



## Full wwPDB EM Validation Report ⓘ

Feb 27, 2025 – 12:14 PM JST

PDB ID : 7DY6  
EMDB ID : EMD-30914  
Title : A refined cryo-EM structure of an Escherichia coli RNAP-promoter open complex (RPo) with SspA  
Authors : Lin, W.  
Deposited on : 2021-01-20  
Resolution : 3.68 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.2

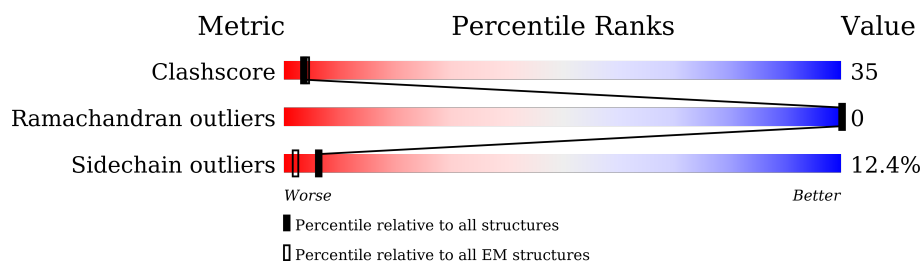
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.68 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	H	63	<div> <div>33%</div> <div>21%</div> <div>79%</div> </div>
2	I	212	<div> <div>31%</div> <div>38%</div> <div>55%</div> <div>5%</div> </div>
2	J	212	<div> <div>28%</div> <div>32%</div> <div>57%</div> <div>7%</div> <div>5%</div> </div>
3	A	329	<div> <div>5%</div> <div>35%</div> <div>30%</div> <div>5%</div> <div>30%</div> </div>
3	B	329	<div> <div>8%</div> <div>31%</div> <div>33%</div> <div>5%</div> <div>31%</div> </div>
3	K	329	<div> <div>20%</div> <div>13%</div> <div>6%</div> <div>80%</div> </div>
4	C	1342	<div> <div>9%</div> <div>47%</div> <div>46%</div> <div>7%</div> </div>
5	D	1407	<div> <div>17%</div> <div>45%</div> <div>45%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
6	F	613	<p>27% 29% 41% 7% 23%</p>
7	G	63	<p>27% 14% 62% 24%</p>
8	E	91	<p>21% 45% 51% 2%</p>

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 35762 atoms, of which 532 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 DNA chain called DNA (63-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	63	Total	C	N	O	P	0	0
			1312	623	256	370	63		

- Molecule 2 is a protein called Stringent starvation protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	206	Total	C	N	O	S	0	0
			1663	1066	279	310	8		
2	J	201	Total	C	N	O	S	0	0
			1629	1046	272	303	8		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	K	67	Total	C	H	N	O	S	0	0
			1050	328	532	88	100	2		
3	A	230	Total	C	N	O	S		0	0
			1787	1112	317	352	6			
3	B	226	Total	C	N	O	S		0	0
			1755	1094	310	345	6			

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	1340	Total	C	N	O	S	0	0
			10569	6632	1841	2053	43		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	516	VAL	ASP	variant	UNP P0A8V2

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	1355	Total	C	N	O	S	0	0
			10468	6579	1863	1976	50		

- Molecule 6 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	472	Total	C	N	O	S	0	0
			3845	2408	685	729	23		

- Molecule 7 is a DNA chain called DNA (63-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	48	Total	C	N	O	P	0	0
			973	469	161	295	48		

- Molecule 8 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	90	Total	C	N	O	S	0	0
			708	430	136	141	1		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
9	D	1	Total	Mg	0
			1	1	

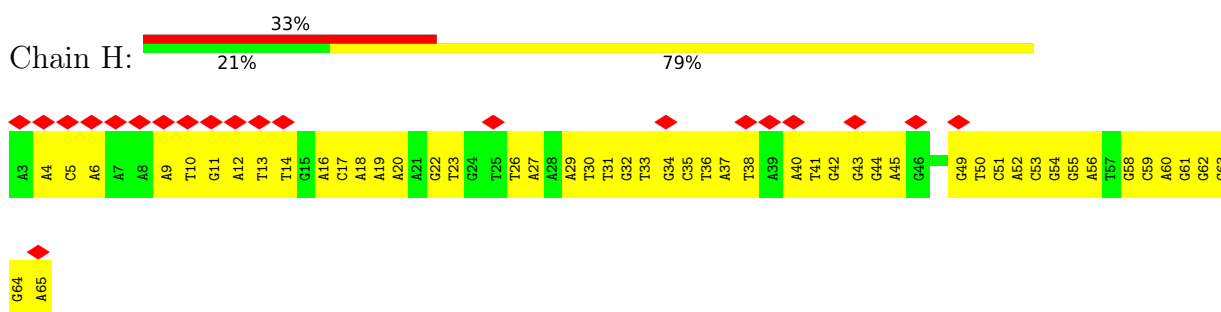
- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	D	2	Total	Zn	0
			2	2	

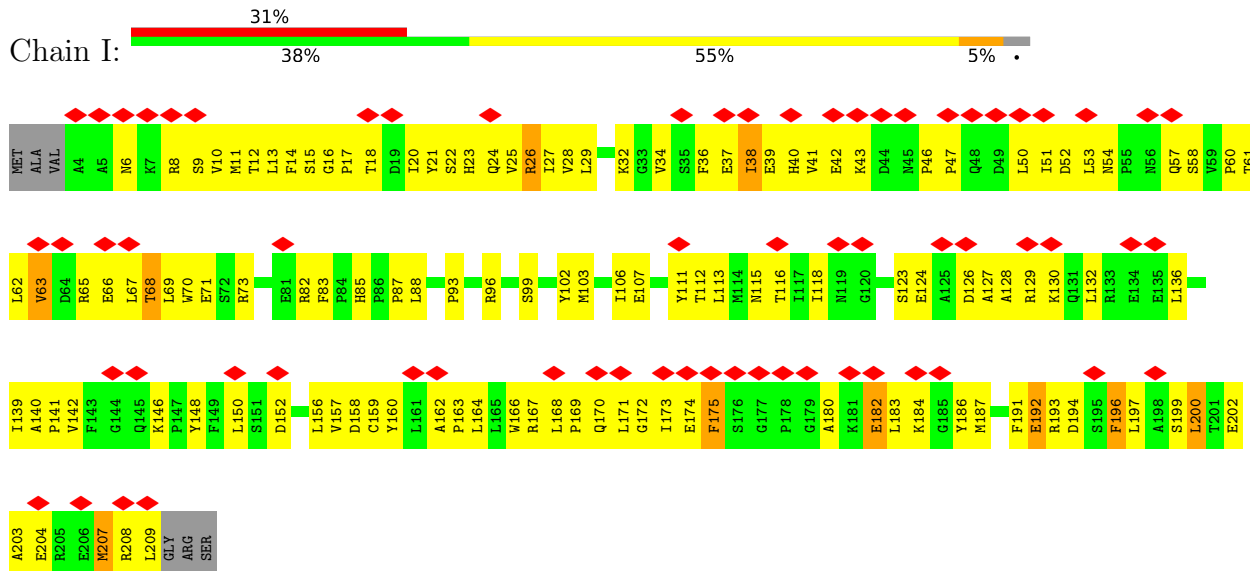
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

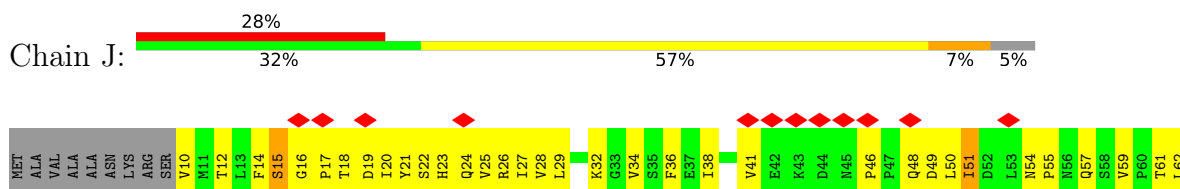
#### • Molecule 1: DNA (63-MER)



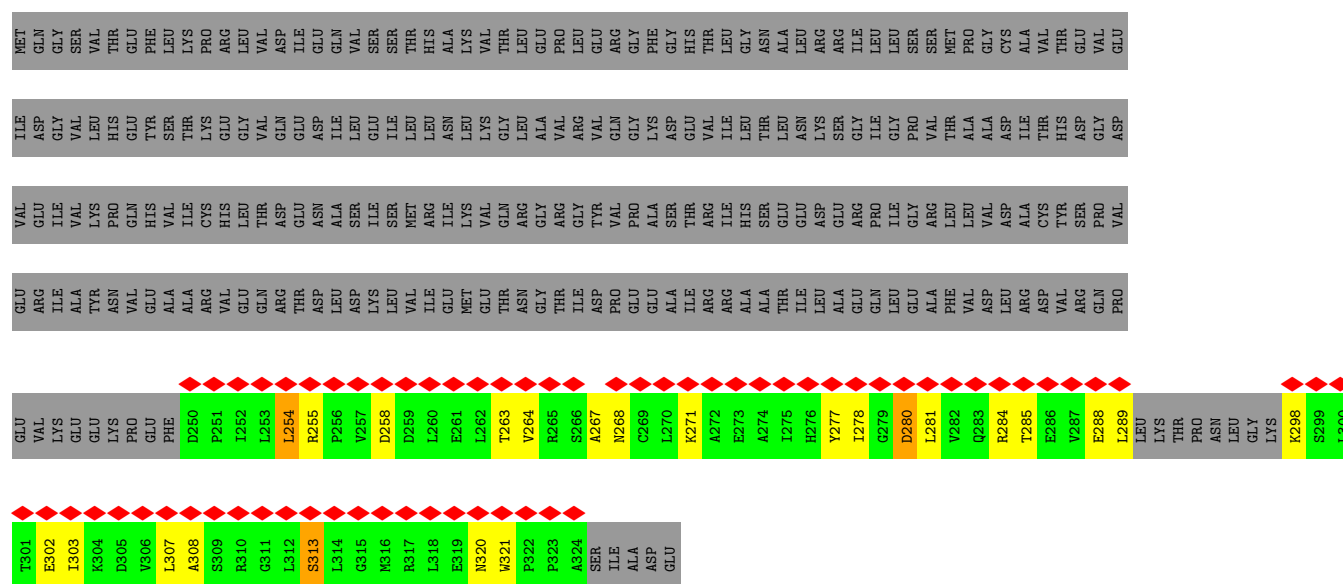
#### • Molecule 2: Stringent starvation protein A



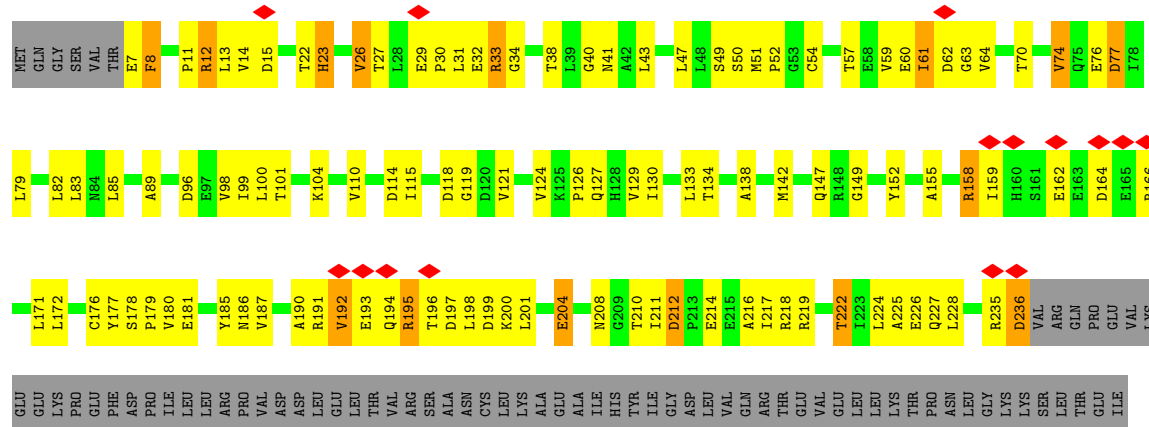
#### • Molecule 2: Stringent starvation protein A



- Molecule 3: DNA-directed RNA polymerase subunit alpha

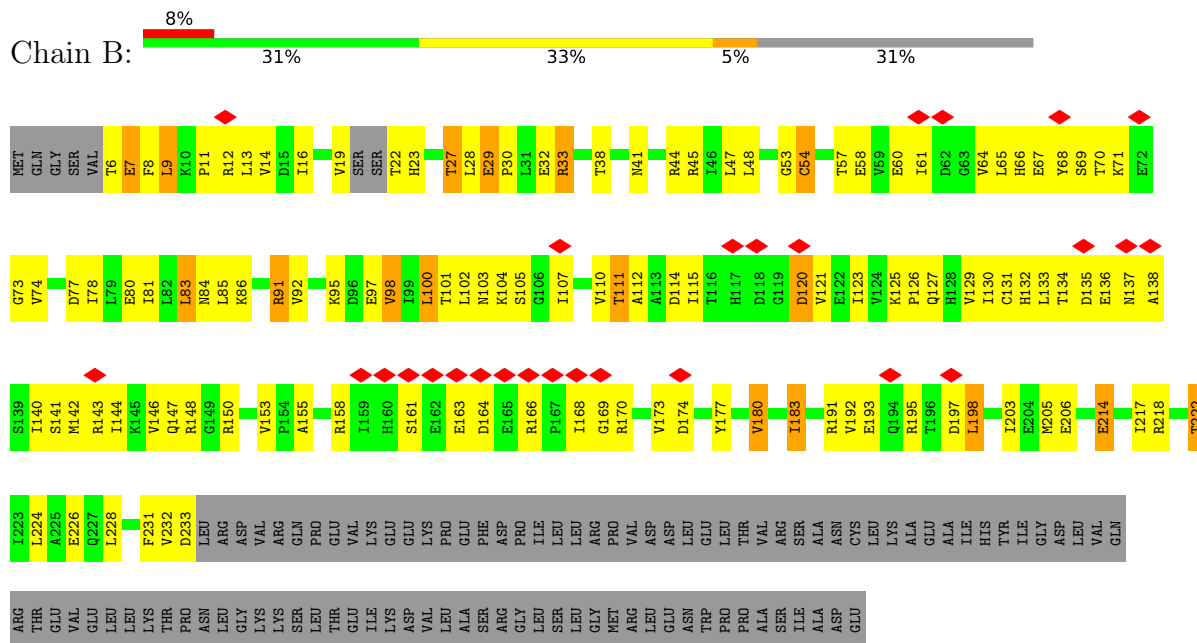


- Molecule 3: DNA-directed RNA polymerase subunit alpha

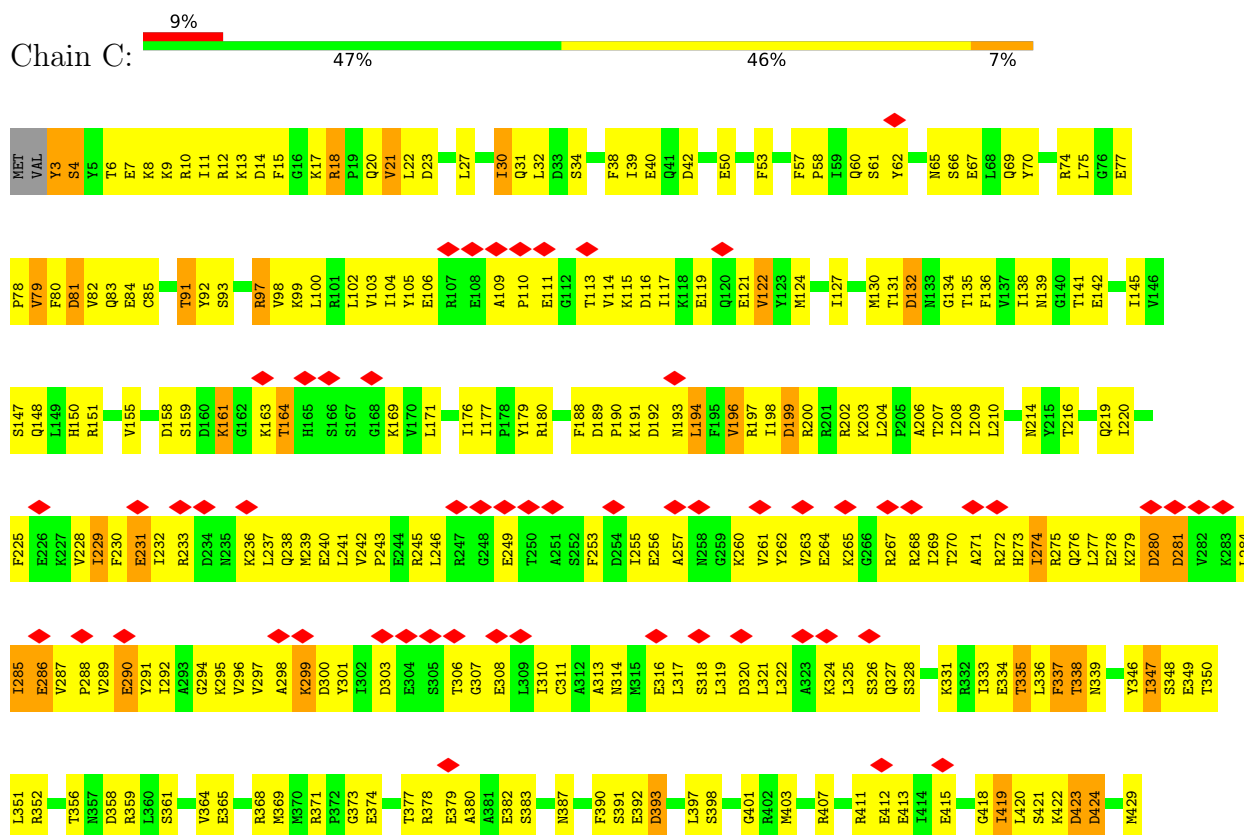


LYS ASP GLN  
VAL VAL LEU  
ALA VAL SER  
SER ARG  
GLY LEU  
SER SER  
LEU LEU  
GLY MET  
MET ARG  
LEU LEU  
GLU LEU  
ASN TRP  
PRO PRO  
PRO ALA  
SER ILE  
ALA ASP  
GLU

• Molecule 3: DNA-directed RNA polymerase subunit alpha



• Molecule 4: DNA-directed RNA polymerase subunit beta

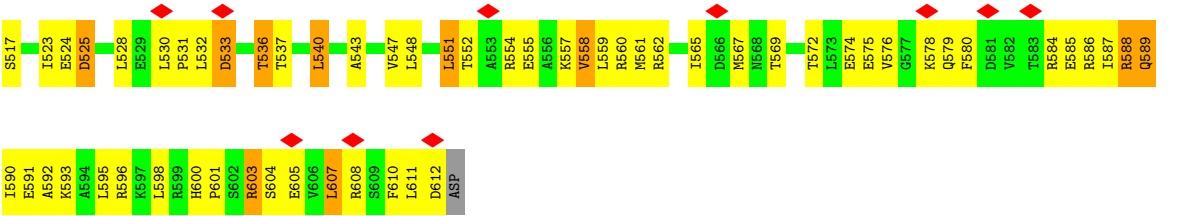




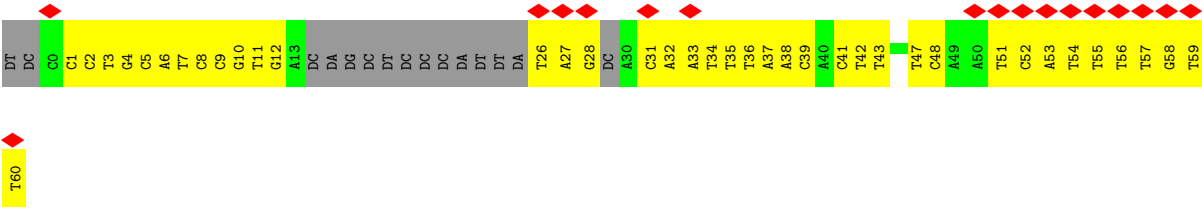
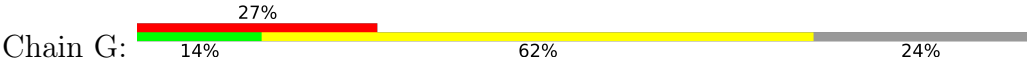








• Molecule 7: DNA (63-MER)



• Molecule 8: DNA-directed RNA polymerase subunit omega



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	60145	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	59	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.170	Depositor
Minimum map value	-0.112	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.026	Depositor
Map size ( $\text{\AA}$ )	261.4, 261.4, 261.4	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.3069999, 1.3069999, 1.3069999	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, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	H	0.69	0/1478	0.93	0/2283
2	I	0.34	0/1704	0.46	0/2313
2	J	0.34	0/1670	0.46	0/2267
3	A	0.47	0/1809	0.53	0/2451
3	B	0.40	0/1776	0.53	0/2406
3	K	0.34	0/524	0.68	0/711
4	C	0.50	0/10738	0.52	0/14488
5	D	0.48	0/10622	0.53	0/14341
6	F	0.34	0/3896	0.49	0/5236
7	G	0.65	0/1084	0.99	0/1664
8	E	0.43	0/710	0.48	0/956
All	All	0.47	0/36011	0.56	0/49116

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1312	0	709	108	0
2	I	1663	0	1646	141	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	1629	0	1613	150	0
3	A	1787	0	1810	100	0
3	B	1755	0	1778	120	0
3	K	518	532	531	14	0
4	C	10569	0	10587	733	0
5	D	10468	0	10635	720	0
6	F	3845	0	3913	392	0
7	G	973	0	550	53	0
8	E	708	0	719	47	0
9	D	1	0	0	0	0
10	D	2	0	0	0	0
All	All	35230	532	34491	2410	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 35.

All (2410) 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:H:42:DG:O6	6:F:106:GLY:HA3	1.40	1.20
6:F:277:MET:O	6:F:281:ARG:HB3	1.43	1.15
4:C:843:THR:HG23	4:C:844:LYS:NZ	1.63	1.13
4:C:993:PRO:HG2	4:C:996:ARG:HB3	1.31	1.13
4:C:843:THR:HG23	4:C:844:LYS:HZ1	1.16	1.09
6:F:139:GLU:O	6:F:142:THR:HG22	1.53	1.07
5:D:1089:LEU:HA	5:D:1096:PRO:HA	1.33	1.07
4:C:238:GLN:HG2	4:C:286:GLU:HG3	1.37	1.06
6:F:476:ARG:HG2	6:F:477:GLU:HG2	1.38	1.05
5:D:1036:ARG:HB3	5:D:1079:LYS:HB3	1.39	1.03
3:B:30:PRO:HB2	3:B:198:LEU:HD12	1.40	1.03
4:C:1296:ASP:OD2	4:C:1320:PRO:HB3	1.58	1.02
1:H:42:DG:H1'	1:H:43:DG:C1'	1.90	1.02
6:F:390:ILE:HD11	6:F:432:THR:HG23	1.40	1.00
5:D:972:LYS:HG3	5:D:1002:VAL:HA	1.44	0.99
3:B:47:LEU:HD12	3:B:183:ILE:HD12	1.44	0.99
4:C:560:PRO:HB2	5:D:776:THR:HG21	1.41	0.98
4:C:595:THR:HG23	4:C:600:THR:HG23	1.44	0.97
5:D:1167:LYS:HE3	5:D:1170:LYS:HB2	1.46	0.97
5:D:559:ALA:HB3	5:D:562:GLU:HG2	1.44	0.97
1:H:42:DG:H1'	1:H:43:DG:H1'	1.43	0.97
5:D:1001:ALA:HA	5:D:1020:TRP:HA	1.47	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:228:VAL:HB	4:C:335:THR:HG23	1.46	0.96
7:G:33:DA:H1'	7:G:34:DT:H5'	1.47	0.96
2:J:28:VAL:HG21	2:J:76:MET:HG3	1.47	0.96
4:C:1004:ASP:HA	4:C:1008:GLN:HG2	1.48	0.95
1:H:42:DG:H2''	1:H:43:DG:O4'	1.67	0.94
7:G:5:DC:H2''	7:G:6:DA:H5'	1.46	0.94
4:C:1157:GLN:HA	4:C:1157:GLN:HE21	1.30	0.94
4:C:1002:LEU:HD23	4:C:1007:LYS:HD3	1.48	0.93
6:F:162:ILE:HD12	6:F:216:LEU:HD11	1.48	0.93
8:E:4:VAL:HG23	8:E:5:THR:HG23	1.50	0.93
2:J:175:PHE:HB3	2:J:180:ALA:HB2	1.50	0.93
4:C:398:SER:HB2	4:C:401:GLY:H	1.32	0.92
5:D:746:LEU:HB3	5:D:758:PRO:HB3	1.51	0.92
5:D:1105:ALA:HB1	5:D:1122:ALA:HB1	1.50	0.92
5:D:337:ARG:HH11	5:D:337:ARG:HG2	1.34	0.92
5:D:1079:LYS:HD3	5:D:1087:ASP:HB3	1.52	0.92
6:F:585:GLU:HA	6:F:588:ARG:HH11	1.33	0.92
5:D:1049:GLN:HB2	5:D:1059:LEU:HD11	1.50	0.91
5:D:368:LEU:HD23	5:D:373:ALA:HB2	1.51	0.91
5:D:1011:VAL:HG21	5:D:1017:VAL:HB	1.51	0.91
4:C:595:THR:HG23	4:C:600:THR:CG2	2.00	0.91
5:D:515:ARG:HH22	5:D:717:VAL:HB	1.35	0.90
6:F:111:LEU:HD11	6:F:115:GLY:HA3	1.52	0.90
4:C:978:VAL:HG12	4:C:979:LEU:HD12	1.53	0.90
6:F:574:GLU:HG2	6:F:588:ARG:HH22	1.33	0.90
2:I:146:LYS:HG3	2:I:150:LEU:HA	1.52	0.89
6:F:166:VAL:HG22	6:F:258:GLN:HG3	1.56	0.88
5:D:980:THR:HB	5:D:997:VAL:HB	1.54	0.88
2:I:124:GLU:HA	2:I:127:ALA:HB3	1.55	0.88
4:C:106:GLU:HG2	4:C:109:ALA:HB3	1.55	0.88
4:C:1327:LEU:HD22	4:C:1337:ILE:HG21	1.56	0.88
6:F:250:LEU:HD22	6:F:254:GLU:HG3	1.54	0.88
3:B:105:SER:HB3	3:B:138:ALA:HB1	1.55	0.88
2:I:46:PRO:HG2	2:I:51:ILE:HD11	1.56	0.87
2:I:82:ARG:HH12	2:J:94:VAL:HG13	1.38	0.87
4:C:876:GLU:HG2	4:C:927:THR:HG22	1.57	0.87
2:I:6:ASN:HD21	2:I:63:VAL:HG12	1.39	0.87
5:D:1031:VAL:HG13	5:D:1080:ILE:HG21	1.57	0.87
3:B:191:ARG:HG3	3:B:193:GLU:H	1.38	0.87
4:C:321:LEU:HD23	4:C:324:LYS:HD2	1.55	0.86
6:F:144:LEU:HA	6:F:147:GLN:HG2	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:60:DA:H1'	1:H:61:DG:H5'	1.56	0.86
5:D:1029:THR:HB	5:D:1121:LEU:HD21	1.57	0.86
6:F:157:ARG:HD2	6:F:159:SER:HB2	1.57	0.86
5:D:1204:VAL:HG21	5:D:1210:ILE:HD11	1.57	0.86
7:G:47:DT:H2''	7:G:48:DC:H5'	1.57	0.86
1:H:17:DC:H1'	1:H:18:DA:H5'	1.58	0.85
1:H:42:DG:C2'	1:H:43:DG:O4'	2.23	0.85
1:H:42:DG:C1'	1:H:43:DG:O4'	2.24	0.85
5:D:870:ASP:HA	5:D:873:GLU:HB3	1.57	0.84
4:C:843:THR:HG22	4:C:845:LEU:HD12	1.59	0.84
5:D:424:ASN:HB2	5:D:434:ILE:HG12	1.59	0.84
6:F:277:MET:O	6:F:281:ARG:CB	2.24	0.84
5:D:747:MET:HG3	5:D:759:ILE:HD11	1.59	0.84
5:D:973:LEU:HB2	5:D:1003:LEU:HD12	1.60	0.84
4:C:979:LEU:HD21	4:C:1011:LEU:HD21	1.59	0.83
2:I:14:PHE:HB3	2:I:50:LEU:HD22	1.59	0.83
6:F:227:GLN:O	6:F:231:THR:HG23	1.78	0.83
5:D:1155:ILE:HG13	5:D:1210:ILE:HB	1.61	0.82
8:E:86:ILE:HB	8:E:90:ARG:HE	1.44	0.82
2:I:26:ARG:HA	2:I:29:LEU:HB3	1.60	0.82
4:C:690:VAL:HG23	4:C:1236:ASN:HB3	1.60	0.82
4:C:843:THR:HG21	4:C:845:LEU:HD13	1.60	0.82
5:D:194:LEU:HD12	5:D:224:LEU:HD22	1.60	0.82
5:D:1005:LYS:HG3	5:D:1011:VAL:HG22	1.61	0.82
2:J:133:ARG:HA	2:J:136:LEU:HG	1.60	0.82
4:C:264:GLU:HB2	4:C:267:ARG:HD3	1.61	0.81
6:F:234:THR:HB	6:F:244:THR:HG23	1.62	0.81
5:D:205:LEU:HB2	5:D:217:LEU:HD12	1.61	0.81
6:F:157:ARG:HG3	6:F:159:SER:H	1.44	0.81
6:F:310:GLU:HB2	6:F:355:ILE:HG21	1.63	0.81
2:I:126:ASP:HA	2:I:129:ARG:HB3	1.61	0.81
3:A:104:LYS:HD3	3:A:110:VAL:HG22	1.63	0.81
3:A:155:ALA:HA	3:A:158:ARG:HD2	1.63	0.80
4:C:843:THR:CG2	4:C:845:LEU:HD12	2.11	0.80
5:D:948:SER:HA	5:D:1022:PRO:HB3	1.62	0.80
6:F:530:LEU:HD23	6:F:531:PRO:HD2	1.64	0.80
5:D:609:TYR:HE1	5:D:614:LEU:HD12	1.47	0.80
5:D:1176:VAL:HG22	5:D:1187:GLU:HG3	1.64	0.79
4:C:1103:VAL:HG21	4:C:1112:ILE:HD11	1.64	0.79
2:I:113:LEU:HD23	2:I:132:LEU:HB2	1.63	0.79
4:C:423:ASP:OD1	4:C:423:ASP:N	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:595:THR:CG2	4:C:600:THR:CG2	2.61	0.79
4:C:843:THR:CG2	4:C:845:LEU:CD1	2.61	0.79
4:C:1160:ASP:OD1	4:C:1161:LEU:N	2.14	0.79
6:F:331:HIS:HA	6:F:334:SER:HB2	1.64	0.79
2:J:129:ARG:HG3	2:J:173:ILE:HG12	1.63	0.78
3:B:166:ARG:HB3	3:B:170:ARG:HG3	1.63	0.78
6:F:137:TYR:HA	6:F:361:ILE:HD11	1.64	0.78
4:C:1117:LEU:HD11	4:C:1182:ILE:HG21	1.63	0.78
2:J:113:LEU:HD23	2:J:132:LEU:HD12	1.64	0.78
4:C:1020:GLU:HB3	4:C:1024:GLU:HB2	1.64	0.78
4:C:736:VAL:HG23	4:C:748:ILE:HA	1.63	0.78
5:D:552:ILE:HD11	5:D:570:LYS:HG3	1.66	0.78
1:H:63:DG:H22	7:G:1:DC:H1'	1.48	0.78
4:C:216:THR:HG22	4:C:219:GLN:HE21	1.49	0.77
5:D:210:SER:HB3	5:D:213:LYS:HB2	1.65	0.77
6:F:490:PRO:HG2	6:F:493:LYS:HE2	1.66	0.77
5:D:1011:VAL:HG12	5:D:1015:GLU:HB3	1.67	0.77
6:F:465:ARG:HH22	7:G:26:DT:H2'	1.50	0.77
6:F:344:LEU:HA	6:F:347:ILE:HG13	1.67	0.77
1:H:4:DA:H1'	1:H:5:DC:H5'	1.66	0.77
5:D:1080:ILE:HD12	5:D:1097:ALA:HB1	1.66	0.77
6:F:138:PRO:HG2	6:F:353:LEU:HD11	1.67	0.77
5:D:337:ARG:HG2	5:D:337:ARG:NH1	1.98	0.77
6:F:144:LEU:HD12	6:F:147:GLN:HB2	1.65	0.77
4:C:393:ASP:N	4:C:393:ASP:OD1	2.14	0.76
4:C:1018:TYR:HA	4:C:1021:LEU:HB2	1.66	0.76
6:F:347:ILE:HA	6:F:350:GLU:HB2	1.67	0.76
2:I:192:GLU:HA	2:I:197:LEU:HD21	1.68	0.76
4:C:471:VAL:HB	4:C:498:ILE:HD11	1.66	0.76
2:I:168:LEU:HB3	2:I:169:PRO:HD3	1.65	0.76
3:B:48:LEU:HD22	5:D:535:ARG:HG3	1.68	0.76
6:F:555:GLU:HG2	6:F:590:ILE:HG22	1.67	0.76
8:E:80:LEU:HA	8:E:83:VAL:HB	1.65	0.76
1:H:42:DG:C1'	1:H:43:DG:C1'	2.64	0.76
2:I:111:TYR:HE1	2:I:164:LEU:HD11	1.51	0.76
4:C:132:ASP:OD1	4:C:132:ASP:N	2.19	0.76
5:D:706:VAL:HG12	5:D:715:LYS:HB3	1.66	0.76
3:A:27:THR:HG21	3:A:200:LYS:HE3	1.68	0.76
6:F:359:LYS:HA	6:F:359:LYS:HE3	1.67	0.75
3:A:190:ALA:HB2	3:A:200:LYS:HG3	1.69	0.75
5:D:337:ARG:HD2	5:D:338:PHE:H	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1144:LEU:HD23	5:D:1237:VAL:HG23	1.66	0.75
5:D:1039:ASP:HB3	5:D:1074:LEU:HB3	1.66	0.75
4:C:57:PHE:HD2	4:C:70:TYR:HB2	1.51	0.75
4:C:839:VAL:HG12	4:C:1049:ILE:HG23	1.69	0.75
5:D:927:GLY:HA2	5:D:930:LEU:HB2	1.69	0.75
1:H:38:DT:H2'	6:F:429:THR:HG21	1.69	0.75
6:F:147:GLN:O	6:F:151:VAL:N	2.20	0.75
4:C:314:ASN:HD21	4:C:352:ARG:HG3	1.51	0.74
7:G:36:DT:H2''	7:G:37:DA:H5'	1.67	0.74
3:B:65:LEU:HD22	3:B:169:GLY:HA3	1.69	0.74
4:C:843:THR:HG22	4:C:844:LYS:N	2.03	0.74
5:D:156:ARG:NH2	5:D:191:SER:OG	2.20	0.74
5:D:573:THR:HG23	5:D:576:ARG:HD2	1.67	0.74
5:D:986:ASP:OD1	5:D:986:ASP:N	2.20	0.74
2:I:6:ASN:HB3	2:I:65:ARG:HA	1.69	0.74
3:A:214:GLU:OE2	3:A:218:ARG:NH2	2.20	0.74
5:D:640:GLY:N	5:D:643:ASP:OD2	2.20	0.74
4:C:424:ASP:OD1	4:C:424:ASP:N	2.21	0.74
3:B:97:GLU:OE2	3:B:147:GLN:NE2	2.20	0.73
4:C:1290:MET:SD	4:C:1294:LYS:NZ	2.58	0.73
5:D:803:VAL:HG11	5:D:1309:ILE:HG22	1.70	0.73
5:D:849:LEU:HA	5:D:856:ILE:HA	1.69	0.73
3:A:191:ARG:NH1	3:A:195:ARG:O	2.21	0.73
4:C:528:ARG:NH2	4:C:576:SER:O	2.21	0.73
1:H:14:DT:H5''	6:F:584:ARG:HD2	1.69	0.73
4:C:164:THR:HG21	4:C:171:LEU:HD12	1.70	0.73
5:D:201:LEU:HD23	5:D:204:GLU:HB2	1.71	0.73
6:F:601:PRO:O	6:F:603:ARG:NH2	2.22	0.73
4:C:131:THR:HG22	4:C:132:ASP:N	2.03	0.73
4:C:272:ARG:HA	4:C:275:ARG:HD2	1.70	0.73
4:C:403:MET:SD	4:C:407:ARG:NH1	2.61	0.73
4:C:546:GLU:HG2	4:C:547:VAL:HG13	1.70	0.73
5:D:661:VAL:HG21	5:D:682:VAL:HG13	1.71	0.73
2:I:126:ASP:O	2:I:130:LYS:N	2.21	0.73
6:F:147:GLN:OE1	6:F:150:ARG:NH2	2.21	0.73
4:C:1246:ARG:NH1	5:D:348:ASP:OD1	2.22	0.73
5:D:7:PHE:O	5:D:11:GLN:N	2.22	0.73
5:D:79:LYS:HG3	6:F:569:THR:HG21	1.70	0.73
4:C:758:ARG:NH1	4:C:762:ASN:OD1	2.21	0.72
4:C:1191:LYS:N	4:C:1194:GLU:OE1	2.21	0.72
5:D:978:ARG:HH12	5:D:999:TYR:HB2	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1144:LEU:HD21	5:D:1236:GLU:HB2	1.70	0.72
6:F:144:LEU:HG	6:F:221:PHE:HE2	1.54	0.72
6:F:268:TYR:O	6:F:272:SER:N	2.22	0.72
4:C:622:ASN:N	4:C:622:ASN:OD1	2.20	0.72
2:I:18:THR:O	2:I:167:ARG:NH2	2.22	0.72
4:C:378:ARG:NH1	4:C:382:GLU:OE2	2.20	0.72
4:C:255:ILE:HG21	4:C:263:VAL:H	1.54	0.72
8:E:39:VAL:HG23	8:E:53:GLU:HG2	1.71	0.72
5:D:278:ARG:NH1	6:F:407:GLU:OE2	2.22	0.72
5:D:1000:GLY:O	5:D:1021:ASP:N	2.20	0.72
5:D:1280:VAL:HG11	5:D:1304:ARG:HH21	1.55	0.72
6:F:346:GLN:O	6:F:350:GLU:N	2.21	0.72
4:C:322:LEU:O	4:C:326:SER:N	2.22	0.72
4:C:615:VAL:HG12	4:C:650:VAL:HA	1.72	0.72
6:F:147:GLN:O	6:F:151:VAL:HG23	1.88	0.72
5:D:849:LEU:HD22	5:D:854:ALA:H	1.53	0.72
6:F:326:TRP:HA	6:F:329:LYS:HB2	1.72	0.72
4:C:100:LEU:HD12	4:C:122:VAL:HG11	1.71	0.72
5:D:352:ARG:NH1	5:D:465:GLN:OE1	2.22	0.72
4:C:3:TYR:N	4:C:7:GLU:OE1	2.23	0.72
4:C:131:THR:HG22	4:C:132:ASP:H	1.55	0.71
5:D:1025:MET:N	5:D:1124:ILE:O	2.23	0.71
4:C:61:SER:OG	4:C:65:ASN:N	2.23	0.71
4:C:1083:GLU:OE1	4:C:1083:GLU:N	2.23	0.71
5:D:425:ARG:NH1	5:D:458:ASN:O	2.23	0.71
1:H:55:DG:OP1	5:D:1311:LYS:NZ	2.23	0.71
4:C:843:THR:CG2	4:C:844:LYS:NZ	2.50	0.71
5:D:1027:VAL:HG21	5:D:1102:PRO:HD2	1.72	0.71
4:C:1019:ASP:O	4:C:1023:HIS:N	2.24	0.71
4:C:1296:ASP:OD2	4:C:1320:PRO:CB	2.37	0.71
5:D:193:ASP:OD1	5:D:193:ASP:N	2.23	0.71
1:H:63:DG:H5"	5:D:1170:LYS:HG2	1.71	0.71
5:D:741:ALA:O	5:D:762:ASN:ND2	2.24	0.71
5:D:829:GLY:HA2	5:D:993:GLU:HB3	1.71	0.71
2:J:54:ASN:OD1	2:J:57:GLN:N	2.24	0.71
4:C:199:ASP:OD1	4:C:199:ASP:N	2.23	0.71
5:D:1001:ALA:HB2	5:D:1020:TRP:HB2	1.71	0.71
3:B:164:ASP:O	3:B:166:ARG:NH1	2.23	0.71
5:D:70:CYS:SG	5:D:71:LEU:N	2.63	0.71
6:F:122:ARG:O	6:F:371:LYS:NZ	2.23	0.71
6:F:161:LEU:HG	6:F:162:ILE:HG23	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:404:LEU:HD22	6:F:439:ILE:HG23	1.73	0.71
6:F:124:GLU:O	6:F:128:ASN:ND2	2.24	0.71
5:D:288:PRO:HB3	6:F:377:LYS:HE3	1.72	0.71
4:C:1164:PHE:HB2	4:C:1168:GLU:HB2	1.73	0.70
5:D:1025:MET:HB3	5:D:1124:ILE:HB	1.73	0.70
5:D:1003:LEU:HA	5:D:1018:ALA:HA	1.73	0.70
6:F:530:LEU:HD22	6:F:532:LEU:H	1.56	0.70
3:B:61:ILE:HG22	3:B:64:VAL:H	1.56	0.70
5:D:958:ILE:HG22	5:D:960:LEU:HD21	1.73	0.70
1:H:30:DT:O4	7:G:32:DA:N6	2.23	0.70
1:H:50:DT:OP2	4:C:542:ARG:NH1	2.24	0.70
5:D:473:THR:OG1	5:D:474:LEU:N	2.21	0.70
5:D:482:ALA:O	5:D:488:ASN:ND2	2.25	0.70
6:F:474:MET:SD	6:F:476:ARG:NH2	2.64	0.70
4:C:348:SER:OG	4:C:349:GLU:OE2	2.10	0.70
6:F:555:GLU:HG2	6:F:590:ILE:CG2	2.22	0.70
5:D:310:GLY:HA2	5:D:314:ARG:HD2	1.74	0.70
5:D:832:LYS:HE3	5:D:1242:ARG:HD3	1.71	0.70
2:I:11:MET:SD	2:I:37:GLU:N	2.64	0.70
2:J:18:THR:O	2:J:167:ARG:NH2	2.25	0.70
4:C:1124:ILE:HG21	4:C:1180:MET:HE3	1.73	0.70
5:D:1032:SER:N	5:D:1117:SER:OG	2.24	0.70
3:K:284:ARG:NH1	3:K:288:GLU:OE1	2.25	0.69
6:F:248:GLU:HA	6:F:251:LYS:HE3	1.74	0.69
4:C:103:VAL:HG12	4:C:116:ASP:HB3	1.73	0.69
4:C:452:ARG:NH2	4:C:584:TYR:O	2.22	0.69
1:H:13:DT:OP2	6:F:586:ARG:NH1	2.25	0.69
4:C:161:LYS:HD3	4:C:161:LYS:H	1.56	0.69
6:F:329:LYS:HD3	6:F:332:ASP:HB2	1.73	0.69
2:I:41:VAL:HG11	2:I:47:PRO:HD3	1.73	0.69
4:C:1017:GLN:O	4:C:1021:LEU:N	2.25	0.69
4:C:979:LEU:HA	4:C:1002:LEU:HD22	1.73	0.69
2:J:41:VAL:HG12	2:J:46:PRO:HB3	1.75	0.69
4:C:557:ARG:NH2	4:C:611:GLU:OE1	2.21	0.69
4:C:975:ILE:HG22	4:C:1010:GLN:HG2	1.74	0.69
4:C:180:ARG:NH2	4:C:393:ASP:O	2.25	0.69
4:C:820:GLU:HB2	4:C:1080:ASN:O	1.93	0.69
5:D:760:THR:O	5:D:760:THR:OG1	2.10	0.69
5:D:1029:THR:HB	5:D:1121:LEU:HD11	1.73	0.69
4:C:297:VAL:HG13	4:C:313:ALA:HA	1.75	0.69
5:D:983:LYS:HE3	5:D:991:THR:HB	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:227:GLN:O	6:F:231:THR:CG2	2.42	0.68
2:J:194:ASP:HA	2:J:197:LEU:HB3	1.74	0.68
5:D:510:LEU:O	5:D:514:THR:HG22	1.92	0.68
5:D:959:LYS:HE3	5:D:985:ILE:HG13	1.75	0.68
6:F:214:PRO:O	6:F:218:ARG:NE	2.26	0.68
2:J:169:PRO:HD3	2:J:208:ARG:HH21	1.58	0.68
4:C:441:GLU:OE1	4:C:442:VAL:N	2.26	0.68
4:C:843:THR:HG21	4:C:845:LEU:CD1	2.22	0.68
2:J:115:ASN:O	2:J:119:ASN:N	2.22	0.68
4:C:99:LYS:NZ	4:C:121:GLU:OE2	2.25	0.68
5:D:17:PHE:HZ	5:D:1353:VAL:HG11	1.59	0.68
5:D:475:GLU:OE2	8:E:28:ARG:NH2	2.27	0.68
5:D:1314:LEU:HB2	5:D:1326:GLN:HE22	1.58	0.68
2:J:129:ARG:HH21	2:J:172:GLY:HA3	1.58	0.68
4:C:699:LEU:HB2	4:C:799:ASN:HD22	1.58	0.68
5:D:827:GLU:HB2	5:D:832:LYS:HG2	1.75	0.68
5:D:1002:VAL:N	5:D:1019:ASN:O	2.26	0.68
5:D:322:ARG:HG2	5:D:323:PRO:HD2	1.75	0.68
4:C:813:GLU:HB2	5:D:461:PHE:HD2	1.59	0.68
5:D:1002:VAL:O	5:D:1019:ASN:N	2.26	0.68
2:J:169:PRO:HD3	2:J:208:ARG:NH2	2.09	0.68
4:C:662:SER:OG	4:C:663:VAL:N	2.25	0.68
5:D:1088:VAL:O	5:D:1097:ALA:N	2.20	0.68
5:D:19:ALA:HA	5:D:1342:ASP:O	1.93	0.67
5:D:438:GLU:OE2	5:D:481:ARG:NH2	2.27	0.67
2:I:88:LEU:HD13	2:I:156:LEU:HD21	1.74	0.67
2:J:168:LEU:HB2	2:J:208:ARG:NH2	2.09	0.67
4:C:1157:GLN:HA	4:C:1157:GLN:NE2	2.06	0.67
5:D:652:GLU:N	5:D:652:GLU:OE1	2.27	0.67
5:D:850:LYS:HB2	5:D:855:ASP:HB2	1.74	0.67
5:D:926:PRO:HG2	5:D:1248:ILE:HD11	1.76	0.67
2:I:112:THR:O	2:I:116:THR:HG23	1.93	0.67
1:H:18:DA:H1'	1:H:19:DA:H5'	1.75	0.67
3:A:192:VAL:HG12	3:A:195:ARG:HB2	1.76	0.67
5:D:955:LYS:HG2	5:D:1010:GLN:HB3	1.76	0.67
2:J:174:GLU:HG2	2:J:175:PHE:H	1.60	0.67
4:C:1267:GLY:HA3	5:D:347:VAL:O	1.94	0.67
5:D:1267:VAL:N	5:D:1301:THR:O	2.22	0.67
2:J:208:ARG:HG2	2:J:209:LEU:H	1.59	0.67
3:B:101:THR:HG22	3:B:143:ARG:HD2	1.77	0.67
6:F:128:ASN:OD1	6:F:131:GLN:NE2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:41:VAL:HG11	2:J:59:VAL:HG11	1.76	0.67
4:C:576:SER:OG	4:C:577:VAL:N	2.27	0.67
5:D:3:ASP:O	5:D:7:PHE:N	2.28	0.67
5:D:925:GLU:HG3	5:D:926:PRO:HD3	1.77	0.67
2:J:71:GLU:HG2	2:J:73:ARG:H	1.59	0.67
4:C:232:ILE:HG23	4:C:237:LEU:HD23	1.76	0.67
4:C:321:LEU:O	4:C:325:LEU:N	2.28	0.67
4:C:379:GLU:N	4:C:379:GLU:OE1	2.28	0.67
3:A:57:THR:HG21	3:A:147:GLN:HE21	1.58	0.67
6:F:283:GLN:HE22	6:F:340:ALA:HB1	1.60	0.67
6:F:146:GLU:O	6:F:150:ARG:NE	2.28	0.66
2:J:180:ALA:HB1	2:J:184:LYS:HD2	1.78	0.66
4:C:97:ARG:HG3	4:C:121:GLU:HB3	1.78	0.66
5:D:716:GLN:HG3	5:D:717:VAL:O	1.95	0.66
5:D:959:LYS:HG3	5:D:985:ILE:HG13	1.77	0.66
3:B:135:ASP:O	3:B:137:ASN:ND2	2.28	0.66
3:B:155:ALA:N	3:B:174:ASP:OD1	2.25	0.66
5:D:638:SER:OG	5:D:639:VAL:N	2.25	0.66
5:D:902:ASP:OD1	5:D:903:LEU:N	2.27	0.66
5:D:1039:ASP:OD2	5:D:1075:ARG:N	2.25	0.66
6:F:338:HIS:HA	6:F:341:LEU:HD11	1.76	0.66
5:D:163:GLU:O	5:D:167:ASP:N	2.23	0.66
5:D:507:VAL:HG21	5:D:598:LYS:HB2	1.77	0.66
5:D:641:ILE:O	5:D:764:ARG:NH2	2.28	0.66
5:D:947:GLU:HG2	5:D:1020:TRP:HH2	1.60	0.66
5:D:1158:GLU:OE1	5:D:1158:GLU:N	2.28	0.66
5:D:1160:SER:OG	5:D:1206:ARG:N	2.29	0.66
2:J:51:ILE:HG22	2:J:57:GLN:HG2	1.78	0.66
2:I:23:HIS:HA	2:I:26:ARG:HG2	1.76	0.66
2:J:147:PRO:HD2	2:J:152:ASP:HA	1.76	0.66
4:C:439:LYS:O	4:C:439:LYS:NZ	2.23	0.66
4:C:1033:ARG:O	4:C:1033:ARG:NE	2.19	0.66
5:D:475:GLU:HG3	8:E:24:ALA:HB1	1.76	0.66
5:D:1063:ASP:OD1	5:D:1103:GLY:HA3	1.96	0.66
6:F:229:VAL:O	6:F:232:ARG:NH1	2.28	0.66
7:G:55:DT:H2'	7:G:56:DT:C2	2.31	0.66
3:B:41:ASN:OD1	3:B:44:ARG:NH2	2.28	0.66
5:D:888:CYS:SG	5:D:889:ASP:N	2.69	0.66
5:D:980:THR:CB	5:D:997:VAL:HB	2.24	0.66
3:A:61:ILE:HB	3:A:64:VAL:HG12	1.77	0.65
5:D:1272:SER:OG	5:D:1286:LYS:NZ	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:595:THR:CG2	4:C:600:THR:HG21	2.25	0.65
5:D:1175:LEU:HD12	5:D:1176:VAL:H	1.61	0.65
3:A:208:ASN:ND2	3:A:210:THR:OG1	2.28	0.65
4:C:843:THR:HG22	4:C:845:LEU:H	1.60	0.65
4:C:1243:MET:HE3	5:D:445:LYS:HB3	1.78	0.65
6:F:460:ILE:HD13	6:F:501:ALA:HB2	1.77	0.65
3:A:155:ALA:O	3:A:159:ILE:HG12	1.97	0.65
5:D:982:LEU:HD21	5:D:997:VAL:HG21	1.79	0.65
6:F:561:MET:HE1	6:F:576:VAL:HG13	1.78	0.65
3:A:74:VAL:HG23	3:A:76:GLU:H	1.62	0.65
4:C:632:ASP:OD1	4:C:632:ASP:N	2.27	0.65
5:D:390:LEU:HD23	5:D:407:VAL:HG11	1.78	0.65
4:C:290:GLU:OE1	4:C:291:TYR:N	2.30	0.65
4:C:453:ILE:HD12	4:C:587:LEU:HD21	1.79	0.65
5:D:611:ILE:HG22	5:D:612:LEU:HD12	1.78	0.65
5:D:1167:LYS:HE3	5:D:1170:LYS:CB	2.26	0.65
3:B:205:MET:HE1	3:B:217:ILE:HG13	1.79	0.65
5:D:1060:VAL:HG22	5:D:1106:ILE:HD13	1.79	0.65
2:J:129:ARG:HA	2:J:173:ILE:HD11	1.78	0.65
4:C:117:ILE:HD11	4:C:488:MET:HA	1.79	0.65
5:D:509:GLY:HA2	5:D:632:ALA:HB2	1.79	0.65
2:I:123:SER:O	2:I:127:ALA:N	2.24	0.64
6:F:158:LEU:HD23	6:F:158:LEU:H	1.62	0.64
2:J:101:LEU:HD22	2:J:104:HIS:HB3	1.79	0.64
4:C:193:ASN:HB3	4:C:350:THR:HG22	1.77	0.64
4:C:1262:LYS:HB2	6:F:524:GLU:OE1	1.96	0.64
5:D:44:ILE:HD11	6:F:450:ILE:HD11	1.80	0.64
8:E:41:GLU:HB2	8:E:49:ILE:HD11	1.78	0.64
4:C:1005:GLU:O	4:C:1008:GLN:HG3	1.98	0.64
5:D:194:LEU:HD21	5:D:234:PRO:HG3	1.80	0.64
3:A:191:ARG:NH2	3:A:196:THR:O	2.29	0.64
4:C:30:ILE:HG22	4:C:31:GLN:HG2	1.80	0.64
5:D:801:VAL:CG2	5:D:917:VAL:HG13	2.28	0.64
6:F:277:MET:O	6:F:281:ARG:N	2.31	0.64
3:B:83:LEU:HD11	5:D:527:LEU:O	1.97	0.64
5:D:73:GLY:O	5:D:76:LYS:NZ	2.27	0.64
5:D:807:LEU:HD12	5:D:1259:GLN:OE1	1.98	0.64
6:F:262:VAL:HG13	6:F:263:PRO:HD2	1.78	0.64
4:C:303:ASP:O	4:C:307:GLY:N	2.31	0.64
4:C:716:ALA:HB3	4:C:784:ALA:HB3	1.80	0.64
5:D:1103:GLY:O	5:D:1124:ILE:HG13	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:558:VAL:HG21	6:F:587:ILE:HD11	1.79	0.64
7:G:11:DT:H2"	7:G:12:DG:H5"	1.79	0.64
2:I:14:PHE:HB2	2:I:50:LEU:HD13	1.78	0.64
2:J:129:ARG:HH11	2:J:129:ARG:HB2	1.62	0.64
4:C:268:ARG:NH2	4:C:269:ILE:O	2.30	0.64
4:C:1164:PHE:HB2	4:C:1168:GLU:CB	2.27	0.64
5:D:836:ARG:NH1	5:D:837:ASP:OD1	2.31	0.64
5:D:134:ASP:OD1	5:D:159:ILE:HG12	1.98	0.64
5:D:450:HIS:NE2	5:D:625:MET:SD	2.71	0.64
6:F:228:TYR:CD2	6:F:229:VAL:HG13	2.33	0.64
2:I:16:GLY:N	2:I:22:SER:OG	2.21	0.63
2:J:137:LEU:HD23	2:J:179:GLY:HA3	1.80	0.63
3:A:11:PRO:HB3	3:A:31:LEU:HD23	1.80	0.63
4:C:245:ARG:HG3	4:C:337:PHE:CZ	2.34	0.63
5:D:960:LEU:HD22	5:D:981:GLU:O	1.99	0.63
6:F:322:MET:HG3	6:F:324:LYS:HD3	1.81	0.63
4:C:60:GLN:HE22	4:C:67:GLU:HG3	1.62	0.63
5:D:1102:PRO:HG2	5:D:1124:ILE:HD11	1.80	0.63
5:D:1167:LYS:HE2	5:D:1174:ARG:HD3	1.79	0.63
4:C:866:ASP:HB3	4:C:872:TYR:CE1	2.33	0.63
5:D:208:THR:HG21	5:D:213:LYS:HE3	1.80	0.63
5:D:232:ASN:OD1	5:D:232:ASN:N	2.31	0.63
5:D:1155:ILE:HG12	5:D:1211:SER:HB3	1.80	0.63
3:A:100:LEU:HD13	3:A:115:ILE:HG21	1.78	0.63
4:C:335:THR:OG1	4:C:336:LEU:N	2.31	0.63
4:C:979:LEU:HD21	4:C:1011:LEU:CD2	2.28	0.63
4:C:1006:GLU:HA	4:C:1009:ASN:HB2	1.80	0.63
5:D:275:ARG:NH2	6:F:403:ASP:OD1	2.30	0.63
3:B:100:LEU:HD23	3:B:144:ILE:HG13	1.81	0.63
4:C:194:LEU:HB3	4:C:206:ALA:HB3	1.81	0.63
4:C:255:ILE:HG12	4:C:263:VAL:HB	1.80	0.63
5:D:1172:LYS:HB3	5:D:1191:PRO:HA	1.80	0.63
3:A:50:SER:HB3	3:B:8:PHE:HZ	1.63	0.63
3:B:135:ASP:OD1	3:B:136:GLU:N	2.32	0.63
5:D:1152:GLU:OE1	5:D:1194:ARG:NH2	2.30	0.63
3:K:263:THR:O	3:K:267:ALA:N	2.30	0.63
3:B:170:ARG:HH11	3:B:170:ARG:HA	1.64	0.63
4:C:667:LEU:HA	4:C:702:THR:HG21	1.80	0.63
4:C:843:THR:HG23	4:C:844:LYS:HZ2	1.57	0.63
1:H:11:DG:N2	7:G:53:DA:N3	2.47	0.63
2:I:96:ARG:NH2	2:J:81:GLU:OE2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:110:VAL:HG23	3:A:133:LEU:HD23	1.81	0.63
5:D:509:GLY:CA	5:D:632:ALA:HB2	2.29	0.63
5:D:799:ARG:NH1	5:D:1146:GLU:OE2	2.32	0.63
5:D:980:THR:O	5:D:997:VAL:N	2.32	0.63
3:B:214:GLU:OE2	3:B:218:ARG:NH2	2.23	0.63
2:I:20:ILE:HD11	2:I:163:PRO:HB2	1.81	0.62
3:B:57:THR:O	3:B:173:VAL:HG12	1.99	0.62
4:C:1339:LEU:HB3	5:D:17:PHE:HD2	1.64	0.62
6:F:144:LEU:HA	6:F:147:GLN:CG	2.28	0.62
7:G:54:DT:O2	7:G:55:DT:H1'	1.99	0.62
5:D:163:GLU:OE1	5:D:163:GLU:N	2.32	0.62
5:D:1111:ASP:OD1	5:D:1112:GLY:N	2.32	0.62
2:I:85:HIS:HB3	6:F:557:LYS:HZ2	1.64	0.62
4:C:1134:GLN:O	4:C:1135:GLN:HG2	1.99	0.62
4:C:1142:ARG:HD3	4:C:1169:VAL:HG21	1.82	0.62
1:H:44:DG:H1'	1:H:45:DA:H5'	1.80	0.62
2:J:191:PHE:HA	2:J:196:PHE:HD2	1.64	0.62
4:C:865:LEU:HD23	4:C:865:LEU:H	1.64	0.62
3:B:104:LYS:NZ	3:B:105:SER:O	2.32	0.62
4:C:198:ILE:HG22	4:C:199:ASP:H	1.64	0.62
4:C:642:SER:HB3	5:D:770:LEU:HD21	1.82	0.62
4:C:982:GLY:HA3	4:C:1002:LEU:HG	1.79	0.62
5:D:210:SER:O	5:D:214:ARG:HG2	2.00	0.62
5:D:1286:LYS:O	5:D:1290:ARG:N	2.27	0.62
8:E:84:THR:HA	8:E:87:ALA:HB3	1.82	0.62
3:B:222:THR:O	3:B:226:GLU:HG2	1.99	0.62
4:C:1012:GLU:HA	4:C:1015:ALA:HB3	1.81	0.62
4:C:268:ARG:CZ	4:C:270:THR:HG22	2.29	0.62
5:D:806:ASP:OD1	5:D:806:ASP:N	2.29	0.62
4:C:242:VAL:HG22	4:C:245:ARG:HE	1.64	0.62
5:D:816:THR:HG22	5:D:818:GLU:H	1.65	0.62
2:I:93:PRO:HD2	5:D:82:GLY:HA3	1.80	0.62
2:J:137:LEU:HA	2:J:140:ALA:HB2	1.81	0.62
4:C:236:LYS:HE2	4:C:236:LYS:HA	1.80	0.62
4:C:545:PHE:CZ	5:D:781:LYS:HD3	2.35	0.62
4:C:549:ASP:OD1	4:C:550:VAL:N	2.32	0.62
4:C:1015:ALA:HA	4:C:1018:TYR:HB3	1.79	0.62
4:C:1338:GLU:O	4:C:1339:LEU:HD23	1.99	0.62
5:D:718:SER:OG	5:D:719:PHE:N	2.28	0.62
5:D:1025:MET:HB3	5:D:1124:ILE:CG2	2.29	0.62
2:I:82:ARG:HH21	6:F:578:LYS:HB3	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:202:GLU:N	2:I:202:GLU:OE1	2.33	0.61
4:C:940:GLU:OE1	4:C:940:GLU:N	2.33	0.61
5:D:1003:LEU:HD22	5:D:1018:ALA:HB1	1.82	0.61
5:D:1080:ILE:HD12	5:D:1097:ALA:CB	2.29	0.61
5:D:1215:GLU:OE1	5:D:1215:GLU:N	2.32	0.61
6:F:97:PRO:O	6:F:101:TYR:N	2.32	0.61
1:H:32:DG:H22	7:G:31:DC:H1'	1.65	0.61
6:F:585:GLU:CG	6:F:588:ARG:HD2	2.31	0.61
4:C:194:LEU:HB3	4:C:206:ALA:CB	2.30	0.61
4:C:415:GLU:OE1	4:C:415:GLU:N	2.27	0.61
4:C:988:LYS:HA	4:C:991:LYS:HG2	1.83	0.61
5:D:1033:GLY:HA2	5:D:1114:GLN:NE2	2.15	0.61
4:C:276:GLN:HA	4:C:279:LYS:HD3	1.81	0.61
4:C:775:GLU:OE1	4:C:775:GLU:N	2.33	0.61
4:C:1157:GLN:HE21	4:C:1157:GLN:CA	2.01	0.61
5:D:17:PHE:O	5:D:1369:ARG:NH2	2.33	0.61
5:D:388:ARG:HB2	5:D:390:LEU:HD13	1.82	0.61
5:D:558:ASP:N	5:D:558:ASP:OD1	2.31	0.61
5:D:1095:MET:HG3	5:D:1096:PRO:O	1.99	0.61
4:C:230:PHE:CE2	4:C:292:ILE:HD12	2.36	0.61
5:D:140:TYR:HB3	6:F:100:MET:HE1	1.82	0.61
2:J:90:PRO:HG2	2:J:96:ARG:HA	1.82	0.61
3:A:14:VAL:HG12	3:A:27:THR:O	2.00	0.61
3:B:83:LEU:HD21	5:D:526:VAL:HG22	1.81	0.61
4:C:119:GLU:HB2	4:C:489:PRO:HD2	1.82	0.61
5:D:314:ARG:HH22	5:D:323:PRO:HG3	1.65	0.61
5:D:966:VAL:HG12	5:D:967:VAL:O	2.01	0.61
5:D:975:ILE:HG12	5:D:998:PRO:O	2.01	0.61
5:D:1178:THR:HG23	5:D:1185:PRO:HA	1.83	0.61
6:F:292:VAL:HA	6:F:297:MET:O	2.00	0.61
1:H:19:DA:H2''	1:H:20:DA:C5'	2.31	0.61
2:J:22:SER:O	2:J:26:ARG:HG3	2.00	0.61
4:C:702:THR:O	4:C:702:THR:OG1	2.04	0.61
4:C:1160:ASP:O	4:C:1161:LEU:HB2	2.00	0.61
5:D:130:MET:HE1	5:D:157:GLN:HB3	1.82	0.61
5:D:808:VAL:HG21	5:D:1359:ALA:HB2	1.83	0.61
6:F:250:LEU:O	6:F:254:GLU:N	2.32	0.61
3:K:258:ASP:OD2	3:K:271:LYS:NZ	2.28	0.61
4:C:12:ARG:NH2	4:C:793:GLU:OE2	2.25	0.61
4:C:1158:LYS:HA	4:C:1158:LYS:NZ	2.16	0.61
5:D:518:VAL:HG12	5:D:707:ILE:HD12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:137:TYR:HA	6:F:361:ILE:CD1	2.31	0.61
6:F:141:ILE:HD13	6:F:224:LEU:HD21	1.83	0.61
8:E:55:GLU:HG3	8:E:56:GLU:HG3	1.81	0.61
2:I:20:ILE:HG12	2:I:24:GLN:HG3	1.82	0.61
2:J:162:ALA:HB3	2:J:163:PRO:HD3	1.82	0.61
3:B:107:ILE:HD13	3:B:135:ASP:HA	1.81	0.61
5:D:273:ILE:O	5:D:277:ASN:HB2	2.00	0.61
5:D:1067:ARG:HH22	5:D:1076:PRO:HD3	1.66	0.61
4:C:10:ARG:NH2	4:C:793:GLU:OE1	2.33	0.61
4:C:231:GLU:HG3	4:C:233:ARG:HG3	1.81	0.61
4:C:1020:GLU:HA	4:C:1024:GLU:H	1.65	0.61
5:D:120:LEU:HD11	7:G:10:DG:H4'	1.82	0.61
5:D:395:LYS:O	5:D:399:LYS:NZ	2.28	0.61
5:D:694:SER:OG	5:D:738:ARG:NE	2.34	0.61
2:I:169:PRO:HA	2:I:173:ILE:H	1.66	0.60
2:J:14:PHE:CD2	2:J:50:LEU:HD13	2.36	0.60
2:J:82:ARG:HG2	2:J:83:PHE:CD1	2.36	0.60
4:C:471:VAL:O	4:C:475:VAL:HG12	2.00	0.60
5:D:998:PRO:HG2	5:D:1025:MET:HE1	1.82	0.60
5:D:1038:THR:HB	5:D:1077:ALA:O	2.00	0.60
5:D:394:ILE:HG12	6:F:532:LEU:HD11	1.83	0.60
6:F:593:LYS:HB3	6:F:596:ARG:HH22	1.65	0.60
2:I:46:PRO:HB3	2:I:50:LEU:HD23	1.82	0.60
6:F:290:LEU:HA	6:F:294:GLN:HB2	1.81	0.60
2:I:46:PRO:CB	2:I:50:LEU:HD23	2.30	0.60
5:D:443:GLU:OE2	5:D:444:GLY:N	2.34	0.60
2:I:111:TYR:CE1	2:I:164:LEU:HD11	2.34	0.60
3:A:27:THR:CG2	3:A:200:LYS:HE3	2.31	0.60
4:C:808:ASN:H	5:D:633:ALA:HB2	1.66	0.60
5:D:1108:GLN:NE2	5:D:1120:THR:O	2.33	0.60
6:F:315:TRP:HH2	6:F:338:HIS:HB2	1.65	0.60
1:H:60:DA:N3	7:G:4:DG:N2	2.49	0.60
2:J:157:VAL:HG13	2:J:158:ASP:OD1	2.02	0.60
6:F:277:MET:HA	6:F:280:VAL:HG22	1.82	0.60
4:C:301:TYR:HB2	4:C:311:CYS:SG	2.41	0.60
5:D:1067:ARG:NH2	5:D:1076:PRO:HD3	2.16	0.60
3:A:179:PRO:HA	3:A:208:ASN:OD1	2.01	0.60
3:B:101:THR:HG22	3:B:143:ARG:CD	2.32	0.60
4:C:27:LEU:O	4:C:528:ARG:NH1	2.35	0.60
4:C:1138:VAL:HG11	4:C:1166:ASP:HA	1.84	0.60
5:D:1012:ALA:HB3	5:D:1015:GLU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:13:LEU:HD11	2:I:60:PRO:HB2	1.84	0.60
2:J:82:ARG:NH2	5:D:91:GLU:OE1	2.34	0.60
3:B:161:SER:O	3:B:163:GLU:HG3	2.02	0.60
4:C:292:ILE:HG22	4:C:317:LEU:HD12	1.83	0.60
5:D:62:PHE:CD1	5:D:247:PRO:HD3	2.36	0.60
2:I:132:LEU:HD23	2:I:173:ILE:HD11	1.82	0.60
5:D:1024:THR:HG22	5:D:1124:ILE:H	1.67	0.60
3:A:235:ARG:HB3	3:B:14:VAL:HG13	1.83	0.59
3:B:107:ILE:HD11	3:B:136:GLU:H	1.66	0.59
3:B:166:ARG:HB3	3:B:170:ARG:CG	2.31	0.59
4:C:230:PHE:HB2	4:C:333:ILE:HB	1.83	0.59
4:C:274:ILE:HA	4:C:277:LEU:CD1	2.32	0.59
4:C:336:LEU:O	4:C:338:THR:HG22	2.02	0.59
1:H:42:DG:O6	6:F:106:GLY:CA	2.34	0.59
3:B:58:GLU:OE2	3:B:170:ARG:NH2	2.35	0.59
4:C:540:ARG:HH22	4:C:567:PRO:HG2	1.67	0.59
4:C:897:PRO:HG2	4:C:898:GLU:OE1	2.03	0.59
5:D:660:GLU:HG2	5:D:685:ILE:HD12	1.83	0.59
5:D:801:VAL:HG21	5:D:917:VAL:HG13	1.84	0.59
5:D:1057:SER:OG	5:D:1059:LEU:HD13	2.02	0.59
5:D:1061:VAL:O	5:D:1103:GLY:HA2	2.02	0.59
6:F:320:ILE:HG13	6:F:330:LEU:HB2	1.84	0.59
2:I:36:PHE:CE2	2:I:38:ILE:HG22	2.37	0.59
4:C:373:GLY:HA3	6:F:94:THR:HB	1.84	0.59
5:D:152:THR:HG22	5:D:153:ASN:H	1.67	0.59
5:D:930:LEU:HD11	5:D:1241:TYR:CD1	2.37	0.59
6:F:127:ILE:O	6:F:131:GLN:HG3	2.02	0.59
6:F:231:THR:OG1	6:F:252:LEU:HB2	2.02	0.59
6:F:574:GLU:O	6:F:578:LYS:NZ	2.26	0.59
5:D:959:LYS:HE3	5:D:985:ILE:HG21	1.84	0.59
2:J:155:SER:OG	2:J:157:VAL:HG12	2.02	0.59
4:C:238:GLN:NE2	4:C:286:GLU:OE2	2.34	0.59
4:C:303:ASP:N	4:C:310:ILE:HG12	2.16	0.59
4:C:1305:TYR:O	4:C:1309:VAL:HG13	2.02	0.59
5:D:217:LEU:O	5:D:221:ILE:HG22	2.03	0.59
4:C:1293:VAL:HG11	4:C:1304:MET:HG2	1.85	0.59
5:D:287:ALA:HB1	5:D:288:PRO:HD2	1.84	0.59
5:D:847:ASP:N	5:D:847:ASP:OD1	2.32	0.59
5:D:947:GLU:HG2	5:D:1020:TRP:CH2	2.37	0.59
5:D:975:ILE:HD11	5:D:977:SER:O	2.03	0.59
2:J:17:PRO:HD3	2:J:41:VAL:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:154:PHE:CE1	2:J:158:ASP:HB2	2.37	0.59
3:B:28:LEU:HD12	3:B:29:GLU:H	1.67	0.59
4:C:66:SER:O	4:C:479:LEU:HD21	2.03	0.59
4:C:1336:ASN:HB2	5:D:25:ALA:HB2	1.85	0.59
5:D:1264:ALA:HB2	5:D:1280:VAL:HG22	1.85	0.59
6:F:231:THR:HB	6:F:248:GLU:O	2.01	0.59
8:E:58:LEU:HD23	8:E:58:LEU:H	1.68	0.59
2:I:96:ARG:HH21	2:J:81:GLU:HG2	1.66	0.59
3:A:155:ALA:HA	3:A:158:ARG:CD	2.32	0.59
4:C:189:ASP:HB2	4:C:190:PRO:HD2	1.84	0.59
4:C:1340:GLU:HG2	5:D:19:ALA:O	2.03	0.59
1:H:59:DC:H1'	1:H:60:DA:H5'	1.85	0.59
5:D:83:VAL:O	5:D:92:VAL:HG22	2.02	0.59
1:H:18:DA:C1'	1:H:19:DA:H5'	2.33	0.59
2:J:23:HIS:O	2:J:27:ILE:HG12	2.03	0.59
3:A:14:VAL:CG1	3:A:27:THR:HB	2.31	0.59
3:A:41:ASN:ND2	4:C:1217:THR:O	2.35	0.58
5:D:127:LEU:HD22	5:D:227:PHE:HE2	1.68	0.58
5:D:673:VAL:HG22	5:D:674:THR:O	2.02	0.58
2:I:42:GLU:OE1	2:I:43:LYS:HD2	2.03	0.58
2:J:28:VAL:O	2:J:32:LYS:HG2	2.03	0.58
3:A:26:VAL:HG21	3:A:217:ILE:HD12	1.84	0.58
5:D:664:ILE:HD13	5:D:681:LYS:HG2	1.85	0.58
5:D:978:ARG:NH1	5:D:999:TYR:HB2	2.18	0.58
6:F:123:ILE:O	6:F:126:GLY:N	2.37	0.58
7:G:52:DC:H5'	7:G:52:DC:H6	1.67	0.58
1:H:42:DG:H2''	1:H:43:DG:OP2	2.03	0.58
4:C:1095:ASP:O	4:C:1096:ILE:HG12	2.02	0.58
5:D:297:ARG:HH11	6:F:100:MET:HE2	1.68	0.58
5:D:1057:SER:HG	5:D:1059:LEU:HD13	1.68	0.58
6:F:227:GLN:HB3	6:F:231:THR:CG2	2.33	0.58
8:E:30:MET:HE1	8:E:49:ILE:CG2	2.33	0.58
1:H:38:DT:C2'	6:F:429:THR:HG21	2.32	0.58
1:H:44:DG:H2''	1:H:45:DA:H5'	1.85	0.58
2:J:32:LYS:NZ	2:J:83:PHE:O	2.22	0.58
3:A:14:VAL:HG22	3:A:15:ASP:H	1.69	0.58
4:C:230:PHE:HE2	4:C:292:ILE:HD12	1.69	0.58
5:D:317:THR:CG2	5:D:320:ASN:HB3	2.34	0.58
5:D:519:ASN:HA	5:D:523:GLU:OE1	2.04	0.58
5:D:1004:ALA:N	5:D:1017:VAL:O	2.30	0.58
2:I:17:PRO:HG3	2:I:40:HIS:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:85:HIS:CE1	6:F:567:MET:HG3	2.39	0.58
2:J:113:LEU:HD23	2:J:132:LEU:CD1	2.32	0.58
3:A:77:ASP:OD1	3:A:77:ASP:N	2.34	0.58
4:C:257:ALA:HB3	4:C:262:TYR:CE2	2.38	0.58
4:C:453:ILE:HD11	4:C:587:LEU:HD11	1.85	0.58
4:C:843:THR:CG2	4:C:844:LYS:N	2.66	0.58
4:C:1297:ASP:OD1	4:C:1300:GLY:N	2.33	0.58
5:D:813:ASP:OD2	5:D:897:HIS:ND1	2.37	0.58
5:D:816:THR:HG23	5:D:818:GLU:OE2	2.02	0.58
2:I:34:VAL:HG11	2:I:83:PHE:HE2	1.68	0.58
4:C:471:VAL:CB	4:C:498:ILE:HD11	2.33	0.58
5:D:490:ILE:HD11	5:D:614:LEU:HD12	1.84	0.58
5:D:1005:LYS:NZ	5:D:1011:VAL:HA	2.19	0.58
6:F:142:THR:HA	6:F:145:LEU:CD2	2.33	0.58
6:F:465:ARG:NH2	7:G:26:DT:H2'	2.19	0.58
6:F:552:THR:OG1	6:F:555:GLU:HB2	2.04	0.58
6:F:598:LEU:O	6:F:604:SER:OG	2.21	0.58
3:B:69:SER:OG	3:B:70:THR:N	2.37	0.58
4:C:155:VAL:HG12	4:C:176:ILE:HG12	1.84	0.58
4:C:320:ASP:O	4:C:324:LYS:N	2.31	0.58
4:C:976:ARG:NE	4:C:989:LEU:HD23	2.19	0.58
5:D:255:LEU:HD23	5:D:261:ALA:HB2	1.85	0.58
1:H:19:DA:H2''	1:H:20:DA:H5''	1.85	0.58
4:C:77:GLU:OE1	4:C:77:GLU:N	2.31	0.58
4:C:278:GLU:N	4:C:278:GLU:OE1	2.36	0.58
4:C:303:ASP:HB2	4:C:308:GLU:O	2.03	0.58
2:I:29:LEU:HD21	2:I:36:PHE:CD2	2.39	0.58
3:A:236:ASP:HA	3:B:16:ILE:HG22	1.85	0.58
4:C:397:LEU:O	4:C:398:SER:OG	2.19	0.58
5:D:973:LEU:O	5:D:1003:LEU:HG	2.02	0.58
6:F:234:THR:CG2	6:F:245:ALA:HA	2.33	0.58
4:C:98:VAL:O	4:C:121:GLU:HA	2.04	0.58
4:C:158:ASP:OD1	4:C:159:SER:N	2.34	0.58
5:D:843:VAL:HG21	5:D:883:ARG:HD3	1.85	0.58
6:F:232:ARG:O	6:F:236:LYS:HB3	2.04	0.58
6:F:297:MET:HG2	6:F:298:PRO:HD2	1.86	0.58
7:G:7:DT:H1'	7:G:8:DC:H5'	1.84	0.58
2:J:29:LEU:HG	2:J:34:VAL:HG11	1.85	0.57
2:J:184:LYS:O	2:J:188:THR:HG22	2.04	0.57
4:C:192:ASP:HB3	4:C:346:TYR:HD1	1.69	0.57
5:D:616:PRO:HA	5:D:619:ILE:HG22	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:268:TYR:HA	6:F:271:ASN:HB2	1.86	0.57
6:F:305:LEU:O	6:F:314:THR:HG21	2.04	0.57
8:E:30:MET:HE1	8:E:49:ILE:HG21	1.86	0.57
3:A:38:THR:OG1	3:B:45:ARG:HD3	2.05	0.57
5:D:1104:LYS:CE	5:D:1124:ILE:HG23	2.34	0.57
5:D:1136:GLY:HA2	5:D:1140:ARG:HB2	1.86	0.57
6:F:146:GLU:HB3	6:F:150:ARG:CZ	2.34	0.57
6:F:150:ARG:HD2	6:F:155:GLU:OE1	2.03	0.57
1:H:40:DA:H3'	1:H:41:DT:H5''	1.86	0.57
4:C:324:LYS:O	4:C:328:SER:HB2	2.04	0.57
6:F:109:GLU:OE1	6:F:109:GLU:N	2.31	0.57
4:C:38:PHE:HE1	4:C:461:GLU:HB2	1.69	0.57
4:C:81:ASP:HB2	4:C:84:GLU:OE1	2.03	0.57
4:C:826:ASP:OD1	4:C:829:THR:HB	2.05	0.57
6:F:246:GLN:O	6:F:250:LEU:HB2	2.04	0.57
3:B:104:LYS:HE3	3:B:114:ASP:OD2	2.03	0.57
4:C:496:LYS:HB3	4:C:497:PRO:HD3	1.85	0.57
4:C:672:GLU:HB3	4:C:1187:PHE:CD1	2.39	0.57
4:C:242:VAL:HG23	4:C:245:ARG:HB2	1.86	0.57
4:C:1022:LYS:HG3	4:C:1023:HIS:HD2	1.67	0.57
5:D:26:SER:HB3	5:D:236:TRP:CE2	2.39	0.57
5:D:320:ASN:O	5:D:321:LYS:HD3	2.05	0.57
5:D:489:ASN:OD1	5:D:489:ASN:N	2.36	0.57
5:D:697:MET:SD	5:D:741:ALA:HB3	2.45	0.57
1:H:37:DA:C2	6:F:423:ARG:HB2	2.39	0.57
2:J:15:SER:O	2:J:41:VAL:HG13	2.05	0.57
5:D:235:GLU:OE1	5:D:235:GLU:N	2.27	0.57
5:D:514:THR:HG21	5:D:596:LEU:HB3	1.87	0.57
5:D:742:GLY:O	5:D:762:ASN:HB3	2.05	0.57
5:D:1229:VAL:O	5:D:1233:ILE:HG12	2.05	0.57
1:H:16:DA:H2''	1:H:17:DC:C6	2.39	0.57
3:A:49:SER:OG	4:C:1083:GLU:OE2	2.21	0.57
3:A:197:ASP:O	3:A:198:LEU:HD23	2.05	0.57
3:B:86:LYS:HE2	3:B:174:ASP:HB2	1.87	0.57
3:B:102:LEU:O	3:B:141:SER:HA	2.05	0.57
4:C:294:GLY:O	4:C:295:LYS:HD3	2.04	0.57
4:C:319:LEU:CD1	4:C:322:LEU:HD12	2.34	0.57
5:D:972:LYS:HD2	5:D:974:VAL:HA	1.86	0.57
5:D:973:LEU:HB2	5:D:1003:LEU:CD1	2.33	0.57
2:J:134:GLU:HA	2:J:137:LEU:HD11	1.86	0.57
3:B:170:ARG:HA	3:B:170:ARG:NH1	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:255:ILE:HG22	4:C:262:TYR:H	1.70	0.57
5:D:134:ASP:O	5:D:138:VAL:HG23	2.05	0.57
5:D:530:PRO:HB2	5:D:581:MET:HE2	1.86	0.57
5:D:810:THR:HG21	5:D:892:PHE:O	2.05	0.57
5:D:857:LEU:HD12	5:D:871:LEU:HD23	1.87	0.57
5:D:1168:GLU:OE2	5:D:1173:ARG:NH1	2.37	0.57
6:F:137:TYR:HD1	6:F:361:ILE:HD13	1.70	0.57
4:C:58:PRO:HB3	4:C:69:GLN:HA	1.85	0.57
4:C:106:GLU:HB2	4:C:114:VAL:HG21	1.87	0.57
4:C:1034:ARG:NH1	4:C:1034:ARG:HB2	2.20	0.57
5:D:155:GLU:OE1	5:D:158:GLN:NE2	2.27	0.57
6:F:288:MET:HG3	6:F:299:LYS:HD3	1.87	0.57
3:A:11:PRO:HA	3:A:30:PRO:HD2	1.87	0.56
4:C:840:SER:O	4:C:1047:LEU:HB2	2.05	0.56
6:F:165:PHE:CE2	6:F:259:PHE:HA	2.40	0.56
6:F:273:MET:HA	6:F:276:MET:HG2	1.86	0.56
7:G:47:DT:C2'	7:G:48:DC:H5'	2.32	0.56
2:J:129:ARG:HG3	2:J:173:ILE:CG1	2.33	0.56
4:C:131:THR:CG2	4:C:132:ASP:H	2.17	0.56
4:C:208:ILE:HD11	4:C:365:GLU:HG2	1.86	0.56
5:D:1011:VAL:HG21	5:D:1017:VAL:CB	2.32	0.56
5:D:1102:PRO:HG2	5:D:1124:ILE:CD1	2.34	0.56
1:H:4:DA:H2	7:G:60:DT:H3	1.52	0.56
2:J:20:ILE:O	2:J:24:GLN:HG3	2.05	0.56
3:B:33:ARG:HB2	3:B:197:ASP:O	2.05	0.56
4:C:1118:GLY:O	4:C:1229:TYR:HB2	2.05	0.56
5:D:847:ASP:OD1	5:D:860:ARG:HD3	2.05	0.56
5:D:986:ASP:OD2	5:D:990:ARG:HB2	2.05	0.56
5:D:1029:THR:CB	5:D:1121:LEU:HD11	2.34	0.56
5:D:1073:ASP:O	5:D:1074:LEU:HD23	2.06	0.56
6:F:131:GLN:HB3	6:F:266:PHE:HZ	1.71	0.56
3:K:280:ASP:N	3:K:280:ASP:OD1	2.38	0.56
5:D:208:THR:CG2	5:D:213:LYS:HE3	2.35	0.56
5:D:557:LYS:HB3	5:D:563:LEU:CD1	2.35	0.56
5:D:706:VAL:HG12	5:D:715:LYS:CB	2.34	0.56
5:D:967:VAL:HA	5:D:973:LEU:HA	1.86	0.56
5:D:1104:LYS:HE2	5:D:1124:ILE:HG23	1.87	0.56
6:F:141:ILE:O	6:F:145:LEU:N	2.32	0.56
6:F:298:PRO:HB2	6:F:301:ASN:HD21	1.71	0.56
6:F:585:GLU:HA	6:F:588:ARG:NH1	2.14	0.56
3:A:186:ASN:OD1	3:A:186:ASN:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:197:ARG:O	4:C:198:ILE:HD13	2.06	0.56
4:C:1022:LYS:HG3	4:C:1023:HIS:CD2	2.41	0.56
5:D:218:THR:HA	5:D:221:ILE:CG2	2.35	0.56
5:D:1025:MET:HB3	5:D:1124:ILE:CB	2.34	0.56
5:D:1055:GLY:O	5:D:1108:GLN:HB2	2.04	0.56
6:F:136:GLU:O	6:F:138:PRO:HD3	2.05	0.56
4:C:264:GLU:HB2	4:C:267:ARG:CD	2.33	0.56
4:C:1010:GLN:HA	4:C:1013:GLN:HB2	1.87	0.56
5:D:516:ASP:HA	5:D:545:HIS:HB2	1.87	0.56
6:F:560:ARG:HD2	6:F:567:MET:HE2	1.88	0.56
7:G:38:DA:H2'	7:G:39:DC:C6	2.41	0.56
2:J:25:VAL:HG12	2:J:29:LEU:HD13	1.88	0.56
4:C:216:THR:O	4:C:220:ILE:HG12	2.05	0.56
4:C:577:VAL:HG23	4:C:661:VAL:O	2.06	0.56
4:C:754:THR:O	4:C:754:THR:OG1	2.20	0.56
5:D:798:ARG:HD2	5:D:798:ARG:O	2.04	0.56
5:D:903:LEU:HD12	5:D:905:ARG:HE	1.70	0.56
5:D:972:LYS:CD	5:D:974:VAL:HA	2.35	0.56
3:A:118:ASP:OD1	3:A:119:GLY:N	2.37	0.56
3:B:80:GLU:OE1	5:D:569:LEU:HD21	2.06	0.56
3:B:107:ILE:CD1	3:B:135:ASP:HA	2.36	0.56
4:C:516:VAL:HG12	4:C:522:SER:OG	2.05	0.56
4:C:529:ARG:HD2	4:C:572:ILE:CG2	2.36	0.56
4:C:1030:GLU:HG3	4:C:1034:ARG:HH12	1.71	0.56
5:D:381:ILE:HD11	5:D:412:LEU:HB2	1.88	0.56
5:D:984:LEU:O	5:D:992:LYS:HB2	2.06	0.56
5:D:1029:THR:HB	5:D:1121:LEU:CD2	2.34	0.56
4:C:130:MET:SD	4:C:134:GLY:HA2	2.46	0.56
4:C:131:THR:CG2	4:C:132:ASP:N	2.69	0.56
4:C:377:THR:HG22	4:C:378:ARG:H	1.71	0.56
5:D:1109:LEU:CD2	5:D:1115:ILE:HG21	2.35	0.56
8:E:73:GLN:O	8:E:77:ALA:N	2.37	0.56
3:B:107:ILE:HG12	3:B:134:THR:O	2.06	0.56
4:C:303:ASP:OD2	4:C:310:ILE:HD11	2.06	0.56
5:D:120:LEU:HB2	5:D:121:PRO:HD3	1.88	0.56
5:D:985:ILE:HG23	5:D:990:ARG:O	2.06	0.56
5:D:1000:GLY:HA3	5:D:1026:PRO:HD2	1.88	0.56
5:D:1005:LYS:CG	5:D:1011:VAL:HG22	2.33	0.56
2:I:63:VAL:HG13	2:I:68:THR:CA	2.36	0.55
4:C:685:MET:CE	4:C:1073:LYS:HD3	2.36	0.55
4:C:1020:GLU:O	4:C:1024:GLU:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:233:LYS:HB3	5:D:235:GLU:OE1	2.06	0.55
5:D:978:ARG:O	5:D:996:LYS:HD2	2.05	0.55
5:D:1105:ALA:CB	5:D:1122:ALA:HB1	2.29	0.55
2:J:54:ASN:ND2	2:J:61:THR:OG1	2.38	0.55
3:K:264:VAL:O	3:K:268:ASN:N	2.39	0.55
3:B:47:LEU:HD12	3:B:183:ILE:CD1	2.27	0.55
5:D:751:ASP:OD1	5:D:751:ASP:N	2.37	0.55
5:D:1167:LYS:NZ	5:D:1170:LYS:HD3	2.21	0.55
2:I:63:VAL:HG13	2:I:68:THR:N	2.22	0.55
4:C:816:ILE:HG22	4:C:817:LEU:O	2.05	0.55
4:C:1016:GLU:O	4:C:1020:GLU:HG2	2.07	0.55
4:C:1041:ASP:N	4:C:1041:ASP:OD1	2.40	0.55
4:C:1124:ILE:HG21	4:C:1180:MET:CE	2.36	0.55
6:F:292:VAL:HG21	6:F:299:LYS:HB3	1.87	0.55
1:H:54:DG:H1	7:G:9:DC:H42	1.54	0.55
4:C:246:LEU:HA	4:C:249:GLU:OE2	2.05	0.55
4:C:471:VAL:CG2	4:C:498:ILE:HD11	2.37	0.55
4:C:1336:ASN:HB3	5:D:23:ALA:O	2.06	0.55
5:D:1087:ASP:O	5:D:1096:PRO:HB3	2.07	0.55
5:D:1150:PRO:CD	5:D:1216:ALA:HB2	2.36	0.55
2:J:116:THR:HA	2:J:120:GLY:HA3	1.87	0.55
2:J:201:THR:HG23	2:J:204:GLU:OE2	2.05	0.55
3:B:54:CYS:SG	3:B:148:ARG:HG2	2.47	0.55
3:B:100:LEU:H	3:B:100:LEU:HD22	1.71	0.55
4:C:285:ILE:HD12	4:C:286:GLU:O	2.07	0.55
4:C:413:GLU:N	4:C:413:GLU:OE1	2.40	0.55
4:C:799:ASN:HB3	4:C:1231:TYR:HD1	1.71	0.55
4:C:896:THR:HB	4:C:897:PRO:HD2	1.87	0.55
4:C:1339:LEU:HD13	5:D:17:PHE:CE2	2.42	0.55
6:F:558:VAL:HG23	6:F:580:PHE:HE2	1.72	0.55
3:A:61:ILE:HB	3:A:64:VAL:CG1	2.36	0.55
3:A:235:ARG:HB3	3:B:14:VAL:CG1	2.37	0.55
4:C:4:SER:O	4:C:7:GLU:N	2.40	0.55
5:D:122:SER:OG	5:D:132:LEU:HD22	2.07	0.55
5:D:426:ALA:HB3	5:D:427:PRO:HD3	1.88	0.55
5:D:1119:ASP:OD1	5:D:1120:THR:N	2.40	0.55
5:D:1168:GLU:HG2	5:D:1169:THR:H	1.71	0.55
6:F:593:LYS:HA	6:F:596:ARG:NH1	2.22	0.55
2:I:17:PRO:HB3	2:I:40:HIS:HB3	1.88	0.55
3:B:111:THR:OG1	3:B:112:ALA:N	2.40	0.55
4:C:596:ASP:N	4:C:596:ASP:OD1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:854:ILE:HG23	4:C:855:PRO:HD2	1.88	0.55
5:D:825:VAL:HG11	5:D:832:LYS:HB2	1.88	0.55
5:D:1068:THR:HG22	5:D:1069:ALA:H	1.71	0.55
1:H:44:DG:C2'	1:H:45:DA:H5'	2.37	0.55
2:J:154:PHE:HE1	2:J:158:ASP:HB2	1.72	0.55
4:C:634:VAL:O	4:C:644:LEU:HD13	2.06	0.55
4:C:699:LEU:HB2	4:C:799:ASN:ND2	2.22	0.55
5:D:707:ILE:HD11	5:D:716:GLN:NE2	2.22	0.55
5:D:860:ARG:O	5:D:862:THR:HG23	2.07	0.55
6:F:214:PRO:CB	6:F:218:ARG:HD3	2.37	0.55
3:B:103:ASN:HA	3:B:141:SER:HA	1.89	0.55
4:C:192:ASP:HB3	4:C:346:TYR:CD1	2.41	0.55
4:C:817:LEU:HD21	4:C:1080:ASN:HD21	1.72	0.55
4:C:1002:LEU:HD23	4:C:1007:LYS:CD	2.30	0.55
5:D:423:LEU:HD23	5:D:466:MET:HE1	1.89	0.55
5:D:820:ILE:HD11	5:D:822:MET:SD	2.47	0.55
5:D:972:LYS:HG3	5:D:1002:VAL:CA	2.30	0.55
5:D:1155:ILE:O	5:D:1156:LEU:HD22	2.05	0.55
6:F:320:ILE:HD11	6:F:331:HIS:HB2	1.87	0.55
2:I:23:HIS:O	2:I:27:ILE:HG13	2.07	0.55
4:C:100:LEU:CD1	4:C:122:VAL:HG11	2.36	0.55
4:C:646:SER:OG	4:C:649:GLN:HB2	2.07	0.55
6:F:137:TYR:CE2	6:F:139:GLU:HB2	2.42	0.55
6:F:138:PRO:CG	6:F:353:LEU:HD11	2.36	0.55
6:F:250:LEU:HD22	6:F:254:GLU:CG	2.32	0.55
6:F:525:ASP:OD2	6:F:528:LEU:HD13	2.07	0.55
1:H:40:DA:H5'	1:H:41:DT:C7	2.37	0.54
2:I:193:ARG:O	2:I:197:LEU:N	2.25	0.54
3:B:100:LEU:HB2	3:B:144:ILE:CG1	2.37	0.54
4:C:348:SER:O	4:C:351:LEU:HB2	2.07	0.54
4:C:906:PHE:HD2	6:F:611:LEU:HD12	1.71	0.54
5:D:664:ILE:CD1	5:D:681:LYS:HG2	2.37	0.54
5:D:857:LEU:HB2	5:D:871:LEU:HD21	1.89	0.54
5:D:1162:ILE:HD12	5:D:1202:GLU:O	2.07	0.54
2:I:41:VAL:CG1	2:I:47:PRO:HD3	2.38	0.54
2:I:204:GLU:HA	2:I:207:MET:HE2	1.89	0.54
2:J:137:LEU:HB3	2:J:179:GLY:HA2	1.88	0.54
4:C:772:SER:N	4:C:775:GLU:OE2	2.29	0.54
5:D:127:LEU:HD22	5:D:227:PHE:CE2	2.41	0.54
5:D:425:ARG:HG2	5:D:426:ALA:H	1.72	0.54
5:D:954:ASN:HB2	5:D:984:LEU:HD21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1032:SER:OG	5:D:1033:GLY:N	2.38	0.54
5:D:1150:PRO:HD3	5:D:1216:ALA:HB2	1.87	0.54
5:D:1286:LYS:HA	5:D:1289:ASN:HB3	1.87	0.54
1:H:13:DT:O2	7:G:51:DT:N3	2.40	0.54
2:J:69:LEU:O	2:J:75:ILE:HD11	2.06	0.54
2:J:139:ILE:O	2:J:142:VAL:HG13	2.07	0.54
4:C:899:GLU:HG2	6:F:540:LEU:HD13	1.89	0.54
4:C:1285:TYR:HB2	5:D:479:GLU:OE2	2.08	0.54
5:D:85:CYS:O	5:D:89:GLY:HA2	2.06	0.54
5:D:841:GLY:CA	5:D:901:ARG:HD3	2.37	0.54
5:D:955:LYS:HG3	5:D:1011:VAL:O	2.08	0.54
6:F:139:GLU:O	6:F:142:THR:CG2	2.43	0.54
6:F:145:LEU:HD22	6:F:228:TYR:OH	2.07	0.54
4:C:470:ARG:HD2	4:C:497:PRO:HB3	1.89	0.54
2:J:16:GLY:HA2	2:J:41:VAL:HG22	1.90	0.54
2:J:140:ALA:CB	2:J:183:LEU:HD23	2.38	0.54
5:D:825:VAL:CG1	5:D:832:LYS:HB2	2.37	0.54
5:D:860:ARG:HD2	5:D:861:ASN:H	1.73	0.54
4:C:179:TYR:HB2	4:C:398:SER:OG	2.08	0.54
5:D:497:GLU:HG2	5:D:498:PRO:HD2	1.90	0.54
6:F:163:THR:HG23	6:F:262:VAL:HG22	1.88	0.54
6:F:585:GLU:CB	6:F:588:ARG:HD2	2.37	0.54
7:G:5:DC:C2'	7:G:6:DA:H5'	2.30	0.54
1:H:14:DT:C5'	6:F:584:ARG:HD2	2.38	0.54
1:H:58:DG:H2''	1:H:59:DC:H5''	1.90	0.54
2:I:132:LEU:O	2:I:136:LEU:HG	2.08	0.54
3:A:12:ARG:HB3	3:A:12:ARG:NH1	2.22	0.54
3:A:23:HIS:NE2	3:A:204:GLU:OE2	2.40	0.54
4:C:11:ILE:HG21	4:C:1159:VAL:HG21	1.87	0.54
4:C:472:GLU:HA	4:C:475:VAL:CG1	2.38	0.54
6:F:341:LEU:O	6:F:345:GLN:HG3	2.08	0.54
6:F:565:ILE:O	6:F:567:MET:HG2	2.07	0.54
2:I:140:ALA:HB3	2:I:141:PRO:HD3	1.88	0.54
3:A:194:GLN:O	3:A:195:ARG:HG2	2.08	0.54
4:C:256:GLU:OE1	4:C:286:GLU:HB2	2.07	0.54
4:C:349:GLU:OE1	4:C:352:ARG:NH1	2.40	0.54
4:C:1105:SER:HB2	5:D:731:ARG:HG3	1.89	0.54
6:F:325:PRO:O	6:F:329:LYS:HB2	2.07	0.54
6:F:572:THR:O	6:F:575:GLU:HB3	2.07	0.54
4:C:1034:ARG:HB2	4:C:1034:ARG:HH11	1.73	0.54
4:C:1340:GLU:HB2	5:D:18:ASP:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:317:THR:HG21	5:D:320:ASN:HB3	1.89	0.54
6:F:503:GLU:HB2	6:F:504:PRO:HD2	1.89	0.54
2:I:12:THR:O	2:I:63:VAL:HG23	2.08	0.54
2:J:10:VAL:HG21	2:J:65:ARG:HD3	1.89	0.54
3:A:82:LEU:HD11	3:A:171:LEU:HD23	1.90	0.54
4:C:84:GLU:OE1	4:C:84:GLU:N	2.39	0.54
4:C:598:VAL:HG12	4:C:628:HIS:NE2	2.23	0.54
4:C:1005:GLU:HB2	4:C:1007:LYS:HG2	1.90	0.54
5:D:894:VAL:HG23	5:D:895:CYS:O	2.07	0.54
5:D:1039:ASP:CB	5:D:1074:LEU:HB3	2.36	0.54
6:F:166:VAL:CG2	6:F:258:GLN:HG3	2.35	0.54
6:F:251:LYS:HA	6:F:254:GLU:HB2	1.89	0.54
6:F:267:ASP:O	6:F:270:VAL:HG22	2.08	0.54
8:E:84:THR:HG23	8:E:88:GLU:OE2	2.08	0.54
2:I:124:GLU:O	2:I:128:ALA:N	2.34	0.53
4:C:98:VAL:HG21	4:C:124:MET:SD	2.47	0.53
4:C:543:ALA:O	4:C:548:ARG:NH1	2.40	0.53
4:C:962:GLU:O	4:C:962:GLU:HG2	2.09	0.53
5:D:661:VAL:CG2	5:D:682:VAL:HG13	2.38	0.53
5:D:707:ILE:HD11	5:D:716:GLN:HE22	1.73	0.53
6:F:158:LEU:HA	6:F:161:LEU:CD2	2.38	0.53
6:F:231:THR:HG21	6:F:252:LEU:HA	1.90	0.53
6:F:586:ARG:NE	6:F:590:ILE:HG12	2.22	0.53
1:H:63:DG:H5"	5:D:1170:LYS:CG	2.37	0.53
2:J:29:LEU:HD23	2:J:36:PHE:CG	2.43	0.53
3:A:228:LEU:HD11	3:B:224:LEU:HD23	1.89	0.53
4:C:12:ARG:HD3	4:C:1183:ALA:HB2	1.90	0.53
4:C:689:ALA:HB1	4:C:1233:LEU:HD12	1.89	0.53
5:D:94:GLN:O	5:D:97:VAL:HG12	2.09	0.53
5:D:288:PRO:CB	6:F:377:LYS:HE3	2.39	0.53
5:D:1060:VAL:HA	5:D:1105:ALA:O	2.09	0.53
6:F:108:VAL:HG21	6:F:381:GLU:O	2.08	0.53
6:F:273:MET:HA	6:F:276:MET:CG	2.39	0.53
3:B:67:GLU:HA	3:B:78:ILE:HD12	1.90	0.53
4:C:79:VAL:HG22	4:C:80:PHE:CD1	2.43	0.53
4:C:281:ASP:N	4:C:281:ASP:OD1	2.40	0.53
4:C:725:GLN:OE1	4:C:735:LYS:HB2	2.08	0.53
4:C:950:GLU:O	4:C:953:LEU:N	2.41	0.53
5:D:227:PHE:CE1	5:D:1337:VAL:HG13	2.44	0.53
5:D:351:GLY:O	5:D:467:ALA:HA	2.08	0.53
5:D:655:SER:HA	5:D:658:GLU:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1003:LEU:HA	5:D:1018:ALA:CB	2.37	0.53
5:D:1031:VAL:HG13	5:D:1080:ILE:HD13	1.89	0.53
6:F:397:ARG:NH2	7:G:26:DT:O4	2.26	0.53
4:C:477:GLU:O	4:C:481:LEU:HB3	2.09	0.53
5:D:38:VAL:HG11	5:D:56:LEU:HD12	1.91	0.53
5:D:1053:LEU:HD22	5:D:1053:LEU:H	1.73	0.53
6:F:456:MET:CE	6:F:497:VAL:HG22	2.39	0.53
1:H:16:DA:H2''	1:H:17:DC:C5	2.42	0.53
1:H:37:DA:H61	6:F:420:GLU:HB3	1.72	0.53
2:I:166:TRP:CZ3	2:I:208:ARG:HD3	2.44	0.53
3:B:60:GLU:HA	3:B:170:ARG:HH12	1.72	0.53
4:C:595:THR:CG2	4:C:600:THR:HG23	2.25	0.53
4:C:988:LYS:CA	4:C:991:LYS:HG2	2.38	0.53
5:D:841:GLY:HA2	5:D:901:ARG:HD3	1.88	0.53
5:D:857:LEU:H	5:D:857:LEU:HD23	1.73	0.53
5:D:1151:LYS:O	5:D:1152:GLU:HG2	2.09	0.53
6:F:320:ILE:HG12	6:F:327:SER:O	2.08	0.53
3:B:48:LEU:HD22	5:D:535:ARG:CG	2.39	0.53
4:C:849:GLU:O	4:C:886:LYS:HG3	2.09	0.53
4:C:1342:GLU:OXT	5:D:16:GLU:HG3	2.08	0.53
5:D:980:THR:CG2	5:D:997:VAL:HB	2.37	0.53
6:F:344:LEU:HA	6:F:347:ILE:CG1	2.39	0.53
6:F:499:LYS:O	6:F:500:ILE:HD13	2.08	0.53
6:F:530:LEU:HB3	6:F:533:ASP:HB2	1.91	0.53
1:H:27:DA:H2'	1:H:27:DA:OP2	2.08	0.53
2:I:54:ASN:ND2	2:I:57:GLN:HA	2.24	0.53
4:C:99:LYS:O	4:C:100:LEU:HD23	2.09	0.53
4:C:1020:GLU:HB3	4:C:1024:GLU:CB	2.36	0.53
5:D:550:VAL:HG23	5:D:552:ILE:HG23	1.91	0.53
6:F:157:ARG:HG2	6:F:160:ASP:CG	2.29	0.53
6:F:163:THR:HG23	6:F:262:VAL:CG2	2.39	0.53
2:J:76:MET:HG2	2:J:156:LEU:HD21	1.91	0.53
2:J:202:GLU:OE1	2:J:203:ALA:N	2.40	0.53
3:B:129:VAL:HG21	3:B:132:HIS:CE1	2.44	0.53
4:C:358:ASP:OD1	4:C:361:SER:HB3	2.09	0.53
4:C:1004:ASP:OD1	4:C:1008:GLN:NE2	2.41	0.53
5:D:1039:ASP:OD1	5:D:1074:LEU:HD22	2.08	0.53
6:F:144:LEU:HD11	6:F:161:LEU:HD12	1.89	0.53
2:I:6:ASN:ND2	2:I:63:VAL:HG12	2.17	0.53
3:K:302:GLU:OE1	3:K:302:GLU:N	2.42	0.53
4:C:38:PHE:HD2	4:C:39:ILE:HG23	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:179:TYR:HB2	4:C:397:LEU:O	2.09	0.53
5:D:959:LYS:NZ	5:D:985:ILE:HG21	2.23	0.53
5:D:1059:LEU:O	5:D:1107:VAL:HG22	2.08	0.53
6:F:160:ASP:O	6:F:265:GLN:NE2	2.40	0.53
6:F:558:VAL:HG21	6:F:587:ILE:CD1	2.39	0.53
2:I:168:LEU:O	2:I:173:ILE:HB	2.09	0.53
3:K:307:LEU:HD12	3:K:308:ALA:N	2.24	0.53
4:C:571:LEU:O	4:C:572:ILE:HD13	2.09	0.53
4:C:857:VAL:HG11	4:C:862:LEU:HD21	1.91	0.53
4:C:961:SER:HA	4:C:1025:PHE:HZ	1.74	0.53
6:F:229:VAL:O	6:F:232:ARG:HG3	2.08	0.53
6:F:313:ASP:O	6:F:316:PHE:HB2	2.09	0.53
2:I:115:ASN:O	2:I:118:ILE:HG22	2.08	0.52
3:A:101:THR:O	3:A:115:ILE:HG23	2.09	0.52
4:C:292:ILE:HG22	4:C:317:LEU:CD1	2.39	0.52
4:C:1222:GLU:OE1	4:C:1222:GLU:N	2.37	0.52
4:C:1252:SER:HB3	4:C:1255:THR:O	2.09	0.52
5:D:1035:VAL:CG1	5:D:1078:LEU:HB3	2.39	0.52
6:F:322:MET:HB3	6:F:324:LYS:HG2	1.90	0.52
6:F:543:ALA:O	6:F:547:VAL:N	2.40	0.52
2:I:129:ARG:NE	2:I:172:GLY:O	2.32	0.52
2:J:49:ASP:O	2:J:50:LEU:HD23	2.10	0.52
2:J:109:ASP:O	2:J:113:LEU:HB2	2.09	0.52
2:J:139:ILE:HG22	2:J:142:VAL:CG2	2.39	0.52
2:J:190:VAL:HG13	2:J:191:PHE:HD1	1.74	0.52
3:A:181:GLU:O	4:C:821:ARG:NH2	2.38	0.52
4:C:714:VAL:O	4:C:767:GLN:NE2	2.41	0.52
4:C:1214:ASP:OD1	4:C:1215:GLY:N	2.43	0.52
2:J:90:PRO:HG2	2:J:96:ARG:CA	2.40	0.52
4:C:241:LEU:CD2	4:C:246:LEU:HD11	2.39	0.52
4:C:299:LYS:NZ	4:C:334:GLU:HB2	2.24	0.52
4:C:843:THR:HG22	4:C:844:LYS:H	1.74	0.52
4:C:1015:ALA:CA	4:C:1018:TYR:HB3	2.39	0.52
4:C:1146:GLN:NE2	4:C:1150:ASP:OD1	2.42	0.52
5:D:869:CYS:O	5:D:873:GLU:N	2.42	0.52
5:D:966:VAL:O	5:D:974:VAL:N	2.31	0.52
6:F:234:THR:HG21	6:F:245:ALA:HA	1.90	0.52
6:F:315:TRP:CH2	6:F:338:HIS:HB2	2.45	0.52
8:E:3:ARG:HA	8:E:3:ARG:HE	1.74	0.52
8:E:56:GLU:O	8:E:58:LEU:HD23	2.10	0.52
3:A:11:PRO:HA	3:A:30:PRO:HG2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:66:HIS:O	3:B:69:SER:HB3	2.09	0.52
4:C:297:VAL:CG1	4:C:313:ALA:HA	2.39	0.52
4:C:728:ASP:OD1	4:C:729:ALA:N	2.42	0.52
4:C:992:LEU:HB3	4:C:997:TRP:HE1	1.75	0.52
5:D:833:GLU:HG2	5:D:838:ARG:HG3	1.90	0.52
6:F:487:MET:O	6:F:488:LEU:HD22	2.10	0.52
1:H:53:DC:H2''	1:H:54:DG:C5'	2.40	0.52
2:I:126:ASP:OD1	2:I:129:ARG:HD2	2.09	0.52
2:J:103:MET:HB2	2:J:160:TYR:CE2	2.45	0.52
4:C:119:GLU:HB2	4:C:489:PRO:CG	2.39	0.52
4:C:545:PHE:CE2	5:D:781:LYS:HD3	2.45	0.52
4:C:631:GLU:OE1	4:C:631:GLU:N	2.42	0.52
4:C:734:ILE:CD1	4:C:777:VAL:HG21	2.40	0.52
4:C:1217:THR:OG1	4:C:1218:GLY:N	2.42	0.52
5:D:847:ASP:HB3	5:D:859:PRO:C	2.29	0.52
6:F:530:LEU:O	6:F:533:ASP:N	2.41	0.52
2:I:17:PRO:HD3	2:I:41:VAL:O	2.09	0.52
5:D:811:GLU:O	5:D:911:LYS:HG3	2.09	0.52
2:J:99:SER:O	2:J:103:MET:HG2	2.10	0.52
2:J:137:LEU:HD23	2:J:179:GLY:CA	2.39	0.52
2:J:185:GLY:O	2:J:189:ARG:HG3	2.09	0.52
3:A:164:ASP:O	3:A:166:ARG:HG3	2.10	0.52
4:C:188:PHE:HE1	4:C:194:LEU:HD12	1.75	0.52
4:C:324:LYS:HA	4:C:327:GLN:HE21	1.74	0.52
4:C:802:VAL:CG2	4:C:1096:ILE:HB	2.40	0.52
4:C:1022:LYS:O	4:C:1026:GLU:HB3	2.10	0.52
5:D:177:ASP:OD1	5:D:179:LYS:HE3	2.08	0.52
5:D:956:GLY:C	5:D:1010:GLN:HG3	2.29	0.52
6:F:276:MET:O	6:F:280:VAL:HG22	2.10	0.52
6:F:489:MET:HB2	6:F:494:ILE:HG13	1.92	0.52
2:I:15:SER:OG	2:I:16:GLY:N	2.43	0.52
4:C:899:GLU:HG2	6:F:540:LEU:CD1	2.40	0.52
5:D:213:LYS:O	5:D:217:LEU:HB2	2.10	0.52
5:D:925:GLU:HG3	5:D:926:PRO:CD	2.37	0.52
3:B:61:ILE:HG21	3:B:64:VAL:HB	1.91	0.52
4:C:18:ARG:HD3	4:C:1188:ASP:OD1	2.10	0.52
4:C:65:ASN:O	4:C:105:TYR:HB2	2.09	0.52
4:C:690:VAL:CG2	4:C:1236:ASN:HB3	2.38	0.52
4:C:1158:LYS:NZ	4:C:1158:LYS:CA	2.73	0.52
5:D:534:GLU:HA	5:D:578:ILE:HD11	1.91	0.52
5:D:981:GLU:HB3	5:D:996:LYS:HE2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1232:TYR:O	5:D:1236:GLU:HG2	2.09	0.52
6:F:572:THR:HB	6:F:575:GLU:HB2	1.92	0.52
1:H:63:DG:N2	7:G:1:DC:H1'	2.21	0.52
3:A:187:VAL:HG23	3:A:199:ASP:HB3	1.91	0.52
4:C:102:LEU:HB2	4:C:489:PRO:HG3	1.91	0.52
4:C:981:ALA:O	4:C:1002:LEU:HD21	2.10	0.52
4:C:1242:LYS:HD2	5:D:465:GLN:NE2	2.25	0.52
4:C:1309:VAL:HG23	4:C:1310:ASP:OD1	2.10	0.52
5:D:475:GLU:O	5:D:479:GLU:HG3	2.10	0.52
6:F:224:LEU:HD22	6:F:259:PHE:CE2	2.45	0.52
2:I:14:PHE:CB	2:I:50:LEU:HD22	2.37	0.51
2:J:85:HIS:HB2	5:D:86:GLU:OE1	2.10	0.51
2:J:140:ALA:HB3	2:J:141:PRO:HD3	1.91	0.51
4:C:782:VAL:O	4:C:783:LEU:HD23	2.10	0.51
5:D:850:LYS:HG2	5:D:857:LEU:HD22	1.92	0.51
5:D:891:ASP:HA	5:D:1281:GLU:OE2	2.10	0.51
5:D:1060:VAL:HG22	5:D:1106:ILE:CD1	2.39	0.51
5:D:1159:ILE:HD12	5:D:1160:SER:H	1.74	0.51
6:F:150:ARG:CB	6:F:155:GLU:HB3	2.40	0.51
6:F:585:GLU:HG2	6:F:588:ARG:HD2	1.91	0.51
2:J:71:GLU:HB3	2:J:74:ILE:HG13	1.90	0.51
4:C:102:LEU:O	4:C:116:ASP:HA	2.11	0.51
4:C:243:PRO:HB3	4:C:277:LEU:HB2	1.92	0.51
4:C:672:GLU:OE2	4:C:1187:PHE:HA	2.10	0.51
4:C:745:GLU:OE2	4:C:1014:LEU:HA	2.10	0.51
4:C:835:GLU:C	4:C:836:LEU:HD12	2.31	0.51
4:C:1017:GLN:HA	4:C:1020:GLU:HB2	1.91	0.51
5:D:709:ARG:NH1	5:D:714:GLU:HB3	2.25	0.51
5:D:1095:MET:SD	5:D:1096:PRO:HD2	2.50	0.51
6:F:310:GLU:CB	6:F:355:ILE:HG21	2.38	0.51
1:H:42:DG:C8	6:F:385:ARG:HG3	2.45	0.51
2:I:34:VAL:HG21	2:I:83:PHE:CD2	2.44	0.51
4:C:615:VAL:CG1	4:C:650:VAL:HA	2.38	0.51
4:C:810:TYR:CE1	5:D:359:PRO:HD2	2.45	0.51
4:C:1012:GLU:OE2	4:C:1016:GLU:HB2	2.10	0.51
5:D:116:PHE:O	5:D:124:ILE:HG13	2.11	0.51
5:D:140:TYR:HB3	6:F:100:MET:CE	2.41	0.51
5:D:795:TYR:CZ	5:D:799:ARG:HD3	2.44	0.51
5:D:959:LYS:CE	5:D:985:ILE:HG21	2.40	0.51
5:D:1044:GLN:HB3	5:D:1071:GLY:HA3	1.92	0.51
6:F:530:LEU:HD23	6:F:531:PRO:CD	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:38:DT:H3'	6:F:429:THR:HG21	1.92	0.51
2:I:26:ARG:CA	2:I:29:LEU:HB3	2.38	0.51
2:J:165:LEU:O	2:J:208:ARG:NH2	2.43	0.51
3:A:100:LEU:HD21	3:A:121:VAL:HG11	1.93	0.51
4:C:1030:GLU:O	4:C:1034:ARG:N	2.44	0.51
4:C:1122:LYS:NZ	4:C:1178:LYS:O	2.27	0.51
4:C:1275:VAL:O	4:C:1279:GLU:HG3	2.10	0.51
6:F:141:ILE:CD1	6:F:224:LEU:HD21	2.40	0.51
6:F:290:LEU:O	6:F:294:GLN:HB2	2.10	0.51
6:F:331:HIS:HA	6:F:334:SER:CB	2.38	0.51
1:H:62:DG:H1'	1:H:63:DG:H5'	1.92	0.51
4:C:189:ASP:OD2	4:C:193:ASN:HB2	2.11	0.51
4:C:356:THR:HG21	4:C:361:SER:O	2.11	0.51
4:C:680:LEU:O	4:C:680:LEU:HD23	2.10	0.51
5:D:1104:LYS:NZ	5:D:1124:ILE:HG23	2.25	0.51
6:F:96:ASP:OD1	6:F:96:ASP:N	2.42	0.51
8:E:76:GLU:HA	8:E:79:GLU:HB2	1.93	0.51
4:C:979:LEU:HD11	4:C:1007:LYS:O	2.11	0.51
5:D:516:ASP:OD2	5:D:547:ARG:NH2	2.40	0.51
5:D:762:ASN:OD1	5:D:765:GLU:HG3	2.10	0.51
6:F:166:VAL:HG12	6:F:260:ARG:NH2	2.25	0.51
7:G:51:DT:H2''	7:G:52:DC:C6	2.46	0.51
8:E:79:GLU:O	8:E:83:VAL:N	2.43	0.51
1:H:37:DA:C2	6:F:425:TYR:HB2	2.44	0.51
2:J:129:ARG:NH2	2:J:171:LEU:O	2.43	0.51
3:B:27:THR:OG1	3:B:28:LEU:N	2.43	0.51
3:B:71:LYS:HB3	3:B:74:VAL:HG21	1.93	0.51
3:B:83:LEU:CD1	5:D:528:THR:HB	2.41	0.51
4:C:260:LYS:HB3	4:C:262:TYR:HE1	1.75	0.51
4:C:303:ASP:HB2	4:C:310:ILE:HD11	1.92	0.51
4:C:1146:GLN:OE1	4:C:1160:ASP:CB	2.58	0.51
4:C:1211:ARG:HD3	4:C:1220:GLN:HE22	1.76	0.51
4:C:1304:MET:O	4:C:1308:ILE:HG12	2.11	0.51
5:D:1215:GLU:CG	5:D:1220:ILE:HD11	2.41	0.51
6:F:234:THR:HG21	6:F:244:THR:O	2.11	0.51
6:F:278:ASP:OD1	6:F:278:ASP:N	2.44	0.51
4:C:225:PHE:HE1	4:C:347:ILE:HG22	1.74	0.51
4:C:268:ARG:HD2	4:C:269:ILE:O	2.11	0.51
4:C:953:LEU:HD11	4:C:1033:ARG:HG3	1.91	0.51
4:C:1106:ARG:H	4:C:1106:ARG:HD2	1.75	0.51
5:D:973:LEU:HD12	5:D:973:LEU:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1037:PHE:HB3	5:D:1041:ILE:HG23	1.93	0.51
6:F:507:MET:SD	6:F:523:ILE:HD11	2.51	0.51
2:I:71:GLU:HG3	2:I:73:ARG:H	1.76	0.51
3:A:51:MET:HE1	3:A:216:ALA:HA	1.93	0.51
4:C:618:GLN:NE2	5:D:770:LEU:HB2	2.25	0.51
4:C:972:PHE:O	4:C:976:ARG:N	2.41	0.51
5:D:857:LEU:HD11	5:D:872:LEU:CD2	2.41	0.51
5:D:983:LYS:CE	5:D:991:THR:HB	2.41	0.51
6:F:347:ILE:HG12	6:F:350:GLU:OE1	2.11	0.51
3:B:105:SER:CB	3:B:138:ALA:HB1	2.33	0.50
4:C:284:LEU:HD12	4:C:285:ILE:H	1.76	0.50
4:C:757:THR:HG23	4:C:765:ILE:HG23	1.91	0.50
4:C:867:GLU:OE1	4:C:867:GLU:N	2.45	0.50
4:C:1159:VAL:HG13	4:C:1160:ASP:N	2.26	0.50
5:D:667:GLN:O	5:D:673:VAL:HG12	2.11	0.50
6:F:164:GLY:O	6:F:260:ARG:NH1	2.44	0.50
4:C:689:ALA:CB	4:C:1233:LEU:HD12	2.41	0.50
4:C:1043:ALA:HB1	4:C:1044:PRO:HD2	1.93	0.50
4:C:1103:VAL:HG11	4:C:1112:ILE:CD1	2.41	0.50
5:D:245:LEU:HD12	5:D:246:PRO:HD3	1.93	0.50
5:D:532:GLU:HG3	5:D:532:GLU:O	2.11	0.50
5:D:557:LYS:HA	5:D:562:GLU:O	2.10	0.50
5:D:704:GLU:HB3	5:D:718:SER:HB2	1.93	0.50
5:D:1046:ILE:HD13	5:D:1060:VAL:O	2.11	0.50
6:F:329:LYS:HD3	6:F:332:ASP:CB	2.39	0.50
6:F:367:ILE:O	6:F:371:LYS:HB2	2.11	0.50
6:F:456:MET:HE1	6:F:497:VAL:HG22	1.92	0.50
2:I:8:ARG:HB2	2:I:10:VAL:HG23	1.92	0.50
4:C:249:GLU:N	4:C:269:ILE:HD11	2.25	0.50
4:C:985:GLU:HA	4:C:988:LYS:CG	2.42	0.50
4:C:1243:MET:HA	5:D:352:ARG:O	2.11	0.50
5:D:6:LYS:HA	5:D:9:LYS:HZ3	1.76	0.50
5:D:1194:ARG:HD3	5:D:1211:SER:OG	2.11	0.50
1:H:55:DG:H2"	1:H:56:DA:H5"	1.94	0.50
3:A:127:GLN:OE1	3:A:127:GLN:N	2.44	0.50
3:B:11:PRO:HB2	3:B:28:LEU:HD11	1.93	0.50
4:C:11:ILE:HG21	4:C:1159:VAL:CG2	2.41	0.50
4:C:99:LYS:HG3	4:C:121:GLU:OE2	2.12	0.50
4:C:114:VAL:HG12	4:C:115:LYS:HD2	1.94	0.50
4:C:1131:MET:CE	4:C:1141:LEU:HD12	2.41	0.50
5:D:337:ARG:HG3	5:D:339:ARG:H	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:747:MET:CG	5:D:759:ILE:HD11	2.37	0.50
6:F:224:LEU:HD22	6:F:259:PHE:HE2	1.75	0.50
6:F:309:ASN:O	6:F:355:ILE:HB	2.12	0.50
6:F:470:MET:O	6:F:474:MET:HB3	2.12	0.50
6:F:591:GLU:O	6:F:595:LEU:HD23	2.12	0.50
2:J:19:ASP:OD2	2:J:21:TYR:HB2	2.12	0.50
3:A:8:PHE:CE1	3:A:32:GLU:HG2	2.46	0.50
4:C:563:THR:HB	4:C:564:PRO:HD2	1.93	0.50
4:C:589:THR:HG23	4:C:590:PRO:HD2	1.93	0.50
5:D:930:LEU:HD11	5:D:1241:TYR:HD1	1.74	0.50
1:H:53:DC:H2''	1:H:54:DG:O5'	2.11	0.50
2:J:148:TYR:HB3	2:J:158:ASP:OD2	2.11	0.50
3:A:47:LEU:O	3:A:180:VAL:HG21	2.12	0.50
3:B:28:LEU:HD12	3:B:29:GLU:N	2.26	0.50
5:D:259:ARG:NH2	6:F:503:GLU:O	2.30	0.50
5:D:1234:VAL:O	5:D:1238:GLN:HB2	2.11	0.50
6:F:262:VAL:HG12	6:F:264:LYS:H	1.75	0.50
2:I:183:LEU:HD12	2:I:183:LEU:O	2.11	0.50
3:A:61:ILE:HG22	3:A:62:ASP:H	1.76	0.50
3:B:60:GLU:O	3:B:142:MET:HA	2.11	0.50
4:C:802:VAL:HG22	4:C:1096:ILE:HB	1.94	0.50
6:F:336:GLU:HA	6:F:339:ARG:HG2	1.94	0.50
2:I:11:MET:CE	2:I:37:GLU:H	2.25	0.50
2:J:132:LEU:CD2	2:J:136:LEU:HD21	2.42	0.50
3:B:19:VAL:HG21	3:B:23:HIS:HD2	1.75	0.50
4:C:287:VAL:HG22	4:C:288:PRO:HD2	1.94	0.50
5:D:72:CYS:SG	5:D:73:GLY:N	2.84	0.50
5:D:355:ILE:HG12	5:D:464:ASP:O	2.11	0.50
6:F:495:ARG:O	6:F:499:LYS:HE3	2.12	0.50
3:A:185:TYR:HD2	3:A:201:LEU:HD11	1.77	0.50
4:C:169:LYS:O	4:C:171:LEU:HG	2.12	0.50
4:C:468:LEU:O	4:C:471:VAL:HG12	2.12	0.50
4:C:594:VAL:HB	4:C:651:ASP:O	2.12	0.50
4:C:1008:GLN:HA	4:C:1011:LEU:CD1	2.42	0.50
4:C:1121:ALA:HB2	4:C:1182:ILE:CG1	2.41	0.50
5:D:86:GLU:HG2	5:D:87:LYS:N	2.27	0.50
6:F:305:LEU:HD13	6:F:318:ALA:HB1	1.93	0.50
8:E:50:ALA:O	8:E:54:ILE:HG12	2.11	0.50
3:A:212:ASP:OD1	3:A:212:ASP:N	2.43	0.49
3:A:224:LEU:HD23	3:B:228:LEU:HD11	1.94	0.49
3:B:120:ASP:OD1	3:B:120:ASP:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:260:LYS:HE2	4:C:261:VAL:O	2.12	0.49
4:C:734:ILE:HD12	4:C:777:VAL:HG21	1.94	0.49
4:C:994:ARG:HG2	4:C:997:TRP:CH2	2.47	0.49
4:C:1270:PHE:CE2	4:C:1290:MET:HG2	2.47	0.49
5:D:555:TYR:HA	5:D:564:VAL:O	2.12	0.49
5:D:975:ILE:HD12	5:D:976:THR:H	1.76	0.49
1:H:33:DT:H72	6:F:441:ARG:HH21	1.77	0.49
2:J:64:ASP:N	2:J:64:ASP:OD1	2.43	0.49
3:A:57:THR:HG21	3:A:147:GLN:NE2	2.26	0.49
3:A:89:ALA:O	3:A:124:VAL:HG12	2.12	0.49
4:C:296:VAL:HA	4:C:316:GLU:HA	1.95	0.49
4:C:672:GLU:HG2	4:C:673:HIS:HD2	1.76	0.49
5:D:18:ASP:OD1	5:D:18:ASP:N	2.44	0.49
5:D:423:LEU:HD12	5:D:468:VAL:HG12	1.92	0.49
5:D:511:TYR:CE2	5:D:515:ARG:HD2	2.47	0.49
5:D:978:ARG:HG3	5:D:998:PRO:HB3	1.94	0.49
5:D:1025:MET:O	5:D:1124:ILE:HB	2.12	0.49
6:F:163:THR:OG1	6:F:260:ARG:HD3	2.12	0.49
6:F:320:ILE:CG1	6:F:330:LEU:HB2	2.42	0.49
6:F:404:LEU:HD22	6:F:439:ILE:CG2	2.40	0.49
1:H:43:DG:H2'	1:H:44:DG:N7	2.26	0.49
4:C:12:ARG:HG3	4:C:1181:PRO:O	2.11	0.49
4:C:150:HIS:CD2	4:C:454:ARG:HG3	2.48	0.49
4:C:231:GLU:OE2	4:C:238:GLN:HB2	2.12	0.49
4:C:834:GLN:NE2	4:C:924:VAL:HG21	2.27	0.49
4:C:1253:LEU:HD13	6:F:525:ASP:HB2	1.93	0.49
5:D:1031:VAL:HA	5:D:1117:SER:HB3	1.92	0.49
5:D:1035:VAL:HG11	5:D:1078:LEU:HB3	1.94	0.49
5:D:1056:LEU:HD23	5:D:1108:GLN:HB3	1.94	0.49
6:F:151:VAL:HG23	6:F:156:ALA:HB3	1.94	0.49
3:B:11:PRO:O	3:B:12:ARG:NE	2.34	0.49
4:C:106:GLU:HG2	4:C:109:ALA:CB	2.36	0.49
4:C:237:LEU:HD12	4:C:289:VAL:HG12	1.95	0.49
5:D:1265:THR:HG22	5:D:1276:GLU:O	2.12	0.49
6:F:297:MET:HG2	6:F:298:PRO:CD	2.42	0.49
6:F:341:LEU:CB	6:F:344:LEU:HD21	2.41	0.49
2:I:62:LEU:HD12	2:I:63:VAL:H	1.77	0.49
2:J:55:PRO:HD2	2:J:70:TRP:CH2	2.47	0.49
2:J:129:ARG:HG3	2:J:173:ILE:CD1	2.42	0.49
3:B:164:ASP:O	3:B:166:ARG:HG3	2.12	0.49
4:C:296:VAL:CG1	4:C:336:LEU:HD12	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:607:SER:OG	4:C:608:ALA:N	2.46	0.49
4:C:843:THR:CG2	4:C:844:LYS:HZ2	2.20	0.49
4:C:843:THR:CG2	4:C:844:LYS:H	2.25	0.49
5:D:165:TYR:CZ	5:D:169:LEU:HD22	2.47	0.49
6:F:164:GLY:O	6:F:260:ARG:HD2	2.12	0.49
6:F:227:GLN:HB3	6:F:231:THR:HG21	1.93	0.49
2:J:201:THR:H	2:J:204:GLU:CG	2.26	0.49
4:C:287:VAL:CG2	4:C:288:PRO:HD2	2.42	0.49
5:D:142:GLU:OE1	6:F:100:MET:HE1	2.13	0.49
5:D:320:ASN:OD1	5:D:321:LYS:N	2.41	0.49
3:K:255:ARG:HB2	3:K:278:ILE:HD12	1.93	0.49
4:C:91:THR:OG1	4:C:92:TYR:N	2.43	0.49
4:C:448:LEU:HD12	4:C:554:HIS:ND1	2.28	0.49
4:C:618:GLN:HE21	5:D:770:LEU:HB2	1.78	0.49
5:D:839:VAL:CG2	5:D:882:VAL:HG11	2.43	0.49
6:F:427:PHE:CE1	6:F:431:ALA:HB2	2.48	0.49
6:F:490:PRO:HD2	6:F:493:LYS:HB2	1.94	0.49
1:H:40:DA:H5'	1:H:41:DT:H72	1.95	0.49
4:C:117:ILE:CD1	4:C:489:PRO:HD3	2.41	0.49
4:C:687:ARG:HB3	4:C:687:ARG:HH11	1.78	0.49
4:C:1339:LEU:HD13	5:D:17:PHE:CD2	2.48	0.49
5:D:980:THR:O	5:D:996:LYS:HD3	2.12	0.49
6:F:102:MET:CE	6:F:388:ILE:HD13	2.43	0.49
7:G:27:DA:H2''	7:G:28:DG:H5'	1.94	0.49
1:H:58:DG:H1	7:G:5:DC:H42	1.61	0.49
2:I:12:THR:O	2:I:62:LEU:HA	2.12	0.49
2:I:146:LYS:CG	2:I:150:LEU:HA	2.33	0.49
3:B:65:LEU:CD2	3:B:169:GLY:HA3	2.41	0.49
4:C:241:LEU:HD23	4:C:246:LEU:HD11	1.94	0.49
4:C:320:ASP:OD1	4:C:320:ASP:N	2.35	0.49
5:D:322:ARG:CG	5:D:323:PRO:HD2	2.42	0.49
5:D:337:ARG:HD2	5:D:338:PHE:N	2.24	0.49
6:F:160:ASP:HA	6:F:264:LYS:HG3	1.93	0.49
6:F:303:ILE:O	6:F:307:THR:HG22	2.13	0.49
1:H:36:DT:O4	6:F:437:GLN:HB2	2.12	0.49
1:H:38:DT:C3'	6:F:429:THR:HG21	2.43	0.49
1:H:44:DG:OP1	6:F:392:LYS:HE2	2.13	0.49
2:I:21:TYR:HB3	2:I:60:PRO:CD	2.43	0.49
2:J:139:ILE:H	2:J:139:ILE:HD12	1.78	0.49
4:C:232:ILE:O	4:C:331:LYS:HD3	2.13	0.49
4:C:397:LEU:HB2	4:C:418:GLY:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:972:PHE:CD2	4:C:994:ARG:HD2	2.47	0.49
5:D:1040:MET:SD	5:D:1078:LEU:HD11	2.52	0.49
6:F:151:VAL:CG2	6:F:156:ALA:HB3	2.43	0.49
6:F:158:LEU:HD13	6:F:213:ASP:N	2.28	0.49
6:F:277:MET:O	6:F:277:MET:HG3	2.12	0.49
7:G:1:DC:H2"	7:G:2:DC:C5	2.47	0.49
2:I:103:MET:O	2:I:107:GLU:HG3	2.13	0.48
2:I:192:GLU:HA	2:I:197:LEU:CD2	2.39	0.48
4:C:279:LYS:HG3	4:C:280:ASP:OD1	2.13	0.48
5:D:62:PHE:O	5:D:98:ARG:HA	2.13	0.48
5:D:870:ASP:HA	5:D:873:GLU:CB	2.34	0.48
5:D:981:GLU:HB3	5:D:996:LYS:CE	2.43	0.48
5:D:1237:VAL:CG1	5:D:1253:ILE:HD13	2.43	0.48
6:F:128:ASN:HA	6:F:131:GLN:NE2	2.27	0.48
6:F:150:ARG:O	6:F:154:GLU:N	2.46	0.48
6:F:305:LEU:CD1	6:F:318:ALA:HB1	2.43	0.48
6:F:428:SER:O	6:F:432:THR:OG1	2.30	0.48
6:F:465:ARG:HH12	7:G:26:DT:H6	1.60	0.48
2:I:187:MET:HB3	2:I:191:PHE:CD1	2.48	0.48
2:J:180:ALA:HB1	2:J:184:LYS:HG3	1.95	0.48
3:B:85:LEU:HD21	3:B:130:ILE:HD13	1.95	0.48
4:C:13:LYS:HD2	4:C:14:ASP:H	1.78	0.48
4:C:229:ILE:HD12	4:C:333:ILE:O	2.13	0.48
4:C:465:ARG:HA	4:C:468:LEU:HB2	1.96	0.48
4:C:979:LEU:HA	4:C:1002:LEU:CD2	2.43	0.48
4:C:1213:TYR:CD1	4:C:1220:GLN:HB2	2.48	0.48
4:C:1321:GLU:OE2	5:D:99:ARG:NH2	2.28	0.48
5:D:6:LYS:HA	5:D:9:LYS:NZ	2.29	0.48
5:D:416:ILE:CG2	5:D:439:PRO:HG2	2.43	0.48
5:D:611:ILE:CG2	5:D:612:LEU:HD12	2.42	0.48
5:D:1138:LEU:HB3	5:D:1139:PRO:HD3	1.95	0.48
6:F:231:THR:HG21	6:F:252:LEU:CA	2.43	0.48
6:F:267:ASP:O	6:F:271:ASN:N	2.42	0.48
8:E:88:GLU:OE2	8:E:88:GLU:N	2.45	0.48
2:I:15:SER:O	2:I:41:VAL:HG22	2.14	0.48
2:I:207:MET:SD	2:I:207:MET:N	2.87	0.48
2:J:51:ILE:HA	2:J:54:ASN:O	2.12	0.48
2:J:161:LEU:HA	2:J:164:LEU:HB3	1.95	0.48
4:C:216:THR:HG22	4:C:219:GLN:NE2	2.23	0.48
4:C:243:PRO:HB3	4:C:277:LEU:CB	2.43	0.48
4:C:632:ASP:O	4:C:647:ARG:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:715:THR:CG2	4:C:782:VAL:HG13	2.43	0.48
4:C:1115:THR:CG2	4:C:1228:GLY:HA3	2.44	0.48
1:H:42:DG:C2'	1:H:43:DG:OP2	2.61	0.48
2:I:58:SER:OG	2:I:70:TRP:HB2	2.14	0.48
2:J:24:GLN:HB3	2:J:76:MET:HE1	1.94	0.48
3:A:29:GLU:HB3	3:A:30:PRO:HD3	1.94	0.48
3:B:103:ASN:HB2	3:B:141:SER:OG	2.13	0.48
4:C:271:ALA:O	4:C:275:ARG:N	2.44	0.48
4:C:1145:ILE:HD11	4:C:1173:ALA:HB2	1.95	0.48
5:D:364:HIS:HB3	5:D:487:THR:CG2	2.43	0.48
5:D:559:ALA:HB3	5:D:562:GLU:CG	2.30	0.48
5:D:615:LYS:HB2	5:D:616:PRO:HD3	1.94	0.48
5:D:1144:LEU:CD2	5:D:1237:VAL:HG23	2.40	0.48
5:D:1327:GLU:OE2	5:D:1330:ARG:HD2	2.13	0.48
8:E:3:ARG:HA	8:E:3:ARG:NE	2.28	0.48
2:J:23:HIS:CD2	2:J:27:ILE:HD11	2.48	0.48
4:C:27:LEU:HD13	4:C:663:VAL:HG11	1.95	0.48
4:C:91:THR:HG21	4:C:503:LYS:NZ	2.28	0.48
4:C:263:VAL:HG12	4:C:264:GLU:H	1.78	0.48
4:C:981:ALA:O	4:C:1002:LEU:HD11	2.13	0.48
4:C:1192:GLU:O	4:C:1196:LYS:HG2	2.14	0.48
4:C:1287:LEU:O	4:C:1287:LEU:HD23	2.14	0.48
4:C:1327:LEU:HD22	4:C:1337:ILE:CG2	2.35	0.48
5:D:154:LEU:HD22	5:D:176:PHE:CE1	2.49	0.48
5:D:211:GLU:O	5:D:215:LYS:HB2	2.14	0.48
5:D:1003:LEU:HA	5:D:1018:ALA:CA	2.40	0.48
5:D:1215:GLU:HG3	5:D:1220:ILE:HD11	1.94	0.48
6:F:141:ILE:CD1	6:F:252:LEU:HD11	2.43	0.48
6:F:151:VAL:HG22	6:F:156:ALA:O	2.14	0.48
2:I:52:ASP:OD1	2:I:52:ASP:N	2.46	0.48
4:C:210:LEU:HD11	4:C:429:MET:CE	2.44	0.48
4:C:1005:GLU:OE1	4:C:1007:LYS:NZ	2.34	0.48
5:D:24:LEU:HD12	5:D:24:LEU:HA	1.69	0.48
5:D:499:ILE:O	5:D:500:ILE:HD13	2.14	0.48
5:D:619:ILE:O	5:D:619:ILE:HG12	2.12	0.48
2:I:8:ARG:HE	2:I:10:VAL:HB	1.78	0.48
2:I:50:LEU:HD12	2:I:54:ASN:HD22	1.77	0.48
3:A:62:ASP:OD1	3:A:63:GLY:N	2.47	0.48
3:B:67:GLU:HA	3:B:78:ILE:CD1	2.43	0.48
4:C:1328:LYS:HE2	5:D:100:GLU:OE1	2.12	0.48
5:D:398:LYS:HD3	6:F:532:LEU:CD2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:552:ILE:HD12	5:D:589:TYR:CD1	2.48	0.48
6:F:158:LEU:HA	6:F:161:LEU:HD21	1.95	0.48
8:E:42:GLU:OE1	8:E:52:ARG:NH2	2.44	0.48
3:A:187:VAL:HA	3:A:200:LYS:O	2.13	0.48
4:C:117:ILE:HD11	4:C:489:PRO:HD3	1.94	0.48
4:C:216:THR:HG23	4:C:219:GLN:H	1.79	0.48
4:C:272:ARG:O	4:C:276:GLN:HG3	2.14	0.48
4:C:413:GLU:HB2	4:C:415:GLU:OE1	2.14	0.48
5:D:1144:LEU:CD2	5:D:1236:GLU:HB2	2.41	0.48
6:F:234:THR:HG23	6:F:235:ILE:H	1.79	0.48
2:I:34:VAL:HG21	2:I:83:PHE:HD2	1.78	0.48
2:J:20:ILE:HG13	2:J:163:PRO:HB2	1.95	0.48
2:J:202:GLU:HA	2:J:205:ARG:NH2	2.28	0.48
4:C:452:ARG:NH1	4:C:458:GLU:OE2	2.35	0.48
5:D:399:LYS:O	5:D:403:ARG:HG3	2.13	0.48
5:D:1042:ASP:OD2	5:D:1048:ARG:HD2	2.14	0.48
5:D:1236:GLU:O	5:D:1239:ASP:N	2.38	0.48
5:D:1314:LEU:HB2	5:D:1326:GLN:NE2	2.26	0.48
6:F:136:GLU:O	6:F:361:ILE:HD11	2.13	0.48
6:F:261:LEU:HG	6:F:262:VAL:H	1.78	0.48
6:F:588:ARG:O	6:F:592:ALA:HB2	2.14	0.48
8:E:72:GLN:O	8:E:72:GLN:NE2	2.40	0.48
1:H:18:DA:C4'	1:H:19:DA:H5'	2.44	0.48
2:I:85:HIS:CE1	6:F:561:MET:HA	2.48	0.48
2:I:174:GLU:OE1	2:I:175:PHE:N	2.41	0.48
4:C:506:PHE:O	4:C:512:SER:OG	2.29	0.48
4:C:877:VAL:HG21	4:C:920:VAL:HG21	1.96	0.48
4:C:953:LEU:O	4:C:953:LEU:HD12	2.13	0.48
4:C:1042:LEU:HD13	4:C:1046:VAL:CG1	2.44	0.48
5:D:237:MET:O	5:D:238:ILE:HD13	2.14	0.48
5:D:423:LEU:HB3	5:D:466:MET:HE1	1.96	0.48
5:D:820:ILE:O	5:D:881:LYS:HA	2.14	0.48
5:D:1025:MET:O	5:D:1124:ILE:HD13	2.13	0.48
5:D:1029:THR:O	5:D:1118:GLY:HA2	2.13	0.48
5:D:1350:ASN:OD1	5:D:1355:ARG:HG3	2.14	0.48
6:F:266:PHE:O	6:F:270:VAL:HG13	2.13	0.48
6:F:315:TRP:CH2	6:F:337:VAL:HB	2.49	0.48
1:H:26:DT:H2''	1:H:27:DA:OP2	2.13	0.47
2:J:102:TYR:HE2	2:J:150:LEU:HD22	1.79	0.47
3:A:7:GLU:HB3	3:B:150:ARG:NH2	2.29	0.47
3:A:190:ALA:CB	3:A:200:LYS:HG3	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:61:SER:HG	4:C:65:ASN:H	1.59	0.47
4:C:270:THR:H	4:C:273:HIS:HB2	1.79	0.47
4:C:835:GLU:O	4:C:835:GLU:HG3	2.11	0.47
5:D:154:LEU:HA	5:D:158:GLN:NE2	2.29	0.47
5:D:255:LEU:HD12	5:D:256:ASP:H	1.79	0.47
5:D:298:MET:SD	6:F:402:LEU:HG	2.53	0.47
5:D:983:LYS:HG2	5:D:985:ILE:HD13	1.96	0.47
5:D:1155:ILE:HD11	5:D:1210:ILE:HG22	1.96	0.47
6:F:136:GLU:CD	6:F:361:ILE:HA	2.33	0.47
6:F:160:ASP:HB3	6:F:264:LYS:HG3	1.95	0.47
6:F:247:GLU:O	6:F:251:LYS:N	2.40	0.47
2:J:46:PRO:HG3	2:J:59:VAL:CG1	2.44	0.47
2:J:103:MET:HB2	2:J:160:TYR:HE2	1.79	0.47
3:A:187:VAL:CG2	3:A:199:ASP:HB3	2.44	0.47
3:A:236:ASP:OD1	3:A:236:ASP:N	2.46	0.47
3:B:47:LEU:HB3	3:B:180:VAL:HG11	1.95	0.47
4:C:21:VAL:HG11	4:C:592:ARG:HD2	1.95	0.47
4:C:685:MET:HE1	4:C:1073:LYS:HD3	1.95	0.47
4:C:840:SER:O	4:C:840:SER:OG	2.25	0.47
4:C:1103:VAL:HG11	4:C:1112:ILE:HD11	1.95	0.47
5:D:722:ILE:O	5:D:722:ILE:HG12	2.13	0.47
6:F:277:MET:HG3	6:F:281:ARG:HB3	1.96	0.47
1:H:42:DG:H8	6:F:385:ARG:HG3	1.79	0.47
3:B:103:ASN:OD1	3:B:141:SER:HB2	2.13	0.47
4:C:109:ALA:HB1	4:C:110:PRO:HD2	1.95	0.47
4:C:188:PHE:CE1	4:C:194:LEU:HD12	2.49	0.47
4:C:964:LEU:HB3	4:C:968:GLU:OE2	2.14	0.47
4:C:1155:VAL:HG12	4:C:1156:ARG:H	1.79	0.47
4:C:1269:ARG:HA	4:C:1269:ARG:HD2	1.66	0.47
6:F:113:ARG:HB2	6:F:426:LYS:CE	2.44	0.47
6:F:128:ASN:O	6:F:132:CYS:HB3	2.14	0.47
6:F:588:ARG:H	6:F:588:ARG:HG2	1.49	0.47
7:G:32:DA:H2''	7:G:33:DA:C5'	2.44	0.47
8:E:70:GLN:O	8:E:74:GLU:HG3	2.14	0.47
1:H:63:DG:H4'	5:D:1170:LYS:HD2	1.96	0.47
3:A:85:LEU:HD21	3:A:130:ILE:HD13	1.95	0.47
4:C:53:PHE:HD1	4:C:468:LEU:HD11	1.79	0.47
4:C:519:ASN:HB3	4:C:521:LEU:H	1.79	0.47
4:C:936:ARG:O	4:C:939:VAL:HG12	2.14	0.47
6:F:414:LYS:HE3	6:F:434:TRP:CZ3	2.49	0.47
1:H:61:DG:H1'	1:H:62:DG:C8	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:13:LEU:CD1	2:I:60:PRO:HB2	2.44	0.47
2:I:13:LEU:HA	2:I:61:THR:O	2.14	0.47
2:J:21:TYR:O	2:J:24:GLN:HB2	2.14	0.47
3:A:227:GLN:NE2	3:B:9:LEU:O	2.47	0.47
3:B:91:ARG:O	3:B:91:ARG:HG2	2.13	0.47
4:C:17:LYS:N	4:C:17:LYS:HD2	2.29	0.47
4:C:985:GLU:O	4:C:989:LEU:HB2	2.14	0.47
5:D:452:LEU:HD13	5:D:500:ILE:HG22	1.96	0.47
6:F:312:SER:OG	6:F:314:THR:HG23	2.14	0.47
8:E:27:ALA:HB2	8:E:50:ALA:CB	2.45	0.47
1:H:40:DA:H3'	1:H:41:DT:C5'	2.44	0.47
3:A:152:TYR:HD1	3:A:176:CYS:HB3	1.79	0.47
4:C:246:LEU:HA	4:C:249:GLU:HG3	1.97	0.47
4:C:817:LEU:HD21	4:C:1080:ASN:ND2	2.29	0.47
4:C:887:VAL:HG23	4:C:913:VAL:HG21	1.96	0.47
5:D:165:TYR:CE1	5:D:169:LEU:HD22	2.50	0.47
6:F:462:LYS:HE2	6:F:462:LYS:HB3	1.56	0.47
1:H:13:DT:OP2	6:F:586:ARG:HD3	2.15	0.47
1:H:32:DG:N2	7:G:31:DC:O2	2.46	0.47
1:H:35:DC:H42	7:G:27:DA:H61	1.62	0.47
1:H:40:DA:OP2	6:F:428:SER:HB2	2.14	0.47
1:H:44:DG:C1'	1:H:45:DA:H5'	2.44	0.47
2:I:21:TYR:HB3	2:I:60:PRO:HD3	1.95	0.47
2:J:201:THR:H	2:J:204:GLU:HG2	1.79	0.47
3:A:236:ASP:HA	3:B:16:ILE:CG2	2.43	0.47
3:B:98:VAL:HG21	3:B:121:VAL:CG2	2.44	0.47
4:C:196:VAL:HG12	4:C:204:LEU:HB2	1.96	0.47
4:C:253:PHE:O	4:C:265:LYS:HG3	2.14	0.47
4:C:263:VAL:HG13	4:C:273:HIS:CE1	2.50	0.47
4:C:276:GLN:HA	4:C:279:LYS:CD	2.44	0.47
4:C:318:SER:O	4:C:321:LEU:HB2	2.14	0.47
4:C:490:GLN:HG3	6:F:472:GLN:HG2	1.95	0.47
4:C:976:ARG:NH2	4:C:989:LEU:HG	2.30	0.47
4:C:978:VAL:CG1	4:C:1007:LYS:HB3	2.44	0.47
4:C:1004:ASP:CA	4:C:1008:GLN:HG2	2.33	0.47
4:C:1099:ASN:OD1	4:C:1100:PRO:HD2	2.15	0.47
5:D:58:CYS:SG	5:D:59:ALA:N	2.88	0.47
5:D:573:THR:OG1	5:D:575:GLY:N	2.47	0.47
5:D:872:LEU:HD22	5:D:877:VAL:CG1	2.45	0.47
5:D:1040:MET:CE	5:D:1107:VAL:HG21	2.45	0.47
5:D:1280:VAL:HG11	5:D:1304:ARG:NH2	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1314:LEU:HD23	5:D:1326:GLN:CD	2.35	0.47
6:F:125:ASP:OD1	6:F:125:ASP:N	2.47	0.47
6:F:320:ILE:CD1	6:F:331:HIS:HB2	2.45	0.47
4:C:39:ILE:HG13	4:C:39:ILE:O	2.15	0.47
4:C:270:THR:O	4:C:273:HIS:HB2	2.15	0.47
4:C:742:TYR:HB3	4:C:743:PRO:HD2	1.96	0.47
4:C:1146:GLN:OE1	4:C:1160:ASP:HB3	2.15	0.47
5:D:8:LEU:HA	5:D:11:GLN:HB3	1.97	0.47
5:D:481:ARG:NH1	8:E:3:ARG:O	2.43	0.47
5:D:844:THR:OG1	5:D:861:ASN:HA	2.15	0.47
5:D:1123:ARG:C	5:D:1124:ILE:HD12	2.35	0.47
6:F:150:ARG:HB2	6:F:155:GLU:HB3	1.97	0.47
6:F:278:ASP:O	6:F:282:THR:HG22	2.15	0.47
6:F:373:ARG:O	6:F:377:LYS:HG3	2.15	0.47
6:F:530:LEU:CD2	6:F:532:LEU:H	2.27	0.47
6:F:572:THR:HB	6:F:575:GLU:CB	2.45	0.47
2:J:101:LEU:HD22	2:J:101:LEU:O	2.14	0.47
4:C:22:LEU:HD12	4:C:23:ASP:H	1.80	0.47
4:C:119:GLU:HB2	4:C:489:PRO:CD	2.43	0.47
4:C:232:ILE:H	4:C:331:LYS:HZ2	1.63	0.47
4:C:993:PRO:HG2	4:C:996:ARG:HD3	1.96	0.47
5:D:255:LEU:HD12	5:D:256:ASP:OD1	2.15	0.47
5:D:759:ILE:CG2	5:D:771:GLN:HB3	2.44	0.47
5:D:982:LEU:HD21	5:D:997:VAL:CG2	2.42	0.47
5:D:1024:THR:HG21	5:D:1123:ARG:HB3	1.97	0.47
5:D:1033:GLY:HA2	5:D:1114:GLN:HE22	1.78	0.47
6:F:142:THR:HA	6:F:145:LEU:HD21	1.97	0.47
7:G:3:DT:H1'	7:G:4:DG:H5'	1.97	0.47
2:I:162:ALA:HB3	2:I:163:PRO:HD3	1.96	0.47
3:A:218:ARG:HG2	3:B:231:PHE:O	2.15	0.47
4:C:38:PHE:CE1	4:C:461:GLU:HB2	2.50	0.47
5:D:34:SER:HA	5:D:102:MET:O	2.15	0.47
5:D:44:ILE:HD11	6:F:450:ILE:CD1	2.42	0.47
5:D:423:LEU:HB3	5:D:466:MET:CE	2.46	0.47
5:D:839:VAL:HG23	5:D:882:VAL:HG11	1.97	0.47
5:D:850:LYS:HE3	5:D:875:ASN:HD21	1.79	0.47
5:D:999:TYR:CD1	5:D:1027:VAL:HA	2.50	0.47
5:D:1143:ASP:OD1	5:D:1148:ARG:HD2	2.14	0.47
6:F:281:ARG:O	6:F:284:GLU:HB3	2.15	0.47
6:F:290:LEU:O	6:F:290:LEU:HD22	2.15	0.47
7:G:26:DT:H2''	7:G:27:DA:OP2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:21:LEU:HD12	8:E:21:LEU:HA	1.70	0.47
3:A:33:ARG:HG3	3:A:34:GLY:N	2.30	0.46
4:C:540:ARG:H	4:C:540:ARG:HG3	1.31	0.46
4:C:964:LEU:HD21	4:C:1021:LEU:HD22	1.97	0.46
4:C:1017:GLN:HE21	4:C:1017:GLN:H	1.62	0.46
5:D:1062:LEU:HD13	5:D:1066:GLU:O	2.15	0.46
6:F:161:LEU:O	6:F:261:LEU:HA	2.15	0.46
6:F:506:SER:O	6:F:509:THR:HG22	2.15	0.46
3:B:100:LEU:HB2	3:B:144:ILE:HD11	1.97	0.46
4:C:1109:ILE:HG13	5:D:740:LEU:HD22	1.96	0.46
4:C:1297:ASP:OD1	4:C:1298:VAL:N	2.49	0.46
5:D:654:ILE:HD11	5:D:743:MET:SD	2.56	0.46
5:D:797:THR:HB	5:D:924:GLY:HA3	1.98	0.46
5:D:857:LEU:HD11	5:D:872:LEU:HD23	1.97	0.46
5:D:1243:LEU:HD12	5:D:1243:LEU:O	2.16	0.46
6:F:354:THR:HG22	6:F:357:GLN:OE1	2.14	0.46
1:H:41:DT:H5"	1:H:41:DT:H6	1.80	0.46
3:A:225:ALA:HB3	3:B:232:VAL:HG11	1.98	0.46
3:B:83:LEU:HD13	5:D:528:THR:HB	1.98	0.46
4:C:104:ILE:O	4:C:114:VAL:HB	2.15	0.46
5:D:122:SER:O	5:D:125:GLY:N	2.49	0.46
5:D:146:VAL:O	5:D:147:ILE:HD13	2.16	0.46
5:D:146:VAL:HG13	5:D:158:GLN:O	2.16	0.46
5:D:955:LYS:CG	5:D:1010:GLN:HB3	2.43	0.46
5:D:981:GLU:HA	5:D:995:TYR:O	2.16	0.46
5:D:1211:SER:OG	5:D:1212:ASP:N	2.49	0.46
6:F:551:LEU:HD22	6:F:551:LEU:HA	1.66	0.46
8:E:84:THR:HA	8:E:87:ALA:CB	2.46	0.46
2:I:8:ARG:CB	2:I:10:VAL:HG23	2.45	0.46
4:C:38:PHE:CD2	4:C:39:ILE:HG23	2.50	0.46
4:C:522:SER:HB2	4:C:687:ARG:HB2	1.98	0.46
4:C:550:VAL:HB	5:D:780:ARG:HH12	1.79	0.46
4:C:595:THR:HG21	4:C:600:THR:CG2	2.42	0.46
4:C:1314:GLN:HB2	8:E:28:ARG:HH12	1.81	0.46
5:D:78:LEU:CD2	5:D:81:ARG:HD2	2.45	0.46
5:D:978:ARG:HH22	5:D:999:TYR:HB2	1.80	0.46
5:D:1031:VAL:O	5:D:1080:ILE:HD13	2.15	0.46
6:F:561:MET:CE	6:F:576:VAL:HG22	2.46	0.46
8:E:19:LEU:HD12	8:E:19:LEU:O	2.15	0.46
4:C:270:THR:OG1	4:C:273:HIS:N	2.31	0.46
4:C:398:SER:HB2	4:C:401:GLY:N	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:818:VAL:HG12	4:C:819:SER:O	2.15	0.46
4:C:975:ILE:HD13	4:C:1014:LEU:CD2	2.46	0.46
4:C:975:ILE:O	4:C:979:LEU:HB2	2.16	0.46
4:C:976:ARG:HB2	4:C:976:ARG:NH1	2.29	0.46
5:D:26:SER:HB3	5:D:236:TRP:CZ2	2.51	0.46
5:D:305:ALA:O	5:D:309:ASN:HB2	2.16	0.46
5:D:653:ILE:HD13	5:D:692:ARG:O	2.15	0.46
7:G:32:DA:H2''	7:G:33:DA:O5'	2.13	0.46
8:E:8:ASP:OD1	8:E:8:ASP:N	2.47	0.46
1:H:22:DG:H2''	1:H:23:DT:H72	1.96	0.46
3:K:320:ASN:O	3:K:320:ASN:ND2	2.48	0.46
4:C:985:GLU:HA	4:C:988:LYS:HG3	1.98	0.46
4:C:1158:LYS:HA	4:C:1158:LYS:CE	2.45	0.46
4:C:1247:SER:HB2	5:D:375:GLU:O	2.14	0.46
5:D:114:ILE:HB	5:D:304:ASP:OD1	2.15	0.46
6:F:133:SER:OG	6:F:136:GLU:OE2	2.32	0.46
6:F:314:THR:O	6:F:318:ALA:N	2.22	0.46
1:H:42:DG:C1'	1:H:43:DG:H1'	2.29	0.46
2:I:166:TRP:CE2	2:I:200:LEU:HD11	2.51	0.46
2:J:113:LEU:CD2	2:J:132:LEU:HB2	2.46	0.46
2:J:139:ILE:HG22	2:J:142:VAL:HG21	1.97	0.46
3:A:8:PHE:HD1	3:A:8:PHE:HA	1.67	0.46
4:C:102:LEU:CB	4:C:489:PRO:HG3	2.45	0.46
4:C:145:ILE:HB	4:C:456:VAL:HG22	1.97	0.46
4:C:249:GLU:O	4:C:269:ILE:HG13	2.15	0.46
4:C:291:TYR:HD2	4:C:292:ILE:HD13	1.81	0.46
4:C:299:LYS:HE2	4:C:334:GLU:CD	2.36	0.46
4:C:483:ASP:OD1	4:C:484:LEU:N	2.49	0.46
4:C:972:PHE:HA	4:C:975:ILE:HG12	1.98	0.46
5:D:88:CYS:O	5:D:90:VAL:N	2.37	0.46
5:D:1042:ASP:CG	5:D:1048:ARG:HD2	2.36	0.46
5:D:1155:ILE:HG12	5:D:1211:SER:CB	2.46	0.46
3:B:112:ALA:O	3:B:115:ILE:HG13	2.16	0.46
4:C:238:GLN:HG2	4:C:286:GLU:CG	2.28	0.46
4:C:588:GLU:CD	4:C:605:TYR:HB3	2.36	0.46
4:C:690:VAL:HG13	4:C:691:PRO:HD2	1.98	0.46
6:F:347:ILE:HA	6:F:350:GLU:OE1	2.16	0.46
6:F:452:ILE:HD11	6:F:457:ILE:CD1	2.46	0.46
6:F:493:LYS:O	6:F:497:VAL:HG23	2.16	0.46
2:J:41:VAL:HB	2:J:46:PRO:HD3	1.98	0.46
3:A:190:ALA:HB2	3:A:200:LYS:CG	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:226:GLU:O	3:A:226:GLU:HG2	2.14	0.46
3:B:57:THR:C	3:B:173:VAL:HG12	2.36	0.46
4:C:60:GLN:OE1	4:C:65:ASN:HA	2.16	0.46
4:C:214:ASN:OD1	4:C:359:ARG:HD2	2.16	0.46
4:C:759:SER:OG	4:C:760:ASN:N	2.49	0.46
4:C:841:ARG:HH11	5:D:257:GLY:HA2	1.81	0.46
5:D:670:SER:HB2	5:D:672:LEU:CD1	2.46	0.46
5:D:850:LYS:HB2	5:D:855:ASP:CB	2.45	0.46
5:D:901:ARG:HG2	5:D:901:ARG:O	2.15	0.46
5:D:977:SER:OG	5:D:978:ARG:N	2.48	0.46
5:D:1161:GLY:HA2	5:D:1180:VAL:HG22	1.98	0.46
2:I:67:LEU:HG	2:I:68:THR:O	2.16	0.46
2:I:203:ALA:O	2:I:207:MET:HE1	2.15	0.46
3:A:79:LEU:O	3:A:83:LEU:HG	2.16	0.46
4:C:202:ARG:HE	4:C:369:MET:HG3	1.81	0.46
4:C:263:VAL:HG13	4:C:273:HIS:HE1	1.81	0.46
4:C:903:ARG:CD	4:C:908:GLU:HB3	2.46	0.46
4:C:1132:LEU:HD23	4:C:1132:LEU:O	2.15	0.46
5:D:51:PRO:HB2	5:D:57:PHE:O	2.16	0.46
5:D:527:LEU:CD2	5:D:548:VAL:HG21	2.45	0.46
6:F:157:ARG:HG3	6:F:159:SER:N	2.23	0.46
2:J:116:THR:HA	2:J:120:GLY:CA	2.45	0.45
2:J:116:THR:HA	2:J:120:GLY:N	2.31	0.45
3:B:12:ARG:O	3:B:13:LEU:HB3	2.16	0.45
4:C:883:LEU:HD11	4:C:920:VAL:HG22	1.97	0.45
4:C:903:ARG:HD2	4:C:908:GLU:HB3	1.98	0.45
4:C:1072:ASN:OD1	4:C:1072:ASN:N	2.49	0.45
4:C:1289:GLU:HB2	4:C:1315:MET:SD	2.56	0.45
5:D:514:THR:HG21	5:D:596:LEU:CB	2.46	0.45
5:D:527:LEU:HB2	5:D:550:VAL:HG12	1.97	0.45
5:D:1314:LEU:HD23	5:D:1326:GLN:OE1	2.16	0.45
6:F:113:ARG:HB2	6:F:426:LYS:HE3	1.98	0.45
6:F:562:ARG:HG2	6:F:591:GLU:OE1	2.16	0.45
2:J:180:ALA:HB1	2:J:184:LYS:CD	2.43	0.45
3:K:280:ASP:OD1	3:K:321:TRP:NE1	2.50	0.45
4:C:694:ARG:O	4:C:694:ARG:HD3	2.15	0.45
4:C:887:VAL:CG2	4:C:913:VAL:HG21	2.47	0.45
4:C:1095:ASP:C	4:C:1096:ILE:HG12	2.36	0.45
4:C:1225:VAL:HG13	5:D:638:SER:HB2	1.98	0.45
4:C:1338:GLU:C	4:C:1339:LEU:HD23	2.36	0.45
5:D:200:GLN:O	5:D:204:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:557:LYS:HB3	5:D:563:LEU:HD13	1.98	0.45
6:F:147:GLN:HB3	6:F:156:ALA:CB	2.46	0.45
6:F:576:VAL:O	6:F:579:GLN:HB3	2.16	0.45
3:B:83:LEU:HD22	3:B:83:LEU:HA	1.66	0.45
4:C:103:VAL:HG12	4:C:116:ASP:CB	2.43	0.45
4:C:136:PHE:O	4:C:142:GLU:HA	2.16	0.45
4:C:591:TYR:OH	4:C:637:ARG:NH2	2.49	0.45
4:C:699:LEU:HD23	4:C:799:ASN:HD21	1.82	0.45
4:C:1254:VAL:HG22	4:C:1255:THR:HG23	1.97	0.45
5:D:609:TYR:CE1	5:D:614:LEU:HD12	2.38	0.45
5:D:1042:ASP:HA	5:D:1046:ILE:O	2.16	0.45
5:D:1161:GLY:HA3	5:D:1178:THR:O	2.16	0.45
6:F:224:LEU:HD11	6:F:252:LEU:HD12	1.97	0.45
8:E:80:LEU:CA	8:E:83:VAL:HB	2.41	0.45
2:I:159:CYS:O	2:I:163:PRO:HD2	2.17	0.45
2:J:48:GLN:O	2:J:51:ILE:HG23	2.15	0.45
2:J:201:THR:N	2:J:204:GLU:OE2	2.50	0.45
4:C:189:ASP:OD1	4:C:189:ASP:N	2.46	0.45
4:C:411:ARG:HG2	4:C:412:GLU:H	1.80	0.45
4:C:538:LEU:HD21	4:C:547:VAL:HG21	1.99	0.45
4:C:811:ASN:O	4:C:1099:ASN:ND2	2.48	0.45
5:D:337:ARG:HH11	5:D:337:ARG:CG	2.13	0.45
5:D:1003:LEU:HD22	5:D:1018:ALA:CB	2.45	0.45
5:D:1069:ALA:O	5:D:1072:LYS:HG3	2.17	0.45
5:D:1327:GLU:HA	7:G:12:DG:OP1	2.16	0.45
6:F:102:MET:HE1	6:F:388:ILE:HD13	1.98	0.45
6:F:144:LEU:CD1	6:F:161:LEU:HD12	2.45	0.45
6:F:559:LEU:HD12	6:F:559:LEU:HA	1.67	0.45
2:J:90:PRO:HG2	2:J:96:ARG:N	2.32	0.45
2:J:158:ASP:OD1	2:J:158:ASP:N	2.50	0.45
2:J:158:ASP:HB3	2:J:186:TYR:OH	2.16	0.45
2:J:175:PHE:CB	2:J:180:ALA:HB2	2.34	0.45
3:A:126:PRO:HG2	3:A:127:GLN:OE1	2.17	0.45
4:C:53:PHE:CD1	4:C:468:LEU:HD11	2.51	0.45
4:C:78:PRO:HB3	4:C:93:SER:O	2.17	0.45
4:C:163:LYS:HG3	4:C:164:THR:N	2.32	0.45
4:C:242:VAL:CG2	4:C:245:ARG:HE	2.30	0.45
4:C:413:GLU:HG3	4:C:415:GLU:OE2	2.17	0.45
5:D:306:LEU:O	5:D:326:SER:HB2	2.16	0.45
5:D:530:PRO:CB	5:D:581:MET:HE2	2.46	0.45
5:D:923:ILE:HD12	5:D:1256:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:30:DT:H2''	1:H:31:DT:O5'	2.17	0.45
1:H:62:DG:H1'	1:H:63:DG:C5'	2.47	0.45
2:I:46:PRO:HB2	2:I:50:LEU:HD23	1.98	0.45
2:I:132:LEU:HD23	2:I:173:ILE:CD1	2.44	0.45
2:J:117:ILE:HG21	2:J:171:LEU:HG	1.98	0.45
2:J:145:GLN:O	2:J:146:LYS:HD2	2.17	0.45
4:C:622:ASN:O	4:C:623:LEU:HD23	2.16	0.45
4:C:971:LEU:O	4:C:975:ILE:HG23	2.16	0.45
5:D:44:ILE:CG1	6:F:450:ILE:HG12	2.46	0.45
5:D:279:LEU:O	5:D:283:LEU:HD13	2.16	0.45
5:D:929:GLN:O	5:D:930:LEU:HD23	2.17	0.45
5:D:950:ILE:O	5:D:1016:THR:HG22	2.17	0.45
5:D:954:ASN:HD21	5:D:992:LYS:HD2	1.80	0.45
5:D:972:LYS:HZ2	5:D:974:VAL:HG23	1.82	0.45
5:D:1001:ALA:CB	5:D:1020:TRP:HB2	2.44	0.45
6:F:97:PRO:O	6:F:100:MET:N	2.49	0.45
6:F:489:MET:CB	6:F:494:ILE:HG13	2.46	0.45
7:G:6:DA:H2''	7:G:7:DT:C7	2.47	0.45
7:G:41:DC:H2''	7:G:42:DT:N3	2.31	0.45
1:H:64:DG:H2''	1:H:65:DA:O5'	2.17	0.45
4:C:745:GLU:OE1	4:C:971:LEU:HD11	2.16	0.45
5:D:1032:SER:OG	5:D:1115:ILE:HG12	2.17	0.45
5:D:1276:GLU:HG2	5:D:1277:GLY:H	1.80	0.45
6:F:275:VAL:HA	6:F:278:ASP:OD2	2.16	0.45
6:F:536:THR:HG22	6:F:610:PHE:HE1	1.80	0.45
6:F:593:LYS:HB3	6:F:596:ARG:NH2	2.31	0.45
8:E:68:GLU:O	8:E:71:GLU:N	2.49	0.45
1:H:26:DT:H71	1:H:27:DA:H62	1.81	0.45
2:I:113:LEU:HD23	2:I:132:LEU:CB	2.41	0.45
2:J:95:ALA:HA	2:J:98:GLU:CD	2.37	0.45
2:J:134:GLU:O	2:J:137:LEU:HD12	2.17	0.45
2:J:166:TRP:CZ2	2:J:200:LEU:HD22	2.52	0.45
4:C:119:GLU:HG2	4:C:489:PRO:O	2.16	0.45
4:C:1148:ALA:HB1	4:C:1180:MET:CE	2.46	0.45
5:D:44:ILE:HD13	5:D:252:LEU:HD23	1.99	0.45
5:D:474:LEU:HD12	5:D:474:LEU:O	2.17	0.45
5:D:614:LEU:HD23	5:D:614:LEU:O	2.17	0.45
5:D:675:ALA:O	5:D:678:ARG:N	2.45	0.45
5:D:921:GLN:O	5:D:925:GLU:HB3	2.16	0.45
6:F:289:LYS:O	6:F:294:GLN:HG3	2.16	0.45
1:H:19:DA:H4'	1:H:20:DA:OP1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:82:ARG:O	2:J:84:PRO:HD3	2.17	0.45
2:J:129:ARG:O	2:J:173:ILE:HD13	2.17	0.45
3:B:98:VAL:HG21	3:B:121:VAL:HG21	1.98	0.45
3:B:153:VAL:HG11	3:B:158:ARG:NH2	2.32	0.45
4:C:1307:ASN:HB3	4:C:1312:ASN:O	2.17	0.45
4:C:1335:ILE:HD12	5:D:1336:ALA:CB	2.47	0.45
5:D:194:LEU:O	5:D:198:CYS:HB2	2.16	0.45
5:D:479:GLU:HG2	8:E:20:VAL:HG21	1.99	0.45
5:D:515:ARG:NH2	5:D:717:VAL:HB	2.18	0.45
6:F:600:HIS:HB3	6:F:601:PRO:HD2	1.99	0.45
1:H:37:DA:N3	6:F:425:TYR:HB2	2.32	0.45
2:J:200:LEU:HA	2:J:204:GLU:OE2	2.16	0.45
3:A:159:ILE:HD11	3:A:172:LEU:CD1	2.47	0.45
4:C:138:ILE:HD13	4:C:138:ILE:HA	1.63	0.45
4:C:524:ILE:O	4:C:524:ILE:HD13	2.17	0.45
4:C:871:VAL:HG22	4:C:872:TYR:H	1.82	0.45
5:D:35:PHE:CD2	5:D:101:ARG:HD3	2.51	0.45
5:D:1269:ALA:HB2	5:D:1274:PHE:HD2	1.82	0.45
6:F:297:MET:HG2	6:F:298:PRO:N	2.32	0.45
6:F:511:ILE:HD11	6:F:517:SER:OG	2.17	0.45
2:J:23:HIS:HA	2:J:26:ARG:NH1	2.32	0.44
2:J:140:ALA:HB2	2:J:183:LEU:HD23	1.98	0.44
3:A:222:THR:N	3:B:232:VAL:HG12	2.32	0.44
3:B:9:LEU:HD12	3:B:195:ARG:HH22	1.81	0.44
3:B:22:THR:O	3:B:22:THR:OG1	2.32	0.44
4:C:421:SER:OG	4:C:422:LYS:N	2.50	0.44
4:C:594:VAL:HG22	4:C:599:VAL:HG22	1.99	0.44
4:C:1319:MET:CG	4:C:1320:PRO:HD2	2.47	0.44
5:D:74:LYS:NZ	5:D:87:LYS:HD3	2.33	0.44
5:D:127:LEU:HD21	5:D:234:PRO:HB3	1.98	0.44
5:D:1027:VAL:CG2	5:D:1102:PRO:HD2	2.44	0.44
5:D:1165:PHE:CE1	5:D:1175:LEU:HD13	2.52	0.44
5:D:1167:LYS:CE	5:D:1170:LYS:HD3	2.46	0.44
1:H:11:DG:H2''	1:H:12:DA:O5'	2.17	0.44
1:H:12:DA:C8	1:H:13:DT:H71	2.52	0.44
1:H:53:DC:H2''	1:H:54:DG:H5'	1.99	0.44
3:B:104:LYS:N	3:B:140:ILE:O	2.41	0.44
4:C:964:LEU:O	4:C:968:GLU:N	2.28	0.44
4:C:1288:GLN:O	4:C:1292:THR:HB	2.16	0.44
5:D:74:LYS:HZ1	5:D:87:LYS:HD3	1.82	0.44
5:D:126:LEU:HD12	5:D:126:LEU:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:245:LEU:HD12	5:D:246:PRO:CD	2.46	0.44
5:D:487:THR:HB	5:D:618:VAL:HG21	1.99	0.44
6:F:561:MET:CE	6:F:576:VAL:HG13	2.46	0.44
1:H:58:DG:H2''	1:H:59:DC:O4'	2.18	0.44
3:A:197:ASP:N	3:A:197:ASP:OD1	2.48	0.44
4:C:179:TYR:HE2	4:C:462:ASN:HD21	1.64	0.44
4:C:299:LYS:HZ1	4:C:334:GLU:HB2	1.83	0.44
4:C:967:LEU:HD23	4:C:967:LEU:O	2.17	0.44
4:C:1303:LYS:HD2	4:C:1303:LYS:HA	1.83	0.44
5:D:958:ILE:CG2	5:D:960:LEU:HD21	2.44	0.44
6:F:346:GLN:O	6:F:350:GLU:HG3	2.17	0.44
6:F:354:THR:O	6:F:358:VAL:HG23	2.16	0.44
4:C:150:HIS:NE2	4:C:454:ARG:HG3	2.33	0.44
4:C:1020:GLU:HB3	4:C:1024:GLU:CG	2.48	0.44
4:C:1151:LEU:CD2	4:C:1198:LEU:HG	2.47	0.44
4:C:1342:GLU:HG3	5:D:18:ASP:OD1	2.17	0.44
5:D:241:VAL:HG23	5:D:241:VAL:O	2.17	0.44
5:D:253:VAL:HG11	6:F:523:ILE:HD12	1.97	0.44
5:D:487:THR:OG1	8:E:5:THR:HG22	2.17	0.44
5:D:959:LYS:O	5:D:983:LYS:HB3	2.18	0.44
5:D:1079:LYS:CD	5:D:1087:ASP:HB3	2.34	0.44
6:F:306:PHE:HB2	6:F:314:THR:OG1	2.16	0.44
8:E:83:VAL:O	8:E:86:ILE:HG13	2.16	0.44
3:A:40:GLY:HA3	3:A:185:TYR:CE2	2.51	0.44
3:B:71:LYS:HB3	3:B:74:VAL:CG2	2.47	0.44
3:B:95:LYS:NZ	3:B:98:VAL:HA	2.32	0.44
4:C:75:LEU:CD2	4:C:127:ILE:HD11	2.47	0.44
4:C:145:ILE:HD13	4:C:512:SER:HA	1.99	0.44
4:C:260:LYS:HA	4:C:260:LYS:HD2	1.89	0.44
4:C:1008:GLN:HA	4:C:1011:LEU:HG	1.99	0.44
4:C:1256:GLN:OE1	6:F:528:LEU:HD21	2.17	0.44
4:C:1339:LEU:HB3	5:D:17:PHE:CD2	2.47	0.44
5:D:1012:ALA:HB3	5:D:1015:GLU:CB	2.47	0.44
6:F:338:HIS:HA	6:F:341:LEU:CD1	2.45	0.44
3:A:79:LEU:HD21	4:C:831:ILE:HD11	1.98	0.44
3:A:192:VAL:HB	3:A:198:LEU:HD12	1.98	0.44
4:C:119:GLU:HB2	4:C:489:PRO:HG2	1.98	0.44
4:C:911:SER:OG	4:C:913:VAL:O	2.36	0.44
5:D:17:PHE:CZ	5:D:1353:VAL:HG11	2.47	0.44
5:D:1156:LEU:HD13	5:D:1156:LEU:HA	1.83	0.44
5:D:1345:ARG:HB3	5:D:1345:ARG:NH1	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:279:ARG:NH2	6:F:350:GLU:OE2	2.50	0.44
2:I:113:LEU:CD2	2:I:132:LEU:HD13	2.48	0.44
2:J:88:LEU:O	2:J:156:LEU:HB2	2.18	0.44
2:J:168:LEU:HB2	2:J:169:PRO:HD3	1.99	0.44
2:J:208:ARG:HG2	2:J:209:LEU:N	2.29	0.44
3:A:27:THR:HG23	3:A:201:LEU:O	2.17	0.44
3:A:192:VAL:CG1	3:A:195:ARG:HB2	2.45	0.44
3:B:95:LYS:HZ1	3:B:98:VAL:HA	1.83	0.44
4:C:976:ARG:O	4:C:980:VAL:HG13	2.17	0.44
4:C:988:LYS:O	4:C:991:LYS:HG2	2.18	0.44
5:D:56:LEU:HD12	5:D:56:LEU:HA	1.85	0.44
5:D:1161:GLY:HA2	5:D:1180:VAL:CG2	2.48	0.44
6:F:144:LEU:HD12	6:F:147:GLN:CB	2.42	0.44
6:F:282:THR:HA	6:F:285:ARG:HG2	1.99	0.44
6:F:333:VAL:O	6:F:337:VAL:HG22	2.18	0.44
8:E:39:VAL:CG1	8:E:40:PRO:HD2	2.48	0.44
8:E:39:VAL:CG2	8:E:53:GLU:HG2	2.45	0.44
2:I:21:TYR:O	2:I:25:VAL:HG23	2.18	0.44
2:I:112:THR:O	2:I:116:THR:CG2	2.63	0.44
3:K:254:LEU:HD12	3:K:254:LEU:H	1.82	0.44
4:C:50:GLU:OE1	4:C:70:TYR:OH	2.36	0.44
4:C:970:GLY:HA2	4:C:973:SER:OG	2.17	0.44
4:C:1105:SER:HA	5:D:736:GLN:OE1	2.17	0.44
5:D:154:LEU:HA	5:D:158:GLN:CD	2.38	0.44
5:D:857:LEU:HB2	5:D:871:LEU:CD2	2.48	0.44
5:D:909:ILE:HD11	5:D:913:GLU:HB3	1.99	0.44
5:D:1154:ALA:HB2	5:D:1213:GLY:O	2.18	0.44
6:F:130:VAL:HG23	6:F:368:GLY:HA3	2.00	0.44
6:F:290:LEU:CA	6:F:294:GLN:HB2	2.47	0.44
8:E:41:GLU:HG3	8:E:43:ASN:H	1.83	0.44
2:I:62:LEU:O	2:I:69:LEU:N	2.45	0.44
3:B:65:LEU:HD22	3:B:168:ILE:O	2.17	0.44
4:C:42:ASP:O	4:C:50:GLU:HG2	2.18	0.44
4:C:975:ILE:CG2	4:C:1010:GLN:HG2	2.46	0.44
4:C:1158:LYS:HA	4:C:1158:LYS:HZ2	1.83	0.44
5:D:500:ILE:HG22	5:D:500:ILE:O	2.17	0.44
5:D:789:LYS:HE3	5:D:931:THR:HA	1.99	0.44
5:D:908:ILE:HG12	5:D:909:ILE:H	1.82	0.44
5:D:1062:LEU:HB2	5:D:1067:ARG:HD3	1.99	0.44
6:F:572:THR:O	6:F:576:VAL:HG23	2.18	0.44
7:G:57:DT:H2''	7:G:58:DG:O5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:6:DA:H1'	7:G:59:DT:O2	2.18	0.43
1:H:9:DA:H2''	1:H:10:DT:O5'	2.18	0.43
2:I:209:LEU:HD11	8:E:87:ALA:O	2.17	0.43
2:J:156:LEU:HD13	2:J:156:LEU:O	2.18	0.43
4:C:15:PHE:CD2	4:C:1190:ALA:HB2	2.53	0.43
4:C:147:SER:HB2	4:C:530:ILE:HD13	1.99	0.43
4:C:271:ALA:O	4:C:275:ARG:HG3	2.18	0.43
4:C:494:ASN:CG	6:F:468:ARG:HD3	2.38	0.43
4:C:632:ASP:OD1	4:C:633:LEU:HD23	2.18	0.43
4:C:1291:LEU:HD21	5:D:1351:VAL:HG22	1.99	0.43
4:C:1296:ASP:OD1	4:C:1297:ASP:N	2.51	0.43
5:D:165:TYR:OH	5:D:169:LEU:HD22	2.18	0.43
5:D:1109:LEU:CD1	5:D:1121:LEU:HD22	2.47	0.43
1:H:58:DG:C2'	1:H:59:DC:H5''	2.48	0.43
2:I:14:PHE:CB	2:I:50:LEU:HD13	2.47	0.43
2:I:20:ILE:CD1	2:I:164:LEU:HG	2.48	0.43
2:J:132:LEU:HD21	2:J:136:LEU:HD21	1.99	0.43
3:K:307:LEU:HD13	3:K:313:SER:HA	1.99	0.43
3:B:123:ILE:HG22	3:B:125:LYS:H	1.83	0.43
4:C:67:GLU:O	4:C:102:LEU:HD12	2.18	0.43
4:C:799:ASN:HB3	4:C:1231:TYR:CD1	2.51	0.43
4:C:843:THR:CG2	4:C:844:LYS:HZ1	2.05	0.43
4:C:1020:GLU:CA	4:C:1024:GLU:H	2.30	0.43
5:D:3:ASP:HA	5:D:6:LYS:HB3	2.00	0.43
5:D:710:ASP:N	5:D:710:ASP:OD1	2.50	0.43
5:D:827:GLU:CG	5:D:832:LYS:HD3	2.48	0.43
5:D:1109:LEU:HD21	5:D:1115:ILE:HG21	1.99	0.43
6:F:306:PHE:HZ	6:F:341:LEU:HD22	1.83	0.43
6:F:390:ILE:CD1	6:F:432:THR:HG23	2.28	0.43
6:F:481:GLU:OE1	6:F:491:GLU:HG3	2.18	0.43
6:F:492:ASP:O	6:F:495:ARG:N	2.52	0.43
1:H:17:DC:H1'	1:H:18:DA:C5'	2.40	0.43
2:J:180:ALA:O	2:J:184:LYS:HG3	2.19	0.43
3:K:298:LYS:HG3	7:G:56:DT:H72	1.99	0.43
4:C:75:LEU:HD21	4:C:127:ILE:HD11	1.99	0.43
4:C:106:GLU:N	4:C:114:VAL:HG21	2.33	0.43
4:C:317:LEU:HD23	4:C:317:LEU:HA	1.85	0.43
4:C:356:THR:CG2	4:C:361:SER:O	2.66	0.43
4:C:380:ALA:O	4:C:383:SER:OG	2.24	0.43
4:C:516:VAL:O	4:C:522:SER:OG	2.37	0.43
4:C:1282:GLY:O	5:D:1360:GLY:HA3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:491:LEU:HB2	5:D:904:ALA:O	2.18	0.43
5:D:1024:THR:HG22	5:D:1124:ILE:N	2.32	0.43
5:D:1024:THR:O	5:D:1026:PRO:HD3	2.19	0.43
6:F:558:VAL:CG2	6:F:587:ILE:HD11	2.47	0.43
7:G:51:DT:H2''	7:G:52:DC:H6	1.82	0.43
3:B:100:LEU:CD2	3:B:144:ILE:HG13	2.46	0.43
4:C:13:LYS:HD2	4:C:14:ASP:N	2.33	0.43
4:C:60:GLN:NE2	4:C:67:GLU:HG3	2.29	0.43
4:C:303:ASP:CG	4:C:310:ILE:HD11	2.39	0.43
4:C:835:GLU:HB2	4:C:1053:TYR:CE1	2.54	0.43
5:D:113:HIS:CE1	5:D:307:LEU:HD13	2.53	0.43
5:D:734:ALA:O	5:D:738:ARG:NH1	2.51	0.43
5:D:1109:LEU:HD22	5:D:1115:ILE:HG21	2.01	0.43
6:F:137:TYR:CZ	6:F:139:GLU:HB2	2.54	0.43
7:G:11:DT:C2'	7:G:12:DG:H5''	2.47	0.43
2:I:12:THR:HB	2:I:63:VAL:HB	1.99	0.43
2:I:27:ILE:HD11	2:I:163:PRO:HG3	2.01	0.43
2:I:182:GLU:N	2:I:182:GLU:OE1	2.52	0.43
3:B:107:ILE:HG23	3:B:134:THR:O	2.17	0.43
4:C:540:ARG:HH22	4:C:567:PRO:CG	2.31	0.43
4:C:985:GLU:CB	4:C:989:LEU:HD13	2.48	0.43
5:D:255:LEU:HD13	5:D:255:LEU:HA	1.67	0.43
5:D:314:ARG:NH2	5:D:323:PRO:HG3	2.33	0.43
6:F:275:VAL:HG13	6:F:278:ASP:OD2	2.19	0.43
2:I:70:TRP:O	2:I:71:GLU:HB2	2.18	0.43
2:J:96:ARG:O	2:J:100:ARG:HB2	2.18	0.43
3:A:100:LEU:HD23	3:A:100:LEU:HA	1.79	0.43
4:C:1115:THR:HG22	4:C:1228:GLY:HA3	2.00	0.43
5:D:141:PHE:CE2	5:D:181:GLY:HA3	2.54	0.43
5:D:228:VAL:HG13	5:D:229:GLN:H	1.82	0.43
5:D:1051:ASP:OD2	5:D:1057:SER:HA	2.18	0.43
6:F:231:THR:HG21	6:F:252:LEU:HB2	2.00	0.43
6:F:341:LEU:HB3	6:F:344:LEU:HD21	2.00	0.43
6:F:586:ARG:O	6:F:590:ILE:HG13	2.19	0.43
1:H:49:DG:C6	4:C:151:ARG:HD2	2.54	0.43
2:I:61:THR:HG23	2:I:68:THR:OG1	2.19	0.43
2:J:113:LEU:HD21	2:J:132:LEU:HB2	1.99	0.43
4:C:34:SER:O	4:C:34:SER:OG	2.32	0.43
4:C:540:ARG:HB2	4:C:540:ARG:HH11	1.83	0.43
4:C:594:VAL:HG23	4:C:652:TYR:HA	2.01	0.43
4:C:976:ARG:HE	4:C:989:LEU:HD23	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1003:THR:OG1	4:C:1005:GLU:OE2	2.28	0.43
4:C:1027:LYS:HA	4:C:1027:LYS:HD3	1.68	0.43
4:C:1082:ILE:H	4:C:1082:ILE:HG13	1.65	0.43
4:C:1260:GLY:CA	4:C:1265:PHE:HA	2.49	0.43
4:C:1308:ILE:HG21	5:D:379:PRO:HB2	2.00	0.43
5:D:688:ALA:O	5:D:692:ARG:HG3	2.18	0.43
5:D:810:THR:HG22	5:D:893:GLY:HA3	2.01	0.43
6:F:231:THR:CB	6:F:252:LEU:HB2	2.49	0.43
6:F:315:TRP:CZ2	6:F:337:VAL:HB	2.54	0.43
6:F:536:THR:O	6:F:540:LEU:N	2.46	0.43
7:G:34:DT:H2''	7:G:35:DT:C5'	2.48	0.43
1:H:37:DA:OP1	1:H:37:DA:H2'	2.18	0.43
1:H:63:DG:C4'	5:D:1170:LYS:HD2	2.49	0.43
2:I:24:GLN:OE1	2:I:160:TYR:HA	2.19	0.43
4:C:844:LYS:NZ	4:C:844:LYS:H	2.17	0.43
4:C:1115:THR:O	4:C:1228:GLY:HA3	2.19	0.43
5:D:978:ARG:NH1	5:D:999:TYR:H	2.17	0.43
6:F:390:ILE:HG21	6:F:435:ILE:HG22	2.01	0.43
6:F:607:LEU:HA	6:F:607:LEU:HD23	1.59	0.43
1:H:12:DA:N1	7:G:51:DT:H72	2.33	0.43
1:H:29:DA:H2''	1:H:30:DT:H5'	2.00	0.43
2:J:165:LEU:O	2:J:168:LEU:HG	2.19	0.43
4:C:232:ILE:HG12	4:C:237:LEU:CD2	2.49	0.43
4:C:298:ALA:HB3	4:C:334:GLU:HB2	2.00	0.43
4:C:453:ILE:CD1	4:C:587:LEU:HD11	2.47	0.43
4:C:985:GLU:O	4:C:989:LEU:HD13	2.19	0.43
4:C:1146:GLN:OE1	4:C:1160:ASP:HB2	2.19	0.43
4:C:1203:ASP:OD1	4:C:1203:ASP:N	2.52	0.43
5:D:911:LYS:HE2	5:D:911:LYS:HB3	1.72	0.43
5:D:1040:MET:HE3	5:D:1107:VAL:HG21	2.00	0.43
5:D:1186:TYR:OH	5:D:1188:GLU:OE1	2.25	0.43
5:D:1229:VAL:HG21	5:D:1306:LEU:HD13	2.00	0.43
6:F:141:ILE:O	6:F:141:ILE:HG22	2.18	0.43
6:F:292:VAL:CG2	6:F:299:LYS:HB3	2.47	0.43
7:G:52:DC:H5'	7:G:52:DC:C6	2.51	0.43
2:I:34:VAL:HG11	2:I:83:PHE:CE2	2.50	0.43
2:I:87:PRO:HD3	6:F:567:MET:SD	2.59	0.43
3:B:95:LYS:HB3	3:B:95:LYS:HE2	1.72	0.43
4:C:179:TYR:HB2	4:C:398:SER:HG	1.82	0.43
4:C:271:ALA:HA	4:C:274:ILE:HB	2.00	0.43
4:C:371:ARG:HB3	4:C:374:GLU:OE2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:473:ARG:HB2	4:C:473:ARG:NH1	2.34	0.43
4:C:540:ARG:HB2	4:C:540:ARG:NH1	2.34	0.43
4:C:850:ILE:HG22	4:C:850:ILE:O	2.19	0.43
4:C:906:PHE:CE2	6:F:608:ARG:HA	2.54	0.43
4:C:1204:LEU:HB3	4:C:1205:PRO:HD2	1.99	0.43
5:D:7:PHE:HD2	5:D:7:PHE:HA	1.69	0.43
5:D:22:ILE:O	5:D:1339:GLY:HA2	2.18	0.43
5:D:294:ASN:ND2	6:F:406:GLN:HE21	2.16	0.43
5:D:709:ARG:HH11	5:D:714:GLU:HB3	1.84	0.43
6:F:530:LEU:HD22	6:F:532:LEU:HB3	2.00	0.43
6:F:611:LEU:HD23	6:F:611:LEU:HA	1.86	0.43
1:H:12:DA:H1'	1:H:13:DT:H5'	2.01	0.42
1:H:20:DA:N6	7:G:43:DT:H3	2.17	0.42
1:H:40:DA:H5'	1:H:41:DT:H73	2.00	0.42
2:J:24:GLN:HB3	2:J:76:MET:CE	2.49	0.42
3:B:205:MET:CE	3:B:217:ILE:HG13	2.48	0.42
4:C:18:ARG:HD2	4:C:18:ARG:N	2.34	0.42
4:C:296:VAL:CG2	4:C:314:ASN:HA	2.48	0.42
4:C:529:ARG:HD2	4:C:572:ILE:HG23	2.01	0.42
4:C:790:ASP:OD1	4:C:791:LEU:HD23	2.19	0.42
5:D:45:ASN:HB3	5:D:48:THR:O	2.19	0.42
5:D:144:TYR:CD1	5:D:180:MET:HB2	2.53	0.42
5:D:573:THR:HG23	5:D:576:ARG:CD	2.41	0.42
5:D:843:VAL:CG2	5:D:883:ARG:HB2	2.49	0.42
5:D:954:ASN:HB2	5:D:984:LEU:CD2	2.49	0.42
5:D:958:ILE:HG22	5:D:960:LEU:CD2	2.45	0.42
6:F:141:ILE:O	6:F:145:LEU:CG	2.67	0.42
6:F:162:ILE:HG22	6:F:260:ARG:O	2.19	0.42
6:F:343:LYS:O	6:F:346:GLN:HB2	2.19	0.42
7:G:27:DA:H2''	7:G:28:DG:C5'	2.49	0.42
2:I:66:GLU:OE1	2:I:67:LEU:HB3	2.19	0.42
2:J:12:THR:O	2:J:62:LEU:HD12	2.19	0.42
2:J:14:PHE:CE2	2:J:50:LEU:HD22	2.54	0.42
3:A:114:ASP:OD1	3:A:114:ASP:N	2.52	0.42
4:C:274:ILE:HA	4:C:277:LEU:HD12	2.01	0.42
4:C:303:ASP:HB3	4:C:306:THR:OG1	2.19	0.42
4:C:674:ASP:HB3	4:C:679:ALA:HB2	2.01	0.42
4:C:906:PHE:CD2	6:F:611:LEU:HD12	2.52	0.42
4:C:1200:LYS:HE3	4:C:1200:LYS:HB2	1.95	0.42
4:C:1211:ARG:HD3	4:C:1220:GLN:NE2	2.34	0.42
5:D:234:PRO:O	5:D:237:MET:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:405:GLU:O	5:D:408:VAL:HG22	2.19	0.42
5:D:709:ARG:CZ	5:D:712:GLN:HB2	2.49	0.42
5:D:1040:MET:CB	5:D:1078:LEU:HD21	2.48	0.42
5:D:1159:ILE:HD12	5:D:1160:SER:N	2.34	0.42
6:F:220:LYS:HD2	6:F:220:LYS:HA	1.47	0.42
8:E:29:GLN:O	8:E:34:GLY:HA2	2.20	0.42
2:I:17:PRO:CG	2:I:40:HIS:HB3	2.49	0.42
4:C:17:LYS:NZ	4:C:1194:GLU:OE2	2.37	0.42
4:C:511:LEU:O	4:C:513:GLN:N	2.53	0.42
4:C:886:LYS:N	4:C:917:SER:OG	2.37	0.42
4:C:1008:GLN:HA	4:C:1011:LEU:HD11	2.00	0.42
4:C:1122:LYS:HG3	4:C:1122:LYS:O	2.19	0.42
5:D:468:VAL:HG23	5:D:468:VAL:O	2.19	0.42
5:D:527:LEU:HD11	5:D:536:LEU:HD22	2.01	0.42
5:D:596:LEU:HA	5:D:596:LEU:HD12	1.82	0.42
6:F:272:SER:O	6:F:276:MET:HG2	2.19	0.42
1:H:18:DA:H4'	1:H:19:DA:OP1	2.19	0.42
2:I:23:HIS:HA	2:I:26:ARG:CG	2.45	0.42
2:J:29:LEU:HD12	2:J:79:LEU:HD13	2.01	0.42
3:A:52:PRO:HA	3:A:149:GLY:O	2.19	0.42
3:B:85:LEU:HD23	3:B:85:LEU:HA	1.81	0.42
4:C:196:VAL:HG22	4:C:197:ARG:H	1.85	0.42
4:C:206:ALA:O	4:C:209:ILE:HG22	2.19	0.42
4:C:299:LYS:NZ	4:C:301:TYR:CZ	2.86	0.42
4:C:1001:GLY:HA3	4:C:1011:LEU:HD13	2.00	0.42
5:D:520:ALA:HB3	5:D:546:ALA:HB2	2.02	0.42
5:D:982:LEU:HD11	5:D:997:VAL:CG2	2.49	0.42
5:D:1042:ASP:OD1	5:D:1042:ASP:N	2.43	0.42
5:D:1358:PRO:HB3	5:D:1366:HIS:CD2	2.55	0.42
6:F:548:LEU:O	6:F:548:LEU:HD23	2.19	0.42
8:E:75:GLN:O	8:E:78:ALA:HB3	2.19	0.42
1:H:50:DT:H5''	1:H:51:DC:OP2	2.20	0.42
2:J:175:PHE:CE2	2:J:183:LEU:HD12	2.55	0.42
3:B:110:VAL:HB	3:B:131:CYS:SG	2.59	0.42
4:C:230:PHE:HE2	4:C:292:ILE:HG23	1.84	0.42
4:C:453:ILE:HD12	4:C:587:LEU:CD2	2.48	0.42
4:C:637:ARG:HG3	4:C:637:ARG:O	2.20	0.42
4:C:885:GLY:HA2	4:C:917:SER:OG	2.20	0.42
4:C:935:THR:HG23	4:C:939:VAL:HG13	2.00	0.42
4:C:1296:ASP:CG	4:C:1320:PRO:HB3	2.32	0.42
5:D:833:GLU:CG	5:D:838:ARG:HG3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:841:GLY:O	5:D:842:ARG:HG3	2.20	0.42
6:F:277:MET:HG3	6:F:281:ARG:CB	2.49	0.42
6:F:471:LEU:HD12	6:F:471:LEU:HA	1.83	0.42
8:E:27:ALA:HB2	8:E:50:ALA:HB2	2.01	0.42
1:H:34:DG:H2''	1:H:35:DC:OP2	2.20	0.42
1:H:51:DC:H2'	1:H:52:DA:C8	2.54	0.42
2:I:39:GLU:O	2:I:41:VAL:HG13	2.20	0.42
2:J:78:TYR:OH	2:J:82:ARG:NH1	2.48	0.42
3:B:100:LEU:HD23	3:B:144:ILE:CG1	2.49	0.42
3:B:129:VAL:HG21	3:B:132:HIS:HE1	1.83	0.42
4:C:274:ILE:O	4:C:277:LEU:HG	2.20	0.42
4:C:935:THR:HG23	4:C:939:VAL:CG1	2.50	0.42
4:C:976:ARG:HH21	4:C:989:LEU:HG	1.84	0.42
4:C:1058:ARG:HE	4:C:1058:ARG:HB3	1.44	0.42
5:D:410:ASP:HA	5:D:413:ASP:OD2	2.20	0.42
5:D:793:SER:O	5:D:793:SER:OG	2.30	0.42
5:D:986:ASP:CG	5:D:992:LYS:HG2	2.40	0.42
5:D:1189:MET:O	5:D:1190:ILE:HG13	2.20	0.42
5:D:1356:LEU:HA	5:D:1356:LEU:HD23	1.63	0.42
6:F:228:TYR:CE2	6:F:229:VAL:HG13	2.54	0.42
6:F:558:VAL:HG23	6:F:580:PHE:CE2	2.53	0.42
2:I:162:ALA:O	2:I:166:TRP:N	2.52	0.42
3:B:81:ILE:O	3:B:84:ASN:N	2.52	0.42
4:C:30:ILE:HG13	4:C:575:LEU:CD2	2.49	0.42
4:C:50:GLU:O	4:C:50:GLU:HG3	2.20	0.42
4:C:145:ILE:HB	4:C:456:VAL:CG2	2.50	0.42
4:C:255:ILE:CG2	4:C:263:VAL:H	2.28	0.42
4:C:331:LYS:HE3	4:C:331:LYS:HB3	1.86	0.42
4:C:834:GLN:HE22	4:C:924:VAL:HG21	1.83	0.42
4:C:1145:ILE:CD1	4:C:1173:ALA:HB2	2.49	0.42
5:D:3:ASP:O	5:D:7:PHE:HB2	2.20	0.42
5:D:527:LEU:HD12	5:D:532:GLU:HG2	2.02	0.42
5:D:668:PHE:HB2	5:D:678:ARG:HG3	2.01	0.42
5:D:959:LYS:CG	5:D:985:ILE:HG13	2.47	0.42
6:F:214:PRO:HB2	6:F:218:ARG:HD3	2.02	0.42
6:F:324:LYS:HB3	6:F:325:PRO:HD2	2.01	0.42
1:H:58:DG:H2''	1:H:59:DC:C5'	2.50	0.42
2:J:72:SER:O	2:J:76:MET:HB3	2.19	0.42
3:A:59:VAL:HG12	3:A:60:GLU:N	2.35	0.42
3:A:98:VAL:HG11	3:A:121:VAL:HG21	2.01	0.42
3:A:98:VAL:HG12	3:A:99:ILE:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:100:LEU:HD23	3:B:144:ILE:CD1	2.49	0.42
4:C:314:ASN:HD22	4:C:351:LEU:HB3	1.84	0.42
4:C:318:SER:O	4:C:321:LEU:N	2.53	0.42
4:C:556:GLY:O	4:C:589:THR:OG1	2.35	0.42
4:C:719:LYS:O	4:C:719:LYS:HG2	2.20	0.42
4:C:1137:GLU:HG3	4:C:1138:VAL:H	1.85	0.42
4:C:1210:ILE:HG22	4:C:1211:ARG:H	1.84	0.42
4:C:1260:GLY:HA3	4:C:1265:PHE:HA	2.00	0.42
4:C:1319:MET:HG3	4:C:1320:PRO:HD2	2.01	0.42
5:D:1263:LYS:NZ	5:D:1315:ALA:O	2.36	0.42
5:D:1280:VAL:HG21	5:D:1304:ARG:HE	1.84	0.42
6:F:150:ARG:HB3	6:F:155:GLU:HB3	2.02	0.42
6:F:491:GLU:O	6:F:491:GLU:HG2	2.20	0.42
2:I:82:ARG:HD3	2:J:93:PRO:HB2	2.02	0.42
4:C:20:GLN:HG3	4:C:20:GLN:O	2.19	0.42
4:C:228:VAL:HG22	4:C:245:ARG:HH11	1.84	0.42
4:C:268:ARG:NH1	4:C:270:THR:HG22	2.34	0.42
4:C:299:LYS:CE	4:C:334:GLU:HB2	2.50	0.42
4:C:368:ARG:O	4:C:368:ARG:HG3	2.19	0.42
5:D:174:ASP:OD1	5:D:175:GLU:N	2.43	0.42
5:D:412:LEU:O	5:D:416:ILE:HG12	2.20	0.42
5:D:801:VAL:HG22	5:D:801:VAL:O	2.20	0.42
5:D:1024:THR:CG2	5:D:1123:ARG:HB3	2.50	0.42
5:D:1029:THR:HB	5:D:1121:LEU:CD1	2.45	0.42
6:F:561:MET:SD	6:F:576:VAL:HG13	2.60	0.42
1:H:20:DA:H61	7:G:43:DT:H3	1.68	0.42
2:I:62:LEU:O	2:I:68:THR:HA	2.20	0.42
2:I:127:ALA:O	2:I:130:LYS:HB2	2.20	0.42
2:J:41:VAL:HB	2:J:46:PRO:N	2.35	0.42
3:A:208:ASN:ND2	3:A:208:ASN:O	2.53	0.42
4:C:34:SER:OG	4:C:455:SER:HB2	2.19	0.42
4:C:145:ILE:HD12	4:C:512:SER:HB2	2.02	0.42
4:C:246:LEU:HA	4:C:249:GLU:CD	2.41	0.42
4:C:637:ARG:HA	4:C:641:GLU:O	2.20	0.42
4:C:822:VAL:O	4:C:822:VAL:HG12	2.20	0.42
4:C:985:GLU:O	4:C:989:LEU:HD22	2.20	0.42
4:C:1141:LEU:O	4:C:1145:ILE:HG13	2.20	0.42
5:D:1062:LEU:CD1	5:D:1067:ARG:HA	2.50	0.42
6:F:347:ILE:O	6:F:350:GLU:HB2	2.20	0.42
7:G:55:DT:H4'	7:G:56:DT:OP1	2.20	0.42
2:I:10:VAL:HG12	2:I:11:MET:H	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:96:ARG:O	2:I:99:SER:HB3	2.20	0.41
2:I:175:PHE:HD1	2:I:175:PHE:HA	1.71	0.41
2:J:194:ASP:HA	2:J:197:LEU:CB	2.47	0.41
4:C:148:GLN:HA	4:C:531:SER:O	2.20	0.41
4:C:191:LYS:O	4:C:193:ASN:ND2	2.53	0.41
4:C:390:PHE:HA	4:C:419:ILE:HG13	2.02	0.41
4:C:465:ARG:HG3	4:C:466:VAL:N	2.35	0.41
4:C:716:ALA:CB	4:C:784:ALA:HB3	2.48	0.41
5:D:426:ALA:HB3	5:D:427:PRO:CD	2.50	0.41
5:D:432:LEU:HD12	5:D:499:ILE:HG12	2.00	0.41
5:D:537:TYR:OH	5:D:634:ARG:NH1	2.53	0.41
5:D:1167:LYS:HZ2	5:D:1170:LYS:HD3	1.84	0.41
5:D:1330:ARG:O	5:D:1330:ARG:HG2	2.20	0.41
6:F:150:ARG:HB2	6:F:150:ARG:HE	1.54	0.41
6:F:402:LEU:HA	6:F:402:LEU:HD12	1.77	0.41
6:F:589:GLN:HA	6:F:592:ALA:HB3	2.02	0.41
2:I:68:THR:C	2:I:69:LEU:HD12	2.41	0.41
2:I:102:TYR:O	2:I:106:ILE:HG13	2.19	0.41
2:J:139:ILE:C	2:J:142:VAL:HG13	2.40	0.41
4:C:194:LEU:HD23	4:C:206:ALA:CB	2.51	0.41
4:C:296:VAL:HG13	4:C:336:LEU:HD12	2.02	0.41
4:C:490:GLN:NE2	6:F:472:GLN:HB3	2.35	0.41
4:C:715:THR:HG23	4:C:784:ALA:O	2.20	0.41
4:C:836:LEU:HD21	4:C:921:PRO:HD3	2.02	0.41
5:D:130:MET:HE1	5:D:157:GLN:CB	2.49	0.41
5:D:152:THR:HB	5:D:154:LEU:CD1	2.50	0.41
5:D:491:LEU:HD12	5:D:904:ALA:O	2.21	0.41
5:D:1029:THR:OG1	5:D:1080:ILE:HD11	2.20	0.41
6:F:141:ILE:O	6:F:145:LEU:CB	2.69	0.41
1:H:22:DG:C2'	1:H:23:DT:H72	2.50	0.41
2:I:183:LEU:O	2:I:186:TYR:HB3	2.20	0.41
2:I:204:GLU:HA	2:I:207:MET:CE	2.50	0.41
3:A:43:LEU:HD23	3:A:43:LEU:HA	1.77	0.41
4:C:479:LEU:HD12	4:C:484:LEU:HD21	2.02	0.41
5:D:291:ILE:HD13	6:F:409:ASN:HB3	2.01	0.41
5:D:572:THR:HG23	5:D:573:THR:O	2.19	0.41
5:D:604:MET:HG2	5:D:604:MET:O	2.20	0.41
5:D:899:TYR:HD2	5:D:909:ILE:HG21	1.85	0.41
5:D:930:LEU:HD11	5:D:1241:TYR:CE1	2.55	0.41
5:D:1109:LEU:HD23	5:D:1109:LEU:HA	1.80	0.41
5:D:1238:GLN:OE1	5:D:1238:GLN:HA	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1314:LEU:HD21	5:D:1331:VAL:HG22	2.02	0.41
2:I:166:TRP:CH2	2:I:208:ARG:HD3	2.55	0.41
2:J:10:VAL:CG1	2:J:65:ARG:HG2	2.50	0.41
2:J:196:PHE:O	2:J:200:LEU:HG	2.20	0.41
3:B:6:THR:C	3:B:7:GLU:HG3	2.40	0.41
4:C:871:VAL:HG22	4:C:872:TYR:N	2.35	0.41
4:C:1223:ARG:O	4:C:1223:ARG:HG3	2.20	0.41
5:D:120:LEU:HD12	5:D:1330:ARG:NH2	2.35	0.41
5:D:377:PHE:CD2	5:D:416:ILE:HD11	2.55	0.41
5:D:536:LEU:HD12	5:D:536:LEU:HA	1.71	0.41
5:D:1144:LEU:HD12	5:D:1144:LEU:O	2.19	0.41
5:D:1164:SER:HA	5:D:1200:GLU:OE2	2.21	0.41
5:D:1190:ILE:HG22	5:D:1191:PRO:O	2.20	0.41
5:D:1259:GLN:HE22	5:D:1262:ARG:NH1	2.17	0.41
5:D:1283:SER:O	5:D:1287:ILE:HB	2.20	0.41
6:F:404:LEU:HD23	6:F:404:LEU:HA	1.75	0.41
6:F:593:LYS:HA	6:F:596:ARG:HH12	1.85	0.41
3:A:193:GLU:OE2	3:A:194:GLN:HB3	2.20	0.41
4:C:419:ILE:HG12	4:C:420:LEU:N	2.34	0.41
4:C:777:VAL:HG11	4:C:783:LEU:HD21	2.01	0.41
4:C:866:ASP:HB3	4:C:872:TYR:CZ	2.56	0.41
5:D:735:ALA:HA	5:D:738:ARG:NH1	2.35	0.41
5:D:827:GLU:HB2	5:D:832:LYS:CG	2.45	0.41
5:D:868:TRP:CZ3	5:D:871:LEU:HD13	2.55	0.41
6:F:347:ILE:O	6:F:351:THR:HG22	2.20	0.41
3:B:23:HIS:ND1	3:B:206:GLU:HG2	2.36	0.41
3:B:126:PRO:HD2	3:B:127:GLN:OE1	2.20	0.41
4:C:109:ALA:HB1	4:C:110:PRO:CD	2.51	0.41
4:C:127:ILE:O	4:C:127:ILE:HG13	2.21	0.41
4:C:658:GLN:HE21	4:C:658:GLN:HB3	1.66	0.41
5:D:114:ILE:O	5:D:114:ILE:HD13	2.20	0.41
5:D:850:LYS:HG3	5:D:855:ASP:HB3	2.02	0.41
5:D:1268:ASN:HA	5:D:1274:PHE:CE2	2.56	0.41
6:F:121:LYS:HA	6:F:121:LYS:HD3	1.93	0.41
6:F:288:MET:CG	6:F:299:LYS:HD3	2.50	0.41
6:F:476:ARG:NH1	6:F:476:ARG:HB3	2.36	0.41
2:I:63:VAL:HG13	2:I:68:THR:HA	2.02	0.41
2:I:148:TYR:HB3	2:I:158:ASP:OD2	2.20	0.41
2:J:10:VAL:HG11	2:J:65:ARG:HG2	2.02	0.41
3:A:61:ILE:HD13	3:A:142:MET:HB3	2.03	0.41
4:C:240:GLU:HG2	4:C:241:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:303:ASP:CB	4:C:310:ILE:HD11	2.51	0.41
4:C:993:PRO:CG	4:C:996:ARG:HD3	2.51	0.41
5:D:287:ALA:HB2	6:F:413:MET:HE1	2.02	0.41
5:D:423:LEU:CD1	5:D:468:VAL:HG12	2.51	0.41
5:D:1150:PRO:HD2	5:D:1216:ALA:HB2	2.03	0.41
5:D:1237:VAL:HG12	5:D:1253:ILE:HD13	2.02	0.41
6:F:225:ARG:HD2	6:F:225:ARG:HA	1.76	0.41
6:F:470:MET:SD	6:F:486:ARG:HG3	2.60	0.41
2:I:17:PRO:HA	2:I:40:HIS:ND1	2.35	0.41
3:B:53:GLY:HA3	3:B:177:TYR:O	2.20	0.41
3:B:65:LEU:HD13	3:B:168:ILE:O	2.19	0.41
4:C:260:LYS:HB3	4:C:262:TYR:CE1	2.56	0.41
5:D:144:TYR:CZ	5:D:180:MET:HE3	2.55	0.41
5:D:460:ASP:OD1	5:D:460:ASP:N	2.35	0.41
5:D:754:ILE:HG22	5:D:755:ILE:O	2.21	0.41
5:D:1023:HIS:O	5:D:1125:PRO:HA	2.21	0.41
5:D:1189:MET:HE2	5:D:1191:PRO:HD3	2.03	0.41
6:F:336:GLU:HA	6:F:339:ARG:CG	2.49	0.41
1:H:38:DT:H4'	6:F:425:TYR:CE2	2.55	0.41
2:I:63:VAL:HG22	2:I:68:THR:HB	2.03	0.41
2:I:139:ILE:HG22	2:I:142:VAL:HG21	2.03	0.41
3:A:11:PRO:CA	3:A:30:PRO:HD2	2.51	0.41
3:A:191:ARG:HD3	3:A:191:ARG:HA	1.83	0.41
3:B:127:GLN:OE1	3:B:127:GLN:N	2.50	0.41
4:C:202:ARG:HG2	4:C:203:LYS:N	2.36	0.41
4:C:239:MET:CE	4:C:241:LEU:HD13	2.51	0.41
4:C:253:PHE:O	4:C:255:ILE:HD12	2.20	0.41
4:C:322:LEU:HA	4:C:325:LEU:HB2	2.02	0.41
4:C:339:ASN:OD1	4:C:339:ASN:N	2.54	0.41
4:C:530:ILE:O	4:C:530:ILE:HG22	2.20	0.41
4:C:672:GLU:HB3	4:C:1187:PHE:CE1	2.55	0.41
4:C:843:THR:HG22	4:C:845:LEU:N	2.31	0.41
4:C:1017:GLN:HE21	4:C:1017:GLN:N	2.19	0.41
4:C:1149:TYR:CG	4:C:1159:VAL:HG11	2.56	0.41
4:C:1164:PHE:HB2	4:C:1168:GLU:HB3	2.02	0.41
5:D:19:ALA:HB1	5:D:1341:ARG:CG	2.50	0.41
5:D:490:ILE:HD11	5:D:609:TYR:CE1	2.55	0.41
5:D:552:ILE:HD12	5:D:589:TYR:CE1	2.55	0.41
5:D:682:VAL:HA	5:D:685:ILE:CG2	2.50	0.41
5:D:805:GLN:HB3	5:D:806:ASP:OD1	2.21	0.41
6:F:139:GLU:HG3	6:F:351:THR:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:371:LYS:HD3	6:F:371:LYS:O	2.21	0.41
6:F:505:ILE:HD13	6:F:505:ILE:HA	1.89	0.41
7:G:54:DT:C2	7:G:55:DT:H1'	2.56	0.41
2:I:26:ARG:HD3	2:I:199:SER:O	2.20	0.41
2:J:187:MET:O	2:J:191:PHE:HB2	2.21	0.41
3:A:52:PRO:HG2	3:A:219:ARG:NH2	2.36	0.41
3:A:133:LEU:HD12	3:A:138:ALA:CB	2.51	0.41
3:A:133:LEU:HD12	3:A:138:ALA:HB1	2.03	0.41
3:B:164:ASP:N	3:B:164:ASP:OD1	2.54	0.41
3:B:192:VAL:O	3:B:192:VAL:HG13	2.21	0.41
4:C:61:SER:HB3	4:C:479:LEU:HD23	2.03	0.41
4:C:616:ILE:HA	4:C:652:TYR:O	2.20	0.41
5:D:92:VAL:HG23	5:D:92:VAL:O	2.20	0.41
5:D:154:LEU:HD22	5:D:176:PHE:HE1	1.85	0.41
5:D:670:SER:O	5:D:672:LEU:HD12	2.21	0.41
5:D:1031:VAL:HG11	5:D:1088:VAL:CG1	2.51	0.41
6:F:283:GLN:HG3	6:F:284:GLU:N	2.35	0.41
8:E:76:GLU:C	8:E:79:GLU:H	2.24	0.41
2:J:137:LEU:HD12	2:J:137:LEU:H	1.86	0.40
4:C:296:VAL:HG21	4:C:314:ASN:HA	2.03	0.40
4:C:387:ASN:HA	4:C:391:SER:HB3	2.03	0.40
4:C:844:LYS:H	4:C:844:LYS:CE	2.34	0.40
4:C:1210:ILE:HD12	4:C:1227:VAL:HG21	2.04	0.40
5:D:279:LEU:O	5:D:279:LEU:HD12	2.21	0.40
5:D:453:VAL:HG12	5:D:457:TYR:HE1	1.86	0.40
5:D:816:THR:OG1	5:D:889:ASP:HB2	2.21	0.40
6:F:160:ASP:O	6:F:264:LYS:HB2	2.21	0.40
7:G:42:DT:H6	7:G:42:DT:H2'	1.66	0.40
8:E:59:ILE:HD13	8:E:59:ILE:HA	1.97	0.40
1:H:19:DA:H2''	1:H:20:DA:O5'	2.21	0.40
2:I:102:TYR:HD2	2:I:157:VAL:HG21	1.86	0.40
3:B:73:GLY:O	3:B:134:THR:HG23	2.21	0.40
4:C:34:SER:O	4:C:457:GLY:HA3	2.21	0.40
4:C:82:VAL:O	4:C:85:CYS:N	2.50	0.40
4:C:899:GLU:O	4:C:902:LEU:N	2.54	0.40
5:D:114:ILE:HB	5:D:304:ASP:CG	2.41	0.40
5:D:447:ILE:HD13	5:D:468:VAL:HG11	2.03	0.40
5:D:850:LYS:CE	5:D:875:ASN:HD21	2.34	0.40
5:D:956:GLY:CA	5:D:1010:GLN:HG3	2.51	0.40
5:D:1078:LEU:HG	5:D:1101:LEU:HD11	2.03	0.40
6:F:127:ILE:H	6:F:127:ILE:HG13	1.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:248:GLU:HA	6:F:251:LYS:HB2	2.03	0.40
6:F:250:LEU:HD23	6:F:250:LEU:HA	1.90	0.40
6:F:479:THR:CG2	6:F:482:GLU:HG3	2.51	0.40
8:E:69:ARG:O	8:E:69:ARG:HG2	2.20	0.40
2:I:9:SER:OG	2:I:65:ARG:NH2	2.54	0.40
2:I:180:ALA:O	2:I:184:LYS:N	2.38	0.40
2:J:41:VAL:HB	2:J:46:PRO:CD	2.51	0.40
2:J:165:LEU:HD13	2:J:165:LEU:HA	1.90	0.40
3:A:27:THR:HA	3:A:201:LEU:O	2.22	0.40
4:C:22:LEU:HB3	4:C:655:VAL:HG11	2.03	0.40
4:C:242:VAL:CG2	4:C:245:ARG:HB2	2.49	0.40
4:C:864:LYS:HD2	4:C:875:ALA:HB1	2.03	0.40
4:C:1114:GLU:O	4:C:1114:GLU:HG2	2.20	0.40
5:D:968:ASN:ND2	5:D:970:SER:OG	2.50	0.40
5:D:972:LYS:HB2	5:D:1002:VAL:HG23	2.03	0.40
6:F:289:LYS:HA	6:F:293:GLU:OE1	2.21	0.40
6:F:586:ARG:HE	6:F:590:ILE:HG12	1.85	0.40
1:H:11:DG:H4'	3:K:264:VAL:HG21	2.03	0.40
1:H:33:DT:H72	6:F:441:ARG:NH2	2.36	0.40
2:I:166:TRP:NE1	2:I:200:LEU:HD21	2.36	0.40
3:B:104:LYS:HB3	3:B:140:ILE:HG23	2.03	0.40
4:C:189:ASP:OD1	4:C:193:ASN:N	2.48	0.40
4:C:200:ARG:HD3	4:C:200:ARG:HA	1.77	0.40
4:C:268:ARG:NH2	4:C:270:THR:HG22	2.36	0.40
4:C:285:ILE:HD12	4:C:286:GLU:N	2.36	0.40
4:C:1020:GLU:O	4:C:1025:PHE:N	2.41	0.40
5:D:297:ARG:NH1	6:F:100:MET:HE2	2.34	0.40
5:D:680:ASN:N	5:D:680:ASN:OD1	2.53	0.40
5:D:955:LYS:HG2	5:D:1010:GLN:CB	2.47	0.40
5:D:955:LYS:NZ	5:D:1012:ALA:HA	2.37	0.40
5:D:1348:LYS:O	5:D:1348:LYS:HG2	2.21	0.40
6:F:166:VAL:HG12	6:F:260:ARG:CZ	2.51	0.40
6:F:343:LYS:HA	6:F:343:LYS:HD3	1.85	0.40
8:E:84:THR:CG2	8:E:88:GLU:OE2	2.69	0.40
2:I:16:GLY:HA2	2:I:17:PRO:HD3	1.90	0.40
2:I:191:PHE:HA	2:I:196:PHE:CD2	2.57	0.40
2:J:55:PRO:HG3	5:D:4:LEU:CD1	2.52	0.40
2:J:167:ARG:HD2	2:J:207:MET:SD	2.61	0.40
4:C:378:ARG:HB3	4:C:379:GLU:OE1	2.21	0.40
4:C:836:LEU:HD13	4:C:1054:LEU:CD1	2.51	0.40
4:C:1066:MET:CE	4:C:1232:MET:HB3	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:120:LEU:HA	5:D:120:LEU:HD23	1.88	0.40
5:D:289:ASP:OD1	5:D:289:ASP:N	2.54	0.40
5:D:490:ILE:HD11	5:D:614:LEU:CD1	2.50	0.40
5:D:527:LEU:HD13	5:D:527:LEU:HA	1.71	0.40
5:D:951:GLN:OE1	5:D:1016:THR:HG23	2.22	0.40
5:D:1247:LYS:HB3	5:D:1247:LYS:HE2	1.78	0.40
6:F:111:LEU:CD1	6:F:115:GLY:HA3	2.37	0.40
6:F:232:ARG:HD2	6:F:236:LYS:HB3	2.03	0.40
6:F:234:THR:HB	6:F:244:THR:CG2	2.41	0.40
6:F:474:MET:HE3	6:F:474:MET:HB2	1.44	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	
2	I	204/212 (96%)	174 (85%)	30 (15%)	0	100	100
2	J	199/212 (94%)	175 (88%)	24 (12%)	0	100	100
3	A	228/329 (69%)	195 (86%)	33 (14%)	0	100	100
3	B	222/329 (68%)	187 (84%)	35 (16%)	0	100	100
3	K	63/329 (19%)	55 (87%)	8 (13%)	0	100	100
4	C	1338/1342 (100%)	1116 (83%)	222 (17%)	0	100	100
5	D	1345/1407 (96%)	1153 (86%)	192 (14%)	0	100	100
6	F	466/613 (76%)	420 (90%)	46 (10%)	0	100	100
8	E	88/91 (97%)	79 (90%)	9 (10%)	0	100	100
All	All	4153/4864 (85%)	3554 (86%)	599 (14%)	0	100	100

There are no Ramachandran outliers to report.

### 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	
2	I	182/187 (97%)	165 (91%)	17 (9%)	7	29
2	J	179/187 (96%)	160 (89%)	19 (11%)	5	25
3	A	198/286 (69%)	172 (87%)	26 (13%)	3	18
3	B	194/286 (68%)	168 (87%)	26 (13%)	3	17
3	K	58/286 (20%)	50 (86%)	8 (14%)	3	17
4	C	1155/1157 (100%)	1013 (88%)	142 (12%)	4	19
5	D	1115/1168 (96%)	977 (88%)	138 (12%)	4	19
6	F	420/540 (78%)	359 (86%)	61 (14%)	2	15
8	E	74/75 (99%)	68 (92%)	6 (8%)	9	34
All	All	3575/4172 (86%)	3132 (88%)	443 (12%)	6	19

All (443) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	26	ARG
2	I	28	VAL
2	I	32	LYS
2	I	38	ILE
2	I	53	LEU
2	I	63	VAL
2	I	68	THR
2	I	152	ASP
2	I	170	GLN
2	I	171	LEU
2	I	175	PHE
2	I	182	GLU
2	I	192	GLU
2	I	194	ASP
2	I	196	PHE
2	I	200	LEU
2	I	207	MET
2	J	15	SER

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Mol	Chain	Res	Type
2	J	38	ILE
2	J	51	ILE
2	J	74	ILE
2	J	81	GLU
2	J	82	ARG
2	J	92	TYR
2	J	106	ILE
2	J	132	LEU
2	J	137	LEU
2	J	139	ILE
2	J	142	VAL
2	J	146	LYS
2	J	153	GLU
2	J	158	ASP
2	J	167	ARG
2	J	183	LEU
2	J	192	GLU
2	J	202	GLU
3	K	254	LEU
3	K	277	TYR
3	K	280	ASP
3	K	281	LEU
3	K	285	THR
3	K	289	LEU
3	K	303	ILE
3	K	313	SER
3	A	8	PHE
3	A	12	ARG
3	A	13	LEU
3	A	22	THR
3	A	23	HIS
3	A	26	VAL
3	A	33	ARG
3	A	54	CYS
3	A	61	ILE
3	A	70	THR
3	A	74	VAL
3	A	77	ASP
3	A	96	ASP
3	A	129	VAL
3	A	134	THR
3	A	158	ARG

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Mol	Chain	Res	Type
3	A	162	GLU
3	A	177	TYR
3	A	178	SER
3	A	192	VAL
3	A	195	ARG
3	A	204	GLU
3	A	211	ILE
3	A	212	ASP
3	A	222	THR
3	A	236	ASP
3	B	7	GLU
3	B	9	LEU
3	B	27	THR
3	B	29	GLU
3	B	32	GLU
3	B	33	ARG
3	B	38	THR
3	B	54	CYS
3	B	68	TYR
3	B	77	ASP
3	B	83	LEU
3	B	91	ARG
3	B	92	VAL
3	B	98	VAL
3	B	100	LEU
3	B	111	THR
3	B	120	ASP
3	B	133	LEU
3	B	146	VAL
3	B	180	VAL
3	B	183	ILE
3	B	198	LEU
3	B	203	ILE
3	B	214	GLU
3	B	222	THR
3	B	233	ASP
4	C	3	TYR
4	C	4	SER
4	C	6	THR
4	C	8	LYS
4	C	9	LYS
4	C	18	ARG

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Mol	Chain	Res	Type
4	C	21	VAL
4	C	30	ILE
4	C	32	LEU
4	C	40	GLU
4	C	62	TYR
4	C	74	ARG
4	C	79	VAL
4	C	81	ASP
4	C	83	GLN
4	C	91	THR
4	C	97	ARG
4	C	111	GLU
4	C	113	THR
4	C	122	VAL
4	C	132	ASP
4	C	135	THR
4	C	139	ASN
4	C	141	THR
4	C	161	LYS
4	C	164	THR
4	C	177	ILE
4	C	194	LEU
4	C	196	VAL
4	C	199	ASP
4	C	207	THR
4	C	229	ILE
4	C	231	GLU
4	C	274	ILE
4	C	280	ASP
4	C	281	ASP
4	C	285	ILE
4	C	286	GLU
4	C	290	GLU
4	C	299	LYS
4	C	300	ASP
4	C	335	THR
4	C	337	PHE
4	C	338	THR
4	C	347	ILE
4	C	364	VAL
4	C	392	GLU
4	C	393	ASP

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Mol	Chain	Res	Type
4	C	419	ILE
4	C	423	ASP
4	C	424	ASP
4	C	439	LYS
4	C	441	GLU
4	C	443	ASP
4	C	448	LEU
4	C	465	ARG
4	C	466	VAL
4	C	468	LEU
4	C	471	VAL
4	C	472	GLU
4	C	473	ARG
4	C	475	VAL
4	C	514	PHE
4	C	522	SER
4	C	524	ILE
4	C	540	ARG
4	C	541	GLU
4	C	622	ASN
4	C	626	GLU
4	C	632	ASP
4	C	663	VAL
4	C	672	GLU
4	C	681	MET
4	C	687	ARG
4	C	694	ARG
4	C	699	LEU
4	C	702	THR
4	C	704	MET
4	C	724	VAL
4	C	740	GLU
4	C	748	ILE
4	C	749	ASP
4	C	750	ILE
4	C	754	THR
4	C	758	ARG
4	C	759	SER
4	C	765	ILE
4	C	779	ARG
4	C	781	ASP
4	C	790	ASP

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Mol	Chain	Res	Type
4	C	791	LEU
4	C	827	ARG
4	C	835	GLU
4	C	841	ARG
4	C	844	LYS
4	C	850	ILE
4	C	851	THR
4	C	865	LEU
4	C	877	VAL
4	C	881	ASP
4	C	890	LYS
4	C	895	LEU
4	C	905	ILE
4	C	915	ASP
4	C	919	ARG
4	C	924	VAL
4	C	946	LEU
4	C	949	GLU
4	C	959	ASP
4	C	962	GLU
4	C	995	ASP
4	C	1008	GLN
4	C	1013	GLN
4	C	1017	GLN
4	C	1018	TYR
4	C	1019	ASP
4	C	1026	GLU
4	C	1028	LYS
4	C	1029	LEU
4	C	1033	ARG
4	C	1037	THR
4	C	1041	ASP
4	C	1047	LEU
4	C	1057	LYS
4	C	1058	ARG
4	C	1096	ILE
4	C	1134	GLN
4	C	1135	GLN
4	C	1157	GLN
4	C	1158	LYS
4	C	1161	LEU
4	C	1174	GLU

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Mol	Chain	Res	Type
4	C	1198	LEU
4	C	1217	THR
4	C	1227	VAL
4	C	1246	ARG
4	C	1254	VAL
4	C	1259	LEU
4	C	1274	GLU
4	C	1289	GLU
4	C	1316	GLU
4	C	1337	ILE
5	D	7	PHE
5	D	9	LYS
5	D	17	PHE
5	D	24	LEU
5	D	39	LYS
5	D	46	TYR
5	D	48	THR
5	D	56	LEU
5	D	80	HIS
5	D	86	GLU
5	D	109	SER
5	D	111	THR
5	D	114	ILE
5	D	134	ASP
5	D	165	TYR
5	D	172	PHE
5	D	186	GLN
5	D	193	ASP
5	D	194	LEU
5	D	205	LEU
5	D	216	LYS
5	D	218	THR
5	D	232	ASN
5	D	237	MET
5	D	242	LEU
5	D	244	VAL
5	D	248	ASP
5	D	255	LEU
5	D	289	ASP
5	D	292	VAL
5	D	301	GLU
5	D	306	LEU

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Mol	Chain	Res	Type
5	D	316	ILE
5	D	337	ARG
5	D	347	VAL
5	D	350	SER
5	D	352	ARG
5	D	353	SER
5	D	368	LEU
5	D	387	LEU
5	D	401	VAL
5	D	404	GLU
5	D	413	ASP
5	D	422	LEU
5	D	424	ASN
5	D	431	ARG
5	D	434	ILE
5	D	460	ASP
5	D	472	LEU
5	D	473	THR
5	D	489	ASN
5	D	506	VAL
5	D	526	VAL
5	D	527	LEU
5	D	528	THR
5	D	532	GLU
5	D	535	ARG
5	D	537	TYR
5	D	545	HIS
5	D	548	VAL
5	D	558	ASP
5	D	563	LEU
5	D	573	THR
5	D	582	ILE
5	D	594	GLN
5	D	603	LYS
5	D	617	THR
5	D	618	VAL
5	D	661	VAL
5	D	674	THR
5	D	678	ARG
5	D	685	ILE
5	D	707	ILE
5	D	709	ARG

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Mol	Chain	Res	Type
5	D	710	ASP
5	D	713	GLU
5	D	721	SER
5	D	724	MET
5	D	746	LEU
5	D	751	ASP
5	D	759	ILE
5	D	760	THR
5	D	765	GLU
5	D	769	VAL
5	D	780	ARG
5	D	797	THR
5	D	806	ASP
5	D	814	CYS
5	D	847	ASP
5	D	849	LEU
5	D	853	THR
5	D	857	LEU
5	D	872	LEU
5	D	885	VAL
5	D	891	ASP
5	D	911	LYS
5	D	918	ILE
5	D	925	GLU
5	D	930	LEU
5	D	961	SER
5	D	981	GLU
5	D	986	ASP
5	D	993	GLU
5	D	999	TYR
5	D	1002	VAL
5	D	1020	TRP
5	D	1024	THR
5	D	1025	MET
5	D	1027	VAL
5	D	1029	THR
5	D	1036	ARG
5	D	1037	PHE
5	D	1042	ASP
5	D	1050	THR
5	D	1054	THR
5	D	1056	LEU

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Mol	Chain	Res	Type
5	D	1082	ASP
5	D	1115	ILE
5	D	1140	ARG
5	D	1167	LYS
5	D	1174	ARG
5	D	1180	VAL
5	D	1202	GLU
5	D	1206	ARG
5	D	1234	VAL
5	D	1235	ASN
5	D	1250	ASP
5	D	1266	ILE
5	D	1275	LEU
5	D	1281	GLU
5	D	1307	LEU
5	D	1309	ILE
5	D	1325	PHE
5	D	1333	THR
5	D	1342	ASP
5	D	1351	VAL
5	D	1365	TYR
5	D	1366	HIS
6	F	90	GLU
6	F	121	LYS
6	F	125	ASP
6	F	131	GLN
6	F	134	VAL
6	F	143	TYR
6	F	152	GLU
6	F	157	ARG
6	F	158	LEU
6	F	160	ASP
6	F	166	VAL
6	F	220	LYS
6	F	225	ARG
6	F	232	ARG
6	F	234	THR
6	F	250	LEU
6	F	255	VAL
6	F	265	GLN
6	F	266	PHE
6	F	268	TYR

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Mol	Chain	Res	Type
6	F	270	VAL
6	F	278	ASP
6	F	281	ARG
6	F	283	GLN
6	F	301	ASN
6	F	320	ILE
6	F	337	VAL
6	F	339	ARG
6	F	341	LEU
6	F	342	GLN
6	F	351	THR
6	F	359	LYS
6	F	361	ILE
6	F	362	ASN
6	F	378	GLU
6	F	384	LEU
6	F	390	ILE
6	F	405	ILE
6	F	429	THR
6	F	433	TRP
6	F	442	SER
6	F	446	GLN
6	F	452	ILE
6	F	465	ARG
6	F	479	THR
6	F	488	LEU
6	F	513	ASP
6	F	525	ASP
6	F	533	ASP
6	F	536	THR
6	F	537	THR
6	F	540	LEU
6	F	551	LEU
6	F	554	ARG
6	F	558	VAL
6	F	588	ARG
6	F	589	GLN
6	F	603	ARG
6	F	605	GLU
6	F	607	LEU
6	F	612	ASP
8	E	18	ASP

*Continued on next page...*

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Mol	Chain	Res	Type
8	E	21	LEU
8	E	46	THR
8	E	48	VAL
8	E	58	LEU
8	E	68	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
2	J	45	ASN
3	A	147	GLN
3	A	194	GLN
3	A	208	ASN
3	B	84	ASN
3	B	93	GLN
3	B	132	HIS
4	C	60	GLN
4	C	120	GLN
4	C	139	ASN
4	C	219	GLN
4	C	314	ASN
4	C	327	GLN
4	C	343	HIS
4	C	463	GLN
4	C	490	GLN
4	C	658	GLN
4	C	659	GLN
4	C	673	HIS
4	C	834	GLN
4	C	856	ASN
4	C	894	GLN
4	C	1017	GLN
4	C	1023	HIS
4	C	1090	ASN
4	C	1111	GLN
4	C	1157	GLN
4	C	1220	GLN
4	C	1268	GLN
4	C	1336	ASN
5	D	186	GLN
5	D	294	ASN
5	D	419	HIS

*Continued on next page...*



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Mol	Chain	Res	Type
5	D	477	GLN
5	D	495	ASN
5	D	560	ASN
5	D	594	GLN
5	D	669	GLN
5	D	777	HIS
5	D	867	GLN
5	D	954	ASN
5	D	1010	GLN
6	F	128	ASN
6	F	131	GLN
6	F	265	GLN
6	F	283	GLN
6	F	342	GLN
6	F	362	ASN
6	F	455	HIS
6	F	464	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

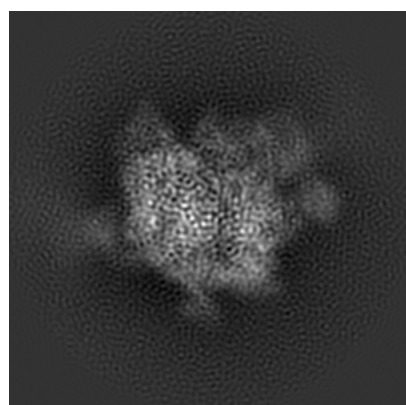
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30914. These allow visual inspection of the internal detail of the map and identification of artifacts.

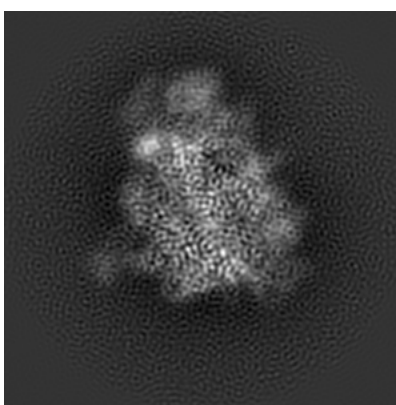
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

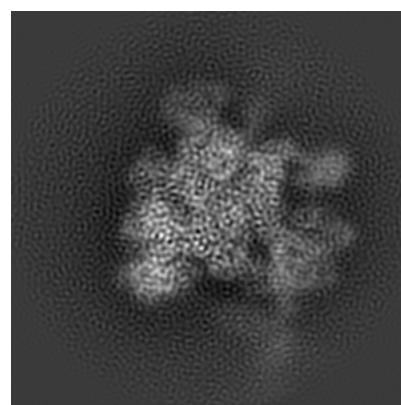
#### 6.1.1 Primary map



X



Y

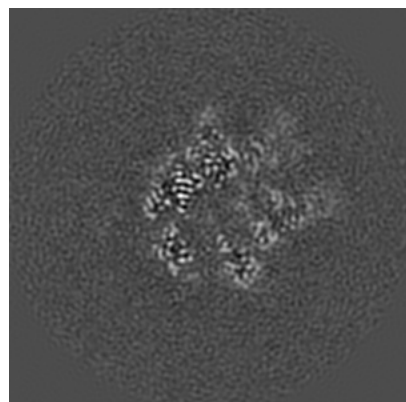


Z

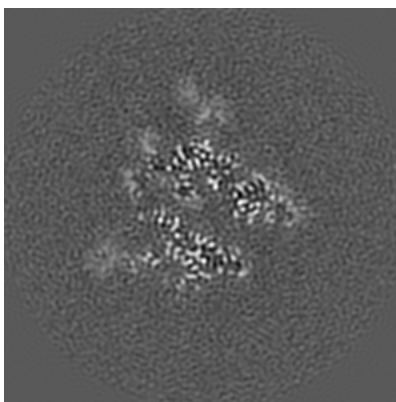
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

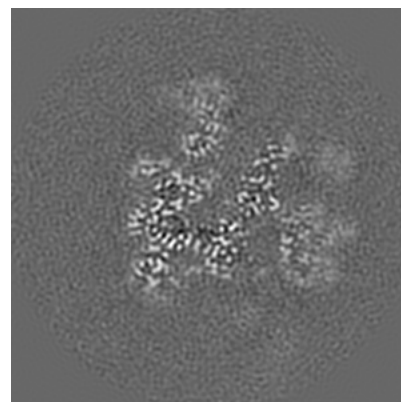
#### 6.2.1 Primary map



X Index: 100



Y Index: 100

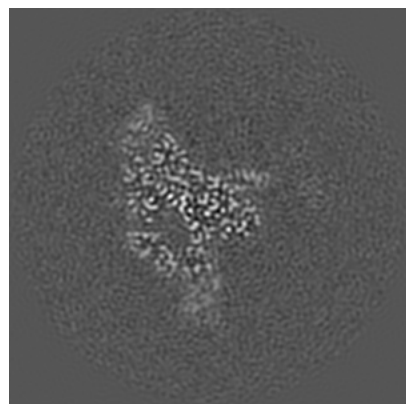


Z Index: 100

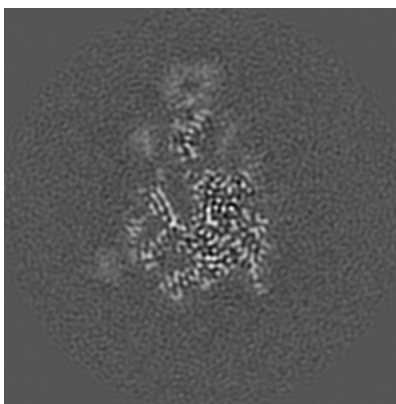
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

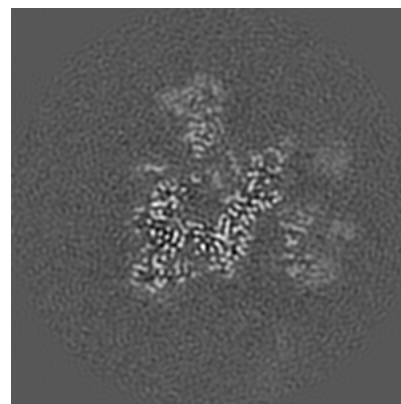
### 6.3.1 Primary map



X Index: 74



Y Index: 87

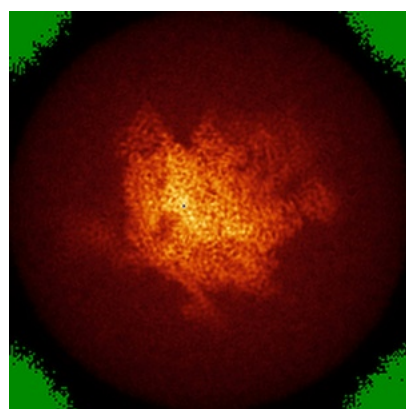


Z Index: 103

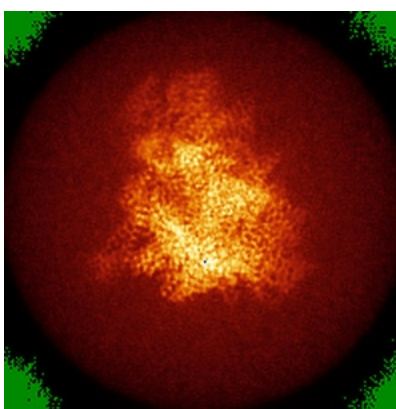
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

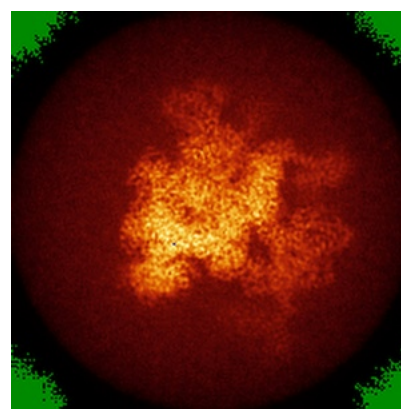
### 6.4.1 Primary map



X



Y

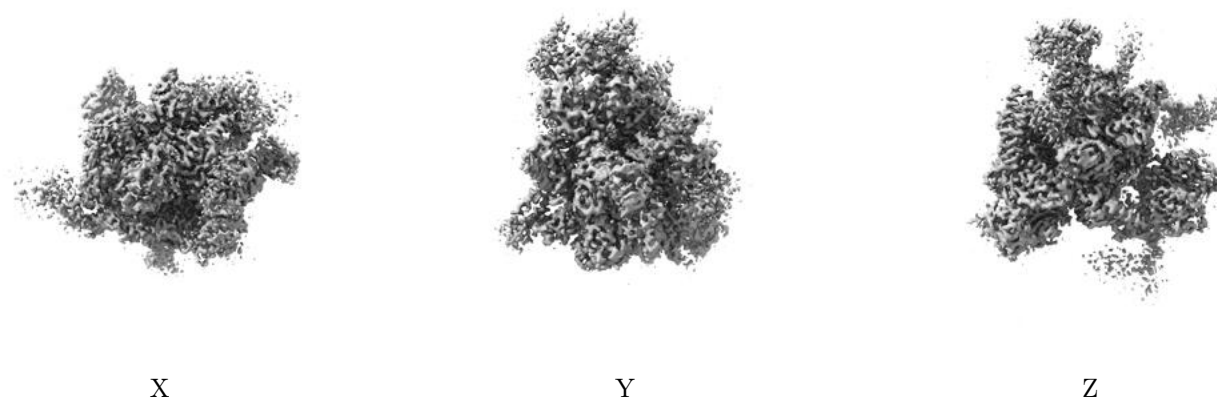


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

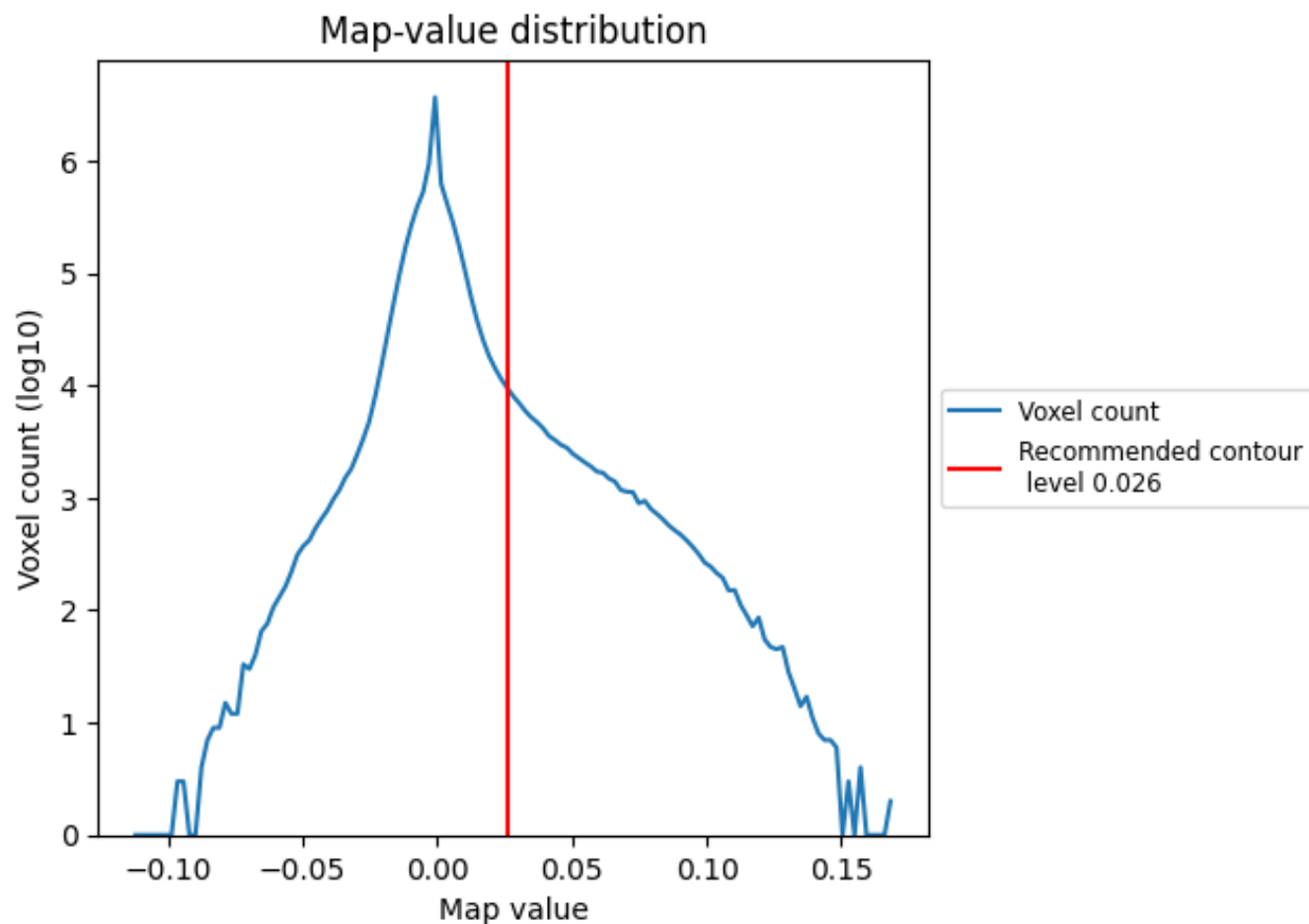
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

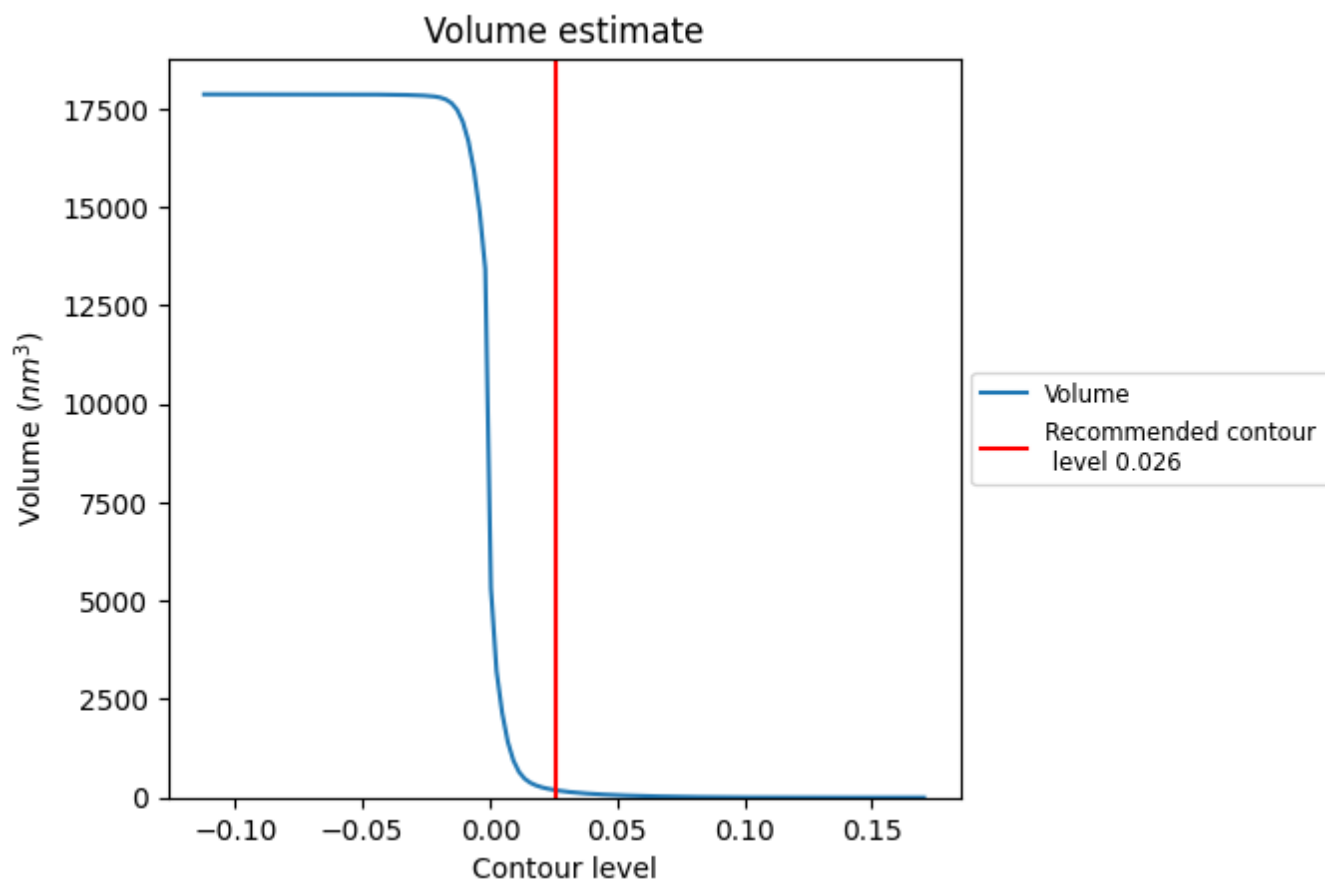
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

## 7.2 Volume estimate [i](#)

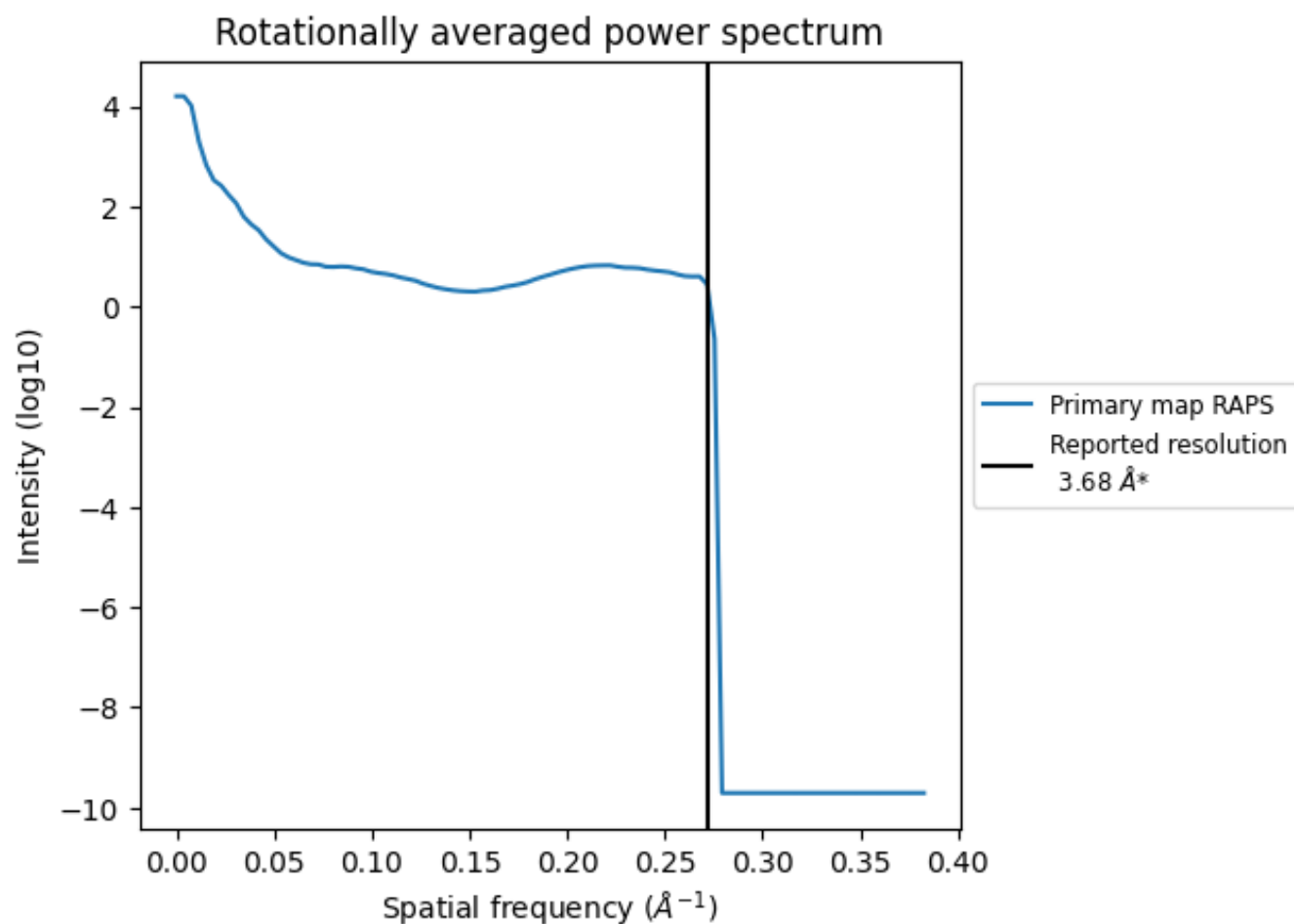


The volume at the recommended contour level is 186 nm<sup>3</sup>; this corresponds to an approximate mass of 168 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.272 Å<sup>-1</sup>

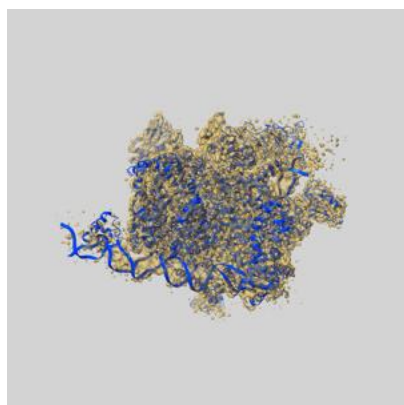
## 8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

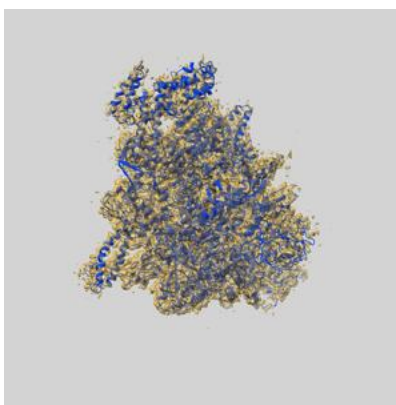
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30914 and PDB model 7DY6. Per-residue inclusion information can be found in section [3](#) on page [6](#).

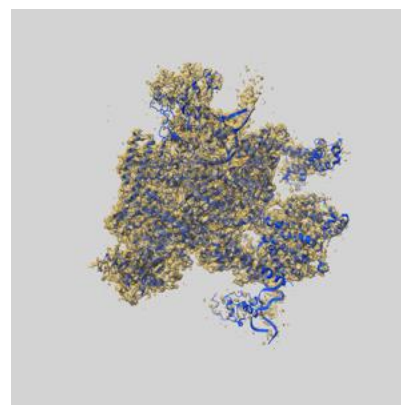
### 9.1 Map-model overlay [i](#)



X



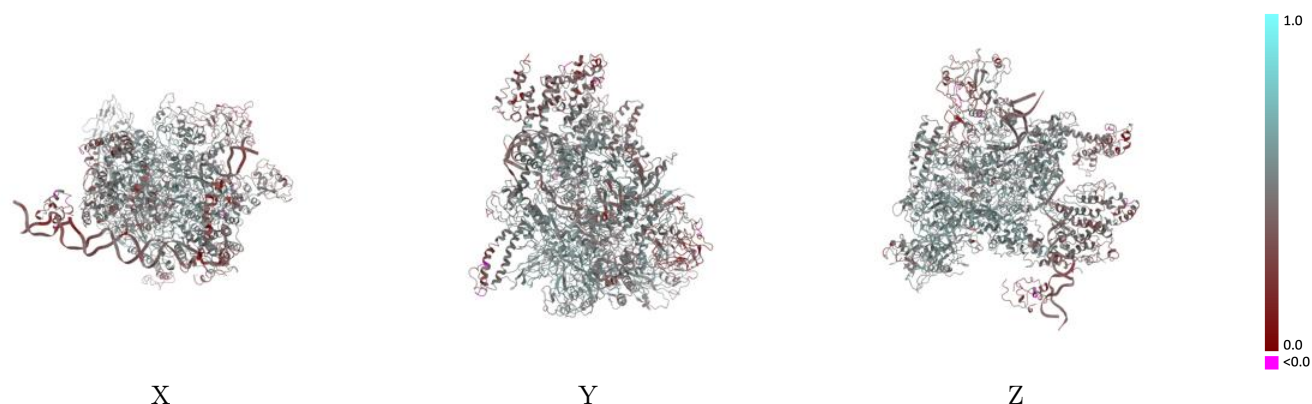
Y



Z

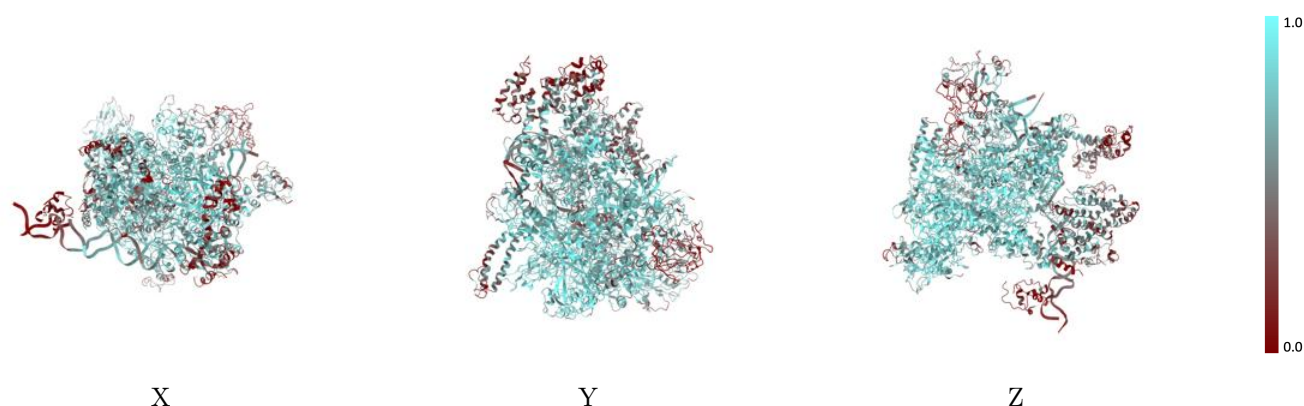
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



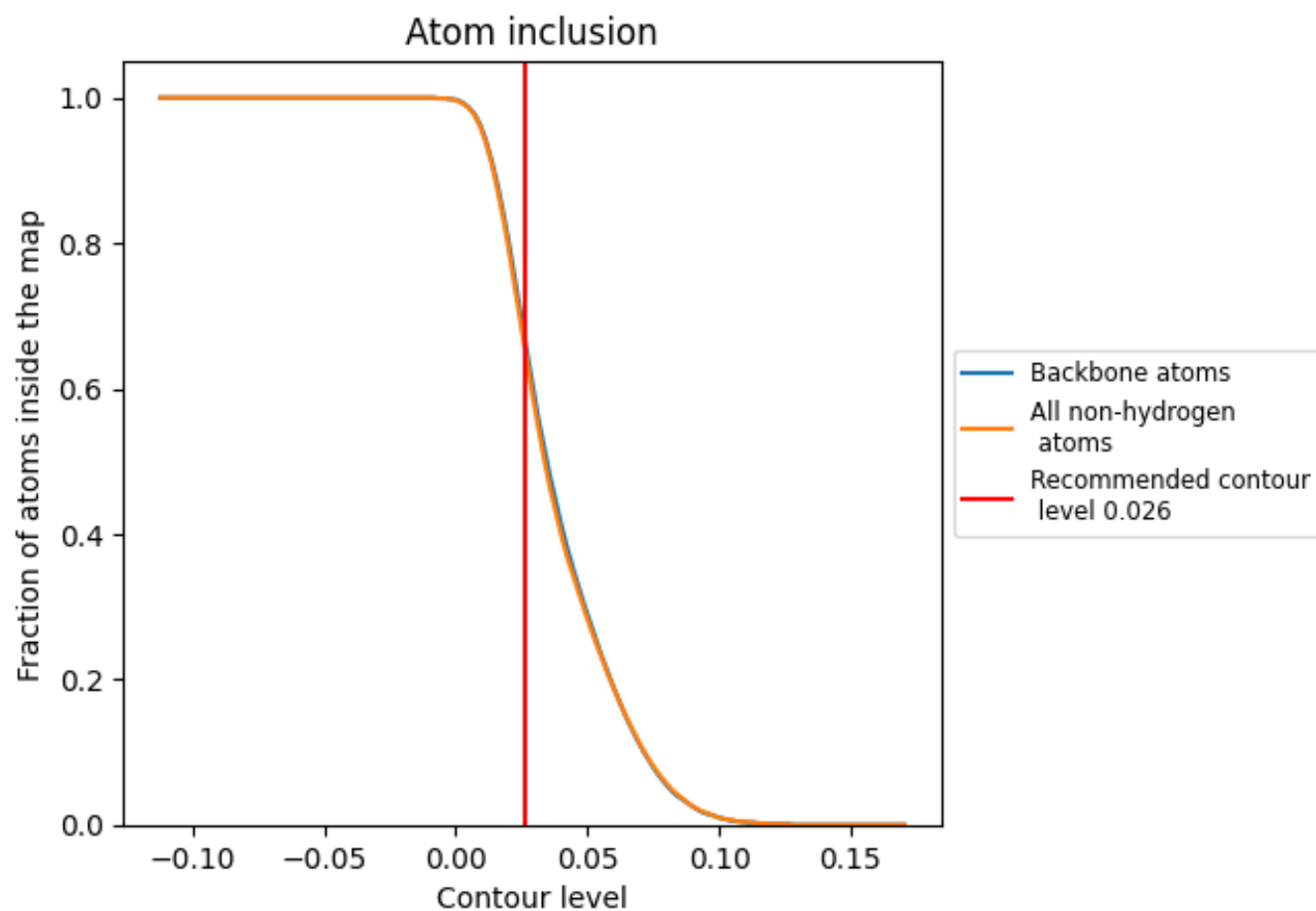
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.026).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6590	<div></div> 0.4740
A	<div></div> 0.7770	<div></div> 0.5270
B	<div></div> 0.6960	<div></div> 0.4880
C	<div></div> 0.7530	<div></div> 0.5080
D	<div></div> 0.6920	<div></div> 0.4910
E	<div></div> 0.6660	<div></div> 0.4910
F	<div></div> 0.5170	<div></div> 0.4240
G	<div></div> 0.5550	<div></div> 0.3680
H	<div></div> 0.5080	<div></div> 0.3730
I	<div></div> 0.5320	<div></div> 0.4350
J	<div></div> 0.5470	<div></div> 0.4360
K	<div></div> 0.0630	<div></div> 0.2560

1.0

0.0

<0.0