



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:08 PM BST

PDB ID : 3ZPZ
EMDB ID: : EMD-2325
Title : Visualizing GroEL-ES in the Act of Encapsulating a Non-Native Substrate Protein
Authors : Chen, D.-H.; Madan, D.; Weaver, J.; Lin, Z.; Schroder, G.F.; Chiu, W.; Rye, H.S.
Deposited on : 2013-03-04
Resolution : 8.90 Å(reported)
Based on PDB ID : 1AON

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
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) : trunk27241

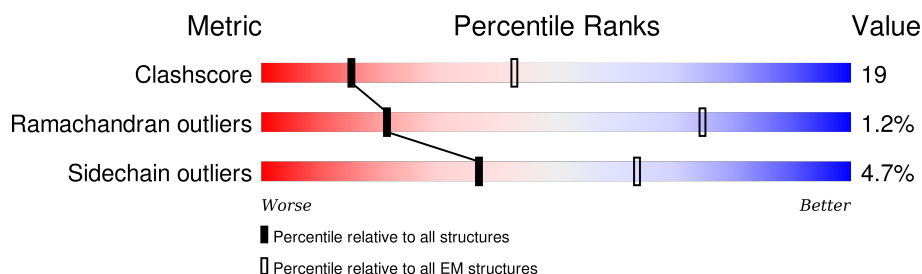
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.90 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

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

Mol	Chain	Length	Quality of chain
1	A	526	63% 34% .
1	B	526	63% 33% .
1	C	526	60% 38% .
1	D	526	60% 36% .
1	E	526	57% 39% .
1	F	526	59% 37% .
1	G	526	60% 37% .
1	H	526	61% 37% .
1	I	526	68% 31% .

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Mol	Chain	Length	Quality of chain
1	J	526	 63% 35% .
1	K	526	 62% 36% .
1	L	526	 68% 30% .
1	M	526	 61% 37% .
1	N	526	 62% 36% .
2	O	97	 65% 27% 8% .
2	P	97	 61% 32% 6% .
2	Q	97	 72% 22% 6% .
2	R	97	 63% 31% 6% .
2	S	97	 56% 38% 6% .
2	T	97	 66% 28% 5% .
2	U	97	 66% 31% .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 59276 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 60 KDA CHAPERONIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	B	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	C	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	D	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	E	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	F	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	G	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	H	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	I	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	J	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	K	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	L	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	M	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		
1	N	525	Total	C	N	O	S	0	1
			3856	2397	666	773	20		

- Molecule 2 is a protein called 10 KDA CHAPERONIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	97	Total	C	N	O	S	0	0
			728	454	127	145	2		

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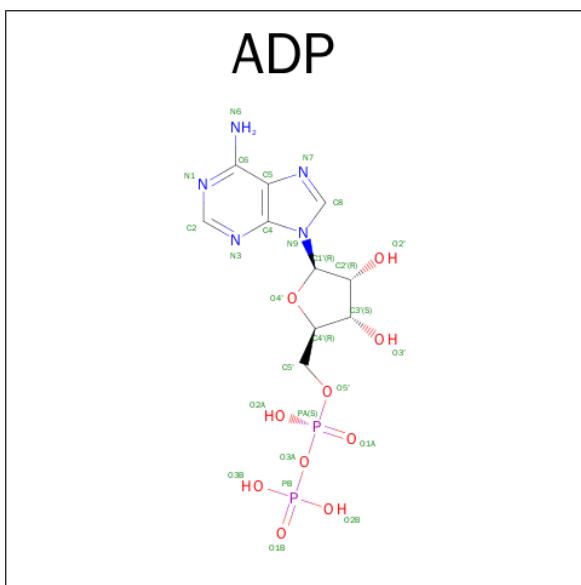
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	97	Total	C	N	O	S	0	0
			728	454	127	145	2		
2	Q	97	Total	C	N	O	S	0	0
			728	454	127	145	2		
2	R	97	Total	C	N	O	S	0	0
			728	454	127	145	2		
2	S	97	Total	C	N	O	S	0	0
			728	454	127	145	2		
2	T	97	Total	C	N	O	S	0	0
			728	454	127	145	2		
2	U	97	Total	C	N	O	S	0	0
			728	454	127	145	2		

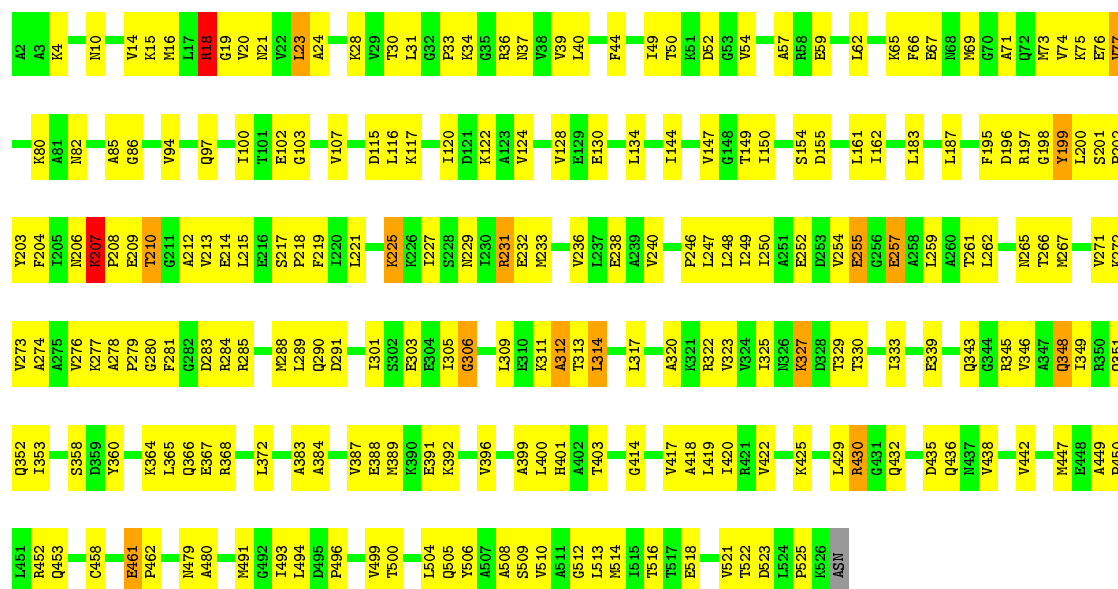
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
3	G	1	Total	Mg	0
			1	1	
3	D	1	Total	Mg	0
			1	1	
3	E	1	Total	Mg	0
			1	1	
3	B	1	Total	Mg	0
			1	1	
3	C	1	Total	Mg	0
			1	1	
3	A	1	Total	Mg	0
			1	1	
3	F	1	Total	Mg	0
			1	1	

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

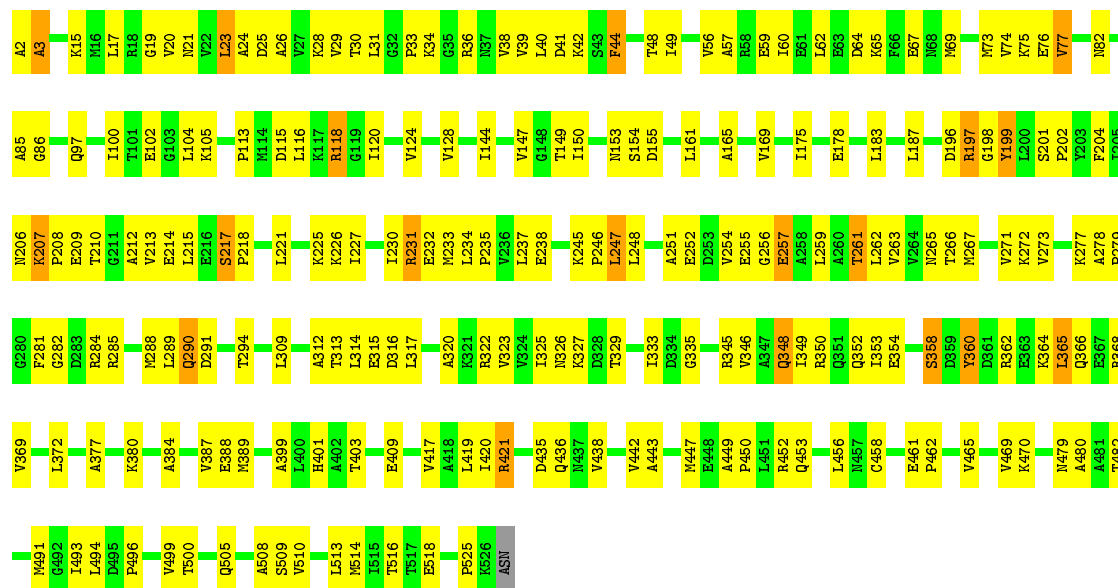


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total 27	C 10	N 5	O 10	P 2	0
4	B	1	Total 27	C 10	N 5	O 10	P 2	0
4	C	1	Total 27	C 10	N 5	O 10	P 2	0
4	D	1	Total 27	C 10	N 5	O 10	P 2	0
4	E	1	Total 27	C 10	N 5	O 10	P 2	0
4	F	1	Total 27	C 10	N 5	O 10	P 2	0
4	G	1	Total 27	C 10	N 5	O 10	P 2	0



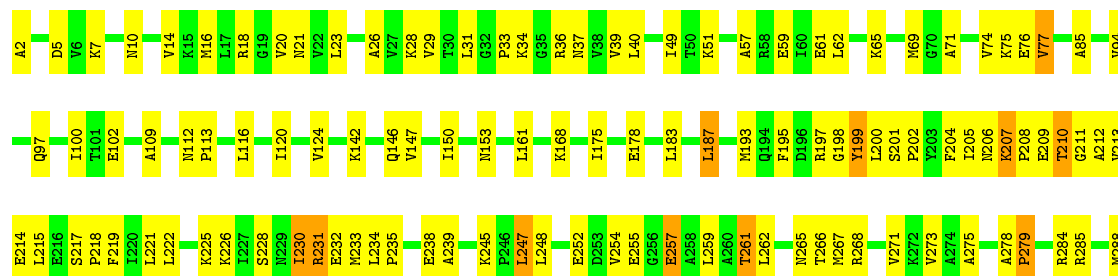
• Molecule 1: 60 KDA CHAPERONIN

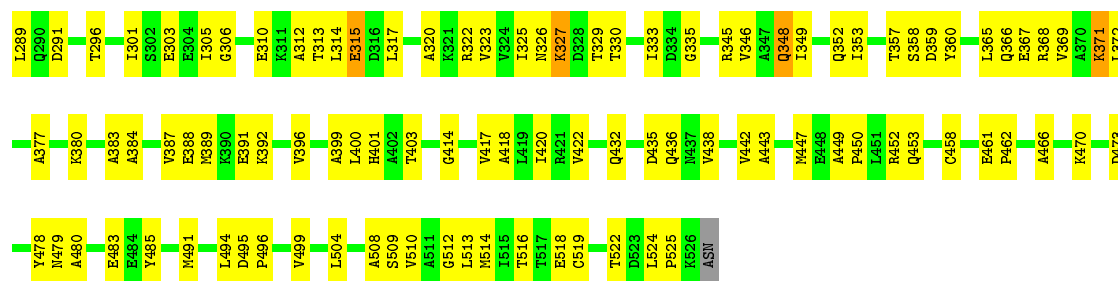
Chain F: 59% 37% •



• Molecule 1: 60 KDA CHAPERONIN

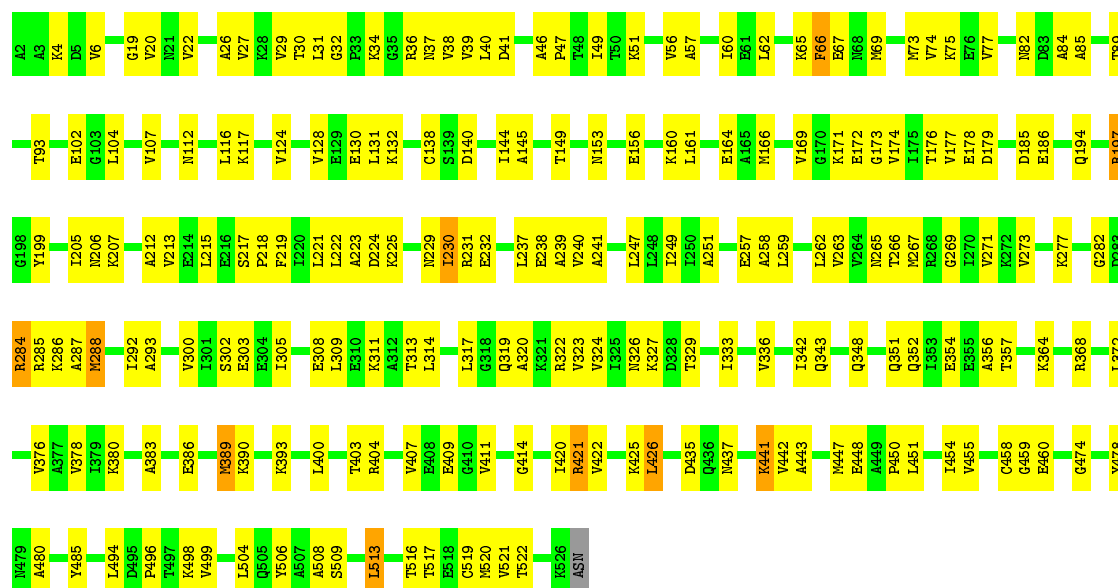
Chain G: 60% 37% •





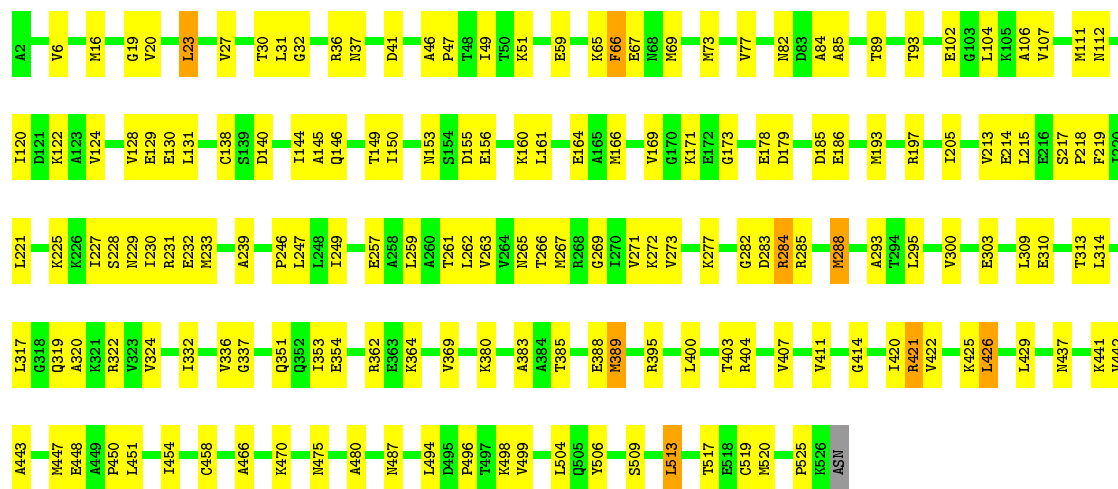
• Molecule 1: 60 KDA CHAPERONIN

Chain H: 61% 37%

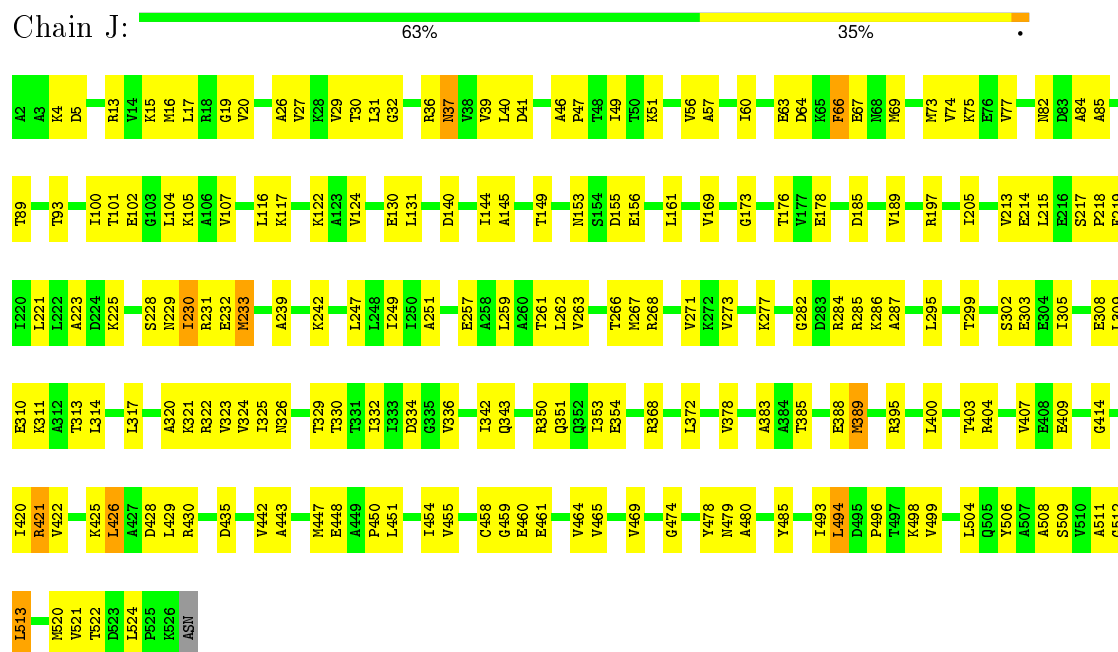


• Molecule 1: 60 KDA CHAPERONIN

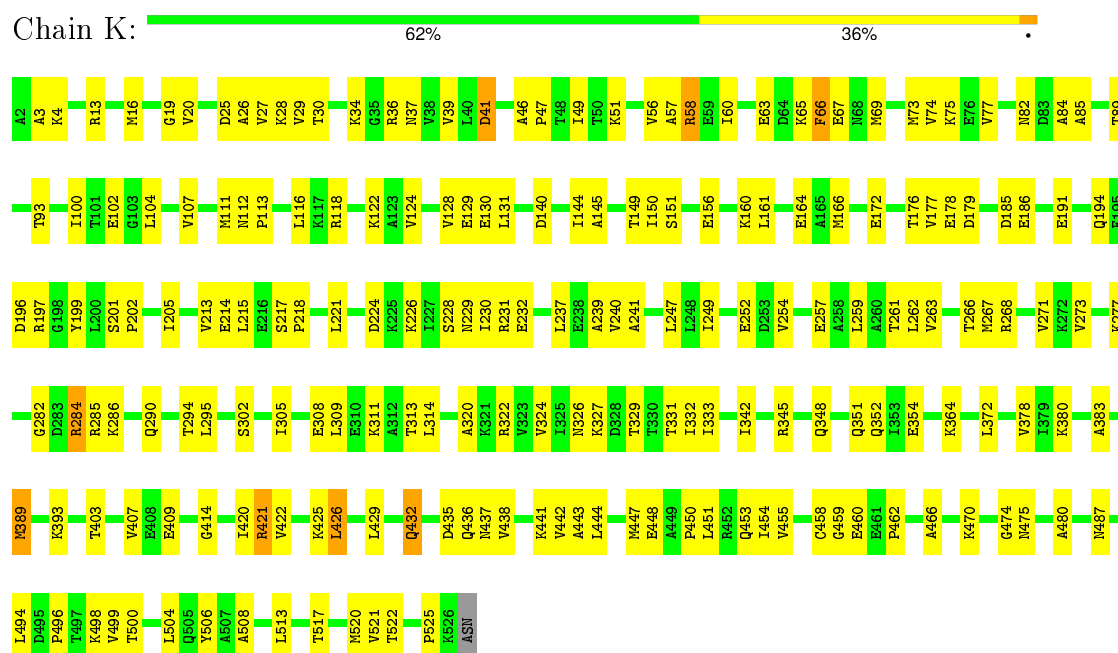
Chain I: 68% 31%



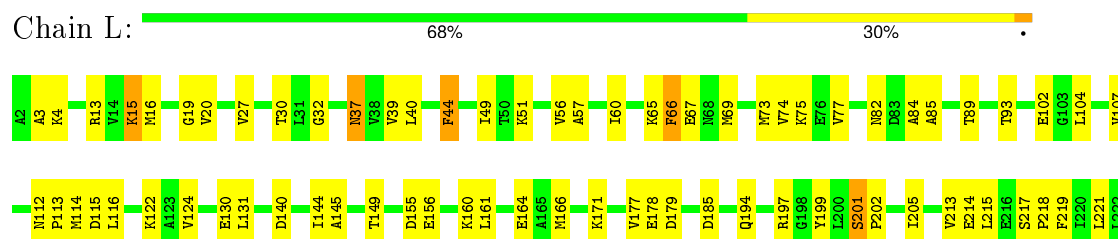
• Molecule 1: 60 KDA CHAPERONIN

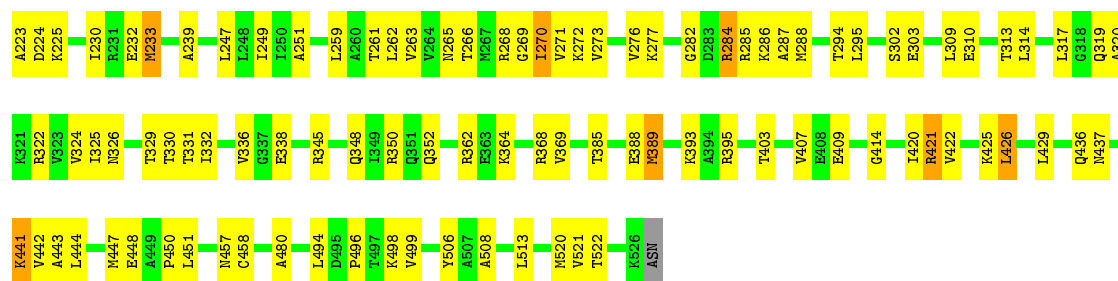


• Molecule 1: 60 KDA CHAPERONIN



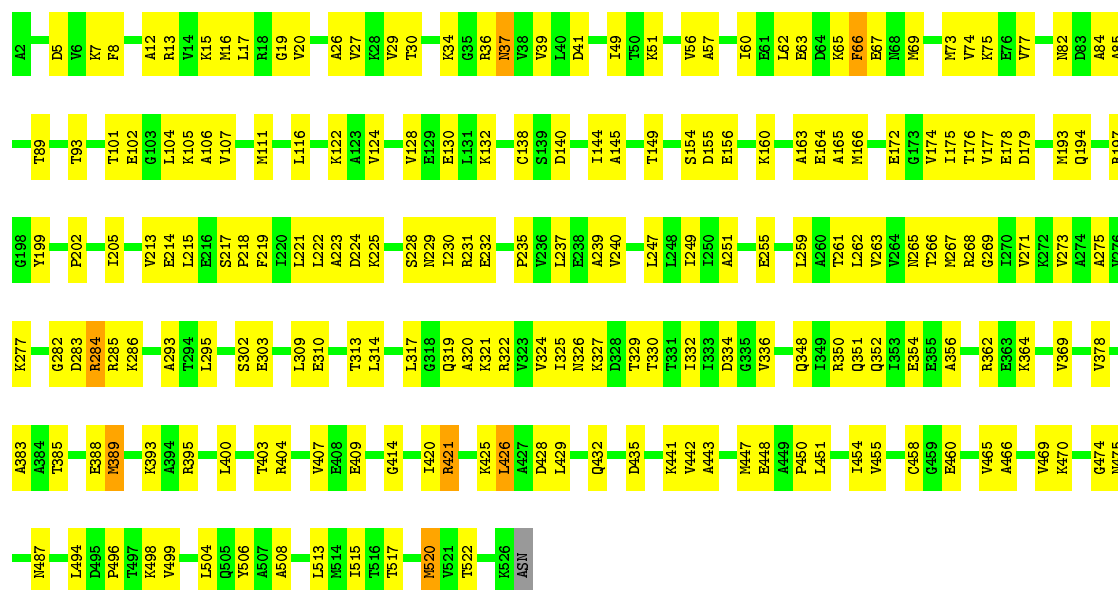
• Molecule 1: 60 KDA CHAPERONIN





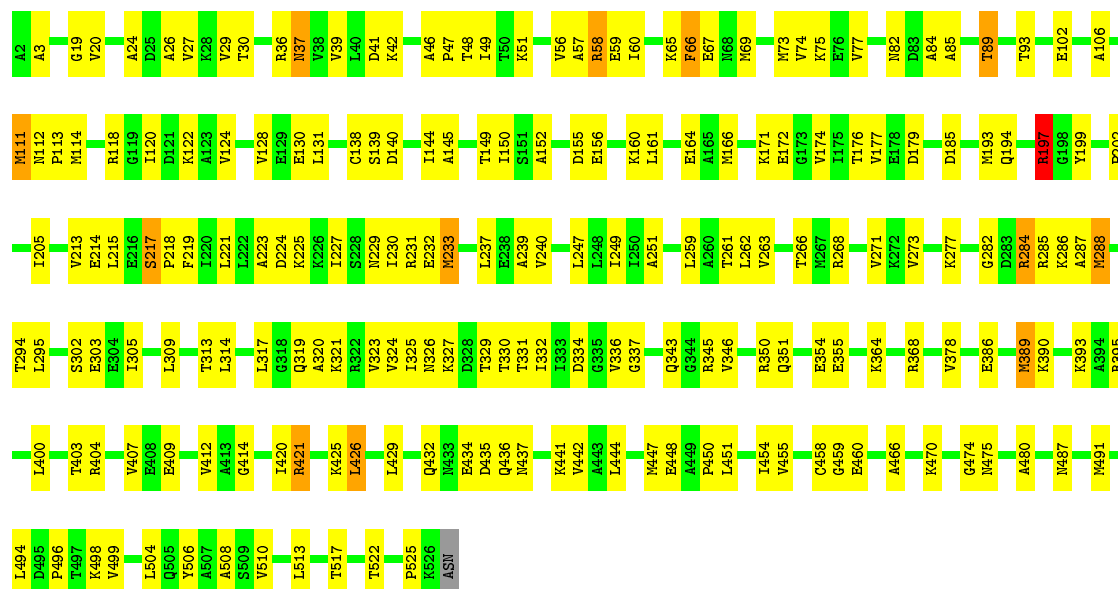
• Molecule 1: 60 KDA CHAPERONIN

Chain M: 61% 37%

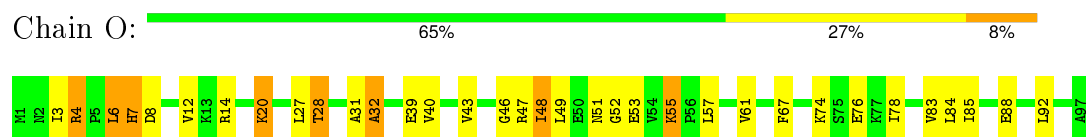


• Molecule 1: 60 KDA CHAPERONIN

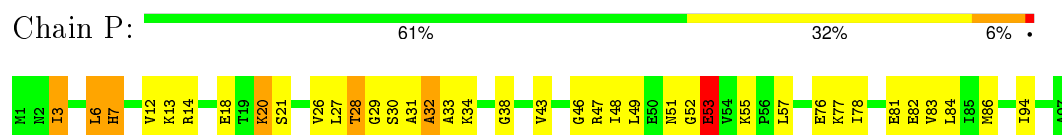
Chain N: 62% 36%



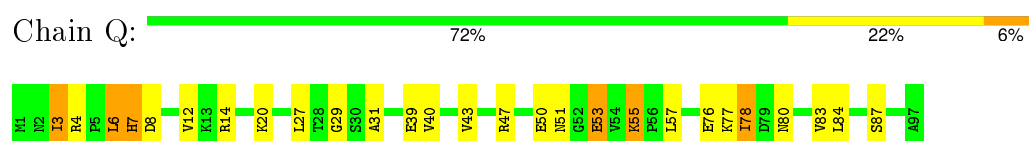
- Molecule 2: 10 KDA CHAPERONIN



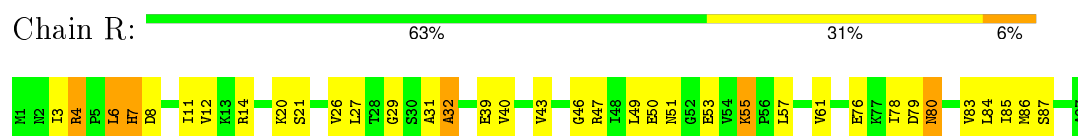
- Molecule 2: 10 KDA CHAPERONIN



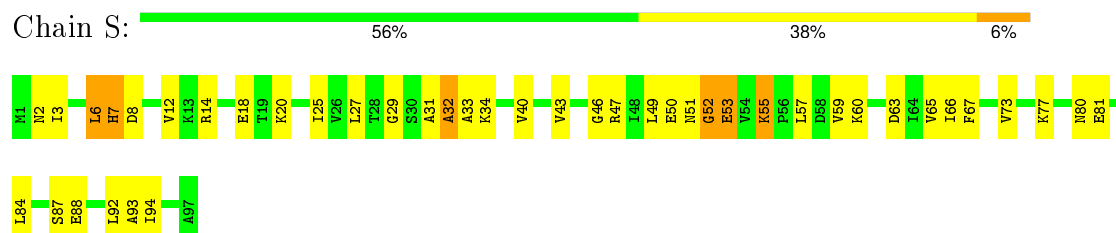
- Molecule 2: 10 KDA CHAPERONIN



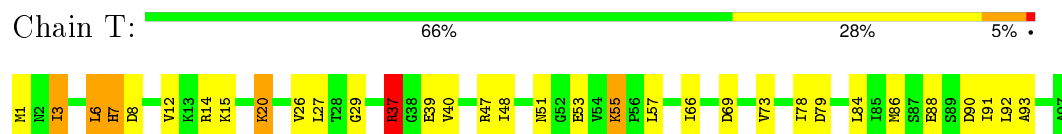
- Molecule 2: 10 KDA CHAPERONIN



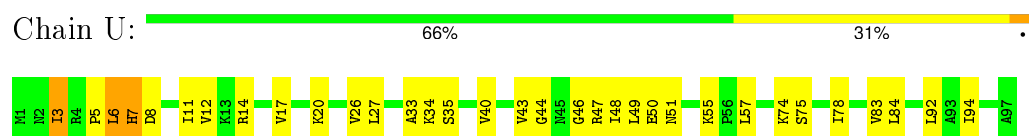
- Molecule 2: 10 KDA CHAPERONIN



- Molecule 2: 10 KDA CHAPERONIN



- Molecule 2: 10 KDA CHAPERONIN



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	EACH MICROGRAPH, Not provided	Depositor
Microscope	JEOL KYOTO-3000SFF	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	60000	Depositor
Image detector	KODAK SO163 FILM	Depositor

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: MG, ADP

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 >2	RMSZ	# Z >2
1	A	0.37	0/3884	0.60	1/5245 (0.0%)
1	B	0.37	0/3884	0.62	0/5245
1	C	0.36	0/3884	0.62	1/5245 (0.0%)
1	D	0.37	0/3884	0.60	0/5245
1	E	0.36	0/3884	0.63	1/5245 (0.0%)
1	F	0.37	0/3884	0.63	0/5245
1	G	0.37	0/3884	0.60	0/5245
1	H	0.36	0/3884	0.57	0/5245
1	I	0.36	0/3884	0.59	0/5245
1	J	0.36	0/3884	0.59	0/5245
1	K	0.36	0/3884	0.58	0/5245
1	L	0.36	0/3884	0.59	0/5245
1	M	0.35	0/3884	0.58	0/5245
1	N	0.36	0/3884	0.59	0/5245
2	O	0.41	0/732	0.69	0/983
2	P	0.40	0/732	0.72	0/983
2	Q	0.40	0/732	0.70	0/983
2	R	0.42	0/732	0.68	0/983
2	S	0.44	0/732	0.71	0/983
2	T	0.41	0/732	0.73	1/983 (0.1%)
2	U	0.42	0/732	0.65	0/983
All	All	0.37	0/59500	0.61	4/80311 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	18	ARG	NE-CZ-NH1	6.63	123.62	120.30
2	T	37	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	A	18	ARG	NE-CZ-NH1	5.21	122.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	18	ARG	NE-CZ-NH1	5.15	122.88	120.30

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	3856	0	3976	164	0
1	B	3856	0	3976	178	0
1	C	3856	0	3976	194	0
1	D	3856	0	3976	187	0
1	E	3856	0	3976	195	0
1	F	3856	0	3976	191	0
1	G	3856	0	3976	184	0
1	H	3856	0	3976	154	0
1	I	3856	0	3976	124	0
1	J	3856	0	3976	151	0
1	K	3856	0	3976	152	0
1	L	3856	0	3976	136	0
1	M	3856	0	3976	146	0
1	N	3856	0	3976	149	0
2	O	728	0	762	30	0
2	P	728	0	762	29	0
2	Q	728	0	762	24	0
2	R	728	0	762	31	0
2	S	728	0	762	31	0
2	T	728	0	762	28	0
2	U	728	0	762	24	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	27	0	12	5	0
4	B	27	0	12	5	0
4	C	27	0	12	5	0
4	D	27	0	12	4	0
4	E	27	0	12	5	0
4	F	27	0	12	4	0
4	G	27	0	12	3	0
All	All	59276	0	61082	2338	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 19.

All (2338) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:352:GLN:HB3	1:C:365:LEU:HD11	1.34	1.08
1:E:352:GLN:HB3	1:E:365:LEU:HD11	1.32	1.06
1:A:352:GLN:HB3	1:A:365:LEU:HD11	1.40	1.03
1:E:39:VAL:HG22	1:E:49:ILE:HG12	1.41	1.01
1:M:85:ALA:HB1	1:M:499:VAL:HG12	1.47	0.95
1:A:322:ARG:HB3	1:A:333:ILE:HD12	1.45	0.95
1:B:39:VAL:HG22	1:B:49:ILE:HG12	1.45	0.95
1:F:161:LEU:HD11	1:F:187:LEU:HB2	1.47	0.94
1:G:161:LEU:HD11	1:G:187:LEU:HB2	1.47	0.93
1:B:322:ARG:HB3	1:B:333:ILE:HD12	1.50	0.93
1:B:161:LEU:HD11	1:B:187:LEU:HB2	1.48	0.92
1:E:161:LEU:HD11	1:E:187:LEU:HB2	1.48	0.92
1:D:161:LEU:HD11	1:D:187:LEU:HB2	1.51	0.92
1:G:352:GLN:HB3	1:G:365:LEU:HD11	1.51	0.91
1:D:39:VAL:HG22	1:D:49:ILE:HG12	1.52	0.91
1:N:122:LYS:HE2	1:N:429:LEU:HD11	1.54	0.89
1:J:85:ALA:HB1	1:J:499:VAL:HG12	1.51	0.89
1:D:262:LEU:HD11	1:D:273:VAL:HB	1.54	0.89
1:E:305:ILE:HG22	1:E:306:GLY:H	1.38	0.89
1:F:513:LEU:HD11	1:G:388:GLU:HA	1.53	0.89
1:F:262:LEU:HD11	1:F:273:VAL:HB	1.54	0.88
1:H:205:ILE:HA	1:H:213:VAL:HG22	1.55	0.87
1:M:122:LYS:HE2	1:M:429:LEU:HD11	1.56	0.86
1:I:205:ILE:HA	1:I:213:VAL:HG22	1.58	0.86
1:J:205:ILE:HA	1:J:213:VAL:HG22	1.58	0.86
1:A:39:VAL:HG22	1:A:49:ILE:HG12	1.57	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:322:ARG:HB3	1:G:333:ILE:HD12	1.59	0.85
1:B:262:LEU:HD11	1:B:273:VAL:HB	1.56	0.85
1:L:205:ILE:HA	1:L:213:VAL:HG22	1.56	0.85
1:L:85:ALA:HB1	1:L:499:VAL:HG12	1.58	0.84
1:J:100:ILE:HD11	1:J:511:ALA:HA	1.60	0.84
1:C:161:LEU:HD11	1:C:187:LEU:HB2	1.57	0.84
1:B:197:ARG:CZ	1:B:279:PRO:HA	2.07	0.83
1:H:85:ALA:HB1	1:H:499:VAL:HG12	1.59	0.83
1:J:122:LYS:HE2	1:J:429:LEU:HD11	1.61	0.82
1:A:161:LEU:HD11	1:A:187:LEU:HB2	1.61	0.82
1:F:479:ASN:HB2	1:F:491:MET:SD	2.19	0.82
1:F:39:VAL:HG22	1:F:49:ILE:HG12	1.61	0.81
1:A:262:LEU:HD11	1:A:273:VAL:HB	1.60	0.81
1:E:69:MET:SD	1:F:41:ASP:HB2	2.19	0.81
1:B:201:SER:HB3	1:B:259:LEU:HD22	1.63	0.81
1:C:40:LEU:HD13	1:C:59:GLU:HG3	1.63	0.81
1:D:352:GLN:HB3	1:D:365:LEU:HD11	1.62	0.81
1:L:122:LYS:HE2	1:L:429:LEU:HD11	1.63	0.81
1:E:197:ARG:HD3	1:E:277:LYS:O	1.80	0.80
1:C:204:PHE:CZ	1:C:213:VAL:HG11	2.16	0.80
1:N:85:ALA:HB1	1:N:499:VAL:HG12	1.62	0.80
1:H:131:LEU:HD12	1:H:422:VAL:HG11	1.64	0.80
1:L:82:ASN:HB2	1:L:89:THR:OG1	1.82	0.80
1:M:420:ILE:HG13	1:M:451:LEU:HD22	1.64	0.79
1:J:82:ASN:HB2	1:J:89:THR:OG1	1.82	0.79
1:G:183:LEU:HD22	1:G:384:ALA:HA	1.63	0.79
1:D:195:PHE:CD1	1:D:197:ARG:HD3	2.17	0.79
1:N:239:ALA:HB1	1:N:314:LEU:HD11	1.64	0.78
1:B:513:LEU:HD11	1:C:388:GLU:HA	1.65	0.78
1:F:322:ARG:HB3	1:F:333:ILE:HD12	1.63	0.78
1:C:322:ARG:HB3	1:C:333:ILE:HD12	1.67	0.77
1:A:212:ALA:HA	1:A:325:ILE:O	1.85	0.77
1:D:212:ALA:HA	1:D:325:ILE:O	1.83	0.77
1:L:39:VAL:HG23	1:M:517:THR:HG21	1.66	0.76
1:E:383:ALA:HB3	1:E:389:MET:SD	2.25	0.76
1:B:40:LEU:HD13	1:B:59:GLU:HG3	1.67	0.76
2:O:47:ARG:HD3	2:O:49:LEU:HD12	1.66	0.76
1:C:266:THR:HA	1:C:271:VAL:O	1.84	0.76
1:H:82:ASN:HB2	1:H:89:THR:OG1	1.86	0.76
1:C:513:LEU:HD11	1:D:388:GLU:HA	1.65	0.76
1:K:63:GLU:HB2	1:L:3:ALA:HB1	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:85:ALA:HB1	1:K:499:VAL:HG12	1.66	0.75
1:A:479:ASN:HB2	1:A:491:MET:SD	2.26	0.75
1:I:122:LYS:HE2	1:I:429:LEU:HD11	1.67	0.75
1:H:420:ILE:HG13	1:H:451:LEU:HD22	1.69	0.75
1:J:351:GLN:O	1:J:354:GLU:HG2	1.87	0.75
1:L:49:ILE:HD11	1:M:73:MET:HE3	1.68	0.74
1:I:82:ASN:HB2	1:I:89:THR:OG1	1.86	0.74
1:K:82:ASN:HB2	1:K:89:THR:OG1	1.87	0.74
1:J:49:ILE:HD11	1:K:73:MET:HE3	1.70	0.74
1:G:200:LEU:HD22	1:G:254:VAL:HB	1.69	0.74
1:B:34:LYS:HD2	1:B:458:CYS:SG	2.28	0.74
1:K:77:VAL:HG22	1:K:506:TYR:HB3	1.67	0.74
2:O:7:HIS:HB2	2:O:46:GLY:O	1.86	0.73
1:N:205:ILE:HA	1:N:213:VAL:HG22	1.68	0.73
1:A:513:LEU:HD11	1:B:388:GLU:HA	1.69	0.73
1:L:414:GLY:N	1:L:494:LEU:HA	2.04	0.73
1:F:212:ALA:HA	1:F:325:ILE:O	1.88	0.73
1:F:199:TYR:CZ	1:F:202:PRO:HA	2.24	0.73
1:E:197:ARG:NH2	1:E:279:PRO:HD3	2.03	0.73
1:L:270:ILE:HG22	1:L:271:VAL:HG23	1.70	0.72
1:I:85:ALA:HB1	1:I:499:VAL:HG12	1.70	0.72
1:C:263:VAL:O	1:C:267:MET:HG2	1.89	0.72
1:F:349:ILE:HG23	1:F:365:LEU:HD21	1.72	0.72
1:E:346:VAL:HA	1:E:349:ILE:HD12	1.72	0.72
1:K:420:ILE:HG13	1:K:451:LEU:HD22	1.72	0.72
1:H:230:ILE:HD12	1:H:258:ALA:HA	1.70	0.72
1:M:205:ILE:HA	1:M:213:VAL:HG22	1.71	0.72
1:G:479:ASN:HB2	1:G:491:MET:SD	2.30	0.71
2:U:3:ILE:HG12	2:U:78:ILE:HD13	1.69	0.71
1:J:230:ILE:H	1:J:230:ILE:CD1	2.03	0.71
1:M:82:ASN:HB2	1:M:89:THR:OG1	1.89	0.71
1:A:34:LYS:HD2	1:A:458:CYS:SG	2.30	0.71
1:G:238:GLU:OE1	2:U:26:VAL:HG23	1.91	0.71
2:R:78:ILE:HD13	2:R:83:VAL:HG21	1.71	0.71
1:C:479:ASN:HB2	1:C:491:MET:SD	2.30	0.71
1:C:346:VAL:HA	1:C:349:ILE:HD12	1.71	0.71
1:C:247:LEU:HB3	1:C:273:VAL:HG13	1.73	0.71
1:D:195:PHE:CE1	1:D:330:THR:HB	2.26	0.71
1:M:221:LEU:HD12	1:M:249:ILE:HG23	1.71	0.71
1:K:205:ILE:HA	1:K:213:VAL:HG22	1.73	0.71
1:G:346:VAL:HA	1:G:349:ILE:HD12	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:420:ILE:HG13	1:N:451:LEU:HD22	1.72	0.70
1:L:221:LEU:HD12	1:L:249:ILE:HG23	1.70	0.70
2:U:78:ILE:HD12	2:U:83:VAL:HG21	1.72	0.70
1:L:239:ALA:HB1	1:L:314:LEU:HD11	1.73	0.70
1:G:199:TYR:CZ	1:G:202:PRO:HA	2.27	0.70
1:E:479:ASN:HB2	1:E:491:MET:SD	2.31	0.70
1:C:285:ARG:O	1:C:289:LEU:HG	1.91	0.70
1:B:212:ALA:HA	1:B:325:ILE:O	1.92	0.70
1:F:77:VAL:HG12	1:F:510:VAL:HG21	1.72	0.70
1:C:39:VAL:HG22	1:C:49:ILE:HG12	1.73	0.70
1:D:266:THR:HA	1:D:271:VAL:O	1.92	0.70
1:G:285:ARG:O	1:G:289:LEU:HG	1.92	0.70
1:G:39:VAL:HG22	1:G:49:ILE:HG12	1.72	0.69
1:L:420:ILE:HG13	1:L:451:LEU:HD22	1.74	0.69
1:F:238:GLU:OE1	2:T:26:VAL:HG23	1.92	0.69
1:I:66:PHE:HA	1:I:69:MET:HE3	1.74	0.69
1:E:291:ASP:HB2	1:E:372:LEU:HD21	1.73	0.69
1:F:346:VAL:HA	1:F:349:ILE:HD12	1.74	0.69
1:B:252:GLU:HA	1:B:285:ARG:NH1	2.07	0.69
1:I:420:ILE:HG13	1:I:451:LEU:HD22	1.74	0.69
1:M:77:VAL:HG22	1:M:506:TYR:HB3	1.75	0.69
1:B:265:ASN:OD1	2:P:27:LEU:HB3	1.92	0.69
1:D:77:VAL:CG1	1:D:510:VAL:HG21	2.22	0.69
1:B:195:PHE:CE1	1:B:330:THR:HB	2.27	0.69
1:G:266:THR:HA	1:G:271:VAL:O	1.91	0.69
1:H:20:VAL:HG23	1:H:74:VAL:HG21	1.73	0.69
1:K:450:PRO:O	1:K:454:ILE:HG12	1.93	0.69
1:H:450:PRO:O	1:H:454:ILE:HG12	1.93	0.69
1:E:262:LEU:HD11	1:E:273:VAL:HB	1.74	0.69
1:A:77:VAL:HG12	1:A:510:VAL:HG21	1.75	0.69
1:M:66:PHE:CZ	1:M:522:THR:HG22	2.28	0.69
1:L:49:ILE:HD11	1:M:73:MET:CE	2.22	0.69
1:J:197:ARG:HG2	1:J:277:LYS:O	1.92	0.69
1:E:261:THR:HG22	2:S:29:GLY:H	1.57	0.69
1:A:265:ASN:OD1	2:O:27:LEU:HB3	1.93	0.68
1:B:352:GLN:HB3	1:B:365:LEU:HD11	1.74	0.68
1:E:252:GLU:HA	1:E:285:ARG:NH1	2.08	0.68
1:B:200:LEU:HD22	1:B:254:VAL:HB	1.74	0.68
1:N:39:VAL:HG22	1:N:49:ILE:HG12	1.76	0.68
1:L:69:MET:HE1	1:L:522:THR:HB	1.76	0.68
1:D:518:GLU:HB2	1:E:36:ARG:HB3	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:217:SER:HA	1:N:320:ALA:O	1.94	0.68
1:M:49:ILE:HD11	1:N:73:MET:HE3	1.74	0.68
1:G:345:ARG:O	1:G:349:ILE:HG13	1.94	0.68
1:D:346:VAL:HA	1:D:349:ILE:HD12	1.74	0.68
1:C:509:SER:HB2	1:D:384:ALA:HB3	1.76	0.68
1:A:352:GLN:CB	1:A:365:LEU:HD11	2.22	0.68
1:G:215:LEU:O	1:G:322:ARG:HA	1.94	0.68
1:E:218:PRO:HD2	1:E:320:ALA:O	1.93	0.68
1:C:73:MET:CE	1:D:49:ILE:HD11	2.25	0.67
1:A:204:PHE:CD1	1:A:266:THR:HB	2.29	0.67
1:I:131:LEU:HD12	1:I:422:VAL:HG11	1.76	0.67
1:E:265:ASN:OD1	2:S:27:LEU:HB3	1.94	0.67
2:P:18:GLU:OE1	2:P:30:SER:HA	1.94	0.67
1:F:225:LYS:CD	1:F:309:LEU:HG	2.24	0.67
1:K:421:ARG:O	1:K:425:LYS:HG2	1.93	0.67
1:M:383:ALA:HB3	1:M:389:MET:HB2	1.76	0.67
1:B:77:VAL:HG12	1:B:510:VAL:HG21	1.77	0.67
1:E:77:VAL:HG12	1:E:510:VAL:HG21	1.76	0.67
1:F:266:THR:HA	1:F:271:VAL:O	1.94	0.67
1:N:69:MET:CE	1:N:522:THR:HB	2.24	0.67
1:G:77:VAL:CG1	1:G:510:VAL:HG21	2.25	0.67
1:M:414:GLY:N	1:M:494:LEU:HA	2.10	0.67
1:D:345:ARG:O	1:D:348:GLN:HG3	1.94	0.67
1:B:57:ALA:O	1:B:75:LYS:HE2	1.95	0.67
1:C:207:LYS:HB3	1:C:208:PRO:HD3	1.77	0.67
1:M:450:PRO:O	1:M:454:ILE:HG12	1.95	0.67
1:H:46:ALA:HB1	1:H:47:PRO:HD2	1.77	0.67
1:D:458:CYS:SG	1:D:480:ALA:HB1	2.34	0.67
1:G:221:LEU:HD11	1:G:301:ILE:HD11	1.77	0.67
1:D:322:ARG:HB3	1:D:333:ILE:HD12	1.75	0.67
1:M:197:ARG:HG2	1:M:277:LYS:O	1.94	0.67
1:E:345:ARG:O	1:E:349:ILE:HG13	1.95	0.67
1:H:73:MET:CE	1:N:49:ILE:HD11	2.25	0.67
2:R:12:VAL:HG12	2:R:40:VAL:HA	1.77	0.67
1:F:261:THR:HB	2:T:29:GLY:H	1.58	0.67
1:F:458:CYS:SG	1:F:480:ALA:HB1	2.35	0.66
1:D:265:ASN:OD1	2:R:27:LEU:HB3	1.95	0.66
1:M:326:ASN:OD1	1:M:329:THR:HB	1.93	0.66
1:H:282:GLY:O	1:H:285:ARG:HG2	1.94	0.66
1:K:313:THR:HG22	1:K:314:LEU:H	1.59	0.66
1:D:77:VAL:HG12	1:D:510:VAL:HG21	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:221:LEU:HD11	1:E:301:ILE:HD11	1.77	0.66
1:G:212:ALA:HA	1:G:325:ILE:O	1.94	0.66
1:J:15:LYS:HE2	1:J:64:ASP:OD1	1.96	0.66
1:K:326:ASN:OD1	1:K:329:THR:HB	1.94	0.66
1:I:84:ALA:O	1:I:498:LYS:HE2	1.95	0.66
1:G:34:LYS:HD2	1:G:458:CYS:SG	2.35	0.66
1:J:214:GLU:HG2	1:J:324:VAL:HG12	1.77	0.66
1:A:150:ILE:HG21	1:A:494:LEU:O	1.96	0.66
1:D:218:PRO:HD2	1:D:320:ALA:O	1.96	0.66
1:J:420:ILE:HG13	1:J:451:LEU:HD22	1.76	0.66
1:D:325:ILE:HG12	1:D:330:THR:HG23	1.78	0.66
1:B:261:THR:HB	2:P:29:GLY:H	1.59	0.66
1:B:215:LEU:O	1:B:322:ARG:HA	1.96	0.66
2:T:37:ARG:CG	2:T:37:ARG:HH11	2.09	0.66
1:C:34:LYS:HD2	1:C:458:CYS:SG	2.36	0.66
1:C:305:ILE:HD11	1:D:203:TYR:CE1	2.30	0.66
1:J:326:ASN:OD1	1:J:329:THR:HB	1.95	0.66
1:N:20:VAL:HG23	1:N:74:VAL:HG21	1.78	0.65
1:D:207:LYS:HB3	1:D:208:PRO:HD3	1.77	0.65
1:E:285:ARG:O	1:E:289:LEU:HG	1.95	0.65
1:D:209:GLU:O	1:D:211:GLY:N	2.29	0.65
1:F:204:PHE:CE1	1:F:266:THR:HB	2.32	0.65
1:M:282:GLY:O	1:M:285:ARG:HG2	1.96	0.65
1:C:432:GLN:HG2	1:C:436:GLN:OE1	1.96	0.65
1:J:69:MET:CE	1:J:522:THR:HB	2.26	0.65
1:B:77:VAL:CG1	1:B:510:VAL:HG21	2.25	0.65
1:J:217:SER:N	1:J:218:PRO:HD3	2.11	0.65
1:E:225:LYS:HB3	1:E:303:GLU:OE2	1.97	0.65
1:N:282:GLY:O	1:N:285:ARG:HG2	1.95	0.65
1:J:20:VAL:HG23	1:J:74:VAL:HG21	1.78	0.65
1:H:326:ASN:OD1	1:H:329:THR:HB	1.97	0.65
1:M:313:THR:HG22	1:M:314:LEU:H	1.61	0.65
1:D:345:ARG:O	1:D:349:ILE:HG13	1.97	0.65
1:E:195:PHE:CE1	1:E:197:ARG:HD2	2.32	0.65
1:D:285:ARG:O	1:D:289:LEU:HG	1.97	0.65
1:G:452:ARG:HB2	1:G:462:PRO:HB3	1.79	0.65
1:N:69:MET:O	1:N:73:MET:HG3	1.97	0.65
1:E:34:LYS:HD2	1:E:458:CYS:SG	2.36	0.65
1:N:450:PRO:O	1:N:454:ILE:HG12	1.97	0.65
1:I:69:MET:O	1:I:73:MET:HG3	1.97	0.65
1:K:176:THR:OG1	1:K:378:VAL:HG12	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:239:ALA:HB1	1:J:314:LEU:HD11	1.78	0.65
1:J:161:LEU:HD21	1:J:185:ASP:HB3	1.79	0.65
2:P:20:LYS:HB3	2:P:27:LEU:HG	1.78	0.64
1:K:266:THR:HG22	1:K:273:VAL:H	1.62	0.64
1:I:450:PRO:O	1:I:454:ILE:HG12	1.97	0.64
1:B:346:VAL:HA	1:B:349:ILE:HD12	1.77	0.64
1:E:458:CYS:SG	1:E:480:ALA:HB1	2.37	0.64
1:J:450:PRO:O	1:J:454:ILE:HG12	1.97	0.64
2:U:47:ARG:HD3	2:U:49:LEU:HD12	1.79	0.64
1:E:345:ARG:O	1:E:348:GLN:HG3	1.97	0.64
1:A:77:VAL:CG1	1:A:510:VAL:HG21	2.28	0.64
1:L:69:MET:CE	1:L:522:THR:HB	2.28	0.64
1:J:4:LYS:HD3	1:J:521:VAL:CG1	2.27	0.64
1:J:13:ARG:HB3	1:J:104:LEU:HD11	1.78	0.64
1:J:69:MET:O	1:J:73:MET:HG3	1.97	0.64
1:K:239:ALA:HB1	1:K:314:LEU:HD11	1.79	0.64
1:G:65:LYS:O	1:G:69:MET:HG3	1.97	0.64
1:A:207:LYS:HB3	1:A:208:PRO:HD3	1.80	0.64
1:H:221:LEU:HD12	1:H:249:ILE:HG23	1.80	0.64
1:B:18:ARG:HB3	1:B:18:ARG:HH11	1.63	0.64
1:H:284:ARG:HB2	1:H:284:ARG:NH1	2.13	0.64
1:K:131:LEU:HD12	1:K:422:VAL:HG11	1.80	0.64
1:D:74:VAL:O	1:D:77:VAL:HG13	1.98	0.64
1:C:305:ILE:HG22	1:C:306:GLY:H	1.63	0.64
1:I:414:GLY:N	1:I:494:LEU:HA	2.12	0.64
1:G:352:GLN:HB3	1:G:365:LEU:CD1	2.24	0.64
1:C:262:LEU:HD21	1:C:274:ALA:HA	1.78	0.64
1:G:74:VAL:O	1:G:77:VAL:HG13	1.97	0.64
1:A:69:MET:HG2	1:B:41:ASP:OD1	1.98	0.64
1:E:305:ILE:HG22	1:E:306:GLY:N	2.12	0.63
1:D:34:LYS:HD2	1:D:458:CYS:SG	2.38	0.63
1:H:426:LEU:HD23	1:H:426:LEU:H	1.63	0.63
1:F:118:ARG:HH11	1:F:118:ARG:CG	2.10	0.63
1:L:20:VAL:HG23	1:L:74:VAL:HG21	1.81	0.63
1:K:403:THR:O	1:K:407:VAL:HG23	1.99	0.63
1:C:77:VAL:HG21	1:C:507:ALA:HA	1.80	0.63
2:S:47:ARG:O	2:S:55:LYS:HD2	1.97	0.63
1:M:13:ARG:HB3	1:M:104:LEU:HD11	1.81	0.63
1:A:74:VAL:O	1:A:77:VAL:HG13	1.98	0.63
1:H:69:MET:O	1:H:73:MET:HG3	1.98	0.63
1:J:420:ILE:HD13	1:J:448:GLU:HA	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:383:ALA:HB3	1:K:389:MET:HB2	1.79	0.63
2:P:52:GLY:O	2:P:53:GLU:HB2	1.98	0.63
1:F:368:ARG:O	1:F:372:LEU:HG	1.98	0.63
1:K:437:ASN:O	1:K:441:LYS:HD2	1.97	0.63
1:C:198:GLY:HA3	1:C:327:LYS:O	1.98	0.63
1:N:217:SER:N	1:N:218:PRO:HD3	2.13	0.63
1:M:49:ILE:HD11	1:N:73:MET:CE	2.28	0.63
1:D:452:ARG:HB2	1:D:462:PRO:HB3	1.80	0.63
1:H:239:ALA:HB1	1:H:314:LEU:HD11	1.81	0.63
1:I:161:LEU:HD21	1:I:185:ASP:HB3	1.79	0.63
1:L:131:LEU:HD12	1:L:422:VAL:HG11	1.81	0.63
1:N:58:ARG:HH11	1:N:58:ARG:CB	2.12	0.63
1:A:57:ALA:O	1:A:75:LYS:HE2	1.97	0.63
1:H:421:ARG:O	1:H:425:LYS:HG2	1.99	0.63
1:G:352:GLN:CB	1:G:365:LEU:HD11	2.27	0.63
1:N:313:THR:HG22	1:N:314:LEU:H	1.64	0.63
1:F:77:VAL:CG1	1:F:510:VAL:HG21	2.28	0.63
1:A:65:LYS:O	1:A:69:MET:HG3	1.98	0.62
1:I:228:SER:O	1:I:257:GLU:HB3	1.98	0.62
1:K:414:GLY:N	1:K:494:LEU:HA	2.14	0.62
1:D:252:GLU:HA	1:D:285:ARG:NH1	2.13	0.62
1:B:198:GLY:HA3	1:B:327:LYS:O	1.99	0.62
2:O:43:VAL:HG13	2:O:57:LEU:HD12	1.80	0.62
1:M:239:ALA:HB1	1:M:314:LEU:HD11	1.80	0.62
1:K:46:ALA:HB1	1:K:47:PRO:HD2	1.81	0.62
1:J:414:GLY:N	1:J:494:LEU:HA	2.15	0.62
1:M:69:MET:HE3	1:M:522:THR:HB	1.80	0.62
1:F:346:VAL:O	1:F:349:ILE:HB	1.99	0.62
1:K:420:ILE:HD13	1:K:448:GLU:HA	1.81	0.62
1:E:199:TYR:CZ	1:E:202:PRO:HA	2.34	0.62
2:S:14:ARG:CD	2:S:34:LYS:HE2	2.29	0.62
2:O:47:ARG:HB3	2:O:55:LYS:CD	2.28	0.62
1:B:74:VAL:O	1:B:77:VAL:HG13	1.99	0.62
1:N:437:ASN:O	1:N:441:LYS:HD2	2.00	0.62
1:B:207:LYS:HB3	1:B:208:PRO:HD3	1.82	0.62
2:P:43:VAL:HG13	2:P:57:LEU:HD12	1.82	0.62
1:E:452:ARG:HB2	1:E:462:PRO:HB3	1.80	0.62
1:N:42:LYS:HE2	1:N:48:THR:OG1	2.00	0.62
1:L:217:SER:N	1:L:218:PRO:HD3	2.15	0.62
1:B:352:GLN:OE1	1:B:365:LEU:HD11	2.00	0.62
1:J:32:GLY:HA2	1:J:454:ILE:HD12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:261:THR:HB	2:R:29:GLY:H	1.64	0.62
1:L:13:ARG:HB3	1:L:104:LEU:HD11	1.81	0.62
1:A:452:ARG:HB2	1:A:462:PRO:HB3	1.81	0.62
1:D:102:GLU:CB	1:D:442:VAL:HG13	2.30	0.62
1:E:18:ARG:HH11	1:E:18:ARG:HG2	1.64	0.62
1:H:217:SER:N	1:H:218:PRO:HD3	2.15	0.62
1:G:206:ASN:HB3	1:G:214:GLU:H	1.64	0.62
1:E:227:ILE:O	1:E:255:GLU:HG2	1.99	0.62
2:P:20:LYS:CB	2:P:27:LEU:HG	2.29	0.62
1:K:459:GLY:HA3	1:L:112:ASN:HD21	1.65	0.62
1:A:346:VAL:HA	1:A:349:ILE:HD12	1.81	0.61
1:F:204:PHE:CD1	1:F:266:THR:HB	2.35	0.61
1:B:458:CYS:SG	1:B:480:ALA:HB1	2.40	0.61
1:J:30:THR:HB	1:J:51:LYS:O	2.00	0.61
1:M:19:GLY:HA3	1:M:67:GLU:O	2.00	0.61
1:I:266:THR:HG22	1:I:273:VAL:H	1.65	0.61
1:C:65:LYS:O	1:C:69:MET:HG3	2.00	0.61
1:C:266:THR:HG22	1:C:273:VAL:H	1.65	0.61
1:N:84:ALA:O	1:N:498:LYS:HE2	2.00	0.61
1:A:206:ASN:HB3	1:A:214:GLU:H	1.66	0.61
1:E:77:VAL:CG1	1:E:510:VAL:HG21	2.30	0.61
1:K:102:GLU:HB2	1:K:442:VAL:HG13	1.82	0.61
1:B:218:PRO:HD2	1:B:320:ALA:O	1.99	0.61
1:B:65:LYS:O	1:B:69:MET:HG3	2.01	0.61
1:I:179:ASP:HA	1:I:389:MET:HE3	1.82	0.61
1:E:352:GLN:CB	1:E:365:LEU:HD11	2.21	0.61
1:C:57:ALA:O	1:C:75:LYS:HE2	2.00	0.61
1:E:279:PRO:HD2	1:E:285:ARG:HB2	1.81	0.61
2:O:47:ARG:HB3	2:O:55:LYS:HD3	1.82	0.61
1:C:305:ILE:HG22	1:C:306:GLY:N	2.16	0.61
2:Q:12:VAL:HG12	2:Q:40:VAL:HA	1.81	0.61
1:A:31:LEU:HD23	1:A:453:GLN:HB3	1.81	0.61
1:F:206:ASN:HB3	1:F:214:GLU:H	1.65	0.61
1:G:326:ASN:OD1	1:G:329:THR:HB	2.01	0.61
1:F:74:VAL:O	1:F:77:VAL:HG13	1.99	0.61
1:H:69:MET:HE3	1:H:522:THR:HB	1.82	0.61
1:D:57:ALA:O	1:D:75:LYS:HE2	2.00	0.61
1:G:193:MET:SD	1:G:371:LYS:HG2	2.41	0.61
1:E:212:ALA:HA	1:E:325:ILE:O	2.01	0.61
1:C:204:PHE:CE2	1:C:213:VAL:HG21	2.36	0.61
1:G:262:LEU:HD11	1:G:273:VAL:HB	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:197:ARG:HE	1:M:277:LYS:HZ3	1.49	0.61
1:G:458:CYS:SG	1:G:480:ALA:HB1	2.41	0.61
1:A:368:ARG:O	1:A:372:LEU:HG	2.01	0.61
1:G:232:GLU:HB3	1:G:310:GLU:OE2	2.01	0.61
1:N:262:LEU:O	1:N:266:THR:HG23	2.01	0.61
1:M:69:MET:O	1:M:73:MET:HG3	2.01	0.60
1:E:18:ARG:CG	1:E:18:ARG:HH11	2.14	0.60
1:G:218:PRO:HD2	1:G:320:ALA:O	2.01	0.60
1:I:313:THR:HG22	1:I:314:LEU:H	1.66	0.60
1:C:452:ARG:HB2	1:C:462:PRO:HB3	1.83	0.60
1:D:198:GLY:HA3	1:D:327:LYS:O	2.01	0.60
1:H:266:THR:HG22	1:H:273:VAL:H	1.67	0.60
1:K:262:LEU:O	1:K:266:THR:HG23	2.00	0.60
1:J:267:MET:O	1:J:268:ARG:HG3	2.01	0.60
1:M:12:ALA:HB1	1:M:520:MET:HG3	1.83	0.60
1:C:225:LYS:HB3	1:C:225:LYS:NZ	2.16	0.60
1:F:42:LYS:HE2	1:F:48:THR:OG1	2.01	0.60
1:C:302:SER:HB2	1:C:305:ILE:HD12	1.84	0.60
1:I:49:ILE:HD11	1:J:73:MET:CE	2.31	0.60
1:D:368:ARG:O	1:D:372:LEU:HG	2.01	0.60
1:F:345:ARG:O	1:F:348:GLN:HG3	2.01	0.60
1:E:74:VAL:O	1:E:77:VAL:HG13	2.02	0.60
1:L:265:ASN:O	1:L:269:GLY:HA3	2.00	0.60
1:C:353:ILE:HG12	1:C:366:GLN:NE2	2.16	0.60
1:A:266:THR:HA	1:A:271:VAL:O	2.01	0.60
1:A:204:PHE:CE1	1:A:266:THR:HB	2.35	0.60
1:B:285:ARG:O	1:B:289:LEU:HG	2.01	0.60
1:B:345:ARG:O	1:B:348:GLN:HG3	2.01	0.60
1:H:130:GLU:HG3	1:H:426:LEU:HD22	1.82	0.60
1:L:197:ARG:HG2	1:L:277:LYS:O	2.01	0.60
1:M:130:GLU:HG3	1:M:426:LEU:CD2	2.32	0.60
1:F:252:GLU:HA	1:F:285:ARG:NH1	2.17	0.60
1:H:437:ASN:O	1:H:441:LYS:HD2	2.01	0.60
1:D:238:GLU:OE1	2:R:26:VAL:HG22	2.01	0.60
1:N:138:CYS:SG	1:N:144:ILE:HD13	2.42	0.60
1:C:31:LEU:HD23	1:C:453:GLN:HB3	1.82	0.60
1:N:174:VAL:HG21	1:N:194:GLN:HB3	1.82	0.60
1:H:32:GLY:HA2	1:H:454:ILE:HD12	1.84	0.60
1:H:271:VAL:HG12	1:H:273:VAL:HG13	1.84	0.60
1:A:18:ARG:HB3	1:A:18:ARG:HH11	1.66	0.60
1:N:176:THR:OG1	1:N:378:VAL:HG12	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:221:LEU:HD12	1:K:249:ILE:HG23	1.84	0.60
1:E:31:LEU:CD1	4:E:1526:ADP:H5'1	2.31	0.60
1:C:204:PHE:CZ	1:C:274:ALA:HB3	2.37	0.59
1:H:414:GLY:N	1:H:494:LEU:HA	2.17	0.59
1:L:77:VAL:HG22	1:L:506:TYR:HB3	1.83	0.59
1:H:197:ARG:HG2	1:H:277:LYS:O	2.00	0.59
1:L:214:GLU:HG2	1:L:324:VAL:HG12	1.84	0.59
1:H:49:ILE:HD11	1:I:73:MET:HE3	1.83	0.59
1:K:30:THR:HG22	1:K:36:ARG:O	2.02	0.59
1:J:169:VAL:HG13	1:J:173:GLY:HA3	1.84	0.59
1:L:232:GLU:HB3	1:L:309:LEU:HB2	1.83	0.59
1:F:215:LEU:O	1:F:322:ARG:HG3	2.02	0.59
1:L:266:THR:HG22	1:L:273:VAL:H	1.67	0.59
1:K:49:ILE:HD11	1:L:73:MET:CE	2.32	0.59
1:J:219:PHE:HB3	1:J:317:LEU:HD23	1.83	0.59
1:N:420:ILE:HD13	1:N:448:GLU:HA	1.85	0.59
1:J:69:MET:HE3	1:J:522:THR:HB	1.84	0.59
1:N:197:ARG:HG2	1:N:277:LYS:O	2.03	0.59
1:J:266:THR:HG22	1:J:273:VAL:H	1.66	0.59
1:F:358:SER:O	1:F:362:ARG:HG2	2.01	0.59
1:H:230:ILE:HD11	1:H:257:GLU:O	2.01	0.59
2:O:20:LYS:HB3	2:O:27:LEU:HG	1.84	0.59
1:N:166:MET:HE2	1:N:171:LYS:HA	1.85	0.59
1:A:218:PRO:HD2	1:A:320:ALA:O	2.02	0.59
1:H:224:ASP:OD2	1:H:286:LYS:HE2	2.02	0.59
1:H:102:GLU:HB2	1:H:442:VAL:HG13	1.83	0.59
1:I:77:VAL:HG22	1:I:506:TYR:HB3	1.82	0.59
1:N:414:GLY:N	1:N:494:LEU:HA	2.18	0.59
1:M:165:ALA:HB1	1:M:175:ILE:HD12	1.85	0.59
1:E:183:LEU:CD2	1:E:384:ALA:HA	2.33	0.59
2:R:43:VAL:HG13	2:R:57:LEU:HD12	1.85	0.59
1:A:432:GLN:HE21	1:A:436:GLN:HE22	1.50	0.59
1:C:352:GLN:HB3	1:C:365:LEU:CD1	2.20	0.59
1:N:266:THR:HG22	1:N:273:VAL:H	1.67	0.59
1:G:284:ARG:HG2	1:G:288:MET:HE2	1.85	0.59
1:F:207:LYS:HB3	1:F:208:PRO:HD3	1.84	0.59
1:C:438:VAL:O	1:C:442:VAL:HG23	2.03	0.59
1:J:49:ILE:HD11	1:K:73:MET:CE	2.32	0.59
1:E:31:LEU:HD12	4:E:1526:ADP:H5'1	1.83	0.59
1:K:217:SER:N	1:K:218:PRO:HD3	2.18	0.59
1:E:195:PHE:O	1:E:329:THR:HG23	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:77:VAL:HG22	1:H:506:TYR:HB3	1.84	0.59
1:C:239:ALA:HB1	1:C:314:LEU:HD23	1.84	0.59
1:E:122:LYS:HE2	1:E:429:LEU:HD11	1.85	0.59
1:H:84:ALA:O	1:H:498:LYS:HE2	2.03	0.58
1:C:345:ARG:O	1:C:348:GLN:HG2	2.03	0.58
1:L:217:SER:HA	1:L:320:ALA:O	2.02	0.58
1:G:239:ALA:HB1	1:G:314:LEU:HD23	1.85	0.58
1:I:197:ARG:HG2	1:I:277:LYS:O	2.03	0.58
1:E:207:LYS:HB3	1:E:208:PRO:HD3	1.85	0.58
1:F:31:LEU:HD23	1:F:453:GLN:HB3	1.85	0.58
1:C:73:MET:HE3	1:D:49:ILE:HD11	1.84	0.58
1:G:213:VAL:HB	1:G:325:ILE:HB	1.84	0.58
1:L:414:GLY:H	1:L:494:LEU:HA	1.68	0.58
1:B:288:MET:HA	1:B:291:ASP:OD1	2.04	0.58
1:B:199:TYR:CZ	1:B:202:PRO:HA	2.38	0.58
1:H:313:THR:HG22	1:H:314:LEU:H	1.68	0.58
1:D:102:GLU:HB3	1:D:442:VAL:HG13	1.86	0.58
1:M:62:LEU:HD13	1:M:67:GLU:HG2	1.84	0.58
1:A:30:THR:HG22	1:A:36:ARG:O	2.03	0.58
1:H:265:ASN:O	1:H:269:GLY:HA3	2.02	0.58
1:A:346:VAL:O	1:A:349:ILE:HB	2.04	0.58
1:D:278:ALA:HB1	1:D:279:PRO:HD2	1.84	0.58
1:C:265:ASN:OD1	2:Q:27:LEU:HB3	2.02	0.58
1:C:231:ARG:HB2	1:C:257:GLU:OE1	2.04	0.58
1:H:161:LEU:HD21	1:H:185:ASP:HB3	1.85	0.58
1:F:34:LYS:HD2	1:F:458:CYS:SG	2.44	0.58
1:J:403:THR:O	1:J:407:VAL:HG23	2.04	0.58
2:T:37:ARG:HG2	2:T:37:ARG:HH11	1.68	0.58
1:H:130:GLU:HG3	1:H:426:LEU:CD2	2.34	0.58
1:A:419:LEU:HD11	1:A:500:THR:HG23	1.85	0.58
1:N:287:ALA:HB1	1:N:368:ARG:CZ	2.33	0.58
1:E:80:LYS:HD2	1:E:506:TYR:CE1	2.39	0.58
1:I:265:ASN:O	1:I:269:GLY:HA3	2.03	0.58
1:A:113:PRO:HB3	1:A:516:THR:HA	1.86	0.58
1:C:345:ARG:O	1:C:349:ILE:HG13	2.03	0.58
1:L:145:ALA:O	1:L:149:THR:HG23	2.03	0.58
1:I:217:SER:N	1:I:218:PRO:HD3	2.19	0.58
1:H:215:LEU:HB3	1:H:218:PRO:HG3	1.86	0.58
1:B:518:GLU:HB2	1:C:36:ARG:CB	2.33	0.58
1:C:518:GLU:HB2	1:D:36:ARG:CB	2.34	0.58
1:I:229:ASN:HD21	1:I:231:ARG:HH12	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:122:LYS:HE3	1:K:429:LEU:HD11	1.86	0.58
1:D:197:ARG:HH22	1:D:250:ILE:HG23	1.68	0.57
2:Q:47:ARG:HB3	2:Q:55:LYS:CG	2.33	0.57
1:L:420:ILE:HD13	1:L:448:GLU:HA	1.86	0.57
1:G:77:VAL:HG12	1:G:510:VAL:HG21	1.86	0.57
1:H:219:PHE:HB3	1:H:317:LEU:HD23	1.86	0.57
1:F:452:ARG:HB2	1:F:462:PRO:HB3	1.86	0.57
1:M:265:ASN:O	1:M:269:GLY:HA3	2.04	0.57
1:E:197:ARG:HH12	1:E:250:ILE:HG12	1.69	0.57
1:C:213:VAL:HB	1:C:325:ILE:HB	1.86	0.57
1:I:420:ILE:HD13	1:I:448:GLU:HA	1.87	0.57
1:K:49:ILE:HD11	1:L:73:MET:HE3	1.86	0.57
1:E:438:VAL:O	1:E:442:VAL:HG23	2.04	0.57
1:I:403:THR:O	1:I:407:VAL:HG23	2.04	0.57
1:H:348:GLN:O	1:H:352:GLN:HG3	2.04	0.57
1:J:228:SER:O	1:J:257:GLU:HB3	2.04	0.57
1:L:313:THR:HG22	1:L:314:LEU:H	1.69	0.57
1:L:69:MET:O	1:L:73:MET:HG3	2.04	0.57
1:D:214:GLU:HB3	1:D:322:ARG:HD2	1.85	0.57
1:C:150:ILE:HG21	1:C:494:LEU:O	2.04	0.57
1:A:36:ARG:HB3	1:G:518:GLU:HB2	1.85	0.57
1:G:57:ALA:O	1:G:75:LYS:HE2	2.04	0.57
1:G:417:VAL:HA	1:G:420:ILE:HG22	1.85	0.57
1:G:147:VAL:HG23	1:G:403:THR:HG22	1.87	0.57
1:K:197:ARG:HG2	1:K:277:LYS:O	2.04	0.57
1:D:438:VAL:O	1:D:442:VAL:HG23	2.05	0.57
1:D:225:LYS:HB3	1:D:303:GLU:OE2	2.05	0.57
1:K:199:TYR:CE1	1:K:202:PRO:HA	2.39	0.57
1:J:230:ILE:H	1:J:230:ILE:HD13	1.68	0.57
1:G:150:ILE:HG21	1:G:494:LEU:O	2.03	0.57
1:C:4:LYS:HG3	1:D:59:GLU:O	2.04	0.57
1:D:305:ILE:HD11	1:E:203:TYR:CD1	2.38	0.57
1:F:150:ILE:HG21	1:F:494:LEU:O	2.04	0.57
1:B:345:ARG:O	1:B:349:ILE:HG13	2.04	0.57
1:L:421:ARG:O	1:L:425:LYS:HG2	2.05	0.57
1:F:178:GLU:O	1:F:380:LYS:HA	2.05	0.57
2:R:47:ARG:HD3	2:R:49:LEU:HD12	1.87	0.57
1:A:285:ARG:O	1:A:289:LEU:HG	2.04	0.57
1:D:199:TYR:HA	1:D:276:VAL:HG12	1.87	0.57
1:B:349:ILE:O	1:B:352:GLN:HB2	2.04	0.57
1:H:73:MET:HE3	1:N:49:ILE:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:313:THR:HG22	1:L:314:LEU:N	2.20	0.56
1:A:31:LEU:HD12	4:A:1526:ADP:H5'1	1.87	0.56
1:M:223:ALA:HB3	1:M:251:ALA:HB2	1.87	0.56
1:D:417:VAL:HA	1:D:420:ILE:HG22	1.87	0.56
2:S:43:VAL:HG13	2:S:57:LEU:HD12	1.86	0.56
1:E:518:GLU:HB2	1:F:36:ARG:CB	2.34	0.56
1:A:215:LEU:O	1:A:322:ARG:HA	2.04	0.56
1:F:266:THR:HG22	1:F:273:VAL:H	1.70	0.56
1:I:271:VAL:HG12	1:I:273:VAL:HG13	1.87	0.56
1:F:285:ARG:O	1:F:289:LEU:HG	2.05	0.56
1:J:221:LEU:HD12	1:J:249:ILE:HG23	1.86	0.56
1:E:57:ALA:O	1:E:75:LYS:HE2	2.05	0.56
1:C:262:LEU:O	1:C:266:THR:HG23	2.05	0.56
1:H:420:ILE:HD13	1:H:448:GLU:HA	1.86	0.56
1:B:213:VAL:HB	1:B:325:ILE:HB	1.88	0.56
1:A:510:VAL:HG13	1:B:385:THR:HG21	1.86	0.56
1:C:458:CYS:SG	1:C:480:ALA:HB1	2.45	0.56
1:I:31:LEU:HG	1:I:454:ILE:HD11	1.87	0.56
1:D:40:LEU:HD13	1:D:59:GLU:HG3	1.88	0.56
1:A:252:GLU:HG3	1:A:285:ARG:HH11	1.70	0.56
1:C:368:ARG:O	1:C:372:LEU:HG	2.06	0.56
1:H:166:MET:HE2	1:H:171:LYS:HA	1.86	0.56
1:M:30:THR:HB	1:M:51:LYS:O	2.03	0.56
1:C:249:ILE:HB	1:C:275:ALA:HB2	1.87	0.56
1:L:102:GLU:HB2	1:L:442:VAL:HG13	1.87	0.56
1:F:509:SER:HB2	1:G:384:ALA:HB3	1.87	0.56
1:F:449:ALA:HA	1:F:452:ARG:HG2	1.86	0.56
1:L:178:GLU:OE2	1:L:322:ARG:HD3	2.05	0.56
1:G:449:ALA:HA	1:G:452:ARG:HG2	1.87	0.56
1:G:225:LYS:HB2	1:G:303:GLU:OE1	2.04	0.56
1:D:65:LYS:HB3	1:D:522:THR:OG1	2.04	0.56
1:F:231:ARG:O	1:F:233:MET:HG2	2.05	0.56
1:H:27:VAL:HG11	1:H:93:THR:HG21	1.88	0.56
1:J:145:ALA:O	1:J:149:THR:HG23	2.05	0.56
1:M:420:ILE:HD13	1:M:448:GLU:HA	1.87	0.56
1:G:204:PHE:CD1	1:G:266:THR:HB	2.41	0.56
1:D:183:LEU:HD22	1:D:384:ALA:HA	1.88	0.56
1:G:14:VAL:O	1:G:18:ARG:HG2	2.06	0.56
1:G:102:GLU:CB	1:G:442:VAL:HG13	2.35	0.56
1:F:57:ALA:O	1:F:75:LYS:HE2	2.05	0.56
1:A:73:MET:SD	1:B:49:ILE:HD11	2.45	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:204:PHE:CE1	1:C:213:VAL:HG11	2.40	0.56
1:E:261:THR:HG22	2:S:29:GLY:N	2.20	0.56
1:B:368:ARG:O	1:B:372:LEU:HG	2.05	0.56
1:D:449:ALA:HA	1:D:452:ARG:HG2	1.88	0.56
1:M:262:LEU:O	1:M:266:THR:HG23	2.06	0.56
1:D:213:VAL:HB	1:D:325:ILE:HB	1.87	0.56
1:N:313:THR:HG22	1:N:314:LEU:N	2.20	0.56
2:R:47:ARG:HB3	2:R:55:LYS:CG	2.36	0.56
1:E:325:ILE:HG12	1:E:330:THR:HG23	1.87	0.56
1:I:49:ILE:HD11	1:J:73:MET:HE2	1.88	0.56
1:I:214:GLU:HG2	1:I:324:VAL:HG12	1.88	0.56
1:A:203:TYR:CZ	1:G:305:ILE:HD11	2.41	0.56
2:P:18:GLU:OE2	2:P:33:ALA:HB3	2.06	0.56
1:I:414:GLY:H	1:I:494:LEU:HA	1.71	0.56
1:M:104:LEU:O	1:M:107:VAL:HG22	2.06	0.56
1:C:225:LYS:HE3	1:C:309:LEU:HG	1.88	0.56
1:K:145:ALA:O	1:K:149:THR:HG23	2.06	0.56
1:M:199:TYR:CE1	1:M:202:PRO:HA	2.41	0.56
2:U:43:VAL:HG13	2:U:57:LEU:HD12	1.87	0.56
1:A:247:LEU:HB2	1:A:273:VAL:HG22	1.88	0.55
1:F:215:LEU:O	1:F:322:ARG:HA	2.06	0.55
1:M:49:ILE:HG21	1:N:513:LEU:HD11	1.88	0.55
1:K:421:ARG:HD2	1:K:474:GLY:O	2.07	0.55
2:S:57:LEU:HD22	2:S:88:GLU:HB2	1.88	0.55
1:H:112:ASN:HD21	1:N:459:GLY:HA3	1.71	0.55
1:C:261:THR:HB	2:Q:29:GLY:H	1.70	0.55
2:S:12:VAL:HG12	2:S:40:VAL:HA	1.87	0.55
1:M:176:THR:OG1	1:M:378:VAL:HG12	2.06	0.55
1:K:230:ILE:CD1	1:K:261:THR:HG21	2.37	0.55
1:G:183:LEU:CD2	1:G:384:ALA:HA	2.33	0.55
1:J:230:ILE:N	1:J:230:ILE:CD1	2.69	0.55
1:F:284:ARG:HG2	1:F:288:MET:HE2	1.87	0.55
1:I:239:ALA:HB1	1:I:314:LEU:HD11	1.87	0.55
1:I:106:ALA:O	1:I:111:MET:HB2	2.06	0.55
1:F:24:ALA:O	1:F:28:LYS:HG3	2.05	0.55
1:H:19:GLY:HA3	1:H:67:GLU:O	2.06	0.55
1:H:176:THR:OG1	1:H:378:VAL:HG12	2.06	0.55
1:F:102:GLU:CB	1:F:442:VAL:HG13	2.36	0.55
1:A:199:TYR:CZ	1:A:202:PRO:HA	2.41	0.55
1:E:449:ALA:HA	1:E:452:ARG:HG2	1.88	0.55
1:L:104:LEU:O	1:L:107:VAL:HG22	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:271:VAL:HG12	1:J:273:VAL:HG13	1.88	0.55
1:I:217:SER:HA	1:I:320:ALA:O	2.05	0.55
1:M:266:THR:HG22	1:M:273:VAL:H	1.70	0.55
1:I:282:GLY:O	1:I:285:ARG:HG2	2.06	0.55
1:B:302:SER:HB2	1:B:305:ILE:HB	1.88	0.55
1:B:150:ILE:HG21	1:B:494:LEU:O	2.06	0.55
2:Q:6:LEU:HD13	2:Q:7:HIS:CD2	2.40	0.55
1:N:111:MET:HG2	1:N:435:ASP:OD1	2.07	0.55
1:I:421:ARG:HA	1:I:421:ARG:NE	2.20	0.55
1:L:403:THR:O	1:L:407:VAL:HG23	2.07	0.55
1:H:138:CYS:SG	1:H:144:ILE:HD13	2.46	0.55
1:A:102:GLU:CB	1:A:442:VAL:HG13	2.36	0.55
1:L:84:ALA:O	1:L:498:LYS:HE2	2.05	0.55
1:B:353:ILE:HG12	1:B:366:GLN:NE2	2.22	0.55
1:K:39:VAL:HG22	1:K:49:ILE:HG12	1.89	0.55
1:N:215:LEU:HB3	1:N:218:PRO:HG3	1.89	0.55
1:F:115:ASP:HA	1:F:118:ARG:NH1	2.22	0.55
1:A:239:ALA:HB1	1:A:314:LEU:HD23	1.88	0.55
1:A:302:SER:OG	1:A:305:ILE:HB	2.06	0.55
1:C:308:GLU:HB2	1:C:311:LYS:HB2	1.87	0.55
1:M:475:ASN:HB2	1:M:487:ASN:HD21	1.71	0.55
1:M:447:MET:O	1:M:450:PRO:HD2	2.06	0.55
1:C:18:ARG:HH11	1:C:18:ARG:HB3	1.72	0.55
1:N:77:VAL:HG21	1:N:510:VAL:HB	1.89	0.55
1:G:124:VAL:HG13	1:G:504:LEU:CD1	2.37	0.55
1:N:421:ARG:O	1:N:425:LYS:HG2	2.07	0.55
1:E:417:VAL:HA	1:E:420:ILE:HG22	1.89	0.55
1:D:211:GLY:O	1:D:326:ASN:HA	2.06	0.55
1:M:107:VAL:HG11	1:M:515:ILE:HG23	1.88	0.55
2:Q:6:LEU:HD13	2:Q:7:HIS:NE2	2.21	0.55
1:F:21:ASN:HD22	1:F:97:GLN:HE22	1.55	0.55
1:B:102:GLU:HB2	1:B:442:VAL:HG13	1.89	0.55
1:A:263:VAL:O	1:A:267:MET:HG2	2.07	0.55
1:I:130:GLU:HG3	1:I:426:LEU:CD2	2.36	0.55
1:J:420:ILE:CD1	1:J:448:GLU:HA	2.37	0.55
1:D:305:ILE:HD11	1:E:203:TYR:CE1	2.42	0.55
1:A:438:VAL:O	1:A:442:VAL:HG23	2.07	0.55
1:M:214:GLU:HG2	1:M:324:VAL:HG12	1.88	0.55
1:G:231:ARG:HB3	1:G:257:GLU:OE1	2.06	0.55
1:C:193:MET:SD	1:C:371:LYS:HB3	2.47	0.55
1:L:140:ASP:O	1:L:144:ILE:HG12	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:GLU:HA	1:A:285:ARG:NH1	2.22	0.55
1:C:249:ILE:HB	1:C:275:ALA:CB	2.36	0.55
2:T:78:ILE:HG22	2:T:79:ASP:OD1	2.06	0.55
1:A:225:LYS:O	1:A:251:ALA:HB1	2.07	0.55
1:I:145:ALA:O	1:I:149:THR:HG23	2.07	0.55
1:K:84:ALA:O	1:K:498:LYS:HE2	2.06	0.55
1:F:227:ILE:O	1:F:255:GLU:HG2	2.07	0.55
1:B:200:LEU:O	1:B:202:PRO:HD3	2.07	0.55
1:K:49:ILE:HG21	1:L:513:LEU:HD11	1.88	0.55
1:N:166:MET:CE	1:N:407:VAL:HG21	2.37	0.55
1:N:214:GLU:HG2	1:N:324:VAL:HG12	1.88	0.55
2:P:6:LEU:HD12	2:P:7:HIS:CD2	2.41	0.55
1:A:183:LEU:CD2	1:A:384:ALA:HA	2.37	0.55
1:L:225:LYS:HD3	1:L:303:GLU:CG	2.37	0.55
2:O:20:LYS:CB	2:O:27:LEU:HG	2.37	0.54
1:F:225:LYS:HD3	1:F:309:LEU:HG	1.88	0.54
1:F:207:LYS:CB	1:F:208:PRO:HD3	2.37	0.54
1:F:165:ALA:O	1:F:169:VAL:HG22	2.08	0.54
1:D:487:ASN:O	1:D:491:MET:HG2	2.07	0.54
1:J:131:LEU:HD12	1:J:422:VAL:HG11	1.89	0.54
1:K:130:GLU:HG3	1:K:426:LEU:HD22	1.89	0.54
1:E:213:VAL:HB	1:E:325:ILE:HB	1.88	0.54
1:B:438:VAL:O	1:B:442:VAL:HG23	2.07	0.54
1:I:466:ALA:O	1:I:470:LYS:HG2	2.06	0.54
1:H:128:VAL:HG12	1:H:132:LYS:HE2	1.90	0.54
1:D:113:PRO:HB2	1:D:516:THR:HG22	1.88	0.54
1:M:400:LEU:HD21	1:M:404:ARG:HE	1.72	0.54
1:C:73:MET:HE1	1:D:49:ILE:HD11	1.88	0.54
1:M:69:MET:CE	1:M:522:THR:HB	2.37	0.54
2:P:20:LYS:HG3	2:P:28:THR:O	2.07	0.54
1:M:39:VAL:HG22	1:M:49:ILE:HG12	1.89	0.54
1:H:217:SER:HA	1:H:320:ALA:O	2.06	0.54
2:P:76:GLU:O	2:P:83:VAL:HG22	2.07	0.54
1:A:385:THR:HG22	1:G:76:GLU:OE2	2.07	0.54
1:D:199:TYR:CZ	1:D:202:PRO:HA	2.42	0.54
1:B:518:GLU:HB2	1:C:36:ARG:HB2	1.89	0.54
1:C:291:ASP:HB2	1:C:372:LEU:HD21	1.89	0.54
1:A:351:GLN:HG2	1:B:210:THR:OG1	2.08	0.54
1:D:296:THR:HG22	1:D:335:GLY:HA3	1.89	0.54
1:N:351:GLN:O	1:N:354:GLU:HG2	2.07	0.54
1:A:383:ALA:HB3	1:A:389:MET:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:212:ALA:HA	1:C:325:ILE:O	2.08	0.54
1:C:229:ASN:HA	1:C:257:GLU:OE2	2.07	0.54
1:F:147:VAL:HG12	1:F:494:LEU:HB2	1.90	0.54
1:B:31:LEU:HD12	4:B:1526:ADP:H5'1	1.90	0.54
1:B:31:LEU:HD22	1:B:94:VAL:HG21	1.88	0.54
1:A:388:GLU:HA	1:G:513:LEU:CD1	2.37	0.54
1:J:57:ALA:O	1:J:75:LYS:HE3	2.07	0.54
1:D:197:ARG:HH22	1:D:250:ILE:HG12	1.73	0.54
1:G:325:ILE:HG12	1:G:330:THR:HG23	1.90	0.54
1:K:140:ASP:O	1:K:144:ILE:HG12	2.08	0.54
1:A:352:GLN:HB3	1:A:365:LEU:CD1	2.26	0.54
1:G:200:LEU:O	1:G:202:PRO:HD3	2.08	0.54
1:G:199:TYR:HB3	1:G:325:ILE:HG21	1.90	0.54
1:I:32:GLY:HA2	1:I:454:ILE:HD12	1.89	0.54
1:F:438:VAL:O	1:F:442:VAL:HG23	2.08	0.54
1:A:40:LEU:HD13	1:A:59:GLU:HG3	1.89	0.54
1:A:365:LEU:HD22	1:A:366:GLN:HE22	1.73	0.54
1:J:100:ILE:CD1	1:J:511:ALA:HA	2.37	0.54
1:L:262:LEU:O	1:L:266:THR:HG23	2.08	0.54
1:D:214:GLU:HA	1:D:323:VAL:O	2.07	0.54
1:J:262:LEU:O	1:J:266:THR:HG23	2.08	0.54
1:B:305:ILE:HG22	1:B:306:GLY:H	1.72	0.54
1:L:458:CYS:SG	1:L:480:ALA:HB1	2.47	0.54
1:F:15:LYS:O	1:F:67:GLU:HG2	2.06	0.54
1:E:339:GLU:O	1:E:343:GLN:HG2	2.08	0.54
1:A:247:LEU:HB3	1:A:273:VAL:HG13	1.90	0.54
2:P:20:LYS:HG2	2:P:27:LEU:HG	1.90	0.54
1:K:58:ARG:HH11	1:K:58:ARG:HB2	1.72	0.54
2:S:66:ILE:HB	2:S:93:ALA:HB3	1.90	0.54
2:O:78:ILE:HD12	2:O:83:VAL:HG21	1.90	0.54
1:N:432:GLN:NE2	1:N:436:GLN:HE22	2.06	0.54
1:D:352:GLN:HB3	1:D:365:LEU:CD1	2.35	0.54
1:L:39:VAL:HG22	1:L:49:ILE:HG12	1.88	0.54
1:H:49:ILE:HD11	1:I:73:MET:CE	2.38	0.54
1:K:447:MET:O	1:K:450:PRO:HD2	2.08	0.54
1:A:203:TYR:CE1	1:G:305:ILE:HD11	2.42	0.54
2:T:6:LEU:HD13	2:T:7:HIS:NE2	2.23	0.54
1:F:518:GLU:HB2	1:G:36:ARG:CB	2.37	0.54
1:C:218:PRO:HD2	1:C:320:ALA:O	2.08	0.54
1:J:84:ALA:O	1:J:498:LYS:HE2	2.07	0.54
1:G:195:PHE:O	1:G:329:THR:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:31:LEU:HG	1:H:454:ILE:HD11	1.91	0.53
1:H:69:MET:CE	1:N:41:ASP:HB2	2.38	0.53
1:N:447:MET:O	1:N:450:PRO:HD2	2.07	0.53
1:L:287:ALA:HB1	1:L:368:ARG:CZ	2.38	0.53
1:G:198:GLY:HA3	1:G:327:LYS:O	2.08	0.53
1:B:204:PHE:CD2	1:B:274:ALA:HB2	2.43	0.53
1:N:102:GLU:HB2	1:N:442:VAL:HG13	1.90	0.53
1:D:247:LEU:HD21	1:D:317:LEU:HD13	1.89	0.53
1:E:278:ALA:HB1	1:E:279:PRO:HD2	1.90	0.53
1:G:266:THR:HG22	1:G:273:VAL:H	1.72	0.53
1:J:494:LEU:HD23	1:J:494:LEU:N	2.22	0.53
1:E:14:VAL:O	1:E:18:ARG:HG3	2.08	0.53
1:C:449:ALA:HA	1:C:452:ARG:HG2	1.90	0.53
1:D:65:LYS:O	1:D:69:MET:HG3	2.08	0.53
2:P:7:HIS:HB2	2:P:46:GLY:O	2.09	0.53
1:K:20:VAL:HG23	1:K:74:VAL:HG21	1.90	0.53
1:F:326:ASN:OD1	1:F:329:THR:HB	2.08	0.53
1:J:77:VAL:HG22	1:J:506:TYR:HB3	1.89	0.53
1:K:69:MET:O	1:K:73:MET:HG3	2.07	0.53
1:J:30:THR:HG22	1:J:36:ARG:O	2.09	0.53
1:G:288:MET:HA	1:G:291:ASP:OD1	2.09	0.53
1:K:466:ALA:O	1:K:470:LYS:HG2	2.09	0.53
1:E:204:PHE:CD2	1:E:274:ALA:HB2	2.43	0.53
1:K:57:ALA:O	1:K:75:LYS:HE3	2.08	0.53
1:I:160:LYS:O	1:I:164:GLU:HG3	2.07	0.53
1:N:66:PHE:CZ	1:N:522:THR:HG22	2.42	0.53
1:F:453:GLN:NE2	1:F:456:LEU:HD23	2.22	0.53
1:D:165:ALA:O	1:D:169:VAL:HG22	2.08	0.53
1:C:215:LEU:O	1:C:322:ARG:HA	2.09	0.53
1:F:257:GLU:O	1:F:261:THR:HG22	2.08	0.53
1:F:115:ASP:O	1:F:436:GLN:HG2	2.09	0.53
1:K:30:THR:HB	1:K:51:LYS:O	2.09	0.53
1:K:217:SER:HA	1:K:320:ALA:O	2.08	0.53
1:C:200:LEU:HD22	1:C:254:VAL:HB	1.91	0.53
1:N:124:VAL:HG13	1:N:504:LEU:CD1	2.39	0.53
1:E:513:LEU:CD1	1:F:388:GLU:HA	2.38	0.53
1:E:513:LEU:HD11	1:F:388:GLU:HA	1.89	0.53
1:I:447:MET:O	1:I:450:PRO:HD2	2.08	0.53
1:J:479:ASN:OD1	1:J:493:ILE:HG13	2.09	0.53
1:B:449:ALA:HA	1:B:452:ARG:HG2	1.91	0.53
2:Q:76:GLU:O	2:Q:83:VAL:HG22	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:140:ASP:O	1:J:144:ILE:HG12	2.09	0.53
1:H:30:THR:HB	1:H:51:LYS:O	2.08	0.53
1:D:220:ILE:HG23	1:D:248:LEU:HD12	1.90	0.53
1:I:233:MET:SD	1:I:309:LEU:HD13	2.49	0.53
2:U:5:PRO:HB2	2:U:44:GLY:HA2	1.91	0.53
1:E:349:ILE:HG22	1:E:353:ILE:HG13	1.91	0.53
1:J:496:PRO:HD2	1:J:499:VAL:HG21	1.91	0.53
1:F:247:LEU:HB3	1:F:273:VAL:HG13	1.91	0.53
1:K:420:ILE:HG13	1:K:451:LEU:CD2	2.39	0.53
1:E:261:THR:CG2	2:S:29:GLY:H	2.21	0.53
1:I:146:GLN:HE21	1:I:150:ILE:HD11	1.74	0.53
1:N:58:ARG:HH11	1:N:58:ARG:HB2	1.73	0.53
1:N:421:ARG:HD2	1:N:474:GLY:O	2.09	0.53
2:Q:77:LYS:C	2:Q:78:ILE:HD13	2.29	0.53
1:N:288:MET:CE	1:N:288:MET:HA	2.39	0.53
1:B:183:LEU:CD2	1:B:384:ALA:HA	2.38	0.53
1:M:496:PRO:HD2	1:M:499:VAL:HG21	1.91	0.52
1:F:213:VAL:HB	1:F:325:ILE:HB	1.90	0.52
1:M:41:ASP:HB2	1:N:69:MET:CE	2.39	0.52
1:B:124:VAL:HG13	1:B:504:LEU:CD1	2.39	0.52
1:A:518:GLU:HB2	1:B:36:ARG:CB	2.39	0.52
1:C:199:TYR:O	1:C:199:TYR:HD1	1.91	0.52
1:D:221:LEU:HD11	1:D:301:ILE:HD11	1.90	0.52
1:J:104:LEU:O	1:J:107:VAL:HG22	2.09	0.52
1:G:65:LYS:HB3	1:G:522:THR:OG1	2.09	0.52
1:C:353:ILE:HG12	1:C:366:GLN:HE22	1.74	0.52
1:B:452:ARG:HB2	1:B:462:PRO:HB3	1.89	0.52
1:D:231:ARG:O	1:D:231:ARG:HD3	2.09	0.52
2:S:50:GLU:HG2	2:S:50:GLU:O	2.09	0.52
1:A:80:LYS:HD2	1:A:506:TYR:CE1	2.44	0.52
1:F:218:PRO:HD2	1:F:320:ALA:O	2.09	0.52
1:A:198:GLY:HA3	1:A:327:LYS:O	2.09	0.52
1:E:150:ILE:HG21	1:E:494:LEU:O	2.08	0.52
1:A:345:ARG:O	1:A:349:ILE:HG13	2.09	0.52
2:T:20:LYS:HG2	2:T:27:LEU:HG	1.89	0.52
1:D:20:VAL:HG13	1:D:74:VAL:HG11	1.91	0.52
1:H:69:MET:CE	1:H:522:THR:HB	2.39	0.52
1:M:414:GLY:H	1:M:494:LEU:HA	1.73	0.52
1:I:421:ARG:O	1:I:425:LYS:HG2	2.10	0.52
1:C:18:ARG:CG	1:C:18:ARG:HH11	2.22	0.52
1:M:421:ARG:O	1:M:425:LYS:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:145:ALA:O	1:H:149:THR:HG23	2.08	0.52
1:E:21:ASN:HD22	1:E:97:GLN:HE22	1.57	0.52
1:A:102:GLU:HB3	1:A:442:VAL:HG13	1.91	0.52
1:G:231:ARG:NH2	1:G:261:THR:HG21	2.24	0.52
1:E:147:VAL:HG23	1:E:403:THR:HG22	1.89	0.52
1:G:230:ILE:HG23	1:G:230:ILE:O	2.10	0.52
1:J:130:GLU:HG3	1:J:426:LEU:HD22	1.91	0.52
1:H:351:GLN:O	1:H:354:GLU:HG2	2.10	0.52
1:D:197:ARG:CZ	1:D:278:ALA:HA	2.40	0.52
1:H:230:ILE:HD13	1:H:230:ILE:H	1.74	0.52
1:A:18:ARG:CB	1:A:18:ARG:HH11	2.23	0.52
1:I:130:GLU:HG3	1:I:426:LEU:HD22	1.92	0.52
2:T:57:LEU:HD22	2:T:88:GLU:HB2	1.92	0.52
1:M:403:THR:O	1:M:407:VAL:HG23	2.10	0.52
1:J:213:VAL:O	1:J:324:VAL:HA	2.10	0.52
1:M:313:THR:HG22	1:M:314:LEU:N	2.24	0.52
1:L:215:LEU:HB3	1:L:218:PRO:HG3	1.90	0.52
1:N:271:VAL:HG12	1:N:273:VAL:HG13	1.92	0.52
1:L:44:PHE:N	1:L:44:PHE:HD1	2.08	0.52
1:N:233:MET:CE	1:N:309:LEU:HD13	2.40	0.52
2:Q:14:ARG:NH2	2:Q:84:LEU:HD21	2.24	0.52
1:E:85:ALA:O	1:E:401:HIS:HB3	2.10	0.52
1:J:19:GLY:HA3	1:J:67:GLU:O	2.10	0.52
1:B:14:VAL:O	1:B:18:ARG:HG2	2.10	0.52
1:L:19:GLY:HA3	1:L:67:GLU:O	2.09	0.52
1:M:319:GLN:O	1:M:336:VAL:HG23	2.09	0.52
1:A:134:LEU:HD11	1:A:425:LYS:NZ	2.25	0.52
1:K:4:LYS:HD2	1:K:521:VAL:CG1	2.39	0.52
1:A:247:LEU:HD21	1:A:317:LEU:HD13	1.91	0.52
1:F:509:SER:CB	1:G:384:ALA:HB3	2.40	0.52
1:K:69:MET:HE3	1:K:522:THR:HB	1.90	0.52
1:I:420:ILE:HG13	1:I:451:LEU:CD2	2.40	0.52
1:J:215:LEU:HB3	1:J:218:PRO:HG3	1.91	0.52
1:F:288:MET:HA	1:F:291:ASP:OD1	2.10	0.52
1:L:149:THR:CG2	1:L:156:GLU:HA	2.40	0.52
1:I:166:MET:CE	1:I:407:VAL:HG21	2.39	0.52
1:K:230:ILE:HD11	1:K:261:THR:HG21	1.90	0.52
1:L:44:PHE:N	1:L:44:PHE:CD1	2.77	0.52
1:B:15:LYS:O	1:B:67:GLU:HG2	2.10	0.52
1:J:458:CYS:SG	1:J:480:ALA:HB1	2.50	0.52
1:J:350:ARG:HA	1:J:353:ILE:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:349:ILE:O	1:D:352:GLN:HB2	2.09	0.52
1:L:271:VAL:HG12	1:L:273:VAL:HG13	1.91	0.52
1:G:252:GLU:HG3	1:G:285:ARG:HH11	1.75	0.52
1:G:77:VAL:HG11	1:G:510:VAL:HG21	1.92	0.52
1:H:247:LEU:H	1:H:273:VAL:HG12	1.75	0.52
1:I:385:THR:HG23	1:I:388:GLU:H	1.75	0.52
1:F:247:LEU:HD21	1:F:317:LEU:HD13	1.91	0.52
1:E:195:PHE:CE1	1:E:330:THR:HB	2.45	0.52
1:F:353:ILE:HG12	1:F:366:GLN:NE2	2.25	0.52
1:H:447:MET:O	1:H:450:PRO:HD2	2.08	0.52
2:O:20:LYS:HD2	2:O:28:THR:O	2.09	0.52
1:C:147:VAL:O	1:C:150:ILE:HG22	2.10	0.52
1:K:149:THR:CG2	1:K:156:GLU:HA	2.40	0.52
1:H:288:MET:HA	1:H:288:MET:HE3	1.92	0.52
1:F:417:VAL:HA	1:F:420:ILE:HG22	1.92	0.52
2:S:52:GLY:O	2:S:53:GLU:HB2	2.08	0.52
1:C:236:VAL:HG22	1:C:312:ALA:O	2.10	0.51
1:F:116:LEU:HD23	1:F:435:ASP:O	2.10	0.51
1:C:124:VAL:HG13	1:C:504:LEU:CD1	2.40	0.51
1:N:284:ARG:NH1	1:N:284:ARG:HB2	2.25	0.51
1:H:287:ALA:HB1	1:H:368:ARG:CZ	2.39	0.51
1:B:479:ASN:HB2	1:B:491:MET:SD	2.49	0.51
1:A:365:LEU:HD22	1:A:366:GLN:NE2	2.24	0.51
1:C:219:PHE:O	1:C:247:LEU:HD22	2.10	0.51
1:D:197:ARG:HH21	1:D:276:VAL:HG23	1.75	0.51
1:F:365:LEU:HD13	1:F:366:GLN:NE2	2.25	0.51
1:I:420:ILE:CD1	1:I:448:GLU:HA	2.39	0.51
1:N:403:THR:O	1:N:407:VAL:HG23	2.10	0.51
1:D:259:LEU:O	1:D:263:VAL:HG23	2.11	0.51
1:C:175:ILE:HG12	1:C:377:ALA:HB3	1.93	0.51
1:M:217:SER:N	1:M:218:PRO:HD3	2.25	0.51
1:K:124:VAL:HG13	1:K:504:LEU:CD1	2.41	0.51
1:E:305:ILE:CG2	1:E:306:GLY:H	2.17	0.51
1:D:352:GLN:OE1	1:D:365:LEU:HD11	2.11	0.51
1:C:513:LEU:CD1	1:D:388:GLU:HA	2.37	0.51
1:H:102:GLU:OE1	1:H:102:GLU:HA	2.11	0.51
2:Q:3:ILE:HG12	2:Q:78:ILE:HG13	1.93	0.51
1:K:295:LEU:HD23	1:K:332:ILE:HD11	1.92	0.51
1:E:65:LYS:HB3	1:E:522:THR:OG1	2.11	0.51
1:K:27:VAL:HG11	1:K:93:THR:HG21	1.92	0.51
1:D:195:PHE:CD1	1:D:197:ARG:HB2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:TYR:O	1:D:199:TYR:HD1	1.94	0.51
1:C:147:VAL:HG12	1:C:494:LEU:HB2	1.91	0.51
1:K:26:ALA:O	1:K:29:VAL:HG22	2.11	0.51
2:S:65:VAL:HG12	2:S:94:ILE:HD13	1.92	0.51
1:L:447:MET:O	1:L:450:PRO:HD2	2.10	0.51
1:E:215:LEU:O	1:E:322:ARG:HA	2.10	0.51
1:F:252:GLU:HG3	1:F:285:ARG:HH11	1.76	0.51
1:K:232:GLU:HB3	1:K:309:LEU:HB2	1.92	0.51
1:H:26:ALA:O	1:H:29:VAL:HG22	2.11	0.51
1:G:349:ILE:O	1:G:352:GLN:HB2	2.10	0.51
1:G:438:VAL:O	1:G:442:VAL:HG23	2.11	0.51
1:F:417:VAL:O	1:F:421:ARG:HB2	2.11	0.51
1:B:417:VAL:HA	1:B:420:ILE:HG22	1.93	0.51
1:N:295:LEU:HD23	1:N:332:ILE:HD11	1.93	0.51
1:B:199:TYR:O	1:B:199:TYR:HD1	1.94	0.51
1:J:66:PHE:CZ	1:J:522:THR:HG22	2.45	0.51
1:M:26:ALA:O	1:M:29:VAL:HG22	2.11	0.51
1:I:232:GLU:HA	1:I:310:GLU:CG	2.41	0.51
1:N:259:LEU:O	1:N:263:VAL:HG23	2.10	0.51
2:R:8:ASP:O	2:R:87:SER:HA	2.11	0.51
1:E:353:ILE:HG12	1:E:366:GLN:HE22	1.75	0.51
1:A:208:PRO:HB2	1:A:212:ALA:HB3	1.91	0.51
1:K:414:GLY:H	1:K:494:LEU:HA	1.75	0.51
1:D:102:GLU:HB2	1:D:442:VAL:HG13	1.93	0.51
1:G:367:GLU:O	1:G:371:LYS:HB2	2.11	0.51
2:S:94:ILE:HG12	2:T:6:LEU:HD23	1.92	0.51
1:I:227:ILE:CD1	1:I:309:LEU:HD11	2.40	0.51
1:J:130:GLU:HG3	1:J:426:LEU:CD2	2.40	0.51
1:M:174:VAL:HG13	1:M:194:GLN:OE1	2.11	0.51
2:P:94:ILE:O	2:Q:4:ARG:HB3	2.11	0.51
1:C:122:LYS:HE2	1:C:429:LEU:HD11	1.93	0.51
1:F:265:ASN:OD1	2:T:27:LEU:HB3	2.11	0.51
1:B:365:LEU:HD23	1:B:366:GLN:HE22	1.75	0.51
1:N:266:THR:HG21	1:N:273:VAL:O	2.11	0.51
1:F:493:ILE:HD13	4:F:1526:ADP:C2	2.46	0.51
1:N:284:ARG:HG2	1:N:364:LYS:NZ	2.26	0.51
1:M:230:ILE:HD11	1:M:261:THR:HG21	1.92	0.51
1:G:40:LEU:HD22	1:G:59:GLU:HG3	1.93	0.51
1:I:437:ASN:O	1:I:441:LYS:HD2	2.10	0.51
1:B:5:ASP:HB2	1:B:524:LEU:HD21	1.92	0.51
1:A:219:PHE:HB2	1:A:247:LEU:CD2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:73:MET:HE1	1:N:49:ILE:HD11	1.93	0.51
1:H:140:ASP:O	1:H:144:ILE:HG12	2.11	0.51
1:E:364:LYS:O	1:E:367:GLU:HB3	2.10	0.51
1:K:19:GLY:HA3	1:K:67:GLU:O	2.11	0.51
1:F:353:ILE:HG12	1:F:366:GLN:HE22	1.75	0.50
2:S:20:LYS:HD2	2:S:27:LEU:HG	1.93	0.50
1:C:509:SER:CB	1:D:384:ALA:HB3	2.39	0.50
1:J:239:ALA:HB1	1:J:314:LEU:CD1	2.41	0.50
1:H:225:LYS:HD3	1:H:303:GLU:CG	2.41	0.50
1:E:419:LEU:HD11	1:E:500:THR:HG23	1.92	0.50
1:B:42:LYS:HE3	1:B:48:THR:OG1	2.10	0.50
1:F:225:LYS:NZ	1:F:225:LYS:HB2	2.26	0.50
1:D:215:LEU:O	1:D:322:ARG:HA	2.11	0.50
1:K:130:GLU:HG3	1:K:426:LEU:CD2	2.41	0.50
1:F:113:PRO:HB3	1:F:516:THR:HA	1.93	0.50
1:H:302:SER:HB2	1:H:305:ILE:HD12	1.94	0.50
2:P:14:ARG:NE	2:P:34:LYS:HE2	2.26	0.50
1:H:509:SER:O	1:H:513:LEU:HD13	2.11	0.50
1:F:85:ALA:O	1:F:401:HIS:HB3	2.11	0.50
1:G:207:LYS:HB3	1:G:208:PRO:HD3	1.92	0.50
2:O:7:HIS:CD2	2:O:48:ILE:HD11	2.46	0.50
2:R:76:GLU:O	2:R:83:VAL:HG22	2.12	0.50
1:F:20:VAL:HG13	1:F:74:VAL:HG11	1.93	0.50
1:A:41:ASP:OD1	1:G:69:MET:HG2	2.11	0.50
1:H:313:THR:HG22	1:H:314:LEU:N	2.26	0.50
1:G:214:GLU:HA	1:G:323:VAL:O	2.11	0.50
1:N:414:GLY:H	1:N:494:LEU:HA	1.76	0.50
1:J:102:GLU:HB2	1:J:442:VAL:HG13	1.92	0.50
1:G:116:LEU:HD23	1:G:435:ASP:O	2.10	0.50
1:G:28:LYS:HG2	1:G:94:VAL:HG22	1.93	0.50
1:D:226:LYS:O	1:D:230:ILE:HD11	2.12	0.50
1:D:195:PHE:O	1:D:329:THR:HG23	2.12	0.50
1:A:147:VAL:O	1:A:150:ILE:HG22	2.11	0.50
1:J:420:ILE:HG13	1:J:451:LEU:CD2	2.42	0.50
1:H:266:THR:HG21	1:H:273:VAL:O	2.12	0.50
1:M:140:ASP:O	1:M:144:ILE:HG12	2.11	0.50
1:M:259:LEU:O	1:M:263:VAL:HG23	2.12	0.50
1:L:294:THR:HG21	1:L:345:ARG:HB2	1.94	0.50
2:S:14:ARG:NE	2:S:34:LYS:HE2	2.27	0.50
1:B:69:MET:SD	1:C:41:ASP:HB2	2.52	0.50
1:C:18:ARG:CB	1:C:18:ARG:HH11	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:409:GLU:OE1	1:K:498:LYS:HA	2.11	0.50
2:P:14:ARG:CD	2:P:34:LYS:HE2	2.42	0.50
2:T:92:LEU:CD1	2:U:74:LYS:HG3	2.41	0.50
1:L:326:ASN:OD1	1:L:329:THR:HB	2.11	0.50
1:N:149:THR:HG22	1:N:156:GLU:HA	1.94	0.50
1:I:295:LEU:HD23	1:I:332:ILE:HD11	1.94	0.50
1:F:65:LYS:O	1:F:69:MET:HG3	2.12	0.50
1:H:284:ARG:CZ	1:H:284:ARG:HB2	2.42	0.50
2:R:4:ARG:C	2:R:4:ARG:HD3	2.31	0.50
1:N:19:GLY:HA3	1:N:67:GLU:O	2.11	0.50
1:H:39:VAL:HG23	1:I:517:THR:HG21	1.94	0.50
1:F:40:LEU:HD13	1:F:59:GLU:HG3	1.92	0.50
1:C:349:ILE:O	1:C:352:GLN:HB2	2.11	0.50
1:A:31:LEU:CD1	4:A:1526:ADP:H5'1	2.42	0.50
1:E:207:LYS:CB	1:E:208:PRO:HD3	2.41	0.50
1:E:518:GLU:HB2	1:F:36:ARG:HB3	1.94	0.50
1:B:134:LEU:HD11	1:B:425:LYS:NZ	2.27	0.50
2:S:18:GLU:CD	2:S:33:ALA:HB3	2.32	0.50
1:D:432:GLN:NE2	1:D:436:GLN:HE22	2.09	0.50
1:I:30:THR:HB	1:I:51:LYS:O	2.12	0.50
1:E:197:ARG:HH21	1:E:279:PRO:HD3	1.75	0.50
1:K:179:ASP:HA	1:K:389:MET:HE3	1.94	0.50
1:I:266:THR:HG21	1:I:273:VAL:O	2.11	0.50
1:F:214:GLU:HA	1:F:323:VAL:O	2.11	0.50
1:I:288:MET:HA	1:I:288:MET:HE3	1.93	0.50
1:G:313:THR:HB	1:G:315:GLU:HG3	1.93	0.50
1:H:232:GLU:HB3	1:H:309:LEU:HB2	1.94	0.50
1:D:234:LEU:N	1:D:235:PRO:HD2	2.26	0.50
1:N:496:PRO:HD2	1:N:499:VAL:HG21	1.94	0.49
1:L:266:THR:HG21	1:L:273:VAL:O	2.12	0.49
1:J:20:VAL:CG2	1:J:74:VAL:HG21	2.42	0.49
1:F:291:ASP:HB2	1:F:372:LEU:HD21	1.94	0.49
1:I:262:LEU:O	1:I:266:THR:HG23	2.12	0.49
1:F:102:GLU:HB2	1:F:442:VAL:HG13	1.94	0.49
1:B:124:VAL:HG21	1:B:508:ALA:CB	2.42	0.49
1:L:348:GLN:O	1:L:352:GLN:HG3	2.12	0.49
1:H:459:GLY:HA3	1:I:112:ASN:HD21	1.77	0.49
1:M:420:ILE:CD1	1:M:448:GLU:HA	2.42	0.49
1:K:420:ILE:CD1	1:K:448:GLU:HA	2.42	0.49
1:A:69:MET:HG2	1:B:41:ASP:CG	2.32	0.49
1:J:149:THR:CG2	1:J:156:GLU:HA	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:210:THR:HG22	1:D:210:THR:O	2.12	0.49
1:K:348:GLN:O	1:K:352:GLN:HG3	2.12	0.49
1:C:206:ASN:HB3	1:C:214:GLU:H	1.77	0.49
1:L:282:GLY:O	1:L:285:ARG:HG2	2.12	0.49
1:F:198:GLY:HA3	1:F:327:LYS:O	2.12	0.49
1:K:259:LEU:O	1:K:263:VAL:HG23	2.11	0.49
1:D:221:LEU:HD13	1:D:317:LEU:HD21	1.94	0.49
1:A:213:VAL:HB	1:A:325:ILE:HB	1.93	0.49
1:A:458:CYS:SG	1:A:480:ALA:HB1	2.52	0.49
1:J:13:ARG:HA	1:J:16:MET:CE	2.42	0.49
1:J:414:GLY:H	1:J:494:LEU:HA	1.76	0.49
1:D:288:MET:HA	1:D:291:ASP:OD1	2.12	0.49
1:G:102:GLU:HB3	1:G:442:VAL:HG13	1.94	0.49
1:L:225:LYS:HD3	1:L:303:GLU:HG3	1.93	0.49
1:A:326:ASN:OD1	1:A:329:THR:HB	2.13	0.49
1:N:420:ILE:CD1	1:N:448:GLU:HA	2.42	0.49
1:B:199:TYR:HA	1:B:276:VAL:HG12	1.94	0.49
1:M:30:THR:HG22	1:M:36:ARG:O	2.11	0.49
1:D:116:LEU:HD23	1:D:435:ASP:O	2.13	0.49
1:L:437:ASN:O	1:L:441:LYS:HD2	2.12	0.49
1:E:124:VAL:HG13	1:E:504:LEU:CD1	2.42	0.49
2:U:17:VAL:HG11	2:U:33:ALA:O	2.11	0.49
1:C:322:ARG:CB	1:C:333:ILE:HD12	2.40	0.49
1:C:28:LYS:HG2	1:C:94:VAL:HG22	1.95	0.49
1:C:33:PRO:HA	1:C:153:ASN:ND2	2.26	0.49
1:F:175:ILE:HG12	1:F:377:ALA:HB3	1.94	0.49
1:I:284:ARG:HG2	1:I:364:LYS:HE2	1.94	0.49
1:G:234:LEU:N	1:G:235:PRO:HD2	2.27	0.49
1:N:225:LYS:HD3	1:N:303:GLU:CG	2.43	0.49
2:Q:43:VAL:HG13	2:Q:57:LEU:HD12	1.93	0.49
1:D:204:PHE:CD2	1:D:274:ALA:HB2	2.48	0.49
1:I:319:GLN:HB2	1:I:336:VAL:HG21	1.95	0.49
1:K:228:SER:O	1:K:257:GLU:HB3	2.12	0.49
1:L:57:ALA:O	1:L:75:LYS:HE3	2.13	0.49
1:H:455:VAL:HG13	1:H:460:GLU:HB2	1.93	0.49
1:G:195:PHE:CE1	1:G:330:THR:HB	2.47	0.49
1:G:247:LEU:HB3	1:G:273:VAL:HG13	1.94	0.49
1:E:102:GLU:HB3	1:E:442:VAL:HG13	1.94	0.49
1:M:166:MET:CE	1:M:407:VAL:HG21	2.42	0.49
1:A:100:ILE:HD13	1:A:514:MET:SD	2.53	0.49
2:U:12:VAL:HG12	2:U:40:VAL:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:287:ALA:HB1	1:J:368:ARG:CZ	2.43	0.49
1:D:247:LEU:HB3	1:D:273:VAL:HG13	1.95	0.49
1:K:69:MET:CE	1:K:522:THR:HB	2.43	0.49
1:D:183:LEU:CD2	1:D:384:ALA:HA	2.43	0.49
1:K:149:THR:HG22	1:K:156:GLU:HA	1.95	0.49
1:A:234:LEU:N	1:A:235:PRO:HD2	2.27	0.49
1:N:302:SER:HB2	1:N:305:ILE:HD12	1.95	0.49
1:A:417:VAL:HA	1:A:420:ILE:HG22	1.94	0.49
1:J:385:THR:HG23	1:J:388:GLU:H	1.77	0.49
2:R:31:ALA:O	2:R:32:ALA:HB2	2.13	0.49
1:A:4:LYS:HD3	1:A:521:VAL:HG12	1.94	0.49
1:A:349:ILE:O	1:A:352:GLN:HB2	2.11	0.49
1:C:69:MET:O	1:C:73:MET:HG3	2.13	0.49
1:D:266:THR:HG22	1:D:273:VAL:H	1.77	0.49
1:D:355:GLU:HG2	1:D:361:ASP:OD2	2.13	0.49
1:G:199:TYR:CE2	1:G:202:PRO:HA	2.48	0.49
1:M:229:ASN:HD21	1:M:231:ARG:NH2	2.11	0.49
1:A:18:ARG:CG	1:A:18:ARG:HH11	2.25	0.49
1:B:305:ILE:N	1:B:305:ILE:CD1	2.76	0.49
1:J:286:LYS:HA	1:J:286:LYS:HE2	1.94	0.49
1:L:27:VAL:HG11	1:L:93:THR:HG21	1.95	0.49
1:E:66:PHE:HA	1:E:69:MET:CE	2.42	0.49
1:J:39:VAL:HG22	1:J:49:ILE:HG12	1.94	0.49
1:C:207:LYS:CB	1:C:208:PRO:HD3	2.42	0.49
1:G:221:LEU:HD11	1:G:301:ILE:CD1	2.42	0.49
1:D:113:PRO:HA	1:D:116:LEU:HD12	1.95	0.49
1:N:232:GLU:HB3	1:N:309:LEU:HB2	1.94	0.49
1:E:65:LYS:HG3	1:E:523:ASP:O	2.12	0.49
1:D:190:VAL:HG11	1:D:194:GLN:OE1	2.12	0.49
1:J:176:THR:OG1	1:J:378:VAL:HG12	2.13	0.49
1:I:124:VAL:HG13	1:I:504:LEU:CD1	2.43	0.49
1:J:63:GLU:HB2	1:K:3:ALA:HB1	1.93	0.49
2:S:6:LEU:HD13	2:S:7:HIS:NE2	2.28	0.49
1:I:351:GLN:O	1:I:354:GLU:HG2	2.11	0.49
1:E:349:ILE:O	1:E:352:GLN:HB2	2.11	0.49
1:A:187:LEU:HD13	1:A:379:ILE:HG12	1.95	0.49
2:O:7:HIS:O	2:O:8:ASP:HB3	2.13	0.49
1:I:496:PRO:HD2	1:I:499:VAL:HG21	1.94	0.49
1:J:230:ILE:CD1	1:J:257:GLU:HG2	2.43	0.49
1:F:453:GLN:HE22	1:F:456:LEU:HD23	1.78	0.49
1:G:102:GLU:HB2	1:G:442:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:342:ILE:HG23	1:K:372:LEU:HD11	1.94	0.49
1:M:230:ILE:CD1	1:M:261:THR:HG21	2.43	0.49
1:M:295:LEU:HD23	1:M:332:ILE:HD11	1.95	0.49
1:D:187:LEU:HD13	1:D:379:ILE:HG12	1.95	0.48
1:H:496:PRO:HD2	1:H:499:VAL:HG21	1.95	0.48
1:G:219:PHE:HB2	1:G:247:LEU:CD2	2.43	0.48
1:H:65:LYS:HB3	1:H:522:THR:HG21	1.95	0.48
1:H:414:GLY:H	1:H:494:LEU:HA	1.76	0.48
1:H:124:VAL:HG13	1:H:504:LEU:CD1	2.43	0.48
1:E:120:ILE:O	1:E:124:VAL:HG23	2.13	0.48
1:F:100:ILE:HD13	1:F:514:MET:SD	2.53	0.48
2:R:14:ARG:NH2	2:R:84:LEU:HD21	2.28	0.48
1:I:221:LEU:HD12	1:I:249:ILE:HG23	1.94	0.48
1:E:247:LEU:HD13	1:E:248:LEU:N	2.28	0.48
1:I:313:THR:HG22	1:I:314:LEU:N	2.27	0.48
1:B:31:LEU:CD1	4:B:1526:ADP:H5'1	2.43	0.48
1:C:124:VAL:HG21	1:C:508:ALA:CB	2.42	0.48
1:M:217:SER:HA	1:M:320:ALA:O	2.13	0.48
1:D:115:ASP:O	1:D:436:GLN:HG2	2.12	0.48
1:L:286:LYS:HE2	1:L:286:LYS:HA	1.95	0.48
1:E:115:ASP:O	1:E:436:GLN:HG2	2.13	0.48
1:M:124:VAL:HG21	1:M:508:ALA:CB	2.43	0.48
2:U:3:ILE:HD13	2:U:11:ILE:HD13	1.95	0.48
1:F:225:LYS:O	1:F:251:ALA:HB1	2.12	0.48
1:C:518:GLU:HB2	1:D:36:ARG:HB2	1.94	0.48
1:A:305:ILE:HG22	1:A:306:GLY:N	2.27	0.48
1:H:229:ASN:HD21	1:H:231:ARG:NH2	2.11	0.48
1:A:124:VAL:HG13	1:A:504:LEU:CD1	2.43	0.48
1:M:466:ALA:O	1:M:470:LYS:HG2	2.13	0.48
2:R:3:ILE:HD13	2:R:11:ILE:CD1	2.44	0.48
1:G:346:VAL:O	1:G:349:ILE:HB	2.13	0.48
1:A:221:LEU:HD13	1:A:317:LEU:HD21	1.94	0.48
1:D:282:GLY:HA2	1:D:285:ARG:HG2	1.94	0.48
1:L:49:ILE:HG21	1:M:513:LEU:HD11	1.95	0.48
2:O:6:LEU:HD13	2:O:7:HIS:CD2	2.49	0.48
1:A:20:VAL:HG13	1:A:74:VAL:HG11	1.94	0.48
1:H:421:ARG:HD2	1:H:474:GLY:O	2.14	0.48
1:E:183:LEU:HD21	1:E:384:ALA:HA	1.95	0.48
1:C:102:GLU:CB	1:C:442:VAL:HG13	2.43	0.48
1:G:147:VAL:HG12	1:G:494:LEU:HB2	1.96	0.48
1:N:57:ALA:O	1:N:75:LYS:HE3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:120:ILE:O	1:D:124:VAL:HG23	2.14	0.48
1:I:27:VAL:HG11	1:I:93:THR:HG21	1.96	0.48
1:C:278:ALA:HB1	1:C:279:PRO:HD2	1.95	0.48
1:E:66:PHE:HA	1:E:69:MET:HE3	1.94	0.48
1:H:20:VAL:CG2	1:H:74:VAL:HG21	2.41	0.48
1:E:199:TYR:HA	1:E:276:VAL:HG12	1.94	0.48
1:J:266:THR:HG21	1:J:273:VAL:O	2.14	0.48
1:N:166:MET:HE1	1:N:407:VAL:HG21	1.94	0.48
1:H:229:ASN:HB3	1:H:232:GLU:OE1	2.14	0.48
1:K:284:ARG:HG2	1:K:364:LYS:NZ	2.28	0.48
1:H:403:THR:O	1:H:407:VAL:HG23	2.13	0.48
1:A:193:MET:SD	1:A:371:LYS:HB3	2.54	0.48
1:J:496:PRO:O	1:J:499:VAL:HG22	2.13	0.48
1:C:20:VAL:HG13	1:C:74:VAL:HG11	1.95	0.48
1:A:272:LYS:HB2	1:A:272:LYS:NZ	2.29	0.48
1:L:30:THR:HB	1:L:51:LYS:O	2.13	0.48
1:C:339:GLU:O	1:C:343:GLN:HG2	2.13	0.48
1:C:228:SER:HA	1:C:255:GLU:HB2	1.95	0.48
1:B:195:PHE:O	1:B:329:THR:HG23	2.13	0.48
1:D:195:PHE:CE1	1:D:197:ARG:HD3	2.49	0.48
1:E:266:THR:HA	1:E:271:VAL:O	2.12	0.48
1:D:518:GLU:HB2	1:E:36:ARG:CB	2.43	0.48
2:S:14:ARG:NH2	2:S:84:LEU:HD21	2.29	0.48
1:L:409:GLU:OE1	1:L:498:LYS:HA	2.14	0.48
1:H:38:VAL:HG13	1:I:519:CYS:HB3	1.94	0.48
2:S:8:ASP:O	2:S:87:SER:HA	2.13	0.48
1:J:233:MET:CE	1:J:309:LEU:HD13	2.43	0.48
1:F:234:LEU:N	1:F:235:PRO:HD2	2.28	0.48
1:H:22:VAL:HG11	1:H:62:LEU:HD21	1.96	0.48
1:D:197:ARG:NE	1:D:277:LYS:O	2.47	0.48
1:C:16:MET:O	1:C:20:VAL:HG23	2.14	0.48
1:B:42:LYS:HB3	1:B:44:PHE:CD2	2.48	0.48
1:I:30:THR:HG22	1:I:36:ARG:O	2.14	0.48
1:J:421:ARG:HD2	1:J:474:GLY:O	2.14	0.48
1:F:447:MET:O	1:F:450:PRO:HD2	2.12	0.48
1:B:447:MET:O	1:B:450:PRO:HD2	2.13	0.48
1:D:279:PRO:HD2	1:D:285:ARG:HB2	1.95	0.48
1:K:213:VAL:O	1:K:324:VAL:HA	2.14	0.48
1:J:31:LEU:HG	1:J:454:ILE:HD11	1.95	0.48
1:H:284:ARG:HE	1:H:364:LYS:NZ	2.12	0.48
1:E:199:TYR:CE1	1:E:202:PRO:HA	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:414:GLY:O	1:D:417:VAL:HG12	2.14	0.48
1:J:149:THR:HG22	1:J:156:GLU:HA	1.96	0.48
1:M:199:TYR:CE2	1:M:327:LYS:HA	2.49	0.48
1:J:282:GLY:O	1:J:285:ARG:HG2	2.14	0.48
1:A:128:VAL:HG21	1:A:505:GLN:HE21	1.78	0.48
1:F:201:SER:HB3	1:F:259:LEU:HD22	1.96	0.48
1:J:101:THR:O	1:J:105:LYS:HG3	2.13	0.48
1:D:150:ILE:HG21	1:D:494:LEU:O	2.14	0.48
1:H:222:LEU:HD13	1:H:293:ALA:HB2	1.94	0.48
1:F:265:ASN:HB3	1:F:271:VAL:HG22	1.95	0.48
1:L:420:ILE:CD1	1:L:448:GLU:HA	2.44	0.48
1:E:18:ARG:HG2	1:E:18:ARG:NH1	2.28	0.48
1:B:33:PRO:HD3	4:B:1526:ADP:C5	2.49	0.48
1:C:417:VAL:HA	1:C:420:ILE:HG22	1.96	0.48
1:J:41:ASP:HB2	1:K:69:MET:CE	2.44	0.47
1:H:230:ILE:N	1:H:230:ILE:CD1	2.77	0.47
1:H:443:ALA:O	1:H:447:MET:HG3	2.14	0.47
1:H:65:LYS:O	1:H:66:PHE:HB2	2.14	0.47
1:K:111:MET:SD	1:K:438:VAL:HG21	2.54	0.47
1:F:217:SER:N	1:F:218:PRO:HD3	2.29	0.47
1:D:272:LYS:HB2	1:D:272:LYS:NZ	2.29	0.47
1:D:21:ASN:HA	1:D:97:GLN:HE22	1.79	0.47
1:N:199:TYR:CE2	1:N:327:LYS:HA	2.49	0.47
1:M:351:GLN:O	1:M:354:GLU:HG2	2.14	0.47
1:E:52:ASP:OD1	1:E:54:VAL:HG12	2.14	0.47
1:C:346:VAL:O	1:C:349:ILE:HB	2.13	0.47
1:D:278:ALA:HB1	1:D:279:PRO:CD	2.43	0.47
1:B:261:THR:HB	2:P:29:GLY:N	2.27	0.47
1:C:74:VAL:O	1:C:77:VAL:HG12	2.13	0.47
1:K:36:ARG:HH12	1:L:113:PRO:HB2	1.79	0.47
1:C:102:GLU:HB3	1:C:442:VAL:HG13	1.96	0.47
1:E:102:GLU:CB	1:E:442:VAL:HG13	2.44	0.47
1:C:199:TYR:HA	1:C:276:VAL:HG12	1.95	0.47
1:H:149:THR:CG2	1:H:156:GLU:HA	2.44	0.47
1:F:419:LEU:HD11	1:F:500:THR:HG23	1.95	0.47
1:G:201:SER:HB3	1:G:259:LEU:HD22	1.95	0.47
1:C:246:PRO:HA	1:C:272:LYS:O	2.14	0.47
2:O:47:ARG:HB3	2:O:55:LYS:HD2	1.96	0.47
1:F:345:ARG:O	1:F:349:ILE:HG13	2.15	0.47
1:N:218:PRO:HG2	1:N:323:VAL:HG12	1.95	0.47
1:E:20:VAL:HG13	1:E:74:VAL:HG11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:SER:CB	1:C:305:ILE:HD12	2.43	0.47
1:H:409:GLU:OE1	1:H:498:LYS:HA	2.15	0.47
1:F:147:VAL:O	1:F:150:ILE:HG22	2.14	0.47
1:M:232:GLU:HB3	1:M:309:LEU:HB2	1.96	0.47
1:I:219:PHE:HB3	1:I:317:LEU:HD23	1.96	0.47
1:H:223:ALA:HB3	1:H:251:ALA:HB2	1.97	0.47
1:J:225:LYS:HD3	1:J:303:GLU:CG	2.45	0.47
1:L:219:PHE:HB3	1:L:317:LEU:HD23	1.96	0.47
1:A:15:LYS:O	1:A:67:GLU:HG2	2.15	0.47
1:B:259:LEU:O	1:B:263:VAL:HG23	2.13	0.47
1:K:496:PRO:O	1:K:499:VAL:HG22	2.14	0.47
1:B:252:GLU:HA	1:B:285:ARG:HH11	1.77	0.47
1:C:115:ASP:O	1:C:436:GLN:HG2	2.14	0.47
1:E:147:VAL:O	1:E:150:ILE:HG22	2.13	0.47
1:N:224:ASP:HB3	1:N:302:SER:HA	1.95	0.47
1:N:286:LYS:HA	1:N:286:LYS:HE2	1.96	0.47
1:C:195:PHE:O	1:C:329:THR:HG23	2.15	0.47
1:C:510:VAL:HG13	1:D:385:THR:HG21	1.97	0.47
1:H:4:LYS:NZ	1:N:59:GLU:HG3	2.29	0.47
1:E:288:MET:HG2	1:E:368:ARG:HE	1.80	0.47
1:E:217:SER:HA	1:E:320:ALA:O	2.14	0.47
1:G:399:ALA:O	1:G:403:THR:HG23	2.15	0.47
1:F:102:GLU:HB3	1:F:442:VAL:HG13	1.95	0.47
1:A:235:PRO:HA	1:A:238:GLU:HG2	1.95	0.47
1:H:225:LYS:HD3	1:H:303:GLU:CD	2.35	0.47
1:F:259:LEU:O	1:F:263:VAL:HG23	2.14	0.47
1:N:221:LEU:HD12	1:N:249:ILE:HG23	1.96	0.47
1:J:478:TYR:HB2	1:J:485:TYR:CE2	2.50	0.47
1:J:40:LEU:HD21	1:J:56:VAL:HG22	1.96	0.47
1:E:198:GLY:HA3	1:E:327:LYS:O	2.14	0.47
1:H:169:VAL:HG13	1:H:173:GLY:HA3	1.97	0.47
1:B:278:ALA:HB1	1:B:279:PRO:HD2	1.97	0.47
1:M:5:ASP:O	1:M:66:PHE:HZ	1.98	0.47
1:H:218:PRO:HG2	1:H:323:VAL:HG12	1.96	0.47
2:R:6:LEU:HD13	2:R:7:HIS:NE2	2.29	0.47
1:K:475:ASN:HB2	1:K:487:ASN:ND2	2.28	0.47
1:E:210:THR:O	1:E:210:THR:HG22	2.15	0.47
1:N:458:CYS:SG	1:N:480:ALA:HB1	2.54	0.47
2:T:91:ILE:O	2:U:6:LEU:HD12	2.13	0.47
1:N:56:VAL:O	1:N:60:ILE:HG12	2.15	0.47
1:H:213:VAL:O	1:H:324:VAL:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:230:ILE:HG13	1:J:261:THR:OG1	2.15	0.47
1:B:287:ALA:HB1	1:B:368:ARG:HH22	1.79	0.47
1:E:30:THR:HG22	1:E:36:ARG:O	2.15	0.47
1:F:118:ARG:HH11	1:F:118:ARG:HG2	1.78	0.47
1:K:150:ILE:HG21	1:K:494:LEU:HD21	1.97	0.47
1:N:434:GLU:HA	1:N:437:ASN:HD22	1.80	0.47
1:K:197:ARG:HE	1:K:277:LYS:HB2	1.80	0.47
1:F:147:VAL:HG23	1:F:403:THR:HG22	1.97	0.47
1:A:120:ILE:O	1:A:124:VAL:HG23	2.14	0.47
1:J:225:LYS:HD3	1:J:303:GLU:CD	2.35	0.47
1:J:383:ALA:HB3	1:J:389:MET:HB2	1.96	0.47
1:L:284:ARG:HG2	1:L:364:LYS:NZ	2.29	0.47
2:T:47:ARG:O	2:T:55:LYS:HE2	2.14	0.47
1:L:325:ILE:HG12	1:L:330:THR:HG23	1.96	0.47
1:B:487:ASN:HB3	1:B:490:ASP:OD1	2.14	0.47
1:C:475:ASN:HB2	1:C:487:ASN:HD21	1.80	0.47
1:J:155:ASP:HB2	1:J:395:ARG:NH2	2.29	0.47
1:B:419:LEU:HD11	1:B:500:THR:HG23	1.96	0.47
1:C:197:ARG:HG2	1:C:277:LYS:O	2.15	0.47
1:N:26:ALA:O	1:N:29:VAL:HG22	2.15	0.47
1:J:230:ILE:N	1:J:230:ILE:HD12	2.30	0.47
1:B:352:GLN:HB3	1:B:365:LEU:CD1	2.43	0.47
2:T:7:HIS:O	2:T:8:ASP:HB3	2.14	0.47
1:M:124:VAL:HG13	1:M:504:LEU:CD1	2.44	0.47
1:J:421:ARG:O	1:J:425:LYS:HG2	2.14	0.47
1:D:147:VAL:HG23	1:D:403:THR:HG22	1.97	0.47
1:D:339:GLU:OE1	1:D:339:GLU:HA	2.15	0.47
1:M:222:LEU:HD13	1:M:293:ALA:HB2	1.96	0.47
1:H:400:LEU:HD21	1:H:404:ARG:HE	1.80	0.47
1:I:509:SER:O	1:I:513:LEU:HD13	2.15	0.47
1:G:31:LEU:HD12	4:G:1526:ADP:H5'1	1.96	0.47
1:G:383:ALA:HB3	1:G:389:MET:HB2	1.97	0.47
1:I:16:MET:O	1:I:20:VAL:HG13	2.14	0.47
1:C:204:PHE:CZ	1:C:213:VAL:HG21	2.49	0.47
1:M:37:ASN:OD1	1:N:513:LEU:HD12	2.15	0.47
1:I:41:ASP:HB2	1:J:69:MET:CE	2.45	0.47
1:K:179:ASP:HA	1:K:389:MET:CE	2.44	0.47
1:E:199:TYR:HD1	1:E:199:TYR:O	1.97	0.47
1:D:305:ILE:HG22	1:D:306:GLY:N	2.30	0.47
1:A:306:GLY:HA3	1:B:264:VAL:HG21	1.97	0.47
1:F:420:ILE:HD11	1:F:470:LYS:CG	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:246:PRO:HA	1:E:272:LYS:O	2.15	0.47
1:I:284:ARG:HG2	1:I:364:LYS:CE	2.45	0.47
1:B:290:GLN:HA	1:B:300:VAL:HG21	1.97	0.47
1:G:447:MET:O	1:G:450:PRO:HD2	2.15	0.47
1:J:459:GLY:HA3	1:K:112:ASN:HD21	1.80	0.47
1:H:174:VAL:HG13	1:H:194:GLN:OE1	2.15	0.47
1:H:383:ALA:HB3	1:H:389:MET:HB2	1.97	0.47
1:E:265:ASN:HB3	1:E:271:VAL:HG22	1.96	0.47
1:B:288:MET:HG2	1:B:368:ARG:HE	1.80	0.47
1:J:16:MET:HG3	1:J:520:MET:SD	2.55	0.47
1:J:447:MET:O	1:J:450:PRO:HD2	2.14	0.47
1:I:247:LEU:H	1:I:273:VAL:HG12	1.78	0.47
1:D:225:LYS:HE3	1:D:309:LEU:HG	1.97	0.47
1:C:288:MET:HA	1:C:291:ASP:OD1	2.15	0.47
1:I:149:THR:CG2	1:I:156:GLU:HA	2.45	0.47
1:B:120:ILE:O	1:B:124:VAL:HG23	2.15	0.47
1:F:226:LYS:C	1:F:226:LYS:HD2	2.36	0.47
1:K:34:LYS:HB2	1:K:458:CYS:SG	2.55	0.47
1:F:3:ALA:HA	1:G:61:GLU:O	2.15	0.47
1:F:73:MET:HE3	1:G:49:ILE:HD11	1.97	0.46
1:B:361:ASP:O	1:B:365:LEU:HB2	2.15	0.46
1:N:140:ASP:O	1:N:144:ILE:HG12	2.15	0.46
1:D:263:VAL:HG13	1:D:267:MET:SD	2.55	0.46
1:H:179:ASP:HA	1:H:389:MET:CE	2.45	0.46
1:I:155:ASP:HB2	1:I:395:ARG:NH2	2.30	0.46
1:F:124:VAL:HG21	1:F:508:ALA:HB1	1.97	0.46
1:B:437:ASN:O	1:B:441:LYS:HG2	2.15	0.46
1:H:34:LYS:HB2	1:H:458:CYS:SG	2.54	0.46
1:J:259:LEU:O	1:J:263:VAL:HG23	2.15	0.46
1:E:266:THR:HG22	1:E:273:VAL:H	1.80	0.46
1:L:69:MET:SD	1:L:520:MET:HE2	2.55	0.46
1:A:33:PRO:HD3	4:A:1526:ADP:C5	2.50	0.46
1:K:215:LEU:CB	1:K:218:PRO:HG3	2.45	0.46
1:B:305:ILE:HG22	1:B:306:GLY:N	2.29	0.46
1:N:77:VAL:CG1	1:N:506:TYR:HB3	2.46	0.46
1:B:26:ALA:O	1:B:29:VAL:HG22	2.15	0.46
1:J:56:VAL:O	1:J:60:ILE:HG12	2.15	0.46
1:L:268:ARG:HG3	1:L:268:ARG:O	2.15	0.46
1:D:178:GLU:O	1:D:380:LYS:HA	2.16	0.46
1:L:179:ASP:HA	1:L:389:MET:CE	2.45	0.46
1:M:34:LYS:HB2	1:M:458:CYS:SG	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:178:GLU:OE2	1:K:322:ARG:HD3	2.16	0.46
1:C:21:ASN:HA	1:C:97:GLN:HE22	1.80	0.46
1:H:57:ALA:O	1:H:75:LYS:HE3	2.15	0.46
1:F:262:LEU:HD11	1:F:273:VAL:CB	2.38	0.46
1:F:199:TYR:HD1	1:F:199:TYR:O	1.98	0.46
1:I:218:PRO:HB3	1:I:246:PRO:HB2	1.97	0.46
1:E:518:GLU:HB2	1:F:36:ARG:HB2	1.97	0.46
1:C:261:THR:CG2	2:Q:29:GLY:H	2.29	0.46
1:F:518:GLU:HB2	1:G:36:ARG:HB3	1.97	0.46
1:K:263:VAL:O	1:K:267:MET:HG2	2.15	0.46
1:B:443:ALA:O	1:B:447:MET:HG3	2.16	0.46
1:G:512:GLY:O	1:G:516:THR:HG23	2.16	0.46
1:A:447:MET:O	1:A:450:PRO:HD2	2.14	0.46
1:N:161:LEU:HD21	1:N:185:ASP:HB3	1.97	0.46
1:K:229:ASN:HD21	1:K:231:ARG:HH12	1.63	0.46
1:M:155:ASP:HB2	1:M:395:ARG:NH2	2.31	0.46
1:G:414:GLY:O	1:G:417:VAL:HG12	2.16	0.46
1:M:247:LEU:HB3	1:M:273:VAL:HG11	1.97	0.46
2:Q:8:ASP:O	2:Q:87:SER:HA	2.14	0.46
1:N:288:MET:HA	1:N:288:MET:HE2	1.97	0.46
1:I:232:GLU:HA	1:I:310:GLU:HG3	1.96	0.46
1:M:144:ILE:HG21	1:M:163:ALA:HA	1.97	0.46
1:J:232:GLU:HA	1:J:310:GLU:HG3	1.97	0.46
1:J:455:VAL:HG13	1:J:460:GLU:HB2	1.97	0.46
1:L:124:VAL:HG21	1:L:508:ALA:CB	2.45	0.46
1:N:30:THR:HB	1:N:51:LYS:O	2.14	0.46
1:G:254:VAL:HG21	1:G:275:ALA:HB1	1.98	0.46
1:E:281:PHE:O	1:E:284:ARG:HB3	2.15	0.46
1:C:112:ASN:ND2	1:D:34:LYS:HG2	2.31	0.46
2:T:37:ARG:NH1	2:T:37:ARG:HG2	2.31	0.46
1:N:145:ALA:O	1:N:149:THR:HG23	2.15	0.46
1:I:124:VAL:O	1:I:128:VAL:HG23	2.15	0.46
1:L:284:ARG:H	1:L:284:ARG:HH11	1.63	0.46
1:H:174:VAL:HG12	1:H:376:VAL:HG13	1.96	0.46
1:C:230:ILE:CG2	1:C:230:ILE:O	2.63	0.46
1:M:128:VAL:HG12	1:M:132:LYS:HE2	1.97	0.46
1:C:383:ALA:HB3	1:C:389:MET:HE2	1.98	0.46
1:J:5:ASP:HB2	1:J:524:LEU:HD23	1.96	0.46
1:N:160:LYS:O	1:N:164:GLU:HG3	2.15	0.46
2:O:14:ARG:NH2	2:O:84:LEU:HD21	2.31	0.46
1:J:325:ILE:HG12	1:J:330:THR:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:496:PRO:HG2	1:F:499:VAL:HG22	1.97	0.46
1:A:219:PHE:O	1:A:247:LEU:HD22	2.14	0.46
1:D:365:LEU:HD23	1:D:366:GLN:HE22	1.81	0.46
1:I:65:LYS:O	1:I:66:PHE:HB2	2.16	0.46
2:U:8:ASP:HB2	2:U:47:ARG:HA	1.98	0.46
1:C:493:ILE:HD13	4:C:1526:ADP:C2	2.51	0.46
1:E:28:LYS:HG2	1:E:94:VAL:HG22	1.97	0.46
1:A:518:GLU:HB2	1:B:36:ARG:HB3	1.96	0.46
1:E:257:GLU:HG3	2:S:31:ALA:CB	2.46	0.46
1:G:100:ILE:HD13	1:G:514:MET:SD	2.56	0.46
1:K:282:GLY:O	1:K:285:ARG:HG2	2.15	0.46
1:F:513:LEU:HD11	1:G:388:GLU:CA	2.36	0.46
1:D:197:ARG:NH2	1:D:276:VAL:HG23	2.30	0.46
1:A:112:ASN:ND2	1:B:34:LYS:HG2	2.31	0.46
2:P:20:LYS:CG	2:P:27:LEU:HG	2.45	0.46
1:I:49:ILE:HD11	1:J:73:MET:HE3	1.96	0.46
1:E:18:ARG:HH11	1:E:18:ARG:CB	2.28	0.46
1:K:459:GLY:HA3	1:L:112:ASN:ND2	2.28	0.46
2:Q:20:LYS:HD3	2:Q:27:LEU:HD11	1.97	0.46
2:Q:47:ARG:HB3	2:Q:55:LYS:HG2	1.96	0.46
1:F:30:THR:HG22	1:F:36:ARG:O	2.16	0.46
2:U:17:VAL:HG22	2:U:35:SER:H	1.81	0.46
2:S:7:HIS:HB2	2:S:46:GLY:O	2.16	0.46
1:J:232:GLU:HB3	1:J:309:LEU:HB2	1.98	0.46
1:B:496:PRO:HG2	1:B:499:VAL:HG22	1.98	0.46
1:H:237:LEU:O	1:H:240:VAL:HG22	2.15	0.46
1:D:261:THR:HB	2:R:29:GLY:N	2.29	0.46
1:C:309:LEU:HD12	1:C:309:LEU:H	1.79	0.46
1:D:23:LEU:C	1:D:23:LEU:HD13	2.36	0.46
1:L:295:LEU:HD23	1:L:332:ILE:HD11	1.98	0.46
1:K:177:VAL:CG1	1:K:393:LYS:HG3	2.46	0.46
1:K:100:ILE:O	1:K:104:LEU:HD13	2.15	0.46
1:F:76:GLU:OE1	1:G:387:VAL:HG13	2.16	0.46
1:I:353:ILE:HD11	1:I:369:VAL:HG21	1.97	0.46
1:D:199:TYR:OH	1:D:211:GLY:HA2	2.16	0.46
1:F:365:LEU:HD22	1:F:365:LEU:O	2.15	0.46
1:F:237:LEU:CD2	2:T:26:VAL:HG21	2.46	0.46
1:C:31:LEU:HD22	1:C:94:VAL:HG21	1.97	0.46
1:K:197:ARG:HE	1:K:277:LYS:CB	2.29	0.46
1:I:421:ARG:HA	1:I:421:ARG:HE	1.80	0.46
2:Q:78:ILE:HG12	2:Q:83:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:290:GLN:HA	1:K:290:GLN:OE1	2.16	0.46
1:B:409:GLU:OE2	1:B:498:LYS:HA	2.16	0.46
1:N:325:ILE:HG12	1:N:330:THR:HG23	1.98	0.46
1:H:177:VAL:CG1	1:H:393:LYS:HG3	2.46	0.46
1:K:432:GLN:HG2	1:K:436:GLN:HE22	1.81	0.46
1:D:232:GLU:HB3	1:D:310:GLU:OE2	2.16	0.46
1:A:38:VAL:HG22	1:G:519:CYS:HB3	1.98	0.46
1:F:246:PRO:HA	1:F:272:LYS:O	2.15	0.46
1:D:77:VAL:HG11	1:D:510:VAL:HG21	1.98	0.46
1:N:20:VAL:CG2	1:N:74:VAL:HG21	2.46	0.46
1:D:207:LYS:HB3	1:D:208:PRO:CD	2.46	0.46
1:I:443:ALA:O	1:I:447:MET:HG3	2.16	0.46
1:A:453:GLN:NE2	1:A:456:LEU:HD23	2.31	0.46
1:C:31:LEU:HD12	4:C:1526:ADP:H5'1	1.98	0.46
1:G:207:LYS:HB3	1:G:208:PRO:CD	2.46	0.46
2:P:47:ARG:HD2	2:P:49:LEU:HD12	1.98	0.46
2:O:12:VAL:HG12	2:O:40:VAL:HA	1.98	0.46
1:I:400:LEU:HD21	1:I:404:ARG:HE	1.81	0.46
1:A:61:GLU:HB3	1:G:2:ALA:O	2.15	0.46
1:E:149:THR:HG23	1:E:155:ASP:C	2.36	0.46
1:C:262:LEU:HD11	1:C:273:VAL:HB	1.97	0.45
1:F:349:ILE:HG21	1:F:369:VAL:HG22	1.99	0.45
1:A:302:SER:CB	1:A:305:ILE:HB	2.46	0.45
1:K:124:VAL:HG21	1:K:508:ALA:CB	2.46	0.45
1:I:102:GLU:HB2	1:I:442:VAL:HG13	1.96	0.45
1:I:458:CYS:SG	1:I:480:ALA:HB1	2.56	0.45
1:L:385:THR:HG23	1:L:388:GLU:H	1.81	0.45
1:C:418:ALA:O	1:C:422:VAL:HG13	2.16	0.45
1:D:240:VAL:HG21	1:D:247:LEU:HD23	1.98	0.45
1:L:270:ILE:HG23	1:M:231:ARG:HH21	1.81	0.45
1:E:284:ARG:HG2	1:E:288:MET:HE2	1.98	0.45
1:B:18:ARG:CB	1:B:18:ARG:HH11	2.26	0.45
1:A:115:ASP:O	1:A:436:GLN:HG2	2.16	0.45
1:G:305:ILE:HG22	1:G:306:GLY:N	2.30	0.45
2:Q:3:ILE:CG1	2:Q:78:ILE:HG13	2.46	0.45
1:M:215:LEU:HB2	1:M:218:PRO:HG3	1.97	0.45
2:R:7:HIS:HB2	2:R:46:GLY:O	2.16	0.45
1:E:201:SER:HB3	1:E:259:LEU:HD22	1.98	0.45
1:A:404:ARG:O	1:A:408:GLU:HG2	2.16	0.45
1:K:455:VAL:HG13	1:K:460:GLU:HB2	1.97	0.45
1:H:263:VAL:O	1:H:267:MET:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:LYS:HB3	1:C:44:PHE:CD2	2.51	0.45
1:L:56:VAL:O	1:L:60:ILE:HG12	2.16	0.45
1:L:82:ASN:HB2	1:L:89:THR:HG1	1.80	0.45
1:K:443:ALA:O	1:K:447:MET:HG3	2.17	0.45
1:J:229:ASN:HB3	1:J:232:GLU:OE1	2.17	0.45
1:K:178:GLU:OE2	1:K:333:ILE:HG21	2.16	0.45
2:T:48:ILE:O	2:T:48:ILE:HG22	2.15	0.45
1:H:178:GLU:OE2	1:H:322:ARG:HD3	2.17	0.45
1:J:400:LEU:HD21	1:J:404:ARG:HE	1.81	0.45
1:J:509:SER:O	1:J:513:LEU:HD13	2.15	0.45
2:T:12:VAL:HA	2:T:39:GLU:O	2.17	0.45
1:C:447:MET:O	1:C:450:PRO:HD2	2.15	0.45
1:C:183:LEU:CD2	1:C:384:ALA:HA	2.47	0.45
1:G:496:PRO:HG2	1:G:499:VAL:HG22	1.97	0.45
1:B:197:ARG:HB2	1:B:197:ARG:HH11	1.81	0.45
1:E:195:PHE:HE1	1:E:330:THR:HB	1.81	0.45
1:J:217:SER:HA	1:J:320:ALA:O	2.17	0.45
1:K:166:MET:CE	1:K:407:VAL:HG21	2.46	0.45
1:A:199:TYR:HA	1:A:276:VAL:HG12	1.98	0.45
1:B:102:GLU:CB	1:B:442:VAL:HG13	2.46	0.45
1:A:518:GLU:HG2	1:B:29:VAL:HB	1.97	0.45
1:N:284:ARG:HG2	1:N:364:LYS:HZ1	1.81	0.45
1:E:124:VAL:HG21	1:E:508:ALA:HB1	1.98	0.45
1:G:33:PRO:HD3	4:G:1526:ADP:C5	2.52	0.45
1:H:177:VAL:HG12	1:H:393:LYS:HE3	1.98	0.45
1:B:225:LYS:HG3	1:B:303:GLU:OE2	2.16	0.45
1:D:496:PRO:HG2	1:D:499:VAL:HG22	1.98	0.45
1:D:443:ALA:O	1:D:447:MET:HG3	2.16	0.45
2:P:31:ALA:O	2:P:32:ALA:HB3	2.17	0.45
1:F:281:PHE:O	1:F:284:ARG:HB3	2.16	0.45
2:R:47:ARG:HB3	2:R:55:LYS:HG2	1.96	0.45
1:C:254:VAL:HG21	1:C:275:ALA:CB	2.47	0.45
1:A:134:LEU:HD11	1:A:425:LYS:HZ2	1.82	0.45
2:R:11:ILE:HG12	2:R:85:ILE:HG12	1.99	0.45
1:L:276:VAL:CG1	1:L:325:ILE:HD13	2.46	0.45
1:A:61:GLU:OE1	1:G:2:ALA:HA	2.17	0.45
1:L:319:GLN:O	1:L:336:VAL:HG23	2.16	0.45
1:N:155:ASP:HB2	1:N:395:ARG:NH2	2.32	0.45
1:C:220:ILE:HD12	1:C:296:THR:HG21	1.99	0.45
1:B:296:THR:HG22	1:B:335:GLY:HA3	1.97	0.45
2:T:20:LYS:CG	2:T:27:LEU:HG	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:199:TYR:CE1	1:F:202:PRO:HA	2.50	0.45
1:L:221:LEU:HD13	1:L:221:LEU:C	2.37	0.45
1:B:353:ILE:HG12	1:B:366:GLN:HE22	1.81	0.45
1:E:24:ALA:O	1:E:28:LYS:HG3	2.16	0.45
1:I:215:LEU:CB	1:I:218:PRO:HG3	2.47	0.45
2:S:57:LEU:C	2:S:59:VAL:H	2.20	0.45
1:K:161:LEU:HD21	1:K:185:ASP:HB3	1.99	0.45
1:F:360:TYR:O	1:F:364:LYS:HG2	2.16	0.45
1:B:100:ILE:HD13	1:B:514:MET:SD	2.56	0.45
2:P:13:LYS:O	2:P:38:GLY:HA2	2.17	0.45
1:G:352:GLN:C	1:G:365:LEU:HD11	2.36	0.45
1:D:252:GLU:HG3	1:D:285:ARG:HH11	1.82	0.45
1:M:221:LEU:C	1:M:221:LEU:HD13	2.36	0.45
1:K:214:GLU:HG2	1:K:324:VAL:HG12	1.97	0.45
1:F:33:PRO:HD3	4:F:1526:ADP:C5	2.51	0.45
2:T:3:ILE:HD11	2:T:78:ILE:HG21	1.97	0.45
1:K:432:GLN:H	1:K:432:GLN:CD	2.19	0.45
1:E:430:ARG:CG	1:E:430:ARG:HH11	2.29	0.45
2:S:67:PHE:HA	2:S:92:LEU:H	1.82	0.45
1:C:15:LYS:O	1:C:67:GLU:HG2	2.15	0.45
1:M:267:MET:O	1:M:268:ARG:HG2	2.17	0.45
1:G:278:ALA:HB1	1:G:279:PRO:HD2	1.99	0.45
1:D:498:LYS:HG3	1:D:501:ARG:NH2	2.32	0.45
1:L:224:ASP:HB3	1:L:302:SER:HA	1.98	0.45
2:T:20:LYS:HB3	2:T:27:LEU:HG	1.98	0.45
1:L:213:VAL:O	1:L:324:VAL:HA	2.16	0.45
1:B:346:VAL:O	1:B:349:ILE:HB	2.17	0.45
1:G:33:PRO:HA	1:G:153:ASN:ND2	2.30	0.45
1:N:326:ASN:OD1	1:N:329:THR:HB	2.16	0.45
1:E:116:LEU:HD23	1:E:435:ASP:O	2.17	0.45
1:C:247:LEU:HB3	1:C:273:VAL:CG1	2.44	0.45
1:E:225:LYS:HE3	1:E:309:LEU:HG	1.99	0.45
1:K:438:VAL:O	1:K:442:VAL:HG23	2.17	0.45
1:F:42:LYS:HB3	1:F:44:PHE:CD2	2.52	0.45
1:N:277:LYS:NZ	1:N:277:LYS:HB2	2.32	0.45
1:A:313:THR:HG22	1:A:314:LEU:H	1.81	0.45
1:B:124:VAL:HG21	1:B:508:ALA:HB1	1.99	0.45
1:L:130:GLU:HG3	1:L:426:LEU:CD2	2.46	0.45
1:H:308:GLU:HB3	1:H:311:LYS:HD3	1.98	0.45
1:A:21:ASN:HA	1:A:97:GLN:HE22	1.81	0.45
1:G:5:ASP:HB2	1:G:524:LEU:HD23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:278:ALA:HB1	1:F:279:PRO:HD2	1.99	0.45
1:H:319:GLN:O	1:H:336:VAL:HG23	2.17	0.45
2:T:14:ARG:CZ	2:T:84:LEU:HD21	2.46	0.45
1:G:368:ARG:O	1:G:372:LEU:HG	2.17	0.45
1:E:236:VAL:HG22	1:E:312:ALA:O	2.17	0.45
1:G:345:ARG:O	1:G:348:GLN:HG3	2.17	0.45
1:F:349:ILE:O	1:F:352:GLN:HB2	2.17	0.45
1:C:399:ALA:O	1:C:403:THR:HG23	2.17	0.45
1:K:458:CYS:SG	1:K:480:ALA:HB1	2.56	0.45
1:L:115:ASP:HB3	1:L:436:GLN:HG3	1.99	0.45
1:N:27:VAL:HG11	1:N:93:THR:HG21	1.99	0.45
1:D:64:ASP:HB3	1:D:67:GLU:HB2	1.99	0.45
1:G:21:ASN:HA	1:G:97:GLN:HE22	1.81	0.45
1:J:124:VAL:HG13	1:J:504:LEU:CD1	2.47	0.45
1:F:365:LEU:HD22	1:F:365:LEU:C	2.37	0.44
1:L:66:PHE:HD1	1:L:520:MET:HE2	1.81	0.44
1:J:17:LEU:HA	1:J:20:VAL:HG12	1.99	0.44
1:K:29:VAL:HB	1:K:36:ARG:HB2	1.98	0.44
1:L:166:MET:CE	1:L:407:VAL:HG21	2.47	0.44
1:N:124:VAL:HG21	1:N:508:ALA:CB	2.47	0.44
1:G:7:LYS:O	1:G:519:CYS:HA	2.17	0.44
1:B:230:ILE:O	1:B:230:ILE:HG23	2.17	0.44
1:F:149:THR:HG23	1:F:155:ASP:C	2.37	0.44
1:K:25:ASP:HA	1:K:28:LYS:HE2	1.98	0.44
1:N:319:GLN:HB2	1:N:336:VAL:HG21	1.99	0.44
1:C:221:LEU:HD11	1:C:301:ILE:HD11	1.99	0.44
1:C:80:LYS:HD2	1:C:506:TYR:CE1	2.52	0.44
1:E:496:PRO:HG2	1:E:499:VAL:HG22	1.98	0.44
1:E:418:ALA:O	1:E:422:VAL:HG13	2.17	0.44
1:M:496:PRO:HD2	1:M:499:VAL:CG2	2.48	0.44
1:K:150:ILE:HG21	1:K:494:LEU:CD2	2.46	0.44
1:D:287:ALA:HB1	1:D:368:ARG:HH22	1.83	0.44
1:E:399:ALA:O	1:E:403:THR:HG23	2.17	0.44
1:J:229:ASN:HD21	1:J:231:ARG:NH1	2.15	0.44
1:K:177:VAL:HG12	1:K:393:LYS:HE3	1.97	0.44
1:H:178:GLU:OE2	1:H:333:ILE:HG21	2.17	0.44
2:O:52:GLY:O	2:O:53:GLU:HB2	2.15	0.44
1:E:447:MET:O	1:E:450:PRO:HD2	2.17	0.44
1:B:313:THR:HG22	1:B:314:LEU:H	1.83	0.44
1:G:228:SER:HA	1:G:255:GLU:HB2	1.99	0.44
1:B:359:ASP:O	1:B:360:TYR:HB2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:346:VAL:O	1:E:349:ILE:HB	2.17	0.44
1:F:262:LEU:O	1:F:266:THR:HG23	2.17	0.44
1:A:325:ILE:HG12	1:A:330:THR:HG23	1.99	0.44
1:E:262:LEU:O	1:E:266:THR:HG23	2.16	0.44
1:L:112:ASN:O	1:L:116:LEU:HG	2.17	0.44
1:A:495:ASP:CG	4:A:1526:ADP:HO2'	2.20	0.44
1:F:33:PRO:HA	1:F:153:ASN:ND2	2.32	0.44
1:D:302:SER:HB2	1:D:305:ILE:HB	1.99	0.44
1:M:247:LEU:H	1:M:273:VAL:HG12	1.81	0.44
1:E:4:LYS:HD2	1:F:59:GLU:O	2.17	0.44
1:E:231:ARG:HG2	1:E:257:GLU:OE1	2.18	0.44
1:G:23:LEU:HD13	1:G:23:LEU:C	2.38	0.44
1:L:161:LEU:HD21	1:L:185:ASP:HB3	1.99	0.44
1:H:160:LYS:O	1:H:164:GLU:HG3	2.17	0.44
1:M:350:ARG:HE	1:M:369:VAL:HG11	1.82	0.44
1:C:349:ILE:HG21	1:C:369:VAL:CG2	2.47	0.44
1:A:221:LEU:HD11	1:A:301:ILE:HD11	1.98	0.44
1:A:205:ILE:HA	1:A:213:VAL:HG22	1.99	0.44
1:G:262:LEU:O	1:G:266:THR:HG23	2.17	0.44
1:E:247:LEU:HB3	1:E:273:VAL:HG22	1.99	0.44
1:G:221:LEU:HD13	1:G:317:LEU:CD2	2.48	0.44
1:L:20:VAL:CG2	1:L:74:VAL:HG21	2.47	0.44
1:G:217:SER:N	1:G:218:PRO:CD	2.79	0.44
1:L:232:GLU:HA	1:L:310:GLU:HG3	1.97	0.44
1:F:231:ARG:O	1:F:233:MET:N	2.50	0.44
1:H:124:VAL:HG21	1:H:508:ALA:CB	2.48	0.44
1:L:443:ALA:O	1:L:447:MET:HG3	2.17	0.44
1:N:30:THR:HG22	1:N:36:ARG:O	2.18	0.44
1:G:21:ASN:HD22	1:G:97:GLN:HE22	1.65	0.44
1:C:400:LEU:C	1:C:400:LEU:HD13	2.37	0.44
1:M:27:VAL:HG11	1:M:93:THR:HG21	1.98	0.44
1:A:496:PRO:HG2	1:A:499:VAL:HG22	1.99	0.44
2:U:14:ARG:NH2	2:U:84:LEU:HD21	2.32	0.44
1:B:351:GLN:HG2	1:C:210:THR:OG1	2.17	0.44
1:E:15:LYS:O	1:E:67:GLU:HG2	2.17	0.44
1:H:199:TYR:CE2	1:H:327:LYS:HA	2.53	0.44
1:B:266:THR:HG22	1:B:273:VAL:H	1.83	0.44
1:A:266:THR:HG22	1:A:273:VAL:H	1.83	0.44
1:N:496:PRO:O	1:N:499:VAL:HG22	2.17	0.44
1:F:362:ARG:HB2	1:F:366:GLN:OE1	2.17	0.44
1:D:257:GLU:O	1:D:261:THR:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:217:SER:N	1:G:218:PRO:HD3	2.32	0.44
1:A:296:THR:HG22	1:A:335:GLY:HA3	1.99	0.44
1:F:518:GLU:HB2	1:G:36:ARG:HB2	1.99	0.44
1:K:191:GLU:OE1	1:K:342:ILE:HG21	2.18	0.44
2:R:3:ILE:HD13	2:R:11:ILE:HD13	1.98	0.44
1:B:85:ALA:O	1:B:401:HIS:HB3	2.18	0.44
1:M:145:ALA:O	1:M:149:THR:HG23	2.18	0.44
1:A:201:SER:HB3	1:A:259:LEU:HD22	2.00	0.44
1:M:465:VAL:O	1:M:469:VAL:HG23	2.17	0.44
1:E:200:LEU:HD23	1:E:254:VAL:O	2.18	0.44
1:H:6:VAL:CG1	1:H:519:CYS:SG	3.05	0.44
1:M:7:LYS:HG2	1:M:66:PHE:CE2	2.53	0.44
1:N:130:GLU:HG3	1:N:426:LEU:CD2	2.48	0.44
1:C:71:ALA:HA	1:C:74:VAL:HG22	1.98	0.44
1:K:36:ARG:HD3	1:L:114:MET:CE	2.48	0.44
1:H:30:THR:HG22	1:H:36:ARG:O	2.17	0.44
1:F:320:ALA:HA	1:F:335:GLY:HA2	1.99	0.44
1:E:162:ILE:HG21	1:E:403:THR:HG21	1.99	0.44
1:M:124:VAL:HG13	1:M:504:LEU:HD13	1.98	0.44
1:E:422:VAL:O	1:E:425:LYS:HB2	2.17	0.44
1:A:23:LEU:C	1:A:23:LEU:HD13	2.38	0.44
1:H:104:LEU:O	1:H:107:VAL:HG22	2.18	0.44
1:F:197:ARG:HG2	1:F:277:LYS:O	2.17	0.44
1:B:116:LEU:HD23	1:B:435:ASP:O	2.17	0.44
1:E:252:GLU:HA	1:E:285:ARG:HH12	1.81	0.44
1:G:247:LEU:CB	1:G:273:VAL:HG22	2.48	0.44
1:N:69:MET:HE3	1:N:522:THR:HB	1.96	0.44
1:B:16:MET:O	1:B:20:VAL:HG23	2.18	0.44
1:G:221:LEU:HD13	1:G:317:LEU:HD21	1.99	0.44
1:J:66:PHE:HD1	1:J:520:MET:HE2	1.83	0.44
1:G:452:ARG:HB2	1:G:462:PRO:CB	2.45	0.44
1:C:311:LYS:O	1:C:312:ALA:HB2	2.18	0.44
2:T:6:LEU:HD13	2:T:7:HIS:CD2	2.53	0.44
1:D:15:LYS:O	1:D:67:GLU:HG2	2.17	0.44
1:L:233:MET:SD	1:L:233:MET:N	2.90	0.44
1:I:104:LEU:O	1:I:107:VAL:HG22	2.18	0.44
1:K:56:VAL:O	1:K:60:ILE:HG12	2.17	0.44
1:N:230:ILE:HD11	1:N:261:THR:HG21	1.99	0.44
1:K:302:SER:HB2	1:K:305:ILE:HG12	1.99	0.44
1:F:183:LEU:CD2	1:F:384:ALA:HA	2.48	0.44
1:F:315:GLU:HG3	1:F:316:ASP:N	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:272:LYS:NZ	1:F:272:LYS:HB2	2.32	0.44
1:C:513:LEU:HD11	1:D:388:GLU:CA	2.44	0.44
1:H:420:ILE:CD1	1:H:448:GLU:HA	2.48	0.44
2:O:6:LEU:HD13	2:O:7:HIS:NE2	2.33	0.44
2:S:47:ARG:HD3	2:S:49:LEU:HD12	2.00	0.44
1:C:231:ARG:O	1:C:233:MET:N	2.51	0.44
1:F:399:ALA:O	1:F:403:THR:HG23	2.17	0.44
1:K:124:VAL:O	1:K:128:VAL:HG23	2.17	0.44
1:B:418:ALA:O	1:B:422:VAL:HG13	2.18	0.44
1:F:105:LYS:HB2	1:F:105:LYS:NZ	2.33	0.44
2:O:67:PHE:HA	2:O:92:LEU:H	1.82	0.44
1:F:17:LEU:HD13	1:F:104:LEU:HD12	2.00	0.44
1:H:342:ILE:HG23	1:H:372:LEU:HD11	2.00	0.44
2:S:77:LYS:HE3	2:S:80:ASN:HA	1.99	0.44
1:D:197:ARG:NH2	1:D:250:ILE:HG23	2.32	0.44
1:M:65:LYS:O	1:M:66:PHE:HB2	2.18	0.44
1:E:247:LEU:HD12	1:E:249:ILE:HG13	2.00	0.44
1:H:69:MET:HE2	1:N:41:ASP:HB2	2.00	0.44
1:L:66:PHE:CZ	1:L:522:THR:HG22	2.53	0.44
2:R:12:VAL:HA	2:R:39:GLU:O	2.17	0.44
1:C:26:ALA:O	1:C:29:VAL:HG22	2.17	0.44
1:B:147:VAL:O	1:B:150:ILE:HG22	2.18	0.44
1:E:117:LYS:HE3	1:E:513:LEU:CD2	2.48	0.44
1:E:215:LEU:HB2	1:E:323:VAL:HG22	1.98	0.44
2:T:92:LEU:HD11	2:U:74:LYS:HG3	2.00	0.44
1:E:509:SER:HB2	1:F:384:ALA:HB3	1.99	0.44
1:I:140:ASP:O	1:I:144:ILE:HG12	2.18	0.44
1:G:210:THR:O	1:G:210:THR:HG22	2.18	0.44
1:B:197:ARG:NH1	1:B:279:PRO:HA	2.33	0.43
1:L:37:ASN:OD1	1:M:513:LEU:HD12	2.19	0.43
1:C:222:LEU:HD23	1:C:289:LEU:HD22	1.99	0.43
1:H:41:ASP:HB2	1:I:69:MET:SD	2.58	0.43
1:K:444:LEU:O	1:K:447:MET:HB2	2.18	0.43
1:I:150:ILE:HG21	1:I:494:LEU:CD2	2.47	0.43
2:O:57:LEU:HD22	2:O:88:GLU:HB2	2.00	0.43
1:E:493:ILE:HD13	4:E:1526:ADP:C2	2.53	0.43
1:F:496:PRO:HG2	1:F:499:VAL:CG2	2.49	0.43
1:C:221:LEU:HD13	1:C:317:LEU:HD21	1.99	0.43
1:B:359:ASP:O	1:B:360:TYR:CB	2.66	0.43
1:H:104:LEU:HA	1:H:107:VAL:HG22	2.00	0.43
1:D:429:LEU:HG	1:D:440:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:351:GLN:HG2	1:F:210:THR:HG23	1.99	0.43
1:I:475:ASN:HB2	1:I:487:ASN:ND2	2.33	0.43
1:B:324:VAL:HB	1:B:331:THR:HB	2.00	0.43
1:D:509:SER:HB3	1:E:388:GLU:OE1	2.18	0.43
1:J:321:LYS:HD2	1:J:334:ASP:OD2	2.17	0.43
1:H:66:PHE:HD1	1:H:520:MET:HE2	1.83	0.43
1:M:475:ASN:HB2	1:M:487:ASN:ND2	2.32	0.43
1:F:19:GLY:HA2	1:F:62:LEU:CD2	2.48	0.43
2:R:6:LEU:HD13	2:R:7:HIS:CE1	2.53	0.43
1:D:432:GLN:HE21	1:D:436:GLN:HE22	1.66	0.43
1:E:432:GLN:HB2	1:E:436:GLN:OE1	2.19	0.43
1:D:399:ALA:O	1:D:403:THR:HG23	2.18	0.43
1:L:40:LEU:N	1:L:40:LEU:HD22	2.33	0.43
1:G:85:ALA:O	1:G:401:HIS:HB3	2.18	0.43
1:M:237:LEU:O	1:M:240:VAL:HG22	2.18	0.43
1:C:130:GLU:O	1:C:134:LEU:HD13	2.18	0.43
1:J:302:SER:HB2	1:J:305:ILE:HD12	2.00	0.43
1:I:178:GLU:OE2	1:I:322:ARG:HD3	2.18	0.43
1:L:201:SER:HA	1:L:202:PRO:HD3	1.92	0.43
1:N:466:ALA:O	1:N:470:LYS:HG2	2.17	0.43
1:B:237:LEU:HD13	2:P:26:VAL:HG11	2.00	0.43
1:B:247:LEU:HB3	1:B:273:VAL:HG13	2.00	0.43
1:N:313:THR:CG2	1:N:314:LEU:H	2.30	0.43
1:H:420:ILE:HG13	1:H:451:LEU:CD2	2.42	0.43
1:L:247:LEU:H	1:L:273:VAL:HG12	1.82	0.43
1:H:230:ILE:CD1	1:H:258:ALA:HA	2.43	0.43
1:L:65:LYS:O	1:L:66:PHE:HB2	2.18	0.43
1:F:309:LEU:H	1:F:309:LEU:HD12	1.83	0.43
1:B:18:ARG:CG	1:B:18:ARG:HH11	2.32	0.43
1:I:179:ASP:HA	1:I:389:MET:CE	2.46	0.43
1:A:414:GLY:HA2	1:A:495:ASP:OD2	2.18	0.43
1:C:31:LEU:CD1	4:C:1526:ADP:H5'1	2.48	0.43
1:B:304:GLU:C	1:B:305:ILE:HD12	2.38	0.43
1:B:33:PRO:HG3	4:B:1526:ADP:C6	2.54	0.43
1:D:248:LEU:C	1:D:248:LEU:HD13	2.39	0.43
2:O:76:GLU:O	2:O:83:VAL:HG22	2.18	0.43
1:A:130:GLU:O	1:A:134:LEU:HD13	2.18	0.43
1:D:33:PRO:HD3	4:D:1526:ADP:C5	2.53	0.43
1:D:31:LEU:HD12	4:D:1526:ADP:H5'1	2.01	0.43
2:O:12:VAL:HA	2:O:39:GLU:O	2.17	0.43
2:T:12:VAL:HG12	2:T:40:VAL:HA	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:336:VAL:HG12	1:J:336:VAL:O	2.18	0.43
1:E:40:LEU:HD13	1:E:59:GLU:HG3	2.00	0.43
1:F:290:GLN:O	1:F:294:THR:HG23	2.17	0.43
1:N:177:VAL:CG1	1:N:393:LYS:HG3	2.48	0.43
1:K:160:LYS:O	1:K:164:GLU:HG3	2.19	0.43
1:E:313:THR:HG22	1:E:314:LEU:H	1.83	0.43
1:C:352:GLN:CB	1:C:365:LEU:HD11	2.25	0.43
1:E:252:GLU:HG3	1:E:285:ARG:HH11	1.84	0.43
1:B:513:LEU:CD1	1:C:388:GLU:HA	2.42	0.43
1:J:39:VAL:HG23	1:K:517:THR:HG21	1.98	0.43
1:F:26:ALA:O	1:F:29:VAL:HG22	2.18	0.43
1:G:40:LEU:HD13	1:G:59:GLU:HG3	2.01	0.43
1:M:138:CYS:SG	1:M:144:ILE:HD13	2.58	0.43
1:D:447:MET:O	1:D:450:PRO:HD2	2.17	0.43
1:M:149:THR:CG2	1:M:156:GLU:HA	2.49	0.43
1:C:100:ILE:HD13	1:C:514:MET:SD	2.58	0.43
1:N:229:ASN:HD21	1:N:231:ARG:HH12	1.66	0.43
1:J:117:LYS:HZ3	1:J:512:GLY:HA3	1.84	0.43
1:B:392:LYS:O	1:B:396:VAL:HG23	2.17	0.43
1:G:392:LYS:O	1:G:396:VAL:HG23	2.18	0.43
1:K:194:GLN:HG3	1:K:331:THR:HB	1.99	0.43
1:E:349:ILE:O	1:E:353:ILE:HG13	2.18	0.43
1:M:496:PRO:O	1:M:499:VAL:HG22	2.18	0.43
1:G:365:LEU:O	1:G:369:VAL:HG23	2.19	0.43
1:D:355:GLU:HG3	1:D:357:THR:H	1.82	0.43
1:M:66:PHE:O	1:M:69:MET:HB2	2.18	0.43
1:K:496:PRO:HD2	1:K:499:VAL:HG21	2.00	0.43
1:C:252:GLU:HG3	1:C:285:ARG:NH1	2.33	0.43
1:G:20:VAL:HG13	1:G:74:VAL:HG11	2.00	0.43
1:C:225:LYS:HZ2	1:C:225:LYS:HB3	1.83	0.43
1:E:31:LEU:HD23	1:E:453:GLN:HB3	2.01	0.43
1:F:144:ILE:O	1:F:147:VAL:HG22	2.17	0.43
1:A:102:GLU:HB2	1:A:442:VAL:HG13	1.99	0.43
1:B:5:ASP:HB2	1:B:524:LEU:CD2	2.48	0.43
1:N:225:LYS:HD3	1:N:303:GLU:CD	2.39	0.43
2:Q:50:GLU:HG2	2:Q:50:GLU:O	2.18	0.43
1:I:23:LEU:C	1:I:23:LEU:CD1	2.87	0.43
1:C:23:LEU:HD13	1:C:23:LEU:C	2.39	0.43
1:I:46:ALA:HB1	1:I:47:PRO:HD2	2.01	0.43
1:C:419:LEU:HD11	1:C:500:THR:HG23	1.99	0.43
1:I:186:GLU:HB2	1:I:380:LYS:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:349:ILE:HG21	1:G:369:VAL:HG22	1.99	0.43
1:A:262:LEU:HD11	1:A:273:VAL:CB	2.41	0.43
2:O:55:LYS:H	2:O:55:LYS:CD	2.32	0.43
1:F:349:ILE:HG21	1:F:369:VAL:CG2	2.48	0.43
2:R:79:ASP:O	2:R:80:ASN:CB	2.66	0.43
1:G:247:LEU:HD13	1:G:248:LEU:N	2.33	0.43
1:G:16:MET:O	1:G:20:VAL:HG23	2.19	0.43
1:H:411:VAL:HB	1:H:494:LEU:HD12	2.00	0.43
2:R:47:ARG:HG2	2:R:49:LEU:H	1.83	0.43
1:E:518:GLU:HG2	1:F:29:VAL:HB	2.01	0.43
1:B:147:VAL:HG12	1:B:494:LEU:HB2	2.00	0.43
1:L:15:LYS:O	1:L:67:GLU:HG2	2.18	0.43
1:E:214:GLU:HA	1:E:323:VAL:O	2.19	0.43
1:F:254:VAL:HG12	1:F:259:LEU:HG	2.00	0.43
1:K:112:ASN:HA	1:K:113:PRO:HD3	1.93	0.43
2:P:3:ILE:HD12	2:P:3:ILE:H	1.82	0.43
1:K:351:GLN:O	1:K:354:GLU:HG2	2.18	0.43
2:P:12:VAL:HG22	2:P:86:MET:SD	2.58	0.43
1:B:432:GLN:HB2	1:B:436:GLN:OE1	2.19	0.43
1:C:113:PRO:HB3	1:C:516:THR:HA	2.01	0.43
1:A:381:VAL:CG1	1:A:392:LYS:HG3	2.49	0.43
2:U:78:ILE:CD1	2:U:83:VAL:HG21	2.47	0.43
1:J:215:LEU:HB2	1:J:323:VAL:CG1	2.49	0.43
1:E:309:LEU:HD12	1:E:309:LEU:H	1.84	0.43
1:E:31:LEU:HD23	1:E:453:GLN:CB	2.49	0.43
1:E:31:LEU:HD22	1:E:94:VAL:HG21	2.01	0.43
1:C:261:THR:CB	2:Q:29:GLY:H	2.32	0.43
1:K:254:VAL:HG12	1:K:259:LEU:HB2	1.99	0.43
1:E:128:VAL:HG21	1:E:505:GLN:HE21	1.83	0.43
1:I:6:VAL:HG13	1:I:519:CYS:SG	2.59	0.43
1:H:458:CYS:SG	1:H:480:ALA:HB1	2.58	0.43
1:K:104:LEU:O	1:K:107:VAL:HG22	2.19	0.43
1:E:19:GLY:HA3	1:E:67:GLU:O	2.19	0.43
1:L:362:ARG:HG2	1:L:362:ARG:HH11	1.84	0.43
1:M:325:ILE:HG12	1:M:330:THR:HG23	2.00	0.43
1:I:19:GLY:HA3	1:I:67:GLU:O	2.17	0.43
1:C:226:LYS:HB2	1:C:253:ASP:HB3	2.00	0.43
1:H:56:VAL:O	1:H:60:ILE:HG12	2.18	0.43
1:B:355:GLU:HG3	1:B:357:THR:H	1.83	0.43
1:A:214:GLU:HA	1:A:323:VAL:O	2.19	0.43
1:B:187:LEU:HD13	1:B:379:ILE:HG12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:ASN:HB3	1:D:49:ILE:CG2	2.48	0.43
1:B:219:PHE:HB3	1:B:317:LEU:HB3	2.01	0.43
1:C:204:PHE:CG	1:C:204:PHE:O	2.71	0.43
1:D:199:TYR:CE1	1:D:202:PRO:HA	2.53	0.43
1:K:66:PHE:CZ	1:K:522:THR:HG22	2.54	0.43
1:F:365:LEU:HD13	1:F:366:GLN:HE22	1.82	0.43
1:A:147:VAL:HG23	1:A:403:THR:HG22	2.01	0.43
1:K:144:ILE:CD1	1:K:407:VAL:HG22	2.49	0.43
1:C:147:VAL:HG23	1:C:403:THR:HG22	2.00	0.43
1:C:288:MET:HG2	1:C:368:ARG:HE	1.83	0.43
1:G:120:ILE:O	1:G:124:VAL:HG23	2.19	0.43
1:A:388:GLU:HA	1:G:513:LEU:HD11	2.01	0.43
1:F:64:ASP:HB3	1:F:67:GLU:HB2	2.00	0.43
1:B:214:GLU:HA	1:B:323:VAL:O	2.18	0.43
2:P:77:LYS:HA	2:P:81:GLU:O	2.18	0.43
1:N:294:THR:HG21	1:N:345:ARG:HB2	2.01	0.43
1:G:187:LEU:C	1:G:187:LEU:CD1	2.87	0.43
1:G:353:ILE:HG12	1:G:366:GLN:HE22	1.84	0.43
1:C:204:PHE:CE1	1:C:274:ALA:HB3	2.54	0.43
1:J:218:PRO:HG2	1:J:323:VAL:HG12	2.00	0.43
1:G:124:VAL:HG21	1:G:508:ALA:CB	2.49	0.43
1:B:64:ASP:HB3	1:B:67:GLU:HB2	2.00	0.43
1:J:233:MET:N	1:J:233:MET:SD	2.92	0.43
1:H:259:LEU:O	1:H:263:VAL:HG23	2.19	0.43
1:E:311:LYS:O	1:E:312:ALA:HB2	2.19	0.43
1:G:418:ALA:O	1:G:422:VAL:HG13	2.18	0.43
1:D:228:SER:HA	1:D:255:GLU:HB2	2.00	0.43
1:I:230:ILE:HG12	1:I:261:THR:OG1	2.19	0.43
1:K:237:LEU:O	1:K:240:VAL:HG22	2.18	0.43
1:G:349:ILE:HG21	1:G:369:VAL:CG2	2.48	0.43
1:L:313:THR:CG2	1:L:314:LEU:H	2.31	0.43
1:G:204:PHE:CE1	1:G:266:THR:HB	2.54	0.43
1:J:15:LYS:O	1:J:67:GLU:HG2	2.19	0.43
1:N:194:GLN:HG3	1:N:331:THR:HB	2.01	0.43
1:B:518:GLU:HB2	1:C:36:ARG:HB3	2.01	0.43
1:F:169:VAL:HG11	1:F:377:ALA:HB2	2.00	0.43
1:H:124:VAL:O	1:H:128:VAL:HG23	2.18	0.43
1:A:19:GLY:HA3	1:A:67:GLU:O	2.19	0.43
2:P:84:LEU:HB3	2:P:86:MET:HE3	2.01	0.43
1:A:85:ALA:O	1:A:401:HIS:HB3	2.18	0.43
1:L:160:LYS:O	1:L:164:GLU:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:82:ASN:HB2	1:N:89:THR:OG1	2.18	0.43
1:I:293:ALA:HB2	1:I:300:VAL:HG13	2.01	0.43
2:O:74:LYS:HG3	2:U:92:LEU:HD11	2.01	0.43
1:E:50:THR:HA	1:E:391:GLU:OE1	2.19	0.43
1:G:296:THR:HG22	1:G:335:GLY:HA3	2.00	0.43
1:A:215:LEU:HB3	1:A:246:PRO:HB2	2.00	0.42
1:B:197:ARG:HB2	1:B:197:ARG:NH1	2.33	0.42
1:G:199:TYR:HB3	1:G:325:ILE:CG2	2.48	0.42
1:F:352:GLN:HB3	1:F:365:LEU:HG	2.01	0.42
1:K:131:LEU:HD21	1:K:500:THR:HG22	2.01	0.42
1:I:411:VAL:HB	1:I:494:LEU:HD12	2.00	0.42
1:E:33:PRO:HD3	4:E:1526:ADP:C5	2.54	0.42
1:F:33:PRO:HG3	4:F:1526:ADP:C6	2.54	0.42
1:F:417:VAL:O	1:F:420:ILE:HG22	2.18	0.42
1:E:4:LYS:HD3	1:E:521:VAL:HG12	2.01	0.42
1:N:199:TYR:CE1	1:N:202:PRO:HA	2.54	0.42
1:B:115:ASP:O	1:B:436:GLN:HG2	2.19	0.42
1:L:338:GLU:HA	1:L:338:GLU:OE1	2.19	0.42
1:E:461:GLU:HG2	1:E:461:GLU:H	1.58	0.42
1:B:461:GLU:HB2	1:B:464:VAL:HB	2.01	0.42
2:U:7:HIS:HB2	2:U:46:GLY:O	2.18	0.42
1:K:65:LYS:O	1:K:66:PHE:HB2	2.19	0.42
2:U:48:ILE:O	2:U:49:LEU:HD23	2.19	0.42
1:K:277:LYS:NZ	1:K:277:LYS:HB2	2.35	0.42
1:F:147:VAL:HA	1:F:150:ILE:HG22	2.01	0.42
1:B:210:THR:HG22	1:B:210:THR:O	2.18	0.42
1:N:177:VAL:HG11	1:N:393:LYS:HG3	2.01	0.42
1:N:487:ASN:O	1:N:491:MET:HG3	2.19	0.42
1:D:76:GLU:OE1	1:E:387:VAL:HG13	2.19	0.42
1:E:392:LYS:O	1:E:396:VAL:HG23	2.18	0.42
1:D:128:VAL:HG21	1:D:505:GLN:HE21	1.84	0.42
1:C:240:VAL:HG11	1:C:247:LEU:HB2	2.02	0.42
1:J:37:ASN:HD22	1:K:517:THR:HA	1.84	0.42
1:M:249:ILE:HB	1:M:275:ALA:CB	2.50	0.42
1:M:37:ASN:HD22	1:N:517:THR:HA	1.85	0.42
1:J:17:LEU:HB2	1:J:104:LEU:CD2	2.49	0.42
1:D:112:ASN:ND2	1:E:34:LYS:HG2	2.33	0.42
1:J:443:ALA:O	1:J:447:MET:HG3	2.19	0.42
1:H:130:GLU:HA	1:H:130:GLU:OE1	2.20	0.42
1:H:277:LYS:HB2	1:H:277:LYS:NZ	2.33	0.42
1:C:257:GLU:HG3	2:Q:31:ALA:CB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:229:ASN:HD21	1:I:231:ARG:NH1	2.17	0.42
1:F:30:THR:CG2	1:F:38:VAL:HG23	2.50	0.42
1:C:18:ARG:HG2	1:C:18:ARG:HH11	1.85	0.42
1:E:206:ASN:HB3	1:E:214:GLU:H	1.84	0.42
1:A:64:ASP:HB3	1:A:67:GLU:HB2	2.01	0.42
1:G:496:PRO:HG2	1:G:499:VAL:CG2	2.49	0.42
1:H:206:ASN:C	1:H:207:LYS:HD2	2.40	0.42
1:J:295:LEU:HD23	1:J:332:ILE:HD11	2.02	0.42
1:B:21:ASN:HA	1:B:97:GLN:HE22	1.84	0.42
1:A:39:VAL:HA	1:A:48:THR:O	2.19	0.42
1:L:420:ILE:HG13	1:L:451:LEU:CD2	2.44	0.42
1:A:71:ALA:HA	1:A:74:VAL:HG22	2.01	0.42
1:D:215:LEU:HB3	1:D:246:PRO:HB2	2.02	0.42
1:B:261:THR:CB	2:P:29:GLY:H	2.26	0.42
1:C:225:LYS:CD	1:C:309:LEU:HG	2.49	0.42
1:C:144:ILE:O	1:C:147:VAL:HG22	2.19	0.42
1:N:193:MET:H	1:N:332:ILE:HG13	1.84	0.42
1:J:308:GLU:HG2	1:J:309:LEU:N	2.35	0.42
1:F:124:VAL:HG21	1:F:508:ALA:CB	2.49	0.42
1:F:23:LEU:CD1	1:F:23:LEU:C	2.88	0.42
1:J:26:ALA:O	1:J:29:VAL:HG22	2.19	0.42
1:M:228:SER:HB3	1:M:255:GLU:OE1	2.20	0.42
1:B:142:LYS:O	1:B:146:GLN:HG3	2.20	0.42
1:M:177:VAL:CG1	1:M:393:LYS:HG3	2.49	0.42
1:D:85:ALA:O	1:D:401:HIS:HB3	2.20	0.42
1:A:197:ARG:HG2	1:A:277:LYS:O	2.18	0.42
1:B:219:PHE:O	1:B:247:LEU:HD22	2.20	0.42
1:F:350:ARG:HA	1:F:353:ILE:HD12	2.01	0.42
1:E:240:VAL:HG21	1:E:247:LEU:HD23	2.02	0.42
1:A:399:ALA:O	1:A:403:THR:HG23	2.20	0.42
1:F:31:LEU:HD12	4:F:1526:ADP:H5'1	2.00	0.42
1:M:271:VAL:HG12	1:M:273:VAL:HG13	2.01	0.42
1:M:421:ARG:HD2	1:M:474:GLY:O	2.20	0.42
1:E:124:VAL:HG21	1:E:508:ALA:CB	2.49	0.42
1:A:124:VAL:HG21	1:A:508:ALA:CB	2.49	0.42
1:D:124:VAL:HG13	1:D:504:LEU:CD1	2.49	0.42
1:N:386:GLU:HG2	1:N:390:LYS:HE2	2.01	0.42
1:L:32:GLY:H	1:L:457:ASN:HD22	1.67	0.42
1:I:225:LYS:HD3	1:I:303:GLU:CG	2.49	0.42
2:O:4:ARG:HB3	2:U:94:ILE:O	2.19	0.42
1:M:284:ARG:HG2	1:M:364:LYS:HE2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:478:TYR:HB2	1:G:485:TYR:CE2	2.54	0.42
1:L:496:PRO:O	1:L:499:VAL:HG22	2.18	0.42
1:H:496:PRO:O	1:H:499:VAL:HG22	2.20	0.42
2:O:6:LEU:HD22	2:O:6:LEU:HA	1.84	0.42
1:B:291:ASP:HB3	1:B:345:ARG:HH21	1.83	0.42
1:B:20:VAL:HG13	1:B:74:VAL:HG11	2.00	0.42
1:D:291:ASP:HB2	1:D:372:LEU:HD21	2.00	0.42
1:A:239:ALA:HB1	1:A:314:LEU:CD2	2.49	0.42
1:G:124:VAL:HG21	1:G:508:ALA:HB1	2.01	0.42
1:C:199:TYR:O	1:C:199:TYR:CD1	2.72	0.42
1:D:496:PRO:HG2	1:D:499:VAL:CG2	2.49	0.42
1:C:221:LEU:HD11	1:C:301:ILE:CD1	2.49	0.42
1:E:496:PRO:HG2	1:E:499:VAL:CG2	2.49	0.42
1:G:478:TYR:OH	1:G:483:GLU:HA	2.20	0.42
1:L:194:GLN:HG3	1:L:331:THR:HB	2.01	0.42
1:M:178:GLU:OE2	1:M:322:ARG:HD3	2.19	0.42
1:C:392:LYS:O	1:C:396:VAL:HG23	2.20	0.42
1:H:386:GLU:HG2	1:H:390:LYS:HE2	2.02	0.42
1:E:103:GLY:O	1:E:107:VAL:HG23	2.20	0.42
1:A:37:ASN:OD1	1:A:51:LYS:HB2	2.19	0.42
1:F:56:VAL:O	1:F:60:ILE:HG12	2.20	0.42
1:I:259:LEU:O	1:I:263:VAL:HG23	2.20	0.42
1:D:418:ALA:O	1:D:422:VAL:HG13	2.19	0.42
1:K:494:LEU:HD23	1:K:494:LEU:N	2.34	0.42
1:M:130:GLU:HA	1:M:130:GLU:OE1	2.19	0.42
1:C:33:PRO:HD3	4:C:1526:ADP:C5	2.54	0.42
2:R:43:VAL:HG23	2:R:61:VAL:HG22	2.01	0.42
1:G:147:VAL:O	1:G:150:ILE:HG22	2.18	0.42
1:E:147:VAL:HG12	1:E:494:LEU:HB2	2.01	0.42
1:I:124:VAL:HG13	1:I:504:LEU:HD13	2.02	0.42
1:F:443:ALA:O	1:F:447:MET:HG3	2.19	0.42
1:D:42:LYS:HB2	1:D:44:PHE:CD2	2.54	0.42
1:C:66:PHE:CZ	1:C:522:THR:HG22	2.55	0.42
1:N:46:ALA:HB1	1:N:47:PRO:HD2	2.02	0.42
1:N:496:PRO:HD2	1:N:499:VAL:CG2	2.49	0.42
1:L:239:ALA:HB1	1:L:314:LEU:CD1	2.46	0.42
1:N:65:LYS:O	1:N:66:PHE:HB2	2.20	0.42
1:N:247:LEU:HB3	1:N:273:VAL:CG1	2.50	0.42
1:M:8:PHE:HA	1:M:12:ALA:HB2	2.01	0.42
1:C:33:PRO:HA	1:C:153:ASN:HD21	1.82	0.42
1:B:302:SER:CB	1:B:305:ILE:HB	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:ILE:HD11	4:B:1526:ADP:N7	2.34	0.42
2:S:31:ALA:O	2:S:32:ALA:HB3	2.19	0.42
1:C:183:LEU:HD22	1:C:384:ALA:HA	2.01	0.42
1:B:360:TYR:O	1:B:364:LYS:HG2	2.19	0.42
1:K:224:ASP:CB	1:K:302:SER:HA	2.50	0.42
1:B:309:LEU:H	1:B:309:LEU:HD12	1.84	0.42
1:C:76:GLU:OE1	1:D:387:VAL:HG13	2.20	0.42
1:N:237:LEU:O	1:N:240:VAL:HG22	2.20	0.42
1:L:177:VAL:CG1	1:L:393:LYS:HG3	2.49	0.42
1:M:106:ALA:O	1:M:111:MET:HB2	2.19	0.42
1:M:116:LEU:HD23	1:M:435:ASP:O	2.19	0.42
1:H:66:PHE:CZ	1:H:522:THR:HG22	2.54	0.42
1:G:71:ALA:HA	1:G:74:VAL:HG22	2.01	0.42
1:N:426:LEU:HD11	1:N:444:LEU:HD21	2.01	0.42
1:M:13:ARG:HA	1:M:16:MET:CE	2.50	0.42
1:H:262:LEU:O	1:H:266:THR:HG23	2.19	0.42
1:K:215:LEU:HB2	1:K:218:PRO:HG3	2.02	0.42
1:D:220:ILE:HD12	1:D:296:THR:HG21	2.02	0.42
1:K:191:GLU:HB3	1:K:295:LEU:HD11	2.02	0.42
1:J:102:GLU:OE1	1:J:102:GLU:HA	2.20	0.42
1:F:120:ILE:O	1:F:124:VAL:HG23	2.19	0.42
1:H:117:LYS:HD2	1:H:516:THR:CG2	2.50	0.42
1:N:400:LEU:HD21	1:N:404:ARG:HE	1.83	0.42
1:M:20:VAL:HG23	1:M:74:VAL:HG21	2.02	0.42
1:M:455:VAL:HG13	1:M:460:GLU:HB2	2.02	0.42
1:F:313:THR:HG22	1:F:314:LEU:H	1.85	0.42
1:E:512:GLY:O	1:E:516:THR:HG23	2.20	0.42
1:M:57:ALA:O	1:M:75:LYS:HE3	2.20	0.42
1:D:265:ASN:HB3	1:D:271:VAL:HG22	2.02	0.42
1:J:49:ILE:HG21	1:K:513:LEU:HD11	2.01	0.42
1:N:420:ILE:HG13	1:N:451:LEU:CD2	2.43	0.42
1:F:69:MET:O	1:F:73:MET:HG3	2.20	0.42
1:D:302:SER:CB	1:D:305:ILE:HB	2.50	0.42
2:P:78:ILE:CD1	2:P:83:VAL:HG21	2.50	0.42
1:A:388:GLU:OE1	1:G:509:SER:HB3	2.20	0.42
1:N:120:ILE:O	1:N:124:VAL:HG23	2.20	0.42
1:E:147:VAL:HA	1:E:150:ILE:HG22	2.02	0.42
1:G:28:LYS:HD2	1:G:453:GLN:CD	2.41	0.42
2:U:6:LEU:HD23	2:U:6:LEU:HA	1.95	0.42
1:G:31:LEU:CD1	4:G:1526:ADP:H5'1	2.50	0.42
1:G:265:ASN:OD1	2:U:27:LEU:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:56:VAL:O	1:M:60:ILE:HG12	2.20	0.42
1:G:37:ASN:OD1	1:G:51:LYS:HB2	2.20	0.42
1:N:112:ASN:HA	1:N:113:PRO:HD3	1.89	0.42
1:F:247:LEU:HD13	1:F:248:LEU:N	2.35	0.41
1:B:247:LEU:HB3	1:B:273:VAL:HG22	2.02	0.41
1:G:219:PHE:O	1:G:247:LEU:HD22	2.20	0.41
1:M:17:LEU:HB2	1:M:104:LEU:CD2	2.49	0.41
1:B:217:SER:N	1:B:218:PRO:HD3	2.35	0.41
1:I:166:MET:HE1	1:I:407:VAL:HG21	2.02	0.41
1:H:179:ASP:HA	1:H:389:MET:HE3	2.01	0.41
1:H:177:VAL:HG11	1:H:393:LYS:HG3	2.02	0.41
1:B:23:LEU:C	1:B:23:LEU:HD13	2.40	0.41
1:M:235:PRO:HG3	1:M:310:GLU:HG3	2.02	0.41
1:I:169:VAL:HG22	1:I:173:GLY:HA3	2.02	0.41
2:S:60:LYS:HG2	2:S:63:ASP:OD2	2.20	0.41
1:A:349:ILE:HG22	1:A:353:ILE:HG13	2.02	0.41
1:E:37:ASN:HB3	1:E:49:ILE:CG2	2.49	0.41
1:F:221:LEU:HD13	1:F:317:LEU:HD21	2.02	0.41
1:B:266:THR:HA	1:B:271:VAL:O	2.20	0.41
2:U:3:ILE:HD13	2:U:11:ILE:HG21	2.03	0.41
2:R:78:ILE:HD13	2:R:83:VAL:CG2	2.44	0.41
1:C:286:LYS:HA	1:C:289:LEU:HD12	2.01	0.41
1:K:266:THR:HG21	1:K:273:VAL:O	2.20	0.41
1:E:10:ASN:O	1:E:14:VAL:HG23	2.19	0.41
1:F:25:ASP:HA	1:F:28:LYS:HD3	2.02	0.41
1:B:28:LYS:HG2	1:B:94:VAL:HG22	2.02	0.41
1:F:19:GLY:HA3	1:F:67:GLU:O	2.20	0.41
1:E:215:LEU:HD22	1:E:246:PRO:HB3	2.01	0.41
1:K:460:GLU:O	1:K:462:PRO:HD3	2.20	0.41
1:E:200:LEU:HD22	1:E:254:VAL:HB	2.02	0.41
2:O:74:LYS:HB2	2:O:85:ILE:HB	2.02	0.41
1:I:362:ARG:HG2	1:I:362:ARG:HH11	1.84	0.41
1:L:155:ASP:HB2	1:L:395:ARG:NH2	2.33	0.41
1:A:228:SER:HA	1:A:255:GLU:HB2	2.01	0.41
1:C:149:THR:HG23	1:C:155:ASP:C	2.40	0.41
1:D:142:LYS:O	1:D:146:GLN:HG3	2.19	0.41
1:G:348:GLN:HE22	1:G:352:GLN:HE21	1.68	0.41
1:B:199:TYR:CD1	1:B:199:TYR:O	2.72	0.41
1:M:443:ALA:O	1:M:447:MET:HG3	2.20	0.41
1:N:426:LEU:CD1	1:N:444:LEU:HD21	2.49	0.41
1:F:288:MET:HG2	1:F:368:ARG:HE	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:291:ASP:HB2	1:F:372:LEU:CD2	2.50	0.41
2:S:73:VAL:HG11	2:S:84:LEU:HD23	2.02	0.41
1:A:313:THR:HG22	1:A:314:LEU:N	2.35	0.41
1:L:287:ALA:HB1	1:L:368:ARG:NH2	2.35	0.41
1:K:20:VAL:CG2	1:K:74:VAL:HG21	2.50	0.41
1:I:504:LEU:HD22	1:I:504:LEU:O	2.20	0.41
1:J:233:MET:HE1	1:J:309:LEU:HD13	2.03	0.41
1:C:21:ASN:HD22	1:C:97:GLN:HE22	1.68	0.41
1:B:496:PRO:HG2	1:B:499:VAL:CG2	2.50	0.41
1:N:321:LYS:HD2	1:N:334:ASP:OD2	2.20	0.41
1:H:478:TYR:HB2	1:H:485:TYR:CE2	2.56	0.41
1:A:28:LYS:HG2	1:A:94:VAL:HG22	2.01	0.41
1:B:165:ALA:O	1:B:169:VAL:HG22	2.20	0.41
1:J:428:ASP:O	1:J:430:ARG:HG2	2.20	0.41
1:F:82:ASN:ND2	1:F:86:GLY:HA2	2.35	0.41
1:A:262:LEU:O	1:A:266:THR:HG23	2.19	0.41
1:B:252:GLU:HG3	1:B:285:ARG:HH11	1.86	0.41
1:D:207:LYS:CB	1:D:208:PRO:HD3	2.45	0.41
1:B:217:SER:N	1:B:218:PRO:CD	2.84	0.41
1:I:277:LYS:NZ	1:I:277:LYS:HB2	2.34	0.41
1:C:199:TYR:CZ	1:C:202:PRO:HA	2.56	0.41
1:H:40:LEU:HD22	1:H:40:LEU:N	2.36	0.41
1:J:46:ALA:HB1	1:J:47:PRO:HD2	2.02	0.41
1:L:350:ARG:HE	1:L:369:VAL:HG11	1.85	0.41
1:K:116:LEU:HD23	1:K:435:ASP:O	2.20	0.41
1:H:116:LEU:HD23	1:H:435:ASP:O	2.20	0.41
1:J:27:VAL:HG11	1:J:93:THR:HG21	2.02	0.41
1:M:84:ALA:O	1:M:498:LYS:HE2	2.20	0.41
1:J:277:LYS:HB2	1:J:277:LYS:NZ	2.36	0.41
1:B:350:ARG:HA	1:B:353:ILE:HD12	2.03	0.41
1:N:444:LEU:O	1:N:447:MET:HB2	2.20	0.41
2:O:43:VAL:HG23	2:O:61:VAL:HG22	2.03	0.41
1:N:409:GLU:OE1	1:N:498:LYS:HA	2.20	0.41
1:C:518:GLU:HB2	1:D:36:ARG:HB3	2.02	0.41
1:L:166:MET:HE2	1:L:171:LYS:HA	2.02	0.41
1:B:209:GLU:O	1:B:210:THR:CB	2.68	0.41
2:S:18:GLU:OE1	2:S:33:ALA:HB3	2.20	0.41
1:G:85:ALA:HB3	1:G:499:VAL:HG12	2.01	0.41
1:M:225:LYS:HD3	1:M:303:GLU:CG	2.49	0.41
1:M:102:GLU:HB2	1:M:442:VAL:HG13	2.01	0.41
1:A:361:ASP:O	1:A:365:LEU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:PHE:CD1	1:B:197:ARG:NH1	2.88	0.41
1:C:231:ARG:HH11	1:C:231:ARG:HD2	1.75	0.41
1:G:466:ALA:O	1:G:470:LYS:HG3	2.21	0.41
1:C:200:LEU:HD12	1:C:200:LEU:N	2.36	0.41
1:C:320:ALA:HA	1:C:335:GLY:HA2	2.02	0.41
1:J:409:GLU:OE1	1:J:498:LYS:HA	2.20	0.41
2:Q:77:LYS:HE3	2:Q:80:ASN:HA	2.01	0.41
1:C:124:VAL:HG21	1:C:508:ALA:HB1	2.03	0.41
1:K:285:ARG:HG3	1:K:286:LYS:N	2.36	0.41
1:G:209:GLU:O	1:G:210:THR:CB	2.69	0.41
2:T:66:ILE:HB	2:T:93:ALA:HB3	2.02	0.41
1:D:100:ILE:HD13	1:D:514:MET:SD	2.61	0.41
1:D:17:LEU:HD13	1:D:104:LEU:HD12	2.03	0.41
1:K:186:GLU:HB2	1:K:380:LYS:HB2	2.03	0.41
1:G:26:ALA:O	1:G:29:VAL:HG22	2.21	0.41
1:D:426:LEU:HB2	1:D:444:LEU:HD21	2.02	0.41
1:M:101:THR:O	1:M:105:LYS:HG3	2.20	0.41
1:A:209:GLU:C	1:A:211:GLY:H	2.23	0.41
1:J:496:PRO:HD2	1:J:499:VAL:CG2	2.49	0.41
1:D:197:ARG:HD2	1:D:279:PRO:HA	2.02	0.41
2:R:12:VAL:HG22	2:R:86:MET:SD	2.60	0.41
1:K:247:LEU:H	1:K:273:VAL:HG12	1.86	0.41
2:Q:12:VAL:HA	2:Q:39:GLU:O	2.21	0.41
1:A:31:LEU:HD12	4:A:1526:ADP:C5'	2.51	0.41
1:C:225:LYS:O	1:C:251:ALA:HB1	2.21	0.41
1:C:24:ALA:O	1:C:28:LYS:HG3	2.21	0.41
1:N:494:LEU:HD23	1:N:494:LEU:N	2.35	0.41
1:A:280:GLY:H	1:A:285:ARG:HB3	1.85	0.41
1:G:10:ASN:O	1:G:14:VAL:HG23	2.21	0.41
1:B:33:PRO:HA	1:B:153:ASN:ND2	2.35	0.41
1:E:414:GLY:O	1:E:417:VAL:HG12	2.21	0.41
1:E:144:ILE:O	1:E:147:VAL:HG22	2.20	0.41
1:D:150:ILE:HD11	4:D:1526:ADP:N7	2.36	0.41
1:H:238:GLU:O	1:H:241:ALA:HB3	2.20	0.41
1:G:432:GLN:HB2	1:G:436:GLN:NE2	2.36	0.41
1:F:128:VAL:HG21	1:F:505:GLN:HE21	1.85	0.41
1:A:451:LEU:HD11	1:A:469:VAL:HG11	2.03	0.41
1:D:313:THR:HG22	1:D:314:LEU:N	2.36	0.41
1:N:455:VAL:HG12	1:N:460:GLU:O	2.21	0.41
1:F:479:ASN:HB3	1:F:482:THR:OG1	2.21	0.41
1:C:204:PHE:CG	1:C:274:ALA:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:LEU:CD1	1:B:388:GLU:HA	2.44	0.41
1:E:288:MET:HA	1:E:291:ASP:OD1	2.20	0.41
1:L:16:MET:HG3	1:L:520:MET:SD	2.60	0.41
1:L:66:PHE:O	1:L:69:MET:HB2	2.20	0.41
1:M:277:LYS:NZ	1:M:277:LYS:HB2	2.35	0.41
1:A:320:ALA:HA	1:A:335:GLY:HA2	2.02	0.41
2:O:78:ILE:CD1	2:O:83:VAL:HG21	2.50	0.41
1:N:124:VAL:O	1:N:128:VAL:HG23	2.21	0.41
1:N:227:ILE:HD11	1:N:309:LEU:HD11	2.03	0.41
1:N:24:ALA:HA	1:N:27:VAL:HG12	2.02	0.41
1:H:6:VAL:HG22	1:H:521:VAL:HG22	2.02	0.41
2:P:84:LEU:HD12	2:P:84:LEU:N	2.36	0.41
1:B:206:ASN:CB	1:B:214:GLU:H	2.34	0.41
1:G:400:LEU:HD13	1:G:400:LEU:C	2.41	0.41
1:M:224:ASP:HB3	1:M:302:SER:HA	2.03	0.41
1:A:231:ARG:O	1:A:233:MET:N	2.53	0.41
1:L:230:ILE:CD1	1:L:261:THR:HG21	2.50	0.41
1:C:123:ALA:HB2	1:C:440:ILE:HG23	2.03	0.41
1:H:517:THR:HA	1:N:37:ASN:HD22	1.85	0.41
1:M:385:THR:HG23	1:M:388:GLU:H	1.86	0.41
1:A:2:ALA:HA	1:B:61:GLU:OE1	2.21	0.41
1:D:161:LEU:HD11	1:D:187:LEU:CB	2.36	0.41
1:E:278:ALA:HB1	1:E:279:PRO:CD	2.49	0.41
1:E:280:GLY:CA	1:E:285:ARG:HH21	2.34	0.41
1:D:195:PHE:HE1	1:D:330:THR:HB	1.83	0.41
1:L:49:ILE:HD11	1:M:73:MET:HE1	2.03	0.41
1:M:66:PHE:CE2	1:M:522:THR:HG22	2.56	0.41
1:G:200:LEU:N	1:G:200:LEU:HD12	2.36	0.41
1:G:222:LEU:HD23	1:G:289:LEU:HD22	2.03	0.41
1:E:16:MET:O	1:E:20:VAL:HG23	2.20	0.41
1:C:150:ILE:HD11	4:C:1526:ADP:C5	2.56	0.41
1:E:33:PRO:HG3	4:E:1526:ADP:C6	2.56	0.41
1:J:247:LEU:H	1:J:273:VAL:HG12	1.86	0.41
1:L:149:THR:HG22	1:L:156:GLU:HA	2.02	0.41
1:B:518:GLU:HG2	1:C:29:VAL:HB	2.03	0.41
1:G:414:GLY:HA2	1:G:495:ASP:OD2	2.20	0.41
1:M:266:THR:HG21	1:M:273:VAL:O	2.21	0.41
1:F:420:ILE:HD11	1:F:470:LYS:HG3	2.01	0.41
1:M:504:LEU:O	1:M:504:LEU:HD22	2.21	0.41
1:I:16:MET:HG3	1:I:520:MET:SD	2.61	0.41
1:B:313:THR:HG22	1:B:314:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:149:THR:HG22	1:M:156:GLU:HA	2.02	0.41
1:M:409:GLU:OE1	1:M:498:LYS:HA	2.21	0.41
1:I:272:LYS:HB2	1:I:272:LYS:HE2	1.92	0.41
1:G:142:LYS:HE2	1:G:146:GLN:OE1	2.20	0.41
2:T:86:MET:HB2	2:T:90:ASP:OD2	2.21	0.41
1:D:54:VAL:HB	1:D:89:THR:HG21	2.03	0.41
1:G:178:GLU:O	1:G:380:LYS:HA	2.21	0.41
1:K:13:ARG:HA	1:K:16:MET:CE	2.51	0.41
1:J:223:ALA:HB3	1:J:251:ALA:HB2	2.03	0.41
1:H:186:GLU:OE1	1:H:380:LYS:HD2	2.20	0.41
2:U:50:GLU:O	2:U:50:GLU:HG2	2.21	0.41
1:E:400:LEU:C	1:E:400:LEU:HD13	2.42	0.41
1:A:236:VAL:HG22	1:A:312:ALA:O	2.19	0.41
1:M:356:ALA:HB1	1:M:362:ARG:HH21	1.85	0.41
1:K:226:LYS:HG3	1:K:252:GLU:HB2	2.03	0.41
1:D:361:ASP:O	1:D:365:LEU:HB2	2.21	0.41
1:C:117:LYS:HE3	1:C:513:LEU:CD2	2.51	0.41
2:R:78:ILE:C	2:R:80:ASN:H	2.24	0.41
1:K:41:ASP:OD1	1:L:69:MET:HG2	2.21	0.41
1:A:36:ARG:CB	1:G:518:GLU:HB2	2.51	0.41
2:Q:7:HIS:O	2:Q:8:ASP:HB3	2.19	0.41
1:N:106:ALA:O	1:N:111:MET:HE2	2.21	0.41
1:L:166:MET:HE3	1:L:407:VAL:HG21	2.02	0.41
1:A:238:GLU:HG3	1:A:239:ALA:N	2.36	0.41
1:F:21:ASN:HA	1:F:97:GLN:HE22	1.86	0.41
2:R:7:HIS:O	2:R:8:ASP:HB3	2.20	0.41
1:E:209:GLU:O	1:E:210:THR:CB	2.69	0.41
1:L:199:TYR:HA	1:L:276:VAL:HG12	2.03	0.41
1:I:138:CYS:SG	1:I:144:ILE:HD13	2.61	0.41
1:M:321:LYS:HD2	1:M:334:ASP:OD2	2.21	0.41
1:N:223:ALA:HB3	1:N:251:ALA:HB2	2.02	0.41
1:D:392:LYS:O	1:D:396:VAL:HG23	2.20	0.41
1:M:160:LYS:O	1:M:164:GLU:HG3	2.20	0.41
1:L:4:LYS:HD2	1:L:521:VAL:HG12	2.03	0.41
1:K:308:GLU:HB3	1:K:311:LYS:HD3	2.03	0.41
1:G:175:ILE:HG12	1:G:377:ALA:HB3	2.03	0.41
1:E:82:ASN:ND2	1:E:86:GLY:HA2	2.36	0.41
1:J:116:LEU:HD23	1:J:435:ASP:O	2.21	0.41
2:O:31:ALA:O	2:O:32:ALA:HB3	2.21	0.41
1:N:179:ASP:HA	1:N:389:MET:CE	2.50	0.41
1:G:112:ASN:HA	1:G:113:PRO:HD3	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:349:ILE:HG22	1:G:353:ILE:HG13	2.02	0.40
1:C:325:ILE:HG12	1:C:330:THR:HG23	2.03	0.40
1:K:66:PHE:HD1	1:K:520:MET:HE2	1.87	0.40
1:H:230:ILE:HD13	1:H:230:ILE:N	2.36	0.40
1:I:65:LYS:O	1:I:66:PHE:CB	2.68	0.40
1:E:219:PHE:HB2	1:E:247:LEU:HD22	2.03	0.40
1:B:199:TYR:CE1	1:B:202:PRO:HA	2.56	0.40
1:H:65:LYS:O	1:H:66:PHE:CB	2.68	0.40
1:M:179:ASP:HA	1:M:389:MET:CE	2.51	0.40
1:D:30:THR:HG22	1:D:36:ARG:O	2.21	0.40
1:D:414:GLY:HA2	1:D:495:ASP:OD2	2.21	0.40
1:C:217:SER:N	1:C:218:PRO:HD3	2.36	0.40
1:I:288:MET:CE	1:I:288:MET:HA	2.51	0.40
1:E:124:VAL:O	1:E:128:VAL:HG23	2.21	0.40
1:G:443:ALA:O	1:G:447:MET:HG3	2.21	0.40
1:N:230:ILE:CD1	1:N:261:THR:HG21	2.51	0.40
1:I:263:VAL:O	1:I:267:MET:HG2	2.20	0.40
1:F:409:GLU:O	1:F:409:GLU:HG2	2.21	0.40
1:K:294:THR:HG21	1:K:345:ARG:HB2	2.03	0.40
1:G:357:THR:HG22	1:G:359:ASP:O	2.21	0.40
1:J:178:GLU:OE2	1:J:322:ARG:HD3	2.21	0.40
1:E:130:GLU:O	1:E:134:LEU:HD13	2.21	0.40
1:F:215:LEU:HB3	1:F:246:PRO:HB2	2.03	0.40
1:L:494:LEU:N	1:L:494:LEU:HD23	2.36	0.40
2:R:78:ILE:O	2:R:79:ASP:HB2	2.21	0.40
1:G:219:PHE:CE2	1:G:245:LYS:HB2	2.56	0.40
1:B:200:LEU:N	1:B:200:LEU:HD12	2.36	0.40
1:A:147:VAL:HG12	1:A:494:LEU:HB2	2.04	0.40
1:J:13:ARG:HB3	1:J:104:LEU:CD1	2.49	0.40
1:M:15:LYS:O	1:M:67:GLU:HA	2.22	0.40
1:J:247:LEU:HB3	1:J:273:VAL:CG1	2.52	0.40
1:N:150:ILE:HG21	1:N:494:LEU:CD2	2.51	0.40
1:D:26:ALA:O	1:D:29:VAL:HG22	2.21	0.40
1:K:199:TYR:CE2	1:K:327:LYS:HA	2.57	0.40
1:G:225:LYS:HD2	1:G:226:LYS:H	1.86	0.40
1:E:21:ASN:HA	1:E:97:GLN:HE22	1.87	0.40
1:I:193:MET:H	1:I:332:ILE:HG13	1.87	0.40
1:L:426:LEU:CD1	1:L:444:LEU:HD21	2.51	0.40
1:A:496:PRO:HG2	1:A:499:VAL:CG2	2.51	0.40
1:G:391:GLU:OE1	1:G:391:GLU:HA	2.22	0.40
1:L:259:LEU:O	1:L:263:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:241:ALA:HB2	1:K:271:VAL:HG21	2.04	0.40
1:N:131:LEU:HD11	1:N:412:VAL:HG11	2.03	0.40
1:L:223:ALA:HB3	1:L:251:ALA:HB2	2.01	0.40
1:A:322:ARG:HG2	1:A:323:VAL:N	2.36	0.40
1:L:496:PRO:HD2	1:L:499:VAL:HG21	2.04	0.40
2:R:78:ILE:HD12	2:R:78:ILE:N	2.35	0.40
1:F:73:MET:CE	1:G:49:ILE:HD11	2.50	0.40
1:B:77:VAL:HG11	1:B:510:VAL:HG21	2.01	0.40
1:E:71:ALA:HA	1:E:74:VAL:HG22	2.04	0.40
1:M:165:ALA:HB1	1:M:175:ILE:CD1	2.49	0.40
1:C:518:GLU:HG2	1:D:29:VAL:HB	2.03	0.40
1:D:147:VAL:O	1:D:150:ILE:HG22	2.21	0.40
1:B:419:LEU:HA	1:B:422:VAL:HG22	2.03	0.40
1:L:40:LEU:HD21	1:L:56:VAL:HG22	2.03	0.40
1:J:124:VAL:HG21	1:J:508:ALA:CB	2.52	0.40
1:N:475:ASN:HB2	1:N:487:ASN:ND2	2.36	0.40
1:D:239:ALA:HB1	1:D:314:LEU:CD2	2.51	0.40
1:C:116:LEU:HD23	1:C:435:ASP:O	2.19	0.40
1:F:465:VAL:O	1:F:469:VAL:HG23	2.22	0.40
1:N:346:VAL:O	1:N:350:ARG:HG2	2.21	0.40
1:E:100:ILE:HD13	1:E:514:MET:SD	2.62	0.40
1:H:205:ILE:HG23	1:H:212:ALA:O	2.21	0.40
1:E:73:MET:SD	1:F:49:ILE:HD11	2.62	0.40
1:E:219:PHE:HB3	1:E:317:LEU:HB3	2.03	0.40
1:N:247:LEU:HB3	1:N:273:VAL:HG11	2.02	0.40
1:I:166:MET:HE2	1:I:171:LYS:HA	2.04	0.40
1:G:420:ILE:HD11	1:G:470:LYS:CG	2.51	0.40
1:K:201:SER:HA	1:K:202:PRO:HD3	1.98	0.40
1:M:193:MET:H	1:M:332:ILE:HG13	1.86	0.40
1:D:147:VAL:HA	1:D:150:ILE:HG22	2.03	0.40
1:D:493:ILE:HD13	4:D:1526:ADP:C2	2.56	0.40
1:F:2:ALA:HA	1:G:61:GLU:OE1	2.22	0.40
1:E:257:GLU:HG3	2:S:31:ALA:HB1	2.03	0.40
1:D:62:LEU:HD23	1:D:67:GLU:HB3	2.04	0.40
1:K:28:LYS:HD2	1:K:453:GLN:OE1	2.21	0.40
1:E:23:LEU:CD1	1:E:23:LEU:C	2.89	0.40
1:J:461:GLU:HB2	1:J:464:VAL:HB	2.03	0.40
2:T:69:ASP:HA	2:T:73:VAL:HG21	2.03	0.40
1:N:219:PHE:HB3	1:N:317:LEU:HD23	2.02	0.40
1:M:348:GLN:O	1:M:352:GLN:HG3	2.22	0.40
1:B:234:LEU:N	1:B:235:PRO:HD2	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:76:GLU:OE1	1:F:387:VAL:HG13	2.22	0.40
1:C:98:ALA:HB3	1:C:446:ALA:HB1	2.02	0.40
1:M:63:GLU:HB2	1:N:3:ALA:HB1	2.03	0.40
1:A:215:LEU:O	1:A:322:ARG:HG3	2.22	0.40
1:B:219:PHE:HB2	1:B:247:LEU:CD2	2.52	0.40
1:B:262:LEU:O	1:B:266:THR:HG23	2.21	0.40
1:J:13:ARG:HA	1:J:16:MET:HE3	2.03	0.40
1:J:13:ARG:HA	1:J:16:MET:HE2	2.02	0.40
1:I:383:ALA:HB3	1:I:389:MET:HB2	2.04	0.40
1:J:426:LEU:N	1:J:426:LEU:HD23	2.37	0.40
1:I:120:ILE:O	1:I:124:VAL:HG23	2.21	0.40
1:C:278:ALA:HB1	1:C:279:PRO:CD	2.52	0.40
1:M:219:PHE:HB3	1:M:317:LEU:HD23	2.03	0.40
1:J:465:VAL:O	1:J:469:VAL:HG23	2.22	0.40
1:J:342:ILE:HG23	1:J:372:LEU:HD11	2.03	0.40
1:G:205:ILE:HG12	1:G:211:GLY:HA2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	523/526 (99%)	503 (96%)	13 (2%)	7 (1%)	15	60
1	B	523/526 (99%)	497 (95%)	19 (4%)	7 (1%)	15	60
1	C	523/526 (99%)	503 (96%)	11 (2%)	9 (2%)	11	55
1	D	523/526 (99%)	505 (97%)	10 (2%)	8 (2%)	13	57
1	E	523/526 (99%)	501 (96%)	14 (3%)	8 (2%)	13	57
1	F	523/526 (99%)	498 (95%)	16 (3%)	9 (2%)	11	55
1	G	523/526 (99%)	506 (97%)	8 (2%)	9 (2%)	11	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	523/526 (99%)	515 (98%)	6 (1%)	2 (0%)	39	80
1	I	523/526 (99%)	511 (98%)	9 (2%)	3 (1%)	30	74
1	J	523/526 (99%)	514 (98%)	8 (2%)	1 (0%)	52	86
1	K	523/526 (99%)	514 (98%)	7 (1%)	2 (0%)	39	80
1	L	523/526 (99%)	510 (98%)	12 (2%)	1 (0%)	52	86
1	M	523/526 (99%)	512 (98%)	10 (2%)	1 (0%)	52	86
1	N	523/526 (99%)	511 (98%)	7 (1%)	5 (1%)	19	65
2	O	95/97 (98%)	88 (93%)	4 (4%)	3 (3%)	5	41
2	P	95/97 (98%)	87 (92%)	4 (4%)	4 (4%)	3	34
2	Q	95/97 (98%)	87 (92%)	5 (5%)	3 (3%)	5	41
2	R	95/97 (98%)	87 (92%)	2 (2%)	6 (6%)	2	25
2	S	95/97 (98%)	86 (90%)	5 (5%)	4 (4%)	3	34
2	T	95/97 (98%)	86 (90%)	5 (5%)	4 (4%)	3	34
2	U	95/97 (98%)	87 (92%)	5 (5%)	3 (3%)	5	41
All	All	7987/8043 (99%)	7708 (96%)	180 (2%)	99 (1%)	21	61

All (99) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	THR
1	A	312	ALA
1	B	210	THR
1	B	232	GLU
1	B	358	SER
1	C	232	GLU
1	C	312	ALA
1	D	210	THR
1	D	233	MET
1	D	312	ALA
1	E	210	THR
1	E	232	GLU
1	E	312	ALA
1	F	3	ALA
1	F	232	GLU
1	F	256	GLY
1	F	312	ALA
1	G	210	THR

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Mol	Chain	Res	Type
1	G	233	MET
1	G	279	PRO
1	I	66	PHE
1	J	66	PHE
1	K	66	PHE
1	L	66	PHE
1	M	66	PHE
1	N	66	PHE
2	O	7	HIS
2	O	32	ALA
2	P	7	HIS
2	Q	7	HIS
2	R	7	HIS
2	R	21	SER
2	R	32	ALA
2	R	51	ASN
2	R	80	ASN
2	S	7	HIS
2	S	51	ASN
2	T	7	HIS
2	T	51	ASN
2	U	7	HIS
2	U	51	ASN
1	A	232	GLU
1	A	282	GLY
1	A	306	GLY
1	A	358	SER
1	B	206	ASN
1	B	360	TYR
1	C	305	ILE
1	C	356	ALA
1	E	207	LYS
1	F	207	LYS
1	F	282	GLY
1	F	358	SER
1	G	207	LYS
1	H	66	PHE
1	H	356	ALA
1	I	525	PRO
2	P	32	ALA
2	R	53	GLU
2	S	52	GLY

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Mol	Chain	Res	Type
2	T	53	GLU
1	A	207	LYS
1	B	312	ALA
1	C	207	LYS
1	C	358	SER
1	D	207	LYS
1	D	358	SER
1	E	306	GLY
1	E	358	SER
1	F	209	GLU
1	F	525	PRO
1	G	312	ALA
1	N	197	ARG
2	P	51	ASN
2	Q	51	ASN
2	T	15	LYS
2	U	20	LYS
1	C	209	GLU
1	C	311	LYS
1	D	525	PRO
1	G	358	SER
2	O	51	ASN
2	Q	53	GLU
2	S	32	ALA
1	E	525	PRO
1	G	109	ALA
1	N	337	GLY
1	N	525	PRO
2	P	53	GLU
1	D	278	ALA
1	D	360	TYR
1	E	233	MET
1	G	230	ILE
1	N	152	ALA
1	B	305	ILE
1	C	230	ILE
1	K	525	PRO
1	I	337	GLY
1	G	525	PRO

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 PDB entries followed by that with respect to all EM entries.

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	404/406 (100%)	384 (95%)	20 (5%)	30	66
1	B	404/406 (100%)	383 (95%)	21 (5%)	29	65
1	C	404/406 (100%)	391 (97%)	13 (3%)	46	76
1	D	404/406 (100%)	383 (95%)	21 (5%)	29	65
1	E	404/406 (100%)	379 (94%)	25 (6%)	23	60
1	F	404/406 (100%)	380 (94%)	24 (6%)	24	61
1	G	404/406 (100%)	385 (95%)	19 (5%)	32	68
1	H	404/406 (100%)	388 (96%)	16 (4%)	38	71
1	I	404/406 (100%)	392 (97%)	12 (3%)	48	77
1	J	404/406 (100%)	388 (96%)	16 (4%)	38	71
1	K	404/406 (100%)	390 (96%)	14 (4%)	43	74
1	L	404/406 (100%)	391 (97%)	13 (3%)	46	76
1	M	404/406 (100%)	391 (97%)	13 (3%)	46	76
1	N	404/406 (100%)	385 (95%)	19 (5%)	32	68
2	O	80/80 (100%)	73 (91%)	7 (9%)	12	45
2	P	80/80 (100%)	71 (89%)	9 (11%)	7	33
2	Q	80/80 (100%)	75 (94%)	5 (6%)	22	59
2	R	80/80 (100%)	75 (94%)	5 (6%)	22	59
2	S	80/80 (100%)	73 (91%)	7 (9%)	12	45
2	T	80/80 (100%)	74 (92%)	6 (8%)	17	53
2	U	80/80 (100%)	75 (94%)	5 (6%)	22	59
All	All	6216/6244 (100%)	5926 (95%)	290 (5%)	37	68

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

Mol	Chain	Res	Type
1	A	18	ARG

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Mol	Chain	Res	Type
1	A	44	PHE
1	A	62	LEU
1	A	77	VAL
1	A	184	GLN
1	A	196	ASP
1	A	199	TYR
1	A	225	LYS
1	A	230	ILE
1	A	231	ARG
1	A	234	LEU
1	A	238	GLU
1	A	247	LEU
1	A	255	GLU
1	A	314	LEU
1	A	315	GLU
1	A	348	GLN
1	A	360	TYR
1	A	385	THR
1	A	461	GLU
1	B	4	LYS
1	B	18	ARG
1	B	41	ASP
1	B	44	PHE
1	B	77	VAL
1	B	168	LYS
1	B	199	TYR
1	B	207	LYS
1	B	232	GLU
1	B	237	LEU
1	B	257	GLU
1	B	261	THR
1	B	267	MET
1	B	302	SER
1	B	305	ILE
1	B	315	GLU
1	B	327	LYS
1	B	348	GLN
1	B	360	TYR
1	B	461	GLU
1	B	490	ASP
1	C	18	ARG
1	C	44	PHE

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Mol	Chain	Res	Type
1	C	199	TYR
1	C	204	PHE
1	C	225	LYS
1	C	230	ILE
1	C	234	LEU
1	C	257	GLU
1	C	261	THR
1	C	313	THR
1	C	315	GLU
1	C	360	TYR
1	C	461	GLU
1	D	42	LYS
1	D	44	PHE
1	D	62	LEU
1	D	77	VAL
1	D	154	SER
1	D	184	GLN
1	D	199	TYR
1	D	225	LYS
1	D	231	ARG
1	D	257	GLU
1	D	261	THR
1	D	267	MET
1	D	302	SER
1	D	314	LEU
1	D	315	GLU
1	D	327	LYS
1	D	348	GLN
1	D	360	TYR
1	D	419	LEU
1	D	461	GLU
1	D	501	ARG
1	E	18	ARG
1	E	23	LEU
1	E	44	PHE
1	E	62	LEU
1	E	77	VAL
1	E	154	SER
1	E	196	ASP
1	E	199	TYR
1	E	207	LYS
1	E	225	LYS

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Mol	Chain	Res	Type
1	E	229	ASN
1	E	231	ARG
1	E	238	GLU
1	E	255	GLU
1	E	257	GLU
1	E	267	MET
1	E	283	ASP
1	E	290	GLN
1	E	314	LEU
1	E	327	LYS
1	E	333	ILE
1	E	348	GLN
1	E	360	TYR
1	E	430	ARG
1	E	461	GLU
1	F	23	LEU
1	F	44	PHE
1	F	77	VAL
1	F	118	ARG
1	F	154	SER
1	F	196	ASP
1	F	197	ARG
1	F	199	TYR
1	F	217	SER
1	F	230	ILE
1	F	231	ARG
1	F	245	LYS
1	F	247	LEU
1	F	257	GLU
1	F	261	THR
1	F	267	MET
1	F	290	GLN
1	F	348	GLN
1	F	354	GLU
1	F	360	TYR
1	F	365	LEU
1	F	389	MET
1	F	421	ARG
1	F	461	GLU
1	G	62	LEU
1	G	77	VAL
1	G	168	LYS

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Mol	Chain	Res	Type
1	G	187	LEU
1	G	197	ARG
1	G	199	TYR
1	G	231	ARG
1	G	247	LEU
1	G	257	GLU
1	G	261	THR
1	G	267	MET
1	G	268	ARG
1	G	315	GLU
1	G	327	LYS
1	G	348	GLN
1	G	360	TYR
1	G	371	LYS
1	G	461	GLU
1	G	473	ASP
1	H	37	ASN
1	H	153	ASN
1	H	172	GLU
1	H	197	ARG
1	H	230	ILE
1	H	284	ARG
1	H	288	MET
1	H	292	ILE
1	H	300	VAL
1	H	343	GLN
1	H	357	THR
1	H	389	MET
1	H	421	ARG
1	H	426	LEU
1	H	441	LYS
1	H	513	LEU
1	I	23	LEU
1	I	37	ASN
1	I	59	GLU
1	I	129	GLU
1	I	153	ASN
1	I	283	ASP
1	I	284	ARG
1	I	288	MET
1	I	389	MET
1	I	421	ARG

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Mol	Chain	Res	Type
1	I	426	LEU
1	I	513	LEU
1	J	37	ASN
1	J	153	ASN
1	J	189	VAL
1	J	230	ILE
1	J	233	MET
1	J	242	LYS
1	J	284	ARG
1	J	299	THR
1	J	311	LYS
1	J	313	THR
1	J	343	GLN
1	J	389	MET
1	J	421	ARG
1	J	426	LEU
1	J	494	LEU
1	J	513	LEU
1	K	37	ASN
1	K	41	ASP
1	K	58	ARG
1	K	118	ARG
1	K	129	GLU
1	K	151	SER
1	K	172	GLU
1	K	196	ASP
1	K	268	ARG
1	K	284	ARG
1	K	389	MET
1	K	421	ARG
1	K	426	LEU
1	K	432	GLN
1	L	15	LYS
1	L	37	ASN
1	L	44	PHE
1	L	201	SER
1	L	233	MET
1	L	270	ILE
1	L	272	LYS
1	L	284	ARG
1	L	288	MET
1	L	389	MET

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Mol	Chain	Res	Type
1	L	421	ARG
1	L	426	LEU
1	L	441	LYS
1	M	37	ASN
1	M	154	SER
1	M	172	GLU
1	M	283	ASP
1	M	284	ARG
1	M	286	LYS
1	M	389	MET
1	M	421	ARG
1	M	426	LEU
1	M	428	ASP
1	M	432	GLN
1	M	441	LYS
1	M	520	MET
1	N	37	ASN
1	N	58	ARG
1	N	89	THR
1	N	111	MET
1	N	114	MET
1	N	118	ARG
1	N	139	SER
1	N	172	GLU
1	N	197	ARG
1	N	217	SER
1	N	233	MET
1	N	268	ARG
1	N	284	ARG
1	N	288	MET
1	N	343	GLN
1	N	355	GLU
1	N	389	MET
1	N	421	ARG
1	N	426	LEU
2	O	3	ILE
2	O	4	ARG
2	O	6	LEU
2	O	20	LYS
2	O	28	THR
2	O	48	ILE
2	O	55	LYS

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Mol	Chain	Res	Type
2	P	3	ILE
2	P	6	LEU
2	P	20	LYS
2	P	21	SER
2	P	28	THR
2	P	48	ILE
2	P	53	GLU
2	P	55	LYS
2	P	82	GLU
2	Q	3	ILE
2	Q	6	LEU
2	Q	53	GLU
2	Q	55	LYS
2	Q	78	ILE
2	R	4	ARG
2	R	6	LEU
2	R	20	LYS
2	R	50	GLU
2	R	55	LYS
2	S	2	ASN
2	S	3	ILE
2	S	6	LEU
2	S	25	ILE
2	S	53	GLU
2	S	55	LYS
2	S	81	GLU
2	T	1	MET
2	T	3	ILE
2	T	6	LEU
2	T	20	LYS
2	T	37	ARG
2	T	55	LYS
2	U	3	ILE
2	U	6	LEU
2	U	34	LYS
2	U	55	LYS
2	U	75	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (146) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN

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Mol	Chain	Res	Type
1	A	82	ASN
1	A	97	GLN
1	A	112	ASN
1	A	146	GLN
1	A	153	ASN
1	A	194	GLN
1	A	352	GLN
1	A	366	GLN
1	A	432	GLN
1	A	436	GLN
1	A	453	GLN
1	A	457	ASN
1	A	475	ASN
1	A	505	GLN
1	B	21	ASN
1	B	82	ASN
1	B	97	GLN
1	B	112	ASN
1	B	146	GLN
1	B	153	ASN
1	B	348	GLN
1	B	366	GLN
1	B	432	GLN
1	B	457	ASN
1	B	475	ASN
1	C	21	ASN
1	C	82	ASN
1	C	97	GLN
1	C	146	GLN
1	C	366	GLN
1	C	457	ASN
1	C	475	ASN
1	C	487	ASN
1	D	21	ASN
1	D	82	ASN
1	D	97	GLN
1	D	112	ASN
1	D	153	ASN
1	D	348	GLN
1	D	366	GLN
1	D	432	GLN
1	D	457	ASN

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Mol	Chain	Res	Type
1	D	475	ASN
1	E	21	ASN
1	E	82	ASN
1	E	97	GLN
1	E	112	ASN
1	E	146	GLN
1	E	153	ASN
1	E	206	ASN
1	E	348	GLN
1	E	366	GLN
1	E	432	GLN
1	E	457	ASN
1	E	475	ASN
1	F	21	ASN
1	F	82	ASN
1	F	97	GLN
1	F	112	ASN
1	F	146	GLN
1	F	153	ASN
1	F	229	ASN
1	F	343	GLN
1	F	348	GLN
1	F	366	GLN
1	F	432	GLN
1	F	453	GLN
1	F	457	ASN
1	F	475	ASN
1	G	21	ASN
1	G	82	ASN
1	G	97	GLN
1	G	112	ASN
1	G	153	ASN
1	G	348	GLN
1	G	352	GLN
1	G	366	GLN
1	G	432	GLN
1	G	457	ASN
1	G	475	ASN
1	H	21	ASN
1	H	153	ASN
1	H	319	GLN
1	H	348	GLN

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Mol	Chain	Res	Type
1	H	433	ASN
1	H	467	ASN
1	I	21	ASN
1	I	37	ASN
1	I	97	GLN
1	I	146	GLN
1	I	153	ASN
1	I	319	GLN
1	I	433	ASN
1	I	436	GLN
1	I	467	ASN
1	I	487	ASN
1	J	21	ASN
1	J	37	ASN
1	J	97	GLN
1	J	146	GLN
1	J	153	ASN
1	J	319	GLN
1	J	343	GLN
1	J	348	GLN
1	J	432	GLN
1	J	433	ASN
1	J	436	GLN
1	K	21	ASN
1	K	37	ASN
1	K	97	GLN
1	K	153	ASN
1	K	319	GLN
1	K	436	GLN
1	L	21	ASN
1	L	37	ASN
1	L	97	GLN
1	L	153	ASN
1	L	319	GLN
1	L	433	ASN
1	L	467	ASN
1	M	21	ASN
1	M	37	ASN
1	M	72	GLN
1	M	97	GLN
1	M	146	GLN
1	M	153	ASN

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Mol	Chain	Res	Type
1	M	319	GLN
1	M	401	HIS
1	M	433	ASN
1	M	436	GLN
1	M	487	ASN
1	N	21	ASN
1	N	37	ASN
1	N	146	GLN
1	N	319	GLN
1	N	343	GLN
1	N	401	HIS
1	N	432	GLN
1	N	436	GLN
1	N	467	ASN
2	O	68	ASN
2	P	68	ASN
2	S	68	ASN
2	T	68	ASN
2	U	68	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 7 are monoatomic - leaving 7 for Mogul analysis.

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	$\# Z > 2$
4	ADP	A	1526	3	24,29,29	1.29	3 (12%)	23,45,45	3.29	6 (26%)
4	ADP	B	1526	3	24,29,29	1.28	3 (12%)	23,45,45	3.25	5 (21%)
4	ADP	C	1526	3	24,29,29	1.28	3 (12%)	23,45,45	3.23	5 (21%)
4	ADP	D	1526	3	24,29,29	1.29	3 (12%)	23,45,45	3.22	5 (21%)
4	ADP	E	1526	3	24,29,29	1.27	3 (12%)	23,45,45	3.28	5 (21%)
4	ADP	F	1526	3	24,29,29	1.27	3 (12%)	23,45,45	3.27	5 (21%)
4	ADP	G	1526	3	24,29,29	1.28	3 (12%)	23,45,45	3.31	5 (21%)

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
4	ADP	A	1526	3	-	0/12/32/32	0/3/3/3
4	ADP	B	1526	3	-	0/12/32/32	0/3/3/3
4	ADP	C	1526	3	-	0/12/32/32	0/3/3/3
4	ADP	D	1526	3	-	0/12/32/32	0/3/3/3
4	ADP	E	1526	3	-	0/12/32/32	0/3/3/3
4	ADP	F	1526	3	-	0/12/32/32	0/3/3/3
4	ADP	G	1526	3	-	0/12/32/32	0/3/3/3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1526	ADP	C5-N7	-2.17	1.31	1.39
4	E	1526	ADP	C5-N7	-2.16	1.31	1.39
4	A	1526	ADP	C5-N7	-2.14	1.31	1.39
4	B	1526	ADP	C5-N7	-2.14	1.31	1.39
4	F	1526	ADP	C5-N7	-2.13	1.31	1.39
4	C	1526	ADP	C5-N7	-2.13	1.31	1.39
4	G	1526	ADP	C5-N7	-2.13	1.31	1.39
4	A	1526	ADP	PA-O2A	-2.08	1.46	1.55
4	D	1526	ADP	PA-O2A	-2.08	1.46	1.55
4	B	1526	ADP	PA-O2A	-2.07	1.46	1.55
4	G	1526	ADP	PA-O2A	-2.06	1.46	1.55
4	E	1526	ADP	PA-O2A	-2.06	1.46	1.55
4	C	1526	ADP	PA-O2A	-2.05	1.46	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1526	ADP	PA-O2A	-2.02	1.46	1.55
4	E	1526	ADP	O4'-C1'	3.34	1.46	1.41
4	G	1526	ADP	O4'-C1'	3.40	1.46	1.41
4	B	1526	ADP	O4'-C1'	3.46	1.46	1.41
4	F	1526	ADP	O4'-C1'	3.48	1.46	1.41
4	C	1526	ADP	O4'-C1'	3.49	1.46	1.41
4	A	1526	ADP	O4'-C1'	3.50	1.46	1.41
4	D	1526	ADP	O4'-C1'	3.59	1.46	1.41

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1526	ADP	N3-C2-N1	-13.22	118.49	128.87
4	G	1526	ADP	N3-C2-N1	-13.16	118.53	128.87
4	F	1526	ADP	N3-C2-N1	-13.15	118.55	128.87
4	E	1526	ADP	N3-C2-N1	-13.13	118.56	128.87
4	D	1526	ADP	N3-C2-N1	-13.11	118.57	128.87
4	B	1526	ADP	N3-C2-N1	-13.08	118.59	128.87
4	C	1526	ADP	N3-C2-N1	-13.06	118.61	128.87
4	E	1526	ADP	O3B-PB-O1B	2.09	117.46	110.63
4	A	1526	ADP	O5'-C5'-C4'	2.10	116.65	109.09
4	G	1526	ADP	O3B-PB-O1B	2.10	117.48	110.63
4	A	1526	ADP	O3B-PB-O1B	2.11	117.53	110.63
4	C	1526	ADP	O3B-PB-O1B	2.12	117.54	110.63
4	B	1526	ADP	O3B-PB-O1B	2.13	117.56	110.63
4	F	1526	ADP	O3B-PB-O1B	2.13	117.59	110.63
4	D	1526	ADP	O3B-PB-O1B	2.14	117.61	110.63
4	E	1526	ADP	O3B-PB-O2B	2.65	117.19	107.44
4	F	1526	ADP	O3B-PB-O2B	2.70	117.36	107.44
4	C	1526	ADP	O3B-PB-O2B	2.70	117.37	107.44
4	G	1526	ADP	O3B-PB-O2B	2.71	117.41	107.44
4	B	1526	ADP	O3B-PB-O2B	2.74	117.50	107.44
4	A	1526	ADP	O3B-PB-O2B	2.75	117.54	107.44
4	D	1526	ADP	O3B-PB-O2B	2.82	117.79	107.44
4	D	1526	ADP	O2B-PB-O1B	3.45	121.89	110.63
4	B	1526	ADP	O2B-PB-O1B	3.53	122.14	110.63
4	A	1526	ADP	O2B-PB-O1B	3.53	122.14	110.63
4	F	1526	ADP	O2B-PB-O1B	3.56	122.23	110.63
4	C	1526	ADP	O2B-PB-O1B	3.57	122.28	110.63
4	G	1526	ADP	O2B-PB-O1B	3.58	122.30	110.63
4	E	1526	ADP	O2B-PB-O1B	3.63	122.47	110.63
4	D	1526	ADP	O4'-C1'-N9	4.40	116.41	108.11

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	C	1526	ADP	O4'-C1'-N9	4.63	116.86	108.11
4	B	1526	ADP	O4'-C1'-N9	4.84	117.24	108.11
4	F	1526	ADP	O4'-C1'-N9	4.92	117.39	108.11
4	E	1526	ADP	O4'-C1'-N9	4.95	117.46	108.11
4	A	1526	ADP	O4'-C1'-N9	4.96	117.48	108.11
4	G	1526	ADP	O4'-C1'-N9	5.40	118.30	108.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1526	ADP	5	0
4	B	1526	ADP	5	0
4	C	1526	ADP	5	0
4	D	1526	ADP	4	0
4	E	1526	ADP	5	0
4	F	1526	ADP	4	0
4	G	1526	ADP	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.