILE:HD12	1:E:278:LYS:CA	2.30	0.41
1:F:180:GLU:HA	1:F:382:VAL:HG12	2.02	0.41
1:F:221:ILE:HG13	1:F:249:LEU:HB3	2.02	0.41
1:F:357:THR:HB	1:F:363:ARG:HD3	2.02	0.41
1:G:283:GLY:H	1:G:286:ARG:NH1	2.18	0.41
1:H:482:GLY:HA3	1:H:493:LEU:HG	2.02	0.41
1:J:174:GLY:HA3	1:J:175:VAL:HA	1.85	0.41
1:J:223:LEU:HD21	1:J:294:ALA:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:419:THR:HA	1:J:422:ARG:HD3	2.02	0.41
1:C:325:THR:O	1:C:332:THR:OG1	2.32	0.41
1:D:202:SER:HA	1:D:203:PRO:HD3	1.86	0.41
1:D:233:ASP:O	1:D:237:ILE:HG13	2.20	0.41
1:E:327:THR:OG1	1:E:328:LYS:N	2.46	0.41
1:I:217:GLU:HG2	1:I:323:LYS:HG2	2.01	0.41
1:K:338:SER:OG	1:K:339:THR:N	2.45	0.41
1:M:165:ASP:HA	1:M:168:ALA:HB3	2.02	0.41
1:C:348:LYS:HE2	1:C:348:LYS:HB3	1.84	0.41
1:D:283:GLY:H	1:D:286:ARG:NH1	2.18	0.41
1:D:334:VAL:HG23	1:D:377:VAL:CB	2.47	0.41
1:E:193:GLY:C	1:E:377:VAL:HG23	2.45	0.41
1:F:113:ASN:HA	1:F:114:PRO:HD3	1.86	0.41
1:H:209:PRO:HA	1:H:212:MET:H	1.85	0.41
1:I:277:ILE:HG22	1:I:278:LYS:N	2.33	0.41
1:I:296:LEU:HG	1:I:343:VAL:HG22	2.02	0.41
1:I:376:GLY:C	1:I:377:VAL:HG23	2.46	0.41
1:L:206:VAL:HB	1:L:212:MET:HA	2.03	0.41
1:L:364:GLU:HA	1:L:367:GLN:HB2	2.02	0.41
1:M:450:LEU:HD21	1:M:509:MET:HE3	2.02	0.41
1:N:104:GLY:O	1:N:108:VAL:HG23	2.21	0.41
1:C:165:ASP:HA	1:C:168:ALA:HB3	2.01	0.41
1:C:209:PRO:HA	1:C:212:MET:H	1.85	0.41
1:C:234:ILE:O	1:C:238:LEU:N	2.49	0.41
1:C:253:GLU:H	1:C:279:ALA:HB2	1.85	0.41
1:F:24:LEU:HD11	1:F:76:ARG:HG3	2.01	0.41
1:F:220:LYS:HA	1:F:320:THR:HA	2.02	0.41
1:F:436:ASP:OD1	1:F:436:ASP:N	2.50	0.41
1:G:285:ARG:NH2	1:G:368:GLU:OE2	2.53	0.41
1:H:73:THR:HA	1:H:76:ARG:HD3	2.02	0.41
1:H:251:MET:HB3	1:H:277:ILE:CG1	2.49	0.41
1:I:194:MET:HE1	1:I:373:LEU:HA	2.02	0.41
1:J:303:ARG:HG2	1:J:305:GLU:HB2	2.01	0.41
1:M:47:ALA:HA	1:M:48:PRO:HD3	1.89	0.41
1:M:119:ARG:O	1:M:119:ARG:NH1	2.53	0.41
1:A:224:VAL:HG12	1:A:225:ASP:H	1.86	0.41
1:A:296:LEU:HG	1:A:343:VAL:HG22	2.02	0.41
1:N:276:ALA:O	1:N:277:ILE:HG22	2.12	0.41
1:C:125:VAL:HG11	1:C:513:VAL:HG21	2.01	0.41
1:G:202:SER:HA	1:G:203:PRO:HD3	1.87	0.41
1:I:365:LYS:HA	1:I:368:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:428:ASP:OD1	1:I:428:ASP:N	2.48	0.41
1:J:306:MET:HB2	1:J:307:GLY:HA2	2.03	0.41
1:J:515:VAL:O	1:J:519:PHE:HB2	2.19	0.41
1:A:209:PRO:HA	1:A:212:MET:H	1.84	0.41
1:A:350:ILE:HG23	1:A:366:LEU:HD22	2.02	0.41
1:A:376:GLY:O	1:A:377:VAL:HG23	2.20	0.41
1:E:165:ASP:HA	1:E:168:ALA:HB3	2.02	0.41
1:F:9:LYS:HG2	1:F:524:VAL:HG13	2.03	0.41
1:F:51:VAL:HG11	1:F:56:THR:HB	2.02	0.41
1:J:169:LYS:HA	1:J:169:LYS:HD2	1.95	0.41
1:A:83:ASN:HB2	1:A:90:THR:HG22	2.02	0.41
1:A:376:GLY:C	1:A:377:VAL:HG23	2.45	0.41
1:N:419:THR:HA	1:N:422:ARG:HD3	2.03	0.41
1:B:47:ALA:HA	1:B:48:PRO:HD3	1.84	0.41
1:B:240:SER:OG	1:B:243:ARG:NH1	2.54	0.41
1:C:433:ARG:HA	1:C:434:MET:HA	1.77	0.41
1:E:175:VAL:HG13	1:E:377:VAL:HG13	2.01	0.41
1:H:218:ASN:N	1:H:322:ALA:O	2.28	0.41
1:J:218:ASN:N	1:J:322:ALA:O	2.37	0.41
1:L:142:ASP:OD1	1:L:142:ASP:N	2.52	0.41
1:A:385:GLN:HB2	1:A:389:GLU:HG2	2.03	0.41
1:A:484:ASN:HB3	1:A:487:THR:HG22	2.03	0.41
1:D:436:ASP:OD1	1:D:436:ASP:N	2.51	0.41
1:E:238:LEU:O	1:E:242:ILE:HG13	2.21	0.41
1:H:293:ILE:HD12	1:H:296:LEU:HD13	2.03	0.41
1:I:237:ILE:HG12	1:I:313:ALA:HB3	2.03	0.41
1:I:482:GLY:HA3	1:I:493:LEU:HG	2.02	0.41
1:K:225:ASP:HB3	1:K:290:LEU:HD21	2.03	0.41
1:M:410:GLU:HB2	1:M:503:LYS:HB2	2.03	0.41
1:A:21:VAL:HG13	1:A:75:VAL:HG21	2.03	0.41
1:A:165:ASP:HA	1:A:168:ALA:HB3	2.02	0.41
1:A:233:ASP:O	1:A:237:ILE:HG13	2.20	0.41
1:N:249:LEU:HD13	1:N:275:VAL:HB	2.03	0.41
1:B:20:GLY:HA3	1:B:68:GLU:HB2	2.03	0.41
1:B:73:THR:HA	1:B:76:ARG:HD3	2.03	0.41
1:B:113:ASN:HA	1:B:114:PRO:HD3	1.91	0.41
1:B:376:GLY:O	1:B:377:VAL:CG2	2.69	0.41
1:B:410:GLU:HB2	1:B:503:LYS:HB2	2.03	0.41
1:C:233:ASP:O	1:C:237:ILE:HG13	2.20	0.41
1:D:186:ASP:OD1	1:D:186:ASP:N	2.52	0.41
1:D:491:GLU:HB3	1:D:496:THR:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:202:SER:N	1:E:203:PRO:CA	2.84	0.41
1:E:251:MET:HG3	1:E:277:ILE:CG1	2.51	0.41
1:F:119:ARG:O	1:F:119:ARG:NH1	2.53	0.41
1:F:306:MET:H	1:F:307:GLY:HA2	1.86	0.41
1:G:206:VAL:HG23	1:G:206:VAL:O	2.21	0.41
1:G:348:LYS:HE2	1:G:348:LYS:HB3	1.87	0.41
1:I:78:ALA:HB2	1:I:515:VAL:HG11	2.03	0.41
1:I:303:ARG:HE	1:I:305:GLU:HB2	1.85	0.41
1:J:310:LEU:HB3	1:J:311:GLU:H	1.66	0.41
1:J:338:SER:OG	1:J:339:THR:N	2.45	0.41
1:K:10:ASP:OD1	1:K:11:MET:N	2.47	0.41
1:K:393:LYS:O	1:K:397:VAL:HG13	2.21	0.41
1:L:428:ASP:OD1	1:L:428:ASP:N	2.54	0.41
1:M:277:ILE:HG22	1:M:278:LYS:N	2.35	0.41
1:A:189:VAL:HB	1:A:379:ILE:HG23	2.03	0.41
1:N:283:GLY:H	1:N:286:ARG:NH1	2.19	0.41
1:N:350:ILE:HG23	1:N:366:LEU:HD22	2.02	0.41
1:B:209:PRO:HA	1:B:212:MET:H	1.86	0.41
1:C:296:LEU:HG	1:C:343:VAL:HG22	2.03	0.41
1:C:364:GLU:HA	1:C:367:GLN:HB2	2.03	0.41
1:E:211:ARG:O	1:E:212:MET:SD	2.79	0.41
1:F:231:ALA:O	1:F:235:ILE:HG23	2.21	0.41
1:K:125:VAL:HG11	1:K:513:VAL:HG21	2.01	0.41
1:K:233:ASP:O	1:K:237:ILE:HG13	2.21	0.41
1:L:348:LYS:HE2	1:L:348:LYS:HB3	1.82	0.41
1:M:363:ARG:HA	1:M:363:ARG:HD2	1.95	0.41
1:C:208:ASP:HA	1:C:209:PRO:HD2	1.91	0.40
1:E:4:GLU:O	1:E:528:GLU:HG3	2.21	0.40
1:E:517:LYS:O	1:E:521:LEU:HB2	2.20	0.40
1:H:9:LYS:HG2	1:H:524:VAL:HG22	2.03	0.40
1:H:65:ASP:HA	1:H:66:PRO:HD3	1.92	0.40
1:B:165:ASP:HA	1:B:168:ALA:HB3	2.03	0.40
1:C:125:VAL:HG23	1:C:509:MET:HE2	2.02	0.40
1:C:206:VAL:O	1:C:206:VAL:HG23	2.21	0.40
1:C:266:ASN:HB3	1:C:272:LEU:HB3	2.03	0.40
1:C:338:SER:OG	1:C:339:THR:N	2.42	0.40
1:D:224:VAL:HG12	1:D:225:ASP:H	1.87	0.40
1:D:394:LYS:O	1:D:398:GLU:HB2	2.21	0.40
1:E:262:THR:O	1:E:266:ASN:ND2	2.30	0.40
1:E:312:GLN:O	1:E:314:THR:HG23	2.22	0.40
1:F:304:ASP:OD1	1:F:304:ASP:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:225:ASP:HB3	1:G:290:LEU:HD21	2.02	0.40
1:I:104:GLY:HA3	1:I:520:LEU:HD21	2.02	0.40
1:I:225:ASP:HB3	1:I:290:LEU:HD21	2.03	0.40
1:J:283:GLY:H	1:J:286:ARG:CZ	2.35	0.40
1:K:125:VAL:HG23	1:K:509:MET:HE2	2.02	0.40
1:A:14:LEU:HB3	1:A:105:MET:HE1	2.04	0.40
1:D:118:VAL:HG21	1:D:517:LYS:HG3	2.02	0.40
1:D:432:ARG:HA	1:D:432:ARG:HD3	1.85	0.40
1:E:505:VAL:O	1:E:509:MET:HB2	2.21	0.40
1:F:189:VAL:HB	1:F:379:ILE:HG23	2.03	0.40
1:H:157:THR:O	1:H:160:GLY:N	2.53	0.40
1:I:410:GLU:HB2	1:I:503:LYS:HB2	2.02	0.40
1:J:202:SER:HB3	1:J:204:TYR:HD1	1.86	0.40
1:K:161:SER:O	1:K:164:SER:OG	2.34	0.40
1:L:376:GLY:C	1:L:377:VAL:HG23	2.46	0.40
1:M:206:VAL:O	1:M:206:VAL:HG23	2.21	0.40
1:M:482:GLY:HA3	1:M:493:LEU:HG	2.04	0.40
1:A:78:ALA:HB2	1:A:515:VAL:HG11	2.04	0.40
1:A:413:VAL:HG13	1:A:502:SER:HB2	2.03	0.40
1:N:123:LYS:HA	1:N:123:LYS:HD2	1.86	0.40
1:N:224:VAL:HG12	1:N:225:ASP:H	1.86	0.40
1:D:159:ILE:HG12	1:D:397:VAL:HG12	2.02	0.40
1:D:193:GLY:CA	1:D:377:VAL:CG1	2.93	0.40
1:E:357:THR:HB	1:E:363:ARG:HD3	2.04	0.40
1:F:237:ILE:HG12	1:F:313:ALA:HB3	2.03	0.40
1:H:224:VAL:HG12	1:H:225:ASP:H	1.87	0.40
1:K:237:ILE:HG12	1:K:313:ALA:HB3	2.02	0.40
1:L:180:GLU:HA	1:L:382:VAL:HG12	2.03	0.40
1:M:17:MET:HB2	1:M:71:GLY:HA3	2.04	0.40
1:C:105:MET:HE3	1:C:519:PHE:CE2	2.57	0.40
1:C:221:ILE:HG13	1:C:249:LEU:HB3	2.03	0.40
1:D:193:GLY:HA3	1:D:377:VAL:HG12	1.98	0.40
1:D:236:THR:OG1	1:D:311:GLU:O	2.40	0.40
1:H:186:ASP:OD1	1:H:186:ASP:N	2.52	0.40
1:I:125:VAL:HG11	1:I:513:VAL:HG21	2.04	0.40
1:J:125:VAL:HG11	1:J:513:VAL:HG21	2.03	0.40
1:L:104:GLY:HA2	1:L:445:ILE:HD13	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	526/552 (95%)	480 (91%)	40 (8%)	6 (1%)	11	41
1	B	526/552 (95%)	473 (90%)	46 (9%)	7 (1%)	9	38
1	C	526/552 (95%)	479 (91%)	40 (8%)	7 (1%)	9	38
1	D	526/552 (95%)	479 (91%)	42 (8%)	5 (1%)	12	43
1	E	526/552 (95%)	472 (90%)	40 (8%)	14 (3%)	4	27
1	F	526/552 (95%)	480 (91%)	42 (8%)	4 (1%)	16	48
1	G	526/552 (95%)	483 (92%)	37 (7%)	6 (1%)	11	41
1	H	526/552 (95%)	478 (91%)	43 (8%)	5 (1%)	12	43
1	I	526/552 (95%)	482 (92%)	39 (7%)	5 (1%)	12	43
1	J	526/552 (95%)	480 (91%)	42 (8%)	4 (1%)	16	48
1	K	526/552 (95%)	478 (91%)	43 (8%)	5 (1%)	12	43
1	L	526/552 (95%)	478 (91%)	43 (8%)	5 (1%)	12	43
1	M	526/552 (95%)	475 (90%)	47 (9%)	4 (1%)	16	48
1	N	526/552 (95%)	480 (91%)	42 (8%)	4 (1%)	16	48
All	All	7364/7728 (95%)	6697 (91%)	586 (8%)	81 (1%)	11	41

All (81) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	ASP
1	A	173	THR
1	A	245	ASN
1	N	158	ASP
1	N	173	THR
1	N	245	ASN
1	N	277	ILE
1	B	158	ASP
1	B	173	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	245	ASN
1	B	281	GLY
1	C	158	ASP
1	C	173	THR
1	C	245	ASN
1	C	277	ILE
1	D	158	ASP
1	D	173	THR
1	D	245	ASN
1	E	173	THR
1	E	247	PRO
1	F	173	THR
1	F	245	ASN
1	G	158	ASP
1	G	173	THR
1	G	245	ASN
1	G	277	ILE
1	H	173	THR
1	H	277	ILE
1	I	158	ASP
1	I	173	THR
1	I	245	ASN
1	J	158	ASP
1	J	173	THR
1	K	158	ASP
1	K	173	THR
1	K	245	ASN
1	K	277	ILE
1	L	158	ASP
1	L	173	THR
1	L	245	ASN
1	L	277	ILE
1	M	173	THR
1	M	245	ASN
1	A	277	ILE
1	B	377	VAL
1	E	232	ARG
1	E	256	GLU
1	E	301	VAL
1	F	377	VAL
1	H	245	ASN
1	J	245	ASN

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Mol	Chain	Res	Type
1	B	280	PRO
1	C	253	GLU
1	C	377	VAL
1	E	202	SER
1	E	314	THR
1	G	377	VAL
1	M	158	ASP
1	D	184	ALA
1	E	158	ASP
1	E	257	GLN
1	G	184	ALA
1	A	184	ALA
1	A	377	VAL
1	B	184	ALA
1	D	157	THR
1	E	253	GLU
1	E	530	LYS
1	F	530	LYS
1	I	530	LYS
1	K	377	VAL
1	C	530	LYS
1	E	184	ALA
1	H	158	ASP
1	L	377	VAL
1	E	171	GLY
1	E	234	ILE
1	J	377	VAL
1	H	377	VAL
1	M	377	VAL
1	I	377	VAL

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	433/445 (97%)	415 (96%)	18 (4%)	<span style="border: 1px solid red; padding: 2px;">26</span>   50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	433/445 (97%)	415 (96%)	18 (4%)	26	50
1	C	433/445 (97%)	417 (96%)	16 (4%)	30	54
1	D	433/445 (97%)	415 (96%)	18 (4%)	26	50
1	E	433/445 (97%)	404 (93%)	29 (7%)	15	41
1	F	433/445 (97%)	415 (96%)	18 (4%)	26	50
1	G	433/445 (97%)	412 (95%)	21 (5%)	23	47
1	H	433/445 (97%)	409 (94%)	24 (6%)	19	45
1	I	433/445 (97%)	413 (95%)	20 (5%)	24	48
1	J	433/445 (97%)	417 (96%)	16 (4%)	30	54
1	K	433/445 (97%)	417 (96%)	16 (4%)	30	54
1	L	433/445 (97%)	413 (95%)	20 (5%)	24	48
1	M	433/445 (97%)	414 (96%)	19 (4%)	25	49
1	N	433/445 (97%)	416 (96%)	17 (4%)	28	52
All	All	6062/6230 (97%)	5792 (96%)	270 (4%)	24	48

All (270) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	74	LEU
1	A	128	LEU
1	A	139	VAL
1	A	170	VAL
1	A	223	LEU
1	A	224	VAL
1	A	255	VAL
1	A	268	LEU
1	A	302	VAL
1	A	305	GLU
1	A	308	VAL
1	A	328	LYS
1	A	343	VAL
1	A	412	VAL
1	A	435	THR
1	A	480	HIS
1	A	521	LEU
1	N	4	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	N	5	LEU
1	N	67	VAL
1	N	74	LEU
1	N	139	VAL
1	N	170	VAL
1	N	223	LEU
1	N	224	VAL
1	N	255	VAL
1	N	302	VAL
1	N	305	GLU
1	N	308	VAL
1	N	328	LYS
1	N	377	VAL
1	N	412	VAL
1	N	435	THR
1	N	521	LEU
1	B	4	GLU
1	B	128	LEU
1	B	139	VAL
1	B	170	VAL
1	B	175	VAL
1	B	223	LEU
1	B	224	VAL
1	B	255	VAL
1	B	278	LYS
1	B	302	VAL
1	B	305	GLU
1	B	308	VAL
1	B	328	LYS
1	B	412	VAL
1	B	435	THR
1	B	492	ASN
1	B	499	ILE
1	B	521	LEU
1	C	105	MET
1	C	139	VAL
1	C	170	VAL
1	C	175	VAL
1	C	223	LEU
1	C	224	VAL
1	C	255	VAL
1	C	268	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	302	VAL
1	C	305	GLU
1	C	308	VAL
1	C	328	LYS
1	C	412	VAL
1	C	435	THR
1	C	446	ILE
1	C	521	LEU
1	D	4	GLU
1	D	5	LEU
1	D	67	VAL
1	D	139	VAL
1	D	170	VAL
1	D	175	VAL
1	D	223	LEU
1	D	224	VAL
1	D	255	VAL
1	D	268	LEU
1	D	277	ILE
1	D	302	VAL
1	D	305	GLU
1	D	308	VAL
1	D	328	LYS
1	D	412	VAL
1	D	435	THR
1	D	521	LEU
1	E	4	GLU
1	E	5	LEU
1	E	74	LEU
1	E	139	VAL
1	E	170	VAL
1	E	201	THR
1	E	204	TYR
1	E	205	PHE
1	E	206	VAL
1	E	207	THR
1	E	211	ARG
1	E	212	MET
1	E	215	GLU
1	E	216	TYR
1	E	245	ASN
1	E	253	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	277	ILE
1	E	290	LEU
1	E	295	ILE
1	E	301	VAL
1	E	308	VAL
1	E	315	ASP
1	E	318	LEU
1	E	328	LYS
1	E	367	GLN
1	E	373	LEU
1	E	412	VAL
1	E	435	THR
1	E	521	LEU
1	F	4	GLU
1	F	5	LEU
1	F	67	VAL
1	F	139	VAL
1	F	170	VAL
1	F	223	LEU
1	F	235	ILE
1	F	242	ILE
1	F	255	VAL
1	F	268	LEU
1	F	277	ILE
1	F	302	VAL
1	F	308	VAL
1	F	318	LEU
1	F	328	LYS
1	F	412	VAL
1	F	435	THR
1	F	521	LEU
1	G	67	VAL
1	G	139	VAL
1	G	170	VAL
1	G	175	VAL
1	G	235	ILE
1	G	242	ILE
1	G	255	VAL
1	G	268	LEU
1	G	302	VAL
1	G	305	GLU
1	G	308	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	318	LEU
1	G	328	LYS
1	G	355	MET
1	G	412	VAL
1	G	435	THR
1	G	467	VAL
1	G	480	HIS
1	G	499	ILE
1	G	521	LEU
1	G	529	LEU
1	H	5	LEU
1	H	74	LEU
1	H	128	LEU
1	H	139	VAL
1	H	170	VAL
1	H	178	MET
1	H	206	VAL
1	H	223	LEU
1	H	224	VAL
1	H	235	ILE
1	H	242	ILE
1	H	255	VAL
1	H	268	LEU
1	H	302	VAL
1	H	305	GLU
1	H	317	VAL
1	H	318	LEU
1	H	328	LYS
1	H	367	GLN
1	H	412	VAL
1	H	435	THR
1	H	460	ASN
1	H	499	ILE
1	H	521	LEU
1	I	5	LEU
1	I	128	LEU
1	I	139	VAL
1	I	170	VAL
1	I	206	VAL
1	I	223	LEU
1	I	224	VAL
1	I	235	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	I	255	VAL
1	I	268	LEU
1	I	277	ILE
1	I	302	VAL
1	I	305	GLU
1	I	308	VAL
1	I	328	LYS
1	I	357	THR
1	I	370	ILE
1	I	412	VAL
1	I	435	THR
1	I	521	LEU
1	J	4	GLU
1	J	5	LEU
1	J	139	VAL
1	J	170	VAL
1	J	175	VAL
1	J	223	LEU
1	J	235	ILE
1	J	242	ILE
1	J	255	VAL
1	J	268	LEU
1	J	302	VAL
1	J	308	VAL
1	J	328	LYS
1	J	412	VAL
1	J	435	THR
1	J	521	LEU
1	K	5	LEU
1	K	139	VAL
1	K	170	VAL
1	K	223	LEU
1	K	235	ILE
1	K	242	ILE
1	K	255	VAL
1	K	268	LEU
1	K	302	VAL
1	K	305	GLU
1	K	308	VAL
1	K	328	LYS
1	K	412	VAL
1	K	435	THR

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Mol	Chain	Res	Type
1	K	521	LEU
1	K	530	LYS
1	L	5	LEU
1	L	170	VAL
1	L	206	VAL
1	L	215	GLU
1	L	223	LEU
1	L	235	ILE
1	L	242	ILE
1	L	255	VAL
1	L	268	LEU
1	L	302	VAL
1	L	305	GLU
1	L	308	VAL
1	L	318	LEU
1	L	328	LYS
1	L	348	LYS
1	L	370	ILE
1	L	412	VAL
1	L	435	THR
1	L	521	LEU
1	L	530	LYS
1	M	5	LEU
1	M	139	VAL
1	M	170	VAL
1	M	223	LEU
1	M	224	VAL
1	M	235	ILE
1	M	255	VAL
1	M	268	LEU
1	M	277	ILE
1	M	302	VAL
1	M	305	GLU
1	M	308	VAL
1	M	318	LEU
1	M	328	LYS
1	M	412	VAL
1	M	435	THR
1	M	480	HIS
1	M	521	LEU
1	M	530	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	69	ASN
1	A	83	ASN
1	A	459	GLN
1	N	6	HIS
1	N	8	ASN
1	N	52	ASN
1	N	69	ASN
1	N	470	ASN
1	B	69	ASN
1	B	475	ASN
1	C	83	ASN
1	D	6	HIS
1	D	8	ASN
1	D	69	ASN
1	D	470	ASN
1	E	77	GLN
1	E	367	GLN
1	F	69	ASN
1	G	52	ASN
1	G	475	ASN
1	H	69	ASN
1	H	83	ASN
1	H	439	GLN
1	I	69	ASN
1	J	18	GLN
1	J	69	ASN
1	K	69	ASN
1	K	484	ASN
1	M	83	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	528/552 (95%)	-0.37	1 (0%) 91 81	64, 175, 274, 319	0
1	B	528/552 (95%)	-0.24	5 (0%) 81 60	49, 165, 283, 325	0
1	C	528/552 (95%)	-0.30	8 (1%) 72 50	50, 166, 284, 318	0
1	D	528/552 (95%)	-0.18	5 (0%) 81 60	55, 153, 262, 292	0
1	E	528/552 (95%)	-0.21	3 (0%) 85 68	26, 159, 234, 301	0
1	F	528/552 (95%)	-0.29	2 (0%) 88 74	69, 184, 271, 303	0
1	G	528/552 (95%)	-0.18	8 (1%) 72 50	55, 193, 280, 315	0
1	H	528/552 (95%)	-0.28	5 (0%) 81 60	57, 182, 288, 319	0
1	I	528/552 (95%)	-0.30	3 (0%) 85 68	57, 192, 299, 325	0
1	J	528/552 (95%)	-0.31	2 (0%) 88 74	84, 203, 315, 369	0
1	K	528/552 (95%)	-0.28	5 (0%) 81 60	71, 189, 307, 340	0
1	L	528/552 (95%)	-0.30	1 (0%) 91 81	70, 185, 310, 357	0
1	M	528/552 (95%)	-0.36	2 (0%) 88 74	81, 207, 326, 366	0
1	N	528/552 (95%)	-0.32	4 (0%) 82 62	77, 194, 294, 335	0
All	All	7392/7728 (95%)	-0.28	54 (0%) 84 65	26, 178, 296, 369	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	277	ILE	5.2
1	D	302	VAL	4.7
1	I	251	MET	4.2
1	B	302	VAL	3.9
1	H	251	MET	3.6
1	G	61	VAL	3.6
1	G	259	ALA	3.4
1	E	203	PRO	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	234	ILE	3.3
1	G	377	VAL	3.3
1	H	148	VAL	3.2
1	J	333	VAL	3.1
1	H	215	GLU	3.1
1	D	477	ASP	3.1
1	E	377	VAL	3.1
1	I	215	GLU	2.9
1	H	302	VAL	2.9
1	D	251	MET	2.9
1	C	215	GLU	2.9
1	J	509	MET	2.8
1	B	251	MET	2.8
1	K	377	VAL	2.7
1	D	215	GLU	2.6
1	C	302	VAL	2.5
1	C	176	VAL	2.5
1	N	251	MET	2.5
1	G	215	GLU	2.5
1	C	255	VAL	2.4
1	A	234	ILE	2.4
1	I	176	VAL	2.4
1	E	61	VAL	2.3
1	M	215	GLU	2.3
1	G	57	ILE	2.3
1	G	4	GLU	2.3
1	M	333	VAL	2.3
1	G	277	ILE	2.3
1	N	277	ILE	2.3
1	N	301	VAL	2.2
1	G	315	ASP	2.2
1	L	519	PHE	2.2
1	K	234	ILE	2.2
1	F	377	VAL	2.2
1	K	334	VAL	2.2
1	C	228	ILE	2.2
1	D	213	ILE	2.2
1	C	234	ILE	2.1
1	K	277	ILE	2.1
1	F	251	MET	2.1
1	K	251	MET	2.1
1	N	125	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	H	301	VAL	2.1
1	B	255	VAL	2.1
1	C	224	VAL	2.0
1	C	259	ALA	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.