



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:12 PM GMT

PDB ID : 1J2Q  
Title : 20S proteasome in complex with calpain-Inhibitor I from archaeoglobus fulgidus  
Authors : Groll, M.; Brandstetter, H.; Bartunik, H.; Bourenkow, G.; Huber, R.  
Deposited on : 2003-01-08  
Resolution : 2.83 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  
<http://wwpdb.org/validation/2016/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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

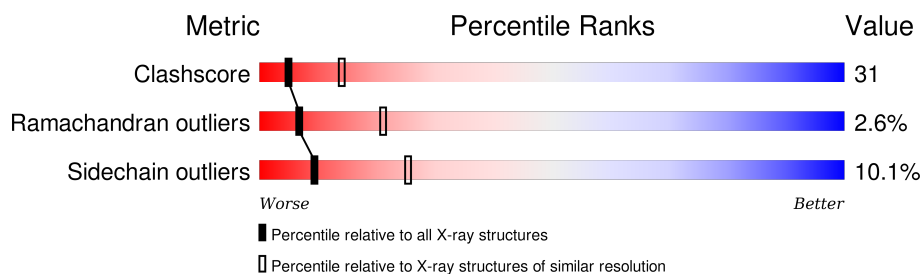
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.83 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	3658 (2.88-2.80)
Ramachandran outliers	100387	3591 (2.88-2.80)
Sidechain outliers	100360	3594 (2.88-2.80)







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	237	
1	B	237	
1	C	237	
1	D	237	
1	E	237	
1	F	237	
1	G	237	

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Mol	Chain	Length	Quality of chain
2	H	202	 45% 47% 8%
2	I	202	 47% 45% 8%
2	J	202	 50% 42% 8%
2	K	202	 50% 43% 7%
2	L	202	 51% 42% 7%
2	M	202	 49% 43% 8%
2	N	202	 50% 42% 8%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 24227 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.

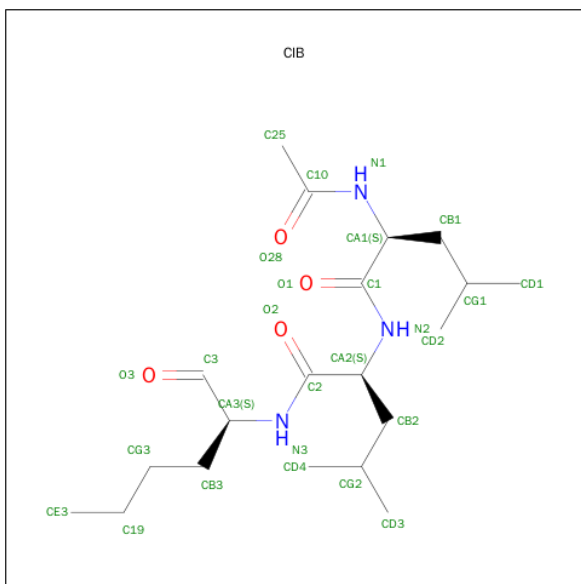
- Molecule 1 is a protein called Proteasome alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	B	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	C	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	D	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	E	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	F	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	G	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			

- Molecule 2 is a protein called Proteasome beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	I	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	J	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	K	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	L	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	M	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	N	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			

- Molecule 3 is 2-ACETYLAMINO-4-METHYL-PENTANOIC ACID [1-(1-FORMYL-PENTYL-CARBAMOYL)-3-METHYL-BUTYL]-AMIDE (three-letter code: CIB) (formula:  $C_{20}H_{37}N_3O_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total	C	N	O	0	0
			27	20	3	4		
3	I	1	Total	C	N	O	0	0
			27	20	3	4		
3	J	1	Total	C	N	O	0	0
			27	20	3	4		
3	K	1	Total	C	N	O	0	0
			27	20	3	4		
3	L	1	Total	C	N	O	0	0
			27	20	3	4		
3	M	1	Total	C	N	O	0	0
			27	20	3	4		
3	N	1	Total	C	N	O	0	0
			27	20	3	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	O	0	0
			4	4		
4	B	7	Total	O	0	0
			7	7		
4	C	9	Total	O	0	0
			9	9		

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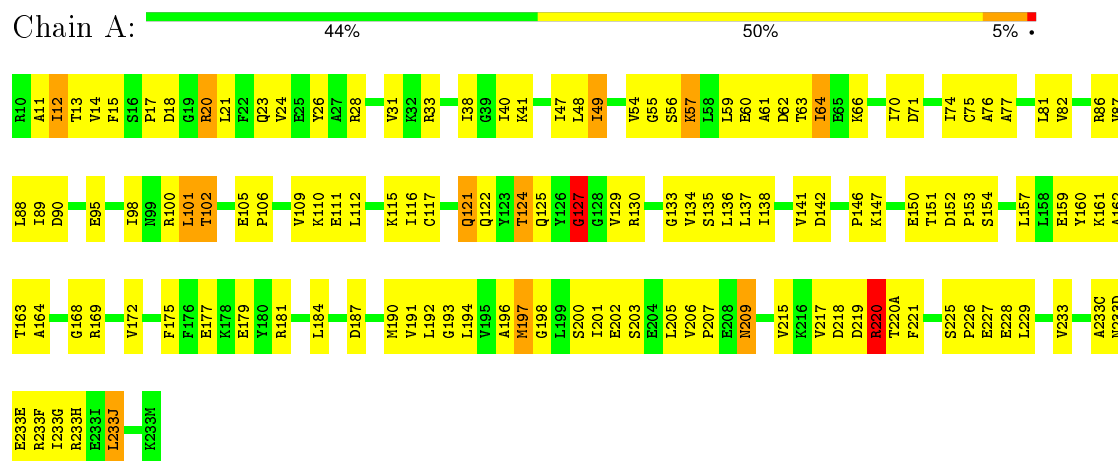
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	4	Total 4	O 4	0	0
4	E	7	Total 7	O 7	0	0
4	F	5	Total 5	O 5	0	0
4	G	5	Total 5	O 5	0	0
4	H	13	Total 13	O 13	0	0
4	I	14	Total 14	O 14	0	0
4	J	5	Total 5	O 5	0	0
4	K	7	Total 7	O 7	0	0
4	L	6	Total 6	O 6	0	0
4	M	12	Total 12	O 12	0	0
4	N	7	Total 7	O 7	0	0

### 3 Residue-property plots

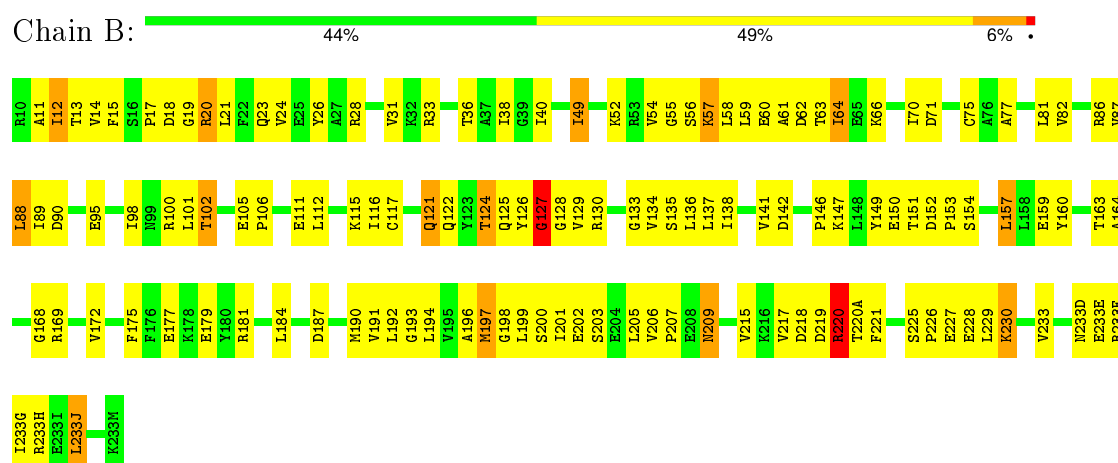
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

#### • Molecule 1: Proteasome alpha subunit

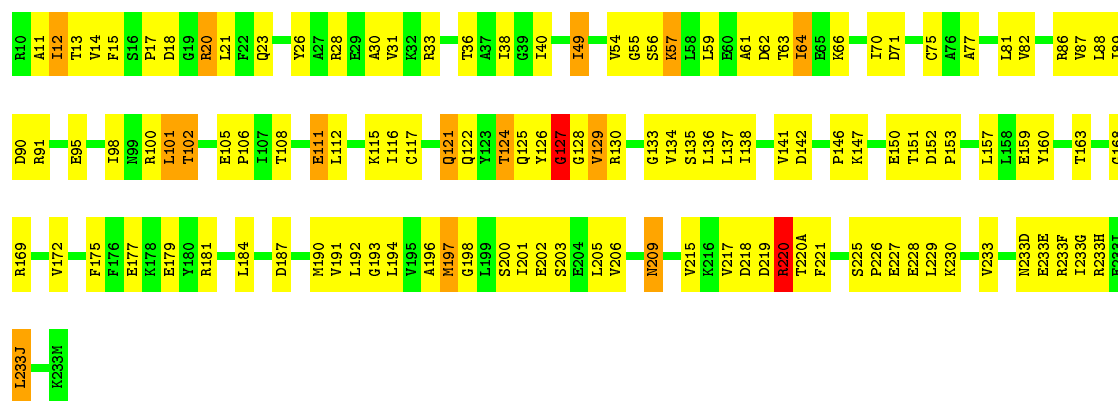


#### • Molecule 1: Proteasome alpha subunit



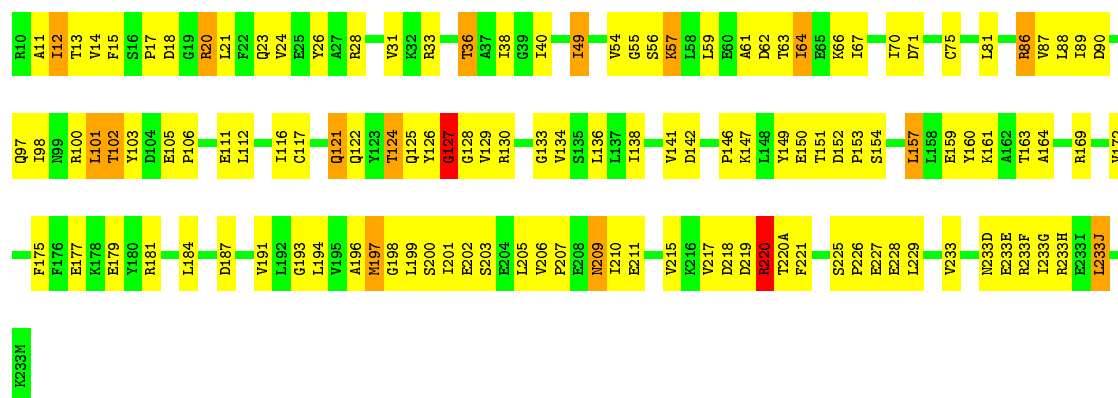
#### • Molecule 1: Proteasome alpha subunit





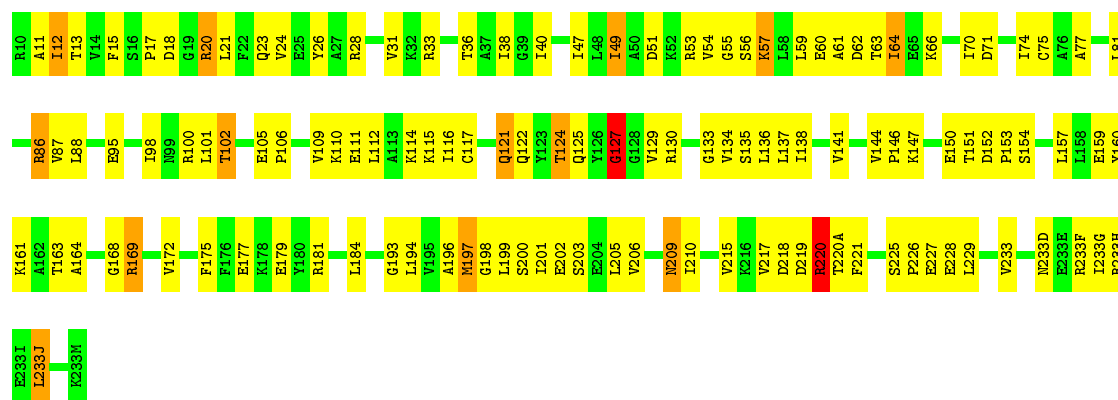
• Molecule 1: Proteasome alpha subunit

Chain D: 48% 45% 6%



• Molecule 1: Proteasome alpha subunit

Chain E: 48% 46% 5%

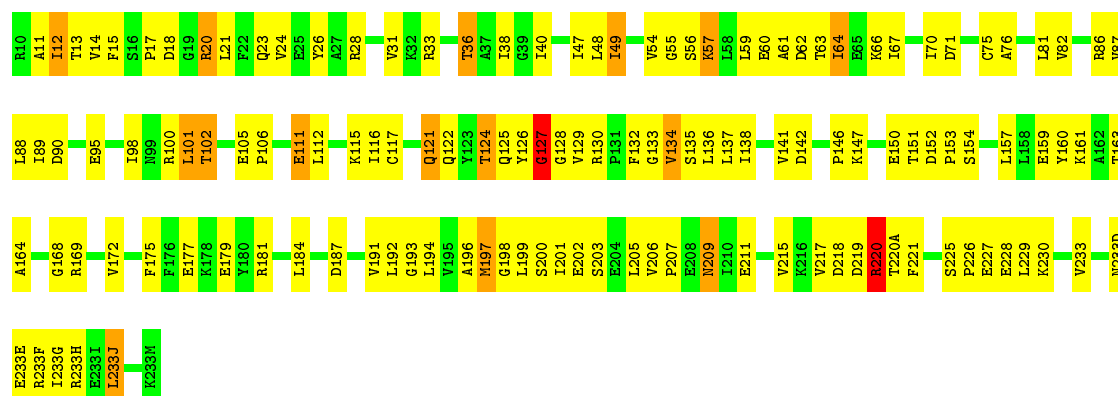


• Molecule 1: Proteasome alpha subunit

Chain F: 47% 46% 6%



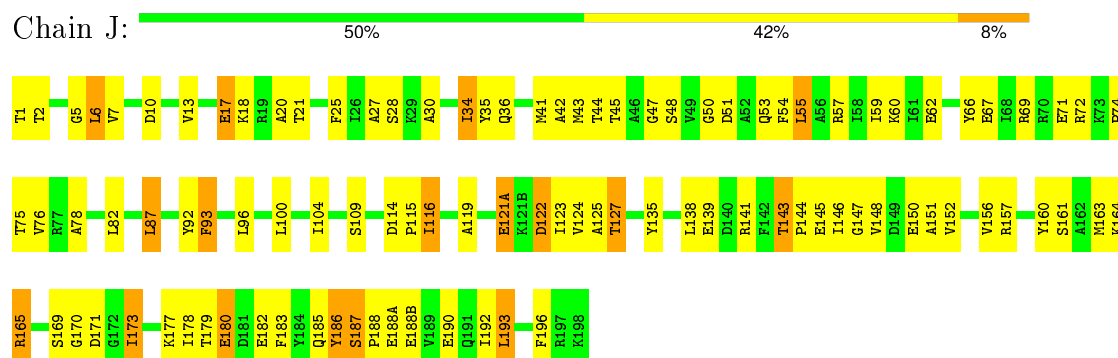




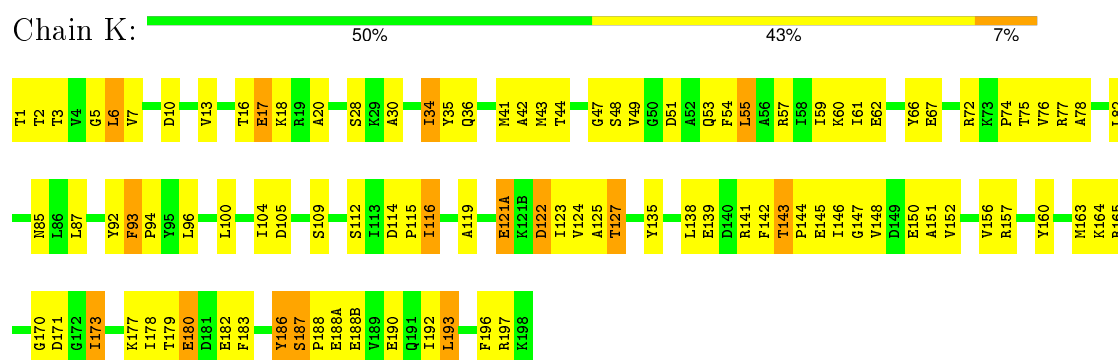
A151	V152	E171	T1
V156	V157	R72	T2
Y160	S161	R73	T3
A162	M163	P74	V4
K164	R165	T75	G5
S169	D171	V76	L6
G170	G171	R77	V7
G172	L173	A78	D10
I174	K175	L82	T16
K177	T178	T83	E17
T179	E180	S84	K18
E181	E182	M85	R19
Y186	S187	L86	A20
P188	E188A	L87	T21
E188B	V189	Y82	M22
I191	L192	P83	P25
L193	K196	P94	L26
F196	R197	Y85	A27
K198	K199	L96	S28
		L100	V29
		G103	A30
		I104	A31
		S109	K32
		D114	K33
		P115	L34
		I116	Y35
		A119	V36
		E121A	R40
		K121B	M41
		D122	A42
		I123	M43
		V124	T44
		A125	T45
		T127	T46
		L132	G47
		Y135	S48
		L138	V49
		E139	G50
		D140	D51
		R141	A52
		F142	Q53
		T143	P54
		P144	L55
		E145	A56
		I146	L58
		G147	I59
		V148	K60
		D149	L61
		E150	E62
			Y66
			E67
			L68
			R69
			P70

A162	M163	K164	R165	S169	G170	D171	G172	L173	D174	K177	L178	T179	E180	D181	E182	Y186	S187	P188	E188A	E188B	V189	E190	Q191	I192	L193	A194	R195	F196	R197	K198	T1	T2	L6	V7	D10	E17	K18	R19	A20	T21	M22	S28	V29	A30	A31	K32	K33	I34	Y35	Q36	M41	A42	M43	T44	S48	V49	G50	D51	A52	Q53	F54	L55	A56	R57	I58	I59	K60	I61	E62	N64	L65	Y66	E67	I68	E71	R72	K73	P74	T75	V76	R77	A78
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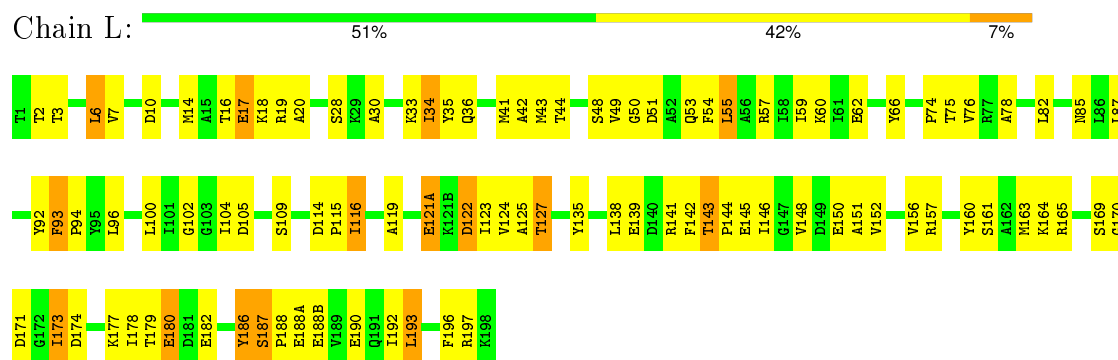
- Molecule 2: Proteasome beta subunit



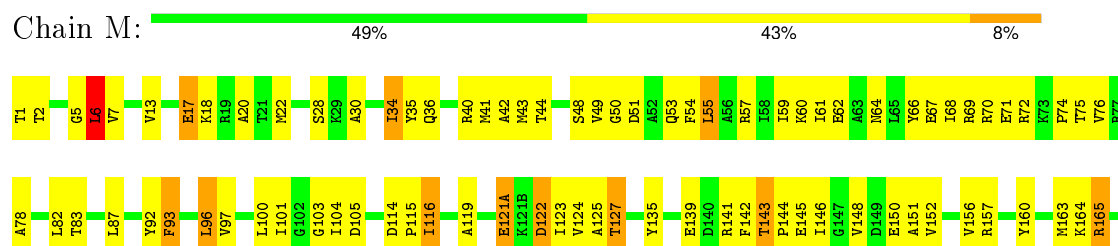
- Molecule 2: Proteasome beta subunit



- Molecule 2: Proteasome beta subunit

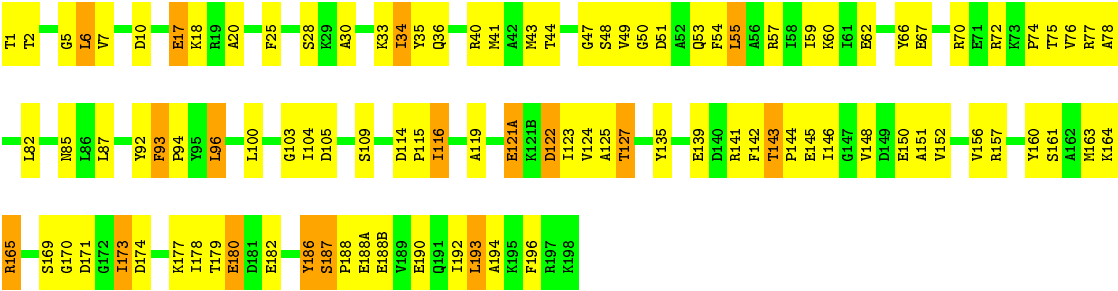


- Molecule 2: Proteasome beta subunit





● Molecule 2: Proteasome beta subunit



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	148.10Å 148.10Å 303.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	16.99 – 2.83	Depositor
% Data completeness (in resolution range)	94.6 (16.99-2.83)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.241 , 0.279	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	24227	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.40	0/1892	0.66	1/2549 (0.0%)
1	B	0.42	0/1892	0.66	1/2549 (0.0%)
1	C	0.41	0/1892	0.65	1/2549 (0.0%)
1	D	0.39	0/1892	0.65	1/2549 (0.0%)
1	E	0.40	0/1892	0.65	1/2549 (0.0%)
1	F	0.40	0/1892	0.64	1/2549 (0.0%)
1	G	0.40	0/1892	0.65	1/2549 (0.0%)
2	H	0.45	0/1573	0.73	1/2121 (0.0%)
2	I	0.45	0/1573	0.72	1/2121 (0.0%)
2	J	0.46	0/1573	0.73	2/2121 (0.1%)
2	K	0.47	0/1573	0.73	2/2121 (0.1%)
2	L	0.44	0/1573	0.73	1/2121 (0.0%)
2	M	0.47	0/1573	0.72	3/2121 (0.1%)
2	N	0.46	0/1573	0.72	1/2121 (0.0%)
All	All	0.43	0/24255	0.69	18/32690 (0.1%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	186	TYR	N-CA-C	6.15	127.60	111.00
2	N	186	TYR	N-CA-C	6.10	127.46	111.00
2	I	186	TYR	N-CA-C	6.07	127.38	111.00
2	M	186	TYR	N-CA-C	6.05	127.33	111.00
2	K	186	TYR	N-CA-C	5.99	127.16	111.00
2	H	186	TYR	N-CA-C	5.94	127.04	111.00
2	L	186	TYR	N-CA-C	5.93	127.02	111.00
1	D	127	GLY	N-CA-C	5.92	127.90	113.10
1	B	127	GLY	N-CA-C	5.70	127.35	113.10
1	G	127	GLY	N-CA-C	5.65	127.22	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	127	GLY	N-CA-C	5.60	127.11	113.10
1	F	127	GLY	N-CA-C	5.51	126.86	113.10
1	E	127	GLY	N-CA-C	5.47	126.78	113.10
1	A	127	GLY	N-CA-C	5.37	126.53	113.10
2	K	183	PHE	N-CA-C	-5.29	96.72	111.00
2	M	183	PHE	N-CA-C	-5.20	96.95	111.00
2	J	183	PHE	N-CA-C	-5.20	96.96	111.00
2	M	6	LEU	CA-CB-CG	5.03	126.87	115.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1866	0	1908	140	0
1	B	1866	0	1908	141	0
1	C	1866	0	1908	134	0
1	D	1866	0	1908	124	0
1	E	1866	0	1908	125	0
1	F	1866	0	1908	118	0
1	G	1866	0	1908	128	0
2	H	1553	0	1582	113	0
2	I	1553	0	1582	101	0
2	J	1553	0	1582	102	0
2	K	1553	0	1582	99	0
2	L	1553	0	1582	92	0
2	M	1553	0	1582	106	0
2	N	1553	0	1582	107	0
3	H	27	0	36	5	0
3	I	27	0	36	4	0
3	J	27	0	36	2	0
3	K	27	0	36	2	0
3	L	27	0	36	2	0
3	M	27	0	36	2	0
3	N	27	0	36	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	4	0	0	1	0
4	B	7	0	0	2	0
4	C	9	0	0	2	0
4	D	4	0	0	0	0
4	E	7	0	0	1	0
4	F	5	0	0	1	0
4	G	5	0	0	1	0
4	H	13	0	0	0	0
4	I	14	0	0	3	0
4	J	5	0	0	1	0
4	K	7	0	0	0	0
4	L	6	0	0	0	0
4	M	12	0	0	4	0
4	N	7	0	0	0	0
All	All	24227	0	24682	1484	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (1484) 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:G:12:ILE:HG21	1:G:127:GLY:HA2	1.21	1.14
1:F:12:ILE:HG21	1:F:127:GLY:HA2	1.23	1.12
1:E:12:ILE:HG21	1:E:127:GLY:HA2	1.18	1.11
2:M:121(A):GLU:HG2	2:M:124:VAL:HB	1.34	1.10
1:B:12:ILE:HG21	1:B:127:GLY:HA2	1.16	1.09
1:A:12:ILE:HG21	1:A:127:GLY:HA2	1.19	1.09
1:C:12:ILE:HG21	1:C:127:GLY:HA2	1.23	1.09
2:K:121(A):GLU:HG2	2:K:124:VAL:HB	1.34	1.08
2:L:121(A):GLU:HG2	2:L:124:VAL:HB	1.33	1.08
1:D:12:ILE:HG21	1:D:127:GLY:HA2	1.16	1.08
2:N:121(A):GLU:HG2	2:N:124:VAL:HB	1.33	1.06
2:J:121(A):GLU:HG2	2:J:124:VAL:HB	1.34	1.04
2:H:121(A):GLU:HG2	2:H:124:VAL:HB	1.34	1.04
2:I:121(A):GLU:HG2	2:I:124:VAL:HB	1.38	1.03
1:B:116:ILE:HD11	1:B:138:ILE:HD11	1.41	1.02
1:C:116:ILE:HD11	1:C:138:ILE:HD11	1.45	0.98
1:F:116:ILE:HD11	1:F:138:ILE:HD11	1.47	0.97
1:E:205:LEU:H	1:E:233(D):ASN:HD21	1.10	0.96
1:A:116:ILE:HD11	1:A:138:ILE:HD11	1.43	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:53:GLN:HE22	2:K:119:ALA:H	1.13	0.95
1:G:81:LEU:HD23	1:G:133:GLY:HA3	1.47	0.94
1:B:12:ILE:HG23	1:B:13:THR:H	1.33	0.94
1:F:205:LEU:H	1:F:233(D):ASN:HD21	1.14	0.94
1:A:81:LEU:HD23	1:A:133:GLY:HA3	1.49	0.94
1:A:205:LEU:H	1:A:233(D):ASN:HD21	1.15	0.94
1:D:116:ILE:HD11	1:D:138:ILE:HD11	1.47	0.94
1:A:20:ARG:HB2	1:A:20:ARG:NH1	1.83	0.93
2:L:7:VAL:HG22	2:L:122:ASP:HA	1.49	0.93
1:G:12:ILE:HG23	1:G:13:THR:H	1.32	0.92
2:H:7:VAL:HG22	2:H:122:ASP:HA	1.52	0.92
1:C:81:LEU:HD23	1:C:133:GLY:HA3	1.52	0.91
2:I:54:PHE:HA	2:I:57:ARG:NH1	1.86	0.91
2:K:7:VAL:HG22	2:K:122:ASP:HA	1.52	0.91
1:G:116:ILE:HD11	1:G:138:ILE:HD11	1.51	0.91
1:D:81:LEU:HD23	1:D:133:GLY:HA3	1.53	0.90
2:J:7:VAL:HG22	2:J:122:ASP:HA	1.53	0.90
1:F:20:ARG:HB2	1:F:20:ARG:NH1	1.87	0.90
1:B:81:LEU:HD23	1:B:133:GLY:HA3	1.54	0.90
2:H:141:ARG:NE	2:H:157:ARG:HE	1.70	0.90
1:B:49:ILE:HD12	1:B:194:LEU:HD13	1.53	0.90
1:D:12:ILE:HG23	1:D:13:THR:H	1.35	0.89
1:C:20:ARG:HB2	1:C:20:ARG:NH1	1.87	0.89
1:A:12:ILE:HG23	1:A:13:THR:H	1.38	0.89
1:G:20:ARG:NH1	1:G:20:ARG:HB2	1.87	0.89
2:I:75:THR:HG23	2:I:78:ALA:H	1.38	0.88
1:G:105:GLU:OE2	2:H:75:THR:HG21	1.73	0.88
2:K:54:PHE:HA	2:K:57:ARG:NH1	1.88	0.88
1:F:81:LEU:HD23	1:F:133:GLY:HA3	1.51	0.88
2:L:54:PHE:HA	2:L:57:ARG:NH1	1.89	0.88
1:F:12:ILE:HG23	1:F:13:THR:H	1.37	0.88
1:C:205:LEU:H	1:C:233(D):ASN:HD21	1.19	0.88
2:I:141:ARG:NE	2:I:157:ARG:HE	1.69	0.88
2:N:141:ARG:NE	2:N:157:ARG:HE	1.72	0.88
1:B:124:THR:CG2	1:C:130:ARG:HH21	1.87	0.87
2:J:141:ARG:NE	2:J:157:ARG:HE	1.72	0.87
1:C:226:PRO:HG2	1:C:227:GLU:OE2	1.73	0.87
2:M:53:GLN:HE22	2:N:119:ALA:H	1.17	0.87
2:N:54:PHE:HA	2:N:57:ARG:NH1	1.89	0.87
1:C:12:ILE:HG23	1:C:13:THR:H	1.39	0.87
1:A:226:PRO:HG2	1:A:227:GLU:OE2	1.75	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:12:ILE:CG2	1:D:127:GLY:HA2	2.03	0.87
2:L:141:ARG:NE	2:L:157:ARG:HE	1.71	0.86
1:G:205:LEU:H	1:G:233(D):ASN:HD21	1.20	0.86
1:D:205:LEU:H	1:D:233(D):ASN:HD21	1.19	0.86
1:E:12:ILE:CG2	1:E:127:GLY:HA2	2.04	0.86
1:E:12:ILE:HG23	1:E:13:THR:H	1.38	0.85
1:B:12:ILE:CG2	1:B:127:GLY:HA2	2.04	0.85
1:E:116:ILE:HD11	1:E:138:ILE:HD11	1.56	0.85
1:E:20:ARG:HB2	1:E:20:ARG:NH1	1.89	0.85
1:A:12:ILE:CG2	1:A:127:GLY:HA2	2.04	0.85
1:B:205:LEU:H	1:B:233(D):ASN:HD21	1.24	0.85
2:I:7:VAL:HG22	2:I:122:ASP:HA	1.58	0.85
2:H:119:ALA:H	2:N:53:GLN:HE22	1.21	0.85
2:M:7:VAL:HG22	2:M:122:ASP:HA	1.59	0.85
1:E:81:LEU:HD23	1:E:133:GLY:HA3	1.59	0.85
2:N:121(A):GLU:CG	2:N:124:VAL:HB	2.07	0.84
1:C:12:ILE:CG2	1:C:127:GLY:HA2	2.07	0.84
1:D:15:PHE:H	1:E:23:GLN:HE22	1.20	0.84
2:M:163:MET:HE2	2:M:170:GLY:HA2	1.60	0.84
2:J:121(A):GLU:CG	2:J:124:VAL:HB	2.07	0.84
1:B:172:VAL:HB	1:B:196:ALA:HB1	1.60	0.84
2:N:75:THR:HG23	2:N:78:ALA:H	1.43	0.84
2:N:7:VAL:HG22	2:N:122:ASP:HA	1.58	0.84
2:I:53:GLN:HE22	2:J:119:ALA:H	1.22	0.83
1:D:20:ARG:NH1	1:D:20:ARG:HB2	1.92	0.83
2:M:121(A):GLU:CG	2:M:124:VAL:HB	2.08	0.83
1:A:49:ILE:HD12	1:A:194:LEU:HD13	1.58	0.83
2:H:54:PHE:HA	2:H:57:ARG:NH1	1.93	0.83
1:F:12:ILE:CG2	1:F:127:GLY:HA2	2.07	0.83
1:A:12:ILE:HG21	1:A:127:GLY:CA	2.08	0.83
1:F:15:PHE:H	1:G:23:GLN:HE22	1.25	0.83
1:E:226:PRO:HG2	1:E:227:GLU:OE2	1.78	0.82
1:G:12:ILE:CG2	1:G:127:GLY:HA2	2.06	0.82
2:H:53:GLN:HE22	2:I:119:ALA:H	1.24	0.82
1:A:172:VAL:HB	1:A:196:ALA:HB1	1.62	0.82
1:E:15:PHE:H	1:F:23:GLN:HE22	1.27	0.82
2:H:121(A):GLU:CG	2:H:124:VAL:HB	2.09	0.81
1:D:226:PRO:HG2	1:D:227:GLU:OE2	1.79	0.81
1:E:172:VAL:HB	1:E:196:ALA:HB1	1.63	0.81
1:F:20:ARG:HB2	1:F:20:ARG:HH11	1.45	0.81
1:A:130:ARG:HH21	1:G:124:THR:CG2	1.93	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:159:GLU:OE2	1:G:63:THR:HG21	1.81	0.81
1:B:226:PRO:HG2	1:B:227:GLU:OE2	1.81	0.81
1:C:28:ARG:O	1:C:31:VAL:HG12	1.81	0.81
1:A:20:ARG:HB2	1:A:20:ARG:HH11	1.45	0.81
1:A:28:ARG:O	1:A:31:VAL:HG12	1.82	0.80
1:B:105:GLU:OE2	2:J:75:THR:HG21	1.80	0.80
2:K:141:ARG:NE	2:K:157:ARG:HE	1.80	0.80
1:G:49:ILE:HD12	1:G:194:LEU:HD13	1.61	0.80
2:J:54:PHE:HA	2:J:57:ARG:NH1	1.95	0.80
1:A:159:GLU:OE2	1:B:63:THR:HG21	1.82	0.80
1:C:172:VAL:HB	1:C:196:ALA:HB1	1.62	0.79
1:F:226:PRO:HG2	1:F:227:GLU:OE2	1.83	0.79
1:B:20:ARG:HB2	1:B:20:ARG:NH1	1.97	0.79
1:F:172:VAL:HB	1:F:196:ALA:HB1	1.64	0.79
2:K:121(A):GLU:CG	2:K:124:VAL:HB	2.12	0.79
1:A:105:GLU:OE2	2:I:75:THR:HG21	1.82	0.79
2:M:141:ARG:NE	2:M:157:ARG:HE	1.81	0.79
2:M:54:PHE:HA	2:M:57:ARG:NH1	1.97	0.79
2:L:53:GLN:HE22	2:M:119:ALA:H	1.27	0.79
1:E:49:ILE:HD12	1:E:194:LEU:HD13	1.65	0.79
1:F:49:ILE:HD12	1:F:194:LEU:HD13	1.64	0.78
2:H:75:THR:HG23	2:H:78:ALA:H	1.49	0.78
1:B:125:GLN:HB2	1:C:130:ARG:HG2	1.63	0.78
2:H:163:MET:CE	2:H:170:GLY:HA2	2.14	0.78
1:G:226:PRO:HG2	1:G:227:GLU:OE2	1.83	0.78
1:D:12:ILE:HG21	1:D:127:GLY:CA	2.07	0.78
1:G:18:ASP:HB2	1:G:20:ARG:NH1	1.99	0.78
2:K:75:THR:HG23	2:K:78:ALA:H	1.47	0.78
1:E:20:ARG:HH11	1:E:20:ARG:HB2	1.48	0.78
2:H:163:MET:HE2	2:H:170:GLY:HA2	1.66	0.78
1:G:172:VAL:HB	1:G:196:ALA:HB1	1.65	0.78
1:C:49:ILE:HD12	1:C:194:LEU:HD13	1.65	0.78
1:D:172:VAL:HB	1:D:196:ALA:HB1	1.64	0.78
1:D:219:ASP:O	1:D:220(A):THR:N	2.17	0.78
2:M:75:THR:HG23	2:M:78:ALA:H	1.49	0.78
1:E:205:LEU:H	1:E:233(D):ASN:ND2	1.81	0.77
1:D:49:ILE:HD12	1:D:194:LEU:HD13	1.65	0.77
1:B:219:ASP:O	1:B:220(A):THR:N	2.18	0.77
2:L:75:THR:HG23	2:L:78:ALA:H	1.49	0.77
1:A:130:ARG:HG2	1:G:125:GLN:HB2	1.65	0.77
2:L:54:PHE:HA	2:L:57:ARG:HH12	1.48	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:121(A):GLU:CG	2:L:124:VAL:HB	2.13	0.76
1:F:28:ARG:O	1:F:31:VAL:HG12	1.86	0.76
2:N:121(A):GLU:HG2	2:N:124:VAL:CB	2.14	0.76
2:I:179:THR:O	2:I:180:GLU:HB2	1.86	0.76
2:L:163:MET:CE	2:L:170:GLY:HA2	2.16	0.76
2:M:179:THR:HG21	4:M:1509:HOH:O	1.83	0.76
1:E:105:GLU:OE2	2:M:75:THR:HG21	1.86	0.75
2:J:163:MET:HE2	2:J:170:GLY:HA2	1.67	0.75
1:C:220:ARG:HG2	1:C:220:ARG:HH21	1.52	0.75
1:D:116:ILE:HD11	1:D:138:ILE:CD1	2.16	0.75
2:L:179:THR:O	2:L:180:GLU:HB2	1.85	0.75
2:M:179:THR:O	2:M:180:GLU:HB2	1.86	0.75
1:C:219:ASP:O	1:C:220(A):THR:N	2.19	0.75
2:I:121(A):GLU:CG	2:I:124:VAL:HB	2.15	0.75
1:G:28:ARG:O	1:G:31:VAL:HG12	1.85	0.75
1:E:12:ILE:HG21	1:E:127:GLY:CA	2.08	0.75
1:C:20:ARG:HB2	1:C:20:ARG:HH11	1.51	0.75
2:H:121(A):GLU:HG2	2:H:124:VAL:CB	2.16	0.74
1:D:220:ARG:HH21	1:D:220:ARG:HG2	1.51	0.74
2:H:179:THR:O	2:H:180:GLU:HB2	1.85	0.74
2:M:49:VAL:HG22	3:M:1501:CIB:HG31	1.69	0.74
1:A:205:LEU:H	1:A:233(D):ASN:ND2	1.85	0.74
2:K:55:LEU:O	2:K:59:ILE:HG12	1.87	0.74
2:M:55:LEU:O	2:M:59:ILE:HG12	1.87	0.74
2:J:121(A):GLU:HG2	2:J:124:VAL:CB	2.14	0.74
1:B:116:ILE:HD11	1:B:138:ILE:CD1	2.16	0.74
1:C:116:ILE:HD11	1:C:138:ILE:CD1	2.17	0.74
2:N:146:ILE:HG13	2:N:150:GLU:HG3	1.69	0.74
2:J:163:MET:CE	2:J:170:GLY:HA2	2.18	0.74
1:E:28:ARG:O	1:E:31:VAL:HG12	1.88	0.74
2:N:163:MET:HE2	2:N:170:GLY:HA2	1.69	0.74
2:K:53:GLN:HE22	2:L:119:ALA:H	1.36	0.74
1:F:205:LEU:H	1:F:233(D):ASN:ND2	1.84	0.74
2:K:179:THR:O	2:K:180:GLU:HB2	1.87	0.74
1:G:12:ILE:HG21	1:G:127:GLY:CA	2.11	0.73
1:F:12:ILE:HG21	1:F:127:GLY:CA	2.11	0.73
2:J:179:THR:O	2:J:180:GLU:HB2	1.88	0.73
2:M:163:MET:CE	2:M:170:GLY:HA2	2.18	0.73
2:L:188(B):GLU:O	2:L:192:ILE:HG13	1.88	0.73
1:B:12:ILE:HG21	1:B:127:GLY:CA	2.09	0.73
1:C:205:LEU:H	1:C:233(D):ASN:ND2	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:VAL:HB	1:C:23:GLN:NE2	2.01	0.73
1:G:20:ARG:HH11	1:G:20:ARG:HB2	1.50	0.73
2:K:163:MET:CE	2:K:170:GLY:HA2	2.18	0.73
1:A:100:ARG:NH2	1:A:106:PRO:HA	2.04	0.73
1:C:15:PHE:H	1:D:23:GLN:HE22	1.34	0.72
2:J:188(B):GLU:O	2:J:192:ILE:HG13	1.88	0.72
1:E:18:ASP:HB2	1:E:20:ARG:NH1	2.05	0.72
1:C:105:GLU:OE2	2:K:75:THR:HG21	1.89	0.72
1:C:12:ILE:HG21	1:C:127:GLY:CA	2.10	0.72
2:L:146:ILE:HG13	2:L:150:GLU:HG3	1.71	0.72
1:A:124:THR:CG2	1:B:130:ARG:HH21	2.03	0.72
1:A:219:ASP:O	1:A:220(A):THR:N	2.22	0.72
1:C:18:ASP:HB2	1:C:20:ARG:NH1	2.05	0.72
1:E:219:ASP:O	1:E:220(A):THR:N	2.22	0.72
2:N:163:MET:CE	2:N:170:GLY:HA2	2.18	0.72
1:F:125:GLN:HB2	1:G:130:ARG:HG2	1.70	0.72
1:G:116:ILE:HD11	1:G:138:ILE:CD1	2.18	0.72
2:N:179:THR:O	2:N:180:GLU:HB2	1.88	0.72
1:B:28:ARG:O	1:B:31:VAL:HG12	1.88	0.72
1:A:116:ILE:HD11	1:A:138:ILE:CD1	2.16	0.71
2:J:55:LEU:O	2:J:59:ILE:HG12	1.90	0.71
1:C:40:ILE:HD11	1:C:193:GLY:HA3	1.72	0.71
1:A:63:THR:HG21	1:G:159:GLU:OE2	1.90	0.71
1:G:105:GLU:CD	2:H:75:THR:HG21	2.11	0.71
1:D:20:ARG:HB2	1:D:20:ARG:HH11	1.55	0.71
1:E:100:ARG:NH2	1:E:106:PRO:HA	2.05	0.71
2:I:163:MET:CE	2:I:170:GLY:HA2	2.21	0.71
1:F:219:ASP:O	1:F:220(A):THR:N	2.24	0.71
2:K:163:MET:HE2	2:K:170:GLY:HA2	1.71	0.71
1:B:220:ARG:H	1:B:220:ARG:HD2	1.55	0.71
2:K:121(A):GLU:HG2	2:K:124:VAL:CB	2.18	0.71
1:D:12:ILE:HG23	1:D:13:THR:N	2.06	0.71
1:E:205:LEU:N	1:E:233(D):ASN:HD21	1.86	0.71
1:E:116:ILE:HD11	1:E:138:ILE:CD1	2.21	0.71
1:B:18:ASP:HB2	1:B:20:ARG:NH1	2.04	0.71
2:L:163:MET:HE2	2:L:170:GLY:HA2	1.71	0.71
2:J:146:ILE:HG13	2:J:150:GLU:HG3	1.73	0.71
1:G:12:ILE:HG23	1:G:13:THR:N	2.04	0.71
1:G:197:MET:O	1:G:200:SER:HB3	1.89	0.71
1:D:40:ILE:HD11	1:D:193:GLY:HA3	1.73	0.71
2:H:146:ILE:HG13	2:H:150:GLU:HG3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:188(B):GLU:O	2:H:192:ILE:HG13	1.91	0.71
1:B:15:PHE:H	1:C:23:GLN:HE22	1.37	0.70
2:I:55:LEU:O	2:I:59:ILE:HG12	1.91	0.70
1:D:205:LEU:H	1:D:233(D):ASN:ND2	1.89	0.70
1:A:220:ARG:H	1:A:220:ARG:HD2	1.56	0.70
1:D:18:ASP:HB2	1:D:20:ARG:NH1	2.05	0.70
1:B:100:ARG:NH2	1:B:106:PRO:HA	2.07	0.70
1:A:181:ARG:O	1:A:184:LEU:HG	1.92	0.70
2:I:54:PHE:HA	2:I:57:ARG:HH12	1.53	0.70
1:G:220:ARG:HH21	1:G:220:ARG:HG2	1.57	0.70
1:A:18:ASP:HB2	1:A:20:ARG:NH1	2.05	0.70
2:M:121(A):GLU:HG2	2:M:124:VAL:CB	2.15	0.70
1:B:12:ILE:HG23	1:B:13:THR:N	2.04	0.70
2:J:54:PHE:HA	2:J:57:ARG:HH12	1.57	0.70
1:G:219:ASP:O	1:G:220(A):THR:N	2.25	0.70
2:J:75:THR:HG23	2:J:78:ALA:H	1.56	0.70
1:D:121:GLN:O	1:D:124:THR:HB	1.91	0.70
1:D:220:ARG:HD2	1:D:220:ARG:H	1.54	0.69
1:F:40:ILE:HD11	1:F:193:GLY:HA3	1.74	0.69
2:H:119:ALA:H	2:N:53:GLN:NE2	1.90	0.69
1:D:105:GLU:OE2	2:L:75:THR:HG21	1.92	0.69
1:D:124:THR:CG2	1:E:130:ARG:HH21	2.04	0.69
2:K:54:PHE:HA	2:K:57:ARG:HH12	1.55	0.69
1:F:116:ILE:HD11	1:F:138:ILE:CD1	2.20	0.69
1:F:205:LEU:N	1:F:233(D):ASN:HD21	1.90	0.69
1:G:220:ARG:H	1:G:220:ARG:HD2	1.57	0.69
2:H:55:LEU:O	2:H:59:ILE:HG12	1.92	0.69
1:C:220:ARG:H	1:C:220:ARG:HD2	1.57	0.69
1:F:124:THR:CG2	1:G:130:ARG:HH21	2.04	0.69
2:I:163:MET:HE2	2:I:170:GLY:HA2	1.73	0.69
1:D:125:GLN:HB2	1:E:130:ARG:HG2	1.73	0.69
1:A:70:ILE:HG21	1:A:112:LEU:HD21	1.75	0.69
1:D:100:ARG:NH2	1:D:106:PRO:HA	2.08	0.69
1:B:38:ILE:HD12	1:B:197:MET:HG2	1.74	0.69
2:H:54:PHE:HA	2:H:57:ARG:HH12	1.56	0.68
1:F:18:ASP:HB2	1:F:20:ARG:NH1	2.08	0.68
2:K:6:LEU:HB3	2:K:123:ILE:HD13	1.75	0.68
2:I:146:ILE:HG13	2:I:150:GLU:HG3	1.76	0.68
1:F:12:ILE:HG23	1:F:13:THR:N	2.09	0.68
2:I:62:GLU:OE2	2:I:82:LEU:HD21	1.93	0.68
2:M:146:ILE:HG13	2:M:150:GLU:HG3	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ILE:HD11	1:A:193:GLY:HA3	1.76	0.68
1:E:125:GLN:HB2	1:F:130:ARG:HG2	1.74	0.68
1:D:28:ARG:O	1:D:31:VAL:HG12	1.93	0.68
2:I:188(B):GLU:O	2:I:192:ILE:HG13	1.94	0.68
2:N:54:PHE:HA	2:N:57:ARG:HH12	1.57	0.68
1:B:40:ILE:HD11	1:B:193:GLY:HA3	1.76	0.68
1:F:17:PRO:HA	1:G:26:TYR:CD1	2.28	0.67
1:G:205:LEU:H	1:G:233(D):ASN:ND2	1.91	0.67
1:A:12:ILE:HG23	1:A:13:THR:N	2.10	0.67
1:C:197:MET:O	1:C:200:SER:HB3	1.94	0.67
1:A:57:LYS:HG2	1:G:177:GLU:OE2	1.94	0.67
1:F:100:ARG:NH2	1:F:106:PRO:HA	2.10	0.67
1:F:105:GLU:OE2	2:N:75:THR:HG21	1.94	0.67
1:B:54:VAL:HG21	1:B:59:LEU:HB2	1.75	0.67
1:B:70:ILE:HG21	1:B:112:LEU:HD21	1.77	0.67
2:K:188(B):GLU:O	2:K:192:ILE:HG13	1.94	0.67
1:D:12:ILE:HG13	1:D:13:THR:N	2.10	0.67
2:H:6:LEU:N	2:H:6:LEU:HD23	2.10	0.67
1:G:124:THR:HG21	4:G:235:HOH:O	1.93	0.67
1:G:54:VAL:HG21	1:G:59:LEU:HB2	1.76	0.67
1:C:100:ARG:NH2	1:C:106:PRO:HA	2.10	0.66
1:C:70:ILE:HG21	1:C:112:LEU:HD21	1.75	0.66
1:D:17:PRO:HA	1:E:26:TYR:CD1	2.31	0.66
2:M:122:ASP:OD1	2:M:123:ILE:N	2.28	0.66
1:E:40:ILE:HD11	1:E:193:GLY:HA3	1.77	0.66
1:E:159:GLU:OE2	1:F:63:THR:HG21	1.94	0.66
1:F:197:MET:O	1:F:200:SER:HB3	1.94	0.66
1:B:121:GLN:O	1:B:124:THR:HB	1.95	0.66
1:E:220:ARG:HD2	1:E:220:ARG:H	1.61	0.66
1:E:124:THR:CG2	1:F:130:ARG:HH21	2.09	0.66
2:K:146:ILE:HG13	2:K:150:GLU:HG3	1.77	0.66
1:E:12:ILE:HG23	1:E:13:THR:N	2.08	0.66
1:B:220:ARG:HH21	1:B:220:ARG:HG2	1.60	0.66
2:L:121(A):GLU:HG2	2:L:124:VAL:CB	2.19	0.66
2:M:188(B):GLU:O	2:M:192:ILE:HG13	1.94	0.66
1:D:194:LEU:O	1:D:205:LEU:HD11	1.95	0.66
1:E:70:ILE:HG21	1:E:112:LEU:HD21	1.78	0.66
2:I:186:TYR:O	2:I:188(B):GLU:HB2	1.95	0.66
2:N:6:LEU:HD23	2:N:6:LEU:N	2.10	0.65
2:J:48:SER:HB3	2:J:51:ASP:HB2	1.78	0.65
1:G:40:ILE:HD11	1:G:193:GLY:HA3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:ARG:HB2	1:B:20:ARG:HH11	1.59	0.65
2:H:186:TYR:O	2:H:188(B):GLU:HB2	1.95	0.65
1:G:40:ILE:HD11	1:G:193:GLY:CA	2.26	0.65
1:A:15:PHE:H	1:B:23:GLN:HE22	1.43	0.65
2:L:62:GLU:OE2	2:L:82:LEU:HD21	1.96	0.65
1:A:194:LEU:O	1:A:205:LEU:HD11	1.97	0.65
1:E:121:GLN:O	1:E:124:THR:HB	1.96	0.65
2:J:62:GLU:OE2	2:J:82:LEU:HD21	1.95	0.65
1:B:197:MET:O	1:B:200:SER:HB3	1.96	0.65
1:D:38:ILE:HD12	1:D:197:MET:HG2	1.79	0.65
2:N:186:TYR:O	2:N:188(B):GLU:HB2	1.96	0.65
1:E:12:ILE:HG13	1:E:13:THR:N	2.11	0.65
1:G:38:ILE:HD12	1:G:197:MET:HG2	1.78	0.65
2:L:6:LEU:N	2:L:6:LEU:HD23	2.12	0.65
1:F:121:GLN:O	1:F:124:THR:HB	1.95	0.65
1:A:23:GLN:HE22	1:G:15:PHE:H	1.42	0.65
1:B:12:ILE:HG13	1:B:13:THR:N	2.11	0.65
1:G:100:ARG:NH2	1:G:106:PRO:HA	2.11	0.65
2:M:62:GLU:OE2	2:M:82:LEU:HD21	1.97	0.65
1:B:181:ARG:O	1:B:184:LEU:HG	1.96	0.65
1:B:49:ILE:CD1	1:B:194:LEU:HD13	2.27	0.64
1:G:70:ILE:HG21	1:G:112:LEU:HD21	1.79	0.64
1:E:40:ILE:HD11	1:E:193:GLY:CA	2.26	0.64
2:N:177:LYS:HE2	2:N:186:TYR:OH	1.95	0.64
1:C:121:GLN:O	1:C:124:THR:HB	1.97	0.64
1:F:220:ARG:H	1:F:220:ARG:HD2	1.61	0.64
2:H:41:MET:HE2	2:H:76:VAL:HG12	1.77	0.64
1:C:12:ILE:HG13	1:C:13:THR:N	2.12	0.64
2:M:54:PHE:HA	2:M:57:ARG:HH12	1.61	0.64
2:M:143:THR:O	2:M:146:ILE:HG22	1.97	0.64
1:A:205:LEU:N	1:A:233(D):ASN:HD21	1.92	0.64
1:C:201:ILE:HD11	1:C:205:LEU:HD23	1.77	0.64
2:N:62:GLU:OE2	2:N:82:LEU:HD21	1.97	0.64
1:B:124:THR:HG23	1:C:130:ARG:HH21	1.63	0.64
2:J:143:THR:O	2:J:146:ILE:HG22	1.97	0.64
1:A:220:ARG:HG2	1:A:220:ARG:HH21	1.62	0.64
1:E:152:ASP:OD1	1:E:153:PRO:HD2	1.97	0.64
1:G:12:ILE:HG13	1:G:13:THR:N	2.13	0.64
1:C:38:ILE:HD12	1:C:197:MET:HG2	1.80	0.64
1:G:205:LEU:N	1:G:233(D):ASN:HD21	1.95	0.64
1:F:40:ILE:HD11	1:F:193:GLY:CA	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:188(B):GLU:O	2:N:192:ILE:HG13	1.98	0.64
1:C:181:ARG:O	1:C:184:LEU:HG	1.98	0.64
1:D:40:ILE:HD11	1:D:193:GLY:CA	2.28	0.64
1:E:225:SER:OG	1:E:228:GLU:HG3	1.98	0.64
1:C:12:ILE:HG23	1:C:13:THR:N	2.10	0.63
3:I:1101:CIB:HD13	2:J:114:ASP:OD1	1.99	0.63
1:F:220:ARG:HH21	1:F:220:ARG:HG2	1.63	0.63
2:K:62:GLU:OE2	2:K:82:LEU:HD21	1.98	0.63
1:G:152:ASP:OD1	1:G:153:PRO:HD2	1.99	0.63
1:E:197:MET:O	1:E:200:SER:HB3	1.98	0.63
1:B:18:ASP:HB2	1:B:20:ARG:HH11	1.62	0.63
1:A:219:ASP:O	1:A:220(A):THR:HG23	1.99	0.63
2:J:152:VAL:O	2:J:156:VAL:HG23	1.98	0.63
1:F:152:ASP:OD1	1:F:153:PRO:HD2	1.99	0.63
1:B:201:ILE:HD11	1:B:205:LEU:HD23	1.81	0.63
1:A:54:VAL:HG21	1:A:59:LEU:HB2	1.80	0.63
1:C:54:VAL:HG21	1:C:59:LEU:HB2	1.80	0.63
1:D:70:ILE:HG21	1:D:112:LEU:HD21	1.81	0.63
1:F:54:VAL:HG21	1:F:59:LEU:HB2	1.81	0.63
2:H:62:GLU:OE2	2:H:82:LEU:HD21	1.99	0.63
2:M:22:MET:HB2	3:M:1501:CIB:HD22	1.81	0.63
1:D:152:ASP:OD1	1:D:153:PRO:HD2	1.98	0.63
2:J:122:ASP:OD1	2:J:123:ILE:N	2.30	0.62
1:C:40:ILE:HD11	1:C:193:GLY:CA	2.28	0.62
1:C:225:SER:OG	1:C:228:GLU:HG3	1.99	0.62
2:K:152:VAL:O	2:K:156:VAL:HG23	1.99	0.62
2:I:121(A):GLU:HG2	2:I:124:VAL:CB	2.22	0.62
1:G:121:GLN:O	1:G:124:THR:HB	2.00	0.62
1:B:225:SER:OG	1:B:228:GLU:HG3	1.99	0.62
1:E:17:PRO:HA	1:F:26:TYR:CD1	2.34	0.62
1:B:205:LEU:H	1:B:233(D):ASN:ND2	1.96	0.62
1:F:225:SER:OG	1:F:228:GLU:HG3	1.99	0.62
2:K:6:LEU:N	2:K:6:LEU:HD23	2.15	0.62
1:G:219:ASP:O	1:G:220(A):THR:HG23	1.99	0.62
1:A:40:ILE:HD11	1:A:193:GLY:CA	2.29	0.62
1:C:124:THR:CG2	1:D:130:ARG:HH21	2.12	0.62
1:D:181:ARG:O	1:D:184:LEU:HG	1.99	0.62
1:E:105:GLU:CD	2:M:75:THR:HG21	2.19	0.62
1:B:194:LEU:O	1:B:205:LEU:HD11	1.99	0.62
2:L:55:LEU:O	2:L:59:ILE:HG12	1.98	0.62
1:A:130:ARG:HH21	1:G:124:THR:HG23	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:136:LEU:O	1:E:150:GLU:HA	1.99	0.62
1:D:220:ARG:NH2	1:D:220:ARG:HG2	2.15	0.62
1:C:220:ARG:NH2	1:C:220:ARG:HG2	2.15	0.62
2:K:186:TYR:O	2:K:188(B):GLU:HB2	1.99	0.62
1:C:136:LEU:O	1:C:150:GLU:HA	2.00	0.62
2:M:43:MET:HA	2:M:100:LEU:O	2.00	0.62
2:I:6:LEU:HB3	2:I:123:ILE:HD13	1.82	0.61
2:I:53:GLN:NE2	2:J:119:ALA:H	1.97	0.61
2:J:6:LEU:N	2:J:6:LEU:HD23	2.15	0.61
1:A:38:ILE:HD12	1:A:197:MET:HG2	1.82	0.61
2:I:41:MET:HE2	2:I:76:VAL:HG12	1.82	0.61
1:A:17:PRO:HA	1:B:26:TYR:CD1	2.36	0.61
1:B:233(F):ARG:O	1:B:233(J):LEU:HB2	2.01	0.61
1:C:125:GLN:HB2	1:D:130:ARG:HG2	1.81	0.61
2:I:104:ILE:HD11	2:I:178:ILE:O	2.00	0.61
2:I:6:LEU:N	2:I:6:LEU:HD23	2.14	0.61
2:N:55:LEU:O	2:N:59:ILE:HG12	2.01	0.61
2:M:6:LEU:HB3	2:M:123:ILE:HD13	1.82	0.61
2:J:186:TYR:O	2:J:188(B):GLU:HB2	2.01	0.61
1:A:121:GLN:O	1:A:124:THR:HB	2.00	0.61
1:E:56:SER:HB3	1:E:59:LEU:HD23	1.82	0.61
1:D:205:LEU:N	1:D:233(D):ASN:HD21	1.96	0.61
2:N:48:SER:HB3	2:N:51:ASP:HB2	1.83	0.61
2:N:6:LEU:HB3	2:N:123:ILE:HD13	1.82	0.61
1:B:14:VAL:HB	1:C:23:GLN:HE22	1.64	0.61
2:N:36:GLN:O	2:N:60:LYS:HE2	2.01	0.61
1:B:56:SER:HB3	1:B:59:LEU:HD23	1.81	0.61
2:K:177:LYS:HE2	2:K:186:TYR:OH	2.01	0.61
2:K:144:PRO:HG2	2:K:145:GLU:OE2	2.01	0.61
2:I:43:MET:HA	2:I:100:LEU:O	2.01	0.61
1:D:136:LEU:O	1:D:150:GLU:HA	2.00	0.60
1:G:18:ASP:HB2	1:G:20:ARG:HH11	1.66	0.60
1:A:225:SER:OG	1:A:228:GLU:HG3	2.01	0.60
1:A:12:ILE:HG13	1:A:13:THR:N	2.16	0.60
1:E:181:ARG:O	1:E:184:LEU:HG	2.02	0.60
1:G:75:CYS:HB3	1:G:221:PHE:CD2	2.37	0.60
1:C:17:PRO:HA	1:D:26:TYR:CD1	2.35	0.60
2:J:43:MET:HA	2:J:100:LEU:O	2.01	0.60
1:B:136:LEU:O	1:B:150:GLU:HA	2.02	0.60
1:C:194:LEU:O	1:C:205:LEU:HD11	2.01	0.60
1:D:18:ASP:HB2	1:D:20:ARG:HH11	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:177:LYS:HE2	2:I:186:TYR:OH	2.02	0.60
1:C:159:GLU:OE2	1:D:63:THR:HG21	2.02	0.60
1:F:181:ARG:O	1:F:184:LEU:HG	2.02	0.60
2:K:41:MET:HE2	2:K:76:VAL:HG12	1.84	0.60
1:E:194:LEU:O	1:E:205:LEU:HD11	2.02	0.60
2:K:122:ASP:OD1	2:K:123:ILE:N	2.35	0.60
2:J:7:VAL:O	2:J:7:VAL:HG23	2.02	0.60
2:L:186:TYR:O	2:L:188(B):GLU:HB2	2.01	0.60
1:B:40:ILE:HD11	1:B:193:GLY:CA	2.31	0.60
2:M:177:LYS:HE2	2:M:186:TYR:OH	2.02	0.60
1:F:161:LYS:HG2	1:G:60:GLU:OE2	2.01	0.60
1:G:136:LEU:O	1:G:150:GLU:HA	2.01	0.60
2:L:122:ASP:OD1	2:L:123:ILE:N	2.32	0.60
1:C:233(F):ARG:O	1:C:233(J):LEU:HB2	2.01	0.60
2:M:6:LEU:N	2:M:6:LEU:HD23	2.18	0.59
2:K:20:ALA:HB3	2:K:28:SER:HB3	1.84	0.59
1:G:181:ARG:O	1:G:184:LEU:HG	2.01	0.59
1:E:219:ASP:O	1:E:220(A):THR:HG23	2.01	0.59
2:M:186:TYR:O	2:M:188(B):GLU:HB2	2.02	0.59
1:D:54:VAL:HG21	1:D:59:LEU:HB2	1.84	0.59
2:J:141:ARG:NH1	2:J:157:ARG:HH11	2.01	0.59
1:A:125:GLN:HB2	1:B:130:ARG:HG2	1.85	0.59
1:C:160:TYR:CD2	1:C:163:THR:HB	2.38	0.59
1:F:12:ILE:HG13	1:F:13:THR:N	2.16	0.59
1:A:20:ARG:NH2	4:A:236:HOH:O	2.34	0.59
1:C:18:ASP:HB2	1:C:20:ARG:HH11	1.66	0.59
1:E:18:ASP:HB2	1:E:20:ARG:HH11	1.67	0.59
2:L:179:THR:O	2:L:180:GLU:CB	2.51	0.59
1:E:220:ARG:HG2	1:E:220:ARG:HH21	1.66	0.59
1:C:177:GLU:OE2	1:D:57:LYS:HG2	2.01	0.59
1:A:161:LYS:HG2	1:B:60:GLU:OE2	2.02	0.59
2:H:6:LEU:HB3	2:H:123:ILE:HD13	1.84	0.59
1:E:201:ILE:HD11	1:E:205:LEU:HD23	1.84	0.59
2:I:152:VAL:O	2:I:156:VAL:HG23	2.03	0.59
2:H:177:LYS:HE2	2:H:186:TYR:OH	2.03	0.59
1:D:197:MET:O	1:D:200:SER:HB3	2.03	0.59
1:A:233(F):ARG:O	1:A:233(J):LEU:HB2	2.03	0.59
2:H:48:SER:HB3	2:H:51:ASP:HB2	1.83	0.59
1:A:18:ASP:HB2	1:A:20:ARG:HH11	1.67	0.59
1:C:205:LEU:N	1:C:233(D):ASN:HD21	1.96	0.59
1:D:225:SER:OG	1:D:228:GLU:HG3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:143:THR:O	2:H:146:ILE:HG22	2.04	0.58
1:F:194:LEU:O	1:F:205:LEU:HD11	2.03	0.58
1:F:56:SER:HB3	1:F:59:LEU:HD23	1.85	0.58
2:H:122:ASP:OD1	2:H:123:ILE:N	2.36	0.58
1:A:124:THR:HG23	1:B:130:ARG:HH21	1.68	0.58
2:H:104:ILE:HD11	2:H:178:ILE:O	2.02	0.58
1:E:61:ALA:O	1:E:64:ILE:HG22	2.02	0.58
1:D:219:ASP:O	1:D:220(A):THR:HG23	2.03	0.58
1:E:122:GLN:C	1:E:124:THR:H	2.05	0.58
2:H:144:PRO:HG2	2:H:145:GLU:OE2	2.03	0.58
2:M:53:GLN:NE2	2:N:119:ALA:H	1.96	0.58
1:C:105:GLU:CD	2:K:75:THR:HG21	2.23	0.58
1:A:75:CYS:HB3	1:A:221:PHE:CD2	2.38	0.58
2:I:141:ARG:HE	2:I:157:ARG:HE	1.50	0.58
2:I:141:ARG:NH1	2:I:157:ARG:HH11	2.01	0.58
2:M:179:THR:O	2:M:180:GLU:CB	2.52	0.58
1:B:136:LEU:HB2	1:B:151:THR:OG1	2.04	0.57
1:C:91:ARG:HD3	4:C:238:HOH:O	2.02	0.57
1:F:75:CYS:HB3	1:F:221:PHE:CD2	2.39	0.57
1:F:18:ASP:HB2	1:F:20:ARG:HH11	1.69	0.57
1:A:105:GLU:CD	2:I:75:THR:HG21	2.24	0.57
1:F:70:ILE:HG21	1:F:112:LEU:HD21	1.85	0.57
2:N:141:ARG:NH1	2:N:157:ARG:HH11	2.01	0.57
2:I:7:VAL:O	2:I:7:VAL:HG23	2.04	0.57
1:B:160:TYR:CD2	1:B:163:THR:HB	2.40	0.57
2:H:114:ASP:HB2	2:H:115:PRO:CD	2.35	0.57
1:F:233(F):ARG:O	1:F:233(J):LEU:HB2	2.05	0.57
1:A:136:LEU:O	1:A:150:GLU:HA	2.05	0.57
2:I:122:ASP:OD1	2:I:123:ILE:N	2.37	0.57
1:D:105:GLU:CD	2:L:75:THR:HG21	2.24	0.57
2:I:143:THR:O	2:I:146:ILE:HG22	2.03	0.57
1:E:64:ILE:HD11	1:E:66:LYS:NZ	2.20	0.57
1:A:177:GLU:OE2	1:B:57:LYS:HG2	2.04	0.57
2:K:179:THR:O	2:K:180:GLU:CB	2.52	0.57
1:A:122:GLN:C	1:A:124:THR:H	2.07	0.57
1:C:56:SER:HB3	1:C:59:LEU:HD23	1.86	0.57
1:C:150:GLU:HG2	1:C:160:TYR:CE1	2.40	0.57
1:E:86:ARG:HD2	4:E:240:HOH:O	2.04	0.57
1:B:75:CYS:HB3	1:B:221:PHE:CD2	2.38	0.57
1:C:219:ASP:O	1:C:220(A):THR:HG23	2.04	0.57
1:E:54:VAL:HG21	1:E:59:LEU:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:104:ILE:HD11	2:L:178:ILE:O	2.04	0.57
1:D:98:ILE:O	1:D:102:THR:CG2	2.52	0.57
1:A:159:GLU:OE2	1:B:63:THR:CG2	2.52	0.56
1:B:219:ASP:O	1:B:220(A):THR:HG23	2.05	0.56
1:C:122:GLN:C	1:C:124:THR:H	2.09	0.56
1:G:122:GLN:C	1:G:124:THR:H	2.08	0.56
1:F:136:LEU:O	1:F:150:GLU:HA	2.06	0.56
1:C:91:ARG:NH2	4:C:238:HOH:O	2.38	0.56
2:N:125:ALA:HB3	2:N:135:TYR:CE1	2.40	0.56
2:N:144:PRO:HG2	2:N:145:GLU:OE2	2.04	0.56
2:I:179:THR:O	2:I:180:GLU:CB	2.53	0.56
2:L:146:ILE:HD11	2:L:151:ALA:HA	1.87	0.56
1:G:98:ILE:O	1:G:102:THR:CG2	2.53	0.56
2:J:53:GLN:NE2	2:K:119:ALA:H	1.94	0.56
2:L:6:LEU:HB3	2:L:123:ILE:HD13	1.85	0.56
1:G:31:VAL:HG21	1:G:135:SER:HB2	1.86	0.56
1:D:75:CYS:HB3	1:D:221:PHE:CD2	2.40	0.56
2:J:6:LEU:HB3	2:J:123:ILE:HD13	1.87	0.56
1:G:179:GLU:HA	1:G:179:GLU:OE2	2.05	0.56
2:J:144:PRO:HG2	2:J:145:GLU:OE2	2.06	0.56
2:M:36:GLN:O	2:M:60:LYS:HE2	2.05	0.56
2:J:104:ILE:HD11	2:J:178:ILE:O	2.05	0.56
1:B:124:THR:HG22	1:C:130:ARG:HH21	1.69	0.56
2:H:179:THR:O	2:H:180:GLU:CB	2.52	0.56
2:L:143:THR:O	2:L:146:ILE:HG22	2.06	0.56
1:B:179:GLU:OE2	1:B:179:GLU:HA	2.05	0.56
1:G:233(F):ARG:O	1:G:233(J):LEU:HB2	2.06	0.56
1:B:202:GLU:O	1:B:203:SER:HB3	2.05	0.56
2:J:177:LYS:HE2	2:J:186:TYR:OH	2.06	0.56
1:A:201:ILE:HD11	1:A:205:LEU:HD23	1.87	0.56
1:B:205:LEU:N	1:B:233(D):ASN:HD21	1.99	0.56
2:I:48:SER:HB3	2:I:51:ASP:HB2	1.87	0.56
2:K:122:ASP:HB2	2:K:142:PHE:CE2	2.41	0.56
2:L:141:ARG:NH1	2:L:157:ARG:HH11	2.03	0.56
1:D:201:ILE:HD11	1:D:205:LEU:HD23	1.88	0.56
1:B:105:GLU:CD	2:J:75:THR:HG21	2.27	0.56
1:G:220:ARG:HG2	1:G:220:ARG:NH2	2.21	0.56
1:A:197:MET:O	1:A:200:SER:HB3	2.06	0.55
1:G:201:ILE:HD11	1:G:205:LEU:HD23	1.89	0.55
1:F:105:GLU:CD	2:N:75:THR:HG21	2.25	0.55
2:H:66:TYR:CD2	2:H:74:PRO:HB3	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:49:VAL:HG22	3:N:1601:CIB:HE33	1.88	0.55
2:M:114:ASP:HB2	2:M:115:PRO:CD	2.36	0.55
1:C:54:VAL:HG22	1:C:55:GLY:N	2.21	0.55
1:C:12:ILE:CG2	1:C:13:THR:H	2.14	0.55
1:D:14:VAL:HB	1:E:23:GLN:NE2	2.21	0.55
2:J:186:TYR:O	2:J:187:SER:HB2	2.06	0.55
1:E:233(F):ARG:O	1:E:233(J):LEU:HB2	2.05	0.55
2:M:116:ILE:CG2	2:M:116:ILE:O	2.53	0.55
1:A:202:GLU:O	1:A:203:SER:HB3	2.07	0.55
2:K:7:VAL:O	2:K:7:VAL:HG23	2.06	0.55
1:D:15:PHE:N	1:E:23:GLN:HE22	2.00	0.55
2:N:41:MET:HE2	2:N:76:VAL:HG12	1.89	0.55
1:E:136:LEU:HB2	1:E:151:THR:HG1	1.71	0.55
2:H:114:ASP:HB2	2:H:115:PRO:HD2	1.88	0.55
1:E:233(D):ASN:O	1:E:233(H):ARG:HG3	2.06	0.55
1:F:201:ILE:HD11	1:F:205:LEU:HD23	1.87	0.55
2:L:7:VAL:O	2:L:7:VAL:HG23	2.05	0.55
2:H:141:ARG:HE	2:H:157:ARG:HE	1.51	0.55
1:D:233(F):ARG:O	1:D:233(J):LEU:HB2	2.06	0.55
2:M:64:ASN:O	2:M:68:ILE:HD13	2.06	0.55
1:E:160:TYR:CD2	1:E:163:THR:HB	2.42	0.55
2:N:152:VAL:O	2:N:156:VAL:HG23	2.06	0.55
1:D:150:GLU:HG2	1:D:160:TYR:CE1	2.41	0.55
1:A:152:ASP:OD1	1:A:153:PRO:HD2	2.07	0.55
2:M:20:ALA:HB3	2:M:28:SER:HB3	1.88	0.55
1:D:122:GLN:C	1:D:124:THR:H	2.10	0.55
2:N:122:ASP:OD1	2:N:123:ILE:N	2.37	0.55
1:F:17:PRO:HA	1:G:26:TYR:CE1	2.42	0.55
1:A:150:GLU:HG2	1:A:160:TYR:CE1	2.40	0.55
2:L:144:PRO:HG2	2:L:145:GLU:OE2	2.08	0.55
1:C:49:ILE:CD1	1:C:194:LEU:HD13	2.34	0.54
2:N:146:ILE:CG1	2:N:150:GLU:HG3	2.36	0.54
2:N:163:MET:HG2	2:N:170:GLY:HA2	1.90	0.54
2:L:177:LYS:HE2	2:L:186:TYR:OH	2.06	0.54
2:M:186:TYR:O	2:M:187:SER:HB2	2.06	0.54
2:H:41:MET:HE1	2:H:76:VAL:HA	1.89	0.54
1:A:56:SER:HB3	1:A:59:LEU:HD23	1.88	0.54
2:L:36:GLN:O	2:L:60:LYS:HE2	2.06	0.54
1:G:225:SER:OG	1:G:228:GLU:HG3	2.07	0.54
2:H:141:ARG:NH1	2:H:157:ARG:HH11	2.05	0.54
1:G:194:LEU:O	1:G:205:LEU:HD11	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:ASP:OD1	1:B:153:PRO:HD2	2.07	0.54
2:L:122:ASP:HB2	2:L:142:PHE:CE2	2.42	0.54
1:G:233(D):ASN:O	1:G:233(H):ARG:HG3	2.07	0.54
1:A:64:ILE:HD11	1:A:66:LYS:NZ	2.22	0.54
1:G:61:ALA:O	1:G:64:ILE:HG22	2.07	0.54
2:L:186:TYR:O	2:L:187:SER:HB2	2.07	0.54
2:M:114:ASP:HB2	2:M:115:PRO:HD2	1.88	0.54
2:L:49:VAL:HG22	3:L:1401:CIB:HG31	1.90	0.54
1:E:31:VAL:HG21	1:E:135:SER:HB2	1.89	0.54
1:F:206:VAL:O	1:F:209:ASN:ND2	2.39	0.54
1:F:122:GLN:C	1:F:124:THR:H	2.11	0.54
2:L:48:SER:HB3	2:L:51:ASP:HB2	1.88	0.54
1:G:150:GLU:HG2	1:G:160:TYR:CE1	2.43	0.54
1:A:179:GLU:OE2	1:A:179:GLU:HA	2.08	0.54
2:M:157:ARG:NH2	2:M:196:PHE:CE2	2.76	0.54
2:J:10:ASP:CG	2:J:148:VAL:HG13	2.28	0.54
2:L:188:PRO:HG2	2:L:188(A):GLU:OE2	2.08	0.54
1:F:101:LEU:O	1:F:101:LEU:HD22	2.08	0.54
2:J:36:GLN:O	2:J:60:LYS:HE2	2.08	0.54
1:C:179:GLU:OE2	1:C:179:GLU:HA	2.07	0.54
1:A:117:CYS:SG	1:A:151:THR:HG22	2.47	0.54
2:K:43:MET:HA	2:K:100:LEU:O	2.08	0.54
2:N:43:MET:HA	2:N:100:LEU:O	2.07	0.54
2:N:170:GLY:O	2:N:171:ASP:HB2	2.08	0.53
1:E:177:GLU:OE2	1:F:57:LYS:HG2	2.07	0.53
1:F:198:GLY:HA3	1:F:233(G):ILE:HD13	1.88	0.53
2:K:104:ILE:HD11	2:K:178:ILE:O	2.08	0.53
1:B:122:GLN:C	1:B:124:THR:H	2.10	0.53
1:D:159:GLU:OE2	1:E:63:THR:HG21	2.08	0.53
1:D:206:VAL:O	1:D:209:ASN:ND2	2.41	0.53
1:F:31:VAL:HG21	1:F:135:SER:HB2	1.91	0.53
2:M:177:LYS:NZ	4:M:1508:HOH:O	2.40	0.53
2:H:7:VAL:O	2:H:7:VAL:HG23	2.07	0.53
2:J:114:ASP:HB2	2:J:115:PRO:CD	2.38	0.53
1:G:160:TYR:CD2	1:G:163:THR:HB	2.44	0.53
1:G:187:ASP:O	1:G:191:VAL:HG23	2.07	0.53
1:E:98:ILE:O	1:E:102:THR:CG2	2.56	0.53
1:G:202:GLU:O	1:G:203:SER:HB3	2.08	0.53
1:G:229:LEU:HD22	1:G:233:VAL:HG23	1.89	0.53
2:J:141:ARG:HE	2:J:157:ARG:HE	1.53	0.53
2:K:141:ARG:NH1	2:K:157:ARG:HH1	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:31:VAL:HG21	1:G:135:SER:CB	2.39	0.53
1:A:220:ARG:NH2	1:A:220:ARG:HG2	2.24	0.53
2:K:143:THR:O	2:K:146:ILE:HG22	2.08	0.53
1:F:98:ILE:O	1:F:102:THR:CG2	2.57	0.53
2:L:152:VAL:O	2:L:156:VAL:HG23	2.08	0.53
1:E:198:GLY:HA3	1:E:233(G):ILE:HD13	1.91	0.53
2:H:163:MET:HG2	2:H:170:GLY:HA2	1.90	0.53
1:A:160:TYR:CD2	1:A:163:THR:HB	2.44	0.53
1:B:98:ILE:O	1:B:102:THR:CG2	2.57	0.53
2:N:116:ILE:O	2:N:116:ILE:CG2	2.57	0.53
1:G:101:LEU:O	1:G:101:LEU:HD22	2.09	0.53
2:N:67:GLU:HA	2:N:72:ARG:O	2.09	0.53
1:F:219:ASP:O	1:F:220(A):THR:HG23	2.08	0.53
2:K:48:SER:HB3	2:K:51:ASP:HB2	1.91	0.53
2:K:2:THR:HA	2:K:127:THR:O	2.09	0.53
1:A:49:ILE:CD1	1:A:194:LEU:HD13	2.34	0.53
2:N:146:ILE:HG13	2:N:150:GLU:CG	2.37	0.53
2:I:93:PHE:HB3	2:J:92:TYR:CZ	2.44	0.53
2:M:190:GLU:HA	2:M:193:LEU:HD22	1.91	0.53
1:B:233(D):ASN:O	1:B:233(H):ARG:HG3	2.10	0.53
1:F:61:ALA:O	1:F:64:ILE:HG22	2.09	0.53
2:J:148:VAL:O	2:J:152:VAL:HG12	2.08	0.53
2:K:190:GLU:HA	2:K:193:LEU:HD22	1.90	0.53
1:C:152:ASP:OD1	1:C:153:PRO:HD2	2.09	0.53
2:I:20:ALA:HB3	2:I:28:SER:HB3	1.91	0.53
1:F:38:ILE:HD12	1:F:197:MET:HG2	1.91	0.52
1:B:17:PRO:HA	1:C:26:TYR:CD1	2.43	0.52
1:B:220:ARG:HG2	1:B:220:ARG:NH2	2.24	0.52
2:J:190:GLU:HA	2:J:193:LEU:HD22	1.91	0.52
2:I:2:THR:HG22	2:I:169:SER:OG	2.09	0.52
2:N:179:THR:O	2:N:180:GLU:CB	2.56	0.52
1:A:61:ALA:O	1:A:64:ILE:HG22	2.09	0.52
2:K:36:GLN:O	2:K:60:LYS:HE2	2.10	0.52
1:G:71:ASP:OD1	1:G:100:ARG:NH2	2.43	0.52
2:H:18:LYS:HB3	2:H:30:ALA:HA	1.91	0.52
1:A:98:ILE:O	1:A:102:THR:CG2	2.58	0.52
1:B:61:ALA:O	1:B:64:ILE:HG22	2.09	0.52
2:L:170:GLY:O	2:L:171:ASP:HB2	2.08	0.52
2:I:146:ILE:CG1	2:I:150:GLU:HG3	2.40	0.52
2:I:66:TYR:CD2	2:I:74:PRO:HB3	2.44	0.52
1:A:206:VAL:O	1:A:209:ASN:ND2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:12:ILE:CG2	1:G:13:THR:H	2.07	0.52
1:F:233(D):ASN:O	1:F:233(H):ARG:HG3	2.10	0.52
2:L:53:GLN:NE2	2:M:119:ALA:H	2.03	0.52
2:I:186:TYR:O	2:I:187:SER:HB2	2.10	0.52
1:D:56:SER:HB3	1:D:59:LEU:HD23	1.90	0.52
2:L:19:ARG:O	2:L:33:LYS:NZ	2.40	0.52
1:A:60:GLU:OE2	1:G:161:LYS:HG2	2.10	0.52
2:I:125:ALA:HB3	2:I:135:TYR:CE1	2.44	0.52
2:N:66:TYR:CD2	2:N:74:PRO:HB3	2.45	0.52
2:N:20:ALA:HB3	2:N:28:SER:HB3	1.92	0.52
2:N:18:LYS:HB3	2:N:30:ALA:HA	1.90	0.52
2:K:125:ALA:HB3	2:K:135:TYR:CE1	2.44	0.52
2:I:36:GLN:O	2:I:60:LYS:HE2	2.08	0.52
2:M:34:ILE:HD13	2:M:35:TYR:N	2.24	0.52
1:D:233(D):ASN:O	1:D:233(H):ARG:HG3	2.09	0.52
2:N:114:ASP:HB2	2:N:115:PRO:HD2	1.92	0.52
1:A:54:VAL:HG22	1:A:55:GLY:N	2.25	0.52
2:J:179:THR:O	2:J:180:GLU:CB	2.56	0.52
2:L:146:ILE:CG1	2:L:150:GLU:HG3	2.38	0.52
2:J:47:GLY:O	3:J:1201:CIB:HA2	2.10	0.52
2:L:43:MET:HA	2:L:100:LEU:O	2.10	0.52
2:I:18:LYS:HB3	2:I:30:ALA:HA	1.92	0.52
2:M:67:GLU:HA	2:M:72:ARG:O	2.09	0.52
2:N:143:THR:O	2:N:146:ILE:HG22	2.09	0.52
1:F:220:ARG:NH2	1:F:220:ARG:HG2	2.24	0.52
1:E:54:VAL:HG22	1:E:55:GLY:N	2.25	0.52
1:F:179:GLU:HA	1:F:179:GLU:OE2	2.10	0.52
2:N:161:SER:O	2:N:164:LYS:HB2	2.10	0.52
1:G:47:ILE:HD12	1:G:47:ILE:N	2.25	0.52
2:L:44:THR:OG1	2:L:100:LEU:HB2	2.10	0.51
2:M:125:ALA:HB3	2:M:135:TYR:CE1	2.45	0.51
2:H:132:LEU:HD21	2:N:25:PHE:CD1	2.44	0.51
1:G:136:LEU:HB2	1:G:151:THR:OG1	2.10	0.51
1:C:61:ALA:O	1:C:64:ILE:HG22	2.10	0.51
2:N:188:PRO:HG2	2:N:188(A):GLU:OE2	2.11	0.51
4:B:236:HOH:O	2:I:68:ILE:HD11	2.10	0.51
2:K:114:ASP:HB2	2:K:115:PRO:CD	2.40	0.51
1:C:187:ASP:O	1:C:191:VAL:HG23	2.10	0.51
2:M:93:PHE:HB3	2:N:92:TYR:CZ	2.45	0.51
1:A:23:GLN:NE2	1:G:14:VAL:HB	2.24	0.51
1:F:160:TYR:CD2	1:F:163:THR:HB	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:54:VAL:HG22	1:G:55:GLY:N	2.25	0.51
1:C:75:CYS:HB3	1:C:221:PHE:CD2	2.46	0.51
1:D:89:ILE:HG13	1:D:90:ASP:N	2.26	0.51
2:L:125:ALA:HB3	2:L:135:TYR:CE1	2.45	0.51
2:I:7:VAL:O	2:I:7:VAL:CG2	2.58	0.51
2:K:157:ARG:NH2	2:K:196:PHE:CE2	2.79	0.51
2:M:44:THR:OG1	2:M:100:LEU:HB2	2.10	0.51
2:M:2:THR:HA	2:M:127:THR:O	2.10	0.51
2:L:190:GLU:HA	2:L:193:LEU:HD22	1.93	0.51
1:A:159:GLU:OE2	1:B:63:THR:CB	2.58	0.51
1:D:61:ALA:O	1:D:64:ILE:HG22	2.11	0.51
1:D:54:VAL:HG22	1:D:55:GLY:N	2.25	0.51
1:C:98:ILE:O	1:C:102:THR:CG2	2.59	0.51
2:H:190:GLU:HA	2:H:193:LEU:HD22	1.93	0.51
1:B:98:ILE:O	1:B:102:THR:HG23	2.11	0.51
2:N:114:ASP:HB2	2:N:115:PRO:CD	2.41	0.51
2:I:114:ASP:HB2	2:I:115:PRO:CD	2.40	0.51
2:J:161:SER:O	2:J:164:LYS:HB2	2.11	0.51
1:G:206:VAL:O	1:G:209:ASN:ND2	2.43	0.51
1:D:160:TYR:CD2	1:D:163:THR:HB	2.45	0.51
2:H:146:ILE:HG13	2:H:150:GLU:CG	2.40	0.51
1:D:187:ASP:O	1:D:191:VAL:HG23	2.11	0.51
1:A:233(D):ASN:O	1:A:233(H):ARG:HG3	2.11	0.50
1:G:49:ILE:HD11	1:G:197:MET:HG3	1.92	0.50
1:A:130:ARG:HH21	1:G:124:THR:HG22	1.75	0.50
1:G:56:SER:HB3	1:G:59:LEU:HD23	1.91	0.50
2:K:2:THR:HG23	2:K:17:GLU:HG3	1.93	0.50
2:I:161:SER:O	2:I:164:LYS:HB2	2.11	0.50
1:F:229:LEU:HD22	1:F:233:VAL:HG23	1.92	0.50
2:M:163:MET:HE2	2:M:170:GLY:CA	2.37	0.50
2:H:41:MET:HE2	2:H:76:VAL:CG1	2.41	0.50
2:J:41:MET:HE2	2:J:76:VAL:HG12	1.91	0.50
2:M:144:PRO:HG2	2:M:145:GLU:OE2	2.10	0.50
2:J:20:ALA:HB3	2:J:28:SER:HB3	1.94	0.50
2:N:104:ILE:HD11	2:N:178:ILE:O	2.10	0.50
1:B:100:ARG:HH22	1:B:106:PRO:CB	2.25	0.50
1:F:98:ILE:O	1:F:102:THR:HG22	2.11	0.50
2:K:93:PHE:HB3	2:L:92:TYR:CZ	2.45	0.50
2:H:157:ARG:NH2	2:H:196:PHE:CE2	2.80	0.50
2:L:141:ARG:HE	2:L:157:ARG:HE	1.56	0.50
2:J:146:ILE:CG1	2:J:150:GLU:HG3	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:146:ILE:CG1	2:H:150:GLU:HG3	2.38	0.50
2:K:146:ILE:CG1	2:K:150:GLU:HG3	2.41	0.50
1:C:215:VAL:HG22	1:C:221:PHE:HA	1.94	0.50
2:L:18:LYS:HB3	2:L:30:ALA:HA	1.94	0.50
2:K:49:VAL:HG22	3:K:1301:CIB:HG31	1.94	0.50
1:C:198:GLY:HA3	1:C:233(G):ILE:HD13	1.93	0.50
2:H:116:ILE:HG22	2:N:50:GLY:HA3	1.94	0.50
1:F:179:GLU:CD	1:F:233(F):ARG:HH12	2.15	0.50
2:M:50:GLY:HA3	2:N:116:ILE:HG22	1.93	0.50
2:J:93:PHE:HB3	2:K:92:TYR:CZ	2.47	0.50
2:M:48:SER:HB3	2:M:51:ASP:HB2	1.92	0.50
2:H:188:PRO:HG2	2:H:188(A):GLU:OE2	2.12	0.50
2:H:34:ILE:HD13	2:H:35:TYR:N	2.27	0.50
1:A:77:ALA:HB3	1:A:137:LEU:HB2	1.92	0.50
2:L:114:ASP:HB2	2:L:115:PRO:CD	2.40	0.50
2:N:157:ARG:NH2	2:N:196:PHE:CE2	2.79	0.50
2:L:157:ARG:NH2	2:L:196:PHE:CE2	2.80	0.50
1:E:136:LEU:HB2	1:E:151:THR:OG1	2.11	0.50
2:N:49:VAL:HG22	3:N:1601:CIB:CE3	2.40	0.50
2:L:33:LYS:HG2	3:L:1401:CIB:H191	1.94	0.50
2:J:2:THR:HG23	2:J:17:GLU:HG3	1.92	0.50
1:A:20:ARG:HB2	1:A:20:ARG:CZ	2.40	0.50
2:N:6:LEU:N	2:N:6:LEU:CD2	2.75	0.50
1:E:150:GLU:HG2	1:E:160:TYR:CE1	2.47	0.50
2:H:36:GLN:O	2:H:60:LYS:HE2	2.12	0.50
1:F:54:VAL:HG22	1:F:55:GLY:N	2.26	0.50
2:J:41:MET:HE1	2:J:76:VAL:HA	1.93	0.50
2:H:93:PHE:CB	2:I:92:TYR:CE2	2.95	0.50
2:M:163:MET:HG2	2:M:170:GLY:HA2	1.94	0.49
2:H:146:ILE:HD11	2:H:151:ALA:HA	1.94	0.49
2:N:186:TYR:O	2:N:187:SER:HB2	2.11	0.49
2:I:49:VAL:HG22	3:I:1101:CIB:HE32	1.94	0.49
2:L:114:ASP:HB2	2:L:115:PRO:HD2	1.92	0.49
1:C:206:VAL:O	1:C:209:ASN:ND2	2.45	0.49
2:H:20:ALA:HB3	2:H:28:SER:HB3	1.94	0.49
2:H:6:LEU:N	2:H:6:LEU:CD2	2.74	0.49
2:J:7:VAL:O	2:J:7:VAL:CG2	2.59	0.49
2:J:146:ILE:HD11	2:J:151:ALA:HA	1.94	0.49
2:I:44:THR:OG1	2:I:100:LEU:HB2	2.12	0.49
1:B:163:THR:OG1	1:B:164:ALA:N	2.45	0.49
1:E:179:GLU:HA	1:E:179:GLU:OE2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:GLU:HG3	1:A:115:LYS:HD3	1.94	0.49
2:M:164:LYS:C	2:M:165:ARG:HG2	2.31	0.49
1:A:26:TYR:CD1	1:G:17:PRO:HA	2.47	0.49
1:F:202:GLU:O	1:F:203:SER:HB3	2.12	0.49
1:B:38:ILE:CD1	1:B:197:MET:HG2	2.42	0.49
2:M:57:ARG:NH1	2:N:85:ASN:HD21	2.10	0.49
2:L:148:VAL:O	2:L:152:VAL:HG12	2.12	0.49
2:I:190:GLU:HA	2:I:193:LEU:HD22	1.93	0.49
2:J:34:ILE:HD13	2:J:35:TYR:N	2.26	0.49
2:J:170:GLY:O	2:J:171:ASP:HB2	2.12	0.49
2:I:163:MET:HG2	2:I:170:GLY:HA2	1.94	0.49
1:B:95:GLU:HG3	1:B:115:LYS:HD3	1.94	0.49
2:L:6:LEU:N	2:L:6:LEU:CD2	2.75	0.49
1:D:49:ILE:CD1	1:D:194:LEU:HD13	2.38	0.49
1:G:24:VAL:HG11	1:G:154:SER:HB3	1.95	0.49
2:L:41:MET:HE2	2:L:76:VAL:HG12	1.95	0.49
1:E:75:CYS:HB3	1:E:221:PHE:CD2	2.47	0.49
1:G:117:CYS:SG	1:G:151:THR:HG22	2.52	0.49
2:H:19:ARG:O	2:H:33:LYS:NZ	2.46	0.49
1:D:101:LEU:HD22	1:D:101:LEU:O	2.13	0.49
1:B:125:GLN:HB2	1:C:130:ARG:CG	2.40	0.49
2:L:163:MET:HG2	2:L:170:GLY:HA2	1.94	0.49
2:I:170:GLY:O	2:I:171:ASP:HB2	2.13	0.49
1:E:117:CYS:SG	1:E:151:THR:HG22	2.53	0.49
2:I:2:THR:HA	2:I:127:THR:O	2.13	0.49
2:H:93:PHE:HB3	2:I:92:TYR:CZ	2.47	0.49
1:B:207:PRO:HD3	1:B:233:VAL:HG11	1.94	0.49
1:A:101:LEU:O	1:A:101:LEU:HD22	2.12	0.49
1:C:20:ARG:CZ	1:C:20:ARG:HB2	2.41	0.49
1:A:71:ASP:OD1	1:A:100:ARG:NH2	2.46	0.49
1:B:141:VAL:HG11	1:B:217:VAL:HA	1.95	0.49
2:N:2:THR:HA	2:N:127:THR:O	2.13	0.49
2:L:14:MET:HE1	2:L:102:GLY:CA	2.42	0.49
2:K:57:ARG:O	2:K:61:ILE:HD13	2.13	0.49
2:H:85:ASN:HD21	2:N:57:ARG:NH1	2.09	0.49
1:D:198:GLY:HA3	1:D:233(G):ILE:HD13	1.95	0.49
1:F:150:GLU:HG2	1:F:160:TYR:CE1	2.47	0.49
2:M:146:ILE:CG1	2:M:150:GLU:HG3	2.42	0.49
1:B:54:VAL:HG22	1:B:55:GLY:N	2.28	0.49
2:K:186:TYR:O	2:K:187:SER:HB2	2.12	0.49
2:I:2:THR:HG23	2:I:17:GLU:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:34:ILE:HD11	2:M:42:ALA:HB1	1.95	0.49
1:F:146:PRO:C	1:F:147:LYS:HG2	2.33	0.49
1:G:81:LEU:HD23	1:G:133:GLY:CA	2.32	0.49
1:F:31:VAL:HG21	1:F:135:SER:CB	2.43	0.49
1:B:215:VAL:HG22	1:B:221:PHE:HA	1.95	0.49
1:A:229:LEU:HD22	1:A:233:VAL:HG23	1.93	0.49
2:M:188:PRO:HG2	2:M:188(A):GLU:OE2	2.12	0.49
1:E:229:LEU:HD22	1:E:233:VAL:HG23	1.93	0.49
2:N:33:LYS:HG2	3:N:1601:CIB:H191	1.95	0.48
2:K:44:THR:OG1	2:K:100:LEU:HB2	2.12	0.48
2:N:160:TYR:CE2	2:N:164:LYS:HE3	2.48	0.48
1:G:89:ILE:HG13	1:G:90:ASP:N	2.28	0.48
2:K:34:ILE:HD13	2:K:35:TYR:N	2.27	0.48
2:J:125:ALA:HB3	2:J:135:TYR:CE1	2.48	0.48
2:L:7:VAL:CG2	2:L:7:VAL:O	2.62	0.48
1:E:220:ARG:HG2	1:E:220:ARG:NH2	2.28	0.48
1:A:177:GLU:O	1:B:57:LYS:HE2	2.13	0.48
2:H:43:MET:HA	2:H:100:LEU:O	2.13	0.48
2:N:190:GLU:HA	2:N:193:LEU:HD22	1.95	0.48
2:J:57:ARG:NH1	2:K:85:ASN:HD21	2.11	0.48
1:E:31:VAL:HG21	1:E:135:SER:CB	2.42	0.48
1:E:218:ASP:OD1	1:E:219:ASP:N	2.43	0.48
2:H:93:PHE:HB2	2:I:92:TYR:CE2	2.48	0.48
2:I:116:ILE:CG2	2:I:116:ILE:O	2.61	0.48
1:E:49:ILE:CD1	1:E:194:LEU:HD13	2.41	0.48
1:A:233(C):ALA:O	1:A:233(G):ILE:HG13	2.13	0.48
2:I:157:ARG:NH2	2:I:196:PHE:CE2	2.80	0.48
2:N:141:ARG:HE	2:N:157:ARG:HE	1.54	0.48
2:M:7:VAL:O	2:M:7:VAL:HG23	2.13	0.48
1:A:31:VAL:HG21	1:A:135:SER:HB2	1.95	0.48
1:C:175:PHE:CZ	1:C:179:GLU:HG3	2.49	0.48
2:H:116:ILE:O	2:H:116:ILE:CG2	2.61	0.48
4:F:235:HOH:O	2:N:75:THR:HG22	2.14	0.48
2:I:22:MET:HG3	3:I:1101:CIB:H253	1.95	0.48
1:G:215:VAL:HG22	1:G:221:PHE:HA	1.96	0.48
2:H:148:VAL:O	2:H:152:VAL:HG12	2.13	0.48
1:E:161:LYS:HG2	1:F:60:GLU:OE2	2.14	0.48
1:E:168:GLY:O	1:E:172:VAL:HG13	2.14	0.48
1:B:15:PHE:N	1:C:23:GLN:HE22	2.08	0.48
2:I:41:MET:HE2	2:I:76:VAL:CG1	2.43	0.48
2:J:157:ARG:NH2	2:J:196:PHE:CE2	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:VAL:HG21	1:A:135:SER:CB	2.44	0.48
2:K:163:MET:HG2	2:K:170:GLY:HA2	1.95	0.48
1:D:98:ILE:O	1:D:102:THR:HG23	2.14	0.48
1:E:215:VAL:HG22	1:E:221:PHE:HA	1.95	0.48
1:E:206:VAL:O	1:E:209:ASN:ND2	2.46	0.48
2:H:67:GLU:HA	2:H:72:ARG:O	2.14	0.48
2:J:5:GLY:O	2:J:124:VAL:HG12	2.13	0.48
2:K:53:GLN:NE2	2:L:119:ALA:H	2.07	0.48
1:E:100:ARG:HH22	1:E:106:PRO:CB	2.27	0.48
1:G:98:ILE:O	1:G:102:THR:HG23	2.12	0.48
1:G:47:ILE:HG22	1:G:48:LEU:N	2.29	0.48
1:D:141:VAL:HG11	1:D:217:VAL:HA	1.96	0.48
2:J:116:ILE:CG2	2:J:116:ILE:O	2.62	0.48
1:B:31:VAL:HG21	1:B:135:SER:CB	2.43	0.48
1:A:23:GLN:HE22	1:G:14:VAL:HB	1.79	0.48
1:C:202:GLU:O	1:C:203:SER:HB3	2.14	0.48
2:L:2:THR:HG22	2:L:169:SER:OG	2.14	0.48
1:D:229:LEU:HD22	1:D:233:VAL:HG23	1.95	0.48
1:E:141:VAL:HG11	1:E:217:VAL:HA	1.94	0.48
1:A:49:ILE:HD11	1:A:197:MET:HG3	1.96	0.48
2:I:6:LEU:N	2:I:6:LEU:CD2	2.77	0.48
2:L:146:ILE:HG13	2:L:150:GLU:CG	2.41	0.48
1:B:71:ASP:OD1	1:B:100:ARG:NH2	2.47	0.48
2:K:114:ASP:HB2	2:K:115:PRO:HD2	1.95	0.48
1:C:141:VAL:HG11	1:C:217:VAL:HA	1.96	0.48
2:L:2:THR:HA	2:L:127:THR:O	2.13	0.48
1:B:100:ARG:HH22	1:B:106:PRO:HB3	1.79	0.47
1:A:141:VAL:HG11	1:A:217:VAL:HA	1.95	0.47
2:H:22:MET:HB2	3:H:1001:CIB:HD22	1.96	0.47
1:B:89:ILE:HG13	1:B:90:ASP:N	2.29	0.47
2:M:152:VAL:O	2:M:156:VAL:HG23	2.14	0.47
2:J:66:TYR:CD2	2:J:74:PRO:HB3	2.49	0.47
2:H:186:TYR:O	2:H:187:SER:HB2	2.13	0.47
2:M:66:TYR:CD2	2:M:74:PRO:HB3	2.48	0.47
2:J:18:LYS:HB3	2:J:30:ALA:HA	1.95	0.47
2:J:188:PRO:HG2	2:J:188(A):GLU:OE2	2.14	0.47
2:K:146:ILE:HG13	2:K:150:GLU:CG	2.44	0.47
1:B:229:LEU:HD22	1:B:233:VAL:HG23	1.97	0.47
2:H:125:ALA:HB3	2:H:135:TYR:CE1	2.49	0.47
1:F:179:GLU:CD	1:F:233(F):ARG:NH1	2.67	0.47
2:H:34:ILE:HD11	2:H:42:ALA:HB1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:2:THR:HA	2:J:127:THR:O	2.14	0.47
2:L:160:TYR:CE2	2:L:164:LYS:HE3	2.50	0.47
2:K:3:THR:HB	2:K:16:THR:HG22	1.97	0.47
1:E:202:GLU:O	1:E:203:SER:HB3	2.14	0.47
1:F:190:MET:O	1:F:194:LEU:HD22	2.14	0.47
1:D:98:ILE:O	1:D:102:THR:HG22	2.14	0.47
2:N:100:LEU:HD12	2:N:100:LEU:HA	1.76	0.47
1:C:168:GLY:O	1:C:172:VAL:HG13	2.14	0.47
1:B:31:VAL:HG21	1:B:135:SER:HB2	1.95	0.47
2:I:76:VAL:HG21	2:I:109:SER:OG	2.15	0.47
1:B:150:GLU:HG2	1:B:160:TYR:CE1	2.49	0.47
1:B:117:CYS:SG	1:B:151:THR:HG22	2.55	0.47
1:G:98:ILE:O	1:G:102:THR:HG22	2.15	0.47
2:K:1:THR:CG2	2:K:2:THR:N	2.77	0.47
2:M:2:THR:HG23	2:M:17:GLU:HG3	1.96	0.47
2:J:67:GLU:HA	2:J:72:ARG:O	2.15	0.47
1:F:141:VAL:HG11	1:F:217:VAL:HA	1.96	0.47
1:A:233(D):ASN:HD22	1:A:233(G):ILE:HD12	1.79	0.47
2:H:53:GLN:NE2	2:I:119:ALA:H	2.00	0.47
2:I:179:THR:HG23	2:I:182:GLU:H	1.80	0.47
2:L:179:THR:HG23	2:L:182:GLU:N	2.30	0.47
2:I:43:MET:HG3	2:I:101:ILE:HG12	1.97	0.47
2:J:44:THR:OG1	2:J:100:LEU:HB2	2.14	0.47
2:K:47:GLY:O	3:K:1301:CIB:HA2	2.15	0.47
2:M:18:LYS:HB3	2:M:30:ALA:HA	1.96	0.47
1:F:190:MET:O	1:F:194:LEU:CD2	2.63	0.47
1:C:218:ASP:OD1	1:C:219:ASP:N	2.45	0.47
1:B:136:LEU:HB2	1:B:151:THR:HG1	1.79	0.47
1:C:81:LEU:HD22	1:C:81:LEU:H	1.80	0.47
1:B:233(D):ASN:HD22	1:B:233(G):ILE:HD12	1.80	0.47
2:J:163:MET:HG2	2:J:170:GLY:HA2	1.97	0.47
2:J:114:ASP:HB2	2:J:115:PRO:HD2	1.96	0.47
1:D:64:ILE:HD11	1:D:66:LYS:NZ	2.30	0.47
1:G:179:GLU:CD	1:G:233(F):ARG:HH12	2.18	0.47
2:I:144:PRO:HG2	2:I:145:GLU:OE2	2.14	0.47
2:K:66:TYR:CD2	2:K:74:PRO:HB3	2.50	0.47
1:C:98:ILE:O	1:C:102:THR:HG22	2.15	0.47
2:K:18:LYS:HB3	2:K:30:ALA:HA	1.95	0.47
2:L:93:PHE:N	2:L:94:PRO:CD	2.78	0.47
1:G:81:LEU:HD22	1:G:81:LEU:H	1.80	0.46
2:M:141:ARG:NH1	2:M:157:ARG:HH11	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:100:ARG:NH2	1:E:106:PRO:CA	2.78	0.46
2:M:146:ILE:HD11	2:M:151:ALA:HA	1.98	0.46
1:F:100:ARG:HH22	1:F:106:PRO:CB	2.28	0.46
1:E:179:GLU:CD	1:E:233(F):ARG:HH12	2.18	0.46
2:L:10:ASP:CG	2:L:148:VAL:HG13	2.35	0.46
2:J:50:GLY:HA3	2:K:116:ILE:HG22	1.96	0.46
2:L:34:ILE:HD11	2:L:42:ALA:HB1	1.97	0.46
1:C:38:ILE:CD1	1:C:197:MET:HG2	2.44	0.46
2:N:7:VAL:HG23	2:N:7:VAL:O	2.15	0.46
1:A:41:LYS:HZ2	1:B:60:GLU:CD	2.18	0.46
1:E:98:ILE:O	1:E:102:THR:HG23	2.15	0.46
2:L:161:SER:O	2:L:164:LYS:HB2	2.16	0.46
1:C:130:ARG:HH11	1:C:130:ARG:HG3	1.79	0.46
2:H:163:MET:HE2	2:H:170:GLY:CA	2.43	0.46
1:F:71:ASP:OD1	1:F:100:ARG:NH2	2.48	0.46
2:I:41:MET:HE1	2:I:76:VAL:HA	1.97	0.46
1:E:110:LYS:NZ	2:M:71:GLU:OE2	2.40	0.46
1:B:229:LEU:O	1:B:230:LYS:C	2.53	0.46
1:D:136:LEU:HB2	1:D:151:THR:OG1	2.15	0.46
2:K:6:LEU:CD2	2:K:6:LEU:N	2.78	0.46
1:B:49:ILE:HD11	1:B:197:MET:HG3	1.98	0.46
1:C:36:THR:HG23	1:C:197:MET:HE3	1.97	0.46
1:B:64:ILE:HD11	1:B:66:LYS:NZ	2.31	0.46
1:C:136:LEU:HB2	1:C:151:THR:OG1	2.14	0.46
2:I:41:MET:CE	2:I:76:VAL:HA	2.46	0.46
2:M:160:TYR:CE2	2:M:164:LYS:HE3	2.49	0.46
2:J:34:ILE:HD11	2:J:42:ALA:HB1	1.97	0.46
2:I:188:PRO:HG2	2:I:188(A):GLU:OE2	2.15	0.46
1:E:169:ARG:HG2	1:E:169:ARG:HH11	1.80	0.46
1:A:63:THR:O	1:A:64:ILE:C	2.54	0.46
1:D:179:GLU:HA	1:D:179:GLU:OE2	2.14	0.46
1:B:207:PRO:HB3	1:B:233:VAL:HG21	1.97	0.46
2:L:34:ILE:HD13	2:L:35:TYR:N	2.29	0.46
2:I:1:THR:HG22	2:I:128:GLY:HA3	1.97	0.46
1:C:81:LEU:HD22	1:C:81:LEU:N	2.30	0.46
1:F:81:LEU:HD23	1:F:133:GLY:CA	2.35	0.46
2:N:122:ASP:HB2	2:N:142:PHE:CE2	2.50	0.46
1:B:63:THR:O	1:B:64:ILE:C	2.54	0.46
2:I:146:ILE:HG13	2:I:150:GLU:CG	2.44	0.46
1:E:163:THR:OG1	1:E:164:ALA:N	2.49	0.46
1:G:163:THR:OG1	1:G:164:ALA:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:50:GLY:HA3	2:M:116:ILE:HG22	1.97	0.46
1:D:12:ILE:CG2	1:D:13:THR:H	2.09	0.46
2:I:122:ASP:HB2	2:I:142:PHE:CE2	2.51	0.46
2:H:41:MET:CE	2:H:76:VAL:HA	2.45	0.46
1:D:175:PHE:CZ	1:D:179:GLU:HG3	2.51	0.46
1:C:108:THR:OG1	1:C:111:GLU:HB2	2.16	0.46
2:N:93:PHE:N	2:N:94:PRO:CD	2.78	0.46
2:K:141:ARG:HE	2:K:157:ARG:HE	1.62	0.46
2:J:146:ILE:HG13	2:J:150:GLU:CG	2.43	0.46
2:K:148:VAL:O	2:K:152:VAL:HG12	2.16	0.46
2:M:100:LEU:HD12	2:M:100:LEU:HA	1.81	0.46
2:K:41:MET:HE2	2:K:76:VAL:CG1	2.46	0.46
1:A:41:LYS:NZ	1:B:60:GLU:CD	2.69	0.46
1:A:98:ILE:O	1:A:102:THR:HG22	2.15	0.46
1:G:95:GLU:HG3	1:G:115:LYS:HD3	1.97	0.46
1:C:229:LEU:HD22	1:C:233:VAL:HG23	1.97	0.46
1:D:62:ASP:N	1:D:62:ASP:OD2	2.48	0.46
2:L:116:ILE:O	2:L:116:ILE:CG2	2.62	0.46
1:A:198:GLY:HA3	1:A:233(G):ILE:HD13	1.98	0.46
2:I:146:ILE:HD11	2:I:151:ALA:HA	1.97	0.46
2:K:10:ASP:CG	2:K:148:VAL:HG13	2.36	0.46
1:D:117:CYS:HB3	1:E:86:ARG:NH2	2.31	0.46
1:F:229:LEU:O	1:F:230:LYS:C	2.54	0.46
2:N:2:THR:HG22	2:N:169:SER:OG	2.16	0.46
2:H:152:VAL:O	2:H:156:VAL:HG23	2.15	0.46
1:G:146:PRO:C	1:G:147:LYS:HG2	2.37	0.46
2:H:2:THR:HG23	2:H:17:GLU:HG3	1.97	0.46
2:L:66:TYR:CD2	2:L:74:PRO:HB3	2.51	0.46
2:M:41:MET:HE2	2:M:76:VAL:HG12	1.97	0.46
1:G:20:ARG:HB2	1:G:20:ARG:CZ	2.44	0.46
2:H:170:GLY:O	2:H:171:ASP:HB2	2.16	0.46
2:H:179:THR:HG23	2:H:182:GLU:H	1.80	0.46
1:A:141:VAL:HG23	1:A:215:VAL:CG1	2.46	0.46
2:J:76:VAL:HG21	2:J:109:SER:OG	2.16	0.46
2:I:67:GLU:HA	2:I:72:ARG:O	2.16	0.46
2:K:160:TYR:CE2	2:K:164:LYS:HE3	2.51	0.46
1:F:49:ILE:HD11	1:F:197:MET:HG3	1.98	0.45
1:A:146:PRO:C	1:A:147:LYS:HG2	2.36	0.45
1:B:218:ASP:OD1	1:B:219:ASP:N	2.46	0.45
2:N:179:THR:HG23	2:N:182:GLU:H	1.82	0.45
1:A:163:THR:OG1	1:A:164:ALA:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:18:LYS:HD3	2:N:174:ASP:OD2	2.16	0.45
2:I:64:ASN:O	2:I:68:ILE:HD13	2.17	0.45
1:D:202:GLU:O	1:D:203:SER:HB3	2.16	0.45
2:K:67:GLU:HA	2:K:72:ARG:O	2.16	0.45
1:F:49:ILE:CD1	1:F:194:LEU:HD13	2.40	0.45
1:C:233(D):ASN:O	1:C:233(H):ARG:HG3	2.16	0.45
1:B:125:GLN:HB3	1:C:130:ARG:CZ	2.47	0.45
1:D:20:ARG:HB2	1:D:20:ARG:CZ	2.46	0.45
2:J:148:VAL:O	2:J:152:VAL:CG1	2.64	0.45
2:H:157:ARG:HG3	2:H:157:ARG:HH21	1.80	0.45
1:A:100:ARG:HH22	1:A:106:PRO:CB	2.29	0.45
1:A:215:VAL:HG22	1:A:221:PHE:HA	1.99	0.45
1:C:64:ILE:HD11	1:C:66:LYS:NZ	2.31	0.45
1:B:146:PRO:C	1:B:147:LYS:HG2	2.37	0.45
1:E:38:ILE:HD12	1:E:197:MET:HG2	1.98	0.45
2:M:122:ASP:HB2	2:M:142:PHE:CE2	2.51	0.45
1:B:168:GLY:O	1:B:172:VAL:HG13	2.16	0.45
1:C:14:VAL:HB	1:D:23:GLN:NE2	2.31	0.45
1:C:71:ASP:OD1	1:C:100:ARG:NH2	2.49	0.45
2:L:3:THR:HB	2:L:16:THR:HG22	1.98	0.45
1:F:24:VAL:HG11	1:F:154:SER:HB3	1.97	0.45
2:H:7:VAL:O	2:H:7:VAL:CG2	2.65	0.45
1:F:100:ARG:HH22	1:F:106:PRO:HB3	1.80	0.45
1:G:111:GLU:CG	2:H:70:ARG:HG2	2.47	0.45
1:E:47:ILE:HD12	1:E:47:ILE:N	2.32	0.45
1:A:218:ASP:OD1	1:A:219:ASP:N	2.46	0.45
1:E:56:SER:HB3	1:E:59:LEU:CD2	2.46	0.45
1:E:179:GLU:CD	1:E:233(F):ARG:NH1	2.70	0.45
1:A:207:PRO:HB3	1:A:233:VAL:HG21	1.97	0.45
1:A:47:ILE:HD12	1:A:47:ILE:N	2.32	0.45
1:D:15:PHE:H	1:E:23:GLN:NE2	2.01	0.45
1:D:100:ARG:HH22	1:D:106:PRO:CB	2.29	0.45
2:L:93:PHE:HB3	2:M:92:TYR:CZ	2.51	0.45
1:B:77:ALA:HB3	1:B:137:LEU:HB2	1.99	0.45
1:D:100:ARG:HH22	1:D:106:PRO:HA	1.82	0.45
1:D:38:ILE:CD1	1:D:197:MET:HG2	2.45	0.45
2:H:156:VAL:HA	2:H:173:ILE:CD1	2.46	0.45
2:K:116:ILE:O	2:K:116:ILE:CG2	2.64	0.45
1:B:187:ASP:O	1:B:191:VAL:HG23	2.16	0.45
2:K:6:LEU:HA	2:K:122:ASP:O	2.17	0.45
1:F:163:THR:OG1	1:F:164:ALA:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ARG:NH2	1:A:106:PRO:CA	2.77	0.45
1:E:122:GLN:C	1:E:124:THR:N	2.69	0.45
1:G:175:PHE:CD2	1:G:199:LEU:CD1	3.00	0.45
2:N:156:VAL:HA	2:N:173:ILE:CD1	2.47	0.45
2:H:49:VAL:HG22	3:H:1001:CIB:HG32	1.98	0.45
2:M:179:THR:HG23	2:M:182:GLU:N	2.32	0.45
1:B:15:PHE:HB3	1:C:26:TYR:HB3	1.99	0.45
1:F:63:THR:O	1:F:64:ILE:C	2.55	0.45
2:I:104:ILE:CD1	2:I:178:ILE:HG22	2.47	0.45
2:N:164:LYS:C	2:N:165:ARG:HG2	2.36	0.45
2:H:2:THR:HG22	2:H:169:SER:OG	2.17	0.45
1:E:12:ILE:CG2	1:E:13:THR:N	2.76	0.44
1:A:38:ILE:CD1	1:A:197:MET:HG2	2.46	0.44
2:M:179:THR:HG23	2:M:182:GLU:H	1.82	0.44
1:A:179:GLU:CD	1:A:233(F):ARG:HH12	2.20	0.44
1:E:175:PHE:CD2	1:E:199:LEU:CD1	3.00	0.44
2:I:18:LYS:HD3	2:I:174:ASP:OD2	2.16	0.44
1:B:24:VAL:HG11	1:B:154:SER:HB3	1.99	0.44
1:B:88:LEU:HD12	1:B:88:LEU:HA	1.84	0.44
1:C:81:LEU:HD23	1:C:133:GLY:CA	2.35	0.44
2:K:7:VAL:O	2:K:7:VAL:CG2	2.65	0.44
1:G:233(D):ASN:HD22	1:G:233(G):ILE:HD12	1.81	0.44
2:N:146:ILE:HD11	2:N:151:ALA:HA	1.98	0.44
1:A:122:GLN:C	1:A:124:THR:N	2.71	0.44
2:M:146:ILE:HG13	2:M:150:GLU:CG	2.45	0.44
1:E:147:LYS:HE2	1:E:159:GLU:OE1	2.17	0.44
1:F:64:ILE:HD11	1:F:66:LYS:NZ	2.32	0.44
1:F:175:PHE:CZ	1:F:179:GLU:HG3	2.52	0.44
1:C:63:THR:O	1:C:64:ILE:C	2.55	0.44
2:L:76:VAL:HG22	2:L:105:ASP:OD1	2.17	0.44
2:H:160:TYR:CE2	2:H:164:LYS:HE3	2.52	0.44
1:B:206:VAL:O	1:B:209:ASN:ND2	2.49	0.44
2:M:6:LEU:N	2:M:6:LEU:CD2	2.80	0.44
1:D:124:THR:HG22	1:E:130:ARG:HH21	1.81	0.44
1:E:17:PRO:HA	1:F:26:TYR:CE1	2.53	0.44
1:C:146:PRO:C	1:C:147:LYS:HG2	2.38	0.44
2:M:125:ALA:HB3	2:M:135:TYR:CD1	2.52	0.44
2:M:93:PHE:HB2	2:N:92:TYR:CE2	2.52	0.44
2:I:114:ASP:HB2	2:I:115:PRO:HD2	1.99	0.44
2:J:41:MET:CE	2:J:76:VAL:HA	2.46	0.44
1:D:149:TYR:HB3	1:D:157:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:122:ASP:HB2	2:H:142:PHE:CE2	2.52	0.44
1:C:31:VAL:HG21	1:C:135:SER:CB	2.48	0.44
2:M:13:VAL:HG21	2:M:151:ALA:HB3	1.97	0.44
1:D:17:PRO:HA	1:E:26:TYR:CE1	2.51	0.44
1:C:141:VAL:HG23	1:C:215:VAL:CG1	2.47	0.44
2:I:83:THR:HG22	2:I:87:LEU:HD22	2.00	0.44
1:G:141:VAL:HG11	1:G:217:VAL:HA	1.99	0.44
2:I:179:THR:HG23	2:I:182:GLU:N	2.32	0.44
1:G:175:PHE:CZ	1:G:179:GLU:HG3	2.52	0.44
2:N:41:MET:HE2	2:N:76:VAL:CG1	2.47	0.44
2:M:18:LYS:HD3	2:M:174:ASP:OD2	2.17	0.44
2:M:104:ILE:HD11	2:M:178:ILE:O	2.17	0.44
1:C:95:GLU:HG3	1:C:115:LYS:HD3	1.99	0.44
1:D:126:TYR:O	1:D:128:GLY:N	2.51	0.44
1:D:146:PRO:C	1:D:147:LYS:HG2	2.38	0.44
1:E:95:GLU:HG3	1:E:115:LYS:HD3	1.99	0.44
2:H:6:LEU:HA	2:H:122:ASP:O	2.18	0.44
1:B:100:ARG:NH2	1:B:106:PRO:CA	2.78	0.44
2:N:148:VAL:O	2:N:152:VAL:HG12	2.18	0.44
1:E:98:ILE:O	1:E:102:THR:HG22	2.18	0.44
1:B:159:GLU:OE2	1:C:63:THR:HG21	2.17	0.44
2:H:33:LYS:HE2	3:H:1001:CIB:H191	1.99	0.44
1:B:52:LYS:HB3	1:B:209:ASN:C	2.38	0.44
1:E:100:ARG:HH22	1:E:106:PRO:HB3	1.82	0.44
1:E:146:PRO:C	1:E:147:LYS:HG2	2.37	0.44
2:K:188:PRO:HG2	2:K:188(A):GLU:OE2	2.18	0.44
1:A:175:PHE:HE1	1:A:192:LEU:CD1	2.31	0.44
1:F:20:ARG:CZ	1:F:20:ARG:HB2	2.46	0.44
2:M:7:VAL:O	2:M:7:VAL:CG2	2.66	0.44
2:J:104:ILE:CD1	2:J:178:ILE:HG22	2.47	0.44
1:G:198:GLY:HA3	1:G:233(G):ILE:HD13	2.00	0.43
1:A:146:PRO:O	1:A:147:LYS:HG2	2.18	0.43
1:D:36:THR:HG23	1:D:197:MET:HE1	2.00	0.43
1:D:215:VAL:HG22	1:D:221:PHE:HA	2.00	0.43
2:M:93:PHE:CB	2:N:92:TYR:CE2	3.00	0.43
1:A:90:ASP:OD2	2:H:69:ARG:HD3	2.17	0.43
1:C:89:ILE:HG13	1:C:90:ASP:N	2.32	0.43
1:E:49:ILE:HD11	1:E:197:MET:HG3	1.99	0.43
2:M:163:MET:SD	2:M:170:GLY:HA2	2.57	0.43
1:B:19:GLY:O	1:C:30:ALA:HB2	2.18	0.43
2:H:25:PHE:CE2	2:H:27:ALA:HA	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:ASP:OD2	1:C:62:ASP:N	2.51	0.43
2:H:141:ARG:NH2	2:H:141:ARG:HG2	2.33	0.43
2:H:163:MET:SD	2:H:170:GLY:HA2	2.58	0.43
1:D:218:ASP:OD1	1:D:219:ASP:N	2.45	0.43
1:G:136:LEU:HB2	1:G:151:THR:HG1	1.82	0.43
2:M:116:ILE:O	2:M:116:ILE:HG22	2.17	0.43
2:K:125:ALA:HB3	2:K:135:TYR:CD1	2.54	0.43
2:J:45:THR:OG1	3:J:1201:CIB:HE31	2.18	0.43
1:F:111:GLU:CG	2:N:70:ARG:HG2	2.48	0.43
2:K:179:THR:HG23	2:K:182:GLU:H	1.84	0.43
1:B:179:GLU:O	1:B:181:ARG:HG3	2.18	0.43
1:D:179:GLU:CD	1:D:233(F):ARG:NH1	2.72	0.43
2:N:116:ILE:O	2:N:116:ILE:HG22	2.17	0.43
2:M:40:ARG:O	2:M:103:GLY:HA3	2.18	0.43
2:L:123:ILE:HG23	2:L:138:LEU:HD13	2.00	0.43
1:G:38:ILE:CD1	1:G:197:MET:HG2	2.48	0.43
1:G:122:GLN:C	1:G:124:THR:N	2.72	0.43
2:J:156:VAL:HA	2:J:173:ILE:CD1	2.48	0.43
2:I:93:PHE:N	2:I:94:PRO:CD	2.81	0.43
2:H:31:ALA:HB1	3:H:1001:CIB:HE31	2.00	0.43
2:M:156:VAL:HG22	2:M:173:ILE:HD11	2.00	0.43
2:H:83:THR:HG22	2:H:87:LEU:HD22	2.00	0.43
2:M:70:ARG:HD3	4:M:1506:HOH:O	2.19	0.43
1:F:47:ILE:N	1:F:47:ILE:HD12	2.32	0.43
2:I:123:ILE:HG23	2:I:138:LEU:HD13	2.00	0.43
1:C:31:VAL:HG21	1:C:135:SER:HB2	1.99	0.43
1:G:168:GLY:O	1:G:172:VAL:HG13	2.18	0.43
1:B:179:GLU:CD	1:B:233(F):ARG:HH12	2.21	0.43
1:D:179:GLU:CD	1:D:233(F):ARG:HH12	2.21	0.43
1:G:179:GLU:CD	1:G:233(F):ARG:NH1	2.72	0.43
1:G:64:ILE:HD11	1:G:66:LYS:NZ	2.34	0.43
1:D:207:PRO:HD3	1:D:233:VAL:HG11	2.00	0.43
2:M:148:VAL:O	2:M:152:VAL:HG12	2.18	0.43
2:H:92:TYR:CZ	2:N:93:PHE:HB3	2.54	0.43
1:A:24:VAL:HG11	1:A:154:SER:HB3	1.99	0.43
1:G:81:LEU:HD22	1:G:81:LEU:N	2.33	0.43
2:H:141:ARG:HH21	2:H:141:ARG:HG2	1.84	0.43
1:G:49:ILE:CD1	1:G:194:LEU:HD13	2.40	0.43
1:G:218:ASP:OD1	1:G:219:ASP:N	2.47	0.43
2:M:1:THR:CG2	2:M:2:THR:N	2.80	0.43
2:H:2:THR:HA	2:H:127:THR:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:34:ILE:HD13	2:I:35:TYR:N	2.32	0.43
1:G:132:PHE:HB3	1:G:134:VAL:HG13	2.01	0.43
1:D:163:THR:OG1	1:D:164:ALA:N	2.50	0.43
1:D:81:LEU:H	1:D:81:LEU:HD22	1.82	0.43
2:I:157:ARG:HH21	2:I:157:ARG:HG3	1.83	0.43
1:A:161:LYS:N	1:B:58:LEU:O	2.31	0.43
2:N:125:ALA:HB3	2:N:135:TYR:CD1	2.54	0.43
1:E:110:LYS:HE2	1:E:114:LYS:NZ	2.33	0.43
2:L:18:LYS:HD3	2:L:174:ASP:OD2	2.19	0.43
1:E:51:ASP:OD2	1:E:53:ARG:HD3	2.19	0.43
2:H:10:ASP:OD1	2:H:147:GLY:HA2	2.19	0.43
1:F:90:ASP:OD2	2:M:69:ARG:HD3	2.19	0.43
1:A:190:MET:O	1:A:194:LEU:CD2	2.66	0.43
2:H:123:ILE:HG23	2:H:138:LEU:HD13	2.00	0.43
1:C:190:MET:O	1:C:194:LEU:HD22	2.19	0.43
2:H:179:THR:HG23	2:H:182:GLU:N	2.34	0.43
2:L:186:TYR:O	2:L:187:SER:CB	2.67	0.43
1:C:141:VAL:CG2	1:C:215:VAL:HG12	2.48	0.43
2:M:76:VAL:HG22	2:M:105:ASP:OD1	2.19	0.43
2:I:34:ILE:HD11	2:I:42:ALA:HB1	2.01	0.43
1:D:67:ILE:HB	1:D:211:GLU:OE2	2.18	0.43
1:G:126:TYR:O	1:G:128:GLY:N	2.52	0.43
1:G:67:ILE:HB	1:G:211:GLU:OE2	2.18	0.43
2:L:197:ARG:HG2	2:L:197:ARG:HH11	1.84	0.43
1:A:62:ASP:N	1:A:62:ASP:OD2	2.52	0.43
1:A:227:GLU:CD	1:A:227:GLU:H	2.23	0.43
2:J:2:THR:HG22	2:J:169:SER:OG	2.18	0.43
2:I:92:TYR:HB2	4:I:1108:HOH:O	2.18	0.43
2:H:197:ARG:HH11	2:H:197:ARG:HG2	1.83	0.43
1:C:190:MET:O	1:C:194:LEU:CD2	2.67	0.42
2:N:179:THR:HG23	2:N:182:GLU:N	2.34	0.42
1:E:71:ASP:OD1	1:E:100:ARG:NH2	2.52	0.42
2:M:186:TYR:O	2:M:187:SER:CB	2.66	0.42
1:A:187:ASP:O	1:A:191:VAL:HG23	2.19	0.42
1:E:62:ASP:OD2	1:E:62:ASP:N	2.52	0.42
2:M:96:LEU:HD22	4:M:1504:HOH:O	2.19	0.42
1:A:12:ILE:CG2	1:A:13:THR:N	2.78	0.42
2:J:141:ARG:NH2	2:J:141:ARG:HG2	2.34	0.42
1:A:64:ILE:HD11	1:A:66:LYS:HZ3	1.84	0.42
1:D:179:GLU:O	1:D:181:ARG:HG3	2.19	0.42
1:A:162:ALA:O	1:B:58:LEU:HB3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:187:ASP:O	1:F:191:VAL:HG23	2.19	0.42
1:A:81:LEU:HD23	1:A:133:GLY:CA	2.35	0.42
2:J:6:LEU:N	2:J:6:LEU:CD2	2.80	0.42
1:D:233(D):ASN:HD22	1:D:233(G):ILE:HD12	1.84	0.42
2:H:57:ARG:O	2:H:61:ILE:HD13	2.19	0.42
1:A:130:ARG:HG3	1:A:130:ARG:HH11	1.85	0.42
2:L:179:THR:HG23	2:L:182:GLU:H	1.82	0.42
2:J:10:ASP:OD1	2:J:147:GLY:HA2	2.19	0.42
1:E:175:PHE:CZ	1:E:179:GLU:HG3	2.54	0.42
3:H:1001:CIB:HD11	4:I:1105:HOH:O	2.17	0.42
1:C:137:LEU:HA	1:C:137:LEU:HD23	1.94	0.42
1:E:77:ALA:HB3	1:E:137:LEU:HB2	2.00	0.42
2:L:122:ASP:HB2	2:L:142:PHE:CZ	2.55	0.42
2:K:179:THR:HG23	2:K:182:GLU:N	2.35	0.42
1:C:179:GLU:CD	1:C:233(F):ARG:HH12	2.23	0.42
2:I:164:LYS:C	2:I:165:ARG:HG2	2.39	0.42
1:G:146:PRO:O	1:G:147:LYS:HG2	2.20	0.42
1:F:111:GLU:HG2	2:N:70:ARG:HG2	2.00	0.42
1:D:161:LYS:HE3	1:E:60:GLU:OE2	2.20	0.42
2:H:3:THR:HB	2:H:16:THR:HG22	2.00	0.42
1:A:74:ILE:HG12	1:A:109:VAL:HG22	2.01	0.42
1:B:81:LEU:HD22	1:B:81:LEU:H	1.84	0.42
1:B:122:GLN:C	1:B:124:THR:N	2.72	0.42
1:B:18:ASP:CB	1:B:20:ARG:NH1	2.79	0.42
1:E:63:THR:O	1:E:64:ILE:C	2.57	0.42
2:N:76:VAL:HG22	2:N:105:ASP:OD1	2.18	0.42
2:N:76:VAL:HG21	2:N:109:SER:OG	2.19	0.42
1:C:229:LEU:O	1:C:230:LYS:C	2.57	0.42
1:B:126:TYR:O	1:B:128:GLY:N	2.53	0.42
1:B:12:ILE:CG2	1:B:13:THR:H	2.08	0.42
2:H:5:GLY:O	2:H:124:VAL:HG12	2.20	0.42
2:H:57:ARG:NH1	2:I:85:ASN:HD21	2.17	0.42
1:C:100:ARG:HH22	1:C:106:PRO:CB	2.33	0.42
2:L:148:VAL:O	2:L:152:VAL:CG1	2.68	0.42
1:F:146:PRO:O	1:F:147:LYS:HG2	2.19	0.42
2:J:67:GLU:O	2:J:71:GLU:N	2.51	0.42
1:C:90:ASP:OD2	2:J:69:ARG:CD	2.68	0.42
2:N:7:VAL:CG2	2:N:7:VAL:O	2.67	0.42
1:A:141:VAL:CG2	1:A:215:VAL:HG12	2.50	0.42
1:F:177:GLU:OE2	1:G:57:LYS:HG2	2.19	0.42
2:M:5:GLY:O	2:M:124:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:179:GLU:CB	1:G:192:LEU:HD11	2.49	0.42
1:B:126:TYR:CD1	1:C:129:VAL:HG23	2.55	0.42
1:F:77:ALA:HB3	1:F:137:LEU:HB2	2.01	0.42
1:B:190:MET:O	1:B:194:LEU:CD2	2.68	0.42
2:N:163:MET:HE2	2:N:170:GLY:CA	2.46	0.42
1:D:100:ARG:HH22	1:D:106:PRO:HB3	1.84	0.42
1:D:175:PHE:CD2	1:D:199:LEU:CD1	3.03	0.42
1:F:215:VAL:HG22	1:F:221:PHE:HA	2.02	0.42
2:K:93:PHE:CB	2:L:92:TYR:CE2	3.03	0.42
1:A:229:LEU:HD22	1:A:233:VAL:CG2	2.50	0.42
2:H:148:VAL:O	2:H:152:VAL:CG1	2.67	0.42
1:D:210:ILE:O	1:D:210:ILE:HG13	2.19	0.42
1:D:227:GLU:CD	1:D:227:GLU:H	2.24	0.42
1:A:130:ARG:CZ	1:G:125:GLN:HB3	2.50	0.42
2:M:55:LEU:HD12	2:M:55:LEU:HA	1.80	0.42
2:I:163:MET:SD	2:I:170:GLY:HA2	2.60	0.42
1:B:179:GLU:CB	1:B:192:LEU:HD11	2.50	0.42
1:F:56:SER:HB3	1:F:59:LEU:CD2	2.50	0.42
1:C:179:GLU:CD	1:C:233(F):ARG:NH1	2.74	0.42
2:N:2:THR:HG23	2:N:17:GLU:HG3	2.01	0.42
2:H:40:ARG:O	2:H:103:GLY:HA3	2.20	0.42
2:K:123:ILE:HG23	2:K:138:LEU:HD13	2.02	0.41
1:B:198:GLY:HA3	1:B:233(G):ILE:HD13	2.01	0.41
1:D:97:GLN:HB3	2:K:61:ILE:HG23	2.01	0.41
2:J:141:ARG:HH21	2:J:141:ARG:HG2	1.83	0.41
4:B:234:HOH:O	2:J:75:THR:HG22	2.19	0.41
1:D:103:TYR:O	1:D:105:GLU:HG3	2.20	0.41
1:D:122:GLN:C	1:D:124:THR:N	2.73	0.41
2:I:33:LYS:HG2	3:I:1101:CIB:H191	2.02	0.41
2:K:76:VAL:HG22	2:K:105:ASP:OD1	2.20	0.41
2:H:93:PHE:N	2:H:93:PHE:CD1	2.88	0.41
2:H:46:ALA:HB2	2:H:127:THR:CG2	2.50	0.41
1:F:137:LEU:HD23	1:F:137:LEU:HA	1.87	0.41
1:B:190:MET:HG2	1:B:194:LEU:CD2	2.50	0.41
2:H:186:TYR:O	2:H:187:SER:O	2.38	0.41
1:E:130:ARG:HH11	1:E:130:ARG:HG3	1.86	0.41
1:B:179:GLU:CD	1:B:233(F):ARG:NH1	2.73	0.41
2:K:41:MET:CE	2:K:76:VAL:HA	2.50	0.41
2:J:93:PHE:CB	2:K:92:TYR:CE2	3.03	0.41
2:L:93:PHE:CB	2:M:92:TYR:CE2	3.03	0.41
2:H:161:SER:O	2:H:164:LYS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:89:ILE:HG13	1:F:90:ASP:N	2.35	0.41
1:B:175:PHE:CD2	1:B:199:LEU:CD1	3.03	0.41
1:F:88:LEU:HD12	1:F:88:LEU:HA	1.86	0.41
2:K:5:GLY:O	2:K:124:VAL:HG12	2.20	0.41
2:J:123:ILE:HG23	2:J:138:LEU:HD13	2.01	0.41
1:A:14:VAL:HB	1:B:23:GLN:NE2	2.35	0.41
1:G:207:PRO:HB3	1:G:233:VAL:HG21	2.01	0.41
2:L:156:VAL:HA	2:L:173:ILE:CD1	2.51	0.41
1:D:71:ASP:OD1	1:D:100:ARG:NH2	2.54	0.41
2:M:186:TYR:O	2:M:188(B):GLU:OE1	2.38	0.41
1:A:179:GLU:CD	1:A:233(F):ARG:NH1	2.74	0.41
1:F:175:PHE:CD2	1:F:199:LEU:CD1	3.03	0.41
1:C:141:VAL:HG23	1:C:215:VAL:HG12	2.02	0.41
1:C:206:VAL:HB	1:C:209:ASN:ND2	2.36	0.41
2:J:18:LYS:HE3	2:J:18:LYS:HB3	1.87	0.41
1:C:90:ASP:OD2	2:J:69:ARG:HD3	2.20	0.41
1:E:210:ILE:O	1:E:210:ILE:HG13	2.18	0.41
1:B:38:ILE:CD1	1:B:197:MET:HE2	2.51	0.41
2:K:57:ARG:NH1	2:L:85:ASN:HD21	2.19	0.41
1:G:130:ARG:HG3	1:G:130:ARG:HH11	1.86	0.41
1:A:70:ILE:HG21	1:A:112:LEU:CD2	2.49	0.41
1:C:122:GLN:C	1:C:124:THR:N	2.72	0.41
2:M:43:MET:HG3	2:M:101:ILE:HG12	2.01	0.41
2:H:18:LYS:HD3	2:H:174:ASP:OD2	2.20	0.41
2:K:93:PHE:CD1	2:K:93:PHE:N	2.88	0.41
1:A:47:ILE:HG22	1:A:48:LEU:N	2.36	0.41
1:C:77:ALA:HB3	1:C:137:LEU:HB2	2.02	0.41
1:D:177:GLU:OE2	1:E:57:LYS:HG2	2.19	0.41
2:N:5:GLY:O	2:N:124:VAL:HG12	2.20	0.41
1:D:81:LEU:HD22	1:D:81:LEU:N	2.35	0.41
1:C:49:ILE:HD11	1:C:197:MET:HG3	2.03	0.41
1:C:179:GLU:CB	1:C:192:LEU:HD11	2.50	0.41
2:N:76:VAL:HG23	2:N:77:ARG:N	2.34	0.41
2:K:100:LEU:HD12	2:K:112:SER:HA	2.01	0.41
2:M:93:PHE:CB	2:N:92:TYR:CZ	3.03	0.41
2:J:164:LYS:C	2:J:165:ARG:HG2	2.39	0.41
1:B:149:TYR:HB3	1:B:157:LEU:HD21	2.02	0.41
2:N:34:ILE:HD13	2:N:35:TYR:N	2.34	0.41
1:F:126:TYR:O	1:F:128:GLY:N	2.54	0.41
1:D:116:ILE:HD12	1:D:136:LEU:HD12	2.03	0.41
1:D:14:VAL:HB	1:E:23:GLN:HE22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:170:GLY:O	2:K:171:ASP:HB2	2.20	0.41
1:A:100:ARG:HH22	1:A:106:PRO:HB3	1.84	0.41
2:K:156:VAL:HG13	2:K:173:ILE:HD13	2.03	0.41
1:A:141:VAL:HG23	1:A:215:VAL:HG12	2.03	0.41
2:N:47:GLY:O	3:N:1601:CIB:HA2	2.20	0.41
1:G:229:LEU:HD22	1:G:233:VAL:CG2	2.49	0.41
2:J:160:TYR:CE2	2:J:164:LYS:HE3	2.55	0.41
2:J:125:ALA:HB3	2:J:135:TYR:CD1	2.55	0.41
2:I:137:VAL:HG22	2:I:158:ALA:HB2	2.03	0.41
1:D:220:ARG:N	1:D:220:ARG:HD2	2.31	0.41
2:N:44:THR:OG1	2:N:100:LEU:HB2	2.20	0.41
2:N:1:THR:HA	2:N:17:GLU:OE1	2.20	0.41
1:E:209:ASN:HD22	1:E:209:ASN:C	2.23	0.41
1:D:207:PRO:HB3	1:D:233:VAL:HG21	2.03	0.41
2:L:20:ALA:HB3	2:L:28:SER:HB3	2.02	0.41
1:E:233(D):ASN:HD22	1:E:233(G):ILE:HD12	1.86	0.41
1:F:204:GLU:OE2	1:F:233(H):ARG:HG2	2.21	0.41
2:H:141:ARG:NE	2:H:157:ARG:NE	2.53	0.41
1:A:147:LYS:HE2	1:A:159:GLU:OE1	2.21	0.41
2:M:59:ILE:HD12	2:M:83:THR:OG1	2.21	0.41
2:J:179:THR:HG23	2:J:182:GLU:N	2.36	0.41
2:J:13:VAL:HG21	2:J:151:ALA:HB3	2.03	0.41
1:E:121:GLN:HB3	1:E:121:GLN:HE21	1.67	0.41
1:C:117:CYS:SG	1:C:151:THR:HG22	2.61	0.41
1:C:179:GLU:CA	1:C:179:GLU:OE2	2.69	0.41
2:N:41:MET:CE	2:N:76:VAL:HA	2.50	0.41
2:N:77:ARG:HG3	2:N:77:ARG:HH21	1.85	0.41
2:N:10:ASP:CG	2:N:148:VAL:HG13	2.41	0.41
1:G:229:LEU:O	1:G:230:LYS:C	2.60	0.41
2:N:114:ASP:OD2	2:N:114:ASP:C	2.59	0.41
2:L:100:LEU:HD12	2:L:100:LEU:HA	1.84	0.41
1:A:76:ALA:HA	1:A:137:LEU:O	2.20	0.41
2:L:2:THR:HG23	2:L:17:GLU:HG3	2.03	0.41
1:C:95:GLU:CG	1:C:115:LYS:HD3	2.51	0.41
2:N:34:ILE:O	2:N:34:ILE:HG23	2.20	0.41
2:J:25:PHE:CE2	2:J:27:ALA:HA	2.56	0.41
1:E:24:VAL:HG11	1:E:154:SER:HB3	2.02	0.41
1:E:74:ILE:HG12	1:E:109:VAL:HG22	2.03	0.41
2:I:77:ARG:HG3	2:I:77:ARG:HH21	1.85	0.41
1:A:110:LYS:NZ	2:I:71:GLU:OE2	2.51	0.41
1:G:76:ALA:HA	1:G:137:LEU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:THR:O	1:E:124:THR:HG23	2.22	0.41
1:B:56:SER:HB3	1:B:59:LEU:CD2	2.48	0.41
1:C:100:ARG:NH2	1:C:106:PRO:CA	2.82	0.41
1:A:17:PRO:HA	1:B:26:TYR:CE1	2.56	0.41
2:N:55:LEU:HD12	2:N:55:LEU:HA	1.87	0.41
1:F:62:ASP:N	1:F:62:ASP:OD2	2.54	0.41
1:G:62:ASP:N	1:G:62:ASP:OD2	2.51	0.41
1:A:190:MET:O	1:A:194:LEU:HD22	2.21	0.40
2:J:6:LEU:HA	2:J:122:ASP:O	2.21	0.40
1:B:190:MET:HG2	1:B:194:LEU:HD21	2.02	0.40
2:M:57:ARG:O	2:M:61:ILE:HD13	2.20	0.40
1:D:124:THR:O	1:D:124:THR:HG23	2.21	0.40
2:K:10:ASP:OD1	2:K:147:GLY:HA2	2.21	0.40
2:K:156:VAL:HA	2:K:173:ILE:CD1	2.51	0.40
2:K:76:VAL:HG21	2:K:109:SER:OG	2.21	0.40
2:K:93:PHE:N	2:K:94:PRO:CD	2.83	0.40
2:L:76:VAL:HG21	2:L:109:SER:OG	2.20	0.40
2:I:31:ALA:HA	4:I:1114:HOH:O	2.20	0.40
1:C:227:GLU:CD	1:C:227:GLU:H	2.24	0.40
1:F:218:ASP:OD1	1:F:219:ASP:N	2.49	0.40
2:H:76:VAL:HG21	2:H:109:SER:OG	2.21	0.40
1:C:117:CYS:HB3	1:D:86:ARG:NH2	2.36	0.40
2:I:193:LEU:HD23	2:I:194:ALA:N	2.35	0.40
1:A:89:ILE:HG13	1:A:90:ASP:N	2.36	0.40
2:J:21:THR:N	4:J:1206:HOH:O	2.54	0.40
1:C:101:LEU:HD22	1:C:101:LEU:O	2.21	0.40
1:G:36:THR:HG23	1:G:197:MET:HE3	2.03	0.40
2:M:170:GLY:O	2:M:171:ASP:HB2	2.20	0.40
1:B:28:ARG:HD3	1:B:152:ASP:OD1	2.21	0.40
2:M:67:GLU:O	2:M:71:GLU:N	2.53	0.40
2:K:34:ILE:HD11	2:K:42:ALA:HB1	2.03	0.40
2:N:193:LEU:HD23	2:N:194:ALA:N	2.37	0.40
2:H:1:THR:CG2	2:H:2:THR:N	2.85	0.40
1:D:146:PRO:O	1:D:147:LYS:HG2	2.21	0.40
1:C:126:TYR:O	1:C:128:GLY:N	2.55	0.40
2:N:40:ARG:O	2:N:103:GLY:HA3	2.21	0.40
2:I:197:ARG:HG2	2:I:197:ARG:HH11	1.86	0.40
1:B:38:ILE:HD11	1:B:197:MET:HE2	2.03	0.40
2:I:123:ILE:HA	2:I:123:ILE:HD13	1.94	0.40
1:F:14:VAL:HB	1:G:23:GLN:NE2	2.36	0.40
1:F:136:LEU:HB2	1:F:151:THR:OG1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:28:ARG:HD3	1:G:152:ASP:OD1	2.22	0.40
2:K:13:VAL:HG21	2:K:151:ALA:HB3	2.03	0.40
2:L:156:VAL:HG13	2:L:173:ILE:HD13	2.02	0.40
2:H:93:PHE:N	2:H:94:PRO:CD	2.84	0.40
2:H:44:THR:OG1	2:H:100:LEU:HB2	2.21	0.40
1:F:95:GLU:HG3	1:F:115:LYS:HD3	2.03	0.40
2:I:10:ASP:OD1	2:I:147:GLY:HA2	2.21	0.40
1:B:177:GLU:OE2	1:C:57:LYS:HG2	2.21	0.40
1:B:62:ASP:OD2	1:B:62:ASP:N	2.53	0.40
2:K:77:ARG:HH21	2:K:77:ARG:HG3	1.85	0.40
2:K:6:LEU:HB3	2:K:123:ILE:CD1	2.50	0.40
2:H:157:ARG:NH2	2:H:157:ARG:HG3	2.36	0.40
1:B:121:GLN:HB3	1:B:121:GLN:HE21	1.64	0.40
1:A:168:GLY:O	1:A:172:VAL:HG13	2.21	0.40
1:F:117:CYS:SG	1:F:151:THR:HG22	2.62	0.40
1:F:164:ALA:HB2	1:F:172:VAL:HG21	2.03	0.40
2:J:55:LEU:HD21	2:J:87:LEU:HD11	2.03	0.40
1:F:100:ARG:NH2	1:F:106:PRO:CA	2.82	0.40
1:E:144:VAL:HG13	1:E:146:PRO:HD2	2.04	0.40
2:K:146:ILE:HD11	2:K:151:ALA:HA	2.04	0.40
1:C:147:LYS:HE2	1:C:159:GLU:OE1	2.22	0.40
1:D:63:THR:O	1:D:64:ILE:C	2.60	0.40
2:I:93:PHE:N	2:I:93:PHE:CD1	2.89	0.40
2:M:93:PHE:CD1	2:M:93:PHE:N	2.90	0.40
2:J:93:PHE:CD1	2:J:93:PHE:N	2.89	0.40
2:J:1:THR:HA	2:J:17:GLU:OE1	2.22	0.40
2:K:18:LYS:HB3	2:K:18:LYS:HE3	1.92	0.40
2:M:41:MET:CE	2:M:76:VAL:HA	2.52	0.40
1:D:24:VAL:HG11	1:D:154:SER:HB3	2.04	0.40
2:J:185:GLN:HB2	2:J:185:GLN:HE21	1.68	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	235/237 (99%)	217 (92%)	10 (4%)	8 (3%)	5	15
1	B	235/237 (99%)	215 (92%)	11 (5%)	9 (4%)	4	12
1	C	235/237 (99%)	213 (91%)	14 (6%)	8 (3%)	5	15
1	D	235/237 (99%)	215 (92%)	12 (5%)	8 (3%)	5	15
1	E	235/237 (99%)	213 (91%)	16 (7%)	6 (3%)	7	21
1	F	235/237 (99%)	217 (92%)	10 (4%)	8 (3%)	5	15
1	G	235/237 (99%)	215 (92%)	12 (5%)	8 (3%)	5	15
2	H	200/202 (99%)	184 (92%)	12 (6%)	4 (2%)	9	29
2	I	200/202 (99%)	188 (94%)	9 (4%)	3 (2%)	13	38
2	J	200/202 (99%)	186 (93%)	11 (6%)	3 (2%)	13	38
2	K	200/202 (99%)	187 (94%)	9 (4%)	4 (2%)	9	29
2	L	200/202 (99%)	188 (94%)	9 (4%)	3 (2%)	13	38
2	M	200/202 (99%)	188 (94%)	9 (4%)	3 (2%)	13	38
2	N	200/202 (99%)	188 (94%)	8 (4%)	4 (2%)	9	29
All	All	3045/3073 (99%)	2814 (92%)	152 (5%)	79 (3%)	7	21

All (79) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	ILE
1	A	127	GLY
1	A	220	ARG
1	B	12	ILE
1	B	127	GLY
1	B	220	ARG
1	C	12	ILE
1	C	127	GLY
1	C	220	ARG
1	D	12	ILE
1	D	127	GLY
1	D	220	ARG
1	E	12	ILE
1	E	127	GLY
1	E	220	ARG
1	F	12	ILE

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Mol	Chain	Res	Type
1	F	127	GLY
1	F	220	ARG
1	G	12	ILE
1	G	127	GLY
1	G	220	ARG
1	A	11	ALA
1	B	11	ALA
1	B	64	ILE
1	C	11	ALA
1	D	11	ALA
1	E	11	ALA
1	F	11	ALA
1	G	11	ALA
2	H	180	GLU
2	I	180	GLU
2	J	180	GLU
2	K	180	GLU
2	L	180	GLU
2	M	180	GLU
2	N	180	GLU
1	A	169	ARG
1	C	64	ILE
1	C	233(E)	GLU
1	F	169	ARG
1	G	169	ARG
2	J	122	ASP
2	K	122	ASP
2	L	122	ASP
1	A	64	ILE
1	A	233(E)	GLU
1	B	169	ARG
1	B	233(E)	GLU
1	C	169	ARG
1	D	169	ARG
1	D	233(E)	GLU
1	F	64	ILE
1	G	233(E)	GLU
2	H	122	ASP
2	M	122	ASP
2	N	122	ASP
1	A	142	ASP
1	B	142	ASP

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Mol	Chain	Res	Type
1	C	142	ASP
1	D	64	ILE
1	D	142	ASP
1	E	64	ILE
1	E	169	ARG
1	F	233(E)	GLU
1	G	64	ILE
1	G	142	ASP
2	I	122	ASP
2	N	96	LEU
2	H	187	SER
2	H	197	ARG
2	I	187	SER
2	J	187	SER
2	K	197	ARG
2	L	187	SER
2	M	187	SER
2	K	187	SER
2	N	187	SER
1	B	230	LYS
1	F	230	LYS

### 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	199/199 (100%)	178 (89%)	21 (11%)	8	23
1	B	199/199 (100%)	177 (89%)	22 (11%)	8	21
1	C	199/199 (100%)	178 (89%)	21 (11%)	8	23
1	D	199/199 (100%)	178 (89%)	21 (11%)	8	23
1	E	199/199 (100%)	178 (89%)	21 (11%)	8	23
1	F	199/199 (100%)	178 (89%)	21 (11%)	8	23
1	G	199/199 (100%)	177 (89%)	22 (11%)	8	21
2	H	164/164 (100%)	149 (91%)	15 (9%)	12	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	I	164/164 (100%)	147 (90%)	17 (10%)	9	24
2	J	164/164 (100%)	149 (91%)	15 (9%)	12	31
2	K	164/164 (100%)	149 (91%)	15 (9%)	12	31
2	L	164/164 (100%)	149 (91%)	15 (9%)	12	31
2	M	164/164 (100%)	148 (90%)	16 (10%)	10	27
2	N	164/164 (100%)	149 (91%)	15 (9%)	12	31
All	All	2541/2541 (100%)	2284 (90%)	257 (10%)	9	25

All (257) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ARG
1	A	21	LEU
1	A	33	ARG
1	A	49	ILE
1	A	57	LYS
1	A	82	VAL
1	A	86	ARG
1	A	87	VAL
1	A	88	LEU
1	A	101	LEU
1	A	102	THR
1	A	111	GLU
1	A	121	GLN
1	A	124	THR
1	A	129	VAL
1	A	134	VAL
1	A	157	LEU
1	A	197	MET
1	A	209	ASN
1	A	220	ARG
1	A	233(J)	LEU
1	B	20	ARG
1	B	21	LEU
1	B	33	ARG
1	B	36	THR
1	B	49	ILE
1	B	57	LYS
1	B	82	VAL
1	B	86	ARG

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Mol	Chain	Res	Type
1	B	87	VAL
1	B	88	LEU
1	B	101	LEU
1	B	102	THR
1	B	111	GLU
1	B	121	GLN
1	B	124	THR
1	B	129	VAL
1	B	134	VAL
1	B	157	LEU
1	B	197	MET
1	B	209	ASN
1	B	220	ARG
1	B	233(J)	LEU
1	C	20	ARG
1	C	21	LEU
1	C	33	ARG
1	C	49	ILE
1	C	57	LYS
1	C	82	VAL
1	C	86	ARG
1	C	87	VAL
1	C	88	LEU
1	C	101	LEU
1	C	102	THR
1	C	111	GLU
1	C	121	GLN
1	C	124	THR
1	C	129	VAL
1	C	134	VAL
1	C	157	LEU
1	C	197	MET
1	C	209	ASN
1	C	220	ARG
1	C	233(J)	LEU
1	D	20	ARG
1	D	21	LEU
1	D	33	ARG
1	D	36	THR
1	D	49	ILE
1	D	57	LYS
1	D	86	ARG

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Mol	Chain	Res	Type
1	D	87	VAL
1	D	88	LEU
1	D	101	LEU
1	D	102	THR
1	D	111	GLU
1	D	121	GLN
1	D	124	THR
1	D	129	VAL
1	D	134	VAL
1	D	157	LEU
1	D	197	MET
1	D	209	ASN
1	D	220	ARG
1	D	233(J)	LEU
1	E	20	ARG
1	E	21	LEU
1	E	33	ARG
1	E	36	THR
1	E	49	ILE
1	E	57	LYS
1	E	86	ARG
1	E	87	VAL
1	E	88	LEU
1	E	101	LEU
1	E	102	THR
1	E	111	GLU
1	E	121	GLN
1	E	124	THR
1	E	129	VAL
1	E	134	VAL
1	E	157	LEU
1	E	197	MET
1	E	209	ASN
1	E	220	ARG
1	E	233(J)	LEU
1	F	20	ARG
1	F	21	LEU
1	F	33	ARG
1	F	36	THR
1	F	49	ILE
1	F	57	LYS
1	F	86	ARG

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Mol	Chain	Res	Type
1	F	87	VAL
1	F	88	LEU
1	F	101	LEU
1	F	102	THR
1	F	111	GLU
1	F	121	GLN
1	F	124	THR
1	F	129	VAL
1	F	134	VAL
1	F	157	LEU
1	F	197	MET
1	F	209	ASN
1	F	220	ARG
1	F	233(J)	LEU
1	G	20	ARG
1	G	21	LEU
1	G	33	ARG
1	G	36	THR
1	G	49	ILE
1	G	57	LYS
1	G	82	VAL
1	G	86	ARG
1	G	87	VAL
1	G	88	LEU
1	G	101	LEU
1	G	102	THR
1	G	111	GLU
1	G	121	GLN
1	G	124	THR
1	G	129	VAL
1	G	134	VAL
1	G	157	LEU
1	G	197	MET
1	G	209	ASN
1	G	220	ARG
1	G	233(J)	LEU
2	H	6	LEU
2	H	17	GLU
2	H	34	ILE
2	H	55	LEU
2	H	87	LEU
2	H	93	PHE

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Mol	Chain	Res	Type
2	H	96	LEU
2	H	116	ILE
2	H	121(A)	GLU
2	H	127	THR
2	H	139	GLU
2	H	143	THR
2	H	165	ARG
2	H	173	ILE
2	H	193	LEU
2	I	2	THR
2	I	6	LEU
2	I	17	GLU
2	I	34	ILE
2	I	55	LEU
2	I	87	LEU
2	I	93	PHE
2	I	96	LEU
2	I	97	VAL
2	I	116	ILE
2	I	121(A)	GLU
2	I	127	THR
2	I	139	GLU
2	I	143	THR
2	I	165	ARG
2	I	173	ILE
2	I	193	LEU
2	J	6	LEU
2	J	17	GLU
2	J	34	ILE
2	J	55	LEU
2	J	87	LEU
2	J	93	PHE
2	J	96	LEU
2	J	116	ILE
2	J	121(A)	GLU
2	J	127	THR
2	J	139	GLU
2	J	143	THR
2	J	165	ARG
2	J	173	ILE
2	J	193	LEU
2	K	6	LEU

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Mol	Chain	Res	Type
2	K	17	GLU
2	K	34	ILE
2	K	55	LEU
2	K	87	LEU
2	K	93	PHE
2	K	96	LEU
2	K	116	ILE
2	K	121(A)	GLU
2	K	127	THR
2	K	139	GLU
2	K	143	THR
2	K	165	ARG
2	K	173	ILE
2	K	193	LEU
2	L	6	LEU
2	L	17	GLU
2	L	34	ILE
2	L	55	LEU
2	L	87	LEU
2	L	93	PHE
2	L	96	LEU
2	L	116	ILE
2	L	121(A)	GLU
2	L	127	THR
2	L	139	GLU
2	L	143	THR
2	L	165	ARG
2	L	173	ILE
2	L	193	LEU
2	M	6	LEU
2	M	17	GLU
2	M	34	ILE
2	M	55	LEU
2	M	87	LEU
2	M	93	PHE
2	M	96	LEU
2	M	97	VAL
2	M	116	ILE
2	M	121(A)	GLU
2	M	127	THR
2	M	139	GLU
2	M	143	THR

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Mol	Chain	Res	Type
2	M	165	ARG
2	M	173	ILE
2	M	193	LEU
2	N	6	LEU
2	N	17	GLU
2	N	34	ILE
2	N	55	LEU
2	N	87	LEU
2	N	93	PHE
2	N	96	LEU
2	N	116	ILE
2	N	121(A)	GLU
2	N	127	THR
2	N	139	GLU
2	N	143	THR
2	N	165	ARG
2	N	173	ILE
2	N	193	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (91) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	121	GLN
1	A	125	GLN
1	A	170	ASN
1	A	209	ASN
1	A	233(D)	ASN
1	B	23	GLN
1	B	121	GLN
1	B	125	GLN
1	B	170	ASN
1	B	209	ASN
1	B	233(D)	ASN
1	C	23	GLN
1	C	121	GLN
1	C	125	GLN
1	C	170	ASN
1	C	209	ASN
1	C	233(D)	ASN
1	D	23	GLN
1	D	121	GLN

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Mol	Chain	Res	Type
1	D	125	GLN
1	D	170	ASN
1	D	209	ASN
1	D	233(D)	ASN
1	E	23	GLN
1	E	121	GLN
1	E	125	GLN
1	E	170	ASN
1	E	209	ASN
1	E	233(D)	ASN
1	F	23	GLN
1	F	121	GLN
1	F	125	GLN
1	F	170	ASN
1	F	209	ASN
1	F	233(D)	ASN
1	G	23	GLN
1	G	121	GLN
1	G	125	GLN
1	G	170	ASN
1	G	209	ASN
1	G	233(D)	ASN
2	H	24	ASN
2	H	36	GLN
2	H	53	GLN
2	H	85	ASN
2	H	98	GLN
2	H	185	GLN
2	H	191	GLN
2	I	24	ASN
2	I	36	GLN
2	I	53	GLN
2	I	85	ASN
2	I	98	GLN
2	I	185	GLN
2	I	191	GLN
2	J	24	ASN
2	J	36	GLN
2	J	53	GLN
2	J	85	ASN
2	J	98	GLN
2	J	185	GLN

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Mol	Chain	Res	Type
2	J	191	GLN
2	K	24	ASN
2	K	36	GLN
2	K	53	GLN
2	K	85	ASN
2	K	98	GLN
2	K	185	GLN
2	K	191	GLN
2	L	24	ASN
2	L	36	GLN
2	L	53	GLN
2	L	85	ASN
2	L	98	GLN
2	L	185	GLN
2	L	191	GLN
2	M	24	ASN
2	M	36	GLN
2	M	53	GLN
2	M	85	ASN
2	M	98	GLN
2	M	185	GLN
2	M	191	GLN
2	N	24	ASN
2	N	36	GLN
2	N	53	GLN
2	N	85	ASN
2	N	98	GLN
2	N	185	GLN
2	N	191	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

7 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	CIB	H	1001	2	25,26,26	0.93	1 (4%)	30,33,33	1.12	2 (6%)
3	CIB	I	1101	2	25,26,26	1.10	2 (8%)	30,33,33	1.47	5 (16%)
3	CIB	J	1201	2	25,26,26	0.92	0	30,33,33	1.24	5 (16%)
3	CIB	K	1301	2	25,26,26	0.87	0	30,33,33	1.08	3 (10%)
3	CIB	L	1401	2	25,26,26	1.04	1 (4%)	30,33,33	1.30	4 (13%)
3	CIB	M	1501	2	25,26,26	0.87	0	30,33,33	0.99	1 (3%)
3	CIB	N	1601	2	25,26,26	0.83	0	30,33,33	0.84	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CIB	H	1001	2	-	0/32/34/34	0/0/0/0
3	CIB	I	1101	2	-	0/32/34/34	0/0/0/0
3	CIB	J	1201	2	-	0/32/34/34	0/0/0/0
3	CIB	K	1301	2	-	0/32/34/34	0/0/0/0
3	CIB	L	1401	2	-	0/32/34/34	0/0/0/0
3	CIB	M	1501	2	-	0/32/34/34	0/0/0/0
3	CIB	N	1601	2	-	0/32/34/34	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	1101	CIB	CA2-N2	-2.33	1.40	1.45
3	I	1101	CIB	CA1-C1	-2.00	1.47	1.52
3	H	1001	CIB	CB2-CA2	2.00	1.60	1.53
3	L	1401	CIB	CB3-CA3	2.27	1.57	1.53



All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	1401	CIB	O28-C10-C25	-3.32	115.96	122.06
3	L	1401	CIB	CB1-CA1-C1	-2.88	103.09	110.60
3	I	1101	CIB	CA1-C1-N2	-2.85	110.21	116.78
3	I	1101	CIB	C2-CA2-N2	-2.80	103.36	111.26
3	M	1501	CIB	O28-C10-C25	-2.70	117.11	122.06
3	K	1301	CIB	O28-C10-C25	-2.59	117.32	122.06
3	J	1201	CIB	CA1-C1-N2	-2.46	111.10	116.78
3	J	1201	CIB	O28-C10-C25	-2.45	117.56	122.06
3	J	1201	CIB	C2-CA2-N2	-2.45	104.37	111.26
3	N	1601	CIB	O28-C10-C25	-2.34	117.77	122.06
3	H	1001	CIB	O28-C10-C25	-2.18	118.07	122.06
3	K	1301	CIB	CB1-CA1-C1	-2.12	105.07	110.60
3	I	1101	CIB	O28-C10-C25	-2.10	118.20	122.06
3	J	1201	CIB	O1-C1-N2	2.06	126.97	122.93
3	L	1401	CIB	CB1-CA1-N1	2.24	116.08	110.49
3	I	1101	CIB	CA1-N1-C10	2.34	129.34	121.37
3	J	1201	CIB	CA2-N2-C1	2.49	127.19	121.62
3	K	1301	CIB	CA3-N3-C2	2.65	127.55	121.63
3	L	1401	CIB	CA3-N3-C2	2.73	127.74	121.63
3	H	1001	CIB	CA3-N3-C2	3.35	129.13	121.63
3	I	1101	CIB	CB1-CA1-N1	4.03	120.56	110.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1001	CIB	5	0
3	I	1101	CIB	4	0
3	J	1201	CIB	2	0
3	K	1301	CIB	2	0
3	L	1401	CIB	2	0
3	M	1501	CIB	2	0
3	N	1601	CIB	4	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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 will therefore be empty.

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

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

### 6.3 Carbohydrates ⓘ

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

### 6.4 Ligands ⓘ

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

### 6.5 Other polymers ⓘ

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