



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:38 PM UTC

PDB ID : 6PSV / pdb_00006psv
EMDB ID : EMD-20465
Title : Escherichia coli RNA polymerase promoter unwinding intermediate (TpreR_{Po})
with TraR and rpsT P2 promoter
Authors : Chen, J.; Chiu, C.E.; Campbell, E.A.; Darst, S.A.
Deposited on : 2019-07-13
Resolution : 3.50 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

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>.

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

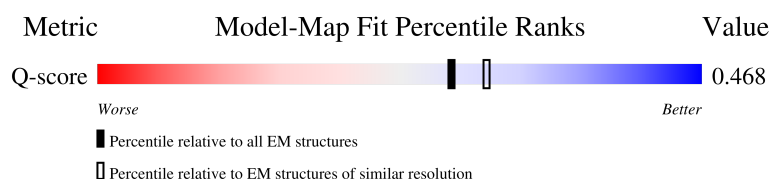
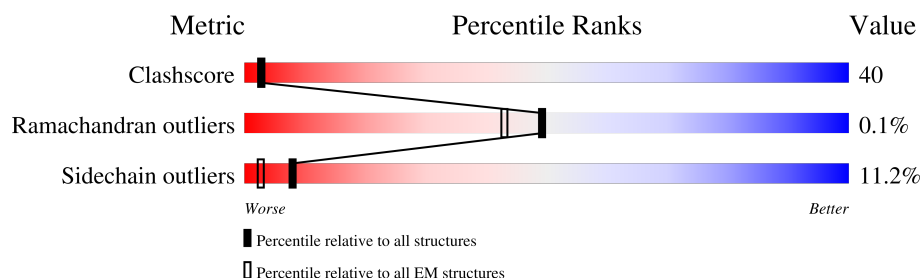
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



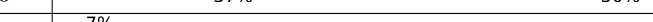
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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 ≥ 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	N	72	
2	G	329	
2	H	329	
2	M	329	

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Mol	Chain	Length	Quality of chain
3	I	1342	
4	J	1430	
5	K	91	
6	L	616	
7	O	85	
8	P	85	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 32487 atoms, of which 156 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Protein TraR.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	72	Total	C	N	O	S	0	0
			571	353	105	108	5		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	228	Total	C	N	O	S	0	0
			1761	1099	312	344	6		
2	H	219	Total	C	N	O	S	0	0
			1664	1040	291	327	6		
2	M	73	Total	C	N	O	S	0	0
			572	362	100	108	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	1340	Total	C	N	O	S	0	0
			10564	6628	1838	2055	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	1345	Total	C	N	O	S	0	0
			10466	6577	1867	1972	50		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	VAL	-	expression tag	UNP P0A8T7
J	1408	LEU	-	expression tag	UNP P0A8T7
J	1409	GLU	-	expression tag	UNP P0A8T7
J	1410	LEU	-	expression tag	UNP P0A8T7
J	1411	GLU	-	expression tag	UNP P0A8T7

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1412	VAL	-	expression tag	UNP P0A8T7
J	1413	LEU	-	expression tag	UNP P0A8T7
J	1414	PHE	-	expression tag	UNP P0A8T7
J	1415	GLN	-	expression tag	UNP P0A8T7
J	1416	GLY	-	expression tag	UNP P0A8T7
J	1417	PRO	-	expression tag	UNP P0A8T7
J	1418	SER	-	expression tag	UNP P0A8T7
J	1419	SER	-	expression tag	UNP P0A8T7
J	1420	GLY	-	expression tag	UNP P0A8T7
J	1421	HIS	-	expression tag	UNP P0A8T7
J	1422	HIS	-	expression tag	UNP P0A8T7
J	1423	HIS	-	expression tag	UNP P0A8T7
J	1424	HIS	-	expression tag	UNP P0A8T7
J	1425	HIS	-	expression tag	UNP P0A8T7
J	1426	HIS	-	expression tag	UNP P0A8T7
J	1427	HIS	-	expression tag	UNP P0A8T7
J	1428	HIS	-	expression tag	UNP P0A8T7
J	1429	HIS	-	expression tag	UNP P0A8T7
J	1430	HIS	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	474	Total	C	N	O	S	0	0
			3846	2409	685	729	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-2	SER	-	expression tag	UNP Q0P6L9
L	-1	GLU	-	expression tag	UNP Q0P6L9
L	0	PHE	-	expression tag	UNP Q0P6L9

- Molecule 7 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	55	Total	C	N	O	P	0	0
			1128	539	211	323	55		

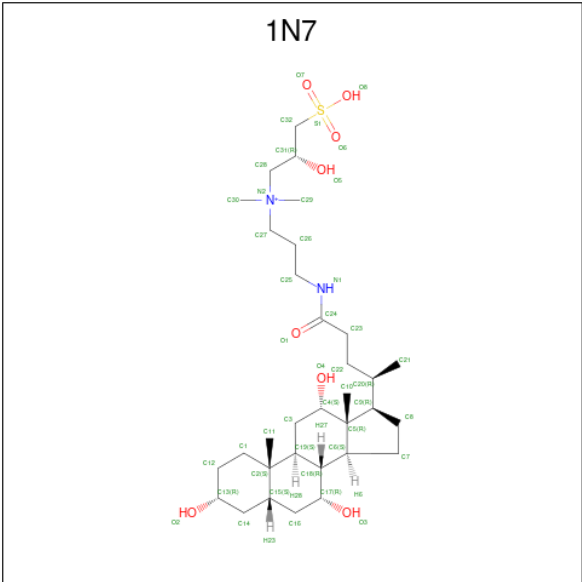
- Molecule 8 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	50	Total	C	N	O	P	0	0
			1020	491	169	310	50		

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
9	N	1	Total	Zn	0
			1	1	
9	J	2	Total	Zn	0
			2	2	

- Molecule 10 is CHAPSO (CCD ID: 1N7) (formula: C₃₂H₅₉N₂O₈S).



Mol	Chain	Residues	Atoms				AltConf
10	N	1	Total	C	H	O	0
			66	24	39	3	
10	I	1	Total	C	H	O	0
			66	24	39	3	
10	J	1	Total	C	H	O	0
			66	24	39	3	

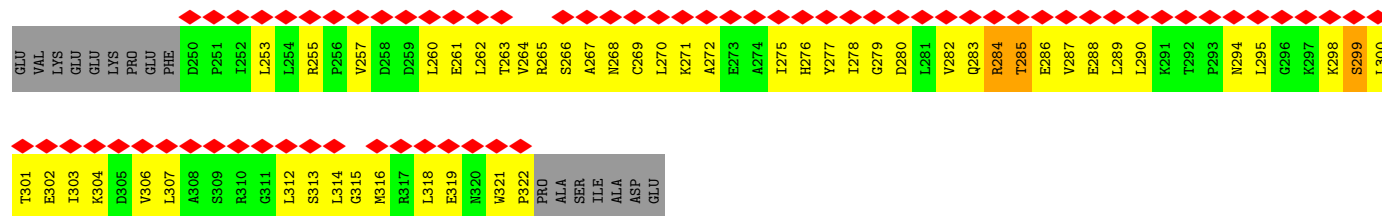
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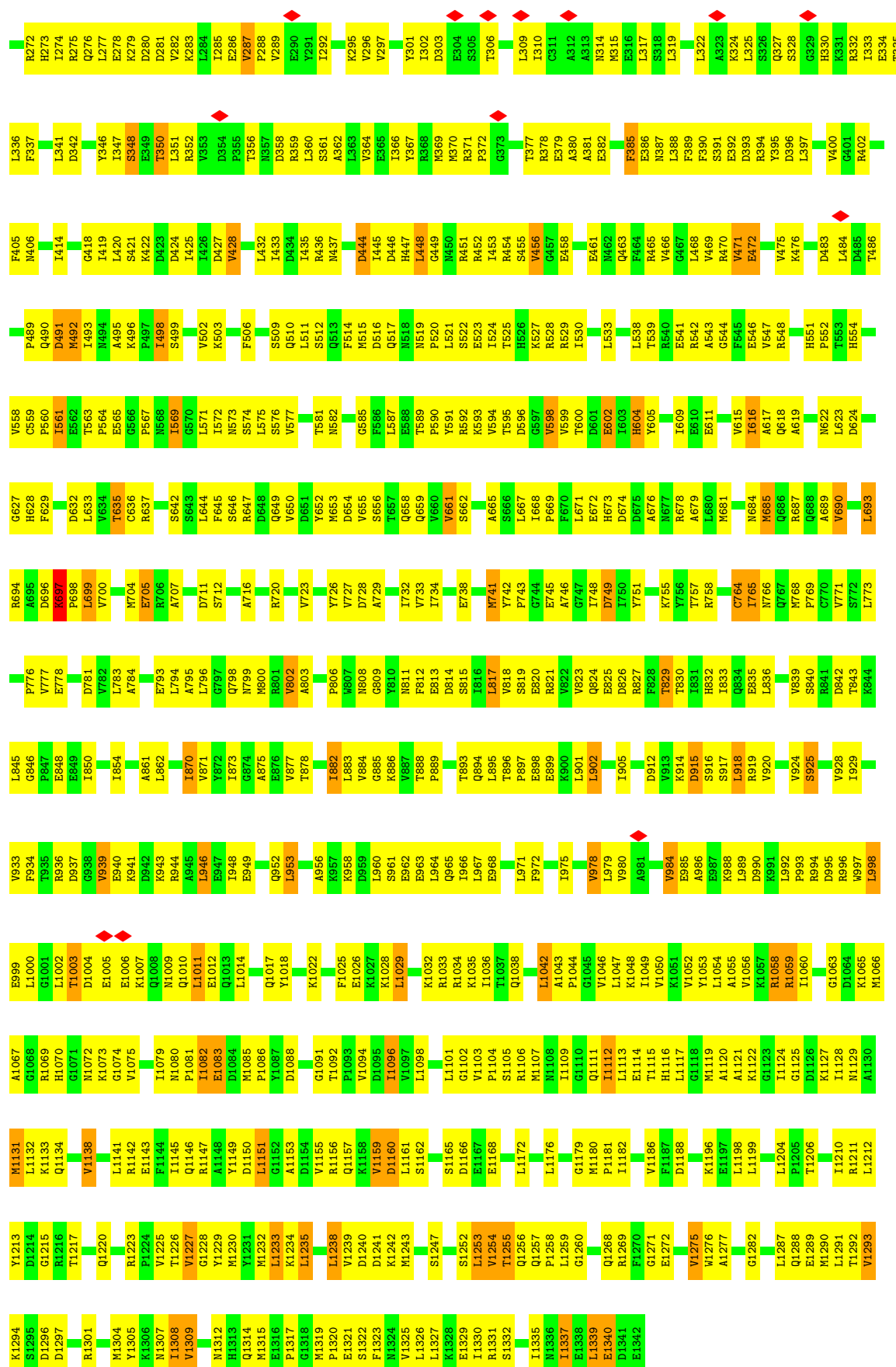
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Mol	Chain	Residues	Atoms				AltConf
10	L	1	Total	C	H	O	0
			66	24	39	3	

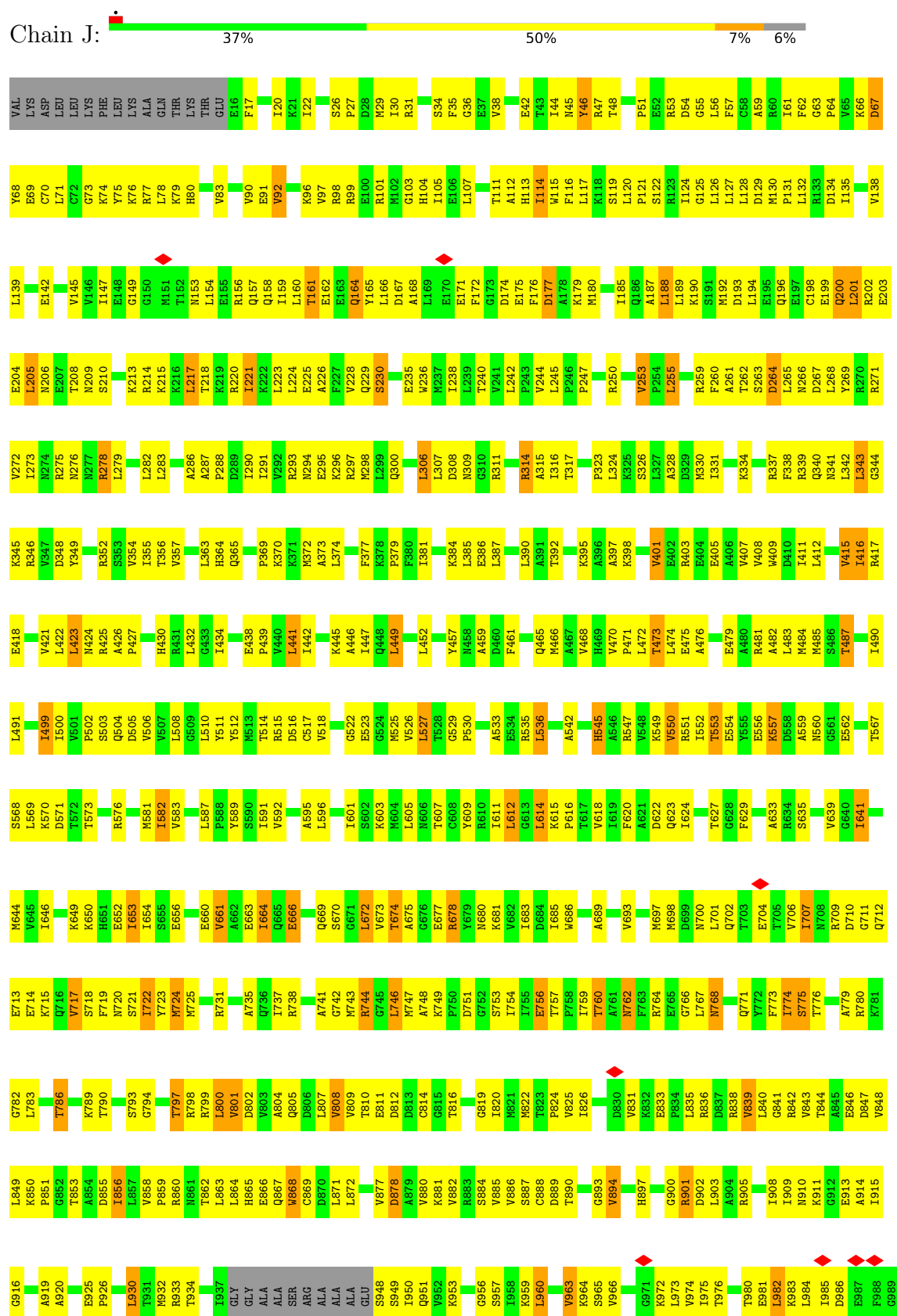
- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

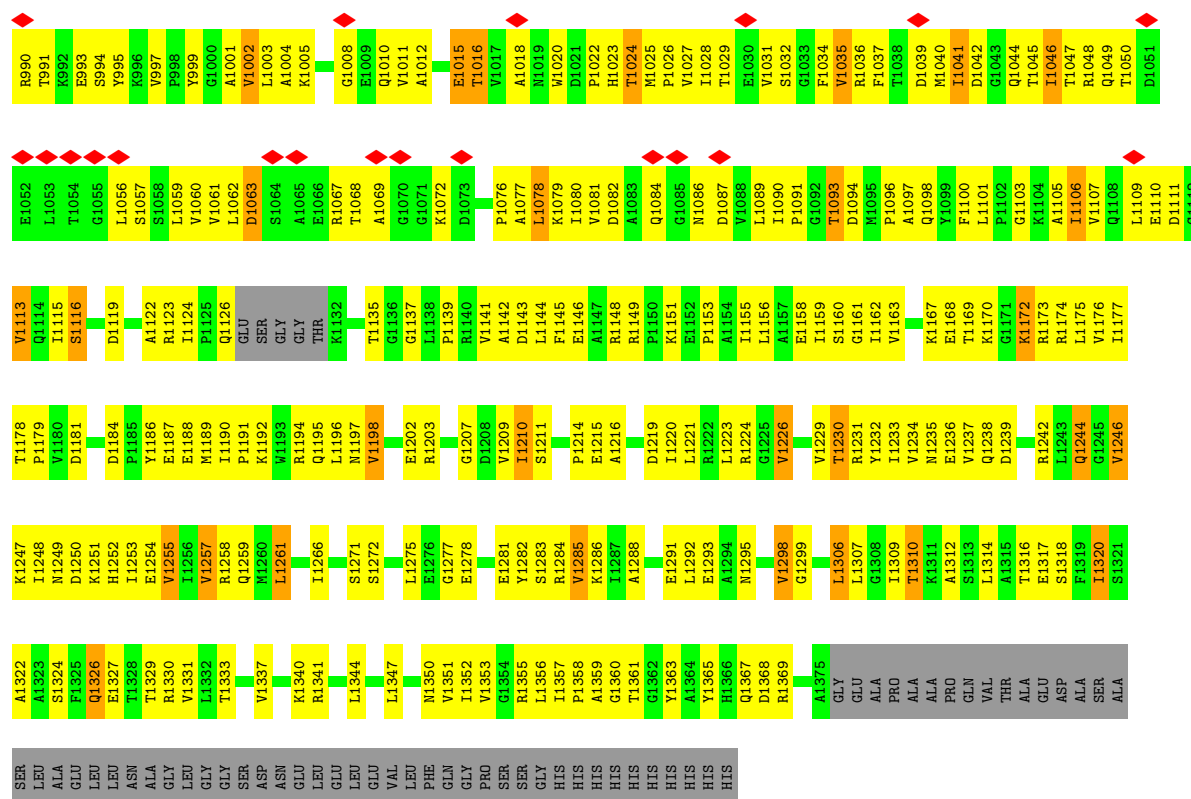
Mol	Chain	Residues	Atoms		AltConf
11	J	1	Total	Mg	0
			1	1	





• Molecule 4: DNA-directed RNA polymerase subunit beta'

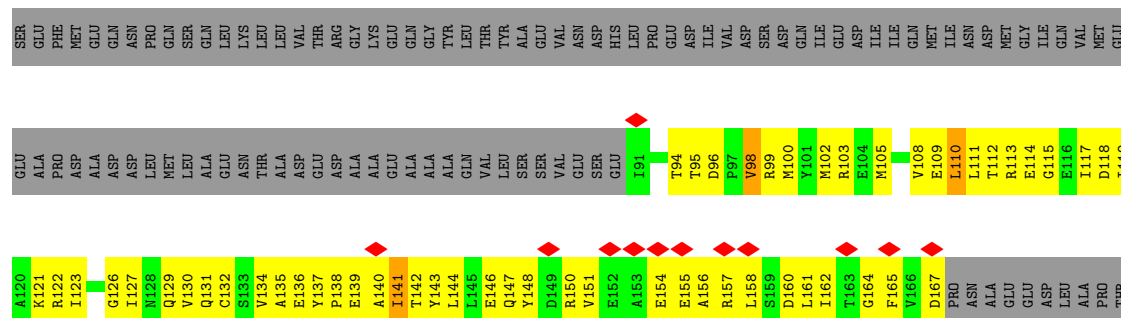




• Molecule 5: DNA-directed RNA polymerase subunit omega



• Molecule 6: RNA polymerase sigma factor RpoD



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	81732	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	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	0.226	Depositor
Minimum map value	-0.146	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 1N7, MG

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	N	0.42	0/581	0.56	0/785
2	G	0.48	0/1783	0.63	0/2417
2	H	0.44	0/1683	0.66	2/2285 (0.1%)
2	M	0.23	0/579	0.51	0/784
3	I	0.49	0/10733	0.63	6/14482 (0.0%)
4	J	0.46	0/10625	0.61	0/14345
5	K	0.36	0/629	0.56	0/847
6	L	0.28	0/3898	0.54	0/5242
7	O	0.25	0/1266	0.44	0/1948
8	P	0.25	0/1138	0.44	0/1752
All	All	0.43	0/32915	0.60	8/44887 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	H	0	1
3	I	0	1
4	J	0	1
6	L	0	2
All	All	0	5

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	516	ASP	N-CA-C	-6.69	99.93	109.96
3	I	1096	ILE	CA-C-N	-5.87	117.39	122.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1096	ILE	C-N-CA	-5.87	117.39	122.96
2	H	194	GLN	CA-C-N	5.47	131.55	121.70
2	H	194	GLN	C-N-CA	5.47	131.55	121.70
3	I	449	GLY	N-CA-C	-5.32	106.36	115.61
3	I	1275	VAL	N-CA-C	-5.25	107.30	111.81
3	I	1131	MET	N-CA-C	-5.19	107.60	114.04

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	12	ARG	Peptide
3	I	81	ASP	Peptide
4	J	177	ASP	Peptide
6	L	110	LEU	Peptide
6	L	500	ILE	Peptide

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	N	571	0	558	45	0
2	G	1761	0	1787	126	0
2	H	1664	0	1672	145	0
2	M	572	0	602	67	0
3	I	10564	0	10571	865	0
4	J	10466	0	10689	926	0
5	K	627	0	634	62	0
6	L	3846	0	3896	432	0
7	O	1128	0	621	78	0
8	P	1020	0	573	63	0
9	J	2	0	0	0	0
9	N	1	0	0	0	0
10	I	27	39	38	6	0
10	J	27	39	37	3	0
10	L	27	39	37	3	0
10	N	27	39	38	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	J	1	0	0	0	0
All	All	32331	156	31753	2594	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 40.

All (2594) 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)
10:L:701:1N7:C19	10:L:701:1N7:C3	1.84	1.55
10:N:102:1N7:C19	10:N:102:1N7:C3	1.82	1.55
10:I:1401:1N7:C3	10:I:1401:1N7:C19	1.83	1.53
10:J:1504:1N7:C19	10:J:1504:1N7:C3	1.84	1.51
4:J:697:MET:HE2	4:J:741:ALA:HB3	1.36	1.04
3:I:103:VAL:HB	3:I:114:VAL:HG11	1.42	1.00
3:I:176:ILE:HD11	3:I:428:VAL:HG21	1.42	1.00
6:L:140:ALA:HB1	6:L:269:LEU:HD13	1.43	0.99
2:M:275:ILE:HG22	2:M:280:ASP:HB3	1.42	0.99
4:J:1215:GLU:HG3	4:J:1220:ILE:HD11	1.45	0.98
6:L:547:VAL:HG11	6:L:607:LEU:HD21	1.46	0.97
6:L:287:ILE:HG12	6:L:337:VAL:HG13	1.47	0.96
6:L:119:ILE:HG23	6:L:375:ALA:HB1	1.47	0.95
3:I:255:ILE:HG22	3:I:262:TYR:HB2	1.47	0.95
6:L:280:VAL:HG22	6:L:347:ILE:HD13	1.47	0.94
2:H:104:LYS:HD2	2:H:110:VAL:HG22	1.47	0.94
4:J:1190:ILE:HG21	4:J:1196:LEU:HD11	1.50	0.94
2:M:300:LEU:HA	2:M:303:ILE:HD12	1.49	0.93
3:I:322:LEU:HD12	3:I:325:LEU:HD11	1.50	0.93
4:J:417:ARG:HB3	5:K:45:LYS:HE2	1.47	0.93
2:H:46:ILE:HD11	2:H:224:LEU:HD13	1.51	0.92
3:I:12:ARG:HG3	3:I:1181:PRO:HB2	1.50	0.92
3:I:839:VAL:HG12	3:I:1049:ILE:HG12	1.52	0.92
4:J:925:GLU:HG3	4:J:926:PRO:HD3	1.52	0.92
6:L:297:MET:HE1	6:L:305:LEU:HD22	1.51	0.91
8:P:41:DT:H1'	8:P:42:DT:H5'	1.51	0.91
6:L:561:MET:HA	6:L:567:MET:HE1	1.50	0.91
4:J:201:LEU:HD22	4:J:217:LEU:HD21	1.52	0.91
6:L:287:ILE:HA	6:L:337:VAL:HG22	1.53	0.91
4:J:559:ALA:HB3	4:J:562:GLU:HB2	1.50	0.91
3:I:633:LEU:HD13	3:I:644:LEU:HD12	1.49	0.90
3:I:289:VAL:HG21	3:I:322:LEU:HD22	1.52	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:95:THR:HA	6:L:100:MET:HE3	1.53	0.90
4:J:661:VAL:HG23	4:J:685:ILE:HD11	1.54	0.90
4:J:701:LEU:HD21	4:J:723:TYR:HB2	1.52	0.90
3:I:155:VAL:HG23	3:I:176:ILE:HG12	1.54	0.89
3:I:1212:LEU:HD22	3:I:1225:VAL:HG21	1.53	0.89
4:J:1109:LEU:HD11	4:J:1113:VAL:HG11	1.54	0.89
4:J:930:LEU:HD22	4:J:1244:GLN:HG3	1.52	0.89
4:J:279:LEU:HD11	4:J:296:LYS:HG2	1.54	0.89
3:I:953:LEU:HD21	3:I:1033:ARG:HG2	1.54	0.89
4:J:1172:LYS:HB3	4:J:1191:PRO:HA	1.53	0.88
3:I:1287:LEU:HD23	4:J:1357:ILE:HD11	1.55	0.88
4:J:338:PHE:HA	4:J:342:LEU:HD12	1.55	0.87
4:J:814:CYS:HB2	4:J:889:ASP:HB3	1.56	0.87
3:I:221:LEU:HD21	3:I:351:LEU:HD11	1.57	0.87
3:I:590:PRO:HB2	3:I:655:VAL:HG11	1.54	0.86
4:J:697:MET:HE3	4:J:738:ARG:HA	1.58	0.86
4:J:79:LYS:HG3	6:L:569:THR:HB	1.58	0.86
2:H:23:HIS:HB2	2:H:206:GLU:HG2	1.58	0.86
6:L:140:ALA:HA	6:L:269:LEU:HD22	1.58	0.86
4:J:975:ILE:HD13	4:J:980:THR:HG21	1.57	0.85
4:J:1090:ILE:HG12	4:J:1097:ALA:HB2	1.58	0.85
4:J:180:MET:HE1	4:J:293:ARG:HE	1.40	0.85
8:P:68:DG:H5''	2:M:294:ASN:HA	1.57	0.85
4:J:253:VAL:HG23	4:J:261:ALA:HB3	1.58	0.85
2:H:98:VAL:HG12	2:H:146:VAL:HG22	1.56	0.85
8:P:40:DC:H1'	8:P:41:DT:H5'	1.58	0.85
4:J:973:LEU:HD22	4:J:1003:LEU:HD12	1.59	0.85
3:I:232:ILE:HG13	3:I:333:ILE:HD11	1.59	0.85
4:J:1144:LEU:HD11	4:J:1236:GLU:HG2	1.59	0.85
7:O:23:DC:O2	8:P:63:DG:N2	2.11	0.84
4:J:1060:VAL:HG22	4:J:1106:ILE:HG12	1.59	0.84
4:J:972:LYS:HD3	4:J:1002:VAL:HB	1.58	0.84
7:O:42:DA:H1'	7:O:43:DA:H5'	1.58	0.84
1:N:52:PHE:HB2	1:N:55:VAL:HG13	1.60	0.84
3:I:29:SER:O	3:I:33:ASP:HB2	1.78	0.83
4:J:205:LEU:HD12	4:J:214:ARG:HB2	1.61	0.83
4:J:117:LEU:HD11	4:J:139:LEU:HD11	1.61	0.83
3:I:623:LEU:HD11	3:I:653:MET:HE1	1.58	0.83
3:I:109:ALA:HB1	3:I:112:GLY:HA3	1.59	0.82
3:I:1243:MET:HE3	4:J:445:LYS:HD3	1.60	0.82
4:J:1161:GLY:HA3	4:J:1179:PRO:HA	1.59	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:78:ILE:HA	2:H:81:ILE:HD12	1.60	0.82
3:I:699:LEU:HB2	3:I:799:ASN:HD22	1.44	0.82
2:M:304:LYS:HD2	2:M:314:LEU:HD11	1.60	0.82
6:L:302:PHE:O	6:L:306:PHE:N	2.11	0.82
2:H:102:LEU:HD13	2:H:115:ILE:HG12	1.59	0.81
6:L:426:LYS:HG2	7:O:52:DA:H3'	1.60	0.81
4:J:831:VAL:HG12	4:J:833:GLU:H	1.43	0.81
4:J:1078:LEU:HG	4:J:1101:LEU:HD11	1.60	0.81
3:I:229:ILE:HD12	3:I:334:GLU:HG2	1.63	0.81
5:K:26:ARG:HD3	5:K:64:LEU:HD21	1.63	0.81
4:J:1176:VAL:HG22	4:J:1187:GLU:HA	1.62	0.81
6:L:437:GLN:HB2	7:O:49:DC:H41	1.45	0.81
6:L:231:THR:HG23	6:L:248:GLU:HB3	1.63	0.81
4:J:1025:MET:HB2	4:J:1124:ILE:HB	1.61	0.81
4:J:1024:THR:HG23	4:J:1123:ARG:HA	1.62	0.80
3:I:28:LEU:HD21	3:I:524:ILE:HD13	1.63	0.80
4:J:515:ARG:HH21	4:J:717:VAL:HB	1.46	0.80
4:J:957:SER:HA	4:J:1010:GLN:HA	1.63	0.80
2:G:179:PRO:HG3	2:G:211:ILE:HG13	1.63	0.80
3:I:829:THR:HB	3:I:1059:ARG:HA	1.62	0.80
4:J:1107:VAL:HG12	4:J:1122:ALA:HB2	1.60	0.80
6:L:102:MET:HE1	6:L:388:ILE:HG21	1.63	0.80
6:L:330:LEU:HD23	6:L:333:VAL:HG11	1.64	0.80
4:J:553:THR:HB	4:J:567:THR:HG22	1.64	0.80
4:J:158:GLN:HG2	4:J:160:LEU:HD21	1.64	0.79
4:J:262:THR:HG23	4:J:266:ASN:HD22	1.46	0.79
6:L:110:LEU:HB2	6:L:111:LEU:HD13	1.62	0.79
4:J:1069:ALA:HA	4:J:1072:LYS:HB3	1.65	0.79
6:L:262:VAL:HG12	6:L:264:LYS:H	1.48	0.79
2:H:201:LEU:HD21	2:H:203:ILE:HD11	1.65	0.79
2:M:279:GLY:HA2	2:M:282:VAL:HG22	1.63	0.79
4:J:1239:ASP:OD1	4:J:1242:ARG:NH2	2.14	0.79
4:J:69:GLU:HG3	4:J:76:LYS:HG2	1.65	0.79
4:J:426:ALA:HB3	4:J:427:PRO:HD3	1.65	0.79
4:J:452:LEU:HD13	4:J:500:ILE:HG22	1.64	0.78
3:I:204:LEU:HD11	3:I:369:MET:HE2	1.63	0.78
3:I:871:VAL:O	3:I:944:ARG:NH2	2.17	0.78
3:I:370:MET:HE2	3:I:388:LEU:HD11	1.66	0.78
3:I:301:TYR:OH	3:I:332:ARG:O	2.02	0.78
3:I:528:ARG:NH2	3:I:576:SER:O	2.16	0.78
6:L:285:ARG:HA	6:L:289:LYS:HD3	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:453:ILE:HD12	3:I:530:ILE:HD12	1.65	0.78
6:L:114:GLU:HA	6:L:117:ILE:HD12	1.64	0.78
4:J:1023:HIS:HA	4:J:1126:GLN:HE21	1.49	0.77
3:I:738:GLU:HA	3:I:741:MET:HE2	1.64	0.77
2:G:93:GLN:HB3	2:G:120:ASP:HB3	1.66	0.77
3:I:88:ARG:NH2	3:I:1035:LYS:O	2.17	0.77
3:I:561:ILE:HD11	3:I:665:ALA:HB1	1.66	0.77
3:I:716:ALA:HB3	3:I:784:ALA:HB3	1.66	0.77
3:I:1294:LYS:NZ	4:J:470:VAL:O	2.17	0.77
3:I:1151:LEU:HD12	3:I:1198:LEU:HD12	1.65	0.77
4:J:130:MET:HE3	4:J:159:ILE:HD11	1.65	0.77
4:J:311:ARG:HH22	4:J:1329:THR:HG21	1.46	0.77
5:K:22:VAL:HG22	5:K:61:ASN:HB2	1.65	0.77
2:M:284:ARG:HB3	2:M:288:GLU:HG2	1.64	0.77
7:O:46:DG:H2''	7:O:47:DG:H5'	1.67	0.77
3:I:24:VAL:HG11	3:I:704:MET:HE1	1.67	0.76
2:M:257:VAL:HG11	2:M:270:LEU:HD23	1.65	0.76
3:I:453:ILE:HG13	3:I:587:LEU:HG	1.66	0.76
4:J:1169:THR:H	4:J:1173:ARG:HA	1.50	0.76
4:J:950:ILE:HD13	4:J:995:TYR:HB3	1.66	0.76
6:L:291:CYS:O	6:L:297:MET:N	2.19	0.76
3:I:565:GLU:HA	3:I:569:ILE:HD11	1.65	0.76
6:L:291:CYS:HA	6:L:295:CYS:HB3	1.67	0.76
4:J:218:THR:HA	4:J:221:ILE:HG22	1.68	0.76
3:I:180:ARG:NH2	3:I:392:GLU:O	2.17	0.75
6:L:394:TYR:OH	6:L:436:ARG:NH1	2.20	0.75
3:I:297:VAL:HA	3:I:335:THR:HA	1.68	0.75
4:J:1059:LEU:HD11	4:J:1110:GLU:HG2	1.68	0.75
4:J:1275:LEU:HD12	4:J:1277:GLY:H	1.50	0.75
3:I:611:GLU:OE2	3:I:637:ARG:NH2	2.20	0.75
3:I:1269:ARG:NH1	4:J:344:GLY:O	2.20	0.75
4:J:115:TRP:O	4:J:119:SER:OG	2.05	0.74
2:M:282:VAL:HG11	2:M:312:LEU:HD12	1.68	0.74
2:G:110:VAL:HG11	2:G:140:ILE:HD11	1.69	0.74
2:H:80:GLU:OE2	4:J:551:ARG:NH2	2.20	0.74
2:H:193:GLU:OE1	2:H:193:GLU:N	2.21	0.74
3:I:1065:LYS:HE2	3:I:1235:LEU:HD12	1.68	0.74
4:J:909:ILE:HD11	4:J:913:GLU:HB3	1.70	0.74
7:O:23:DC:N3	8:P:63:DG:N1	2.35	0.74
3:I:56:VAL:HG11	3:I:468:LEU:HD13	1.70	0.74
6:L:379:MET:O	6:L:383:ASN:ND2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:47:LEU:HD23	2:G:51:MET:HE3	1.70	0.73
3:I:211:ARG:NH1	3:I:215:TYR:O	2.20	0.73
4:J:1059:LEU:HB2	4:J:1107:VAL:HG22	1.68	0.73
6:L:330:LEU:HA	6:L:333:VAL:HG12	1.69	0.73
4:J:799:ARG:NH2	4:J:1146:GLU:OE2	2.21	0.73
8:P:14:DA:H2'	8:P:15:DC:H5'	1.70	0.73
4:J:317:THR:HG22	4:J:323:PRO:HA	1.70	0.73
4:J:518:VAL:HG11	4:J:707:ILE:HD13	1.68	0.73
6:L:316:PHE:HE2	6:L:334:SER:HA	1.52	0.73
4:J:308:ASP:HB3	4:J:328:ALA:HB3	1.70	0.73
3:I:1002:LEU:HD12	3:I:1003:THR:H	1.53	0.73
4:J:278:ARG:NH1	6:L:403:ASP:OD1	2.16	0.73
2:G:102:LEU:HD11	2:G:110:VAL:HG21	1.70	0.72
4:J:926:PRO:HB3	4:J:1246:VAL:HG11	1.69	0.72
3:I:812:PHE:O	4:J:504:GLN:NE2	2.22	0.72
8:P:18:DT:H2'	8:P:19:DT:H71	1.72	0.72
3:I:1196:LYS:HG3	3:I:1206:THR:HG23	1.71	0.72
4:J:1036:ARG:HH21	4:J:1081:VAL:HG11	1.55	0.72
2:M:255:ARG:HB2	2:M:278:ILE:HG13	1.72	0.72
3:I:794:LEU:HD21	3:I:796:LEU:HD21	1.72	0.72
6:L:377:LYS:O	6:L:381:GLU:HG2	1.90	0.72
3:I:595:THR:HG22	3:I:596:ASP:H	1.55	0.72
3:I:12:ARG:NH2	3:I:793:GLU:OE1	2.22	0.72
4:J:1158:GLU:HG3	4:J:1186:TYR:OH	1.90	0.72
3:I:896:THR:HG22	3:I:897:PRO:HD2	1.71	0.71
3:I:1116:HIS:HE1	4:J:641:ILE:H	1.38	0.71
3:I:444:ASP:N	3:I:444:ASP:OD1	2.19	0.71
3:I:1176:LEU:HD22	3:I:1181:PRO:HD3	1.73	0.71
3:I:943:LYS:HA	3:I:946:LEU:HD23	1.73	0.71
4:J:405:GLU:O	4:J:408:VAL:HG12	1.90	0.71
4:J:957:SER:OG	4:J:1008:GLY:O	2.09	0.71
10:N:102:1N7:C3	10:N:102:1N7:C18	2.66	0.71
2:G:160:HIS:N	2:G:162:GLU:OE1	2.24	0.71
4:J:1158:GLU:HA	4:J:1223:LEU:HD11	1.71	0.71
6:L:562:ARG:HG3	6:L:576:VAL:HG21	1.73	0.71
3:I:1143:GLU:OE2	3:I:1147:ARG:NH1	2.22	0.71
6:L:573:LEU:HD22	8:P:55:DT:H3'	1.72	0.71
2:G:29:GLU:HB3	2:G:30:PRO:HD3	1.72	0.70
2:H:67:GLU:HG2	2:H:68:TYR:HD1	1.53	0.70
3:I:1142:ARG:NH2	3:I:1161:LEU:O	2.24	0.70
4:J:825:VAL:HG12	4:J:833:GLU:HB2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:16:ILE:HG13	2:H:26:VAL:HG22	1.73	0.70
4:J:644:MET:HG2	4:J:722:ILE:HD12	1.74	0.70
4:J:981:GLU:OE1	4:J:983:LYS:NZ	2.22	0.70
2:M:263:THR:OG1	2:M:302:GLU:OE2	2.06	0.70
5:K:76:GLU:HA	5:K:79:GLU:HB2	1.74	0.70
3:I:593:LYS:O	3:I:600:THR:OG1	2.08	0.70
8:P:56:DG:H2''	8:P:57:DT:H71	1.71	0.70
2:G:20:SER:OG	2:G:21:SER:N	2.23	0.70
4:J:147:ILE:HG22	4:J:188:LEU:HG	1.72	0.70
1:N:48:ARG:NH2	1:N:62:GLN:OE1	2.24	0.70
4:J:139:LEU:HD21	4:J:185:ILE:HG13	1.74	0.70
2:H:212:ASP:N	2:H:212:ASP:OD1	2.23	0.70
3:I:98:VAL:HG21	3:I:124:MET:HE3	1.73	0.70
4:J:198:CYS:HB2	4:J:221:ILE:HD11	1.73	0.70
4:J:482:ALA:O	5:K:16:ARG:NH1	2.24	0.70
3:I:124:MET:HB2	3:I:498:ILE:HD12	1.73	0.69
4:J:661:VAL:CG2	4:J:685:ILE:HD11	2.22	0.69
6:L:391:ALA:HB3	6:L:405:ILE:HD13	1.73	0.69
1:N:62:GLN:O	1:N:66:GLU:HG2	1.92	0.69
1:N:6:ASP:OD2	3:I:1106:ARG:NH1	2.24	0.69
4:J:819:GLY:HA3	4:J:882:VAL:O	1.93	0.69
6:L:220:LYS:NZ	6:L:223:GLU:OE1	2.24	0.69
6:L:305:LEU:HD21	6:L:319:ALA:HB2	1.74	0.69
6:L:344:LEU:HA	6:L:347:ILE:HD12	1.72	0.69
6:L:479:THR:HG23	6:L:482:GLU:H	1.57	0.69
3:I:346:TYR:O	3:I:350:THR:OG1	2.10	0.69
3:I:745:GLU:HG3	3:I:1017:GLN:HB3	1.74	0.69
4:J:878:ASP:OD2	4:J:878:ASP:N	2.26	0.69
6:L:606:VAL:HG23	6:L:607:LEU:HD22	1.74	0.69
3:I:27:LEU:O	3:I:528:ARG:NH1	2.25	0.69
3:I:905:ILE:HG12	6:L:598:LEU:HD12	1.73	0.69
4:J:490:ILE:HD11	4:J:614:LEU:HD12	1.75	0.69
7:O:55:DC:H6	7:O:55:DC:H5'	1.56	0.69
3:I:241:LEU:N	3:I:283:LYS:O	2.23	0.69
3:I:560:PRO:O	4:J:780:ARG:NH2	2.24	0.69
4:J:128:LEU:HD11	4:J:189:LEU:HD21	1.73	0.69
6:L:96:ASP:O	6:L:100:MET:HG2	1.92	0.69
10:L:701:1N7:C3	10:L:701:1N7:C18	2.66	0.69
1:N:6:ASP:OD1	3:I:678:ARG:NH2	2.26	0.69
3:I:886:LYS:NZ	3:I:916:SER:O	2.25	0.69
3:I:979:LEU:HD11	3:I:1011:LEU:HD11	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:192:VAL:HB	2:G:198:LEU:HD12	1.73	0.68
3:I:1006:GLU:OE2	3:I:1009:ASN:ND2	2.26	0.68
6:L:285:ARG:HG3	6:L:289:LYS:HE2	1.73	0.68
3:I:314:ASN:O	3:I:352:ARG:NH1	2.23	0.68
3:I:548:ARG:NH2	3:I:567:PRO:O	2.26	0.68
4:J:355:ILE:HD13	4:J:466:MET:HE3	1.76	0.68
4:J:884:SER:HB2	4:J:886:VAL:HG12	1.75	0.68
4:J:964:LYS:O	4:J:976:THR:OG1	2.10	0.68
3:I:3:TYR:O	3:I:8:LYS:NZ	2.25	0.68
4:J:154:LEU:HD12	4:J:176:PHE:CZ	2.29	0.68
4:J:475:GLU:HG2	5:K:24:ALA:HB1	1.74	0.68
4:J:559:ALA:CB	4:J:562:GLU:HB2	2.23	0.68
2:G:224:LEU:HD23	2:H:228:LEU:HD11	1.76	0.68
4:J:518:VAL:HG11	4:J:707:ILE:CD1	2.24	0.68
6:L:547:VAL:CG1	6:L:607:LEU:HD21	2.24	0.68
3:I:1105:SER:HB2	4:J:731:ARG:HG3	1.74	0.68
3:I:741:MET:HG2	3:I:746:ALA:HB1	1.75	0.68
4:J:381:ILE:HD11	4:J:412:LEU:HD13	1.74	0.68
4:J:1020:TRP:HE1	4:J:1022:PRO:HB3	1.58	0.68
6:L:586:ARG:HE	7:O:25:DA:H5"	1.59	0.68
3:I:395:TYR:CE2	3:I:420:LEU:HD22	2.29	0.68
4:J:17:PHE:HZ	4:J:1353:VAL:HG21	1.59	0.68
3:I:120:GLN:HG2	3:I:490:GLN:HE22	1.58	0.67
4:J:1069:ALA:HB1	4:J:1072:LYS:HD3	1.75	0.67
7:O:73:DC:H2"	7:O:74:DC:H5"	1.74	0.67
3:I:989:LEU:HD13	3:I:1000:LEU:HD11	1.75	0.67
4:J:510:LEU:O	4:J:514:THR:HG22	1.94	0.67
4:J:974:VAL:HA	4:J:1001:ALA:O	1.94	0.67
6:L:130:VAL:O	6:L:134:VAL:HG23	1.93	0.67
6:L:291:CYS:HA	6:L:295:CYS:CB	2.24	0.67
10:I:1401:1N7:C3	10:I:1401:1N7:C18	2.67	0.67
4:J:47:ARG:NH2	7:O:44:DA:OP1	2.22	0.67
2:G:192:VAL:CB	2:G:198:LEU:HD12	2.25	0.67
3:I:65:ASN:O	3:I:105:TYR:N	2.25	0.67
4:J:825:VAL:CG1	4:J:833:GLU:HB2	2.24	0.67
3:I:96:LEU:HD23	3:I:124:MET:HG3	1.75	0.67
3:I:233:ARG:O	3:I:238:GLN:NE2	2.27	0.67
3:I:560:PRO:HB3	4:J:776:THR:HG21	1.75	0.67
3:I:180:ARG:O	3:I:396:ASP:N	2.18	0.67
2:H:205:MET:HE1	2:H:217:ILE:HG13	1.75	0.67
3:I:57:PHE:HD2	3:I:70:TYR:HB2	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:870:ILE:HD13	3:I:1050:VAL:HG11	1.77	0.67
4:J:965:SER:OG	4:J:966:VAL:N	2.24	0.67
2:G:84:ASN:ND2	2:G:130:ILE:O	2.23	0.67
6:L:126:GLY:O	6:L:130:VAL:HG23	1.95	0.67
3:I:68:LEU:HD23	3:I:475:VAL:HG11	1.77	0.67
4:J:975:ILE:HG21	4:J:980:THR:HG21	1.76	0.67
4:J:985:ILE:HD13	4:J:991:THR:HA	1.77	0.67
6:L:606:VAL:O	6:L:609:SER:OG	2.08	0.67
3:I:175:ARG:HG2	3:I:177:ILE:HG13	1.77	0.66
3:I:324:LYS:O	3:I:327:GLN:NE2	2.23	0.66
4:J:527:LEU:HD23	4:J:533:ALA:HB2	1.77	0.66
2:M:275:ILE:CG2	2:M:280:ASP:HB3	2.21	0.66
6:L:148:TYR:HA	6:L:161:LEU:HD11	1.76	0.66
10:N:102:1N7:C3	10:N:102:1N7:C2	2.70	0.66
3:I:243:PRO:HB3	3:I:277:LEU:HD23	1.76	0.66
3:I:301:TYR:O	3:I:310:ILE:HB	1.95	0.66
3:I:964:LEU:HG	3:I:968:GLU:OE2	1.95	0.66
4:J:168:ALA:HA	4:J:171:GLU:HB3	1.76	0.66
3:I:1103:VAL:HG11	3:I:1112:ILE:HG13	1.78	0.66
3:I:1276:TRP:HH2	4:J:798:ARG:HG2	1.60	0.66
4:J:185:ILE:O	4:J:189:LEU:HG	1.95	0.66
3:I:1314:GLN:OE1	5:K:28:ARG:NH2	2.28	0.66
3:I:23:ASP:OD1	3:I:23:ASP:N	2.28	0.66
3:I:257:ALA:HB3	3:I:282:VAL:HG21	1.78	0.66
3:I:933:VAL:HG23	3:I:1050:VAL:HG22	1.75	0.66
4:J:768:ASN:OD1	4:J:768:ASN:N	2.29	0.66
3:I:1010:GLN:O	3:I:1014:LEU:HG	1.96	0.66
6:L:135:ALA:HB1	6:L:253:SER:HA	1.77	0.66
7:O:33:DA:H2'	7:O:33:DA:OP2	1.95	0.66
3:I:1080:ASN:HD22	3:I:1085:MET:HE3	1.61	0.66
4:J:265:LEU:HD11	4:J:330:MET:SD	2.35	0.66
4:J:842:ARG:NH2	4:J:1254:GLU:OE1	2.29	0.66
6:L:162:ILE:HG23	6:L:260:ARG:O	1.95	0.66
4:J:844:THR:OG1	4:J:860:ARG:O	2.11	0.65
4:J:1059:LEU:HD13	4:J:1107:VAL:HG23	1.76	0.65
3:I:69:GLN:HE21	3:I:101:ARG:HD2	1.61	0.65
3:I:875:ALA:O	3:I:877:VAL:HG13	1.96	0.65
3:I:902:LEU:HD21	6:L:611:LEU:HG	1.78	0.65
4:J:154:LEU:HD12	4:J:176:PHE:HZ	1.59	0.65
4:J:614:LEU:HD22	5:K:7:GLN:HG3	1.77	0.65
4:J:1050:THR:HG23	4:J:1057:SER:HA	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:726:TYR:CE2	3:I:728:ASP:HB2	2.31	0.65
6:L:234:THR:OG1	6:L:248:GLU:OE1	2.15	0.65
4:J:514:THR:OG1	4:J:576:ARG:HG3	1.95	0.65
4:J:888:CYS:SG	4:J:889:ASP:N	2.65	0.65
2:G:98:VAL:HG11	2:G:121:VAL:CG2	2.27	0.65
2:H:125:LYS:NZ	2:H:127:GLN:OE1	2.29	0.65
3:I:1340:GLU:HG2	4:J:1341:ARG:NH2	2.12	0.65
4:J:1077:ALA:HB2	4:J:1100:PHE:HA	1.77	0.65
5:K:59:ILE:O	5:K:63:ILE:HB	1.97	0.65
6:L:387:VAL:HG11	6:L:409:ASN:OD1	1.97	0.65
6:L:572:THR:O	6:L:576:VAL:HG23	1.97	0.65
4:J:128:LEU:HD21	4:J:189:LEU:HD23	1.78	0.65
4:J:603:LYS:O	4:J:607:THR:HG23	1.96	0.65
2:M:253:LEU:HD11	2:M:282:VAL:HG21	1.79	0.65
3:I:177:ILE:HG12	3:I:183:TRP:HE3	1.60	0.65
3:I:693:LEU:HB2	3:I:829:THR:O	1.97	0.64
3:I:1305:TYR:O	3:I:1309:VAL:HG13	1.97	0.64
4:J:511:TYR:HE2	4:J:724:MET:HG2	1.60	0.64
8:P:43:DT:H2''	8:P:44:DT:H71	1.79	0.64
1:N:14:GLN:O	1:N:18:THR:HG22	1.97	0.64
3:I:561:ILE:HD11	3:I:665:ALA:CB	2.27	0.64
3:I:885:GLY:HA2	3:I:917:SER:HB3	1.78	0.64
4:J:822:MET:HE2	4:J:838:ARG:O	1.97	0.64
7:O:56:DC:H6	7:O:56:DC:H5'	1.61	0.64
2:G:80:GLU:OE2	3:I:768:MET:HE1	1.97	0.64
3:I:325:LEU:HA	3:I:328:SER:HB2	1.80	0.64
3:I:884:VAL:HG23	3:I:918:LEU:HD23	1.77	0.64
4:J:1232:TYR:HD2	4:J:1233:ILE:HD12	1.62	0.64
6:L:289:LYS:O	6:L:293:GLU:HB3	1.98	0.64
3:I:241:LEU:HB3	3:I:283:LYS:HA	1.80	0.64
4:J:430:HIS:HB3	4:J:925:GLU:HG2	1.80	0.64
6:L:216:LEU:O	6:L:220:LYS:HG2	1.98	0.64
2:H:92:VAL:HG23	2:H:121:VAL:HG12	1.80	0.64
2:H:105:SER:OG	2:H:106:GLY:N	2.30	0.64
3:I:245:ARG:HB3	3:I:337:PHE:CZ	2.32	0.64
3:I:1042:LEU:HB3	3:I:1046:VAL:HG13	1.78	0.64
6:L:291:CYS:O	6:L:296:LYS:N	2.30	0.64
2:M:302:GLU:O	2:M:306:VAL:HG23	1.98	0.64
3:I:391:SER:CB	3:I:394:ARG:HB2	2.28	0.64
3:I:489:PRO:HA	3:I:492:MET:HE2	1.79	0.64
4:J:425:ARG:HG2	4:J:426:ALA:H	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:295:CYS:SG	6:L:329:LYS:HB2	2.38	0.64
3:I:81:ASP:OD1	3:I:84:GLU:HB2	1.98	0.64
3:I:130:MET:SD	3:I:134:GLY:HA2	2.38	0.64
3:I:400:VAL:HG21	3:I:452:ARG:HD2	1.79	0.64
8:P:60:DA:H2''	8:P:61:DT:H5'	1.80	0.64
1:N:64:TYR:HD1	3:I:341:LEU:HD22	1.62	0.64
3:I:894:GLN:HG2	4:J:77:ARG:HH22	1.63	0.64
3:I:956:ALA:HB1	3:I:1032:LYS:HG2	1.79	0.64
4:J:910:ASN:OD1	5:K:15:ASN:HA	1.97	0.64
6:L:286:LEU:HD11	6:L:336:GLU:HB3	1.78	0.64
1:N:46:GLU:HG2	1:N:49:ARG:HH22	1.63	0.64
1:N:52:PHE:HB2	1:N:55:VAL:CG1	2.27	0.64
2:G:211:ILE:HG23	2:G:216:ALA:HB2	1.80	0.64
3:I:390:PHE:HA	3:I:419:ILE:CD1	2.27	0.64
3:I:565:GLU:HA	3:I:569:ILE:CD1	2.28	0.64
4:J:848:VAL:HB	4:J:858:VAL:HG22	1.79	0.64
6:L:141:ILE:HD12	6:L:256:PHE:CD1	2.31	0.64
6:L:147:GLN:HB3	6:L:161:LEU:HD21	1.79	0.64
6:L:282:THR:HG23	6:L:285:ARG:HH21	1.63	0.64
3:I:387:ASN:HA	3:I:391:SER:OG	1.98	0.63
3:I:733:VAL:HG13	3:I:748:ILE:HD13	1.80	0.63
4:J:1141:VAL:HG22	4:J:1237:VAL:HG23	1.80	0.63
6:L:227:GLN:O	6:L:231:THR:OG1	2.11	0.63
2:H:12:ARG:HA	2:H:14:VAL:H	1.64	0.63
4:J:398:LYS:HD2	6:L:532:LEU:CD2	2.28	0.63
4:J:847:ASP:HB3	4:J:856:ILE:CG2	2.28	0.63
6:L:165:PHE:HB2	6:L:167:ASP:OD1	1.97	0.63
4:J:17:PHE:CZ	4:J:1353:VAL:HG21	2.33	0.63
4:J:797:THR:O	4:J:801:VAL:HG13	1.98	0.63
6:L:224:LEU:HD13	6:L:256:PHE:HE1	1.63	0.63
6:L:303:ILE:HA	6:L:306:PHE:HB3	1.80	0.63
2:M:316:MET:HE1	2:M:318:LEU:HD22	1.79	0.63
3:I:979:LEU:HD23	3:I:1000:LEU:HD12	1.80	0.63
3:I:1026:GLU:HA	3:I:1029:LEU:HD23	1.80	0.63
10:L:701:1N7:C3	10:L:701:1N7:C2	2.73	0.63
4:J:709:ARG:HB3	4:J:711:GLY:HA3	1.80	0.63
4:J:948:SER:O	4:J:948:SER:OG	2.17	0.63
6:L:344:LEU:HD11	6:L:355:ILE:HG13	1.81	0.63
1:N:48:ARG:HH12	1:N:59:VAL:HA	1.61	0.63
2:G:208:ASN:OD1	2:G:210:THR:HG23	1.99	0.63
3:I:1104:PRO:HG2	4:J:725:MET:CE	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:573:LEU:HB2	6:L:587:ILE:HD11	1.81	0.63
3:I:391:SER:O	3:I:395:TYR:N	2.31	0.63
4:J:291:ILE:HD11	6:L:380:VAL:HG11	1.81	0.63
4:J:573:THR:OG1	4:J:576:ARG:HD2	1.99	0.63
4:J:949:SER:OG	4:J:1018:ALA:O	2.16	0.63
6:L:552:THR:OG1	6:L:597:LYS:NZ	2.26	0.63
3:I:225:PHE:HB2	3:I:336:LEU:HD22	1.81	0.63
3:I:742:TYR:HB3	3:I:743:PRO:HD2	1.80	0.63
4:J:314:ARG:HD2	4:J:315:ALA:H	1.63	0.63
3:I:929:ILE:HD13	3:I:1055:ALA:HB2	1.80	0.62
4:J:1357:ILE:HG22	4:J:1359:ALA:H	1.64	0.62
6:L:146:GLU:O	6:L:150:ARG:HG3	1.99	0.62
2:G:184:ALA:HB2	3:I:1091:GLY:HA3	1.81	0.62
3:I:994:ARG:HA	3:I:997:TRP:CD2	2.34	0.62
4:J:202:ARG:HA	4:J:205:LEU:HD23	1.80	0.62
4:J:550:VAL:HG23	4:J:552:ILE:HG23	1.79	0.62
6:L:95:THR:HA	6:L:100:MET:CE	2.29	0.62
3:I:5:TYR:HA	3:I:8:LYS:HE2	1.80	0.62
10:I:1401:1N7:C3	10:I:1401:1N7:C2	2.72	0.62
4:J:56:LEU:O	4:J:250:ARG:NH2	2.28	0.62
4:J:129:ASP:HB2	4:J:220:ARG:HH21	1.63	0.62
4:J:710:ASP:N	4:J:711:GLY:HA3	2.13	0.62
4:J:847:ASP:HB3	4:J:856:ILE:HG21	1.80	0.62
4:J:1173:ARG:NH1	4:J:1192:LYS:HE2	2.15	0.62
6:L:548:LEU:HD12	6:L:560:ARG:HE	1.64	0.62
3:I:225:PHE:CE2	3:I:347:ILE:HB	2.33	0.62
3:I:362:ALA:O	3:I:366:ILE:HG13	1.99	0.62
4:J:826:ILE:HG12	4:J:831:VAL:HG22	1.81	0.62
1:N:27:ILE:HD11	4:J:680:ASN:HB3	1.80	0.62
3:I:525:THR:O	3:I:529:ARG:HG3	1.98	0.62
3:I:667:LEU:HD23	3:I:704:MET:HB3	1.82	0.62
3:I:707:ALA:O	3:I:711:ASP:HB2	1.99	0.62
4:J:418:GLU:HG3	5:K:48:VAL:HG21	1.81	0.62
4:J:782:GLY:O	4:J:786:THR:HG23	1.99	0.62
2:G:70:THR:HG23	3:I:729:ALA:HB3	1.82	0.62
2:H:64:VAL:CG1	2:H:69:SER:HB2	2.30	0.62
3:I:59:ILE:HG21	3:I:472:GLU:HB2	1.82	0.62
3:I:591:TYR:HB3	3:I:652:TYR:HB3	1.80	0.62
3:I:1138:VAL:O	3:I:1142:ARG:HG3	1.99	0.62
4:J:689:ALA:O	4:J:693:VAL:HG23	2.00	0.62
6:L:315:TRP:CZ2	6:L:341:LEU:HD11	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:57:THR:HG22	2:G:58:GLU:HG3	1.81	0.62
3:I:453:ILE:HD11	3:I:587:LEU:HD11	1.81	0.62
4:J:215:LYS:O	4:J:218:THR:HG22	1.98	0.62
4:J:288:PRO:HD2	4:J:291:ILE:HD12	1.81	0.62
5:K:54:ILE:HD13	5:K:59:ILE:HB	1.82	0.62
3:I:575:LEU:HD12	3:I:587:LEU:HD21	1.80	0.62
4:J:117:LEU:HD11	4:J:139:LEU:CD1	2.29	0.62
4:J:412:LEU:O	4:J:415:VAL:HG22	1.99	0.62
4:J:508:LEU:HD13	4:J:725:MET:HG2	1.82	0.62
6:L:301:ASN:O	6:L:304:THR:HG22	2.00	0.62
3:I:1242:LYS:HD2	4:J:465:GLN:HE22	1.64	0.62
4:J:652:GLU:O	4:J:656:GLU:HG3	2.00	0.62
4:J:742:GLY:O	4:J:762:ASN:HB3	1.98	0.62
3:I:257:ALA:HB2	3:I:285:ILE:HG22	1.81	0.62
3:I:1125:GLY:HA3	3:I:1179:GLY:H	1.65	0.62
3:I:1304:MET:SD	3:I:1315:MET:HB3	2.39	0.62
4:J:681:LYS:O	4:J:685:ILE:HG23	2.00	0.62
4:J:1037:PHE:HZ	4:J:1110:GLU:HA	1.64	0.62
1:N:56:THR:O	1:N:57:LEU:HD23	2.00	0.61
2:H:228:LEU:O	2:H:232:VAL:HG23	2.00	0.61
3:I:67:GLU:O	3:I:103:VAL:HG22	2.00	0.61
3:I:1042:LEU:HB3	3:I:1046:VAL:CG1	2.30	0.61
4:J:1173:ARG:HG3	4:J:1192:LYS:HD3	1.82	0.61
5:K:58:LEU:O	5:K:59:ILE:HD13	2.00	0.61
6:L:114:GLU:HA	6:L:117:ILE:CD1	2.28	0.61
2:G:98:VAL:HG11	2:G:121:VAL:HG21	1.82	0.61
2:H:76:GLU:OE1	2:H:132:HIS:N	2.27	0.61
4:J:747:MET:HE3	4:J:775:SER:HB2	1.81	0.61
4:J:1047:THR:HG23	4:J:1049:GLN:HB2	1.81	0.61
4:J:1060:VAL:CG2	4:J:1106:ILE:HG12	2.30	0.61
6:L:366:SER:O	6:L:369:GLU:HG3	2.00	0.61
6:L:530:LEU:O	6:L:533:ASP:N	2.31	0.61
3:I:229:ILE:CD1	3:I:334:GLU:HG2	2.29	0.61
3:I:391:SER:HB2	3:I:394:ARG:HB2	1.82	0.61
4:J:46:TYR:HD1	6:L:500:ILE:HD12	1.63	0.61
4:J:424:ASN:HB2	4:J:434:ILE:HG12	1.83	0.61
3:I:232:ILE:HG13	3:I:333:ILE:CD1	2.29	0.61
4:J:474:LEU:HD23	5:K:28:ARG:HG2	1.82	0.61
6:L:389:SER:OG	7:O:54:DT:H4'	2.00	0.61
2:G:183:ILE:CD1	2:G:205:MET:HB2	2.31	0.61
4:J:411:ILE:O	4:J:415:VAL:HG13	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:1238:GLN:HB3	4:J:1242:ARG:HH12	1.65	0.61
2:G:86:LYS:NZ	3:I:826:ASP:OD2	2.33	0.61
2:H:30:PRO:HG3	2:H:192:VAL:HG11	1.81	0.61
4:J:130:MET:HE2	4:J:134:ASP:HB3	1.82	0.61
4:J:397:ALA:O	4:J:401:VAL:HG13	2.00	0.61
6:L:290:LEU:O	6:L:294:GLN:HB3	2.00	0.61
4:J:225:GLU:O	4:J:229:GLN:HG2	2.01	0.61
4:J:1059:LEU:HB2	4:J:1107:VAL:CG2	2.30	0.61
6:L:261:LEU:HB2	6:L:266:PHE:HD1	1.64	0.61
6:L:277:MET:HE3	6:L:281:ARG:HH22	1.64	0.61
3:I:102:LEU:HB3	3:I:489:PRO:HG3	1.82	0.61
4:J:1209:VAL:O	4:J:1210:ILE:HD13	2.00	0.61
6:L:108:VAL:HG13	6:L:109:GLU:O	2.00	0.61
8:P:44:DT:H2''	8:P:45:DA:C8	2.34	0.61
1:N:20:ILE:HG12	4:J:754:ILE:HD13	1.83	0.61
3:I:136:PHE:CD2	3:I:145:ILE:HD13	2.36	0.61
4:J:985:ILE:HD11	4:J:991:THR:HG22	1.82	0.61
4:J:1005:LYS:HE2	4:J:1011:VAL:HG22	1.83	0.61
6:L:316:PHE:CD1	6:L:337:VAL:HG11	2.35	0.61
6:L:425:TYR:OH	7:O:50:DA:O3'	2.12	0.61
1:N:48:ARG:NH2	4:J:677:GLU:OE1	2.34	0.61
3:I:122:VAL:HG21	3:I:493:ILE:CG2	2.31	0.61
3:I:235:ASN:OD1	3:I:238:GLN:NE2	2.25	0.61
4:J:1105:ALA:HA	4:J:1123:ARG:O	2.01	0.61
4:J:1368:ASP:OD1	4:J:1369:ARG:N	2.34	0.61
6:L:150:ARG:NE	6:L:155:GLU:OE1	2.34	0.61
3:I:994:ARG:HG2	3:I:997:TRP:CH2	2.36	0.60
4:J:615:LYS:HE3	5:K:4:VAL:HG21	1.83	0.60
4:J:1155:ILE:HG12	4:J:1190:ILE:CD1	2.31	0.60
6:L:162:ILE:HG22	6:L:164:GLY:N	2.16	0.60
7:O:40:DC:H1'	7:O:41:DT:H5'	1.83	0.60
3:I:24:VAL:HG12	3:I:25:PRO:HD2	1.82	0.60
3:I:71:VAL:HB	3:I:99:LYS:O	2.02	0.60
3:I:250:THR:HA	3:I:268:ARG:HA	1.81	0.60
3:I:214:ASN:HD21	3:I:359:ARG:HD2	1.66	0.60
4:J:1044:GLN:O	4:J:1067:ARG:HD3	2.01	0.60
6:L:249:ILE:HG22	6:L:250:LEU:HD22	1.82	0.60
4:J:51:PRO:HB2	4:J:57:PHE:O	2.02	0.60
4:J:83:VAL:O	4:J:92:VAL:HG12	2.01	0.60
4:J:210:SER:O	4:J:214:ARG:NH1	2.35	0.60
6:L:286:LEU:O	6:L:290:LEU:HD13	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:347:ILE:HA	6:L:350:GLU:OE1	2.01	0.60
2:M:279:GLY:O	2:M:283:GLN:HG3	2.01	0.60
3:I:75:LEU:HD12	3:I:94:ALA:HB3	1.83	0.60
3:I:1085:MET:HE2	3:I:1086:PRO:HD3	1.83	0.60
3:I:1305:TYR:CE1	4:J:379:PRO:HG3	2.36	0.60
4:J:69:GLU:OE2	4:J:76:LYS:NZ	2.34	0.60
4:J:70:CYS:SG	4:J:73:GLY:N	2.73	0.60
4:J:196:GLN:HA	4:J:199:GLU:OE1	2.01	0.60
4:J:807:LEU:HD12	4:J:1259:GLN:OE1	2.01	0.60
4:J:1082:ASP:OD1	4:J:1086:ASN:N	2.29	0.60
3:I:123:TYR:OH	3:I:126:GLU:OE2	2.16	0.60
3:I:1101:LEU:HD13	4:J:504:GLN:HB2	1.83	0.60
4:J:885:VAL:HG23	4:J:894:VAL:HG21	1.83	0.60
6:L:383:ASN:HB2	6:L:412:LEU:HD21	1.84	0.60
6:L:452:ILE:HG13	6:L:457:ILE:HG13	1.84	0.60
3:I:104:ILE:HG13	3:I:115:LYS:HG3	1.82	0.60
3:I:213:LEU:HD11	3:I:422:LYS:HG3	1.84	0.60
3:I:1007:LYS:HA	3:I:1010:GLN:HE21	1.65	0.60
3:I:1339:LEU:HG	4:J:17:PHE:CD2	2.37	0.60
4:J:514:THR:HG21	4:J:596:LEU:HB2	1.84	0.60
4:J:1047:THR:HG22	4:J:1060:VAL:O	2.02	0.60
6:L:330:LEU:HD23	6:L:333:VAL:CG1	2.31	0.60
2:M:303:ILE:O	2:M:307:LEU:HD13	2.01	0.60
1:N:12:THR:O	1:N:16:THR:HG23	2.01	0.60
3:I:105:TYR:HA	3:I:114:VAL:HA	1.82	0.60
3:I:936:ARG:HG2	3:I:937:ASP:H	1.65	0.60
3:I:1297:ASP:O	3:I:1301:ARG:HB2	2.01	0.60
4:J:142:GLU:OE2	6:L:103:ARG:NH2	2.35	0.60
4:J:515:ARG:NH2	4:J:717:VAL:HB	2.16	0.60
4:J:810:THR:CG2	4:J:893:GLY:HA3	2.32	0.60
4:J:950:ILE:HD13	4:J:995:TYR:CB	2.31	0.60
4:J:1155:ILE:CD1	4:J:1210:ILE:HB	2.32	0.60
3:I:1005:GLU:OE1	3:I:1005:GLU:N	2.32	0.60
3:I:1109:ILE:O	3:I:1113:LEU:HD12	2.01	0.60
4:J:385:LEU:CD2	4:J:411:ILE:HG13	2.30	0.60
6:L:141:ILE:HG23	6:L:144:LEU:HD23	1.84	0.60
6:L:227:GLN:HG2	6:L:252:LEU:HA	1.83	0.60
2:H:35:PHE:HA	2:H:38:THR:CG2	2.32	0.60
3:I:139:ASN:O	3:I:141:THR:HG23	2.01	0.60
3:I:277:LEU:O	3:I:281:ASP:HA	2.02	0.60
3:I:390:PHE:HA	3:I:419:ILE:HD11	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:524:ILE:HD11	3:I:712:SER:HB3	1.83	0.60
3:I:1070:HIS:NE2	3:I:1114:GLU:OE1	2.23	0.60
3:I:1326:LEU:O	3:I:1330:ILE:HG13	2.02	0.60
4:J:308:ASP:HB3	4:J:328:ALA:CB	2.31	0.60
4:J:530:PRO:HB2	4:J:581:MET:CE	2.32	0.60
4:J:670:SER:OG	4:J:672:LEU:HD13	2.02	0.60
4:J:963:VAL:HG22	4:J:980:THR:OG1	2.02	0.60
6:L:118:ASP:O	6:L:122:ARG:HG3	2.01	0.60
6:L:231:THR:HG23	6:L:248:GLU:CB	2.32	0.60
2:H:118:ASP:HB3	2:H:121:VAL:HG22	1.83	0.59
3:I:13:LYS:CB	3:I:1180:MET:HE3	2.31	0.59
3:I:1319:MET:HE1	4:J:1353:VAL:CG2	2.31	0.59
4:J:309:ASN:HD21	4:J:324:LEU:HB2	1.67	0.59
4:J:1175:LEU:O	4:J:1188:GLU:N	2.35	0.59
2:H:51:MET:HE1	2:H:219:ARG:CB	2.32	0.59
3:I:1234:LYS:HE2	3:I:1238:LEU:HD11	1.84	0.59
4:J:71:LEU:H	4:J:90:VAL:HG21	1.66	0.59
4:J:168:ALA:O	4:J:172:PHE:N	2.31	0.59
4:J:824:PRO:HB2	4:J:831:VAL:HG11	1.83	0.59
4:J:1046:ILE:C	4:J:1062:LEU:HG	2.26	0.59
4:J:530:PRO:HB2	4:J:581:MET:HE2	1.82	0.59
4:J:1173:ARG:NH2	4:J:1196:LEU:HG	2.17	0.59
4:J:1221:LEU:CD2	4:J:1306:LEU:HB2	2.31	0.59
1:N:64:TYR:O	1:N:68:GLN:HG2	2.02	0.59
3:I:242:VAL:HB	3:I:245:ARG:HG3	1.85	0.59
3:I:1319:MET:HE3	3:I:1320:PRO:HD2	1.85	0.59
4:J:843:VAL:HG23	4:J:863:LEU:HD12	1.83	0.59
2:M:283:GLN:O	2:M:315:GLY:HA2	2.02	0.59
2:M:298:LYS:O	2:M:301:THR:HG22	2.02	0.59
3:I:1103:VAL:HG11	3:I:1112:ILE:CD1	2.32	0.59
4:J:262:THR:HG22	4:J:263:SER:O	2.03	0.59
4:J:553:THR:CB	4:J:567:THR:HG22	2.32	0.59
4:J:844:THR:HG23	4:J:864:LEU:HD21	1.83	0.59
6:L:335:GLU:HG3	6:L:336:GLU:OE1	2.03	0.59
7:O:73:DC:H2''	7:O:74:DC:C5'	2.31	0.59
2:M:268:ASN:O	2:M:271:LYS:HB3	2.02	0.59
2:H:208:ASN:OD1	2:H:210:THR:HG23	2.03	0.59
6:L:277:MET:HG3	6:L:281:ARG:HH12	1.67	0.59
6:L:585:GLU:HB3	7:O:27:DT:H71	1.84	0.59
2:M:255:ARG:HB2	2:M:278:ILE:CD1	2.33	0.59
2:H:83:LEU:HD11	4:J:526:VAL:HB	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:190:ALA:O	2:H:198:LEU:HB2	2.02	0.59
3:I:395:TYR:HE2	3:I:420:LEU:HD22	1.67	0.59
4:J:422:LEU:CD1	4:J:471:PRO:HG3	2.33	0.59
4:J:663:GLU:O	4:J:666:GLU:HG3	2.03	0.59
3:I:241:LEU:HD21	3:I:277:LEU:HD11	1.85	0.59
3:I:257:ALA:CB	3:I:282:VAL:HG21	2.33	0.59
3:I:896:THR:CG2	3:I:897:PRO:HD2	2.33	0.59
3:I:1247:SER:O	4:J:348:ASP:HB3	2.03	0.59
4:J:850:LYS:HD2	4:J:851:PRO:HD2	1.85	0.59
2:G:154:PRO:O	2:G:158:ARG:HG3	2.02	0.59
3:I:1259:LEU:HD11	6:L:524:GLU:HB3	1.85	0.59
4:J:224:LEU:O	4:J:228:VAL:HG12	2.03	0.59
4:J:260:PHE:O	6:L:505:ILE:N	2.35	0.59
2:G:57:THR:HG22	2:G:58:GLU:CG	2.33	0.59
2:H:24:ALA:HB2	2:H:213:PRO:HG2	1.84	0.59
3:I:195:PHE:C	3:I:206:ALA:HB2	2.28	0.59
3:I:940:GLU:OE1	3:I:940:GLU:N	2.35	0.59
3:I:960:LEU:HB3	3:I:1025:PHE:HD1	1.68	0.59
4:J:438:GLU:HG3	4:J:485:MET:CE	2.33	0.59
4:J:1350:ASN:HD22	4:J:1358:PRO:HD3	1.68	0.59
4:J:306:LEU:HD22	4:J:306:LEU:O	2.02	0.58
4:J:822:MET:CE	4:J:838:ARG:HB3	2.33	0.58
4:J:1036:ARG:HA	4:J:1111:ASP:OD2	2.03	0.58
6:L:127:ILE:O	6:L:131:GLN:HG3	2.01	0.58
2:G:134:THR:HG21	3:I:727:VAL:O	2.02	0.58
2:H:74:VAL:HG22	2:H:133:LEU:CD2	2.33	0.58
4:J:1046:ILE:HA	4:J:1061:VAL:HA	1.86	0.58
4:J:1046:ILE:HA	4:J:1062:LEU:H	1.67	0.58
5:K:53:GLU:HB3	5:K:59:ILE:HG12	1.85	0.58
2:M:304:LYS:HD2	2:M:314:LEU:CD1	2.32	0.58
3:I:646:SER:H	3:I:649:GLN:HE21	1.49	0.58
3:I:823:VAL:HG22	3:I:1060:ILE:CG2	2.33	0.58
4:J:290:ILE:HD13	6:L:381:GLU:OE1	2.03	0.58
4:J:1175:LEU:HD23	4:J:1190:ILE:HG13	1.86	0.58
6:L:137:TYR:CD2	6:L:140:ALA:HB2	2.38	0.58
8:P:47:DC:H2"	8:P:48:DC:C6	2.38	0.58
3:I:525:THR:HG21	3:I:687:ARG:HD3	1.85	0.58
3:I:745:GLU:HB2	3:I:1017:GLN:CG	2.33	0.58
4:J:1047:THR:CG2	4:J:1060:VAL:HB	2.32	0.58
6:L:273:MET:HB3	6:L:362:ASN:HD21	1.67	0.58
2:G:102:LEU:HD11	2:G:110:VAL:CG2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:32:GLU:HB3	2:H:35:PHE:HD2	1.67	0.58
3:I:1120:ALA:HB2	3:I:1199:LEU:HD12	1.84	0.58
6:L:117:ILE:HG23	6:L:421:TYR:CD2	2.39	0.58
6:L:470:MET:HG2	6:L:486:ARG:HD2	1.85	0.58
8:P:66:DT:H2'	8:P:67:DT:H71	1.84	0.58
3:I:245:ARG:HD2	3:I:337:PHE:CE2	2.39	0.58
4:J:1049:GLN:HG2	4:J:1050:THR:H	1.69	0.58
4:J:1174:ARG:HG2	4:J:1189:MET:CE	2.33	0.58
6:L:227:GLN:OE1	6:L:251:LYS:HB3	2.04	0.58
6:L:484:ALA:HB2	6:L:494:ILE:HD13	1.84	0.58
6:L:585:GLU:HG2	7:O:27:DT:O4	2.03	0.58
3:I:106:GLU:OE2	3:I:115:LYS:HB3	2.03	0.58
3:I:1111:GLN:HG3	3:I:1230:MET:CE	2.34	0.58
4:J:79:LYS:HG3	6:L:569:THR:CB	2.32	0.58
2:H:35:PHE:HA	2:H:38:THR:HG22	1.86	0.58
2:H:215:GLU:OE1	2:H:218:ARG:NH2	2.30	0.58
3:I:676:ALA:HB3	4:J:779:ALA:CB	2.33	0.58
3:I:685:MET:SD	3:I:1073:LYS:HG2	2.44	0.58
3:I:948:ILE:O	3:I:952:GLN:HG3	2.03	0.58
4:J:814:CYS:CB	4:J:889:ASP:HB3	2.31	0.58
6:L:487:MET:O	6:L:488:LEU:HD23	2.04	0.58
8:P:34:DT:H2''	8:P:35:DA:C5	2.39	0.58
3:I:348:SER:HA	3:I:351:LEU:HD12	1.85	0.58
3:I:590:PRO:HG3	3:I:605:TYR:HE1	1.69	0.58
3:I:697:LYS:HA	3:I:795:ALA:HB2	1.85	0.58
4:J:398:LYS:HD2	6:L:532:LEU:HD21	1.84	0.58
4:J:1026:PRO:HB2	4:J:1028:ILE:HG23	1.84	0.58
6:L:117:ILE:O	6:L:121:LYS:HG3	2.04	0.58
6:L:496:LYS:O	6:L:500:ILE:HG12	2.04	0.58
6:L:552:THR:HB	6:L:555:GLU:HB3	1.86	0.58
1:N:8:ALA:HB2	4:J:783:LEU:HD12	1.84	0.58
3:I:72:SER:OG	3:I:73:TYR:N	2.37	0.58
3:I:220:ILE:HG22	3:I:221:LEU:HD23	1.85	0.58
3:I:681:MET:HE3	3:I:1073:LYS:HE3	1.86	0.58
4:J:131:PRO:HG2	4:J:134:ASP:OD2	2.04	0.58
4:J:311:ARG:NH2	4:J:1329:THR:HG21	2.18	0.58
4:J:527:LEU:HD22	4:J:550:VAL:HG12	1.85	0.58
4:J:697:MET:CE	4:J:738:ARG:HA	2.33	0.58
3:I:888:THR:HG23	3:I:916:SER:HB2	1.84	0.57
4:J:846:GLU:HG2	4:J:881:LYS:HB3	1.86	0.57
5:K:10:VAL:CG2	5:K:16:ARG:HG3	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:175:ARG:HD2	3:I:177:ILE:HD11	1.84	0.57
3:I:189:ASP:OD1	3:I:193:ASN:N	2.36	0.57
3:I:256:GLU:HB3	3:I:261:VAL:HA	1.86	0.57
3:I:1213:TYR:CE1	3:I:1220:GLN:HB2	2.39	0.57
4:J:1187:GLU:OE2	4:J:1189:MET:HE3	2.04	0.57
10:J:1504:1N7:C3	10:J:1504:1N7:C2	2.76	0.57
6:L:137:TYR:CZ	6:L:139:GLU:HB3	2.39	0.57
6:L:341:LEU:HD23	6:L:344:LEU:HD22	1.85	0.57
2:H:134:THR:HG23	2:H:136:GLU:HB2	1.86	0.57
3:I:28:LEU:HD22	3:I:527:LYS:HD2	1.85	0.57
3:I:463:GLN:O	3:I:466:VAL:HG12	2.04	0.57
3:I:964:LEU:HD22	3:I:1025:PHE:HB3	1.86	0.57
3:I:1120:ALA:HB1	3:I:1198:LEU:HD23	1.86	0.57
4:J:824:PRO:HB2	4:J:831:VAL:CG1	2.34	0.57
4:J:1162:ILE:HG13	4:J:1202:GLU:O	2.03	0.57
8:P:18:DT:C2'	8:P:19:DT:H71	2.34	0.57
2:M:255:ARG:HB2	2:M:278:ILE:CG1	2.34	0.57
2:H:14:VAL:HG22	2:H:28:LEU:HD12	1.85	0.57
3:I:263:VAL:HG12	3:I:264:GLU:H	1.68	0.57
3:I:924:VAL:HG23	3:I:1056:VAL:HG21	1.86	0.57
4:J:26:SER:HB3	4:J:236:TRP:CZ2	2.40	0.57
4:J:334:LYS:O	4:J:340:GLN:HB2	2.03	0.57
6:L:288:MET:HA	6:L:291:CYS:SG	2.45	0.57
6:L:390:ILE:HG21	6:L:435:ILE:HG22	1.84	0.57
7:O:29:DA:H2''	7:O:30:DC:C5'	2.35	0.57
7:O:69:DT:H6	7:O:69:DT:H5'	1.69	0.57
2:M:298:LYS:HA	2:M:301:THR:HG22	1.84	0.57
2:G:211:ILE:CG2	2:G:216:ALA:HB2	2.34	0.57
3:I:599:VAL:HG21	3:I:623:LEU:HD21	1.85	0.57
5:K:45:LYS:O	5:K:49:ILE:HG12	2.04	0.57
6:L:426:LYS:CB	7:O:52:DA:H5''	2.34	0.57
1:N:30:HIS:CD2	1:N:32:ILE:HG13	2.38	0.57
4:J:132:LEU:HA	4:J:135:ILE:HD13	1.87	0.57
4:J:153:ASN:ND2	4:J:171:GLU:OE2	2.37	0.57
6:L:102:MET:CE	6:L:388:ILE:HD13	2.35	0.57
6:L:244:THR:HA	6:L:247:GLU:OE1	2.05	0.57
2:M:279:GLY:HA2	2:M:282:VAL:CG2	2.35	0.57
2:H:102:LEU:HB3	2:H:142:MET:HG2	1.85	0.57
2:H:185:TYR:HA	2:H:202:VAL:O	2.04	0.57
3:I:558:VAL:HG13	3:I:573:ASN:HB3	1.86	0.57
3:I:617:ALA:HA	3:I:636:CYS:SG	2.45	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:514:THR:CG2	4:J:596:LEU:HB2	2.35	0.57
4:J:999:TYR:OH	4:J:1028:ILE:HG12	2.04	0.57
4:J:1031:VAL:HG23	4:J:1080:ILE:HG21	1.85	0.57
4:J:1307:LEU:HD22	4:J:1312:ALA:HA	1.85	0.57
4:J:1327:GLU:O	4:J:1331:VAL:HG23	2.04	0.57
3:I:196:VAL:HG23	3:I:206:ALA:HA	1.87	0.57
4:J:128:LEU:HD23	4:J:192:MET:CE	2.35	0.57
4:J:271:ARG:NH1	4:J:316:ILE:HG21	2.20	0.57
4:J:1161:GLY:CA	4:J:1179:PRO:HA	2.32	0.57
6:L:98:VAL:CA	6:L:402:LEU:HD11	2.34	0.57
7:O:37:DA:H2"	7:O:38:DG:C8	2.39	0.57
2:G:197:ASP:O	2:G:198:LEU:HD23	2.05	0.57
3:I:122:VAL:HG21	3:I:493:ILE:HG21	1.86	0.57
3:I:817:LEU:HD13	3:I:1085:MET:HE1	1.86	0.57
4:J:430:HIS:CD2	4:J:432:LEU:HD12	2.40	0.57
4:J:1238:GLN:HB3	4:J:1242:ARG:NH1	2.19	0.57
6:L:165:PHE:CD1	6:L:259:PHE:HA	2.40	0.57
2:G:52:PRO:HG2	2:G:219:ARG:HE	1.70	0.57
3:I:1287:LEU:CD2	4:J:1357:ILE:HD11	2.32	0.57
4:J:198:CYS:CB	4:J:221:ILE:HD11	2.34	0.57
6:L:285:ARG:O	6:L:289:LYS:HB2	2.04	0.57
6:L:560:ARG:HG3	6:L:565:ILE:CG2	2.35	0.57
3:I:901:LEU:HD13	6:L:565:ILE:HD11	1.87	0.56
3:I:960:LEU:HB3	3:I:1025:PHE:CD1	2.40	0.56
4:J:385:LEU:HD21	4:J:411:ILE:HG13	1.85	0.56
4:J:1179:PRO:HD2	4:J:1184:ASP:HA	1.87	0.56
7:O:25:DA:C2'	7:O:26:DT:H5"	2.35	0.56
1:N:27:ILE:HD11	4:J:680:ASN:CB	2.36	0.56
3:I:57:PHE:HE2	3:I:100:LEU:HD21	1.68	0.56
3:I:979:LEU:HD11	3:I:1011:LEU:CD1	2.35	0.56
4:J:438:GLU:HG3	4:J:485:MET:HE1	1.87	0.56
6:L:213:ASP:HB2	6:L:214:PRO:HD2	1.86	0.56
6:L:288:MET:HB3	6:L:302:PHE:CZ	2.40	0.56
3:I:56:VAL:HG13	3:I:57:PHE:CD1	2.39	0.56
3:I:359:ARG:HH22	3:I:382:GLU:HG2	1.70	0.56
3:I:965:GLN:HA	3:I:968:GLU:CD	2.29	0.56
4:J:20:ILE:HD13	4:J:1320:ILE:HD12	1.86	0.56
4:J:54:ASP:HB2	4:J:61:ILE:HD11	1.87	0.56
4:J:298:MET:CE	6:L:402:LEU:HB3	2.35	0.56
4:J:384:LYS:HG2	4:J:411:ILE:HG23	1.87	0.56
4:J:502:PRO:HB3	4:J:506:VAL:HB	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:552:ILE:HD11	4:J:570:LYS:HZ3	1.71	0.56
4:J:984:LEU:CB	4:J:993:GLU:HB2	2.35	0.56
4:J:1031:VAL:CG2	4:J:1080:ILE:HG21	2.35	0.56
4:J:1162:ILE:HA	4:J:1203:ARG:HA	1.87	0.56
4:J:1226:VAL:HA	4:J:1229:VAL:HG12	1.87	0.56
4:J:1322:ALA:HB3	4:J:1331:VAL:HG11	1.87	0.56
6:L:285:ARG:HG3	6:L:289:LYS:CE	2.35	0.56
6:L:313:ASP:CG	6:L:316:PHE:HB3	2.30	0.56
8:P:66:DT:C2'	8:P:67:DT:H71	2.35	0.56
2:G:11:PRO:O	2:G:30:PRO:HD2	2.05	0.56
2:G:180:VAL:HG12	2:G:207:THR:HG22	1.87	0.56
3:I:850:ILE:HD13	3:I:886:LYS:HB2	1.87	0.56
3:I:1112:ILE:HD11	4:J:639:VAL:HG13	1.87	0.56
4:J:202:ARG:HA	4:J:205:LEU:CD2	2.36	0.56
4:J:202:ARG:O	4:J:205:LEU:HD23	2.05	0.56
4:J:288:PRO:HG2	4:J:291:ILE:HG13	1.86	0.56
5:K:52:ARG:O	5:K:56:GLU:HG2	2.05	0.56
6:L:585:GLU:OE1	6:L:588:ARG:HD2	2.06	0.56
3:I:302:ILE:HG22	3:I:309:LEU:HA	1.87	0.56
3:I:366:ILE:O	3:I:369:MET:HE3	2.05	0.56
3:I:1085:MET:HE2	3:I:1085:MET:HA	1.88	0.56
4:J:134:ASP:HB3	4:J:159:ILE:HD11	1.88	0.56
4:J:1168:GLU:HG3	4:J:1173:ARG:CG	2.36	0.56
7:O:46:DG:C2'	7:O:47:DG:H5'	2.34	0.56
2:M:278:ILE:O	2:M:282:VAL:HG13	2.05	0.56
2:H:45:ARG:O	2:H:49:SER:OG	2.21	0.56
4:J:759:ILE:HD11	4:J:774:ILE:CG2	2.35	0.56
4:J:1189:MET:O	4:J:1191:PRO:HD3	2.06	0.56
6:L:339:ARG:O	6:L:342:GLN:HG3	2.06	0.56
6:L:572:THR:HB	8:P:55:DT:H5''	1.87	0.56
6:L:573:LEU:HG	6:L:584:ARG:HG2	1.87	0.56
4:J:1298:VAL:HG13	4:J:1299:GLY:O	2.05	0.56
4:J:1359:ALA:O	4:J:1363:TYR:HB2	2.06	0.56
2:G:130:ILE:HG22	2:G:131:CYS:SG	2.46	0.56
3:I:81:ASP:O	3:I:83:GLN:N	2.39	0.56
4:J:707:ILE:CD1	4:J:714:GLU:HB3	2.36	0.56
4:J:743:MET:HE3	4:J:760:THR:HA	1.88	0.56
4:J:1063:ASP:OD2	4:J:1103:GLY:HA3	2.05	0.56
6:L:295:CYS:O	6:L:326:TRP:HB2	2.05	0.56
2:H:219:ARG:O	2:H:223:ILE:HG13	2.06	0.56
3:I:210:LEU:CD2	3:I:220:ILE:HG12	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:689:ALA:HB2	3:I:1233:LEU:HB3	1.88	0.56
3:I:1296:ASP:OD1	3:I:1321:GLU:HB3	2.06	0.56
4:J:121:PRO:HB2	4:J:126:LEU:CD2	2.36	0.56
4:J:683:ILE:HD11	4:J:756:GLU:HA	1.88	0.56
6:L:573:LEU:HG	6:L:584:ARG:HB3	1.88	0.56
3:I:1141:LEU:O	3:I:1145:ILE:HG12	2.06	0.56
6:L:384:LEU:O	6:L:387:VAL:HG12	2.06	0.56
7:O:69:DT:H2'	7:O:70:DT:H72	1.88	0.56
4:J:317:THR:HG22	4:J:323:PRO:CA	2.35	0.55
4:J:700:ASN:O	4:J:704:GLU:HB2	2.05	0.55
8:P:52:DT:H2''	8:P:53:DT:C5	2.41	0.55
1:N:3:ASP:O	1:N:6:ASP:N	2.35	0.55
3:I:369:MET:CE	3:I:370:MET:HG2	2.36	0.55
3:I:468:LEU:O	3:I:471:VAL:HG12	2.05	0.55
4:J:1175:LEU:CD2	4:J:1190:ILE:HG13	2.37	0.55
6:L:547:VAL:HG23	6:L:548:LEU:HD23	1.88	0.55
2:H:98:VAL:HG21	2:H:121:VAL:HG11	1.87	0.55
3:I:44:GLU:N	3:I:44:GLU:OE2	2.39	0.55
3:I:377:THR:HB	3:I:380:ALA:HB3	1.89	0.55
3:I:988:LYS:O	3:I:992:LEU:HD22	2.06	0.55
4:J:722:ILE:HG23	4:J:737:ILE:HD12	1.89	0.55
6:L:397:ARG:HB2	6:L:443:ILE:HD13	1.89	0.55
6:L:604:SER:HA	6:L:607:LEU:HD23	1.89	0.55
8:P:34:DT:H2''	8:P:35:DA:N7	2.20	0.55
1:N:46:GLU:HA	1:N:49:ARG:NH2	2.21	0.55
2:H:33:ARG:NH1	3:I:1081:PRO:HG3	2.21	0.55
3:I:194:LEU:HD12	3:I:206:ALA:CB	2.36	0.55
3:I:369:MET:HE1	3:I:370:MET:HG2	1.89	0.55
3:I:845:LEU:HD21	3:I:889:PRO:O	2.06	0.55
3:I:1260:GLY:HA2	4:J:346:ARG:NH1	2.20	0.55
4:J:42:GLU:O	4:J:55:GLY:HA3	2.06	0.55
4:J:556:GLU:OE1	4:J:556:GLU:N	2.39	0.55
4:J:1035:VAL:HG23	4:J:1113:VAL:O	2.07	0.55
4:J:1145:PHE:O	4:J:1309:ILE:HG23	2.06	0.55
4:J:1167:LYS:HD3	4:J:1170:LYS:HD2	1.87	0.55
6:L:110:LEU:CB	6:L:111:LEU:HD13	2.34	0.55
6:L:225:ARG:O	6:L:229:VAL:HG22	2.06	0.55
6:L:313:ASP:OD1	6:L:316:PHE:HB3	2.07	0.55
7:O:33:DA:H2''	7:O:34:DA:C8	2.41	0.55
7:O:49:DC:H2''	7:O:50:DA:OP1	2.05	0.55
8:P:41:DT:C1'	8:P:42:DT:H5'	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:214:ASN:ND2	3:I:359:ARG:HD2	2.21	0.55
3:I:689:ALA:CB	3:I:1233:LEU:HB3	2.37	0.55
4:J:511:TYR:CE2	4:J:724:MET:HG2	2.40	0.55
8:P:20:DC:H2''	8:P:21:DA:C8	2.42	0.55
8:P:49:DT:H2''	8:P:50:DT:H71	1.89	0.55
2:H:51:MET:HE1	2:H:219:ARG:HB3	1.87	0.55
3:I:201:ARG:NH2	3:I:370:MET:O	2.40	0.55
3:I:633:LEU:HD13	3:I:644:LEU:CD1	2.32	0.55
3:I:806:PRO:O	4:J:633:ALA:HA	2.07	0.55
6:L:429:THR:HA	7:O:53:DT:C7	2.37	0.55
3:I:367:TYR:CZ	3:I:371:ARG:HG3	2.41	0.55
3:I:802:VAL:HG21	3:I:1098:LEU:HD12	1.88	0.55
4:J:35:PHE:CE2	4:J:101:ARG:HG2	2.42	0.55
4:J:759:ILE:HD11	4:J:774:ILE:HG21	1.89	0.55
4:J:973:LEU:HD22	4:J:1003:LEU:CD1	2.34	0.55
4:J:1155:ILE:HD13	4:J:1210:ILE:HB	1.87	0.55
2:G:47:LEU:CD2	2:G:220:ALA:HB2	2.37	0.55
2:H:98:VAL:HG21	2:H:121:VAL:CG1	2.37	0.55
3:I:67:GLU:HB3	3:I:103:VAL:CG2	2.36	0.55
3:I:1138:VAL:HA	3:I:1141:LEU:HB2	1.87	0.55
3:I:1319:MET:HE1	4:J:1353:VAL:HG22	1.87	0.55
4:J:1170:LYS:N	4:J:1172:LYS:O	2.39	0.55
4:J:1197:ASN:OD1	4:J:1211:SER:HA	2.06	0.55
2:M:257:VAL:HG11	2:M:270:LEU:CD2	2.36	0.55
2:H:79:LEU:HD23	2:H:80:GLU:H	1.72	0.55
3:I:16:GLY:HA2	3:I:1188:ASP:O	2.07	0.55
3:I:671:LEU:O	3:I:674:ASP:HB2	2.06	0.55
3:I:975:ILE:O	3:I:978:VAL:HG12	2.07	0.55
4:J:1190:ILE:CG2	4:J:1196:LEU:HD21	2.37	0.55
8:P:50:DT:H2''	8:P:51:DC:C5	2.42	0.55
3:I:5:TYR:HA	3:I:8:LYS:CE	2.37	0.55
3:I:102:LEU:CB	3:I:489:PRO:HG3	2.36	0.55
3:I:207:THR:HG21	3:I:351:LEU:HD23	1.88	0.55
3:I:995:ASP:O	3:I:998:LEU:HD22	2.06	0.55
4:J:850:LYS:CD	4:J:851:PRO:HD2	2.36	0.55
4:J:1141:VAL:HG22	4:J:1237:VAL:CG2	2.37	0.55
6:L:544:THR:O	6:L:548:LEU:HG	2.07	0.55
8:P:60:DA:C2'	8:P:61:DT:H71	2.37	0.55
3:I:356:THR:HG21	3:I:361:SER:OG	2.06	0.54
3:I:658:GLN:NE2	3:I:704:MET:SD	2.80	0.54
4:J:316:ILE:O	4:J:324:LEU:HD13	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:407:VAL:O	4:J:411:ILE:HG12	2.07	0.54
4:J:1079:LYS:HA	4:J:1098:GLN:CB	2.37	0.54
6:L:290:LEU:C	6:L:294:GLN:HB3	2.32	0.54
6:L:585:GLU:CB	7:O:27:DT:H71	2.37	0.54
3:I:21:VAL:HG11	3:I:592:ARG:CZ	2.38	0.54
3:I:558:VAL:CG1	3:I:573:ASN:HB3	2.37	0.54
3:I:669:PRO:HG3	3:I:1069:ARG:NH2	2.23	0.54
3:I:673:HIS:CD2	4:J:766:GLY:HA2	2.42	0.54
3:I:1086:PRO:HD2	3:I:1094:VAL:CG2	2.37	0.54
4:J:1042:ASP:HA	4:J:1046:ILE:O	2.07	0.54
6:L:290:LEU:HD23	6:L:294:GLN:OE1	2.07	0.54
2:H:181:GLU:HA	4:J:535:ARG:NH1	2.22	0.54
3:I:297:VAL:HA	3:I:335:THR:HG22	1.88	0.54
4:J:1048:ARG:NE	4:J:1048:ARG:HA	2.22	0.54
4:J:1271:SER:OG	4:J:1298:VAL:HG12	2.07	0.54
4:J:64:PRO:HG3	4:J:91:GLU:O	2.07	0.54
4:J:98:ARG:O	4:J:247:PRO:HD2	2.07	0.54
4:J:370:LYS:HZ3	4:J:441:LEU:HB3	1.72	0.54
4:J:773:PHE:O	4:J:776:THR:HG22	2.07	0.54
10:J:1504:1N7:H31	10:J:1504:1N7:H5	1.90	0.54
6:L:311:THR:HG21	6:L:348:GLU:OE2	2.06	0.54
6:L:429:THR:HA	7:O:53:DT:H72	1.90	0.54
1:N:19:GLY:C	4:J:754:ILE:HD11	2.32	0.54
3:I:870:ILE:HD13	3:I:1050:VAL:CG1	2.38	0.54
4:J:664:ILE:CD1	4:J:681:LYS:HG2	2.38	0.54
4:J:833:GLU:CD	4:J:1242:ARG:HD3	2.33	0.54
4:J:1146:GLU:OE1	4:J:1310:THR:HG22	2.08	0.54
6:L:226:ALA:O	6:L:230:VAL:HG12	2.06	0.54
6:L:399:LEU:HD13	6:L:443:ILE:HG12	1.89	0.54
6:L:561:MET:CA	6:L:567:MET:HE1	2.33	0.54
7:O:66:DG:H2''	7:O:67:DA:C5'	2.38	0.54
2:H:42:ALA:HB1	2:H:224:LEU:HD21	1.90	0.54
3:I:221:LEU:HD22	3:I:225:PHE:CE2	2.43	0.54
3:I:496:LYS:HE3	8:P:34:DT:H5''	1.90	0.54
3:I:633:LEU:HA	3:I:645:PHE:O	2.08	0.54
4:J:38:VAL:HG13	4:J:55:GLY:O	2.08	0.54
4:J:128:LEU:HA	4:J:192:MET:HE1	1.90	0.54
4:J:822:MET:HE1	4:J:838:ARG:HE	1.71	0.54
4:J:1153:PRO:HA	4:J:1214:PRO:O	2.08	0.54
7:O:56:DC:H5'	7:O:56:DC:C6	2.41	0.54
3:I:1234:LYS:HE2	3:I:1238:LEU:CD1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:153:ASN:O	4:J:154:LEU:HD23	2.07	0.54
4:J:205:LEU:HD12	4:J:214:ARG:CB	2.36	0.54
4:J:953:LYS:HB2	4:J:993:GLU:OE2	2.07	0.54
4:J:1107:VAL:HA	4:J:1122:ALA:HB2	1.90	0.54
6:L:105:MET:HE1	7:O:55:DC:C6	2.42	0.54
1:N:20:ILE:HG12	4:J:754:ILE:CD1	2.37	0.54
3:I:176:ILE:HD13	3:I:405:PHE:HE1	1.72	0.54
3:I:194:LEU:HD12	3:I:206:ALA:HB3	1.89	0.54
3:I:581:THR:HG22	3:I:585:GLY:HA2	1.90	0.54
3:I:1276:TRP:CE2	4:J:801:VAL:HG21	2.43	0.54
4:J:810:THR:HG21	4:J:893:GLY:HA3	1.90	0.54
4:J:1047:THR:CG2	4:J:1049:GLN:HB2	2.38	0.54
6:L:165:PHE:CE1	6:L:259:PHE:HA	2.42	0.54
2:H:64:VAL:HG11	2:H:78:ILE:HD12	1.89	0.54
3:I:124:MET:HE2	3:I:493:ILE:CD1	2.38	0.54
3:I:1260:GLY:HA2	4:J:346:ARG:HH12	1.71	0.54
4:J:147:ILE:HD11	4:J:179:LYS:NZ	2.22	0.54
4:J:473:THR:CG2	4:J:476:ALA:H	2.21	0.54
4:J:582:ILE:HD13	4:J:623:GLN:O	2.08	0.54
4:J:826:ILE:CG1	4:J:831:VAL:HG22	2.38	0.54
4:J:1036:ARG:NH2	4:J:1081:VAL:HG11	2.23	0.54
4:J:1168:GLU:HG3	4:J:1173:ARG:HG2	1.90	0.54
5:K:22:VAL:CG2	5:K:61:ASN:HB2	2.37	0.54
5:K:50:ALA:O	5:K:54:ILE:HG12	2.08	0.54
6:L:312:SER:O	6:L:315:TRP:NE1	2.41	0.54
2:M:255:ARG:O	2:M:278:ILE:N	2.40	0.54
1:N:20:ILE:N	4:J:754:ILE:HD11	2.22	0.54
3:I:236:LYS:NZ	3:I:288:PRO:HB3	2.22	0.54
3:I:347:ILE:H	3:I:347:ILE:HD12	1.73	0.54
4:J:812:ASP:O	4:J:897:HIS:ND1	2.32	0.54
4:J:1179:PRO:CD	4:J:1184:ASP:HA	2.38	0.54
4:J:1357:ILE:HG22	4:J:1359:ALA:N	2.23	0.54
6:L:150:ARG:HB3	6:L:155:GLU:OE1	2.08	0.54
2:H:74:VAL:HG22	2:H:133:LEU:HD23	1.88	0.53
3:I:727:VAL:HG21	3:I:771:VAL:O	2.07	0.53
3:I:798:GLN:OE1	3:I:827:ARG:HD2	2.08	0.53
3:I:1124:ILE:O	3:I:1128:ILE:HG13	2.07	0.53
4:J:887:SER:O	4:J:887:SER:OG	2.23	0.53
6:L:415:ALA:HB2	6:L:434:TRP:HB2	1.90	0.53
6:L:425:TYR:CE2	6:L:429:THR:HB	2.44	0.53
2:G:150:ARG:NH2	2:H:32:GLU:OE2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:109:PRO:HB3	2:H:132:HIS:CD2	2.44	0.53
3:I:221:LEU:HD11	3:I:314:ASN:HB3	1.89	0.53
3:I:242:VAL:HG11	3:I:245:ARG:CZ	2.38	0.53
3:I:533:LEU:HD21	3:I:571:LEU:HD13	1.90	0.53
3:I:619:ALA:HB2	3:I:654:ASP:HB2	1.91	0.53
3:I:1102:GLY:O	3:I:1106:ARG:HB2	2.08	0.53
3:I:1321:GLU:OE2	4:J:99:ARG:NH2	2.42	0.53
6:L:584:ARG:HD3	6:L:584:ARG:H	1.73	0.53
7:O:67:DA:H2''	7:O:68:DA:C8	2.43	0.53
2:H:29:GLU:OE1	2:H:200:LYS:HD2	2.08	0.53
3:I:56:VAL:CG1	3:I:468:LEU:HD13	2.38	0.53
3:I:289:VAL:HG21	3:I:322:LEU:CD2	2.32	0.53
3:I:359:ARG:O	3:I:362:ALA:HB3	2.08	0.53
3:I:542:ARG:HH21	7:O:63:DT:C5'	2.21	0.53
4:J:709:ARG:C	4:J:711:GLY:HA3	2.33	0.53
4:J:1197:ASN:HB2	4:J:1210:ILE:O	2.08	0.53
5:K:27:ALA:HA	5:K:46:THR:HG22	1.90	0.53
6:L:291:CYS:CA	6:L:295:CYS:HB3	2.38	0.53
6:L:573:LEU:HD23	6:L:574:GLU:H	1.73	0.53
2:H:14:VAL:HG22	2:H:28:LEU:CD1	2.38	0.53
3:I:829:THR:CB	3:I:1059:ARG:HA	2.36	0.53
3:I:861:ALA:C	3:I:862:LEU:HD23	2.34	0.53
3:I:1103:VAL:HG11	3:I:1112:ILE:CG1	2.38	0.53
4:J:308:ASP:HA	4:J:326:SER:OG	2.08	0.53
4:J:311:ARG:NH2	8:P:21:DA:OP1	2.41	0.53
6:L:285:ARG:CA	6:L:289:LYS:HD3	2.35	0.53
6:L:287:ILE:HG23	6:L:337:VAL:HG13	1.89	0.53
2:M:304:LYS:CD	2:M:314:LEU:HD11	2.37	0.53
2:G:79:LEU:CD1	3:I:693:LEU:HD11	2.38	0.53
2:G:179:PRO:HG3	2:G:211:ILE:CG1	2.38	0.53
2:H:205:MET:CE	2:H:217:ILE:HG13	2.39	0.53
3:I:104:ILE:HG12	3:I:116:ASP:O	2.08	0.53
3:I:124:MET:HE2	3:I:493:ILE:HD13	1.91	0.53
3:I:158:ASP:OD1	3:I:159:SER:N	2.41	0.53
3:I:1340:GLU:HG2	4:J:1341:ARG:HH22	1.72	0.53
4:J:259:ARG:CZ	6:L:505:ILE:HD11	2.39	0.53
4:J:801:VAL:HG12	4:J:920:ALA:CB	2.38	0.53
4:J:1025:MET:HG2	4:J:1124:ILE:O	2.08	0.53
6:L:141:ILE:HD12	6:L:256:PHE:CE1	2.43	0.53
6:L:312:SER:OG	6:L:314:THR:HG22	2.09	0.53
6:L:453:PRO:HG2	7:O:44:DA:OP2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:95:LYS:HE2	2:G:120:ASP:OD2	2.09	0.53
2:H:79:LEU:HD23	2:H:80:GLU:N	2.24	0.53
3:I:302:ILE:CG2	3:I:309:LEU:HD12	2.38	0.53
3:I:1104:PRO:HG2	4:J:725:MET:HE3	1.89	0.53
4:J:218:THR:HA	4:J:221:ILE:CG2	2.38	0.53
3:I:897:PRO:HB3	6:L:564:GLY:HA3	1.89	0.53
3:I:992:LEU:O	3:I:997:TRP:NE1	2.39	0.53
3:I:1075:VAL:HG12	4:J:461:PHE:O	2.09	0.53
4:J:275:ARG:HD3	4:J:298:MET:HG2	1.91	0.53
8:P:60:DA:H2'	8:P:61:DT:H71	1.88	0.53
3:I:76:GLY:HA3	3:I:95:PRO:HD2	1.90	0.53
3:I:230:PHE:HZ	3:I:295:LYS:HE3	1.74	0.53
3:I:1043:ALA:HB1	3:I:1044:PRO:HD2	1.91	0.53
3:I:1082:ILE:H	3:I:1082:ILE:HD12	1.73	0.53
3:I:1213:TYR:CD1	3:I:1220:GLN:HB2	2.43	0.53
6:L:113:ARG:CD	6:L:426:LYS:HE2	2.38	0.53
6:L:297:MET:HE1	6:L:305:LEU:CD2	2.33	0.53
2:M:321:TRP:CD2	2:M:322:PRO:HA	2.43	0.53
3:I:145:ILE:HA	3:I:511:LEU:O	2.09	0.53
3:I:963:GLU:O	3:I:967:LEU:HG	2.08	0.53
4:J:282:LEU:HD12	4:J:295:GLU:HG2	1.91	0.53
4:J:286:ALA:HB1	6:L:373:ARG:NH1	2.24	0.53
4:J:866:GLU:N	4:J:866:GLU:OE1	2.42	0.53
4:J:960:LEU:HB2	4:J:963:VAL:HG21	1.89	0.53
6:L:216:LEU:HA	6:L:219:GLU:HG2	1.91	0.53
6:L:476:ARG:HG3	6:L:477:GLU:H	1.73	0.53
2:G:42:ALA:O	2:G:46:ILE:HG12	2.09	0.53
3:I:1212:LEU:HD22	3:I:1225:VAL:CG2	2.34	0.53
3:I:1238:LEU:H	3:I:1238:LEU:HD22	1.74	0.53
4:J:111:THR:HG21	4:J:300:GLN:HA	1.91	0.53
4:J:591:ILE:HG22	4:J:592:VAL:HG13	1.91	0.53
4:J:793:SER:O	4:J:797:THR:HG22	2.09	0.53
6:L:98:VAL:N	6:L:402:LEU:HD11	2.24	0.53
6:L:353:LEU:HD22	6:L:357:GLN:OE1	2.09	0.53
6:L:560:ARG:HG3	6:L:565:ILE:HG21	1.90	0.53
4:J:384:LYS:HE3	4:J:415:VAL:HG12	1.90	0.52
4:J:551:ARG:HA	4:J:568:SER:O	2.09	0.52
4:J:902:ASP:HB3	4:J:905:ARG:O	2.09	0.52
5:K:36:ASP:OD1	5:K:36:ASP:N	2.42	0.52
6:L:126:GLY:O	6:L:129:GLN:NE2	2.26	0.52
6:L:288:MET:HE2	6:L:289:LYS:NZ	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:280:ASP:O	2:M:284:ARG:NH1	2.42	0.52
2:G:183:ILE:HD13	2:G:205:MET:HB2	1.91	0.52
2:H:31:LEU:HD11	2:H:39:LEU:HD12	1.91	0.52
3:I:172:TYR:O	3:I:432:LEU:HD11	2.09	0.52
3:I:225:PHE:CZ	3:I:347:ILE:HB	2.45	0.52
3:I:230:PHE:HA	3:I:239:MET:HA	1.90	0.52
3:I:420:LEU:HD23	3:I:420:LEU:O	2.09	0.52
3:I:602:GLU:O	3:I:602:GLU:HG3	2.08	0.52
3:I:964:LEU:HD22	3:I:1025:PHE:CB	2.40	0.52
4:J:614:LEU:HD23	5:K:5:THR:HG21	1.91	0.52
4:J:833:GLU:OE2	4:J:1242:ARG:HD3	2.10	0.52
4:J:848:VAL:HB	4:J:858:VAL:CG2	2.39	0.52
4:J:972:LYS:HZ2	4:J:1004:ALA:HA	1.73	0.52
6:L:233:ASP:N	6:L:233:ASP:OD1	2.41	0.52
3:I:19:PRO:HA	3:I:1156:ARG:HD2	1.90	0.52
3:I:101:ARG:HA	3:I:118:LYS:O	2.09	0.52
4:J:287:ALA:HB1	4:J:288:PRO:HD2	1.91	0.52
4:J:516:ASP:HB3	4:J:573:THR:HG21	1.90	0.52
4:J:706:VAL:HG12	4:J:715:LYS:HG3	1.90	0.52
4:J:1047:THR:HB	4:J:1062:LEU:CD2	2.39	0.52
4:J:1173:ARG:HB2	4:J:1192:LYS:HD2	1.92	0.52
4:J:1306:LEU:C	4:J:1307:LEU:HD12	2.34	0.52
2:H:15:ASP:O	2:H:26:VAL:HG13	2.08	0.52
3:I:165:HIS:ND1	3:I:167:SER:HB3	2.25	0.52
3:I:177:ILE:HG12	3:I:183:TRP:CE3	2.44	0.52
4:J:287:ALA:HB2	6:L:413:MET:HE1	1.91	0.52
4:J:844:THR:OG1	4:J:862:THR:OG1	2.28	0.52
4:J:1144:LEU:HD11	4:J:1236:GLU:CG	2.37	0.52
4:J:1178:THR:HG22	4:J:1184:ASP:HB2	1.91	0.52
1:N:37:CYS:HB2	1:N:58:CYS:HB3	1.91	0.52
2:G:85:LEU:CD2	2:G:130:ILE:HD13	2.40	0.52
4:J:512:TYR:CE2	4:J:635:SER:HB2	2.44	0.52
4:J:675:ALA:O	4:J:678:ARG:HG3	2.08	0.52
4:J:850:LYS:O	4:J:853:THR:N	2.33	0.52
4:J:885:VAL:HG23	4:J:894:VAL:CG2	2.38	0.52
4:J:1027:VAL:HG21	4:J:1122:ALA:HB3	1.92	0.52
4:J:1041:ILE:HD12	4:J:1045:THR:OG1	2.09	0.52
4:J:1162:ILE:O	4:J:1178:THR:N	2.34	0.52
4:J:1281:GLU:OE1	4:J:1283:SER:HB2	2.09	0.52
5:K:62:GLN:O	5:K:66:VAL:HG23	2.10	0.52
6:L:123:ILE:O	6:L:127:ILE:HD12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:151:VAL:HG13	6:L:156:ALA:O	2.10	0.52
7:O:39:DG:H2''	7:O:40:DC:H5'	1.89	0.52
2:H:17:GLU:HB2	2:H:25:LYS:O	2.10	0.52
3:I:211:ARG:HH12	3:I:216:THR:HA	1.75	0.52
3:I:637:ARG:HA	3:I:642:SER:HA	1.90	0.52
3:I:1212:LEU:HD11	3:I:1227:VAL:HG21	1.91	0.52
4:J:473:THR:HG22	4:J:476:ALA:H	1.74	0.52
4:J:1232:TYR:CD2	4:J:1233:ILE:HD12	2.45	0.52
6:L:354:THR:O	6:L:358:VAL:HG23	2.10	0.52
6:L:508:GLU:HA	6:L:518:HIS:HB3	1.91	0.52
3:I:155:VAL:HG23	3:I:176:ILE:CG1	2.34	0.52
4:J:116:PHE:O	4:J:124:ILE:HG13	2.10	0.52
4:J:975:ILE:HD13	4:J:980:THR:CG2	2.35	0.52
4:J:1155:ILE:HD12	4:J:1155:ILE:O	2.09	0.52
4:J:1284:ARG:HH12	4:J:1288:ALA:HB2	1.75	0.52
4:J:1363:TYR:O	4:J:1367:GLN:HG2	2.08	0.52
2:G:45:ARG:NH2	3:I:1215:GLY:O	2.43	0.52
3:I:569:ILE:CD1	4:J:783:LEU:HD23	2.40	0.52
3:I:893:THR:O	3:I:894:GLN:HB2	2.10	0.52
3:I:1254:VAL:HG13	3:I:1255:THR:HG23	1.92	0.52
3:I:1297:ASP:OD2	3:I:1319:MET:N	2.43	0.52
4:J:516:ASP:N	4:J:516:ASP:OD1	2.43	0.52
4:J:799:ARG:HA	4:J:802:ASP:OD1	2.08	0.52
4:J:810:THR:O	4:J:810:THR:OG1	2.27	0.52
4:J:1090:ILE:HG22	4:J:1091:PRO:HD2	1.91	0.52
6:L:343:LYS:O	6:L:347:ILE:HG13	2.10	0.52
2:G:12:ARG:HG2	2:H:230:ALA:CB	2.40	0.52
2:G:16:ILE:HG22	2:G:26:VAL:HG13	1.91	0.52
2:G:229:GLU:HA	2:G:232:VAL:HG12	1.92	0.52
3:I:370:MET:CE	3:I:388:LEU:HD11	2.36	0.52
3:I:840:SER:OG	3:I:848:GLU:O	2.26	0.52
4:J:131:PRO:O	4:J:135:ILE:HD12	2.09	0.52
4:J:1063:ASP:O	4:J:1067:ARG:HB3	2.10	0.52
6:L:130:VAL:HG13	6:L:365:MET:CG	2.40	0.52
6:L:585:GLU:O	6:L:589:GLN:HB2	2.09	0.52
1:N:73:ALA:HB3	3:I:169:LYS:HG3	1.91	0.52
3:I:43:PRO:HB2	3:I:44:GLU:OE2	2.10	0.52
3:I:58:PRO:HB2	3:I:67:GLU:OE2	2.09	0.52
3:I:593:LYS:HD3	3:I:604:HIS:CE1	2.45	0.52
3:I:820:GLU:O	3:I:824:GLN:HG3	2.10	0.52
3:I:961:SER:O	3:I:965:GLN:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:511:TYR:HA	4:J:595:ALA:O	2.10	0.52
4:J:859:PRO:HG2	4:J:862:THR:CG2	2.40	0.52
2:H:44:ARG:HH11	2:H:185:TYR:HE1	1.57	0.51
3:I:172:TYR:CD2	3:I:436:ARG:HD3	2.45	0.51
3:I:241:LEU:HD22	3:I:285:ILE:CG2	2.40	0.51
3:I:519:ASN:OD1	3:I:796:LEU:HD22	2.10	0.51
3:I:980:VAL:HA	3:I:984:VAL:HB	1.92	0.51
3:I:1088:ASP:OD1	3:I:1088:ASP:N	2.39	0.51
3:I:1257:GLN:NE2	3:I:1296:ASP:OD2	2.35	0.51
4:J:1059:LEU:HD11	4:J:1110:GLU:CG	2.39	0.51
6:L:551:LEU:HB2	6:L:556:ALA:HB2	1.91	0.51
6:L:554:ARG:NH2	6:L:582:VAL:HG11	2.25	0.51
6:L:605:GLU:OE1	6:L:606:VAL:HG13	2.09	0.51
2:H:60:GLU:OE2	2:H:65:LEU:HD21	2.11	0.51
3:I:228:VAL:O	3:I:334:GLU:HA	2.10	0.51
3:I:757:THR:HG22	3:I:765:ILE:HG12	1.91	0.51
3:I:836:LEU:CD1	3:I:1054:LEU:HD13	2.40	0.51
3:I:898:GLU:OE2	6:L:541:ARG:HG2	2.11	0.51
4:J:822:MET:HE2	4:J:838:ARG:HB3	1.93	0.51
4:J:836:ARG:HA	4:J:869:CYS:SG	2.49	0.51
6:L:470:MET:CG	6:L:486:ARG:HD2	2.39	0.51
1:N:16:THR:O	1:N:20:ILE:HG13	2.09	0.51
3:I:202:ARG:HD2	8:P:18:DT:OP1	2.10	0.51
3:I:596:ASP:OD1	3:I:596:ASP:N	2.42	0.51
3:I:966:ILE:HG12	10:I:1401:1N7:C16	2.41	0.51
3:I:979:LEU:CD2	3:I:1000:LEU:HD12	2.40	0.51
3:I:1075:VAL:HG21	4:J:354:VAL:HG11	1.92	0.51
4:J:114:ILE:HG21	4:J:308:ASP:OD1	2.09	0.51
4:J:268:LEU:O	4:J:272:VAL:HG23	2.10	0.51
4:J:1184:ASP:OD1	4:J:1184:ASP:N	2.32	0.51
4:J:1266:ILE:CD1	4:J:1285:VAL:HG21	2.41	0.51
6:L:143:TYR:HD2	6:L:269:LEU:HD21	1.74	0.51
6:L:148:TYR:HE1	6:L:158:LEU:HD23	1.75	0.51
6:L:335:GLU:O	6:L:339:ARG:HG3	2.10	0.51
2:G:180:VAL:HG12	2:G:207:THR:CG2	2.40	0.51
2:H:107:ILE:HG13	2:H:108:GLY:N	2.26	0.51
3:I:175:ARG:HG3	3:I:184:LEU:O	2.10	0.51
3:I:188:PHE:HA	3:I:194:LEU:HA	1.93	0.51
3:I:421:SER:OG	3:I:422:LYS:N	2.43	0.51
3:I:1102:GLY:O	3:I:1106:ARG:HD3	2.11	0.51
3:I:1291:LEU:CD2	4:J:1351:VAL:HG13	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:1155:ILE:CD1	4:J:1211:SER:H	2.23	0.51
6:L:271:ASN:O	6:L:275:VAL:HG12	2.10	0.51
2:G:53:GLY:O	2:G:148:ARG:HA	2.11	0.51
3:I:115:LYS:HG3	3:I:116:ASP:H	1.76	0.51
3:I:239:MET:HG2	3:I:240:GLU:O	2.10	0.51
3:I:1254:VAL:O	4:J:99:ARG:NH2	2.34	0.51
4:J:164:GLN:O	4:J:167:ASP:HB3	2.10	0.51
4:J:512:TYR:CD2	4:J:635:SER:HB2	2.46	0.51
4:J:706:VAL:CG1	4:J:715:LYS:HG3	2.41	0.51
4:J:1040:MET:SD	4:J:1078:LEU:HD23	2.51	0.51
6:L:311:THR:HA	6:L:344:LEU:HD21	1.92	0.51
6:L:360:ASP:O	6:L:364:ARG:HG2	2.11	0.51
6:L:392:LYS:O	6:L:395:THR:HG23	2.11	0.51
2:G:12:ARG:HB3	2:G:12:ARG:NH1	2.25	0.51
2:G:210:THR:OG1	2:G:211:ILE:N	2.43	0.51
2:G:222:THR:HB	2:H:232:VAL:HG13	1.92	0.51
3:I:115:LYS:NZ	3:I:484:LEU:HB3	2.26	0.51
3:I:385:PHE:CE1	3:I:386:GLU:HG2	2.46	0.51
3:I:1018:TYR:CZ	3:I:1022:LYS:HE3	2.45	0.51
3:I:1111:GLN:HG3	3:I:1230:MET:HE1	1.92	0.51
3:I:1120:ALA:HB2	3:I:1199:LEU:CD1	2.41	0.51
4:J:62:PHE:CD1	4:J:247:PRO:HD3	2.46	0.51
4:J:807:LEU:HD23	4:J:808:VAL:N	2.25	0.51
4:J:1056:LEU:HD23	4:J:1057:SER:O	2.09	0.51
5:K:39:VAL:HG23	5:K:40:PRO:HD2	1.92	0.51
6:L:348:GLU:OE2	6:L:354:THR:HA	2.10	0.51
2:G:8:PHE:O	2:G:9:LEU:HD23	2.11	0.51
3:I:519:ASN:O	3:I:523:GLU:HG3	2.11	0.51
3:I:565:GLU:HA	3:I:569:ILE:CG1	2.41	0.51
3:I:1308:ILE:HD11	4:J:472:LEU:HB3	1.92	0.51
3:I:1308:ILE:HG21	4:J:379:PRO:HB2	1.92	0.51
4:J:158:GLN:O	4:J:160:LEU:HG	2.10	0.51
4:J:681:LYS:HE3	4:J:685:ILE:CG2	2.41	0.51
4:J:1090:ILE:HB	4:J:1093:THR:OG1	2.11	0.51
2:H:52:PRO:HG3	2:H:150:ARG:HD3	1.91	0.51
3:I:53:PHE:CD1	3:I:468:LEU:HD11	2.46	0.51
3:I:228:VAL:HG12	3:I:239:MET:HE3	1.91	0.51
3:I:324:LYS:HA	3:I:327:GLN:CG	2.41	0.51
3:I:854:ILE:HD11	3:I:885:GLY:CA	2.40	0.51
3:I:1101:LEU:CD1	4:J:504:GLN:HB2	2.40	0.51
4:J:147:ILE:HD13	4:J:187:ALA:HB1	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:615:LYS:HB3	4:J:616:PRO:HD3	1.92	0.51
4:J:794:GLY:HA2	4:J:797:THR:CG2	2.40	0.51
4:J:934:THR:HA	4:J:1137:GLY:HA3	1.93	0.51
7:O:40:DC:H1'	7:O:41:DT:C5'	2.41	0.51
8:P:57:DT:H1'	8:P:58:DC:H5''	1.93	0.51
2:G:8:PHE:HE2	2:H:223:ILE:HD13	1.75	0.51
2:H:136:GLU:HG2	2:H:137:ASN:H	1.76	0.51
3:I:84:GLU:OE1	3:I:88:ARG:HG3	2.10	0.51
3:I:301:TYR:HB3	3:I:330:HIS:CD2	2.46	0.51
3:I:1066:MET:HE1	3:I:1096:ILE:HD11	1.92	0.51
3:I:1104:PRO:HG2	4:J:725:MET:HE1	1.93	0.51
4:J:128:LEU:HD23	4:J:192:MET:HE3	1.92	0.51
4:J:490:ILE:O	4:J:491:LEU:HD23	2.10	0.51
4:J:826:ILE:HG13	4:J:831:VAL:HG13	1.93	0.51
6:L:102:MET:SD	6:L:105:MET:HE2	2.51	0.51
6:L:388:ILE:HA	6:L:405:ILE:HD12	1.92	0.51
2:H:194:GLN:HA	2:H:195:ARG:C	2.35	0.51
3:I:178:PRO:HB3	3:I:397:LEU:HD12	1.93	0.51
3:I:276:GLN:HA	3:I:279:LYS:HE3	1.92	0.51
3:I:389:PHE:O	3:I:419:ILE:HD11	2.11	0.51
3:I:667:LEU:CD2	3:I:704:MET:HB3	2.41	0.51
3:I:1321:GLU:O	3:I:1325:VAL:HG23	2.11	0.51
4:J:267:ASP:OD2	4:J:324:LEU:HD21	2.11	0.51
4:J:482:ALA:O	4:J:483:LEU:HD23	2.11	0.51
4:J:644:MET:HE3	4:J:764:ARG:HB2	1.91	0.51
6:L:115:GLY:HA2	6:L:118:ASP:OD2	2.11	0.51
6:L:216:LEU:O	6:L:219:GLU:HG2	2.11	0.51
7:O:66:DG:H2''	7:O:67:DA:H5'	1.92	0.51
2:H:112:ALA:O	2:H:115:ILE:HG13	2.10	0.50
3:I:242:VAL:HG11	3:I:245:ARG:NE	2.26	0.50
3:I:257:ALA:HB2	3:I:285:ILE:CG2	2.41	0.50
3:I:559:CYS:CB	3:I:662:SER:HB3	2.41	0.50
4:J:128:LEU:HD11	4:J:189:LEU:CD2	2.41	0.50
4:J:279:LEU:HD23	4:J:283:LEU:HG	1.91	0.50
4:J:1162:ILE:HG13	4:J:1202:GLU:C	2.36	0.50
4:J:1257:VAL:HG13	4:J:1261:LEU:HD21	1.93	0.50
6:L:256:PHE:HA	6:L:259:PHE:CD2	2.46	0.50
2:H:89:ALA:O	2:H:124:VAL:HG23	2.10	0.50
3:I:31:GLN:HG3	3:I:527:LYS:HB3	1.93	0.50
3:I:195:PHE:CA	3:I:206:ALA:HB2	2.41	0.50
3:I:483:ASP:HB2	3:I:486:THR:OG1	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:598:VAL:HA	3:I:627:GLY:O	2.10	0.50
3:I:1337:ILE:HB	4:J:22:ILE:HG13	1.93	0.50
4:J:370:LYS:HA	4:J:441:LEU:HD12	1.93	0.50
6:L:573:LEU:HG	6:L:584:ARG:CB	2.41	0.50
2:M:266:SER:OG	2:M:303:ILE:HD11	2.11	0.50
3:I:448:LEU:HD12	3:I:554:HIS:ND1	2.27	0.50
3:I:1002:LEU:HD12	3:I:1003:THR:N	2.22	0.50
3:I:1122:LYS:HA	3:I:1179:GLY:HA2	1.92	0.50
3:I:1153:ALA:O	3:I:1155:VAL:HG13	2.11	0.50
3:I:1291:LEU:HD21	4:J:1351:VAL:HG13	1.93	0.50
4:J:201:LEU:CD2	4:J:217:LEU:HD21	2.34	0.50
4:J:449:LEU:HD13	4:J:466:MET:SD	2.52	0.50
4:J:709:ARG:HH11	4:J:710:ASP:H	1.57	0.50
4:J:1307:LEU:CD2	4:J:1312:ALA:HA	2.40	0.50
7:O:55:DC:H5'	7:O:55:DC:C6	2.43	0.50
3:I:230:PHE:CZ	3:I:295:LYS:HE3	2.45	0.50
3:I:264:GLU:OE2	3:I:265:LYS:HB3	2.11	0.50
3:I:272:ARG:O	3:I:276:GLN:HG3	2.11	0.50
3:I:741:MET:HG2	3:I:746:ALA:CB	2.40	0.50
3:I:832:HIS:ND1	3:I:1058:ARG:HD2	2.26	0.50
3:I:1066:MET:HE1	3:I:1096:ILE:CD1	2.42	0.50
3:I:1096:ILE:HD12	3:I:1232:MET:SD	2.51	0.50
4:J:516:ASP:HA	4:J:545:HIS:HB2	1.93	0.50
4:J:583:VAL:HG13	4:J:587:LEU:HD22	1.92	0.50
3:I:962:GLU:O	3:I:966:ILE:HG13	2.10	0.50
4:J:1061:VAL:HB	4:J:1103:GLY:HA2	1.94	0.50
6:L:96:ASP:H	6:L:100:MET:HE3	1.76	0.50
6:L:575:GLU:O	6:L:578:LYS:HG2	2.11	0.50
2:H:30:PRO:HG2	2:H:192:VAL:HG21	1.93	0.50
3:I:207:THR:HG21	3:I:351:LEU:CD2	2.41	0.50
3:I:402:ARG:NE	3:I:406:ASN:OD1	2.45	0.50
3:I:1127:LYS:O	3:I:1131:MET:HE3	2.12	0.50
4:J:707:ILE:HD11	4:J:714:GLU:HB3	1.93	0.50
4:J:986:ASP:OD1	4:J:986:ASP:N	2.42	0.50
4:J:1040:MET:CE	4:J:1046:ILE:HD13	2.41	0.50
4:J:1063:ASP:O	4:J:1067:ARG:N	2.43	0.50
4:J:1079:LYS:HD3	4:J:1087:ASP:OD1	2.12	0.50
4:J:1178:THR:CG2	4:J:1184:ASP:HB2	2.42	0.50
6:L:346:GLN:O	6:L:350:GLU:HG3	2.11	0.50
7:O:51:DT:H2'	7:O:52:DA:C8	2.47	0.50
2:H:22:THR:O	2:H:213:PRO:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:105:SER:HB2	2:H:139:SER:HB2	1.93	0.50
3:I:1319:MET:HE2	3:I:1323:PHE:CD2	2.47	0.50
4:J:475:GLU:O	4:J:479:GLU:HG3	2.12	0.50
4:J:848:VAL:CG2	4:J:880:VAL:HG13	2.42	0.50
4:J:910:ASN:HB3	5:K:15:ASN:OD1	2.11	0.50
4:J:984:LEU:HB2	4:J:993:GLU:HB2	1.93	0.50
4:J:1024:THR:CG2	4:J:1123:ARG:HA	2.38	0.50
5:K:53:GLU:HB3	5:K:59:ILE:CG1	2.42	0.50
7:O:28:DG:H2''	7:O:29:DA:C5'	2.41	0.50
2:H:16:ILE:CG1	2:H:26:VAL:HG22	2.42	0.50
2:H:64:VAL:HG13	2:H:69:SER:HB2	1.94	0.50
3:I:310:ILE:O	3:I:324:LYS:NZ	2.41	0.50
3:I:461:GLU:OE2	3:I:465:ARG:NH2	2.43	0.50
4:J:260:PHE:HB2	6:L:504:PRO:HB3	1.93	0.50
4:J:491:LEU:HD11	4:J:609:TYR:CE2	2.47	0.50
4:J:808:VAL:HG22	4:J:914:ALA:HA	1.93	0.50
4:J:839:VAL:CG2	4:J:882:VAL:HG11	2.41	0.50
4:J:1041:ILE:H	4:J:1045:THR:HG1	1.59	0.50
4:J:1173:ARG:HH22	4:J:1196:LEU:HG	1.77	0.50
6:L:102:MET:HE1	6:L:388:ILE:HD13	1.94	0.50
6:L:136:GLU:HB3	6:L:361:ILE:HD13	1.93	0.50
6:L:262:VAL:HG13	6:L:263:PRO:HD2	1.93	0.50
1:N:64:TYR:CD1	3:I:341:LEU:HD22	2.47	0.50
2:H:59:VAL:O	2:H:171:LEU:HB2	2.11	0.50
3:I:74:ARG:NH1	3:I:97:ARG:HG3	2.27	0.50
3:I:905:ILE:CD1	6:L:595:LEU:HB2	2.42	0.50
3:I:953:LEU:HD21	3:I:1033:ARG:CG	2.34	0.50
4:J:112:ALA:HA	4:J:238:ILE:HD13	1.93	0.50
4:J:1047:THR:HG22	4:J:1060:VAL:HB	1.92	0.50
6:L:227:GLN:NE2	6:L:231:THR:OG1	2.45	0.50
6:L:548:LEU:HD13	6:L:560:ARG:HD2	1.94	0.50
3:I:104:ILE:HD11	3:I:116:ASP:CB	2.41	0.49
3:I:499:SER:O	3:I:503:LYS:HG3	2.12	0.49
3:I:808:ASN:H	4:J:633:ALA:HB2	1.77	0.49
3:I:1282:GLY:HA3	5:K:17:PHE:CE1	2.47	0.49
4:J:264:ASP:OD1	4:J:264:ASP:N	2.44	0.49
4:J:298:MET:HE1	6:L:402:LEU:HB3	1.93	0.49
4:J:422:LEU:CD2	4:J:484:MET:HE1	2.42	0.49
4:J:957:SER:N	4:J:985:ILE:O	2.30	0.49
4:J:1059:LEU:O	4:J:1106:ILE:HA	2.12	0.49
5:K:4:VAL:HG23	5:K:5:THR:OG1	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:311:THR:HA	6:L:344:LEU:CD2	2.42	0.49
6:L:584:ARG:O	6:L:587:ILE:HG13	2.12	0.49
8:P:52:DT:H2''	8:P:53:DT:C7	2.42	0.49
2:G:12:ARG:HB3	2:G:12:ARG:CZ	2.41	0.49
3:I:13:LYS:HB2	3:I:1180:MET:HE3	1.94	0.49
3:I:109:ALA:HB1	3:I:112:GLY:CA	2.35	0.49
4:J:483:LEU:CD2	5:K:16:ARG:HD3	2.42	0.49
4:J:1327:GLU:HB2	8:P:21:DA:H4'	1.93	0.49
3:I:241:LEU:HD23	3:I:282:VAL:O	2.12	0.49
3:I:1289:GLU:HB3	3:I:1315:MET:HE1	1.94	0.49
4:J:653:ILE:HG21	4:J:693:VAL:CG2	2.42	0.49
4:J:824:PRO:HG2	4:J:826:ILE:HD11	1.93	0.49
5:K:79:GLU:HG2	5:K:79:GLU:O	2.12	0.49
6:L:291:CYS:HA	6:L:295:CYS:H	1.76	0.49
6:L:425:TYR:HH	7:O:50:DA:C3'	2.21	0.49
7:O:35:DG:N2	8:P:52:DT:O2	2.45	0.49
3:I:360:LEU:O	3:I:364:VAL:HG23	2.12	0.49
3:I:905:ILE:HD11	6:L:595:LEU:HB2	1.94	0.49
3:I:936:ARG:HB3	3:I:939:VAL:CG2	2.43	0.49
3:I:1112:ILE:CD1	4:J:639:VAL:HG13	2.41	0.49
4:J:111:THR:CG2	4:J:300:GLN:HA	2.42	0.49
4:J:204:GLU:O	4:J:208:THR:OG1	2.20	0.49
5:K:3:ARG:NE	5:K:5:THR:O	2.39	0.49
5:K:30:MET:SD	5:K:37:PRO:HB3	2.52	0.49
3:I:829:THR:O	3:I:829:THR:OG1	2.29	0.49
3:I:1271:GLY:O	3:I:1275:VAL:HG23	2.13	0.49
3:I:1307:ASN:HB3	3:I:1312:ASN:O	2.12	0.49
4:J:421:VAL:HG13	4:J:439:PRO:HG3	1.92	0.49
4:J:515:ARG:O	4:J:545:HIS:HB3	2.13	0.49
4:J:712:GLN:HG2	4:J:713:GLU:N	2.28	0.49
6:L:162:ILE:N	6:L:262:VAL:HG23	2.27	0.49
6:L:284:GLU:HG3	6:L:306:PHE:CE1	2.48	0.49
6:L:305:LEU:O	6:L:315:TRP:HB2	2.12	0.49
2:G:11:PRO:HG3	2:G:31:LEU:HD21	1.94	0.49
3:I:147:SER:HB2	3:I:530:ILE:HD13	1.94	0.49
3:I:732:ILE:HD11	3:I:769:PRO:HB3	1.93	0.49
3:I:814:ASP:O	3:I:1074:GLY:HA2	2.12	0.49
3:I:885:GLY:HA2	3:I:917:SER:CB	2.41	0.49
3:I:1211:ARG:HG3	3:I:1211:ARG:O	2.11	0.49
4:J:1172:LYS:HG2	4:J:1191:PRO:HG3	1.94	0.49
5:K:59:ILE:HG23	5:K:64:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:162:ILE:CA	6:L:262:VAL:HG23	2.43	0.49
6:L:242:HIS:N	6:L:245:ALA:HB2	2.27	0.49
6:L:479:THR:HG22	6:L:482:GLU:OE1	2.12	0.49
2:G:189:ALA:HB1	2:G:191:ARG:HH12	1.77	0.49
3:I:941:LYS:NZ	3:I:949:GLU:OE1	2.24	0.49
3:I:1075:VAL:CG1	4:J:461:PHE:HB3	2.43	0.49
4:J:255:LEU:HD21	6:L:523:ILE:CD1	2.43	0.49
4:J:982:LEU:O	4:J:994:SER:HA	2.12	0.49
5:K:10:VAL:HG21	5:K:16:ARG:HG3	1.93	0.49
6:L:489:MET:HB2	6:L:494:ILE:HD11	1.95	0.49
2:M:262:LEU:HD21	2:M:303:ILE:HA	1.95	0.49
2:G:85:LEU:HD23	2:G:130:ILE:HD13	1.94	0.49
3:I:196:VAL:HG21	3:I:209:ILE:HD11	1.95	0.49
3:I:491:ASP:OD1	3:I:491:ASP:N	2.44	0.49
4:J:206:ASN:O	4:J:209:ASN:ND2	2.45	0.49
5:K:16:ARG:O	5:K:16:ARG:HG2	2.12	0.49
6:L:113:ARG:CZ	6:L:426:LYS:HD3	2.43	0.49
6:L:480:PRO:HA	6:L:483:LEU:HB2	1.94	0.49
2:G:102:LEU:HD21	2:G:114:ASP:HB2	1.95	0.49
3:I:98:VAL:HG21	3:I:124:MET:CE	2.41	0.49
3:I:367:TYR:CE2	3:I:371:ARG:HG3	2.48	0.49
3:I:581:THR:CG2	3:I:585:GLY:HA2	2.42	0.49
3:I:671:LEU:HD11	3:I:679:ALA:HB1	1.94	0.49
3:I:998:LEU:HD23	3:I:999:GLU:N	2.28	0.49
3:I:1026:GLU:OE1	3:I:1029:LEU:HD21	2.13	0.49
2:M:257:VAL:HG13	2:M:276:HIS:O	2.13	0.49
2:M:298:LYS:CA	2:M:301:THR:HG22	2.42	0.49
2:H:61:ILE:HG12	2:H:142:MET:HB3	1.94	0.49
3:I:158:ASP:HB3	3:I:173:ASN:OD1	2.13	0.49
3:I:965:GLN:HA	3:I:968:GLU:OE1	2.13	0.49
4:J:34:SER:OG	4:J:35:PHE:N	2.45	0.49
4:J:646:ILE:HD12	4:J:762:ASN:HD21	1.78	0.49
4:J:925:GLU:CG	4:J:926:PRO:HD3	2.32	0.49
6:L:213:ASP:O	6:L:216:LEU:HG	2.12	0.49
6:L:269:LEU:O	6:L:273:MET:HE3	2.12	0.49
6:L:276:MET:O	6:L:280:VAL:HG23	2.13	0.49
3:I:315:MET:HA	3:I:315:MET:HE3	1.95	0.48
3:I:471:VAL:HG21	3:I:493:ILE:HG13	1.95	0.48
3:I:894:GLN:HG2	4:J:77:ARG:NH2	2.25	0.48
4:J:75:TYR:HB3	4:J:80:HIS:HD2	1.78	0.48
4:J:646:ILE:HD12	4:J:762:ASN:ND2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:800:LEU:CD1	4:J:1309:ILE:HD12	2.43	0.48
4:J:965:SER:HB2	4:J:975:ILE:HA	1.95	0.48
4:J:1177:ILE:HD12	4:J:1186:TYR:CD2	2.48	0.48
4:J:1215:GLU:CG	4:J:1220:ILE:HD11	2.32	0.48
6:L:162:ILE:HG13	6:L:165:PHE:CZ	2.48	0.48
6:L:391:ALA:CB	6:L:405:ILE:HD13	2.43	0.48
2:G:190:ALA:HB2	2:G:200:LYS:CB	2.43	0.48
4:J:129:ASP:HB2	4:J:220:ARG:NH2	2.28	0.48
4:J:171:GLU:HG2	4:J:172:PHE:CD1	2.47	0.48
4:J:253:VAL:HG21	6:L:523:ILE:HG21	1.95	0.48
4:J:416:ILE:HG13	4:J:441:LEU:HD21	1.94	0.48
6:L:448:ARG:HH22	6:L:501:ALA:HA	1.78	0.48
6:L:587:ILE:HD12	6:L:588:ARG:N	2.28	0.48
7:O:23:DC:OP1	2:M:264:VAL:HG21	2.14	0.48
3:I:751:TYR:CE2	3:I:783:LEU:HD12	2.48	0.48
3:I:1043:ALA:O	3:I:1046:VAL:HG12	2.14	0.48
3:I:1291:LEU:O	4:J:345:LYS:HE3	2.12	0.48
4:J:218:THR:CA	4:J:221:ILE:HG22	2.41	0.48
4:J:888:CYS:HB3	4:J:1258:ARG:NH1	2.28	0.48
4:J:1142:ALA:O	4:J:1146:GLU:HG2	2.13	0.48
4:J:1330:ARG:HA	4:J:1333:THR:HG22	1.95	0.48
6:L:491:GLU:H	6:L:494:ILE:HD12	1.78	0.48
6:L:502:LYS:HD3	6:L:502:LYS:HA	1.56	0.48
6:L:595:LEU:O	6:L:599:ARG:HG2	2.13	0.48
2:M:277:TYR:HB2	2:M:280:ASP:CG	2.38	0.48
1:N:26:LYS:O	1:N:27:ILE:HD13	2.13	0.48
2:H:41:ASN:OD1	3:I:1217:THR:HG23	2.14	0.48
3:I:37:LYS:HE2	3:I:37:LYS:HA	1.94	0.48
3:I:188:PHE:CE1	3:I:194:LEU:HB3	2.48	0.48
3:I:220:ILE:HG22	3:I:221:LEU:CD2	2.43	0.48
3:I:576:SER:OG	3:I:577:VAL:N	2.45	0.48
3:I:799:ASN:OD1	3:I:799:ASN:N	2.43	0.48
3:I:901:LEU:CD1	6:L:565:ILE:HD11	2.44	0.48
4:J:56:LEU:HB3	4:J:250:ARG:HH12	1.79	0.48
4:J:975:ILE:HG21	4:J:980:THR:CG2	2.43	0.48
4:J:1246:VAL:HG12	4:J:1247:LYS:H	1.78	0.48
5:K:66:VAL:O	5:K:70:GLN:HG3	2.14	0.48
6:L:248:GLU:HA	6:L:251:LYS:HE2	1.94	0.48
2:G:13:LEU:HA	2:G:28:LEU:HA	1.95	0.48
2:H:92:VAL:HA	2:H:121:VAL:HA	1.94	0.48
2:H:158:ARG:HE	2:H:172:LEU:CD1	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:162:GLY:H	3:I:170:VAL:HG12	1.78	0.48
3:I:221:LEU:CD1	3:I:314:ASN:HB3	2.43	0.48
3:I:228:VAL:C	3:I:229:ILE:HD13	2.38	0.48
3:I:395:TYR:CD2	3:I:419:ILE:HG13	2.49	0.48
3:I:594:VAL:HG22	3:I:599:VAL:HG22	1.94	0.48
3:I:685:MET:SD	3:I:1073:LYS:HE2	2.54	0.48
3:I:971:LEU:CD2	3:I:1018:TYR:HB2	2.43	0.48
3:I:985:GLU:O	3:I:989:LEU:HB2	2.13	0.48
3:I:1086:PRO:HD2	3:I:1094:VAL:HG22	1.96	0.48
4:J:56:LEU:CD2	4:J:269:TYR:HB3	2.43	0.48
4:J:59:ALA:HA	4:J:63:GLY:O	2.12	0.48
4:J:134:ASP:O	4:J:138:VAL:HG12	2.13	0.48
4:J:145:VAL:HG22	4:J:159:ILE:HA	1.94	0.48
4:J:253:VAL:CG2	4:J:261:ALA:HB3	2.38	0.48
4:J:395:LYS:HD3	6:L:536:THR:HG21	1.96	0.48
6:L:162:ILE:HG13	6:L:165:PHE:CE2	2.49	0.48
3:I:301:TYR:OH	3:I:333:ILE:HA	2.13	0.48
3:I:896:THR:HG22	3:I:897:PRO:CD	2.42	0.48
3:I:902:LEU:HD21	6:L:611:LEU:CG	2.44	0.48
4:J:1035:VAL:HG21	4:J:1109:LEU:CD2	2.43	0.48
5:K:9:ALA:HB1	5:K:19:LEU:HD13	1.95	0.48
3:I:83:GLN:O	3:I:87:ILE:HG13	2.12	0.48
3:I:255:ILE:CG2	3:I:262:TYR:HB2	2.31	0.48
3:I:402:ARG:HG3	3:I:406:ASN:HD21	1.79	0.48
3:I:1288:GLN:NE2	3:I:1317:PRO:HG3	2.28	0.48
4:J:27:PRO:O	4:J:31:ARG:HG3	2.13	0.48
4:J:121:PRO:HB2	4:J:126:LEU:HD21	1.96	0.48
4:J:226:ALA:O	4:J:230:SER:OG	2.29	0.48
4:J:259:ARG:HB3	6:L:505:ILE:CD1	2.43	0.48
4:J:841:GLY:HA3	4:J:901:ARG:HG2	1.96	0.48
4:J:1079:LYS:HA	4:J:1098:GLN:HB2	1.96	0.48
4:J:1178:THR:HB	4:J:1184:ASP:HB2	1.94	0.48
6:L:141:ILE:HG21	6:L:256:PHE:CE1	2.49	0.48
8:P:35:DA:H2"	8:P:36:DT:C4	2.48	0.48
1:N:16:THR:HG22	4:J:748:ALA:HB3	1.96	0.48
2:G:49:SER:OG	2:G:50:SER:N	2.46	0.48
2:G:70:THR:CG2	3:I:729:ALA:HB3	2.44	0.48
2:H:14:VAL:HG13	2:H:28:LEU:CD1	2.44	0.48
3:I:958:LYS:O	3:I:961:SER:OG	2.22	0.48
4:J:75:TYR:HB3	4:J:80:HIS:CD2	2.49	0.48
4:J:174:ASP:HB3	4:J:175:GLU:OE2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:235:GLU:OE1	4:J:235:GLU:N	2.39	0.48
4:J:294:ASN:HD22	6:L:406:GLN:HE21	1.61	0.48
4:J:1077:ALA:CB	4:J:1100:PHE:HA	2.43	0.48
5:K:26:ARG:HH21	5:K:38:LEU:HD13	1.79	0.48
6:L:419:PHE:HB2	6:L:430:TYR:CD2	2.49	0.48
2:M:257:VAL:HA	2:M:260:LEU:CD1	2.43	0.48
1:N:67:ARG:O	1:N:70:LYS:HB3	2.14	0.48
2:G:29:GLU:HB3	2:G:30:PRO:CD	2.43	0.48
2:G:190:ALA:HB2	2:G:200:LYS:HB3	1.96	0.48
3:I:196:VAL:HG23	3:I:206:ALA:CB	2.44	0.48
3:I:391:SER:HB3	3:I:394:ARG:HB2	1.94	0.48
3:I:757:THR:O	3:I:765:ILE:HG23	2.14	0.48
3:I:1326:LEU:HD22	4:J:342:LEU:HD11	1.96	0.48
4:J:97:VAL:CG2	4:J:101:ARG:HE	2.27	0.48
4:J:849:LEU:HD13	4:J:856:ILE:HA	1.95	0.48
4:J:893:GLY:O	4:J:894:VAL:HG23	2.13	0.48
6:L:118:ASP:O	6:L:121:LYS:HB2	2.14	0.48
6:L:302:PHE:CE2	6:L:306:PHE:HB2	2.49	0.48
6:L:327:SER:HA	6:L:330:LEU:HD12	1.95	0.48
7:O:27:DT:H2"	7:O:28:DG:H8	1.79	0.48
3:I:229:ILE:HG21	3:I:240:GLU:OE2	2.13	0.48
3:I:341:LEU:HG	3:I:342:ASP:OD1	2.14	0.48
3:I:622:ASN:C	3:I:623:LEU:HD12	2.38	0.48
3:I:1129:ASN:O	3:I:1133:LYS:HB2	2.13	0.48
4:J:103:GLY:CA	4:J:244:VAL:HG22	2.44	0.48
4:J:373:ALA:HB3	4:J:441:LEU:HD11	1.95	0.48
4:J:1040:MET:HE3	4:J:1046:ILE:HD13	1.96	0.48
5:K:10:VAL:HG22	5:K:16:ARG:HG3	1.95	0.48
6:L:117:ILE:HG22	6:L:121:LYS:NZ	2.29	0.48
6:L:141:ILE:HD12	6:L:256:PHE:CG	2.48	0.48
3:I:45:GLY:HA3	3:I:46:GLN:HA	1.58	0.47
3:I:229:ILE:HB	3:I:240:GLU:CG	2.44	0.47
3:I:877:VAL:CG2	3:I:920:VAL:HG21	2.44	0.47
3:I:882:ILE:H	3:I:882:ILE:HD12	1.78	0.47
3:I:1098:LEU:HD23	3:I:1098:LEU:HA	1.47	0.47
3:I:1119:MET:HB2	3:I:1228:GLY:CA	2.44	0.47
4:J:122:SER:OG	4:J:125:GLY:HA3	2.14	0.47
4:J:913:GLU:O	4:J:915:ILE:HG23	2.14	0.47
6:L:252:LEU:HG	6:L:256:PHE:CE2	2.49	0.47
3:I:43:PRO:C	3:I:46:GLN:HE22	2.21	0.47
3:I:287:VAL:HG23	3:I:292:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:342:ASP:O	3:I:437:ASN:ND2	2.47	0.47
3:I:824:GLN:NE2	3:I:1082:ILE:HD11	2.30	0.47
3:I:972:PHE:CD1	3:I:975:ILE:HD12	2.49	0.47
3:I:1272:GLU:OE1	4:J:798:ARG:NH1	2.46	0.47
4:J:135:ILE:HA	4:J:138:VAL:HG12	1.96	0.47
4:J:867:GLN:HG2	4:J:868:TRP:N	2.29	0.47
6:L:266:PHE:O	6:L:270:VAL:HG23	2.14	0.47
8:P:59:DA:H2''	8:P:60:DA:O5'	2.15	0.47
2:H:16:ILE:HG12	2:H:17:GLU:H	1.78	0.47
2:H:65:LEU:O	2:H:65:LEU:HD22	2.14	0.47
2:H:213:PRO:O	2:H:216:ALA:N	2.47	0.47
3:I:181:GLY:HA3	3:I:395:TYR:CD1	2.50	0.47
3:I:517:GLN:O	3:I:517:GLN:HG2	2.15	0.47
3:I:519:ASN:HB3	3:I:522:SER:H	1.78	0.47
3:I:519:ASN:HD21	3:I:796:LEU:HD13	1.79	0.47
3:I:764:CYS:HB2	3:I:833:ILE:HD11	1.97	0.47
3:I:1124:ILE:HD11	3:I:1198:LEU:HG	1.95	0.47
4:J:44:ILE:HG13	6:L:450:ILE:HG22	1.96	0.47
4:J:68:TYR:C	4:J:92:VAL:HG23	2.39	0.47
4:J:71:LEU:N	4:J:90:VAL:HG21	2.27	0.47
4:J:278:ARG:NE	6:L:407:GLU:OE2	2.46	0.47
4:J:425:ARG:HD3	4:J:459:ALA:HB2	1.97	0.47
4:J:653:ILE:HG21	4:J:693:VAL:HG22	1.96	0.47
4:J:1011:VAL:HG12	4:J:1012:ALA:O	2.14	0.47
5:K:10:VAL:HG13	5:K:16:ARG:HB2	1.96	0.47
6:L:94:THR:O	6:L:100:MET:HE1	2.14	0.47
6:L:294:GLN:O	6:L:329:LYS:HE2	2.14	0.47
8:P:51:DC:H2''	8:P:52:DT:C6	2.49	0.47
2:H:105:SER:HB2	2:H:139:SER:CB	2.43	0.47
3:I:28:LEU:HD21	3:I:524:ILE:CD1	2.41	0.47
3:I:195:PHE:HA	3:I:206:ALA:HB2	1.97	0.47
3:I:233:ARG:HB2	3:I:238:GLN:CD	2.39	0.47
3:I:524:ILE:HD11	3:I:712:SER:CB	2.44	0.47
3:I:985:GLU:O	3:I:989:LEU:N	2.48	0.47
4:J:105:ILE:HD12	4:J:242:LEU:HD22	1.95	0.47
4:J:147:ILE:HG13	4:J:177:ASP:OD1	2.13	0.47
4:J:609:TYR:HE1	4:J:614:LEU:HD12	1.79	0.47
4:J:1207:GLY:HA2	4:J:1223:LEU:HB3	1.96	0.47
6:L:279:ARG:O	6:L:283:GLN:HG2	2.14	0.47
7:O:63:DT:H2''	7:O:64:DT:C6	2.49	0.47
2:M:298:LYS:HA	2:M:301:THR:CG2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:8:ALA:CB	4:J:783:LEU:HD12	2.45	0.47
1:N:15:LEU:HD23	1:N:15:LEU:O	2.13	0.47
2:G:218:ARG:O	2:G:222:THR:HG22	2.14	0.47
3:I:12:ARG:HH22	3:I:698:PRO:HD2	1.80	0.47
3:I:98:VAL:CG2	3:I:124:MET:HE3	2.42	0.47
3:I:256:GLU:CB	3:I:261:VAL:HA	2.43	0.47
3:I:367:TYR:CD1	3:I:381:ALA:HA	2.50	0.47
4:J:1156:LEU:HD11	4:J:1224:ARG:HH21	1.80	0.47
4:J:1356:LEU:HD12	4:J:1365:TYR:CD2	2.49	0.47
6:L:593:LYS:O	6:L:596:ARG:HB2	2.13	0.47
7:O:29:DA:H2''	7:O:30:DC:O4'	2.14	0.47
8:P:19:DT:H2''	8:P:20:DC:C6	2.50	0.47
2:G:23:HIS:CB	2:G:206:GLU:HA	2.45	0.47
3:I:44:GLU:O	3:I:46:GLN:NE2	2.47	0.47
3:I:96:LEU:HD23	3:I:124:MET:O	2.13	0.47
3:I:105:TYR:HB3	3:I:109:ALA:O	2.14	0.47
3:I:269:ILE:H	3:I:269:ILE:HD12	1.79	0.47
3:I:444:ASP:O	3:I:447:HIS:HB2	2.14	0.47
3:I:632:ASP:HA	3:I:647:ARG:HE	1.80	0.47
3:I:809:GLY:O	4:J:357:VAL:HG11	2.15	0.47
3:I:1101:LEU:HD23	4:J:725:MET:SD	2.55	0.47
3:I:1101:LEU:O	4:J:731:ARG:HG2	2.14	0.47
3:I:1103:VAL:HG11	3:I:1112:ILE:HD11	1.97	0.47
3:I:1223:ARG:NH2	4:J:721:SER:OG	2.26	0.47
3:I:1331:ARG:HA	3:I:1335:ILE:O	2.15	0.47
4:J:364:HIS:HB3	4:J:487:THR:CG2	2.45	0.47
4:J:820:ILE:HD11	4:J:822:MET:SD	2.54	0.47
4:J:1226:VAL:O	4:J:1230:THR:HG22	2.14	0.47
4:J:1237:VAL:CG1	4:J:1253:ILE:HD13	2.45	0.47
6:L:119:ILE:HB	6:L:379:MET:CE	2.45	0.47
6:L:344:LEU:HG	6:L:355:ILE:HD11	1.95	0.47
6:L:391:ALA:HB2	6:L:439:ILE:HD11	1.97	0.47
2:G:61:ILE:HG12	2:G:142:MET:HB3	1.96	0.47
2:H:51:MET:HE1	2:H:219:ARG:HB2	1.95	0.47
3:I:216:THR:CG2	3:I:219:GLN:H	2.27	0.47
3:I:237:LEU:HD11	3:I:322:LEU:CD1	2.44	0.47
3:I:272:ARG:HA	3:I:275:ARG:HG3	1.97	0.47
3:I:378:ARG:HG3	3:I:379:GLU:N	2.30	0.47
3:I:593:LYS:HD2	3:I:652:TYR:HE1	1.80	0.47
3:I:768:MET:HB3	3:I:768:MET:HE2	1.66	0.47
3:I:803:ALA:HB2	3:I:1094:VAL:HG11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:1004:ASP:OD1	3:I:1004:ASP:N	2.42	0.47
4:J:180:MET:HE1	4:J:293:ARG:NE	2.20	0.47
4:J:198:CYS:O	4:J:202:ARG:HG2	2.14	0.47
4:J:949:SER:OG	4:J:950:ILE:N	2.45	0.47
4:J:949:SER:HA	4:J:1020:TRP:CH2	2.50	0.47
6:L:130:VAL:HG13	6:L:365:MET:HG2	1.96	0.47
6:L:212:ILE:N	6:L:216:LEU:HD21	2.30	0.47
6:L:290:LEU:CA	6:L:294:GLN:HB3	2.44	0.47
6:L:324:LYS:H	6:L:327:SER:CB	2.28	0.47
6:L:327:SER:HA	6:L:330:LEU:CD1	2.45	0.47
6:L:344:LEU:HG	6:L:355:ILE:CD1	2.44	0.47
6:L:409:ASN:O	6:L:413:MET:HG3	2.14	0.47
6:L:488:LEU:C	6:L:489:MET:HE3	2.40	0.47
6:L:573:LEU:HB3	8:P:56:DG:OP2	2.15	0.47
7:O:32:DA:H2"	7:O:33:DA:H8	1.80	0.47
2:M:284:ARG:CB	2:M:288:GLU:HG2	2.40	0.47
2:M:300:LEU:HD13	2:M:300:LEU:O	2.13	0.47
1:N:20:ILE:HD13	4:J:746:LEU:HD13	1.97	0.47
3:I:734:ILE:O	3:I:734:ILE:HG13	2.14	0.47
3:I:912:ASP:OD1	3:I:912:ASP:N	2.45	0.47
4:J:53:ARG:HA	4:J:54:ASP:HA	1.54	0.47
4:J:1107:VAL:HA	4:J:1122:ALA:CB	2.45	0.47
4:J:1221:LEU:HD23	4:J:1306:LEU:HB2	1.97	0.47
3:I:117:ILE:C	3:I:118:LYS:HG3	2.40	0.47
3:I:204:LEU:CD1	3:I:369:MET:HE2	2.39	0.47
3:I:1160:ASP:OD1	3:I:1162:SER:HB3	2.15	0.47
4:J:1159:ILE:HD12	4:J:1160:SER:H	1.79	0.47
8:P:68:DG:OP1	2:M:295:LEU:N	2.47	0.47
2:G:90:VAL:HG11	2:G:146:VAL:HG21	1.97	0.47
2:G:111:THR:HA	2:G:129:VAL:HA	1.96	0.47
3:I:6:THR:HB	3:I:781:ASP:OD1	2.15	0.47
3:I:319:LEU:O	3:I:322:LEU:HB3	2.14	0.47
3:I:629:PHE:CE2	3:I:650:VAL:HG21	2.50	0.47
3:I:1151:LEU:HD22	3:I:1151:LEU:HA	1.68	0.47
5:K:14:GLY:O	5:K:15:ASN:HB3	2.15	0.47
6:L:137:TYR:HD2	6:L:140:ALA:HB2	1.78	0.47
6:L:297:MET:HE2	6:L:301:ASN:C	2.40	0.47
6:L:305:LEU:HD11	6:L:322:MET:HE1	1.97	0.47
6:L:484:ALA:CB	6:L:494:ILE:HD13	2.45	0.47
2:M:298:LYS:O	2:M:302:GLU:HG3	2.15	0.47
3:I:125:GLY:H	3:I:495:ALA:HB1	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:878:THR:HG22	3:I:925:SER:HB3	1.96	0.46
4:J:20:ILE:HD13	4:J:1320:ILE:CD1	2.45	0.46
4:J:872:LEU:HD11	4:J:877:VAL:HB	1.98	0.46
4:J:948:SER:OG	4:J:1022:PRO:HG3	2.15	0.46
4:J:982:LEU:O	4:J:982:LEU:HD23	2.15	0.46
4:J:1158:GLU:HG3	4:J:1186:TYR:CZ	2.50	0.46
4:J:1251:LYS:O	4:J:1255:VAL:HG12	2.14	0.46
6:L:157:ARG:N	6:L:160:ASP:OD2	2.48	0.46
2:H:41:ASN:O	2:H:45:ARG:HG3	2.15	0.46
3:I:272:ARG:HA	3:I:275:ARG:CG	2.44	0.46
3:I:530:ILE:HG13	3:I:575:LEU:HB2	1.97	0.46
3:I:996:ARG:HD3	3:I:996:ARG:HA	1.67	0.46
3:I:1276:TRP:CZ2	4:J:801:VAL:HG21	2.51	0.46
4:J:271:ARG:O	4:J:275:ARG:HG3	2.15	0.46
4:J:719:PHE:HA	4:J:724:MET:HE2	1.96	0.46
4:J:909:ILE:HD11	4:J:913:GLU:CB	2.43	0.46
4:J:1060:VAL:HG23	4:J:1106:ILE:HG23	1.97	0.46
4:J:1194:ARG:HG2	4:J:1195:GLN:N	2.29	0.46
6:L:316:PHE:CE2	6:L:334:SER:HA	2.41	0.46
6:L:506:SER:O	6:L:509:THR:HG22	2.16	0.46
7:O:39:DG:H2''	7:O:40:DC:C5'	2.46	0.46
1:N:52:PHE:HE2	4:J:673:VAL:HG12	1.81	0.46
3:I:104:ILE:C	3:I:114:VAL:HG12	2.41	0.46
3:I:178:PRO:HG3	3:I:395:TYR:CE1	2.51	0.46
3:I:391:SER:O	3:I:394:ARG:N	2.48	0.46
3:I:727:VAL:O	3:I:727:VAL:HG13	2.16	0.46
4:J:105:ILE:HD12	4:J:242:LEU:CD2	2.45	0.46
4:J:130:MET:CE	4:J:159:ILE:HD11	2.40	0.46
4:J:132:LEU:HA	4:J:135:ILE:CD1	2.45	0.46
4:J:220:ARG:NH1	4:J:224:LEU:HD11	2.30	0.46
4:J:841:GLY:O	4:J:901:ARG:HB3	2.15	0.46
4:J:850:LYS:HG3	4:J:851:PRO:N	2.30	0.46
4:J:1045:THR:O	4:J:1061:VAL:HG13	2.15	0.46
4:J:1209:VAL:HB	4:J:1211:SER:O	2.14	0.46
4:J:1327:GLU:OE2	4:J:1330:ARG:HB2	2.14	0.46
5:K:27:ALA:O	5:K:46:THR:HG21	2.14	0.46
6:L:112:THR:O	6:L:115:GLY:N	2.47	0.46
6:L:151:VAL:HG11	6:L:158:LEU:HA	1.97	0.46
6:L:248:GLU:HG3	6:L:251:LYS:HZ1	1.80	0.46
1:N:5:ALA:HB2	3:I:681:MET:SD	2.55	0.46
2:G:124:VAL:HG13	2:G:125:LYS:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:154:PRO:C	2:G:158:ARG:HG3	2.41	0.46
3:I:164:THR:HG21	3:I:171:LEU:HG	1.96	0.46
3:I:738:GLU:HA	3:I:741:MET:CE	2.40	0.46
3:I:1026:GLU:O	3:I:1029:LEU:HG	2.15	0.46
3:I:1282:GLY:CA	4:J:1360:GLY:HA3	2.46	0.46
4:J:268:LEU:HD21	4:J:324:LEU:HD22	1.97	0.46
4:J:314:ARG:HD3	4:J:314:ARG:HA	1.70	0.46
4:J:395:LYS:HD3	6:L:536:THR:CG2	2.45	0.46
4:J:570:LYS:HG3	4:J:589:TYR:CD2	2.50	0.46
4:J:702:GLN:O	4:J:718:SER:HB3	2.16	0.46
4:J:984:LEU:HB3	4:J:993:GLU:HB2	1.96	0.46
4:J:1035:VAL:HG21	4:J:1109:LEU:HD23	1.98	0.46
6:L:117:ILE:HG22	6:L:121:LYS:HZ1	1.80	0.46
6:L:290:LEU:HA	6:L:294:GLN:HB3	1.98	0.46
6:L:452:ILE:HD11	6:L:457:ILE:HG12	1.98	0.46
6:L:551:LEU:HD13	6:L:555:GLU:OE2	2.16	0.46
7:O:47:DG:H2''	7:O:48:DG:OP2	2.16	0.46
8:P:37:DG:H1'	8:P:38:DC:H5'	1.97	0.46
2:H:102:LEU:HD21	2:H:130:ILE:HD13	1.97	0.46
2:H:113:ALA:HB2	2:H:126:PRO:HB3	1.96	0.46
3:I:278:GLU:O	3:I:281:ASP:HB3	2.15	0.46
3:I:289:VAL:CG2	3:I:322:LEU:HD22	2.35	0.46
3:I:322:LEU:HA	3:I:325:LEU:HG	1.97	0.46
3:I:656:SER:O	3:I:659:GLN:HB2	2.16	0.46
3:I:1028:LYS:HB2	3:I:1028:LYS:HE3	1.60	0.46
4:J:822:MET:HE1	4:J:838:ARG:NE	2.29	0.46
4:J:825:VAL:O	4:J:825:VAL:HG13	2.15	0.46
4:J:902:ASP:C	4:J:903:LEU:HG	2.41	0.46
4:J:1284:ARG:NH1	4:J:1288:ALA:HB2	2.30	0.46
6:L:265:GLN:HA	6:L:268:TYR:CB	2.45	0.46
6:L:286:LEU:HD23	6:L:340:ALA:HB2	1.98	0.46
2:M:269:CYS:SG	2:M:295:LEU:HD12	2.55	0.46
2:M:299:SER:O	2:M:302:GLU:HB2	2.15	0.46
3:I:105:TYR:CD1	3:I:114:VAL:HG13	2.50	0.46
3:I:229:ILE:HB	3:I:240:GLU:HG3	1.98	0.46
3:I:453:ILE:CD1	3:I:530:ILE:HD12	2.40	0.46
3:I:468:LEU:HD23	3:I:468:LEU:HA	1.48	0.46
3:I:509:SER:OG	3:I:510:GLN:N	2.45	0.46
3:I:559:CYS:SG	3:I:662:SER:HB3	2.55	0.46
4:J:44:ILE:CG1	6:L:450:ILE:HG22	2.45	0.46
6:L:311:THR:HG22	6:L:344:LEU:HD21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:P:37:DG:H2''	8:P:38:DC:H5'	1.96	0.46
2:M:286:GLU:OE2	2:M:314:LEU:HD13	2.16	0.46
2:G:13:LEU:HB3	2:H:231:PHE:HE1	1.81	0.46
3:I:149:LEU:HA	3:I:452:ARG:O	2.15	0.46
3:I:198:ILE:HG22	3:I:199:ASP:H	1.79	0.46
3:I:243:PRO:CB	3:I:277:LEU:HD23	2.44	0.46
3:I:544:GLY:O	3:I:548:ARG:HD2	2.15	0.46
3:I:564:PRO:O	3:I:569:ILE:HG12	2.15	0.46
3:I:681:MET:CE	3:I:1073:LYS:HE3	2.45	0.46
6:L:328:GLU:N	6:L:328:GLU:OE1	2.49	0.46
6:L:334:SER:O	6:L:338:HIS:HB2	2.16	0.46
6:L:574:GLU:HA	6:L:584:ARG:HG2	1.98	0.46
8:P:17:DA:C8	8:P:18:DT:H72	2.50	0.46
8:P:53:DT:H2''	8:P:54:DT:OP2	2.16	0.46
3:I:346:TYR:CD2	3:I:433:ILE:HG23	2.51	0.46
3:I:395:TYR:HD2	3:I:419:ILE:HG13	1.80	0.46
3:I:673:HIS:ND1	3:I:1113:LEU:HD13	2.30	0.46
4:J:161:THR:HG22	4:J:162:GLU:H	1.80	0.46
4:J:422:LEU:HD11	4:J:471:PRO:HG3	1.97	0.46
6:L:299:LYS:O	6:L:303:ILE:HG22	2.14	0.46
6:L:481:GLU:O	6:L:485:GLU:HG2	2.15	0.46
7:O:27:DT:H2''	7:O:28:DG:C8	2.51	0.46
2:M:264:VAL:HA	2:M:267:ALA:HB3	1.98	0.46
3:I:161:LYS:HA	3:I:170:VAL:CG1	2.46	0.46
3:I:843:THR:OG1	3:I:846:GLY:O	2.20	0.46
3:I:1105:SER:CB	4:J:731:ARG:HG3	2.42	0.46
4:J:46:TYR:CD1	6:L:500:ILE:HD12	2.49	0.46
4:J:801:VAL:HG12	4:J:920:ALA:HB1	1.97	0.46
4:J:835:LEU:HD13	4:J:835:LEU:O	2.16	0.46
4:J:1037:PHE:CZ	4:J:1110:GLU:HA	2.48	0.46
4:J:1069:ALA:O	4:J:1072:LYS:HD3	2.15	0.46
4:J:1176:VAL:HA	4:J:1186:TYR:O	2.15	0.46
4:J:1293:GLU:OE1	4:J:1298:VAL:HA	2.16	0.46
6:L:140:ALA:CA	6:L:269:LEU:HD22	2.40	0.46
6:L:283:GLN:HB3	6:L:340:ALA:HB1	1.98	0.46
6:L:525:ASP:OD2	6:L:527:THR:OG1	2.18	0.46
2:H:105:SER:HB2	2:H:139:SER:OG	2.15	0.46
3:I:225:PHE:HB2	3:I:336:LEU:CD2	2.45	0.46
4:J:147:ILE:HD13	4:J:187:ALA:CB	2.45	0.46
4:J:149:GLY:HA2	4:J:177:ASP:OD2	2.16	0.46
4:J:660:GLU:O	4:J:663:GLU:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:25:ARG:NH1	5:K:64:LEU:HD13	2.31	0.46
6:L:141:ILE:HA	6:L:144:LEU:HB3	1.97	0.46
6:L:276:MET:HE1	6:L:279:ARG:HE	1.80	0.46
6:L:391:ALA:HB3	6:L:405:ILE:CD1	2.42	0.46
2:G:28:LEU:HG	2:H:231:PHE:HZ	1.81	0.45
2:G:47:LEU:O	2:G:180:VAL:HG21	2.16	0.45
2:G:110:VAL:CG1	2:G:131:CYS:HB2	2.46	0.45
2:G:150:ARG:HD3	2:H:5:VAL:O	2.17	0.45
3:I:60:GLN:O	3:I:476:LYS:HG2	2.16	0.45
3:I:178:PRO:HG3	3:I:395:TYR:HE1	1.81	0.45
3:I:303:ASP:HB3	3:I:306:THR:HG23	1.99	0.45
4:J:54:ASP:OD1	4:J:54:ASP:N	2.49	0.45
4:J:74:LYS:HG3	4:J:75:TYR:CE1	2.51	0.45
4:J:356:THR:HG23	4:J:446:ALA:HB1	1.98	0.45
4:J:385:LEU:HD23	4:J:411:ILE:HG13	1.97	0.45
4:J:390:LEU:CD2	4:J:407:VAL:HB	2.46	0.45
4:J:515:ARG:NH2	4:J:717:VAL:O	2.49	0.45
4:J:800:LEU:HD12	4:J:800:LEU:HA	1.65	0.45
4:J:836:ARG:O	4:J:840:LEU:HB2	2.16	0.45
4:J:1047:THR:HG21	4:J:1060:VAL:HB	1.97	0.45
7:O:33:DA:H2''	7:O:34:DA:N7	2.31	0.45
8:P:57:DT:H2''	8:P:58:DC:C5'	2.46	0.45
3:I:58:PRO:HB3	3:I:69:GLN:HB3	1.97	0.45
3:I:990:ASP:N	3:I:990:ASP:OD1	2.50	0.45
4:J:1047:THR:HB	4:J:1062:LEU:HD23	1.97	0.45
2:G:8:PHE:C	2:G:9:LEU:HD23	2.40	0.45
2:G:52:PRO:HG2	2:G:219:ARG:NE	2.31	0.45
2:H:46:ILE:CD1	2:H:224:LEU:HD22	2.47	0.45
2:H:197:ASP:O	2:H:198:LEU:HD13	2.16	0.45
3:I:1111:GLN:HG3	3:I:1230:MET:HE2	1.98	0.45
3:I:1151:LEU:HD11	3:I:1198:LEU:HA	1.97	0.45
4:J:193:ASP:OD1	4:J:194:LEU:N	2.49	0.45
4:J:218:THR:O	4:J:221:ILE:HG22	2.16	0.45
4:J:349:TYR:CD2	4:J:472:LEU:HD11	2.51	0.45
4:J:1139:PRO:O	4:J:1143:ASP:N	2.35	0.45
4:J:1275:LEU:HG	4:J:1278:GLU:HB2	1.97	0.45
6:L:236:LYS:HD2	6:L:236:LYS:HA	1.78	0.45
7:O:23:DC:H2''	7:O:24:DC:C6	2.51	0.45
2:G:31:LEU:HD23	2:G:31:LEU:HA	1.78	0.45
2:G:47:LEU:HD21	2:G:220:ALA:HB2	1.97	0.45
2:H:133:LEU:HD23	2:H:133:LEU:HA	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:29:SER:O	3:I:33:ASP:CB	2.59	0.45
3:I:161:LYS:HA	3:I:170:VAL:HG12	1.99	0.45
3:I:223:LEU:HD12	3:I:223:LEU:HA	1.62	0.45
3:I:369:MET:HE3	3:I:369:MET:HB3	1.69	0.45
3:I:1109:ILE:HG12	4:J:644:MET:CE	2.47	0.45
3:I:1165:SER:OG	3:I:1166:ASP:N	2.50	0.45
4:J:74:LYS:HG3	4:J:75:TYR:CD1	2.51	0.45
4:J:121:PRO:HB2	4:J:126:LEU:HD23	1.97	0.45
4:J:135:ILE:O	4:J:139:LEU:HG	2.15	0.45
4:J:355:ILE:CD1	4:J:466:MET:HE3	2.43	0.45
4:J:1039:ASP:O	4:J:1076:PRO:HA	2.15	0.45
4:J:1292:LEU:O	4:J:1295:ASN:N	2.50	0.45
7:O:45:DA:H2''	7:O:46:DG:H5''	1.98	0.45
2:G:190:ALA:HB2	2:G:200:LYS:HE3	1.99	0.45
3:I:24:VAL:CG1	3:I:25:PRO:HD2	2.46	0.45
3:I:243:PRO:HA	3:I:277:LEU:HD23	1.98	0.45
3:I:543:ALA:HA	3:I:544:GLY:HA3	1.69	0.45
3:I:778:GLU:O	3:I:781:ASP:HB3	2.16	0.45
3:I:854:ILE:HD11	3:I:885:GLY:HA3	1.98	0.45
3:I:966:ILE:HG12	10:I:1401:1N7:H26	1.99	0.45
4:J:309:ASN:ND2	4:J:324:LEU:HB2	2.30	0.45
4:J:1010:GLN:O	4:J:1010:GLN:HG3	2.16	0.45
4:J:1178:THR:CB	4:J:1184:ASP:HB2	2.46	0.45
4:J:1257:VAL:O	4:J:1261:LEU:HG	2.16	0.45
6:L:261:LEU:HB3	6:L:266:PHE:HB2	1.98	0.45
3:I:668:ILE:HD12	3:I:671:LEU:HD13	1.98	0.45
3:I:689:ALA:HB3	3:I:796:LEU:HB3	1.99	0.45
3:I:1291:LEU:HB2	4:J:345:LYS:HE3	1.99	0.45
4:J:156:ARG:HG3	4:J:157:GLN:N	2.30	0.45
4:J:514:THR:HG21	4:J:596:LEU:CG	2.47	0.45
4:J:718:SER:OG	4:J:720:ASN:HB2	2.16	0.45
4:J:749:LYS:HE3	4:J:753:SER:OG	2.17	0.45
4:J:800:LEU:HD13	4:J:1309:ILE:HD12	1.97	0.45
4:J:985:ILE:HD13	4:J:991:THR:CA	2.46	0.45
6:L:113:ARG:HD2	6:L:426:LYS:HE2	1.98	0.45
6:L:462:LYS:HD3	6:L:487:MET:HE3	1.99	0.45
7:O:32:DA:H2''	7:O:33:DA:C8	2.52	0.45
8:P:52:DT:H2''	8:P:53:DT:H71	1.99	0.45
2:G:13:LEU:HB3	2:H:231:PHE:CE1	2.51	0.45
3:I:57:PHE:CD2	3:I:70:TYR:HB2	2.48	0.45
3:I:185:ASP:HB2	3:I:197:ARG:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:755:LYS:HA	3:I:755:LYS:CE	2.47	0.45
3:I:996:ARG:HA	3:I:998:LEU:HD22	1.99	0.45
3:I:1242:LYS:HD2	4:J:465:GLN:NE2	2.31	0.45
4:J:46:TYR:CE2	6:L:453:PRO:HD3	2.52	0.45
4:J:160:LEU:HD22	4:J:164:GLN:CD	2.42	0.45
4:J:560:ASN:OD1	4:J:560:ASN:N	2.50	0.45
7:O:25:DA:H2'	7:O:26:DT:C6	2.52	0.45
8:P:48:DC:H2''	8:P:49:DT:C6	2.51	0.45
2:G:91:ARG:NH1	2:G:210:THR:O	2.50	0.45
2:G:118:ASP:OD2	2:G:119:GLY:N	2.44	0.45
2:H:11:PRO:HB2	2:H:28:LEU:HD11	1.98	0.45
3:I:575:LEU:CD1	3:I:587:LEU:HD21	2.46	0.45
3:I:577:VAL:HG23	3:I:661:VAL:O	2.17	0.45
3:I:672:GLU:HG2	3:I:673:HIS:CD2	2.51	0.45
4:J:120:LEU:HG	4:J:1330:ARG:HG3	1.98	0.45
4:J:291:ILE:HG22	6:L:406:GLN:HE22	1.82	0.45
4:J:911:LYS:HG3	4:J:911:LYS:O	2.15	0.45
4:J:993:GLU:HB3	4:J:995:TYR:CE2	2.52	0.45
4:J:1029:THR:HG21	4:J:1115:ILE:CD1	2.47	0.45
6:L:99:ARG:O	6:L:103:ARG:HG3	2.17	0.45
6:L:298:PRO:HB2	6:L:301:ASN:OD1	2.17	0.45
2:G:64:VAL:HG22	2:G:78:ILE:CD1	2.47	0.45
2:G:192:VAL:HG22	2:G:193:GLU:H	1.82	0.45
2:H:78:ILE:HA	2:H:81:ILE:CD1	2.40	0.45
3:I:175:ARG:HE	3:I:175:ARG:HB2	1.50	0.45
3:I:241:LEU:HD22	3:I:285:ILE:HG23	1.97	0.45
3:I:360:LEU:HD21	3:I:378:ARG:HD3	1.99	0.45
3:I:506:PHE:O	3:I:512:SER:OG	2.26	0.45
3:I:565:GLU:H	3:I:565:GLU:HG3	1.57	0.45
3:I:590:PRO:HB2	3:I:655:VAL:CG1	2.36	0.45
3:I:830:THR:HG23	3:I:832:HIS:HE1	1.82	0.45
3:I:884:VAL:CG2	3:I:918:LEU:HD23	2.43	0.45
3:I:986:ALA:HA	3:I:989:LEU:HB2	1.99	0.45
4:J:522:GLY:HA3	4:J:542:ALA:HA	1.99	0.45
4:J:549:LYS:HG3	4:J:571:ASP:OD1	2.17	0.45
4:J:709:ARG:HD3	4:J:710:ASP:H	1.80	0.45
4:J:1174:ARG:HG2	4:J:1189:MET:HE1	1.97	0.45
6:L:265:GLN:HA	6:L:268:TYR:HB2	1.97	0.45
6:L:322:MET:CG	6:L:324:LYS:HG2	2.47	0.45
6:L:574:GLU:HG2	6:L:584:ARG:CD	2.47	0.45
2:M:269:CYS:O	2:M:272:ALA:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:45:ARG:HG2	2:H:38:THR:HB	1.98	0.45
2:G:79:LEU:HD11	3:I:693:LEU:HD11	1.98	0.45
2:H:11:PRO:HB2	2:H:14:VAL:HG22	1.98	0.45
3:I:529:ARG:NH1	3:I:574:SER:OG	2.49	0.45
3:I:835:GLU:OE2	3:I:1053:TYR:OH	2.26	0.45
4:J:69:GLU:N	4:J:92:VAL:HG23	2.32	0.45
4:J:97:VAL:HG21	4:J:101:ARG:HE	1.81	0.45
4:J:514:THR:O	4:J:514:THR:HG23	2.17	0.45
4:J:985:ILE:HG23	4:J:990:ARG:O	2.16	0.45
4:J:1069:ALA:CB	4:J:1072:LYS:HD3	2.43	0.45
6:L:392:LYS:HD2	7:O:56:DC:O5'	2.16	0.45
6:L:544:THR:HA	6:L:547:VAL:HG22	1.99	0.45
2:G:166:ARG:N	2:G:167:PRO:HD2	2.32	0.44
2:H:84:ASN:ND2	4:J:551:ARG:HH12	2.15	0.44
3:I:28:LEU:HD13	3:I:133:ASN:O	2.17	0.44
3:I:231:GLU:N	3:I:238:GLN:O	2.23	0.44
3:I:815:SER:OG	4:J:357:VAL:HG23	2.17	0.44
3:I:995:ASP:OD1	3:I:995:ASP:N	2.48	0.44
3:I:1072:ASN:OD1	3:I:1072:ASN:N	2.50	0.44
4:J:36:GLY:HA3	4:J:61:ILE:HG23	1.99	0.44
4:J:487:THR:HG22	4:J:618:VAL:CG1	2.48	0.44
4:J:611:ILE:HG22	4:J:612:LEU:CD1	2.47	0.44
4:J:1198:VAL:HB	4:J:1210:ILE:HG23	1.97	0.44
5:K:13:ILE:HD12	5:K:54:ILE:HD12	1.99	0.44
6:L:98:VAL:HA	6:L:402:LEU:HD11	1.99	0.44
7:O:29:DA:H2'	7:O:30:DC:C6	2.52	0.44
8:P:37:DG:C2'	8:P:38:DC:H5'	2.46	0.44
8:P:48:DC:OP2	8:P:48:DC:H2'	2.17	0.44
2:M:265:ARG:HH21	2:M:294:ASN:HB2	1.82	0.44
1:N:48:ARG:C	1:N:48:ARG:HD3	2.42	0.44
3:I:120:GLN:CG	3:I:490:GLN:HE22	2.27	0.44
3:I:188:PHE:CD1	3:I:194:LEU:HB3	2.53	0.44
3:I:237:LEU:HD11	3:I:322:LEU:HD11	1.98	0.44
3:I:448:LEU:HD12	3:I:554:HIS:CE1	2.52	0.44
3:I:633:LEU:HD22	3:I:644:LEU:HB3	1.99	0.44
3:I:975:ILE:HG12	3:I:1014:LEU:HD12	1.99	0.44
3:I:993:PRO:HB2	3:I:995:ASP:OD1	2.17	0.44
3:I:1048:LYS:HB2	3:I:1048:LYS:HE3	1.53	0.44
3:I:1146:GLN:NE2	3:I:1150:ASP:OD1	2.50	0.44
3:I:1308:ILE:CG2	4:J:379:PRO:HB2	2.48	0.44
4:J:523:GLU:OE1	4:J:547:ARG:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:1282:TYR:O	4:J:1286:LYS:HB2	2.17	0.44
4:J:1307:LEU:CB	4:J:1312:ALA:HB2	2.47	0.44
4:J:1347:LEU:O	4:J:1351:VAL:HG23	2.18	0.44
5:K:51:LEU:HA	5:K:51:LEU:HD13	1.67	0.44
5:K:76:GLU:O	5:K:79:GLU:HB3	2.15	0.44
6:L:607:LEU:HD22	6:L:607:LEU:H	1.82	0.44
7:O:41:DT:H2''	7:O:42:DA:OP2	2.17	0.44
8:P:68:DG:OP1	8:P:68:DG:H3'	2.18	0.44
2:G:231:PHE:HZ	2:H:201:LEU:CD2	2.30	0.44
2:H:32:GLU:HB3	2:H:35:PHE:CD2	2.50	0.44
2:H:211:ILE:HD11	2:H:215:GLU:CB	2.48	0.44
3:I:230:PHE:CZ	3:I:295:LYS:HG3	2.53	0.44
3:I:898:GLU:CD	6:L:541:ARG:HG2	2.42	0.44
3:I:1277:ALA:HB3	4:J:434:ILE:HD12	1.99	0.44
4:J:201:LEU:HD23	4:J:201:LEU:HA	1.65	0.44
6:L:150:ARG:HB3	6:L:155:GLU:CD	2.43	0.44
6:L:167:ASP:HB2	6:L:212:ILE:N	2.33	0.44
6:L:519:LEU:O	6:L:519:LEU:HD23	2.18	0.44
6:L:540:LEU:HD23	6:L:610:PHE:CD2	2.52	0.44
2:G:124:VAL:O	2:G:126:PRO:HD3	2.17	0.44
2:H:32:GLU:HG3	2:H:33:ARG:N	2.32	0.44
2:H:47:LEU:CD2	2:H:220:ALA:HB2	2.47	0.44
3:I:217:THR:O	3:I:221:LEU:HG	2.17	0.44
3:I:221:LEU:HB3	3:I:336:LEU:CD2	2.47	0.44
3:I:985:GLU:HG2	3:I:988:LYS:HE2	2.00	0.44
4:J:514:THR:HG21	4:J:596:LEU:HD12	2.00	0.44
4:J:620:PHE:O	4:J:624:ILE:HB	2.18	0.44
4:J:1096:PRO:HB2	4:J:1098:GLN:OE1	2.18	0.44
4:J:1163:VAL:HA	4:J:1177:ILE:HA	1.97	0.44
4:J:1317:GLU:HG2	4:J:1318:SER:N	2.32	0.44
6:L:254:GLU:O	6:L:257:LYS:HB3	2.18	0.44
7:O:45:DA:H2''	7:O:46:DG:C5'	2.48	0.44
2:G:79:LEU:O	2:G:79:LEU:HD22	2.17	0.44
2:H:102:LEU:HB3	2:H:142:MET:CG	2.47	0.44
3:I:252:SER:O	3:I:252:SER:OG	2.30	0.44
3:I:529:ARG:HD3	3:I:572:ILE:HG22	2.00	0.44
4:J:165:TYR:CD2	4:J:166:LEU:HD22	2.52	0.44
4:J:253:VAL:HG21	6:L:523:ILE:HD12	1.99	0.44
4:J:356:THR:HG23	4:J:446:ALA:CB	2.47	0.44
4:J:557:LYS:HA	4:J:562:GLU:O	2.17	0.44
4:J:801:VAL:O	4:J:805:GLN:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:1286:LYS:HE3	4:J:1286:LYS:HB3	1.89	0.44
5:K:59:ILE:CG2	5:K:64:LEU:HD11	2.47	0.44
6:L:148:TYR:CA	6:L:161:LEU:HD11	2.44	0.44
6:L:231:THR:CG2	6:L:248:GLU:HB3	2.41	0.44
8:P:57:DT:H2"	8:P:58:DC:H5"	1.98	0.44
2:G:43:LEU:O	2:G:47:LEU:HG	2.17	0.44
2:G:47:LEU:HD23	2:G:220:ALA:HB2	1.99	0.44
2:G:48:LEU:HD23	2:G:48:LEU:HA	1.70	0.44
2:G:83:LEU:HD23	3:I:694:ARG:CZ	2.47	0.44
2:G:176:CYS:O	2:G:178:SER:N	2.51	0.44
3:I:58:PRO:HB3	3:I:69:GLN:HA	1.99	0.44
3:I:106:GLU:HB2	3:I:109:ALA:HB3	2.00	0.44
3:I:269:ILE:HG23	3:I:273:HIS:HB2	2.00	0.44
3:I:283:LYS:O	3:I:283:LYS:HG2	2.17	0.44
3:I:529:ARG:HG2	3:I:529:ARG:HH11	1.81	0.44
3:I:966:ILE:HG12	10:I:1401:1N7:H25	1.98	0.44
3:I:1035:LYS:HB2	3:I:1035:LYS:HE3	1.74	0.44
3:I:1103:VAL:HB	3:I:1104:PRO:HD3	1.99	0.44
3:I:1119:MET:HB2	3:I:1228:GLY:HA2	2.00	0.44
3:I:1165:SER:O	3:I:1168:GLU:HB2	2.18	0.44
3:I:1255:THR:O	3:I:1257:GLN:N	2.50	0.44
4:J:168:ALA:HA	4:J:171:GLU:OE1	2.18	0.44
4:J:200:GLN:HG3	4:J:201:LEU:N	2.33	0.44
4:J:338:PHE:CE1	4:J:1352:ILE:HD13	2.53	0.44
4:J:902:ASP:O	4:J:903:LEU:HG	2.17	0.44
4:J:919:ALA:HA	4:J:1252:HIS:HD1	1.82	0.44
6:L:102:MET:HE1	6:L:388:ILE:CG2	2.42	0.44
6:L:367:ILE:HD12	6:L:367:ILE:HA	1.78	0.44
6:L:559:LEU:HD12	6:L:559:LEU:HA	1.76	0.44
7:O:32:DA:H2"	7:O:33:DA:OP2	2.17	0.44
8:P:66:DT:H2"	8:P:67:DT:C6	2.53	0.44
2:H:31:LEU:HD12	2:H:35:PHE:HB3	2.00	0.44
3:I:563:THR:OG1	3:I:564:PRO:HD2	2.18	0.44
3:I:645:PHE:HB3	3:I:649:GLN:HG3	1.99	0.44
3:I:700:VAL:CG2	3:I:1117:LEU:HD23	2.48	0.44
3:I:817:LEU:HD23	3:I:817:LEU:HA	1.65	0.44
3:I:894:GLN:HG3	3:I:895:LEU:H	1.82	0.44
4:J:836:ARG:NH1	4:J:840:LEU:HD22	2.33	0.44
4:J:963:VAL:CG1	4:J:975:ILE:HG12	2.48	0.44
4:J:1011:VAL:CG1	4:J:1015:GLU:HB2	2.48	0.44
6:L:399:LEU:CD1	6:L:447:ALA:HB2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:551:LEU:HB3	6:L:555:GLU:OE1	2.17	0.44
6:L:573:LEU:HG	6:L:584:ARG:CG	2.47	0.44
7:O:24:DC:H2''	7:O:25:DA:O4'	2.18	0.44
2:G:14:VAL:HG22	2:G:27:THR:HB	2.00	0.44
2:H:104:LYS:HG3	2:H:114:ASP:HB3	1.99	0.44
3:I:91:THR:HA	3:I:137:VAL:O	2.18	0.44
3:I:262:TYR:OH	3:I:280:ASP:OD1	2.30	0.44
3:I:745:GLU:HB2	3:I:1017:GLN:HG3	2.00	0.44
3:I:820:GLU:O	3:I:820:GLU:HG2	2.18	0.44
3:I:877:VAL:HG23	3:I:920:VAL:HG21	2.00	0.44
4:J:166:LEU:HA	4:J:166:LEU:HD13	1.83	0.44
4:J:217:LEU:O	4:J:217:LEU:HD13	2.18	0.44
4:J:900:GLY:HA3	4:J:1251:LYS:HE3	2.00	0.44
4:J:981:GLU:HG2	4:J:982:LEU:N	2.33	0.44
6:L:399:LEU:HD23	6:L:403:ASP:HB3	2.00	0.44
6:L:453:PRO:HG2	7:O:44:DA:P	2.57	0.44
6:L:470:MET:HE3	6:L:486:ARG:NH1	2.32	0.44
6:L:574:GLU:HA	6:L:584:ARG:CG	2.48	0.44
2:G:31:LEU:HB2	2:G:199:ASP:O	2.17	0.44
2:G:192:VAL:CG2	2:G:198:LEU:HD12	2.48	0.44
3:I:144:VAL:HG21	3:I:527:LYS:HG2	2.00	0.44
4:J:147:ILE:HD11	4:J:179:LYS:HZ3	1.81	0.44
4:J:865:HIS:O	4:J:869:CYS:HB2	2.18	0.44
5:K:48:VAL:O	5:K:52:ARG:HG3	2.17	0.44
3:I:10:ARG:HD2	3:I:1181:PRO:CG	2.48	0.43
3:I:1124:ILE:HD12	3:I:1198:LEU:HD21	2.00	0.43
4:J:104:HIS:HA	4:J:242:LEU:O	2.17	0.43
4:J:288:PRO:HB3	6:L:377:LYS:HB2	1.99	0.43
6:L:110:LEU:O	6:L:110:LEU:HD12	2.17	0.43
6:L:330:LEU:HA	6:L:333:VAL:CG1	2.44	0.43
6:L:415:ALA:HB2	6:L:434:TRP:CB	2.48	0.43
2:M:282:VAL:HB	2:M:313:SER:O	2.18	0.43
2:G:23:HIS:HB2	2:G:206:GLU:HA	1.99	0.43
3:I:466:VAL:O	3:I:469:VAL:HG22	2.18	0.43
3:I:1258:PRO:HG3	4:J:348:ASP:OD1	2.17	0.43
4:J:905:ARG:N	4:J:905:ARG:HD2	2.34	0.43
4:J:1115:ILE:HG21	4:J:1119:ASP:OD2	2.18	0.43
4:J:1145:PHE:HB3	4:J:1309:ILE:HD13	1.99	0.43
7:O:22:DT:H6	7:O:22:DT:H5'	1.84	0.43
8:P:67:DT:H4'	2:M:265:ARG:CZ	2.49	0.43
2:M:255:ARG:O	2:M:278:ILE:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:45:ARG:HD3	3:I:1083:GLU:CB	2.48	0.43
3:I:250:THR:HG22	3:I:268:ARG:CB	2.47	0.43
3:I:699:LEU:CB	3:I:799:ASN:HD22	2.23	0.43
4:J:536:LEU:HD12	4:J:536:LEU:HA	1.73	0.43
4:J:666:GLU:O	4:J:669:GLN:HB2	2.18	0.43
4:J:965:SER:OG	4:J:973:LEU:HG	2.18	0.43
4:J:1078:LEU:CG	4:J:1101:LEU:HD11	2.41	0.43
6:L:287:ILE:HD11	6:L:340:ALA:HB3	2.00	0.43
6:L:585:GLU:CD	6:L:588:ARG:HD2	2.43	0.43
2:H:64:VAL:HG11	2:H:69:SER:HB2	1.99	0.43
2:H:65:LEU:O	2:H:65:LEU:HD13	2.19	0.43
3:I:34:SER:OG	3:I:455:SER:HB2	2.18	0.43
3:I:261:VAL:HG23	3:I:261:VAL:O	2.18	0.43
3:I:528:ARG:NH2	3:I:575:LEU:HD23	2.34	0.43
3:I:1034:ARG:O	3:I:1038:GLN:HB3	2.19	0.43
4:J:203:GLU:OE2	4:J:203:GLU:HA	2.18	0.43
4:J:210:SER:HB2	4:J:213:LYS:CG	2.49	0.43
4:J:421:VAL:HG13	4:J:439:PRO:CG	2.48	0.43
4:J:623:GLN:O	4:J:627:THR:HG22	2.18	0.43
4:J:1173:ARG:HD2	4:J:1174:ARG:O	2.17	0.43
5:K:73:GLN:O	5:K:77:ALA:N	2.51	0.43
6:L:261:LEU:CB	6:L:266:PHE:HB2	2.48	0.43
6:L:287:ILE:HG23	6:L:337:VAL:CG1	2.49	0.43
6:L:293:GLU:O	6:L:293:GLU:HG2	2.19	0.43
6:L:571:TYR:HB2	6:L:576:VAL:HG22	2.00	0.43
2:G:49:SER:OG	2:G:50:SER:OG	2.14	0.43
3:I:196:VAL:HG21	3:I:209:ILE:CD1	2.48	0.43
3:I:489:PRO:CA	3:I:492:MET:HE2	2.47	0.43
3:I:615:VAL:HG13	3:I:615:VAL:O	2.18	0.43
4:J:1109:LEU:HD11	4:J:1113:VAL:CG1	2.36	0.43
6:L:393:LYS:HA	6:L:393:LYS:HD3	1.89	0.43
6:L:452:ILE:CG1	6:L:457:ILE:HG13	2.49	0.43
6:L:463:LEU:HG	6:L:487:MET:HE1	2.00	0.43
6:L:509:THR:HG23	6:L:509:THR:O	2.19	0.43
6:L:593:LYS:HA	6:L:596:ARG:HB2	1.99	0.43
2:M:300:LEU:HA	2:M:303:ILE:CD1	2.34	0.43
2:G:154:PRO:HA	2:G:174:ASP:HB3	1.99	0.43
2:H:51:MET:HB3	2:H:178:SER:HB2	1.99	0.43
2:H:109:PRO:HB3	2:H:132:HIS:HD2	1.83	0.43
2:H:140:ILE:HD12	2:H:140:ILE:HA	1.79	0.43
2:H:192:VAL:HG23	2:H:192:VAL:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:255:ILE:O	3:I:262:TYR:N	2.51	0.43
3:I:325:LEU:O	3:I:328:SER:HB3	2.18	0.43
3:I:594:VAL:HG12	3:I:595:THR:O	2.18	0.43
3:I:616:ILE:O	3:I:636:CYS:HB3	2.17	0.43
3:I:883:LEU:HD11	3:I:920:VAL:HG22	2.01	0.43
3:I:1106:ARG:NH1	4:J:731:ARG:HH12	2.16	0.43
4:J:57:PHE:HZ	4:J:266:ASN:HD21	1.67	0.43
4:J:294:ASN:ND2	6:L:406:GLN:HE21	2.16	0.43
4:J:819:GLY:CA	4:J:882:VAL:O	2.64	0.43
4:J:836:ARG:HH12	4:J:840:LEU:HD22	1.83	0.43
4:J:1149:ARG:HG2	4:J:1216:ALA:CB	2.48	0.43
4:J:1219:ASP:O	4:J:1223:LEU:HB2	2.19	0.43
6:L:102:MET:O	6:L:105:MET:HG3	2.18	0.43
6:L:151:VAL:HG22	6:L:156:ALA:HB3	1.99	0.43
6:L:267:ASP:HA	6:L:270:VAL:HB	1.99	0.43
6:L:573:LEU:HD22	8:P:56:DG:OP2	2.18	0.43
8:P:67:DT:H2''	8:P:68:DG:OP2	2.18	0.43
2:G:80:GLU:O	2:G:80:GLU:HG2	2.18	0.43
3:I:205:PRO:O	3:I:208:ILE:HG23	2.18	0.43
3:I:830:THR:HG23	3:I:832:HIS:CE1	2.53	0.43
3:I:1006:GLU:HA	3:I:1009:ASN:HB3	1.99	0.43
3:I:1067:ALA:HB2	3:I:1073:LYS:HA	2.01	0.43
3:I:1292:THR:HG22	3:I:1297:ASP:HB2	2.01	0.43
4:J:67:ASP:OD1	4:J:67:ASP:N	2.45	0.43
4:J:418:GLU:HG3	5:K:48:VAL:CG2	2.49	0.43
4:J:438:GLU:OE2	4:J:481:ARG:NH2	2.43	0.43
6:L:280:VAL:HG11	6:L:355:ILE:CG2	2.49	0.43
8:P:56:DG:C2'	8:P:57:DT:H71	2.43	0.43
8:P:60:DA:H2''	8:P:61:DT:C5'	2.48	0.43
2:H:78:ILE:HG12	2:H:81:ILE:HD12	2.01	0.43
2:H:134:THR:CG2	2:H:136:GLU:HB2	2.49	0.43
3:I:324:LYS:HA	3:I:327:GLN:HG3	1.99	0.43
3:I:928:VAL:HG13	3:I:1052:VAL:HG13	2.01	0.43
4:J:210:SER:OG	4:J:213:LYS:HD2	2.18	0.43
4:J:759:ILE:HG23	4:J:771:GLN:HB3	2.00	0.43
4:J:847:ASP:HB3	4:J:856:ILE:HG23	1.99	0.43
6:L:143:TYR:CD2	6:L:269:LEU:HD21	2.53	0.43
6:L:569:THR:HG22	6:L:570:ASP:H	1.84	0.43
3:I:161:LYS:HD3	3:I:161:LYS:H	1.83	0.43
3:I:624:ASP:OD1	3:I:628:HIS:HB2	2.18	0.43
3:I:646:SER:H	3:I:649:GLN:NE2	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:934:PHE:O	3:I:1049:ILE:N	2.47	0.43
3:I:1075:VAL:HG12	4:J:461:PHE:HB3	2.01	0.43
7:O:69:DT:H2''	7:O:70:DT:O5'	2.19	0.43
2:G:73:GLY:O	2:G:134:THR:N	2.44	0.43
2:G:79:LEU:HD23	2:G:79:LEU:HA	1.75	0.43
3:I:104:ILE:HD11	3:I:116:ASP:HB2	2.00	0.43
3:I:136:PHE:HD2	3:I:145:ILE:HD13	1.83	0.43
3:I:184:LEU:HG	3:I:185:ASP:N	2.34	0.43
3:I:1002:LEU:HD21	3:I:1007:LYS:HB3	2.00	0.43
4:J:22:ILE:HG22	4:J:1340:LYS:O	2.19	0.43
4:J:365:GLN:HA	4:J:438:GLU:H	1.84	0.43
4:J:1361:THR:HG21	5:K:20:VAL:HG11	2.01	0.43
6:L:414:LYS:HE3	6:L:434:TRP:CZ3	2.54	0.43
6:L:489:MET:HE3	6:L:489:MET:N	2.34	0.43
8:P:17:DA:H2''	8:P:18:DT:O5'	2.19	0.43
2:M:285:THR:HG22	2:M:286:GLU:H	1.83	0.43
3:I:658:GLN:HG2	3:I:658:GLN:O	2.19	0.42
4:J:45:ASN:HB3	4:J:48:THR:O	2.18	0.42
4:J:190:LYS:HE3	4:J:190:LYS:HB3	1.83	0.42
4:J:831:VAL:HG12	4:J:833:GLU:N	2.23	0.42
4:J:859:PRO:HG2	4:J:862:THR:HG21	2.00	0.42
4:J:972:LYS:CD	4:J:1002:VAL:HB	2.39	0.42
4:J:1316:THR:HG22	4:J:1318:SER:H	1.84	0.42
6:L:297:MET:HE3	6:L:326:TRP:CH2	2.54	0.42
2:G:25:LYS:HA	2:G:203:ILE:O	2.19	0.42
2:G:201:LEU:HD12	2:G:202:VAL:N	2.34	0.42
3:I:35:PHE:CD2	3:I:130:MET:HB3	2.54	0.42
3:I:181:GLY:CA	3:I:395:TYR:HA	2.49	0.42
3:I:741:MET:CG	3:I:746:ALA:HB1	2.46	0.42
3:I:777:VAL:HG11	3:I:783:LEU:CD2	2.49	0.42
3:I:812:PHE:CE2	3:I:813:GLU:HG2	2.53	0.42
3:I:823:VAL:HG22	3:I:1060:ILE:HG21	2.00	0.42
3:I:1149:TYR:CD2	3:I:1159:VAL:HG11	2.54	0.42
4:J:260:PHE:CB	6:L:504:PRO:HB3	2.49	0.42
4:J:343:LEU:HD11	4:J:1352:ILE:HG12	2.01	0.42
4:J:649:LYS:O	4:J:653:ILE:HB	2.19	0.42
4:J:1040:MET:HE3	4:J:1046:ILE:HG21	2.01	0.42
6:L:276:MET:SD	6:L:279:ARG:NH2	2.92	0.42
8:P:20:DC:H2''	8:P:21:DA:H8	1.83	0.42
2:M:261:GLU:OE2	2:M:261:GLU:HA	2.19	0.42
3:I:232:ILE:HG12	3:I:237:LEU:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:1058:ARG:HE	3:I:1058:ARG:HB3	1.44	0.42
3:I:1122:LYS:HG2	3:I:1229:TYR:CZ	2.54	0.42
4:J:54:ASP:HB2	4:J:61:ILE:CD1	2.49	0.42
4:J:363:LEU:HD12	4:J:363:LEU:O	2.19	0.42
4:J:369:PRO:HG2	4:J:372:MET:HB2	2.01	0.42
4:J:529:GLY:HA2	4:J:551:ARG:O	2.19	0.42
4:J:612:LEU:HA	4:J:612:LEU:HD12	1.83	0.42
4:J:660:GLU:OE2	4:J:685:ILE:HB	2.19	0.42
4:J:674:THR:OG1	4:J:675:ALA:N	2.52	0.42
4:J:1036:ARG:HE	4:J:1081:VAL:HG21	1.84	0.42
4:J:1037:PHE:HB3	4:J:1040:MET:SD	2.59	0.42
4:J:1163:VAL:CG2	4:J:1175:LEU:HD11	2.49	0.42
6:L:584:ARG:HA	6:L:587:ILE:HG13	2.00	0.42
1:N:49:ARG:CZ	1:N:49:ARG:HB3	2.49	0.42
2:G:224:LEU:HD23	2:H:228:LEU:CD1	2.48	0.42
2:H:49:SER:O	2:H:151:GLY:HA3	2.19	0.42
3:I:346:TYR:CE1	3:I:436:ARG:HG3	2.55	0.42
3:I:826:ASP:OD1	3:I:829:THR:HG21	2.19	0.42
3:I:854:ILE:CG2	3:I:915:ASP:HB2	2.50	0.42
3:I:1332:SER:CB	4:J:245:LEU:HD13	2.50	0.42
4:J:374:LEU:O	4:J:374:LEU:HG	2.19	0.42
4:J:474:LEU:CD1	5:K:47:THR:HG22	2.49	0.42
4:J:766:GLY:O	4:J:767:LEU:HD12	2.18	0.42
4:J:814:CYS:SG	4:J:816:THR:HG22	2.60	0.42
4:J:1067:ARG:HG3	4:J:1068:THR:O	2.20	0.42
4:J:1163:VAL:HG22	4:J:1175:LEU:HD11	2.00	0.42
4:J:1248:ILE:HG22	4:J:1249:ASN:N	2.34	0.42
6:L:226:ALA:HA	6:L:229:VAL:HG22	2.00	0.42
6:L:463:LEU:HA	6:L:463:LEU:HD23	1.58	0.42
1:N:26:LYS:C	1:N:27:ILE:HD13	2.44	0.42
3:I:211:ARG:HH11	3:I:220:ILE:HD12	1.85	0.42
3:I:216:THR:HG22	3:I:219:GLN:HB2	2.02	0.42
3:I:359:ARG:HH22	3:I:382:GLU:CG	2.31	0.42
3:I:397:LEU:N	3:I:418:GLY:O	2.53	0.42
3:I:470:ARG:HD3	3:I:470:ARG:HA	1.65	0.42
3:I:757:THR:CG2	3:I:765:ILE:HG12	2.49	0.42
3:I:1141:LEU:HD12	3:I:1141:LEU:HA	1.61	0.42
3:I:1256:GLN:OE1	6:L:528:LEU:HD23	2.19	0.42
4:J:418:GLU:HB2	5:K:45:LYS:CG	2.49	0.42
4:J:500:ILE:HG22	4:J:500:ILE:O	2.19	0.42
4:J:1025:MET:SD	4:J:1126:GLN:HG2	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:1032:SER:CB	4:J:1116:SER:HA	2.49	0.42
6:L:582:VAL:CG2	6:L:586:ARG:HB3	2.49	0.42
2:H:151:GLY:O	2:H:177:TYR:HB2	2.20	0.42
2:H:152:TYR:HE2	2:H:154:PRO:HG3	1.84	0.42
3:I:5:TYR:CD2	3:I:776:PRO:HG2	2.54	0.42
3:I:127:ILE:O	3:I:127:ILE:HG13	2.19	0.42
3:I:241:LEU:HD13	3:I:285:ILE:HG12	2.02	0.42
3:I:794:LEU:CD2	3:I:796:LEU:HD21	2.46	0.42
4:J:475:GLU:H	4:J:475:GLU:HG3	1.64	0.42
4:J:804:ALA:O	4:J:916:GLY:HA3	2.20	0.42
4:J:999:TYR:CD2	4:J:1026:PRO:HG2	2.54	0.42
4:J:1281:GLU:HG2	4:J:1283:SER:H	1.84	0.42
4:J:1347:LEU:HG	4:J:1357:ILE:HG23	2.02	0.42
6:L:138:PRO:HG2	6:L:351:THR:O	2.19	0.42
6:L:157:ARG:HG2	6:L:158:LEU:N	2.35	0.42
7:O:22:DT:H2''	7:O:23:DC:OP2	2.19	0.42
7:O:74:DC:H5'	7:O:74:DC:H6	1.85	0.42
2:M:253:LEU:CD1	2:M:282:VAL:HG21	2.49	0.42
2:M:300:LEU:HD22	2:M:303:ILE:HB	2.01	0.42
1:N:21:ASN:O	1:N:25:GLN:HG3	2.20	0.42
2:G:224:LEU:CD2	2:H:228:LEU:HD11	2.46	0.42
2:H:74:VAL:HG22	2:H:133:LEU:HD21	2.02	0.42
3:I:76:GLY:N	3:I:95:PRO:O	2.44	0.42
3:I:82:VAL:HG22	3:I:92:TYR:CD2	2.54	0.42
3:I:99:LYS:HE2	3:I:99:LYS:HB2	1.82	0.42
3:I:811:ASN:HA	3:I:815:SER:HB2	2.00	0.42
3:I:1002:LEU:HG	3:I:1007:LYS:HB2	2.01	0.42
3:I:1080:ASN:OD1	3:I:1081:PRO:HD2	2.19	0.42
4:J:130:MET:O	4:J:135:ILE:HD11	2.19	0.42
4:J:255:LEU:HA	4:J:255:LEU:HD22	1.82	0.42
4:J:698:MET:O	4:J:702:GLN:HG2	2.19	0.42
4:J:1181:ASP:N	4:J:1181:ASP:OD1	2.51	0.42
4:J:1306:LEU:HG	4:J:1307:LEU:N	2.34	0.42
4:J:1314:LEU:HD21	4:J:1326:GLN:CB	2.50	0.42
6:L:126:GLY:O	6:L:129:GLN:HG3	2.20	0.42
6:L:253:SER:O	6:L:256:PHE:HB2	2.19	0.42
1:N:48:ARG:HG2	4:J:672:LEU:O	2.19	0.42
2:G:57:THR:CB	2:G:147:GLN:HE21	2.32	0.42
2:G:229:GLU:O	2:G:232:VAL:HG12	2.19	0.42
2:H:120:ASP:OD1	2:H:121:VAL:HG13	2.19	0.42
3:I:245:ARG:HB3	3:I:337:PHE:CE2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:817:LEU:HD13	3:I:1085:MET:CE	2.50	0.42
3:I:914:LYS:HE2	3:I:914:LYS:HB3	1.62	0.42
3:I:1253:LEU:HA	3:I:1253:LEU:HD23	1.65	0.42
3:I:1320:PRO:HB2	4:J:345:LYS:NZ	2.34	0.42
4:J:650:LYS:O	4:J:654:ILE:HG23	2.20	0.42
4:J:1048:ARG:HH22	4:J:1057:SER:CB	2.33	0.42
4:J:1347:LEU:HG	4:J:1357:ILE:CG2	2.50	0.42
6:L:280:VAL:HG11	6:L:355:ILE:HG23	2.02	0.42
6:L:344:LEU:CD1	6:L:355:ILE:HG13	2.49	0.42
6:L:390:ILE:HD12	6:L:435:ILE:HG21	2.01	0.42
7:O:29:DA:H2'	7:O:30:DC:H6	1.85	0.42
2:M:275:ILE:HG22	2:M:280:ASP:CB	2.31	0.42
2:M:318:LEU:HG	2:M:319:GLU:H	1.85	0.42
2:H:11:PRO:HB2	2:H:28:LEU:CD1	2.50	0.42
2:H:23:HIS:CB	2:H:206:GLU:HG2	2.39	0.42
3:I:213:LEU:HD21	3:I:422:LYS:O	2.20	0.42
3:I:371:ARG:HD2	3:I:371:ARG:HA	1.80	0.42
3:I:1268:GLN:NE2	4:J:352:ARG:HE	2.18	0.42
4:J:500:ILE:HG23	4:J:500:ILE:HD12	1.77	0.42
4:J:1155:ILE:HD11	4:J:1211:SER:H	1.84	0.42
4:J:1322:ALA:CB	4:J:1331:VAL:HG11	2.48	0.42
5:K:21:LEU:HD23	5:K:21:LEU:HA	1.82	0.42
6:L:129:GLN:NE2	6:L:130:VAL:HG23	2.34	0.42
6:L:336:GLU:O	6:L:339:ARG:HB2	2.20	0.42
6:L:401:PHE:CZ	6:L:405:ILE:HD11	2.54	0.42
2:G:185:TYR:HB2	2:G:201:LEU:HD11	2.02	0.42
2:G:191:ARG:H	2:G:191:ARG:HD2	1.84	0.42
3:I:24:VAL:HG11	3:I:704:MET:CE	2.45	0.42
3:I:269:ILE:HG22	3:I:274:ILE:HD11	2.02	0.42
3:I:551:HIS:ND1	3:I:552:PRO:HD2	2.34	0.42
3:I:720:ARG:HH21	3:I:749:ASP:CG	2.28	0.42
4:J:128:LEU:HD23	4:J:192:MET:HE1	2.02	0.42
4:J:153:ASN:C	4:J:154:LEU:HD23	2.43	0.42
4:J:412:LEU:O	4:J:416:ILE:HG12	2.20	0.42
4:J:499:ILE:HA	4:J:499:ILE:HD12	1.83	0.42
4:J:505:ASP:HB2	4:J:629:PHE:HE1	1.85	0.42
4:J:622:ASP:OD2	4:J:622:ASP:N	2.51	0.42
4:J:686:TRP:CE3	4:J:686:TRP:HA	2.54	0.42
4:J:932:MET:HG2	4:J:933:ARG:HG3	2.02	0.42
8:P:19:DT:H2''	8:P:20:DC:H6	1.85	0.42
2:G:27:THR:CG2	2:G:200:LYS:HG3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:102:LEU:HB3	2:G:142:MET:HG3	2.01	0.41
2:G:222:THR:CB	2:H:232:VAL:HG13	2.50	0.41
2:H:205:MET:HE2	2:H:205:MET:HB3	1.78	0.41
2:H:211:ILE:HD11	2:H:215:GLU:HG3	2.02	0.41
3:I:13:LYS:HB3	3:I:1180:MET:HE3	2.02	0.41
3:I:38:PHE:HA	3:I:48:GLY:HA2	2.00	0.41
3:I:184:LEU:HD21	3:I:186:PHE:HE2	1.84	0.41
3:I:402:ARG:NH2	3:I:424:ASP:OD1	2.52	0.41
3:I:452:ARG:HH22	3:I:458:GLU:CD	2.28	0.41
3:I:813:GLU:HB2	4:J:461:PHE:HD2	1.85	0.41
3:I:1063:GLY:HA2	3:I:1075:VAL:CG2	2.50	0.41
4:J:130:MET:HE2	4:J:134:ASP:CB	2.47	0.41
4:J:438:GLU:HG3	4:J:485:MET:HE3	2.02	0.41
4:J:809:VAL:HG23	4:J:915:ILE:HG23	2.02	0.41
4:J:824:PRO:CB	4:J:831:VAL:HG11	2.50	0.41
6:L:140:ALA:CB	6:L:269:LEU:HD13	2.31	0.41
6:L:261:LEU:HB2	6:L:266:PHE:CD1	2.49	0.41
6:L:344:LEU:O	6:L:347:ILE:HB	2.20	0.41
6:L:602:SER:O	6:L:603:ARG:HD2	2.20	0.41
7:O:34:DA:H1'	7:O:35:DG:C8	2.56	0.41
2:M:287:VAL:HA	2:M:290:LEU:HB3	2.02	0.41
2:H:207:THR:OG1	2:H:208:ASN:N	2.50	0.41
3:I:136:PHE:CE2	3:I:145:ILE:HD13	2.55	0.41
3:I:274:ILE:H	3:I:274:ILE:HD12	1.85	0.41
3:I:346:TYR:CE2	3:I:433:ILE:HG23	2.55	0.41
3:I:360:LEU:HA	3:I:360:LEU:HD23	1.66	0.41
3:I:432:LEU:HA	3:I:432:LEU:HD12	1.74	0.41
3:I:848:GLU:OE1	3:I:888:THR:HG22	2.19	0.41
3:I:1290:MET:HG3	3:I:1294:LYS:HE2	2.02	0.41
4:J:69:GLU:CG	4:J:76:LYS:HG2	2.44	0.41
4:J:127:LEU:O	4:J:127:LEU:HD12	2.20	0.41
4:J:210:SER:HB2	4:J:213:LYS:HB2	2.02	0.41
4:J:255:LEU:HD21	6:L:523:ILE:HD11	2.02	0.41
4:J:409:TRP:HA	4:J:409:TRP:CE3	2.55	0.41
4:J:709:ARG:NH1	4:J:710:ASP:HB3	2.34	0.41
4:J:843:VAL:HG22	4:J:863:LEU:HA	2.01	0.41
4:J:985:ILE:CD1	4:J:991:THR:HG22	2.48	0.41
4:J:1082:ASP:OD2	4:J:1084:GLN:HB2	2.20	0.41
6:L:269:LEU:C	6:L:273:MET:HE3	2.45	0.41
6:L:491:GLU:HG2	6:L:491:GLU:O	2.20	0.41
2:G:192:VAL:HG21	2:G:198:LEU:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:238:GLN:HA	3:I:286:GLU:HA	2.01	0.41
3:I:241:LEU:HD23	3:I:282:VAL:HG23	2.02	0.41
3:I:358:ASP:OD1	3:I:358:ASP:N	2.52	0.41
3:I:840:SER:O	3:I:1047:LEU:HB2	2.20	0.41
3:I:898:GLU:OE2	6:L:541:ARG:HA	2.21	0.41
4:J:34:SER:OG	4:J:36:GLY:O	2.34	0.41
4:J:113:HIS:HB3	4:J:116:PHE:HD2	1.85	0.41
4:J:193:ASP:OD2	4:J:196:GLN:HG2	2.20	0.41
4:J:959:LYS:HD2	4:J:959:LYS:HA	1.76	0.41
4:J:1170:LYS:CD	4:J:1174:ARG:HH21	2.33	0.41
4:J:1178:THR:HG22	4:J:1184:ASP:O	2.21	0.41
4:J:1230:THR:HG23	4:J:1231:ARG:H	1.85	0.41
6:L:142:THR:O	6:L:146:GLU:HG2	2.20	0.41
2:M:321:TRP:CE3	2:M:322:PRO:HA	2.56	0.41
1:N:14:GLN:HB2	10:N:102:1N7:C21	2.50	0.41
2:H:14:VAL:HG13	2:H:28:LEU:HD13	2.01	0.41
2:H:77:ASP:HB3	2:H:79:LEU:CD2	2.51	0.41
2:H:195:ARG:NH1	2:H:198:LEU:HD11	2.35	0.41
3:I:59:ILE:HD12	3:I:475:VAL:HB	2.02	0.41
3:I:369:MET:SD	3:I:370:MET:HG2	2.60	0.41
3:I:520:PRO:HB2	3:I:794:LEU:HD13	2.02	0.41
4:J:269:TYR:O	4:J:273:ILE:HG13	2.21	0.41
4:J:447:ILE:HD11	4:J:468:VAL:CG2	2.50	0.41
4:J:502:PRO:HB3	4:J:506:VAL:CB	2.50	0.41
6:L:487:MET:C	6:L:488:LEU:HD23	2.44	0.41
2:G:36:GLY:C	2:G:187:VAL:HG11	2.45	0.41
2:H:153:VAL:HA	2:H:154:PRO:HD3	1.91	0.41
3:I:10:ARG:HG3	3:I:1176:LEU:CD2	2.51	0.41
3:I:229:ILE:HG23	3:I:334:GLU:HG2	2.03	0.41
3:I:288:PRO:O	3:I:292:ILE:HG13	2.19	0.41
3:I:546:GLU:O	3:I:546:GLU:HG2	2.20	0.41
3:I:672:GLU:OE1	3:I:672:GLU:N	2.40	0.41
3:I:1290:MET:HA	3:I:1294:LYS:HG3	2.03	0.41
4:J:26:SER:O	4:J:29:MET:HB3	2.20	0.41
4:J:73:GLY:CA	4:J:76:LYS:HE2	2.50	0.41
4:J:107:LEU:HA	4:J:276:ASN:HD21	1.85	0.41
4:J:474:LEU:HD11	5:K:47:THR:HG22	2.02	0.41
4:J:522:GLY:HA2	4:J:525:MET:HE3	2.02	0.41
4:J:811:GLU:HG3	4:J:812:ASP:H	1.85	0.41
4:J:990:ARG:HA	4:J:990:ARG:HD2	1.88	0.41
4:J:1250:ASP:O	4:J:1254:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:39:VAL:CG2	5:K:40:PRO:HD2	2.51	0.41
6:L:119:ILE:CG2	6:L:375:ALA:HB1	2.35	0.41
6:L:316:PHE:HZ	6:L:333:VAL:HG13	1.86	0.41
2:M:264:VAL:HG12	2:M:268:ASN:ND2	2.36	0.41
2:M:270:LEU:HD21	2:M:275:ILE:O	2.20	0.41
2:G:134:THR:HG22	3:I:773:LEU:HD12	2.01	0.41
2:H:44:ARG:O	2:H:48:LEU:HB2	2.21	0.41
3:I:147:SER:HB3	3:I:454:ARG:O	2.20	0.41
3:I:169:LYS:HD3	3:I:436:ARG:NH2	2.35	0.41
3:I:229:ILE:HG23	3:I:334:GLU:CG	2.50	0.41
3:I:446:ASP:HA	3:I:451:ARG:HD2	2.03	0.41
3:I:905:ILE:HD12	3:I:905:ILE:HA	1.90	0.41
4:J:198:CYS:HA	4:J:221:ILE:CD1	2.50	0.41
4:J:282:LEU:HD23	4:J:282:LEU:HA	1.86	0.41
4:J:387:LEU:HA	4:J:387:LEU:HD23	1.86	0.41
4:J:423:LEU:HD23	4:J:449:LEU:HD12	2.02	0.41
4:J:438:GLU:HA	4:J:439:PRO:HD3	1.93	0.41
4:J:683:ILE:HD13	4:J:683:ILE:HA	1.88	0.41
4:J:735:ALA:O	4:J:738:ARG:HB3	2.19	0.41
4:J:1107:VAL:CG1	4:J:1122:ALA:HB2	2.40	0.41
4:J:1145:PHE:HB3	4:J:1309:ILE:HG21	2.01	0.41
4:J:1155:ILE:HG12	4:J:1190:ILE:HD11	2.02	0.41
4:J:1230:THR:HG23	4:J:1231:ARG:N	2.36	0.41
6:L:586:ARG:NE	7:O:25:DA:H5"	2.31	0.41
1:N:5:ALA:HB3	3:I:678:ARG:CZ	2.51	0.41
2:H:200:LYS:O	2:H:200:LYS:HG2	2.19	0.41
3:I:27:LEU:HG	3:I:711:ASP:OD2	2.20	0.41
3:I:135:THR:HG21	3:I:515:MET:SD	2.61	0.41
3:I:151:ARG:CZ	3:I:445:ILE:HG21	2.50	0.41
3:I:414:ILE:H	3:I:414:ILE:HG12	1.70	0.41
3:I:452:ARG:HH11	3:I:452:ARG:HD3	1.74	0.41
3:I:699:LEU:HD13	3:I:1121:ALA:HB3	2.02	0.41
3:I:1063:GLY:O	3:I:1075:VAL:HG23	2.21	0.41
4:J:744:ARG:HE	4:J:744:ARG:HB2	1.48	0.41
4:J:956:GLY:HA2	4:J:986:ASP:HA	2.03	0.41
4:J:1168:GLU:HA	4:J:1173:ARG:HG2	2.02	0.41
6:L:571:TYR:HB3	6:L:575:GLU:HB3	2.01	0.41
7:O:23:DC:N4	8:P:63:DG:O6	2.51	0.41
1:N:34:VAL:HG21	1:N:56:THR:HA	2.03	0.41
2:G:230:ALA:CB	2:H:11:PRO:HD2	2.51	0.41
3:I:75:LEU:HD11	3:I:127:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:86:GLN:HA	3:I:140:GLY:HA2	2.02	0.41
3:I:126:GLU:O	3:I:126:GLU:HG2	2.21	0.41
3:I:296:VAL:O	3:I:336:LEU:N	2.47	0.41
3:I:803:ALA:HB2	3:I:1227:VAL:HG13	2.03	0.41
3:I:899:GLU:HA	3:I:899:GLU:OE2	2.20	0.41
4:J:747:MET:HG2	4:J:759:ILE:HG12	2.03	0.41
4:J:822:MET:HE3	4:J:822:MET:HB3	1.90	0.41
4:J:901:ARG:HG3	4:J:902:ASP:O	2.21	0.41
6:L:136:GLU:OE1	6:L:361:ILE:HG12	2.20	0.41
6:L:265:GLN:O	6:L:268:TYR:HB3	2.21	0.41
6:L:347:ILE:O	6:L:350:GLU:HB2	2.20	0.41
6:L:470:MET:HG2	6:L:486:ARG:HH11	1.86	0.41
7:O:25:DA:H2'	7:O:26:DT:H6	1.85	0.41
7:O:46:DG:H8	7:O:46:DG:H5'	1.86	0.41
2:G:74:VAL:HA	2:G:132:HIS:O	2.21	0.41
2:G:198:LEU:HD23	2:G:198:LEU:HA	1.76	0.41
2:G:205:MET:HE2	2:G:205:MET:HB3	1.76	0.41
2:H:16:ILE:HD11	2:H:214:GLU:HB3	2.01	0.41
2:H:157:THR:HG22	2:H:157:THR:O	2.21	0.41
2:H:178:SER:HA	2:H:179:PRO:HD3	1.88	0.41
3:I:100:LEU:HD23	3:I:100:LEU:HA	1.73	0.41
3:I:115:LYS:HZ2	3:I:484:LEU:HB3	1.85	0.41
3:I:201:ARG:HH12	3:I:372:PRO:HG3	1.84	0.41
3:I:379:GLU:OE1	3:I:382:GLU:HB3	2.21	0.41
3:I:696:ASP:O	3:I:697:LYS:HB3	2.21	0.41
3:I:1293:VAL:HG11	3:I:1304:MET:HG2	2.03	0.41
3:I:1326:LEU:HD11	4:J:331:ILE:HG23	2.01	0.41
3:I:1329:GLU:OE2	4:J:330:MET:HE2	2.20	0.41
4:J:159:ILE:O	4:J:160:LEU:HD23	2.21	0.41
4:J:198:CYS:CA	4:J:221:ILE:HD11	2.51	0.41
4:J:307:LEU:HD23	4:J:307:LEU:HA	1.83	0.41
4:J:334:LYS:HE2	4:J:339:ARG:HH21	1.85	0.41
4:J:338:PHE:O	4:J:343:LEU:HD22	2.20	0.41
4:J:364:HIS:CD2	5:K:4:VAL:HG12	2.56	0.41
4:J:490:ILE:HD11	4:J:609:TYR:CE1	2.56	0.41
4:J:504:GLN:OE1	4:J:731:ARG:NH2	2.54	0.41
4:J:649:LYS:O	4:J:653:ILE:HD13	2.20	0.41
4:J:919:ALA:HB2	4:J:1255:VAL:HG11	2.02	0.41
4:J:953:LYS:HD3	4:J:995:TYR:OH	2.21	0.41
4:J:1049:GLN:HG2	4:J:1050:THR:N	2.35	0.41
4:J:1059:LEU:CD1	4:J:1110:GLU:HG2	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:1176:VAL:HG13	4:J:1186:TYR:O	2.20	0.41
5:K:9:ALA:HB2	5:K:55:GLU:OE1	2.21	0.41
5:K:26:ARG:NH2	5:K:53:GLU:OE2	2.53	0.41
6:L:122:ARG:HG3	6:L:122:ARG:H	1.64	0.41
6:L:311:THR:HG22	6:L:355:ILE:HG12	2.03	0.41
6:L:394:TYR:HH	6:L:436:ARG:NH1	2.14	0.41
6:L:426:LYS:HB2	7:O:52:DA:H5"	2.03	0.41
6:L:470:MET:HE3	6:L:486:ARG:HH11	1.85	0.41
6:L:483:LEU:HD23	6:L:483:LEU:HA	1.76	0.41
6:L:571:TYR:HB2	6:L:576:VAL:CG2	2.51	0.41
6:L:578:LYS:HG3	6:L:579:GLN:N	2.35	0.41
7:O:25:DA:C8	7:O:26:DT:H72	2.56	0.41
7:O:51:DT:H2"	7:O:52:DA:OP1	2.18	0.41
2:M:270:LEU:HD12	2:M:270:LEU:HA	1.71	0.41
2:M:289:LEU:O	2:M:295:LEU:HD22	2.21	0.41
2:H:57:THR:HG22	2:H:58:GLU:HG2	2.03	0.41
3:I:198:ILE:HG22	3:I:199:ASP:N	2.35	0.41
3:I:237:LEU:HD23	3:I:289:VAL:HB	2.03	0.41
3:I:678:ARG:NH2	3:I:1106:ARG:HG3	2.35	0.41
3:I:821:ARG:HD2	3:I:825:GLU:OE2	2.21	0.41
3:I:1134:GLN:HE21	3:I:1134:GLN:HB3	1.60	0.41
4:J:1190:ILE:HG21	4:J:1196:LEU:HD21	2.03	0.41
5:K:13:ILE:CD1	5:K:54:ILE:HD12	2.50	0.41
6:L:147:GLN:HA	6:L:150:ARG:HD3	2.03	0.41
6:L:257:LYS:O	6:L:257:LYS:HG2	2.21	0.41
2:G:234:LEU:HD23	2:G:234:LEU:HA	1.82	0.40
2:H:10:LYS:HB3	2:H:11:PRO:HD2	2.03	0.40
2:H:90:VAL:HG22	2:H:123:ILE:HD13	2.03	0.40
3:I:593:LYS:HD2	3:I:652:TYR:CE1	2.55	0.40
3:I:678:ARG:HA	3:I:678:ARG:HD3	1.61	0.40
3:I:755:LYS:HA	3:I:755:LYS:HE3	2.03	0.40
3:I:960:LEU:HD21	3:I:1028:LYS:HB3	2.03	0.40
3:I:1322:SER:OG	4:J:342:LEU:HD23	2.20	0.40
4:J:262:THR:CG2	4:J:266:ASN:HB2	2.51	0.40
4:J:355:ILE:HG21	4:J:466:MET:HB2	2.03	0.40
4:J:369:PRO:HA	4:J:442:ILE:O	2.22	0.40
4:J:1314:LEU:HD21	4:J:1326:GLN:HB2	2.03	0.40
6:L:324:LYS:H	6:L:327:SER:HB2	1.86	0.40
6:L:380:VAL:O	6:L:384:LEU:HG	2.21	0.40
6:L:390:ILE:HG21	6:L:435:ILE:CG2	2.51	0.40
6:L:511:ILE:HG23	6:L:511:ILE:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:555:GLU:OE1	6:L:556:ALA:N	2.54	0.40
8:P:13:DG:H2''	8:P:14:DA:OP2	2.21	0.40
8:P:57:DT:C2'	8:P:58:DC:H5''	2.50	0.40
8:P:65:DT:C6	8:P:66:DT:H72	2.56	0.40
2:G:183:ILE:HD12	2:G:205:MET:HB2	2.03	0.40
2:H:100:LEU:HB2	2:H:144:ILE:HG23	2.03	0.40
3:I:322:LEU:O	3:I:325:LEU:HG	2.20	0.40
3:I:705:GLU:H	3:I:705:GLU:HG2	1.48	0.40
3:I:1256:GLN:HB3	3:I:1301:ARG:HH12	1.86	0.40
4:J:96:LYS:HE3	4:J:96:LYS:HB2	1.76	0.40
4:J:126:LEU:HD12	4:J:223:LEU:HD23	2.03	0.40
4:J:135:ILE:HD12	4:J:135:ILE:H	1.86	0.40
4:J:449:LEU:HD11	4:J:457:TYR:HE2	1.86	0.40
4:J:490:ILE:HD11	4:J:609:TYR:HE1	1.86	0.40
4:J:1047:THR:N	4:J:1060:VAL:O	2.34	0.40
4:J:1172:LYS:HB3	4:J:1191:PRO:CA	2.36	0.40
6:L:141:ILE:HA	6:L:144:LEU:CB	2.51	0.40
6:L:288:MET:HB3	6:L:302:PHE:CE2	2.56	0.40
6:L:288:MET:HE2	6:L:289:LYS:HZ2	1.83	0.40
2:M:253:LEU:HB3	2:M:321:TRP:CZ2	2.57	0.40
2:M:265:ARG:HE	2:M:294:ASN:HD22	1.69	0.40
3:I:136:PHE:CZ	3:I:456:VAL:HG21	2.56	0.40
3:I:230:PHE:CE1	3:I:292:ILE:HG23	2.56	0.40
3:I:590:PRO:HG3	3:I:605:TYR:CE1	2.52	0.40
3:I:593:LYS:HD3	3:I:604:HIS:NE2	2.37	0.40
3:I:986:ALA:HA	3:I:989:LEU:CB	2.52	0.40
4:J:330:MET:O	4:J:337:ARG:HG2	2.21	0.40
4:J:373:ALA:O	4:J:377:PHE:HD2	2.04	0.40
4:J:510:LEU:HD21	4:J:624:ILE:HG12	2.03	0.40
4:J:557:LYS:HB3	4:J:557:LYS:HE2	1.71	0.40
4:J:1173:ARG:HD2	4:J:1174:ARG:N	2.36	0.40
6:L:320:ILE:HG12	6:L:330:LEU:HB3	2.03	0.40
1:N:52:PHE:CZ	4:J:677:GLU:HG2	2.56	0.40
2:H:48:LEU:HD13	2:H:183:ILE:HD13	2.04	0.40
2:H:172:LEU:HD13	2:H:172:LEU:HA	1.98	0.40
3:I:135:THR:OG1	3:I:142:GLU:OE2	2.40	0.40
3:I:317:LEU:HD23	3:I:317:LEU:HA	1.84	0.40
3:I:324:LYS:O	3:I:327:GLN:HG3	2.21	0.40
3:I:541:GLU:HG3	3:I:542:ARG:N	2.37	0.40
3:I:565:GLU:HA	3:I:569:ILE:HG12	2.03	0.40
3:I:618:GLN:HB2	3:I:635:THR:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:326:SER:O	4:J:330:MET:HG3	2.22	0.40
4:J:490:ILE:CD1	4:J:614:LEU:HD12	2.49	0.40
4:J:951:GLN:OE1	4:J:1016:THR:HB	2.22	0.40
4:J:1034:PHE:O	4:J:1080:ILE:HD12	2.21	0.40
4:J:1151:LYS:HA	4:J:1151:LYS:HD3	1.75	0.40
2:M:255:ARG:HB2	2:M:278:ILE:HD11	2.02	0.40
2:G:57:THR:HG22	2:G:58:GLU:HG2	2.04	0.40
3:I:180:ARG:NH2	3:I:393:ASP:HA	2.36	0.40
3:I:528:ARG:HH11	3:I:528:ARG:HG2	1.86	0.40
3:I:596:ASP:OD1	3:I:598:VAL:HG23	2.21	0.40
3:I:690:VAL:HG11	3:I:830:THR:HG21	2.03	0.40
3:I:985:GLU:CD	3:I:988:LYS:HD2	2.47	0.40
3:I:1252:SER:OG	3:I:1253:LEU:N	2.54	0.40
4:J:298:MET:HE3	4:J:298:MET:HB2	1.62	0.40
4:J:314:ARG:HD2	4:J:315:ALA:N	2.32	0.40
4:J:1230:THR:O	4:J:1234:VAL:HG23	2.21	0.40
6:L:95:THR:O	6:L:95:THR:HG23	2.22	0.40
6:L:276:MET:CE	6:L:279:ARG:HH21	2.34	0.40
6:L:450:ILE:HG13	6:L:450:ILE:O	2.21	0.40
7:O:66:DG:H2'	7:O:67:DA:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	N	70/72 (97%)	66 (94%)	4 (6%)	0	100	100
2	G	226/329 (69%)	192 (85%)	34 (15%)	0	100	100
2	H	215/329 (65%)	185 (86%)	30 (14%)	0	100	100
2	M	71/329 (22%)	68 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	I	1338/1342 (100%)	1164 (87%)	170 (13%)	4 (0%)	36	67
4	J	1339/1430 (94%)	1202 (90%)	137 (10%)	0	100	100
5	K	77/91 (85%)	66 (86%)	10 (13%)	1 (1%)	9	39
6	L	468/616 (76%)	433 (92%)	35 (8%)	0	100	100
All	All	3804/4538 (84%)	3376 (89%)	423 (11%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	82	VAL
5	K	61	ASN
3	I	81	ASP
3	I	1059	ARG
3	I	697	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	N	61/61 (100%)	52 (85%)	9 (15%)	3	17
2	G	194/286 (68%)	172 (89%)	22 (11%)	5	25
2	H	181/286 (63%)	157 (87%)	24 (13%)	4	20
2	M	65/286 (23%)	62 (95%)	3 (5%)	24	50
3	I	1154/1157 (100%)	1015 (88%)	139 (12%)	5	23
4	J	1128/1189 (95%)	991 (88%)	137 (12%)	5	22
5	K	67/75 (89%)	61 (91%)	6 (9%)	9	32
6	L	418/543 (77%)	391 (94%)	27 (6%)	15	42
All	All	3268/3883 (84%)	2901 (89%)	367 (11%)	8	25

All (367) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	10	SER
1	N	12	THR
1	N	16	THR
1	N	20	ILE
1	N	34	VAL
1	N	42	ASN
1	N	46	GLU
1	N	48	ARG
1	N	59	VAL
2	G	17	GLU
2	G	18	GLN
2	G	19	VAL
2	G	56	VAL
2	G	78	ILE
2	G	79	LEU
2	G	85	LEU
2	G	92	VAL
2	G	99	ILE
2	G	110	VAL
2	G	124	VAL
2	G	129	VAL
2	G	131	CYS
2	G	133	LEU
2	G	140	ILE
2	G	147	GLN
2	G	168	ILE
2	G	173	VAL
2	G	187	VAL
2	G	203	ILE
2	G	210	THR
2	G	211	ILE
2	H	6	THR
2	H	16	ILE
2	H	46	ILE
2	H	65	LEU
2	H	71	LYS
2	H	76	GLU
2	H	78	ILE
2	H	83	LEU
2	H	98	VAL
2	H	111	THR
2	H	114	ASP
2	H	121	VAL

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Mol	Chain	Res	Type
2	H	123	ILE
2	H	125	LYS
2	H	127	GLN
2	H	134	THR
2	H	146	VAL
2	H	183	ILE
2	H	188	GLU
2	H	195	ARG
2	H	207	THR
2	H	210	THR
2	H	212	ASP
2	H	224	LEU
3	I	4	SER
3	I	6	THR
3	I	13	LYS
3	I	21	VAL
3	I	22	LEU
3	I	23	ASP
3	I	29	SER
3	I	30	ILE
3	I	39	ILE
3	I	47	TYR
3	I	59	ILE
3	I	85	CYS
3	I	87	ILE
3	I	91	THR
3	I	104	ILE
3	I	116	ASP
3	I	118	LYS
3	I	130	MET
3	I	155	VAL
3	I	194	LEU
3	I	213	LEU
3	I	216	THR
3	I	220	ILE
3	I	228	VAL
3	I	232	ILE
3	I	242	VAL
3	I	255	ILE
3	I	263	VAL
3	I	287	VAL
3	I	348	SER

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Mol	Chain	Res	Type
3	I	350	THR
3	I	385	PHE
3	I	425	ILE
3	I	427	ASP
3	I	428	VAL
3	I	435	ILE
3	I	444	ASP
3	I	448	LEU
3	I	456	VAL
3	I	471	VAL
3	I	472	GLU
3	I	491	ASP
3	I	492	MET
3	I	498	ILE
3	I	502	VAL
3	I	514	PHE
3	I	521	LEU
3	I	538	LEU
3	I	539	THR
3	I	547	VAL
3	I	561	ILE
3	I	569	ILE
3	I	582	ASN
3	I	589	THR
3	I	598	VAL
3	I	602	GLU
3	I	604	HIS
3	I	609	ILE
3	I	616	ILE
3	I	635	THR
3	I	661	VAL
3	I	684	ASN
3	I	685	MET
3	I	690	VAL
3	I	693	LEU
3	I	697	LYS
3	I	699	LEU
3	I	705	GLU
3	I	723	VAL
3	I	741	MET
3	I	749	ASP
3	I	758	ARG

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Mol	Chain	Res	Type
3	I	764	CYS
3	I	765	ILE
3	I	766	ASN
3	I	800	MET
3	I	802	VAL
3	I	817	LEU
3	I	818	VAL
3	I	819	SER
3	I	829	THR
3	I	842	ASP
3	I	870	ILE
3	I	873	ILE
3	I	882	ILE
3	I	902	LEU
3	I	915	ASP
3	I	918	LEU
3	I	919	ARG
3	I	925	SER
3	I	939	VAL
3	I	946	LEU
3	I	953	LEU
3	I	978	VAL
3	I	984	VAL
3	I	998	LEU
3	I	1003	THR
3	I	1011	LEU
3	I	1012	GLU
3	I	1029	LEU
3	I	1036	ILE
3	I	1042	LEU
3	I	1058	ARG
3	I	1079	ILE
3	I	1082	ILE
3	I	1083	GLU
3	I	1092	THR
3	I	1107	MET
3	I	1112	ILE
3	I	1115	THR
3	I	1132	LEU
3	I	1138	VAL
3	I	1151	LEU
3	I	1157	GLN

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Mol	Chain	Res	Type
3	I	1159	VAL
3	I	1160	ASP
3	I	1172	LEU
3	I	1182	ILE
3	I	1186	VAL
3	I	1204	LEU
3	I	1210	ILE
3	I	1226	THR
3	I	1227	VAL
3	I	1233	LEU
3	I	1235	LEU
3	I	1238	LEU
3	I	1239	VAL
3	I	1240	ASP
3	I	1241	ASP
3	I	1253	LEU
3	I	1254	VAL
3	I	1255	THR
3	I	1293	VAL
3	I	1308	ILE
3	I	1309	VAL
3	I	1327	LEU
3	I	1337	ILE
3	I	1339	LEU
3	I	1340	GLU
4	J	30	ILE
4	J	46	TYR
4	J	66	LYS
4	J	67	ASP
4	J	78	LEU
4	J	92	VAL
4	J	114	ILE
4	J	161	THR
4	J	164	GLN
4	J	188	LEU
4	J	200	GLN
4	J	201	LEU
4	J	205	LEU
4	J	217	LEU
4	J	221	ILE
4	J	230	SER
4	J	240	THR

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Mol	Chain	Res	Type
4	J	253	VAL
4	J	255	LEU
4	J	264	ASP
4	J	278	ARG
4	J	297	ARG
4	J	306	LEU
4	J	314	ARG
4	J	341	ASN
4	J	343	LEU
4	J	386	GLU
4	J	392	THR
4	J	401	VAL
4	J	403	ARG
4	J	415	VAL
4	J	416	ILE
4	J	423	LEU
4	J	441	LEU
4	J	449	LEU
4	J	473	THR
4	J	487	THR
4	J	499	ILE
4	J	503	SER
4	J	517	CYS
4	J	527	LEU
4	J	536	LEU
4	J	545	HIS
4	J	550	VAL
4	J	553	THR
4	J	554	GLU
4	J	557	LYS
4	J	569	LEU
4	J	582	ILE
4	J	601	ILE
4	J	605	LEU
4	J	612	LEU
4	J	614	LEU
4	J	641	ILE
4	J	653	ILE
4	J	661	VAL
4	J	664	ILE
4	J	666	GLU
4	J	672	LEU

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Mol	Chain	Res	Type
4	J	674	THR
4	J	678	ARG
4	J	707	ILE
4	J	717	VAL
4	J	722	ILE
4	J	724	MET
4	J	744	ARG
4	J	746	LEU
4	J	751	ASP
4	J	756	GLU
4	J	757	THR
4	J	760	THR
4	J	762	ASN
4	J	768	ASN
4	J	774	ILE
4	J	775	SER
4	J	786	THR
4	J	789	LYS
4	J	790	THR
4	J	797	THR
4	J	800	LEU
4	J	801	VAL
4	J	808	VAL
4	J	839	VAL
4	J	855	ASP
4	J	856	ILE
4	J	868	TRP
4	J	871	LEU
4	J	878	ASP
4	J	890	THR
4	J	894	VAL
4	J	901	ARG
4	J	908	ILE
4	J	930	LEU
4	J	960	LEU
4	J	963	VAL
4	J	982	LEU
4	J	997	VAL
4	J	1002	VAL
4	J	1015	GLU
4	J	1016	THR
4	J	1024	THR

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Mol	Chain	Res	Type
4	J	1035	VAL
4	J	1041	ILE
4	J	1046	ILE
4	J	1063	ASP
4	J	1078	LEU
4	J	1089	LEU
4	J	1093	THR
4	J	1094	ASP
4	J	1106	ILE
4	J	1113	VAL
4	J	1116	SER
4	J	1135	THR
4	J	1148	ARG
4	J	1172	LYS
4	J	1198	VAL
4	J	1210	ILE
4	J	1226	VAL
4	J	1230	THR
4	J	1235	ASN
4	J	1244	GLN
4	J	1246	VAL
4	J	1255	VAL
4	J	1257	VAL
4	J	1261	LEU
4	J	1272	SER
4	J	1285	VAL
4	J	1291	GLU
4	J	1298	VAL
4	J	1306	LEU
4	J	1310	THR
4	J	1320	ILE
4	J	1324	SER
4	J	1326	GLN
4	J	1337	VAL
4	J	1344	LEU
4	J	1355	ARG
5	K	20	VAL
5	K	36	ASP
5	K	48	VAL
5	K	51	LEU
5	K	55	GLU
5	K	58	LEU

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Mol	Chain	Res	Type
6	L	98	VAL
6	L	132	CYS
6	L	141	ILE
6	L	154	GLU
6	L	233	ASP
6	L	249	ILE
6	L	261	LEU
6	L	304	THR
6	L	335	GLU
6	L	410	ILE
6	L	416	VAL
6	L	442	SER
6	L	449	THR
6	L	452	ILE
6	L	457	ILE
6	L	462	LYS
6	L	466	ILE
6	L	476	ARG
6	L	487	MET
6	L	489	MET
6	L	494	ILE
6	L	502	LYS
6	L	523	ILE
6	L	524	GLU
6	L	528	LEU
6	L	590	ILE
6	L	598	LEU
2	M	284	ARG
2	M	285	THR
2	M	299	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	N	30	HIS
2	G	37	HIS
2	G	132	HIS
2	G	137	ASN
2	H	84	ASN
2	H	128	HIS
2	H	227	GLN
3	I	46	GLN

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Mol	Chain	Res	Type
3	I	65	ASN
3	I	69	GLN
3	I	214	ASN
3	I	314	ASN
3	I	330	HIS
3	I	463	GLN
3	I	517	GLN
3	I	618	GLN
3	I	620	ASN
3	I	622	ASN
3	I	628	HIS
3	I	677	ASN
3	I	686	GLN
3	I	752	ASN
3	I	761	GLN
3	I	856	ASN
3	I	1010	GLN
3	I	1116	HIS
3	I	1134	GLN
3	I	1135	GLN
3	I	1146	GLN
3	I	1244	HIS
3	I	1268	GLN
4	J	45	ASN
4	J	266	ASN
4	J	341	ASN
4	J	465	GLN
4	J	488	ASN
4	J	665	GLN
4	J	680	ASN
4	J	951	GLN
4	J	1023	HIS
4	J	1049	GLN
4	J	1114	GLN
4	J	1126	GLN
4	J	1244	GLN
4	J	1249	ASN
4	J	1295	ASN
4	J	1350	ASN
6	L	246	GLN
6	L	406	GLN
6	L	437	GLN

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Mol	Chain	Res	Type
6	L	464	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
10	1N7	J	1504	-	30,30,46	5.20	19 (63%)	47,48,72	2.17	12 (25%)
10	1N7	L	701	-	30,30,46	5.24	15 (50%)	47,48,72	2.34	18 (38%)
10	1N7	I	1401	-	30,30,46	5.11	15 (50%)	47,48,72	2.58	21 (44%)
10	1N7	N	102	-	30,30,46	5.00	15 (50%)	47,48,72	2.42	17 (36%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	1N7	J	1504	-	-	3/7/72/92	0/4/4/4
10	1N7	L	701	-	-	4/7/72/92	0/4/4/4
10	1N7	I	1401	-	-	2/7/72/92	0/4/4/4
10	1N7	N	102	-	-	2/7/72/92	0/4/4/4

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	L	701	1N7	C3-C19	18.84	1.84	1.53
10	J	1504	1N7	C3-C19	18.79	1.84	1.53
10	I	1401	1N7	C3-C19	18.34	1.83	1.53
10	N	102	1N7	C3-C19	17.76	1.82	1.53
10	L	701	1N7	C3-C4	12.47	1.73	1.53
10	I	1401	1N7	C3-C4	12.45	1.73	1.53
10	J	1504	1N7	C3-C4	12.07	1.72	1.53
10	N	102	1N7	C3-C4	11.84	1.72	1.53
10	L	701	1N7	C5-C4	-9.54	1.39	1.54
10	I	1401	1N7	C5-C4	-9.21	1.40	1.54
10	N	102	1N7	C5-C4	-9.06	1.40	1.54
10	J	1504	1N7	C5-C4	-8.94	1.40	1.54
10	I	1401	1N7	C2-C19	-7.84	1.42	1.56
10	N	102	1N7	C2-C19	-7.59	1.42	1.56
10	L	701	1N7	C2-C19	-7.47	1.43	1.56
10	J	1504	1N7	C2-C19	-7.36	1.43	1.56
10	L	701	1N7	C8-C7	6.00	1.70	1.54
10	N	102	1N7	C8-C7	5.62	1.69	1.54
10	J	1504	1N7	C8-C7	5.62	1.69	1.54
10	I	1401	1N7	C8-C7	5.55	1.69	1.54
10	N	102	1N7	C5-C9	5.00	1.63	1.55
10	J	1504	1N7	C2-C15	4.65	1.62	1.55
10	L	701	1N7	O4-C4	-4.39	1.36	1.43
10	L	701	1N7	C7-C6	4.29	1.63	1.54
10	J	1504	1N7	O4-C4	-4.15	1.36	1.43
10	I	1401	1N7	C5-C9	4.14	1.62	1.55
10	N	102	1N7	O4-C4	-3.99	1.37	1.43
10	J	1504	1N7	C5-C9	3.96	1.62	1.55
10	J	1504	1N7	C18-C6	-3.87	1.46	1.53
10	L	701	1N7	C5-C6	-3.76	1.49	1.55
10	L	701	1N7	C5-C9	3.70	1.61	1.55
10	I	1401	1N7	O4-C4	-3.62	1.37	1.43
10	L	701	1N7	C14-C15	-3.61	1.48	1.53
10	N	102	1N7	C2-C15	3.52	1.60	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	I	1401	1N7	C14-C15	-3.48	1.48	1.53
10	J	1504	1N7	C5-C6	-3.34	1.49	1.55
10	I	1401	1N7	C18-C6	-3.34	1.47	1.53
10	L	701	1N7	C2-C15	3.31	1.60	1.55
10	I	1401	1N7	C2-C15	3.22	1.60	1.55
10	I	1401	1N7	C5-C6	-3.19	1.50	1.55
10	N	102	1N7	C18-C6	-3.11	1.47	1.53
10	I	1401	1N7	C7-C6	3.09	1.60	1.54
10	J	1504	1N7	C7-C6	3.09	1.60	1.54
10	N	102	1N7	C5-C6	-3.00	1.50	1.55
10	N	102	1N7	C14-C15	-2.88	1.49	1.53
10	N	102	1N7	C7-C6	2.77	1.60	1.54
10	J	1504	1N7	C14-C15	-2.66	1.49	1.53
10	J	1504	1N7	C14-C13	2.63	1.56	1.52
10	J	1504	1N7	C10-C5	2.58	1.58	1.54
10	I	1401	1N7	O2-C13	-2.54	1.36	1.43
10	L	701	1N7	C18-C6	-2.52	1.49	1.53
10	N	102	1N7	O2-C13	-2.41	1.36	1.43
10	L	701	1N7	O2-C13	-2.37	1.36	1.43
10	N	102	1N7	C10-C5	2.31	1.58	1.54
10	J	1504	1N7	C11-C2	2.29	1.58	1.54
10	J	1504	1N7	O2-C13	-2.27	1.36	1.43
10	L	701	1N7	C12-C13	2.27	1.56	1.51
10	L	701	1N7	C14-C13	2.14	1.55	1.52
10	I	1401	1N7	C1-C2	2.14	1.57	1.54
10	I	1401	1N7	C10-C5	2.12	1.57	1.54
10	J	1504	1N7	C1-C12	2.07	1.57	1.53
10	N	102	1N7	C1-C2	2.06	1.57	1.54
10	J	1504	1N7	C1-C2	2.05	1.57	1.54
10	J	1504	1N7	C12-C13	2.05	1.56	1.51

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	1504	1N7	C7-C6-C18	-7.80	107.66	118.36
10	I	1401	1N7	C7-C6-C18	-5.81	110.39	118.36
10	I	1401	1N7	C9-C5-C4	-5.81	112.44	117.67
10	N	102	1N7	C9-C5-C4	-5.51	112.71	117.67
10	L	701	1N7	C9-C5-C4	-5.46	112.75	117.67
10	J	1504	1N7	C16-C15-C14	-5.44	105.01	111.23
10	L	701	1N7	C21-C20-C9	-5.15	105.16	112.88
10	N	102	1N7	C21-C20-C22	-5.01	102.58	110.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	N	102	1N7	C19-C3-C4	-5.01	107.74	114.29
10	L	701	1N7	C2-C19-C18	4.85	117.24	111.84
10	N	102	1N7	C7-C6-C18	-4.79	111.78	118.36
10	L	701	1N7	C6-C5-C4	4.74	111.75	107.42
10	I	1401	1N7	C5-C6-C18	4.63	120.58	114.72
10	N	102	1N7	C9-C5-C6	4.53	104.66	100.11
10	I	1401	1N7	C19-C3-C4	-4.35	108.60	114.29
10	N	102	1N7	C5-C6-C18	4.17	120.00	114.72
10	L	701	1N7	C3-C19-C18	-4.14	104.77	110.89
10	I	1401	1N7	C19-C18-C17	-4.13	106.66	111.86
10	I	1401	1N7	C14-C13-C12	-4.00	105.74	110.62
10	N	102	1N7	C3-C19-C18	-3.95	105.06	110.89
10	N	102	1N7	C2-C19-C18	3.88	116.16	111.84
10	J	1504	1N7	C7-C6-C5	3.82	107.24	103.54
10	J	1504	1N7	C9-C5-C6	3.79	103.92	100.11
10	I	1401	1N7	C3-C19-C18	-3.68	105.44	110.89
10	I	1401	1N7	C16-C15-C2	-3.67	108.76	112.66
10	I	1401	1N7	C9-C5-C6	3.66	103.78	100.11
10	L	701	1N7	C22-C20-C9	3.59	117.78	110.33
10	L	701	1N7	C19-C18-C17	-3.57	107.36	111.86
10	I	1401	1N7	C8-C7-C6	-3.55	98.20	105.14
10	J	1504	1N7	C9-C5-C4	-3.47	114.54	117.67
10	I	1401	1N7	C6-C5-C4	3.44	110.56	107.42
10	I	1401	1N7	C15-C14-C13	-3.43	107.53	112.71
10	I	1401	1N7	C2-C19-C18	3.42	115.65	111.84
10	L	701	1N7	C15-C14-C13	-3.40	107.58	112.71
10	N	102	1N7	C14-C13-C12	-3.39	106.48	110.62
10	N	102	1N7	C16-C15-C2	-3.31	109.14	112.66
10	L	701	1N7	C19-C2-C15	3.20	112.95	108.51
10	N	102	1N7	C8-C9-C20	-3.15	107.41	112.18
10	I	1401	1N7	C14-C15-C2	3.11	115.97	112.66
10	J	1504	1N7	C5-C6-C18	3.10	118.64	114.72
10	I	1401	1N7	C19-C2-C15	3.06	112.77	108.51
10	L	701	1N7	C11-C2-C19	3.06	115.29	111.18
10	I	1401	1N7	C11-C2-C15	-3.06	105.33	110.44
10	N	102	1N7	C11-C2-C1	-3.04	103.47	108.31
10	I	1401	1N7	C3-C4-C5	-2.92	108.30	111.26
10	L	701	1N7	C11-C2-C15	-2.91	105.58	110.44
10	J	1504	1N7	C10-C5-C6	2.86	115.68	111.20
10	I	1401	1N7	C8-C9-C20	-2.76	107.99	112.18
10	I	1401	1N7	C1-C12-C13	-2.75	106.84	110.48
10	N	102	1N7	C8-C7-C6	-2.72	99.82	105.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	701	1N7	C7-C6-C18	-2.65	114.72	118.36
10	N	102	1N7	C6-C5-C4	2.64	109.83	107.42
10	J	1504	1N7	C11-C2-C1	-2.64	104.11	108.31
10	J	1504	1N7	C8-C9-C20	-2.62	108.21	112.18
10	L	701	1N7	C10-C5-C4	-2.61	106.45	109.06
10	N	102	1N7	C1-C12-C13	-2.58	107.06	110.48
10	L	701	1N7	C14-C15-C2	-2.49	110.00	112.66
10	J	1504	1N7	C10-C5-C9	-2.41	107.43	111.20
10	L	701	1N7	C7-C8-C9	-2.39	100.47	105.14
10	L	701	1N7	C21-C20-C22	-2.37	106.66	110.34
10	J	1504	1N7	C11-C2-C19	2.37	114.36	111.18
10	L	701	1N7	C5-C6-C18	2.32	117.66	114.72
10	I	1401	1N7	C21-C20-C22	-2.31	106.77	110.34
10	I	1401	1N7	C11-C2-C1	-2.26	104.71	108.31
10	L	701	1N7	C11-C2-C1	-2.18	104.84	108.31
10	J	1504	1N7	C19-C18-C17	-2.15	109.15	111.86
10	N	102	1N7	C22-C20-C9	2.12	114.73	110.33
10	N	102	1N7	C3-C4-C5	-2.08	109.15	111.26

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	N	102	1N7	C21-C20-C22-C23
10	J	1504	1N7	C9-C20-C22-C23
10	L	701	1N7	C22-C20-C9-C5
10	J	1504	1N7	C21-C20-C22-C23
10	L	701	1N7	C21-C20-C9-C5
10	I	1401	1N7	C21-C20-C22-C23
10	N	102	1N7	C9-C20-C22-C23
10	I	1401	1N7	C9-C20-C22-C23
10	L	701	1N7	C21-C20-C9-C8
10	L	701	1N7	C22-C20-C9-C8
10	J	1504	1N7	C20-C22-C23-C24

There are no ring outliers.

4 monomers are involved in 16 short contacts:

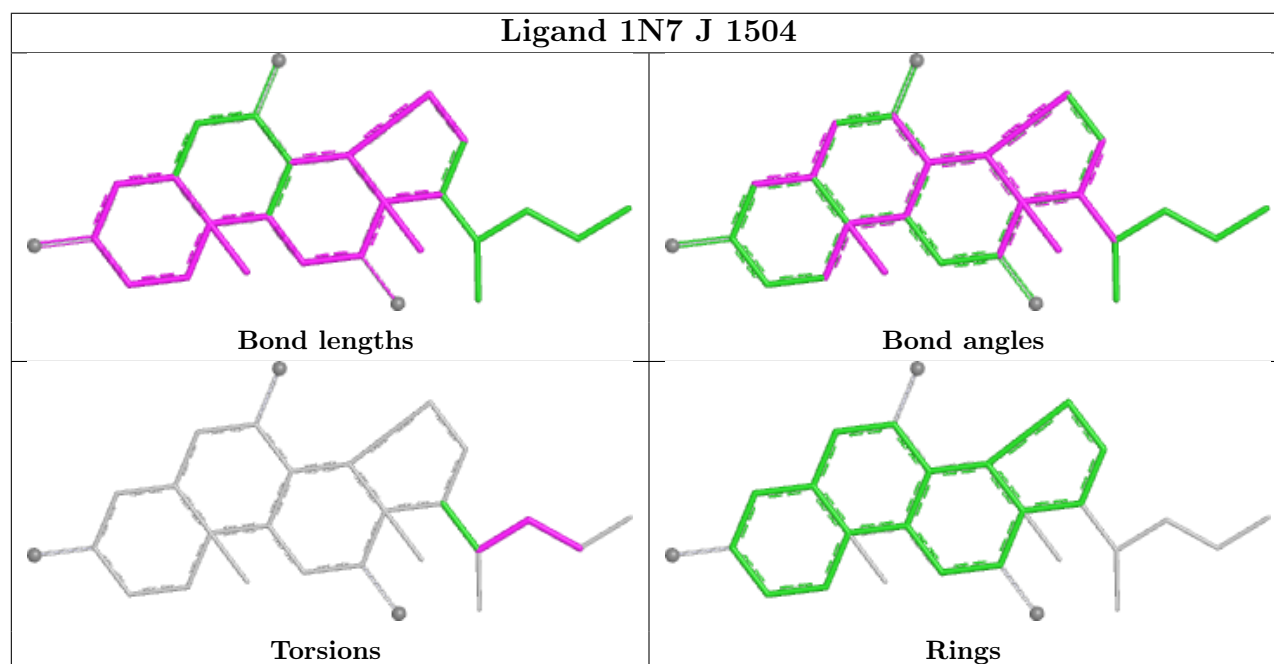
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	J	1504	1N7	3	0
10	L	701	1N7	3	0

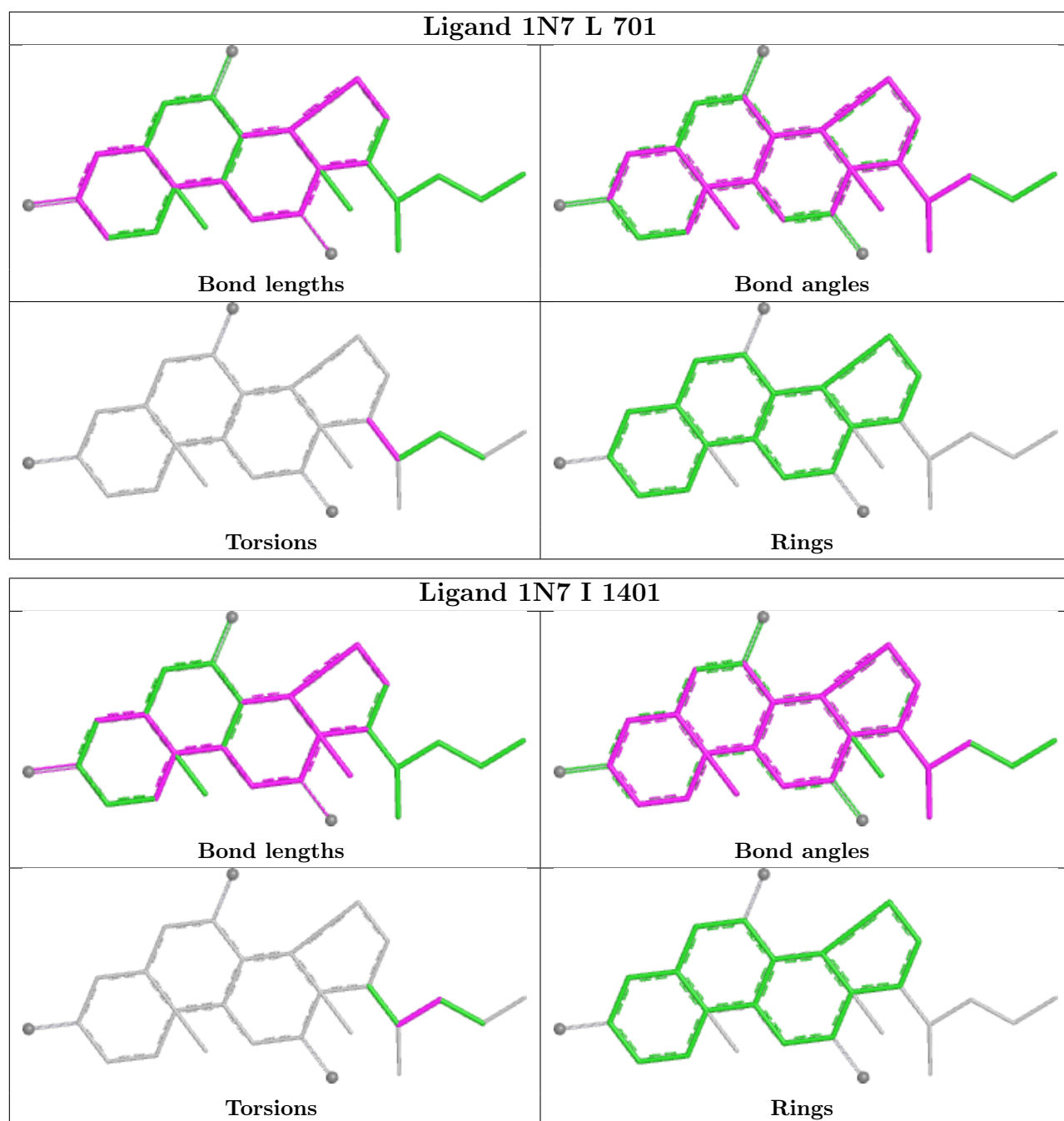
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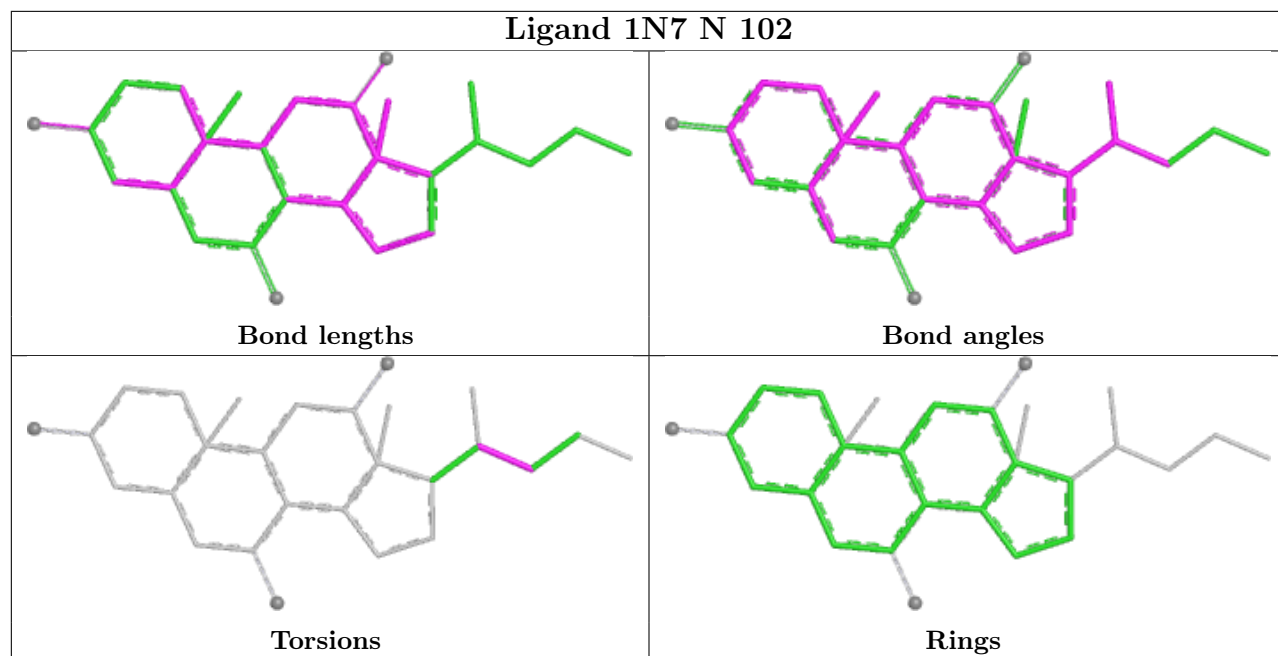
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	I	1401	1N7	6	0
10	N	102	1N7	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

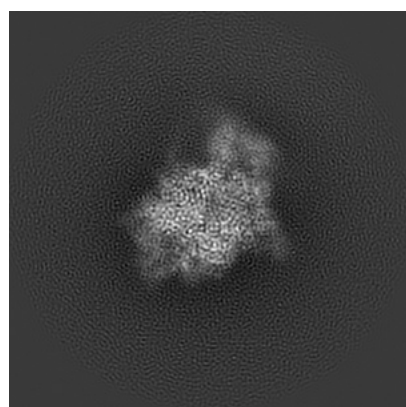
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20465. These allow visual inspection of the internal detail of the map and identification of artifacts.

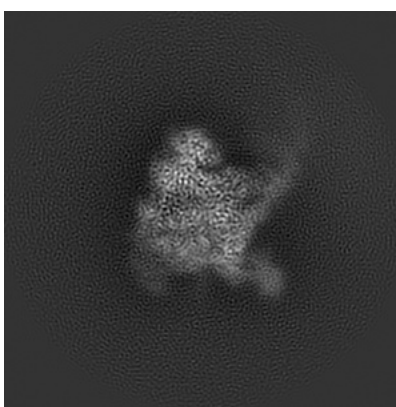
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

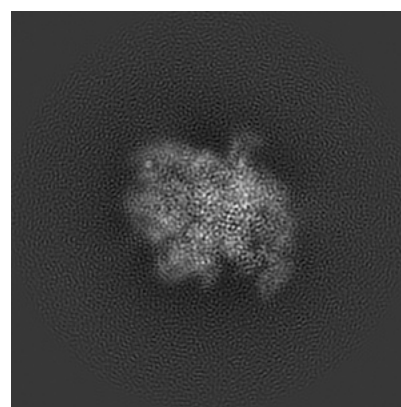
6.1.1 Primary map



X



Y

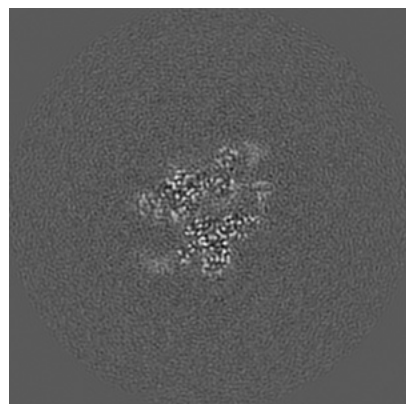


Z

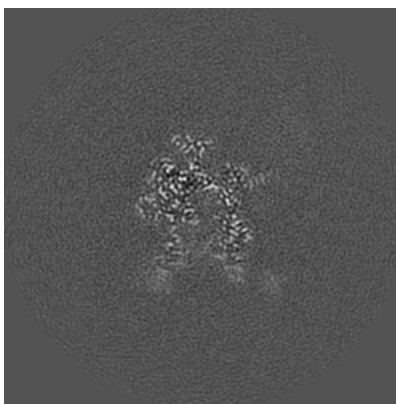
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

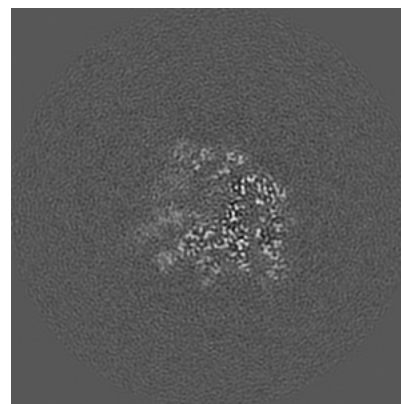
6.2.1 Primary map



X Index: 128



Y Index: 128

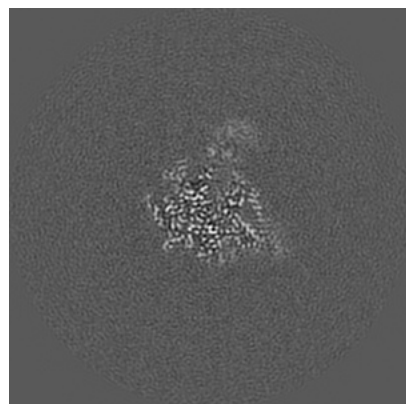


Z Index: 128

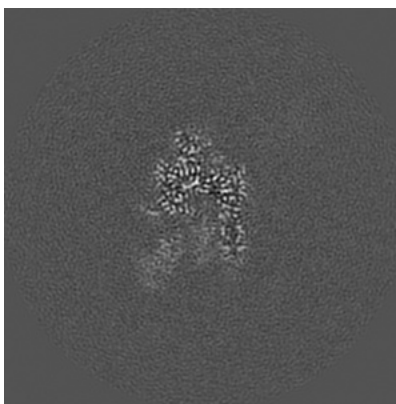
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

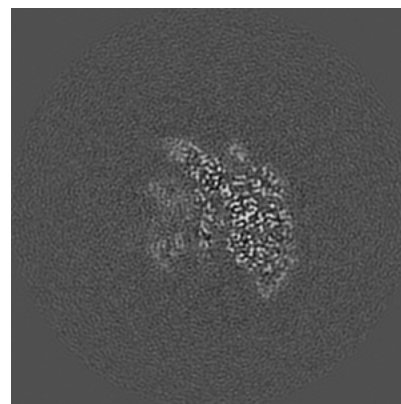
6.3.1 Primary map



X Index: 146



Y Index: 123

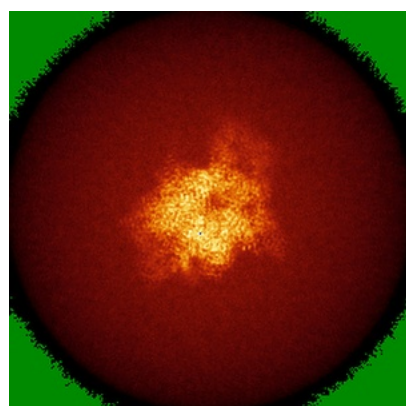


Z Index: 120

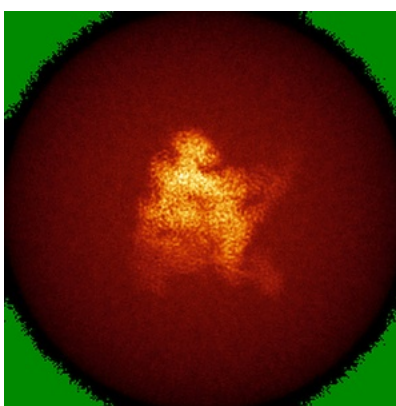
The images above show the largest variance slices of the map in three orthogonal directions.

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

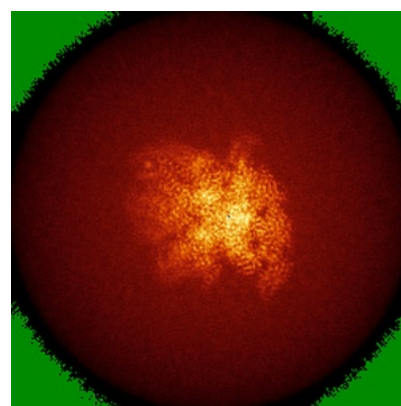
6.4.1 Primary map



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

This section was not generated.

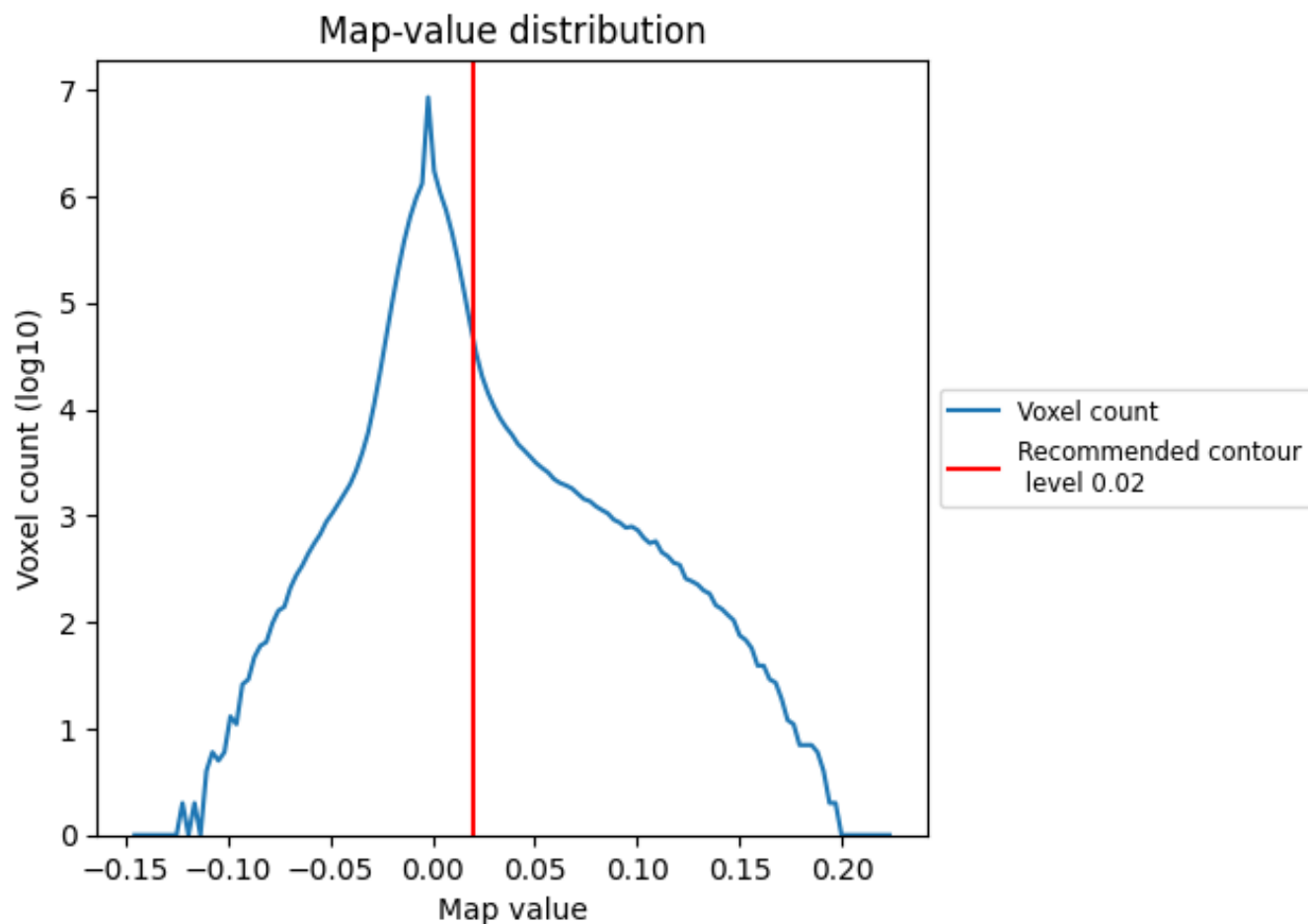
6.6 Mask visualisation

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

7 Map analysis [i](#)

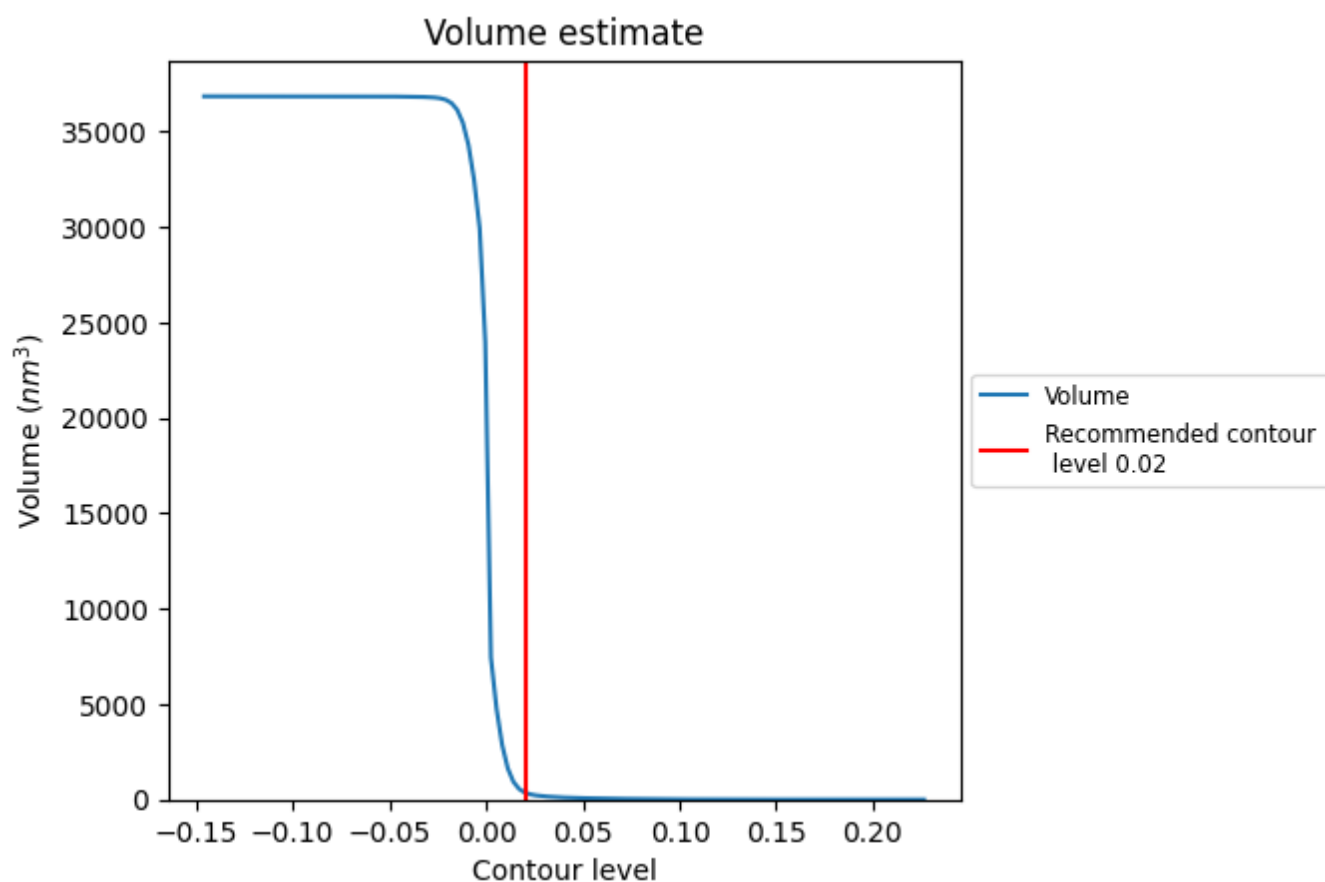
This section contains the results of statistical analysis of the map.

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.

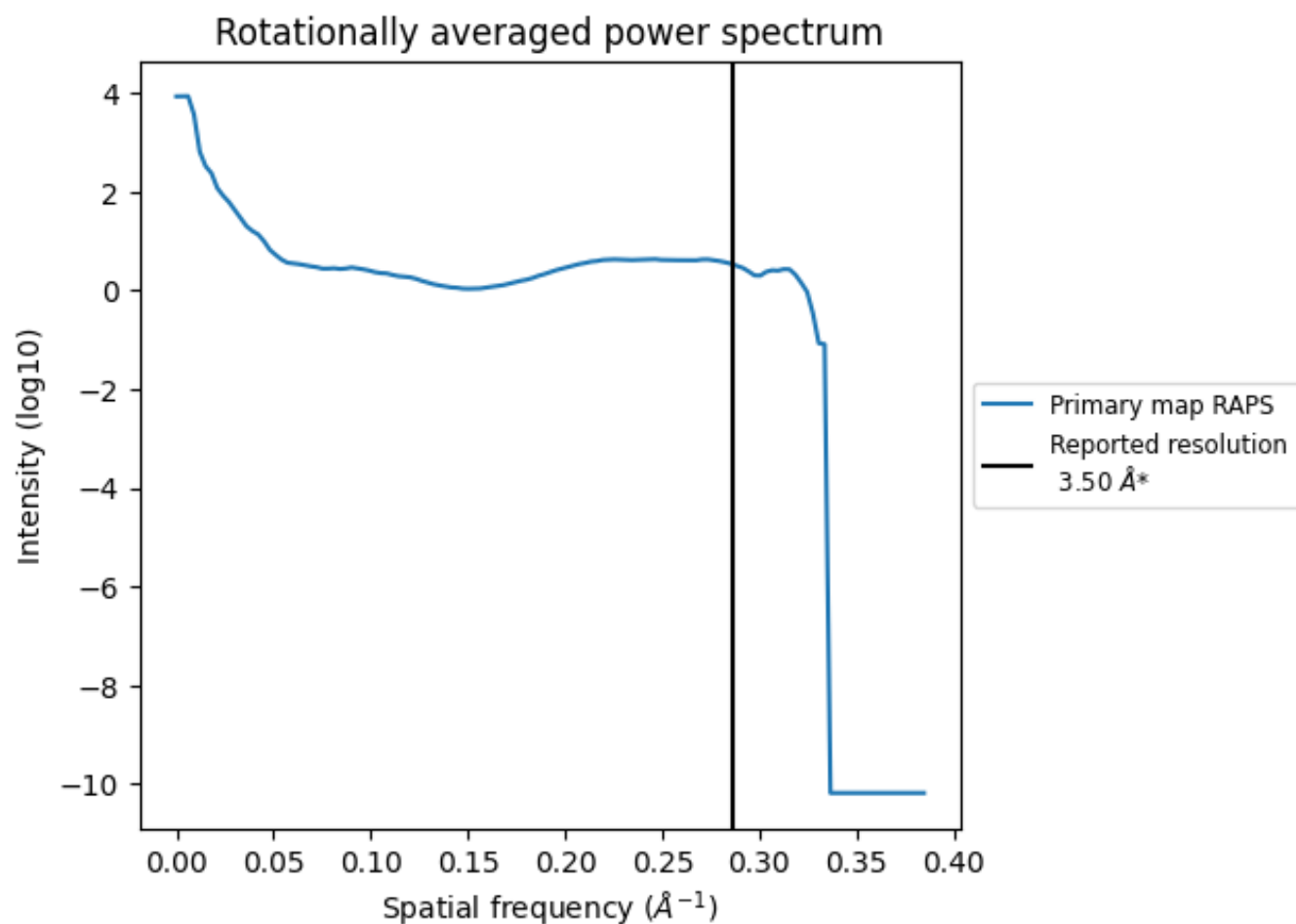
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 368 nm³; this corresponds to an approximate mass of 332 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 ⓘ

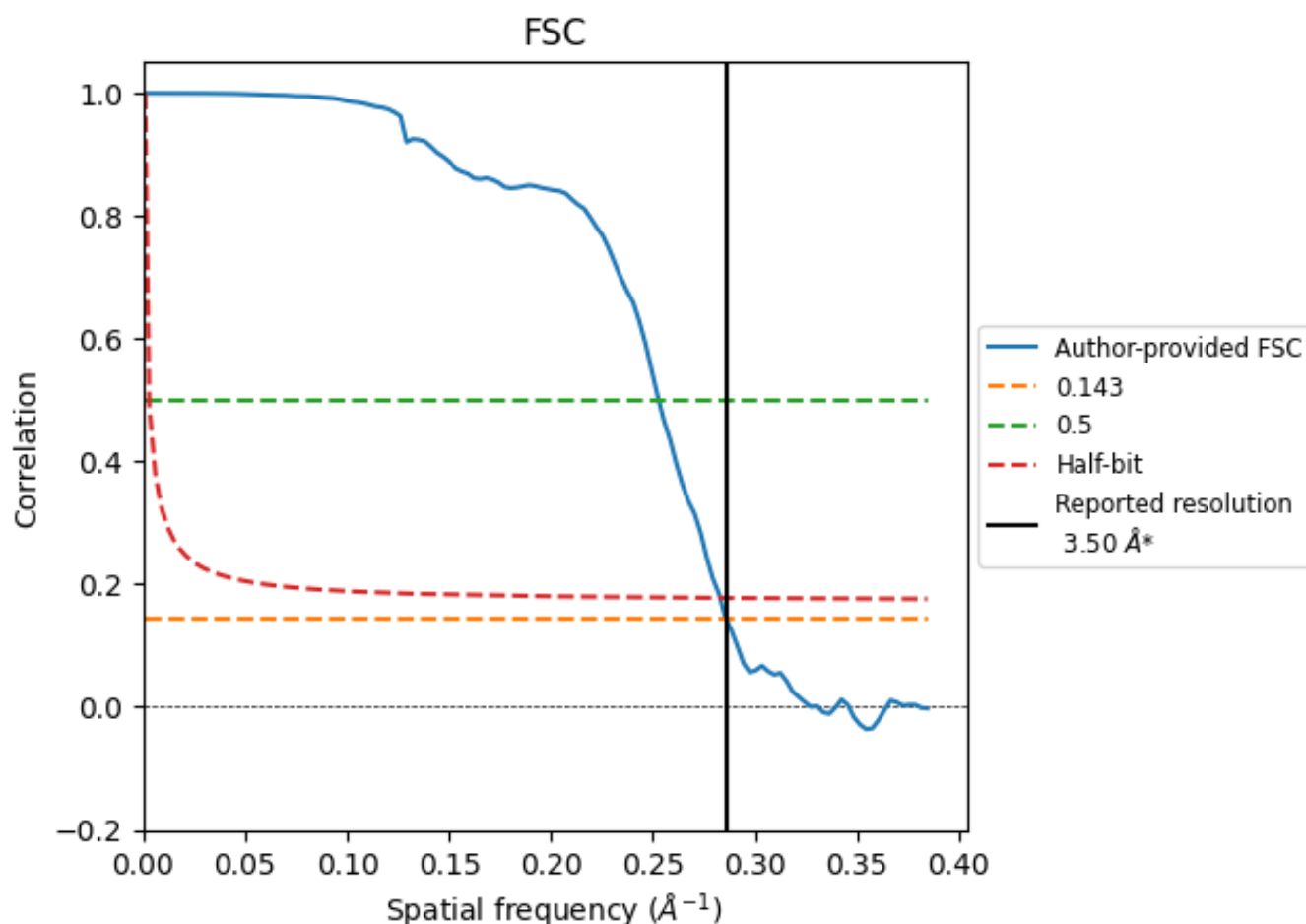


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

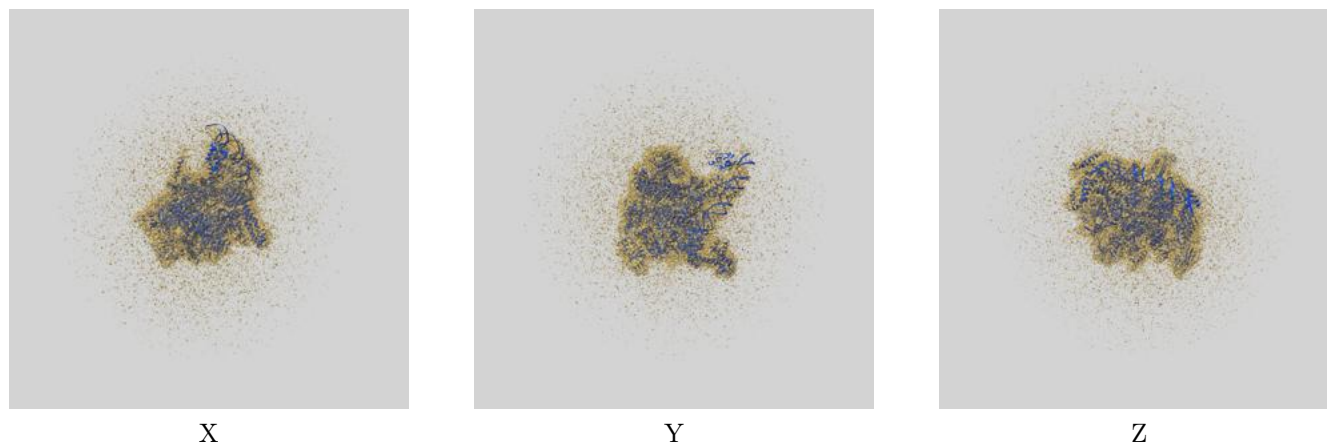
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.50	3.96	3.53
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

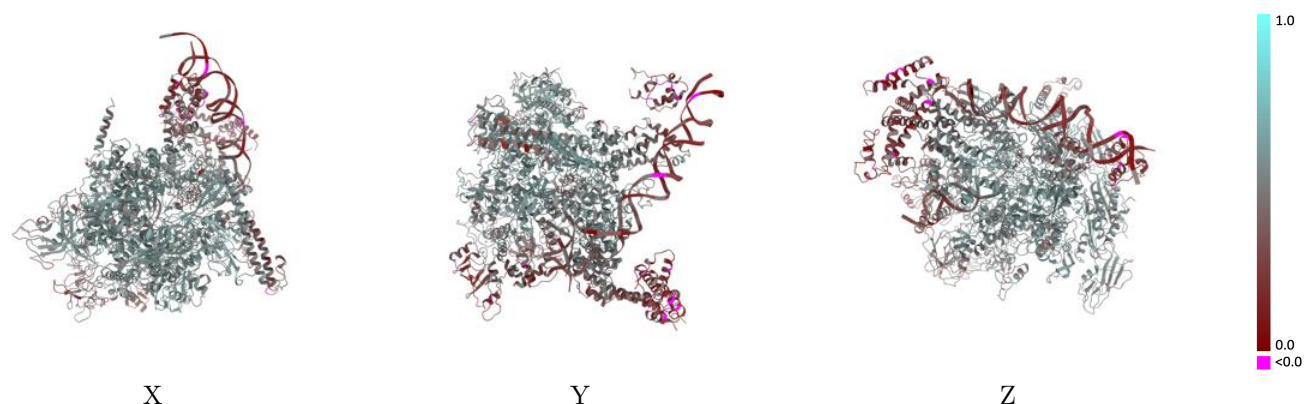
This section contains information regarding the fit between EMDB map EMD-20465 and PDB model 6PSV. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



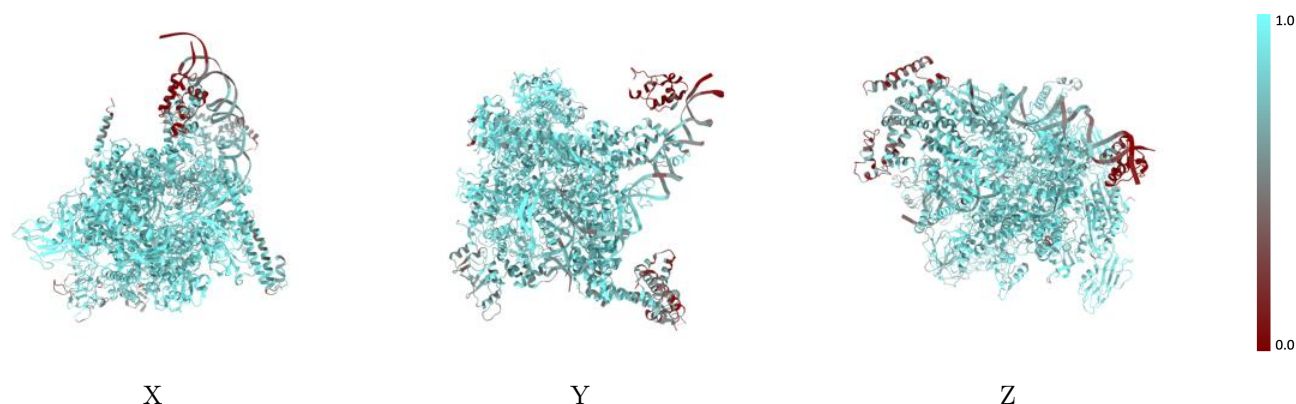
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



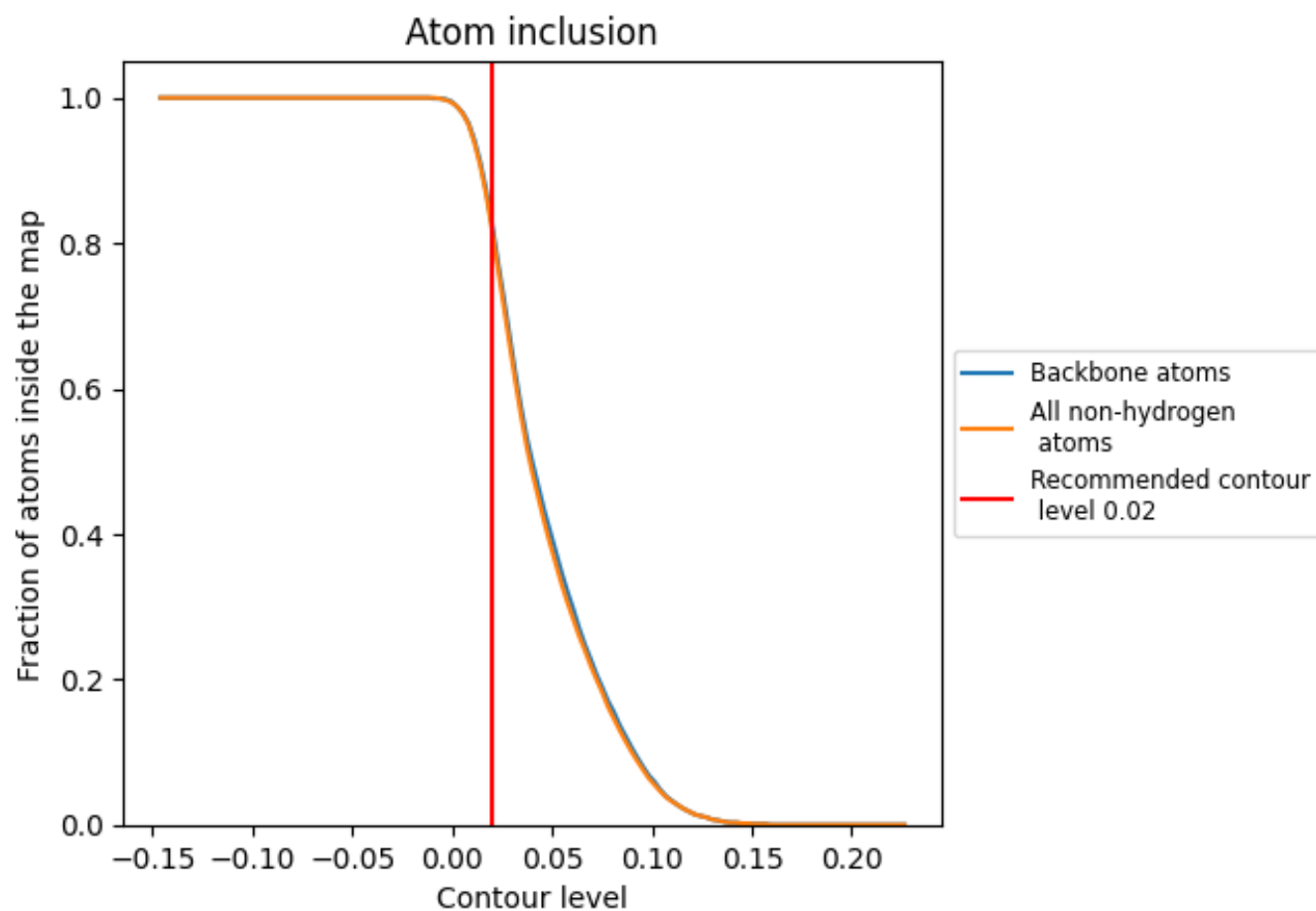
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 82% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8190	0.4680
G	0.8980	0.5330
H	0.8990	0.5120
I	0.8720	0.5020
J	0.8750	0.5050
K	0.7690	0.5000
L	0.7030	0.3630
M	0.0890	0.2660
N	0.8760	0.5060
O	0.6300	0.2580
P	0.5790	0.2620

1.0
0.0
<0.0