



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 03:30 PM UTC

PDB ID : 7MEI / pdb_00007mei
EMDB ID : EMD-23789
Title : Composite structure of EC+EC
Authors : Yang, C.; Murakami, K.
Deposited on : 2021-04-06
Resolution : 3.54 Å(reported)
Based on initial models : 5FMF, 3PO2, 5C4J

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
MolProbity : 4-5-2 with Phenix2.0
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

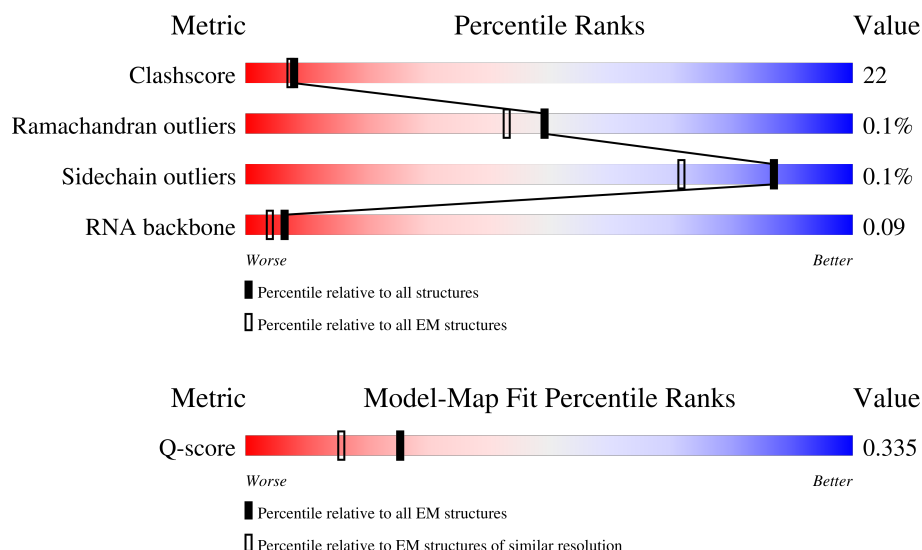
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.54 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.



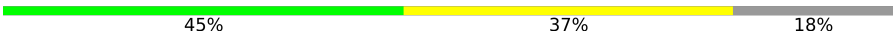
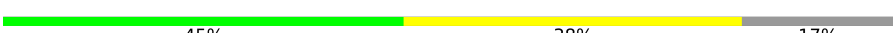
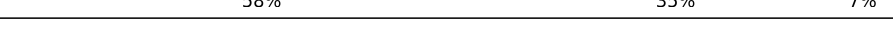
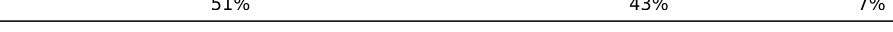
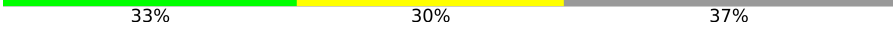
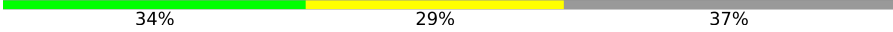
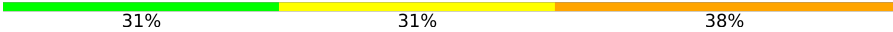
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12891 (3.04 - 4.04)

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	74	
2	O	74	
3	A	1733	

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Mol	Chain	Length	Quality of chain
3	a	1733	
4	B	1224	
4	b	1224	
5	C	318	
5	c	318	
6	D	221	
6	d	221	
7	E	215	
7	e	215	
8	F	155	
8	f	155	
9	G	171	
9	g	171	
10	H	146	
10	h	146	
11	I	122	
11	i	122	
12	J	70	
12	j	70	
13	K	120	
13	k	120	
14	L	70	
14	l	70	
15	r	16	
16	R	15	

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Mol	Chain	Length	Quality of chain
17	Q	735	22%7%71%
18	M	400	21%13%66%

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 69281 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a DNA chain called DNA (74-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	74	Total	C	N	O	P	0	0
			1519	727	290	428	74		

- Molecule 2 is a DNA chain called DNA (74-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	74	Total	C	N	O	P	0	0
			1524	730	263	457	74		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	1425	Total	C	N	O	S	0	0
			11189	7046	1955	2126	62		
3	A	1425	Total	C	N	O	S	0	0
			11167	7036	1948	2121	62		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	1160	Total	C	N	O	S	0	0
			9197	5805	1614	1723	55		
4	B	1166	Total	C	N	O	S	0	0
			9227	5823	1619	1729	56		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	265	Total	C	N	O	S	0	0
			2086	1312	347	414	13		
5	C	265	Total	C	N	O	S	0	0
			2086	1312	347	414	13		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	168	Total	C	N	O	S	0	0
			1331	822	237	270	2		
6	D	168	Total	C	N	O	S	0	0
			1331	822	237	270	2		

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	e	214	Total	C	N	O	S	0	0
			1752	1111	309	321	11		
7	E	214	Total	C	N	O	S	0	0
			1752	1111	309	321	11		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	f	87	Total	C	N	O	S	0	0
			705	451	119	132	3		
8	F	87	Total	C	N	O	S	0	0
			705	451	119	132	3		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	g	171	Total	C	N	O	S	0	0
			1339	861	222	248	8		
9	G	171	Total	C	N	O	S	0	0
			1335	858	221	248	8		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	h	135	Total	C	N	O	S	0	0
			1080	679	182	214	5		
10	H	135	Total	C	N	O	S	0	0
			1080	679	182	214	5		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	i	114	Total	C	N	O	S	0	0
			927	571	168	178	10		
11	I	114	Total	C	N	O	S	0	0
			927	571	168	178	10		

- Molecule 12 is a protein called DNA-directed RNA polymerases II subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	j	66	Total	C	N	O	S	0	0
			540	345	94	95	6		
12	J	66	Total	C	N	O	S	0	0
			540	345	94	95	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	k	115	Total	C	N	O	S	0	0
			924	593	157	172	2		
13	K	115	Total	C	N	O	S	0	0
			924	593	157	172	2		

- Molecule 14 is a protein called DNA-directed RNA polymerases II subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	l	44	Total	C	N	O	S	0	0
			352	217	70	61	4		
14	L	44	Total	C	N	O	S	0	0
			352	217	70	61	4		

- Molecule 15 is a RNA chain called RNA (5'-R(P*AP*AP*CP*UP*AP*GP*UP*UP*AP*A P*GP*AP*GP*GP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	r	16	Total	C	N	O	P	0	0
			333	150	55	112	16		

- Molecule 16 is a RNA chain called RNA (5'-R(P*UP*CP*GP*AP*GP*AP*GP*GP*AP*U P*CP*CP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	15	Total	C	N	O	P	0	0
			312	141	56	100	15		

- Molecule 17 is a protein called Transcription initiation factor IIF subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	214	Total	C	N	O	S	0	0
			1619	1017	297	299	6		

- Molecule 18 is a protein called Transcription initiation factor IIF subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	135	Total	C	N	O	S	0	0
			1106	694	197	210	5		

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	a	2	Total	Zn	0
			2	2	
19	b	1	Total	Zn	0
			1	1	
19	c	1	Total	Zn	0
			1	1	
19	i	2	Total	Zn	0
			2	2	
19	j	1	Total	Zn	0
			1	1	
19	l	1	Total	Zn	0
			1	1	
19	A	2	Total	Zn	0
			2	2	
19	B	1	Total	Zn	0
			1	1	
19	C	1	Total	Zn	0
			1	1	
19	I	2	Total	Zn	0
			2	2	
19	J	1	Total	Zn	0
			1	1	
19	L	1	Total	Zn	0
			1	1	

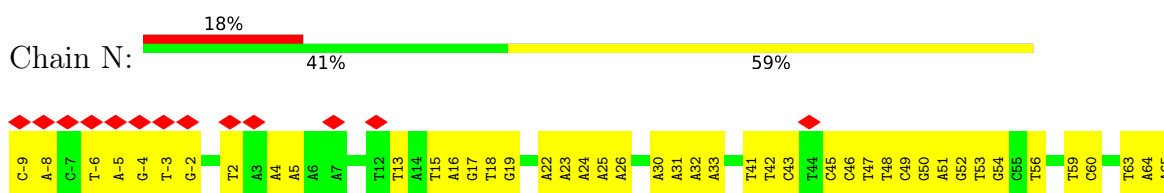
- Molecule 20 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
20	a	2	Total 2	Mg 2	0
20	A	1	Total 1	Mg 1	0
20	R	1	Total 1	Mg 1	0

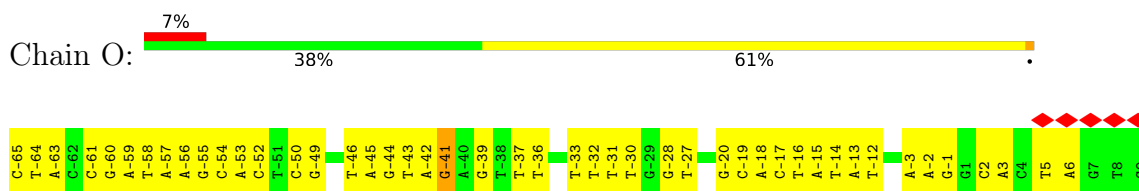
3 Residue-property plots

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

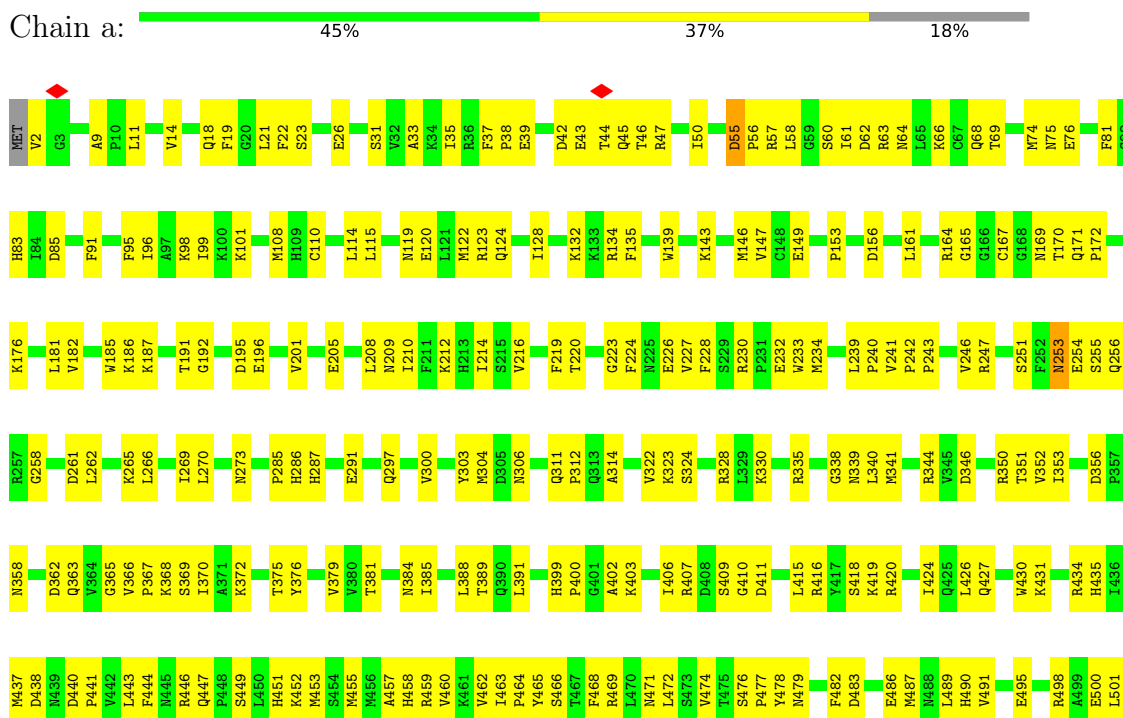
• Molecule 1: DNA (74-MER)



• Molecule 2: DNA (74-MER)

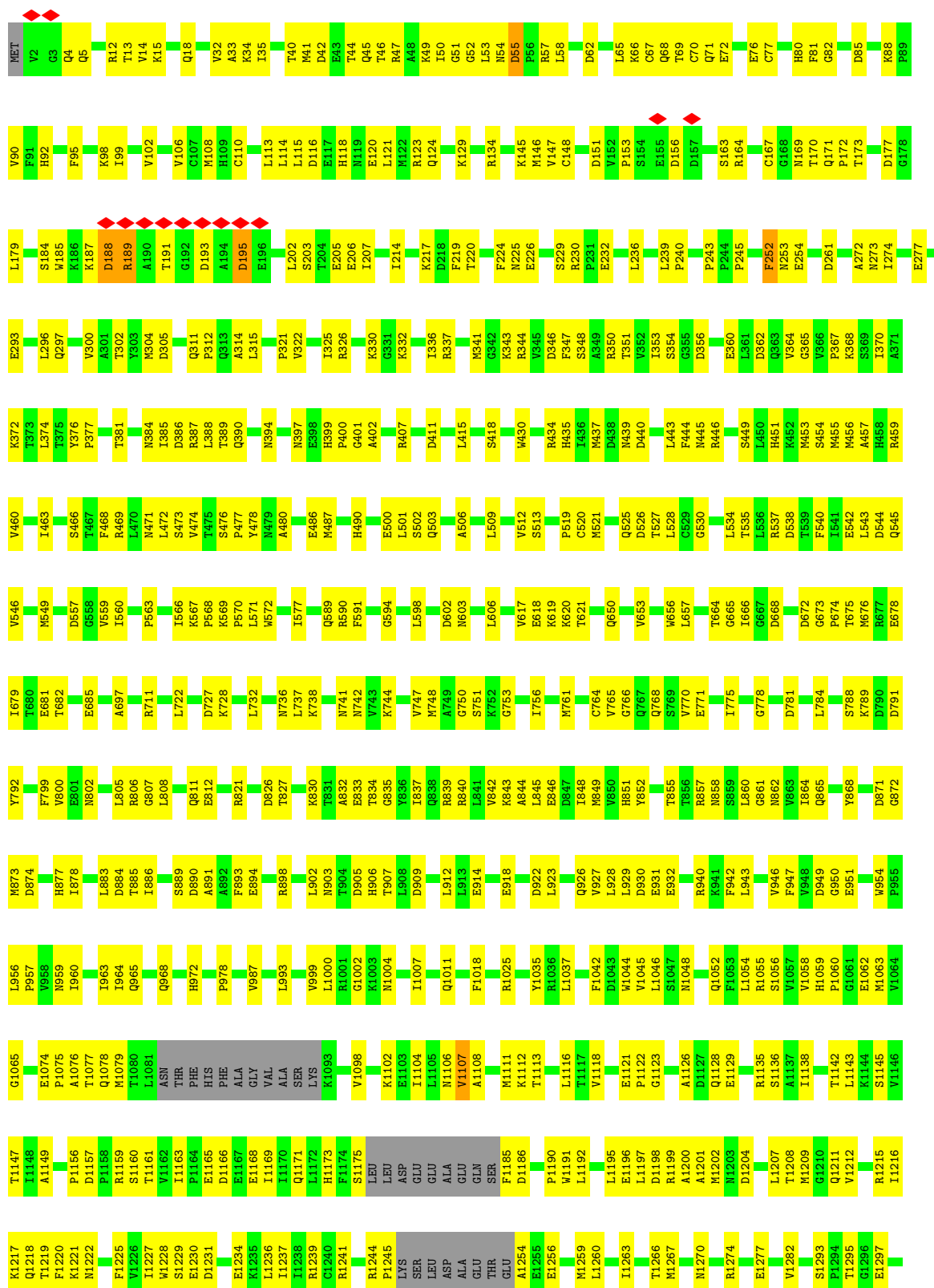


• Molecule 3: DNA-directed RNA polymerase subunit



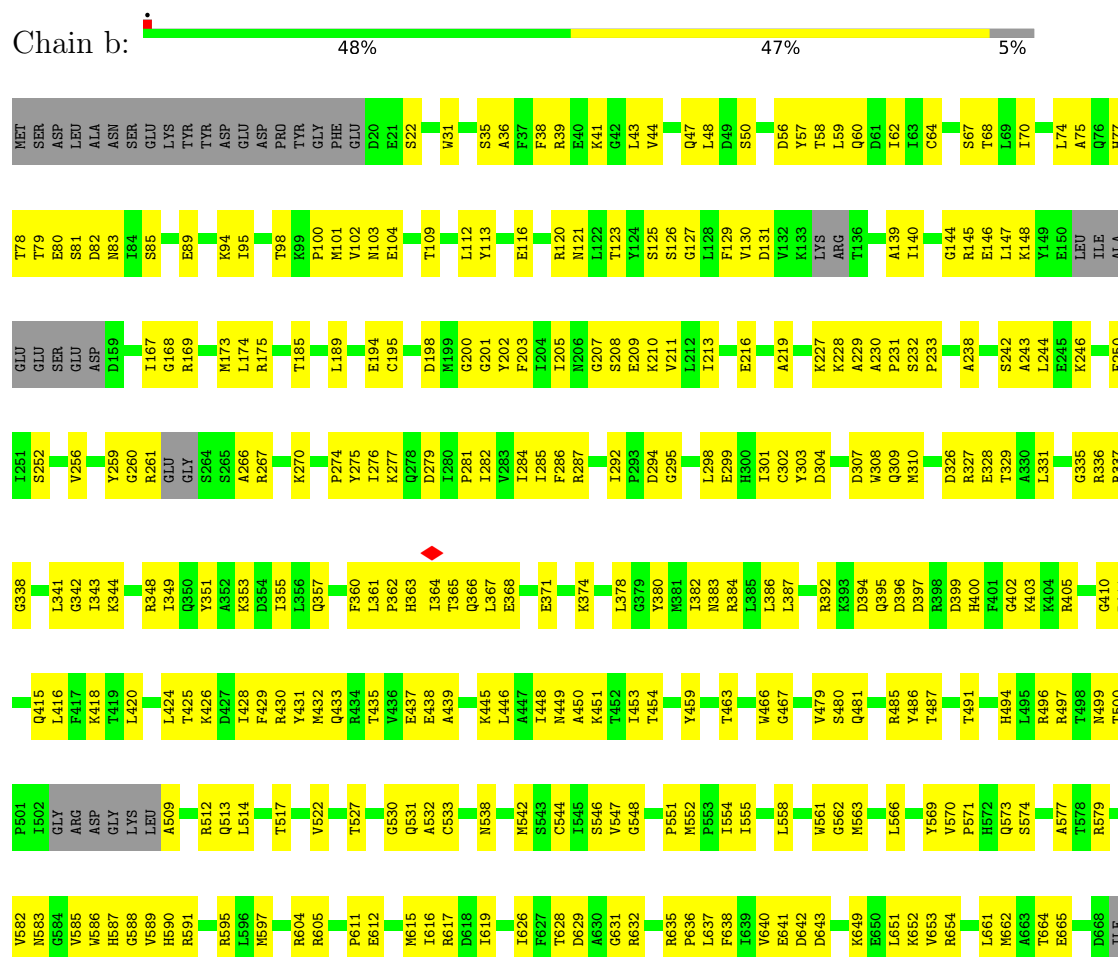
- Molecule 3: DNA-directed RNA polymerase subunit

Chain A:  48% 34% 18%

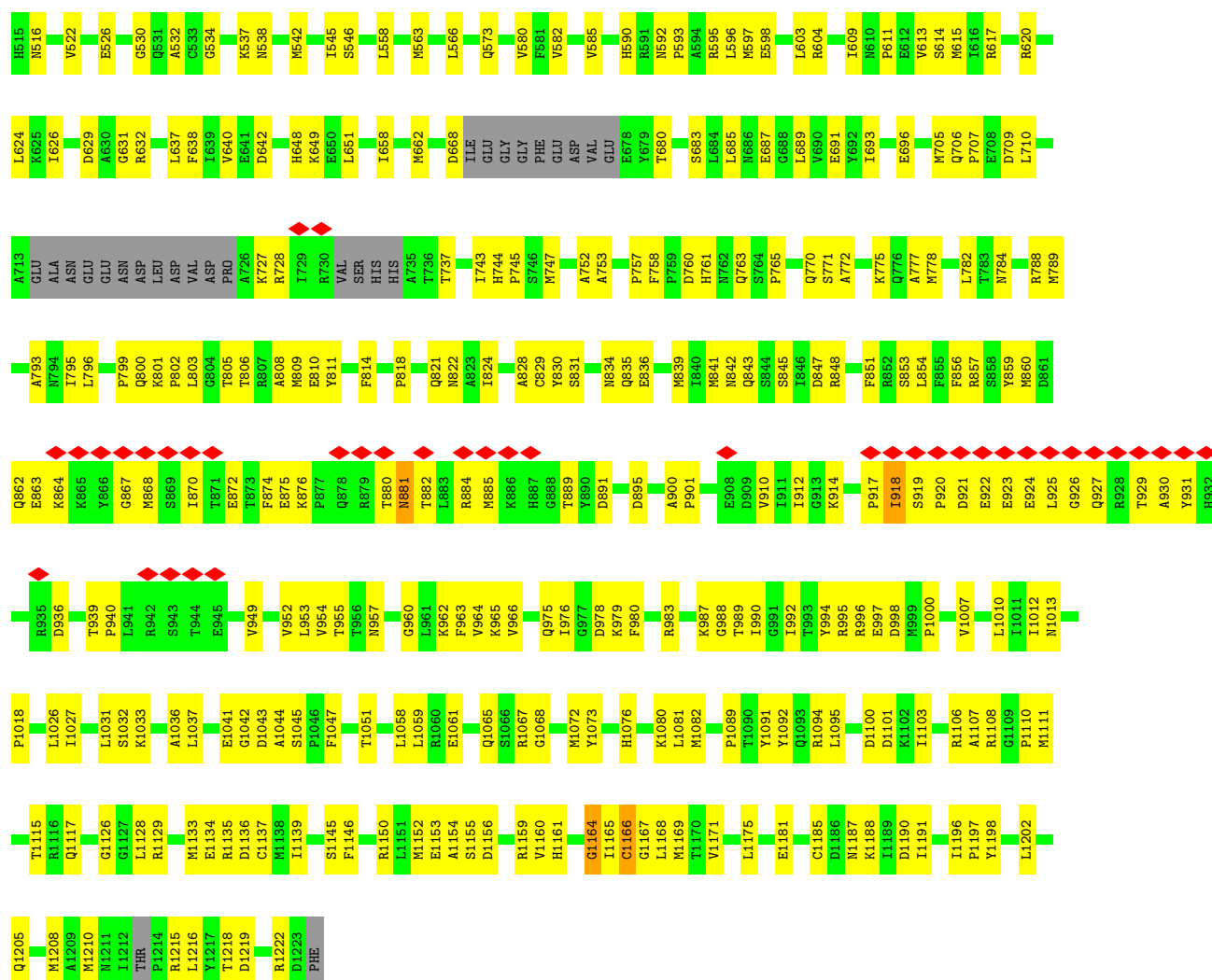


ASP	SER	SER	PHE	ALA	F1402	W1304
GLU	THR	PRO	SER	ASP	E1403	V1305
GLU	PRO	SER	PRO	LEU	E1404	L1306
GLU	SER	TYR	THR	ASP	T1405	E1307
HIS	PRO	SER	SER	VAL		T1308
ASN	SER	PRO	PRO	LYS	I1408	
	TYR	THR	THR	ASP		V1311
ASN	SER	SER	TYR	GLU	E1417	N1312
ASN	PRO	PRO	SER	LEU		L1313
ASN	THR	SER	PRO	MET	D1420	S1314
SER	SER	TYR	THR	PHE	E1421	E1315
PRO	PRO	SER	SER	SER	R1422	V1316
SER	PRO	PRO	PRO	PRO		M1317
TYR	TYR	THR	ALA	LEU	S1425	T1318
TYR	SER	SER	TYR	VAL	E1426	V1319
PRO	PRO	PRO	SER	ASP		
THR	THR	SER	PRO	SER	I1429	I1322
SER	TYR	THR	THR	GLY	L1430	
PRO	PRO	SER	SER	SER	G1431	R1326
LYS	SER	PRO	PRO	ASN	Q1432	
TYR	TYR	THR	THR	ASP	M1433	T1329
SER	SER	SER	TYR	ALA	A1434	N1330
PRO	PRO	PRO	SER	MET	P1435	S1331
THR	THR	SER	PRO	ALA	I1436	F1332
GLU	TYR	TYR	THR	GLY	G1437	
PRO	PRO	SER	PRO	PHE	T1438	I1335
SER	PRO	PRO	PRO	GLY	G1439	
TYR	THR	THR	SER	THR		L1339
SER	SER	SER	TYR	ALA	V1443	
PRO	PRO	PRO	SER	TYR	M1444	V1352
THR	THR	SER	PRO	GLY	I1445	
SER	SER	TYR	THR	GLY		
HIS	TYR	THR	THR	ALA	M1454	D1359
GLU	ASN	PRO	SER	ASP	PRO	G1360
GLU	PRO	THR	THR	ASP		S1361
GLU	TYR	THR	SER	TYR	GLU	Y1362
GLU	SER	SER	TYR	GLY	GLN	V1363
GLU	PRO	PRO	SER	GLY	LYS	N1364
GLU	THR	SER	PRO	ALA	ILE	V1365
GLU	TYR	THR	THR	THR	THR	R1366
PRO	PRO	SER	SER	SER	GLU	H1367
PRO	PRO	PRO	PRO	ILE	ILE	M1368
TYR	THR	THR	SER	PHE	GLU	
SER	PRO	SER	TYR	GLY	ASP	D1373
SER	PRO	PRO	THR	ALA	GLY	
GLU	PRO	PRO	TYR	GLY	GLN	T1376
TYR	TYR	SER	THR	GLY	ASP	T1377
PRO	SER	SER	SER	GLU	GLY	
GLY	PRO	PRO	PRO	ALA	GLY	V1384
TYR	THR	THR	SER	PRO	VAL	T1385
SER	SER	SER	TYR	THR	THR	R1386
PRO	PRO	PRO	SER	SER	PRO	H1387
GLY	SER	GLY	PRO	PRO	TYR	G1388
SER	SER	TYR	THR	GLY	SER	F1389
PRO	PRO	SER	SER	PHE	ASN	M1390
ALA	PRO	PRO	PRO	GLY	GLU	
TYR	THR	THR	TYR	VAL	SER	L1397
GLU	TYR	SER	TYR	SER	GLY	M1398
SER	SER	SER	TYR	SER	LEU	R1399
PRO	PRO	PRO	PRO	SER	VAL	
LYS	ALA	ALA	PRO	PRO	ASN	C1400
GLN	TYR	TYR	THR	TYR	GLY	S1401

• Molecule 4: DNA-directed RNA polymerase subunit beta

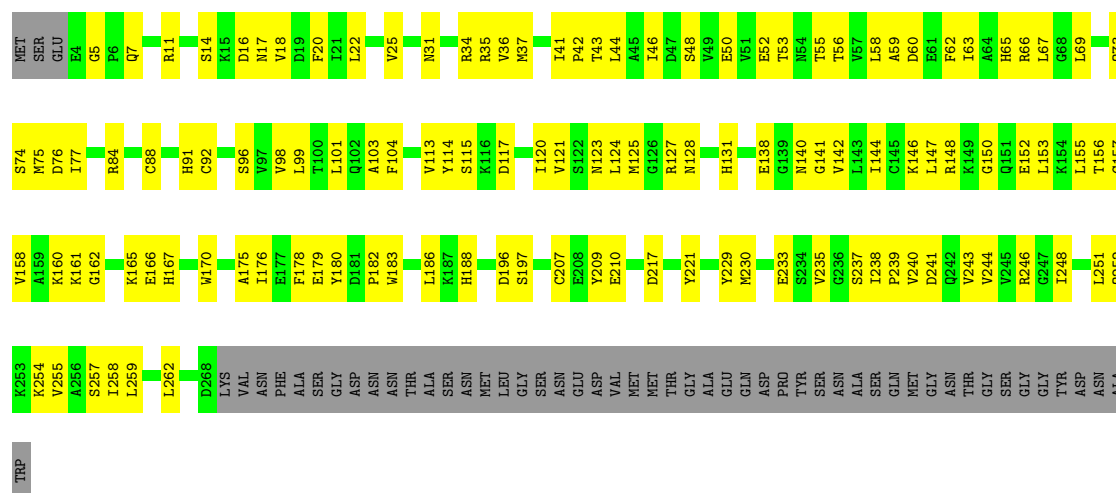






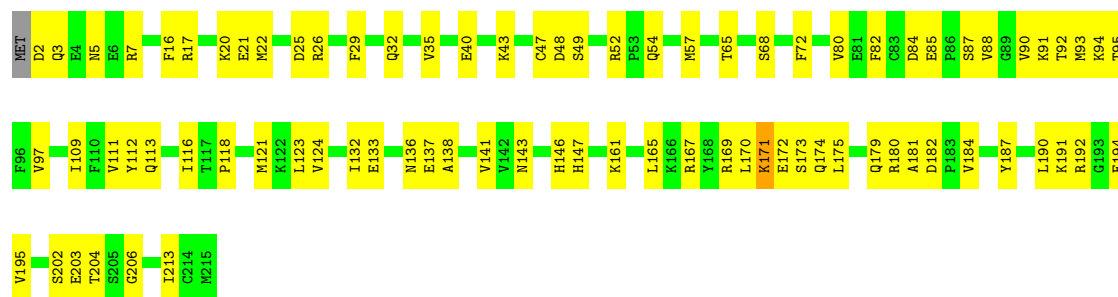
• Molecule 5: DNA-directed RNA polymerase II subunit RPB3

Chain c: 45% 38% 17%



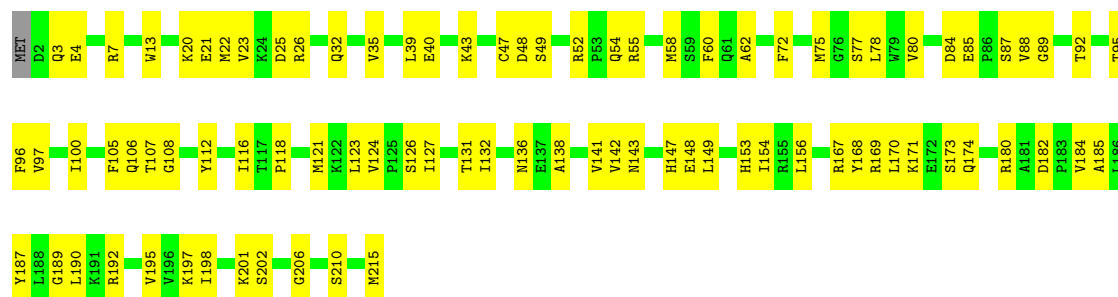
• Molecule 5: DNA-directed RNA polymerase II subunit RPB3





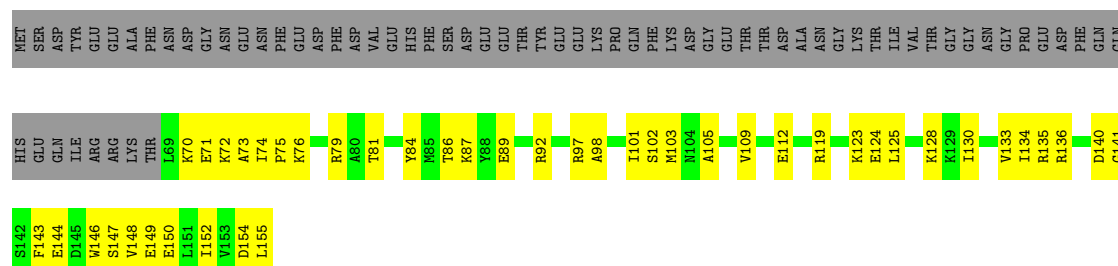
- Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 59% 40%



- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain f: 28% 28% 44%

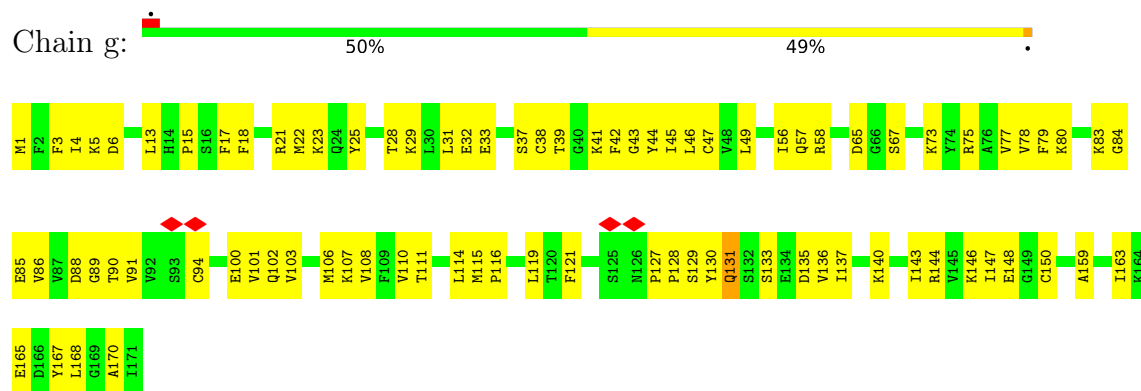


- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC2

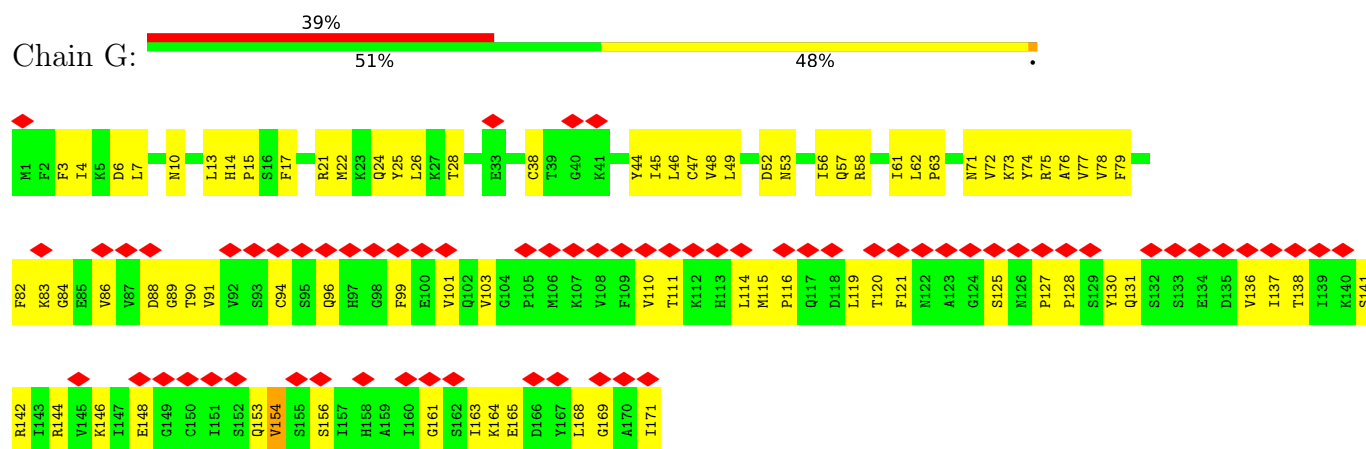
Chain F: 33% 23% 44%



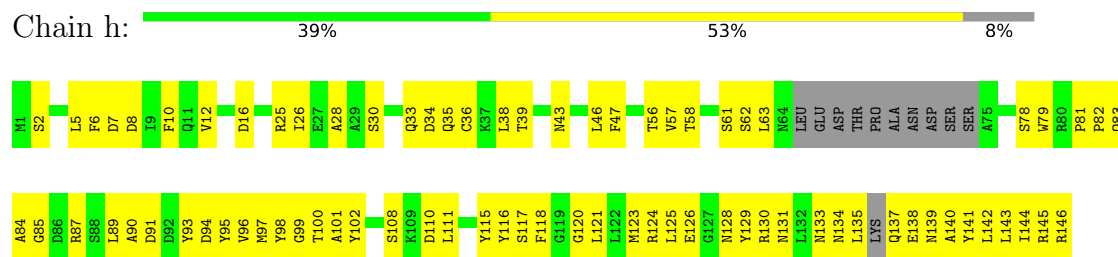
- Molecule 9: DNA-directed RNA polymerase II subunit RPB7



- Molecule 9: DNA-directed RNA polymerase II subunit RPB7



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC3

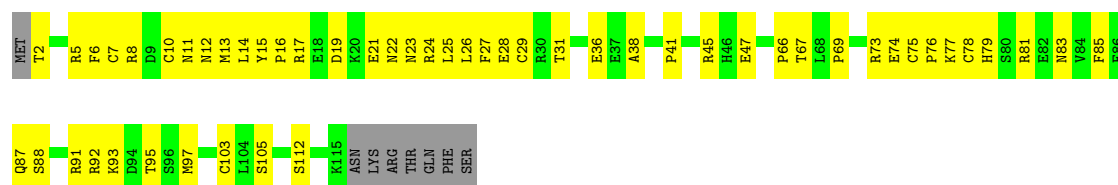


- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC3



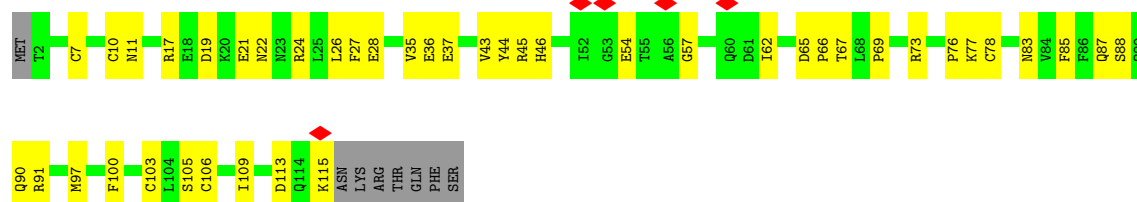
- Molecule 11: DNA-directed RNA polymerase II subunit RPB9

Chain i: 



- Molecule 11: DNA-directed RNA polymerase II subunit RPB9

Chain I: 



- Molecule 12: DNA-directed RNA polymerases II subunit RPABC5

Chain j: 



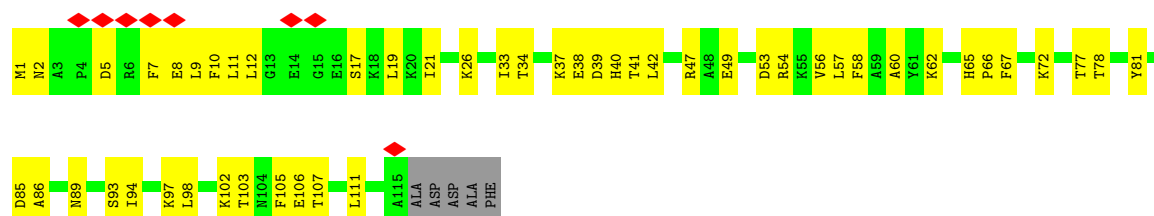
- Molecule 12: DNA-directed RNA polymerases II subunit RPABC5

Chain J: 



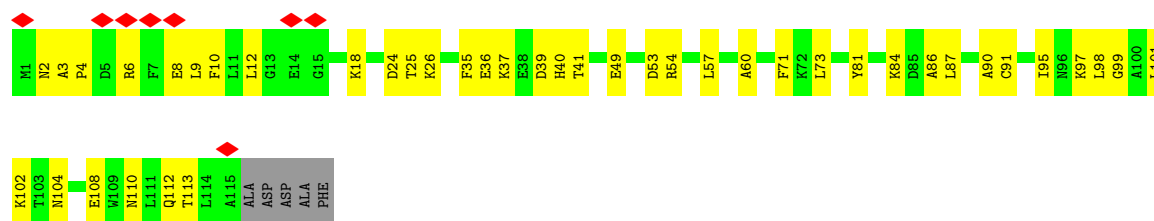
- Molecule 13: DNA-directed RNA polymerase II subunit RPB11

Chain k: 



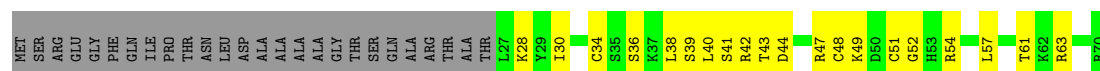
- Molecule 13: DNA-directed RNA polymerase II subunit RPB11

Chain K: 



• Molecule 14: DNA-directed RNA polymerases II subunit RPABC4

Chain I: 34% 29% 37%



• Molecule 14: DNA-directed RNA polymerases II subunit RPABC4

Chain L: 33% 30% 37%



• Molecule 15: RNA (5'-R(P*AP*AP*CP*UP*AP*GP*UP*UP*AP*AP*GP*AP*GP*GP*UP*U)-3')

Chain r: 31% 31% 38%



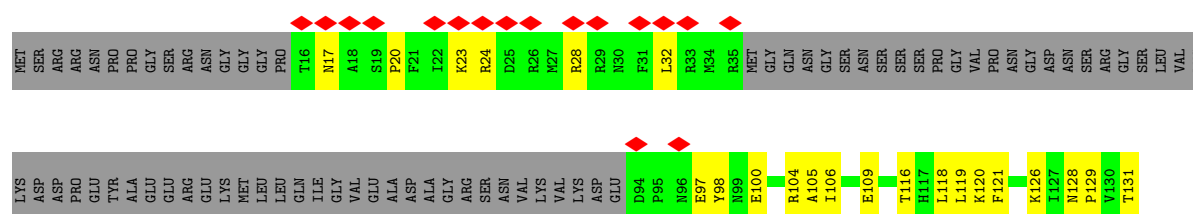
• Molecule 16: RNA (5'-R(P*UP*CP*GP*AP*GP*AP*GP*GP*AP*UP*CP*CP*CP*AP*A)-3')

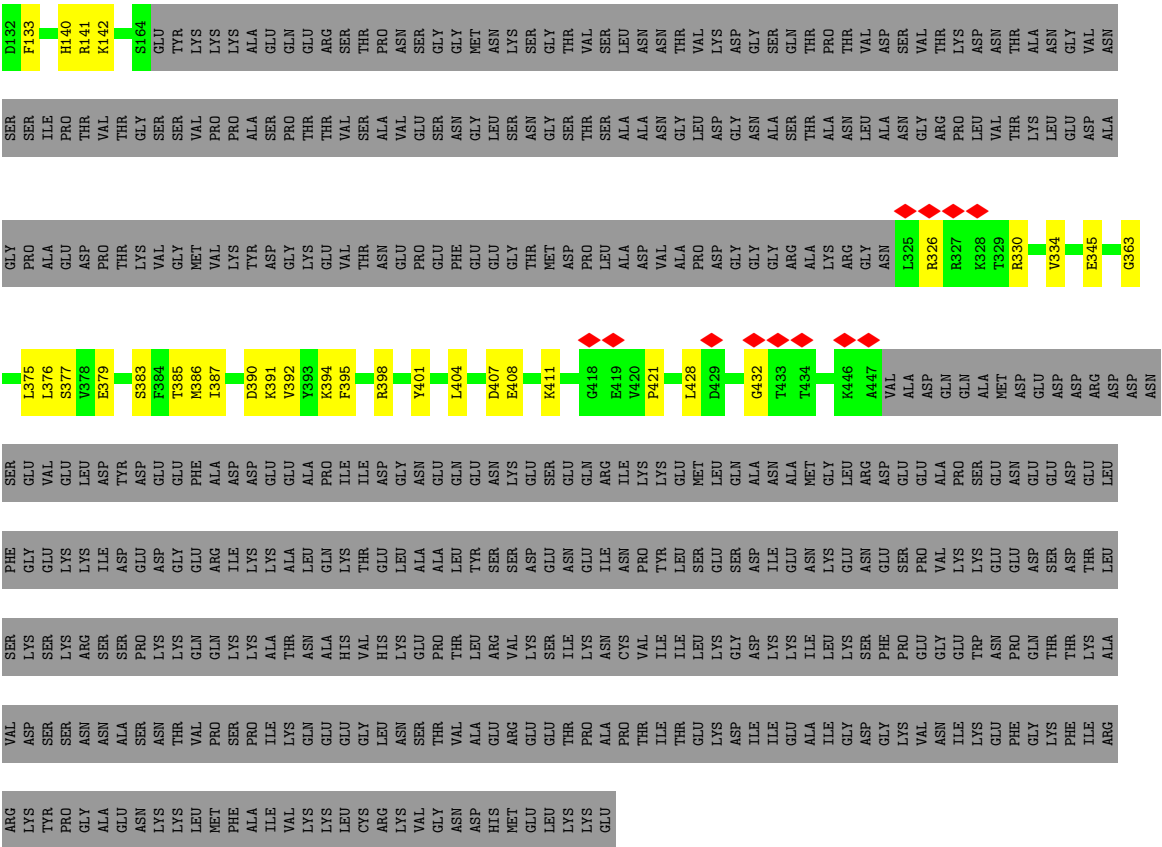
Chain R: 20% 13% 73% 13%



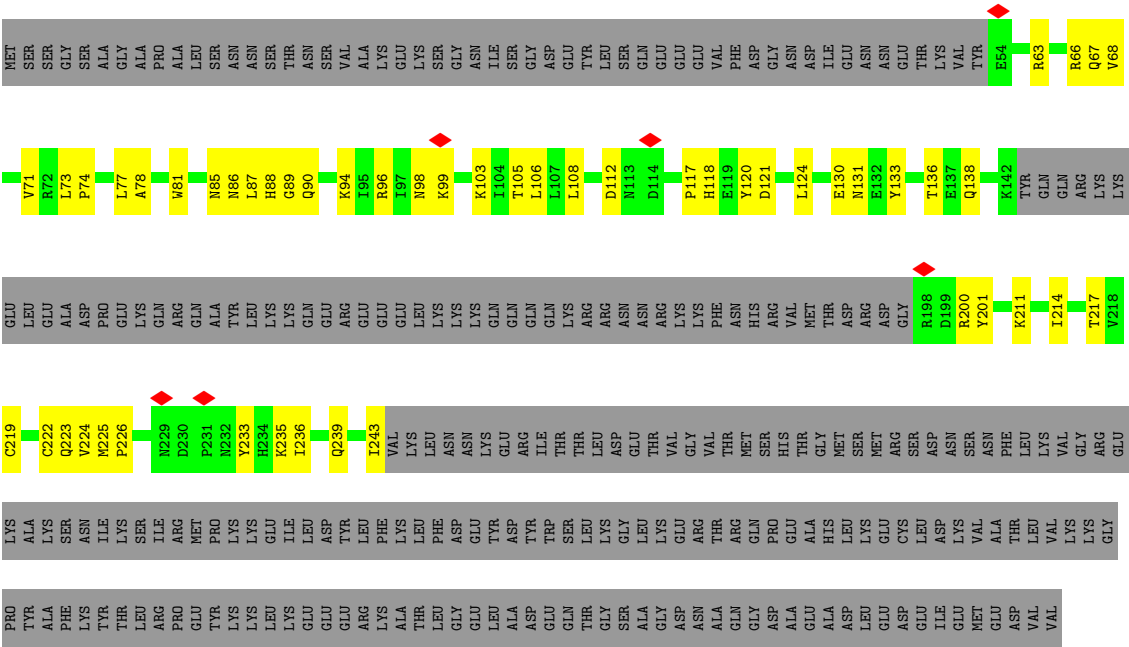
• Molecule 17: Transcription initiation factor IIF subunit alpha

Chain Q: 22% 7% 71%





● Molecule 18: Transcription initiation factor IIF subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	57690	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	1750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.061	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0088	Depositor
Map size ($\text{\AA}$)	367.2, 367.2, 367.2	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	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, 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	0.23	0/1709	0.37	0/2633
2	O	0.35	0/1706	0.59	2/2635 (0.1%)
3	A	0.27	0/11368	0.49	2/15383 (0.0%)
3	a	0.29	0/11390	0.52	4/15408 (0.0%)
4	B	0.28	0/9402	0.55	7/12680 (0.1%)
4	b	0.31	0/9371	0.55	3/12636 (0.0%)
5	C	0.25	0/2124	0.44	0/2879
5	c	0.28	0/2124	0.43	0/2879
6	D	0.14	0/1339	0.39	0/1793
6	d	0.16	0/1339	0.46	0/1793
7	E	0.23	0/1788	0.42	0/2406
7	e	0.26	0/1788	0.48	0/2406
8	F	0.29	0/717	0.54	0/967
8	f	0.31	0/717	0.52	0/967
9	G	0.19	0/1363	0.48	0/1840
9	g	0.23	0/1367	0.55	0/1844
10	H	0.24	0/1097	0.46	0/1484
10	h	0.25	0/1097	0.47	0/1484
11	I	0.19	0/945	0.40	0/1273
11	i	0.20	0/945	0.42	0/1273
12	J	0.36	0/549	0.59	0/738
12	j	0.35	0/549	0.54	0/738
13	K	0.25	0/942	0.44	0/1272
13	k	0.26	0/942	0.43	0/1272
14	L	0.20	0/354	0.71	0/468
14	l	0.24	0/354	0.61	0/468
15	r	0.64	0/370	1.01	3/572 (0.5%)
16	R	0.48	0/347	0.74	0/536
17	Q	0.17	0/1648	0.41	1/2226 (0.0%)
18	M	0.15	0/1124	0.43	0/1517
All	All	0.27	0/70875	0.51	22/96470 (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
3	A	0	3
3	a	0	1
4	B	0	3
4	b	0	1
7	e	0	1
9	G	0	1
9	g	0	2
All	All	0	12

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1166	CYS	CB-CA-C	-9.03	96.70	110.88
15	r	40	U	C2'-C3'-O3'	-8.46	101.01	113.70
15	r	47	U	C1'-C2'-O2'	-8.18	96.13	108.40
2	O	-39	DG	C2'-C3'-O3'	-8.00	99.50	111.50
17	Q	421	PRO	N-CA-CB	7.67	110.17	103.27
4	B	79	THR	CA-C-N	6.44	133.29	121.70
4	B	79	THR	C-N-CA	6.44	133.29	121.70
4	b	1210	MET	N-CA-C	-5.69	106.31	113.20
3	a	253	ASN	CA-C-N	-5.27	115.25	121.90
3	a	253	ASN	C-N-CA	-5.27	115.25	121.90
4	B	918	ILE	CA-C-N	5.26	131.17	121.70
4	B	918	ILE	C-N-CA	5.26	131.17	121.70
3	a	1107	VAL	CA-C-N	5.26	131.16	121.70
3	a	1107	VAL	C-N-CA	5.26	131.16	121.70
4	B	1164	GLY	O-C-N	-5.18	116.74	122.24
4	B	1167	GLY	N-CA-C	-5.17	107.67	115.32
4	b	918	ILE	CA-C-N	5.16	130.99	121.70
4	b	918	ILE	C-N-CA	5.16	130.99	121.70
15	r	40	U	C1'-C2'-O2'	5.14	116.11	108.40
2	O	-41	DG	C4'-C3'-O3'	-5.11	102.34	110.00
3	A	1107	VAL	CA-C-N	5.10	130.89	121.70
3	A	1107	VAL	C-N-CA	5.10	130.89	121.70

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	252	PHE	Peptide
3	A	55	ASP	Peptide
3	A	750	GLY	Peptide
4	B	363	HIS	Peptide
4	B	510	LYS	Peptide
4	B	881	ASN	Peptide
9	G	154	VAL	Peptide
3	a	55	ASP	Peptide
4	b	868	MET	Peptide
7	e	171	LYS	Peptide
9	g	131	GLN	Peptide
9	g	56	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	1519	0	833	50	0
2	O	1524	0	844	45	0
3	A	11167	0	11188	497	0
3	a	11189	0	11225	604	0
4	B	9227	0	9201	419	0
4	b	9197	0	9180	512	0
5	C	2086	0	2045	95	0
5	c	2086	0	2045	101	0
6	D	1331	0	1345	54	0
6	d	1331	0	1345	65	0
7	E	1752	0	1776	68	0
7	e	1752	0	1776	72	0
8	F	705	0	731	34	0
8	f	705	0	731	41	0
9	G	1335	0	1346	60	0
9	g	1339	0	1357	78	0
10	H	1080	0	1049	58	0
10	h	1080	0	1049	96	0
11	I	927	0	881	36	0
11	i	927	0	880	56	0
12	J	540	0	553	38	0
12	j	540	0	553	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	K	924	0	934	45	0
13	k	924	0	934	50	0
14	L	352	0	375	20	0
14	l	352	0	374	14	0
15	r	333	0	172	8	0
16	R	312	0	165	12	0
17	Q	1619	0	1452	43	0
18	M	1106	0	1099	47	0
19	A	2	0	0	0	0
19	B	1	0	0	0	0
19	C	1	0	0	0	0
19	I	2	0	0	0	0
19	J	1	0	0	0	0
19	L	1	0	0	0	0
19	a	2	0	0	0	0
19	b	1	0	0	0	0
19	c	1	0	0	0	0
19	i	2	0	0	0	0
19	j	1	0	0	0	0
19	l	1	0	0	0	0
20	A	1	0	0	0	0
20	R	1	0	0	0	0
20	a	2	0	0	0	0
All	All	69281	0	67438	3034	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 22.

All (3034) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:65:DA:H61	2:O:-65:DC:N4	1.48	1.10
1:N:65:DA:N6	2:O:-65:DC:H42	1.48	1.09
12:J:8:PHE:H	12:J:49:MET:HE1	1.27	0.97
4:B:510:LYS:HG3	4:B:511:PRO:HD3	1.45	0.97
3:a:372:LYS:HD2	13:k:2:ASN:HB2	1.50	0.93
14:L:48:CYS:SG	14:L:51:CYS:HB2	2.09	0.92
3:a:208:LEU:HD23	3:a:212:LYS:HZ2	1.34	0.92
3:A:110:CYS:HB3	3:A:167:CYS:SG	2.09	0.92
3:A:802:ASN:HD21	3:A:806:ARG:HB2	1.35	0.91
4:b:102:VAL:HG12	4:b:112:LEU:HD21	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:47:GLN:HE22	4:b:173:MET:HG3	1.36	0.91
4:B:763:GLN:HG2	4:B:765:PRO:HD2	1.54	0.90
4:B:334:ILE:HA	4:B:347:LYS:HG3	1.52	0.89
3:a:346:ASP:H	4:b:1154:ALA:HB1	1.33	0.89
4:b:85:SER:HB3	4:b:139:ALA:H	1.36	0.89
10:h:56:THR:HB	10:h:145:ARG:HB2	1.53	0.89
1:N:49:DC:O2	2:O:-49:DG:N2	2.06	0.88
1:N:50:DG:H1	2:O:-50:DC:H5	1.19	0.88
4:b:842:ASN:HA	4:b:999:MET:HE1	1.56	0.88
10:h:144:ILE:O	10:h:145:ARG:NH1	2.05	0.88
4:b:1117:GLN:NE2	4:b:1156:ASP:OD1	2.07	0.87
3:a:353:ILE:HD13	3:a:487:MET:HE1	1.57	0.87
3:a:311:GLN:HG2	3:a:312:PRO:HD3	1.57	0.86
3:A:148:CYS:HB2	3:A:171:GLN:HE22	1.41	0.86
3:A:1266:THR:O	3:A:1270:ASN:HB2	1.76	0.86
3:A:397:ASN:O	13:K:2:ASN:ND2	2.08	0.85
4:B:799:PRO:HB2	4:B:818:PRO:HG2	1.59	0.85
17:Q:105:ALA:HB1	18:M:87:LEU:HD12	1.59	0.84
10:H:55:LEU:HA	10:H:146:ARG:HH12	1.42	0.84
14:L:28:LYS:HB2	14:L:39:SER:HA	1.57	0.84
4:b:829:CYS:HA	4:b:834:ASN:HD21	1.43	0.83
9:G:91:VAL:HG22	9:G:101:VAL:HG22	1.61	0.82
4:b:82:ASP:H	4:b:83:ASN:HA	1.44	0.81
11:i:19:ASP:HB3	11:i:24:ARG:H	1.44	0.81
4:b:175:ARG:NH2	4:b:198:ASP:O	2.12	0.81
12:j:8:PHE:H	12:j:49:MET:HE1	1.46	0.81
1:N:65:DA:N1	2:O:-65:DC:N3	2.29	0.80
10:h:85:GLY:O	10:h:87:ARG:NH1	2.13	0.80
4:b:260:GLY:HA3	4:b:266:ALA:HB3	1.63	0.80
7:e:52:ARG:O	7:e:54:GLN:NE2	2.14	0.80
3:a:961:ARG:HG3	3:a:965:GLN:HE22	1.45	0.80
4:b:48:LEU:HD12	4:b:173:MET:HE1	1.64	0.80
3:A:202:LEU:HB3	3:A:207:ILE:HD11	1.62	0.80
4:B:805:THR:OG1	4:B:809:MET:SD	2.39	0.80
3:a:55:ASP:HA	3:a:58:LEU:HD23	1.64	0.79
10:h:39:THR:HB	10:h:124:ARG:HB3	1.64	0.79
10:h:137:GLN:NE2	10:h:139:ASN:OD1	2.15	0.79
4:B:880:THR:HA	4:B:931:TYR:H	1.47	0.79
4:b:448:ILE:HD12	4:b:451:LYS:HD3	1.65	0.79
3:a:353:ILE:HG22	3:a:468:PHE:HB2	1.65	0.79
11:i:12:ASN:HD22	11:i:31:THR:HG21	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:75:ALA:HB2	4:B:83:ASN:H	1.48	0.78
5:c:50:GLU:HB2	5:c:156:THR:HB	1.66	0.78
10:h:95:TYR:H	10:h:145:ARG:NH1	1.80	0.78
3:a:119:ASN:HB3	3:a:122:MET:HE1	1.66	0.78
3:a:440:ASP:H	3:a:460:VAL:HG12	1.47	0.78
3:a:1002:GLY:HA3	3:a:1007:ILE:HG21	1.66	0.78
8:F:125:LEU:HA	8:F:130:ILE:HD11	1.64	0.78
4:b:394:ASP:HB2	11:i:91:ARG:HH22	1.49	0.77
4:B:526:GLU:O	4:B:538:ASN:ND2	2.17	0.77
6:D:153:ARG:HH22	6:D:160:VAL:HA	1.49	0.77
8:F:97:ARG:HD2	8:F:100:GLN:HE22	1.49	0.77
4:B:246:LYS:HE2	4:B:249:ARG:HD2	1.67	0.77
9:g:38:CYS:HA	9:g:44:TYR:HA	1.67	0.77
4:b:416:LEU:HD21	4:b:467:GLY:H	1.47	0.77
3:a:635:ARG:NH2	3:a:876:ALA:O	2.17	0.77
10:H:80:ARG:HD3	10:H:81:PRO:HD2	1.67	0.77
7:e:91:LYS:HD3	7:e:94:LYS:HD3	1.67	0.77
4:B:829:CYS:HA	4:B:834:ASN:HD21	1.48	0.77
10:h:82:PRO:O	10:h:87:ARG:NH2	2.17	0.76
3:A:368:LYS:HD3	13:K:3:ALA:HA	1.66	0.76
6:d:206:GLU:OE2	6:d:209:ARG:NH2	2.17	0.76
3:a:1407:GLU:N	3:a:1407:GLU:OE1	2.17	0.76
3:a:251:SER:H	3:a:258:GLY:HA3	1.49	0.76
4:b:336:ARG:NH1	4:b:351:TYR:OH	2.18	0.76
4:b:50:SER:HG	4:b:410:GLY:H	1.31	0.76
4:b:416:LEU:HD13	4:b:466:TRP:HE3	1.49	0.76
3:A:367:PRO:HB3	3:A:466:SER:HA	1.67	0.76
3:A:1430:LEU:HB3	3:A:1432:GLN:HE22	1.51	0.76
3:a:346:ASP:OD1	4:b:1106:ARG:NH2	2.19	0.76
3:a:587:HIS:NE2	3:a:969:GLN:OE1	2.17	0.76
3:a:590:ARG:NH2	3:a:620:LYS:O	2.18	0.76
9:G:21:ARG:HH22	9:G:25:TYR:HB2	1.49	0.76
4:B:85:SER:HB3	4:B:138:GLU:HB3	1.68	0.75
4:B:841:MET:HE1	4:B:980:PHE:HE2	1.51	0.75
17:Q:106:ILE:HG22	18:M:87:LEU:HD11	1.69	0.75
4:b:209:GLU:OE1	4:b:788:ARG:NH2	2.19	0.75
4:b:604:ARG:NH2	4:b:615:MET:SD	2.59	0.75
12:j:7:CYS:HB3	12:j:10:CYS:SG	2.26	0.75
3:a:1385:THR:OG1	3:a:1388:GLY:N	2.19	0.75
4:b:348:ARG:HG2	4:b:351:TYR:H	1.52	0.75
4:b:1076:HIS:O	5:c:31:ASN:ND2	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:h:83:GLN:O	10:h:87:ARG:NH1	2.19	0.75
16:R:14:C:O2	16:R:14:C:O2'	2.02	0.74
10:h:99:GLY:HA3	10:h:118:PHE:HD1	1.52	0.74
4:B:526:GLU:OE2	4:B:753:ALA:N	2.20	0.74
10:h:123:MET:HE1	10:h:125:LEU:HB2	1.69	0.74
14:L:61:THR:HG22	14:L:63:ARG:H	1.50	0.74
4:b:416:LEU:HD13	4:b:466:TRP:CE3	2.22	0.74
4:b:428:ILE:O	4:b:445:LYS:NZ	2.19	0.74
6:d:148:LEU:HA	6:d:151:PHE:HD2	1.51	0.74
3:a:367:PRO:HG2	3:a:370:ILE:HB	1.69	0.74
4:b:232:SER:O	4:b:261:ARG:NH2	2.20	0.74
4:b:757:PRO:HD3	4:b:983:ARG:HE	1.50	0.74
6:D:139:LYS:NZ	6:D:143:ASN:OD1	2.21	0.74
4:b:1165:ILE:HD12	4:b:1187:ASN:HD22	1.52	0.74
4:b:1165:ILE:N	4:b:1190:ASP:OD1	2.18	0.73
3:A:1420:ASP:OD2	3:A:1422:ARG:NH1	2.21	0.73
3:a:120:GLU:HB3	3:a:124:GLN:HE22	1.53	0.73
9:g:88:ASP:HB3	9:g:144:ARG:HG3	1.70	0.73
12:J:10:CYS:SG	12:J:11:GLY:N	2.60	0.73
3:a:350:ARG:HB2	4:b:1128:LEU:HD21	1.70	0.73
4:b:35:SER:HA	4:b:811:TYR:HE1	1.53	0.73
3:a:110:CYS:HB3	3:a:167:CYS:SG	2.28	0.73
12:j:7:CYS:SG	12:j:9:SER:OG	2.46	0.73
4:b:821:GLN:HE22	4:b:851:PHE:HA	1.53	0.73
9:g:165:GLU:HB3	9:g:168:LEU:HD12	1.70	0.73
4:B:978:ASP:OD2	4:B:1094:ARG:NH2	2.21	0.73
3:A:252:PHE:O	3:A:254:GLU:N	2.21	0.73
4:B:74:LEU:HA	4:B:85:SER:HA	1.69	0.73
6:D:152:SER:HB2	6:D:155:ARG:HH21	1.54	0.73
3:a:1100:ARG:NH2	3:a:1330:ASN:OD1	2.21	0.73
6:D:64:VAL:HG23	6:D:68:ARG:HH22	1.53	0.73
3:A:18:GLN:HB3	4:B:1215:ARG:HB2	1.70	0.73
3:a:254:GLU:HG2	3:a:255:SER:H	1.53	0.72
4:b:795:ILE:HB	4:b:854:LEU:HB2	1.71	0.72
10:h:93:TYR:HB3	10:h:145:ARG:HH21	1.54	0.72
12:J:1:MET:HA	12:J:57:ILE:HG23	1.69	0.72
4:b:74:LEU:HA	4:b:85:SER:HA	1.70	0.72
5:c:162:GLY:HA3	5:c:170:TRP:CE2	2.24	0.72
3:A:15:LYS:HD3	4:B:1219:ASP:HA	1.72	0.72
4:b:1104:HIS:NE2	4:b:1126:GLY:O	2.20	0.72
3:a:191:THR:OG1	3:a:196:GLU:O	2.08	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:1329:THR:HG22	3:a:1331:SER:H	1.55	0.72
3:A:40:THR:HG22	3:A:53:LEU:HB2	1.72	0.72
4:B:842:ASN:ND2	4:B:845:SER:OG	2.21	0.72
3:a:940:ARG:HH21	3:a:944:ARG:HH21	1.33	0.72
6:d:149:THR:O	6:d:221:TYR:OH	2.07	0.72
3:A:368:LYS:HZ2	13:K:4:PRO:HD3	1.55	0.72
5:C:177:GLU:HB2	5:C:231:ASN:HB3	1.71	0.72
9:g:4:ILE:HG22	9:g:77:VAL:HA	1.72	0.71
3:A:855:THR:OG1	3:A:857:ARG:NH1	2.23	0.71
6:D:39:ASN:ND2	6:D:41:GLN:OE1	2.23	0.71
3:A:1208:THR:OG1	3:A:1211:GLN:OE1	2.07	0.71
4:B:384:ARG:HH21	4:B:387:LEU:HD11	1.55	0.71
4:b:664:THR:HG1	4:b:678:GLU:N	1.87	0.71
5:C:165:LYS:HE2	13:K:9:LEU:HD11	1.69	0.71
6:D:70:PHE:O	6:D:74:GLN:NE2	2.23	0.71
4:b:809:MET:N	4:b:809:MET:SD	2.63	0.71
16:R:13:U:H5''	16:R:14:C:H5''	1.73	0.71
4:b:763:GLN:HG3	4:b:765:PRO:HD2	1.71	0.71
8:f:89:GLU:OE2	8:f:136:ARG:NH2	2.21	0.71
3:A:273:ASN:HA	3:A:296:LEU:HD21	1.73	0.71
4:B:190:TYR:HE2	4:B:196:PRO:HD3	1.56	0.71
4:B:806:THR:HG23	4:B:808:ALA:H	1.56	0.71
4:b:43:LEU:O	4:b:496:ARG:NH2	2.24	0.71
9:G:47:CYS:SG	9:G:48:VAL:N	2.62	0.71
4:b:509:ALA:N	4:b:513:GLN:O	2.24	0.71
6:d:32:GLU:HG2	9:g:41:LYS:HE3	1.71	0.71
7:e:202:SER:N	7:e:206:GLY:O	2.22	0.71
2:O:-50:DC:H2'	2:O:-49:DG:C8	2.25	0.70
4:B:365:THR:HG21	4:B:370:PHE:HB2	1.73	0.70
10:H:81:PRO:O	10:H:87:ARG:NH2	2.24	0.70
3:a:226:GLU:OE2	3:a:230:ARG:NH2	2.24	0.70
10:h:57:VAL:HG12	10:h:144:ILE:HG22	1.72	0.70
3:a:114:LEU:HD11	3:a:171:GLN:HE22	1.54	0.70
13:k:65:HIS:HD2	13:k:67:PHE:HB2	1.54	0.70
14:l:47:ARG:NH1	14:l:48:CYS:O	2.25	0.70
17:Q:375:LEU:HB2	17:Q:387:ILE:HB	1.72	0.70
3:a:205:GLU:OE1	3:a:205:GLU:N	2.22	0.70
4:b:1163:CYS:O	4:b:1167:GLY:N	2.22	0.70
3:A:474:VAL:HA	3:A:521:MET:HE1	1.74	0.70
4:B:234:ILE:HG21	4:B:257:LYS:HD2	1.73	0.70
4:b:227:LYS:HB3	4:b:395:GLN:HE21	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:747:VAL:HG12	3:A:753:GLY:HA3	1.73	0.70
3:a:1255:GLU:HB3	3:a:1259:MET:HE1	1.72	0.70
14:L:47:ARG:HH21	14:L:54:ARG:HE	1.40	0.70
4:B:822:ASN:O	12:J:48:ARG:NH2	2.24	0.70
4:B:287:ARG:NH1	4:B:324:ILE:O	2.23	0.70
3:a:43:GLU:OE1	3:a:43:GLU:N	2.25	0.70
3:a:862:ASN:HD22	7:e:174:GLN:HA	1.55	0.70
3:a:1335:ILE:HG23	3:a:1339:LEU:HD12	1.74	0.70
14:L:31:CYS:HA	14:L:56:LEU:HA	1.74	0.70
3:a:830:LYS:NZ	3:a:1077:THR:O	2.23	0.69
3:A:365:GLY:HA3	3:A:469:ARG:HB3	1.74	0.69
18:M:96:ARG:NH2	18:M:103:LYS:O	2.25	0.69
4:b:41:LYS:NZ	4:b:544:CYS:SG	2.66	0.69
9:g:49:LEU:HD12	9:g:75:ARG:HG2	1.74	0.69
3:A:1397:LEU:HD23	3:A:1429:ILE:HD11	1.75	0.69
1:N:52:DG:H2'	1:N:53:DT:C6	2.27	0.69
3:a:551:TYR:O	13:k:62:LYS:NZ	2.24	0.69
3:A:69:THR:HA	3:A:71:GLN:HE22	1.57	0.69
9:g:37:SER:HB3	9:g:45:ILE:HB	1.75	0.69
3:A:871:ASP:OD2	3:A:1366:ARG:NH2	2.25	0.69
4:b:1033:LYS:NZ	4:b:1087:PHE:O	2.24	0.69
4:b:1156:ASP:HB3	4:b:1198:TYR:H	1.57	0.69
4:B:582:VAL:O	4:B:585:VAL:HG12	1.92	0.69
1:N:42:DT:H2''	1:N:43:DC:H5''	1.75	0.69
3:a:1282:VAL:HG12	3:a:1308:THR:HA	1.73	0.69
4:b:287:ARG:NH2	4:b:292:ILE:O	2.26	0.69
4:b:969:ARG:HH12	5:c:60:ASP:H	1.41	0.69
4:B:313:MET:HE1	4:B:390:LEU:HD13	1.74	0.69
4:b:357:GLN:NE2	4:b:367:LEU:O	2.26	0.69
6:d:145:MET:HA	6:d:148:LEU:HB2	1.75	0.69
8:f:128:LYS:HD2	8:f:149:GLU:HA	1.74	0.69
3:A:1059:HIS:ND1	8:F:86:THR:OG1	2.23	0.69
3:a:1107:VAL:HA	3:a:1108:ALA:HB3	1.75	0.69
5:c:41:ILE:HD12	5:c:42:PRO:HD2	1.75	0.69
4:B:757:PRO:HD3	4:B:983:ARG:HE	1.59	0.69
10:H:97:MET:HE1	10:H:118:PHE:CG	2.27	0.68
3:a:407:ARG:NE	3:a:411:ASP:OD2	2.24	0.68
3:A:1136:SER:HB2	3:A:1274:ARG:HH22	1.57	0.68
13:K:95:ILE:HD12	13:K:98:LEU:HD11	1.75	0.68
3:a:14:VAL:H	3:a:1432:GLN:HE22	1.40	0.68
3:a:795:GLU:OE1	3:a:795:GLU:N	2.22	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:50:SER:OG	4:b:410:GLY:N	2.24	0.68
4:B:510:LYS:O	4:B:512:ARG:N	2.27	0.68
3:A:821:ARG:HD3	4:B:514:LEU:HB2	1.76	0.68
3:a:1162:VAL:HG11	11:i:41:PRO:HG3	1.76	0.68
4:b:430:ARG:NH2	4:b:433:GLN:OE1	2.27	0.68
7:e:118:PRO:HA	7:e:121:MET:HE2	1.76	0.68
3:A:346:ASP:H	4:B:1154:ALA:HB1	1.58	0.68
3:A:454:SER:O	3:A:455:MET:HE2	1.93	0.68
3:A:883:LEU:HD23	3:A:885:THR:H	1.58	0.68
5:C:10:ILE:HD12	5:C:20:PHE:HB3	1.75	0.68
9:G:4:ILE:HD12	9:G:49:LEU:HD11	1.75	0.68
3:a:265:LYS:HD3	3:a:322:VAL:HG21	1.75	0.68
3:a:1100:ARG:NH2	3:a:1351:GLU:OE1	2.27	0.68
7:e:124:VAL:HG23	7:e:132:ILE:HB	1.76	0.68
12:j:10:CYS:SG	12:j:11:GLY:N	2.67	0.68
3:a:85:ASP:O	3:a:273:ASN:ND2	2.26	0.68
4:b:996:ARG:NH2	12:j:10:CYS:O	2.26	0.68
9:g:1:MET:N	9:g:80:LYS:O	2.25	0.68
11:i:78:CYS:SG	11:i:105:SER:OG	2.51	0.68
4:B:44:VAL:HG11	4:B:200:GLY:HA2	1.75	0.68
4:B:82:ASP:H	4:B:83:ASN:HA	1.57	0.68
4:B:542:MET:HE1	4:B:747:MET:HB3	1.75	0.68
4:B:611:PRO:HG2	4:B:685:LEU:HD21	1.75	0.68
4:B:642:ASP:HA	4:B:649:LYS:HE3	1.76	0.67
3:a:330:LYS:HA	3:a:1405:THR:HG21	1.74	0.67
4:b:574:SER:HB3	4:b:577:ALA:HB2	1.76	0.67
10:h:135:LEU:HD13	10:h:137:GLN:HB3	1.77	0.67
3:a:717:ASN:OD1	3:a:720:ARG:NH2	2.27	0.67
4:b:244:LEU:HB2	4:b:250:PHE:CD2	2.30	0.67
3:A:884:ASP:OD2	3:A:1025:ARG:NE	2.27	0.67
4:B:706:GLN:HB2	4:B:709:ASP:HB3	1.77	0.67
8:F:85:MET:HE3	8:F:153:VAL:HG12	1.77	0.67
3:a:119:ASN:OD1	3:a:120:GLU:N	2.27	0.67
8:f:76:LYS:O	8:f:79:ARG:NE	2.28	0.67
3:a:1110:ASN:O	3:a:1112:LYS:NZ	2.26	0.67
3:A:1159:ARG:HH12	3:A:1186:ASP:HB2	1.60	0.67
3:a:209:ASN:HA	3:a:212:LYS:HZ3	1.59	0.67
3:A:788:SER:HB2	11:I:69:PRO:HG3	1.77	0.67
3:A:1126:ALA:HA	3:A:1304:TRP:HD1	1.60	0.67
3:a:830:LYS:NZ	3:a:1079:MET:O	2.21	0.67
3:a:1216:ILE:O	3:a:1219:THR:OG1	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:h:33:GLN:HG3	10:h:36:CYS:H	1.60	0.67
4:B:72:GLU:HA	4:B:87:LYS:HA	1.77	0.67
3:a:609:ASP:OD1	3:a:969:GLN:NE2	2.28	0.66
3:A:46:THR:O	3:A:47:ARG:NE	2.28	0.66
4:B:365:THR:O	4:B:374:LYS:NZ	2.28	0.66
3:a:291:GLU:N	3:a:291:GLU:OE1	2.28	0.66
10:h:2:SER:HG	10:h:61:SER:HG	1.42	0.66
2:O:-61:DC:H2''	2:O:-60:DG:H5'	1.75	0.66
4:b:894:ASP:OD1	4:b:895:ASP:N	2.27	0.66
5:c:103:ALA:HB3	5:c:153:LEU:HB3	1.76	0.66
4:b:617:ARG:HE	4:b:619:ILE:HG22	1.59	0.66
3:A:868:TYR:HD1	3:A:1058:VAL:HG21	1.60	0.66
18:M:124:LEU:HD23	18:M:222:CYS:HB3	1.76	0.66
3:a:951:GLU:OE2	3:a:953:ASN:N	2.28	0.66
8:f:149:GLU:OE2	8:f:149:GLU:N	2.21	0.66
3:A:311:GLN:HG2	3:A:312:PRO:HD3	1.77	0.66
3:A:528:LEU:HD11	3:A:619:LYS:HB3	1.76	0.66
3:A:1161:THR:HG22	3:A:1163:ILE:H	1.60	0.66
4:B:864:LYS:H	4:B:872:GLU:HG3	1.61	0.66
7:E:97:VAL:HA	7:E:100:ILE:HD12	1.77	0.66
3:a:567:LYS:HD3	10:h:95:TYR:HA	1.78	0.66
4:b:997:GLU:HB2	5:c:35:ARG:HG2	1.77	0.66
4:B:930:ALA:HA	4:B:931:TYR:C	2.20	0.66
3:a:147:VAL:HA	3:a:170:THR:HA	1.78	0.66
3:a:451:HIS:CD2	3:a:453:MET:HB2	2.31	0.66
4:B:1161:HIS:HB3	4:B:1191:ILE:HD11	1.77	0.66
9:G:148:GLU:H	9:G:161:GLY:HA2	1.60	0.66
3:a:1229:SER:OG	3:a:1233:ASP:OD2	2.14	0.66
11:i:29:CYS:SG	11:i:31:THR:OG1	2.51	0.66
4:B:839:MET:HG3	4:B:1012:ILE:HG22	1.77	0.66
3:A:830:LYS:NZ	3:A:1079:MET:O	2.28	0.66
4:B:172:ILE:HD11	4:B:178:ASN:HB2	1.78	0.66
4:B:771:SER:O	4:B:775:LYS:NZ	2.29	0.66
10:H:33:GLN:HG3	10:H:36:CYS:H	1.61	0.66
3:a:114:LEU:O	3:a:164:ARG:NH2	2.28	0.66
4:B:210:LYS:NZ	4:B:480:SER:O	2.29	0.66
6:D:165:GLN:HA	6:D:168:LYS:HE3	1.76	0.66
3:A:81:PHE:HE1	3:A:243:PRO:HD3	1.60	0.65
3:A:390:GLN:NE2	3:A:394:ASN:OD1	2.29	0.65
4:b:210:LYS:NZ	4:b:481:GLN:O	2.29	0.65
3:A:1318:THR:HG22	7:E:141:VAL:HG11	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:f:125:LEU:HA	8:f:130:ILE:HD11	1.76	0.65
3:A:569:LYS:NZ	5:C:221:TYR:O	2.29	0.65
5:C:10:ILE:HG21	13:K:112:GLN:HG3	1.79	0.65
3:a:402:ALA:HA	3:a:434:ARG:HA	1.79	0.65
3:a:1312:ASN:OD1	3:a:1313:LEU:N	2.29	0.65
4:b:307:ASP:OD1	4:b:308:TRP:N	2.29	0.65
4:b:357:GLN:HE21	4:b:368:GLU:HA	1.60	0.65
3:A:1107:VAL:HA	3:A:1108:ALA:HB3	1.78	0.65
3:a:513:SER:HB2	3:a:520:CYS:HB2	1.79	0.65
4:b:310:MET:N	4:b:310:MET:SD	2.68	0.65
4:B:884:ARG:NH2	4:B:936:ASP:O	2.30	0.65
1:N:45:DC:H2'	1:N:46:DC:H4'	1.78	0.65
3:a:56:PRO:O	3:a:66:LYS:NZ	2.30	0.65
13:k:81:TYR:HE2	13:k:86:ALA:HB2	1.62	0.65
3:A:356:ASP:HB2	3:A:469:ARG:HD2	1.79	0.65
3:A:1111:MET:SD	3:A:1331:SER:OG	2.52	0.65
7:E:136:ASN:HD21	7:E:138:ALA:HB3	1.60	0.65
3:a:871:ASP:OD2	3:a:1366:ARG:NH2	2.29	0.65
13:k:8:GLU:OE1	13:k:37:LYS:NZ	2.30	0.65
4:B:796:LEU:HA	4:B:853:SER:HA	1.79	0.65
6:D:139:LYS:HA	6:D:142:LYS:HE3	1.78	0.65
7:E:124:VAL:HG13	7:E:132:ILE:HB	1.79	0.65
3:a:365:GLY:HA3	3:a:469:ARG:HB2	1.78	0.65
9:G:153:GLN:HG3	9:G:154:VAL:H	1.60	0.65
3:a:841:LEU:HD11	3:a:1105:LEU:HD23	1.78	0.65
3:a:873:MET:O	3:a:1366:ARG:NH1	2.27	0.65
4:b:60:GLN:HE22	4:b:95:ILE:H	1.45	0.65
4:b:757:PRO:HG3	4:b:983:ARG:HH21	1.61	0.65
7:e:21:GLU:OE1	7:e:146:HIS:NE2	2.30	0.65
4:B:173:MET:HB3	4:B:176:SER:HB3	1.79	0.65
4:B:363:HIS:O	4:B:365:THR:N	2.29	0.65
6:d:62:ALA:HB1	6:d:66:ARG:HH12	1.60	0.64
6:d:127:ASP:HA	6:d:130:LEU:HD12	1.77	0.64
3:A:802:ASN:ND2	3:A:807:GLY:O	2.29	0.64
9:g:115:MET:HG3	9:g:116:PRO:HD2	1.79	0.64
3:a:18:GLN:HB3	4:b:1215:ARG:HB2	1.79	0.64
6:d:183:LEU:HD21	9:g:86:VAL:HG12	1.77	0.64
9:g:84:GLY:N	9:g:147:ILE:O	2.29	0.64
3:A:4:GLN:O	4:B:1159:ARG:NH2	2.31	0.64
4:b:499:ASN:OD1	4:b:500:THR:N	2.30	0.64
3:A:1128:GLN:OE1	3:A:1304:TRP:NE1	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:493:SER:OG	4:B:497:ARG:NH2	2.31	0.64
18:M:138:GLN:HG3	18:M:211:LYS:HB3	1.78	0.64
3:a:186:LYS:HG3	3:a:187:LYS:H	1.62	0.64
3:a:857:ARG:HH22	7:e:170:LEU:HD21	1.63	0.64
4:b:573:GLN:OE1	4:b:573:GLN:N	2.30	0.64
5:C:148:ARG:HH12	12:J:65:PRO:HD2	1.61	0.64
4:b:605:ARG:NE	4:b:691:GLU:OE2	2.31	0.64
4:b:1024:ALA:HA	4:b:1027:ILE:HG22	1.80	0.64
4:B:79:THR:HB	4:B:81:SER:H	1.63	0.64
3:a:865:GLN:NE2	3:a:1373:ASP:OD2	2.31	0.64
9:g:37:SER:O	9:g:45:ILE:N	2.30	0.64
3:a:483:ASP:HA	4:b:988:GLY:HA2	1.79	0.64
4:b:424:LEU:O	4:b:428:ILE:HG13	1.98	0.64
4:b:635:ARG:NH2	4:b:742:GLU:OE2	2.30	0.64
4:B:334:ILE:HG13	4:B:335:GLY:H	1.60	0.64
4:B:604:ARG:NH1	4:B:691:GLU:OE2	2.30	0.64
4:B:1033:LYS:HD2	4:B:1059:LEU:HD11	1.80	0.64
6:D:40:HIS:HB2	9:G:73:LYS:HZ2	1.62	0.64
4:b:997:GLU:OE1	4:b:997:GLU:N	2.30	0.64
7:E:88:VAL:HG21	7:E:116:ILE:HG12	1.80	0.64
3:a:757:ASN:O	3:a:761:MET:HG2	1.98	0.64
14:l:30:ILE:O	14:l:57:LEU:N	2.30	0.64
3:A:226:GLU:HG2	3:A:230:ARG:HE	1.63	0.64
4:b:230:ALA:HA	4:b:261:ARG:HH12	1.62	0.63
7:e:92:THR:O	7:e:95:THR:OG1	2.16	0.63
9:g:119:LEU:HD22	9:g:133:SER:HB2	1.79	0.63
4:B:822:ASN:OD1	12:J:48:ARG:NH2	2.31	0.63
17:Q:376:LEU:HD12	18:M:71:VAL:HG21	1.78	0.63
4:b:950:ASP:OD2	4:b:969:ARG:NH2	2.24	0.63
14:l:42:ARG:HG2	14:l:43:THR:HG23	1.80	0.63
1:N:17:DG:H2''	1:N:18:DT:H5'	1.78	0.63
3:A:77:CYS:SG	3:A:80:HIS:CE1	2.80	0.63
9:G:52:ASP:OD1	9:G:53:ASN:N	2.32	0.63
14:L:40:LEU:HD12	14:L:44:ASP:HB2	1.80	0.63
10:h:63:LEU:HD13	10:h:141:TYR:HD2	1.63	0.63
13:k:12:LEU:HA	13:k:37:LYS:HG3	1.79	0.63
3:A:1444:MET:HB3	8:F:133:VAL:HG23	1.78	0.63
4:B:1135:ARG:NH2	4:B:1136:ASP:OD1	2.31	0.63
3:a:443:LEU:HD21	3:a:501:LEU:HG	1.80	0.63
4:b:487:THR:OG1	4:b:777:ALA:O	2.14	0.63
3:a:464:PRO:HB2	3:a:465:TYR:HD2	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:209:GLU:OE1	4:B:788:ARG:NH2	2.25	0.63
18:M:226:PRO:HG3	18:M:236:ILE:HD11	1.80	0.63
3:a:1151:GLU:HB2	3:a:1194:ARG:HB3	1.80	0.63
3:a:1199:ARG:NH1	3:a:1231:ASP:O	2.28	0.63
4:b:930:ALA:HA	4:b:931:TYR:C	2.23	0.63
3:A:453:MET:O	3:A:454:SER:OG	2.17	0.63
3:A:567:LYS:HB3	3:A:568:PRO:HD3	1.80	0.63
3:A:1197:LEU:HB2	3:A:1236:LEU:HB3	1.81	0.63
4:B:563:MET:HE1	4:B:590:HIS:HB2	1.80	0.63
4:b:694:ASP:OD1	4:b:696:GLU:N	2.32	0.63
3:A:526:ASP:OD1	3:A:527:THR:N	2.31	0.63
4:B:980:PHE:HE1	4:B:1094:ARG:HG3	1.64	0.63
3:A:826:ASP:OD2	3:A:827:THR:N	2.31	0.63
3:a:384:ASN:HB2	3:a:388:LEU:HD23	1.81	0.62
3:a:848:ILE:HD11	3:a:856:THR:HG22	1.79	0.62
14:l:61:THR:HG22	14:l:63:ARG:H	1.64	0.62
3:A:146:MET:O	3:A:171:GLN:N	2.32	0.62
3:A:473:SER:OG	3:A:650:GLN:OE1	2.18	0.62
4:B:1072:MET:HB3	4:B:1081:LEU:HD12	1.81	0.62
8:F:86:THR:N	8:F:89:GLU:OE2	2.29	0.62
3:a:379:VAL:O	3:a:384:ASN:ND2	2.32	0.62
3:a:534:LEU:HD12	3:a:656:TRP:CD2	2.33	0.62
4:b:361:LEU:HG	4:b:363:HIS:HD2	1.63	0.62
4:b:486:TYR:OH	4:b:794:ASN:ND2	2.31	0.62
4:b:577:ALA:HB1	4:b:589:VAL:HG11	1.80	0.62
8:f:97:ARG:NH1	8:f:124:GLU:OE2	2.32	0.62
3:A:55:ASP:HA	3:A:58:LEU:HD23	1.81	0.62
7:E:169:ARG:NH2	8:F:142:SER:OG	2.31	0.62
9:G:21:ARG:O	9:G:22:MET:HE2	1.99	0.62
14:L:30:ILE:HB	14:L:57:LEU:HB2	1.82	0.62
4:b:259:TYR:O	4:b:267:ARG:NH2	2.31	0.62
6:d:53:SER:OG	6:d:153:ARG:NH1	2.32	0.62
11:i:76:PRO:HB2	11:i:77:LYS:HG3	1.81	0.62
3:A:959:ASN:OD1	3:A:960:ILE:N	2.32	0.62
9:G:46:LEU:HB2	9:G:77:VAL:HG13	1.81	0.62
10:H:8:ASP:OD1	10:H:9:ILE:N	2.31	0.62
5:c:148:ARG:NH2	12:j:63:TYR:O	2.33	0.62
7:e:88:VAL:HB	7:e:116:ILE:HG23	1.79	0.62
7:e:171:LYS:O	7:e:173:SER:N	2.32	0.62
4:B:194:GLU:HA	4:B:784:ASN:HD22	1.65	0.62
6:D:148:LEU:O	6:D:152:SER:OG	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:62:ALA:O	7:E:77:SER:OG	2.15	0.62
17:Q:97:GLU:OE2	18:M:96:ARG:NH1	2.32	0.62
3:a:44:THR:N	3:a:45:GLN:HA	2.14	0.62
3:a:185:TRP:HA	3:a:187:LYS:HZ1	1.64	0.62
6:d:145:MET:O	6:d:145:MET:HE3	1.99	0.62
11:i:17:ARG:N	11:i:26:LEU:O	2.23	0.62
11:i:19:ASP:OD2	11:i:24:ARG:NH1	2.32	0.62
3:A:367:PRO:HG2	3:A:370:ILE:HG12	1.81	0.62
3:A:1433:MET:HE1	3:A:1439:GLY:HA2	1.81	0.62
4:B:20:ASP:OD1	4:B:21:GLU:N	2.33	0.62
6:D:123:LEU:HG	6:D:145:MET:HE1	1.81	0.62
3:a:760:GLN:HG2	3:a:765:VAL:HA	1.80	0.62
4:B:104:GLU:OE2	4:B:110:HIS:HE1	1.82	0.62
4:b:824:ILE:N	4:b:1009:ASP:OD2	2.33	0.62
4:B:841:MET:HE2	4:B:990:ILE:HG12	1.82	0.62
8:F:116:ASP:OD2	8:F:119:ARG:N	2.29	0.62
3:a:254:GLU:HG2	3:a:255:SER:N	2.15	0.62
4:b:227:LYS:HB3	4:b:395:GLN:NE2	2.15	0.62
4:b:882:THR:OG1	4:b:885:MET:HB2	2.00	0.62
3:A:169:ASN:OD1	3:A:170:THR:N	2.31	0.62
4:B:327:ARG:HG2	17:Q:398:ARG:HH12	1.64	0.62
13:K:8:GLU:HA	13:K:37:LYS:HZ3	1.65	0.62
9:g:6:ASP:HA	9:g:75:ARG:HA	1.81	0.62
10:h:8:ASP:OD2	10:h:30:SER:OG	2.12	0.62
10:h:83:GLN:OE1	10:h:87:ARG:NH1	2.33	0.62
3:A:500:GLU:OE2	4:B:1146:PHE:N	2.31	0.62
4:B:1134:GLU:N	4:B:1134:GLU:OE1	2.28	0.62
17:Q:141:ARG:NH1	17:Q:345:GLU:O	2.33	0.62
3:a:1079:MET:HE1	3:a:1097:GLY:HA2	1.79	0.62
5:c:75:MET:HE1	5:c:239:PRO:HD3	1.82	0.62
5:c:235:VAL:HG21	12:j:6:ARG:HH22	1.65	0.62
9:g:143:ILE:HG23	9:g:170:ALA:HB2	1.81	0.62
3:A:203:SER:O	3:A:206:GLU:HG2	2.00	0.62
3:A:384:ASN:HB2	3:A:388:LEU:HD13	1.82	0.62
3:A:512:VAL:HA	3:A:519:PRO:HA	1.80	0.62
4:B:867:GLY:HA3	4:B:868:MET:C	2.25	0.62
4:B:1106:ARG:NH2	4:B:1110:PRO:O	2.32	0.62
7:E:147:HIS:HE1	7:E:149:LEU:HD13	1.65	0.62
11:I:45:ARG:HE	11:I:46:HIS:H	1.46	0.62
4:b:906:SER:OG	4:b:907:GLY:N	2.33	0.61
12:j:45:CYS:SG	12:j:46:CYS:N	2.73	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:334:ILE:HG13	4:B:335:GLY:N	2.15	0.61
3:a:95:PHE:HB3	3:a:234:MET:HE3	1.82	0.61
3:a:247:ARG:HB3	3:a:262:LEU:HD11	1.81	0.61
3:a:939:ASP:OD2	3:a:1023:ARG:NH1	2.32	0.61
4:b:31:TRP:HB3	4:b:807:ARG:NH2	2.15	0.61
3:A:827:THR:HA	3:A:830:LYS:HG2	1.81	0.61
3:a:848:ILE:HD13	3:a:864:ILE:HD13	1.83	0.61
4:b:1096:ARG:O	4:b:1097:HIS:ND1	2.33	0.61
4:b:1134:GLU:OE1	4:b:1134:GLU:N	2.31	0.61
3:A:789:LYS:NZ	11:I:67:THR:OG1	2.32	0.61
3:A:834:THR:OG1	3:A:1076:ALA:HB1	2.00	0.61
3:A:1044:TRP:O	3:A:1048:ASN:ND2	2.33	0.61
3:a:770:VAL:HG22	3:a:771:GLU:OE1	2.00	0.61
3:a:1156:PRO:HA	3:a:1190:PRO:HA	1.82	0.61
4:b:31:TRP:HB3	4:b:807:ARG:HH22	1.64	0.61
4:b:923:GLU:O	4:b:928:ARG:NH2	2.31	0.61
6:d:203:SER:OG	6:d:205:ASP:OD1	2.17	0.61
3:A:598:LEU:O	10:H:25:ARG:NH2	2.27	0.61
3:A:894:GLU:HB2	3:A:898:ARG:HB2	1.81	0.61
3:a:306:ASN:OD1	3:a:324:SER:N	2.30	0.61
3:a:959:ASN:OD1	3:a:960:ILE:N	2.33	0.61
3:a:1209:MET:HA	3:a:1212:VAL:HG22	1.81	0.61
3:a:1318:THR:HG22	7:e:141:VAL:HG11	1.83	0.61
18:M:223:GLN:NE2	18:M:224:VAL:O	2.33	0.61
3:a:1148:ILE:HB	3:a:1196:GLU:OE1	2.00	0.61
3:a:533:LYS:HE3	3:a:662:PHE:HB2	1.82	0.61
3:a:973:ILE:HD11	3:a:1036:ARG:HB2	1.83	0.61
5:c:235:VAL:HG13	5:c:237:SER:H	1.66	0.61
8:f:144:GLU:OE2	8:f:146:TRP:NE1	2.34	0.61
3:A:502:SER:OG	3:A:503:GLN:NE2	2.29	0.61
3:A:885:THR:O	3:A:940:ARG:NH1	2.32	0.61
3:A:134:ARG:NH2	3:A:220:THR:O	2.33	0.61
3:A:865:GLN:NE2	3:A:1373:ASP:OD2	2.26	0.61
4:b:121:ASN:HA	4:b:207:GLY:HA3	1.83	0.61
5:c:73:GLN:OE1	5:c:74:SER:N	2.34	0.61
10:h:89:LEU:HD22	10:h:91:ASP:HB3	1.83	0.61
13:k:17:SER:OG	13:k:19:LEU:O	2.19	0.61
3:A:1200:ALA:O	3:A:1204:ASP:HB2	2.00	0.61
4:B:344:LYS:HZ2	4:B:347:LYS:HA	1.65	0.61
4:B:795:ILE:O	4:B:854:LEU:N	2.32	0.61
4:B:857:ARG:NH1	4:B:859:TYR:OH	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:875:GLU:OE2	4:B:881:ASN:ND2	2.34	0.61
5:c:14:SER:HB2	5:c:17:ASN:H	1.64	0.61
5:C:240:VAL:O	5:C:243:VAL:HG22	2.01	0.61
3:a:811:GLN:H	3:a:811:GLN:CD	2.08	0.60
4:b:36:ALA:HA	4:b:39:ARG:HG2	1.83	0.60
4:b:1065:GLN:OE1	4:b:1068:GLY:N	2.34	0.60
14:l:41:SER:N	14:l:44:ASP:OD2	2.32	0.60
3:A:886:ILE:HD11	3:A:943:LEU:HB3	1.84	0.60
4:B:287:ARG:NH2	4:B:294:ASP:OD1	2.30	0.60
7:E:55:ARG:HA	7:E:58:MET:HE3	1.81	0.60
4:b:44:VAL:HG11	4:b:200:GLY:HA2	1.81	0.60
4:b:661:LEU:HD11	4:b:684:LEU:HD11	1.82	0.60
3:A:1142:THR:O	3:A:1145:SER:OG	2.19	0.60
17:Q:379:GLU:N	17:Q:383:SER:O	2.25	0.60
3:A:81:PHE:CE1	3:A:243:PRO:HD3	2.35	0.60
13:K:36:GLU:OE1	13:K:36:GLU:N	2.34	0.60
3:a:765:VAL:HB	3:a:800:VAL:HG11	1.83	0.60
4:b:242:SER:OG	4:b:252:SER:O	2.20	0.60
12:J:44:TYR:HA	12:J:47:ARG:HB3	1.83	0.60
3:a:1209:MET:HE1	3:a:1228:TRP:HB2	1.83	0.60
7:e:20:LYS:HB3	7:e:35:VAL:HG12	1.83	0.60
9:g:65:ASP:OD1	9:g:67:SER:OG	2.17	0.60
11:i:10:CYS:SG	11:i:31:THR:OG1	2.60	0.60
4:B:114:PRO:HG3	4:B:181:LEU:HD11	1.84	0.60
4:B:341:LEU:HB3	4:B:344:LYS:HD2	1.82	0.60
9:G:84:GLY:HA2	9:G:146:LYS:HD2	1.84	0.60
18:M:106:LEU:N	18:M:120:TYR:O	2.27	0.60
3:a:39:GLU:HG3	3:a:50:ILE:HG21	1.82	0.60
3:a:372:LYS:NZ	13:k:1:MET:O	2.28	0.60
4:b:210:LYS:HE3	4:b:480:SER:HB2	1.83	0.60
4:b:706:GLN:HB3	4:b:709:ASP:HB3	1.82	0.60
4:b:1112:GLN:HG2	4:b:1115:THR:HG22	1.83	0.60
6:d:152:SER:O	6:d:221:TYR:OH	2.09	0.60
10:h:56:THR:O	10:h:145:ARG:N	2.34	0.60
10:h:101:ALA:HA	10:h:116:TYR:HA	1.83	0.60
4:B:1037:LEU:O	12:J:47:ARG:NH1	2.35	0.60
4:B:1160:VAL:HG11	4:B:1169:MET:HE3	1.83	0.60
5:C:162:GLY:HA3	5:C:170:TRP:CE2	2.37	0.60
10:H:12:VAL:HG12	10:H:53:ASP:H	1.65	0.60
3:a:208:LEU:HD23	3:a:212:LYS:NZ	2.11	0.60
3:A:840:ARG:NH1	3:A:1384:VAL:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:295:GLY:HA3	11:I:11:ASN:HB3	1.84	0.60
4:B:296:GLU:O	4:B:300:HIS:ND1	2.28	0.60
9:G:154:VAL:O	9:G:156:SER:N	2.34	0.60
17:Q:126:LYS:HD3	18:M:130:GLU:HB2	1.84	0.60
1:N:46:DC:H5'	1:N:47:DT:H2'	1.83	0.60
3:a:42:ASP:HB3	3:a:45:GLN:HB2	1.83	0.60
3:a:444:PHE:O	3:a:455:MET:HA	2.02	0.60
5:c:75:MET:HE1	5:c:239:PRO:CD	2.32	0.60
9:g:83:LYS:HE2	9:g:150:CYS:HB3	1.84	0.60
3:A:1385:THR:OG1	3:A:1388:GLY:N	2.31	0.60
4:B:1010:LEU:HD11	4:B:1092:TYR:HE2	1.65	0.60
9:G:89:GLY:HA3	9:G:103:VAL:HG22	1.83	0.60
3:a:62:ASP:OD1	3:a:63:ARG:NH1	2.35	0.60
3:a:1044:TRP:O	3:a:1048:ASN:ND2	2.34	0.60
3:A:618:GLU:HG3	3:A:620:LYS:H	1.65	0.60
3:A:1113:THR:O	3:A:1330:ASN:ND2	2.35	0.60
3:a:576:GLN:O	3:a:579:SER:OG	2.19	0.60
3:a:1055:ARG:NE	8:f:154:ASP:OD2	2.34	0.60
4:b:551:PRO:O	4:b:554:ILE:HG12	2.01	0.60
10:h:137:GLN:NE2	10:h:139:ASN:O	2.32	0.60
11:i:15:TYR:N	11:i:28:GLU:O	2.35	0.60
3:A:32:VAL:O	3:A:57:ARG:NH1	2.35	0.60
3:A:590:ARG:NH2	3:A:620:LYS:HB3	2.17	0.60
3:A:1063:MET:HE3	3:A:1436:ILE:HG23	1.83	0.60
4:B:146:GLU:HG2	4:B:147:LEU:H	1.65	0.60
4:B:801:LYS:O	12:J:52:THR:OG1	2.18	0.60
4:B:924:GLU:HG2	4:B:925:LEU:HD12	1.83	0.60
3:a:1192:LEU:HB3	3:a:1241:ARG:HE	1.66	0.59
3:A:871:ASP:OD1	3:A:872:GLY:N	2.34	0.59
3:A:1168:GLU:O	3:A:1171:GLN:NE2	2.35	0.59
5:C:167:HIS:CE1	5:C:169:LYS:HG3	2.37	0.59
11:I:78:CYS:SG	11:I:105:SER:OG	2.60	0.59
3:a:563:PRO:HG3	3:a:570:PRO:HB3	1.84	0.59
4:b:1112:GLN:N	4:b:1117:GLN:O	2.34	0.59
9:g:86:VAL:HA	9:g:146:LYS:HA	1.83	0.59
7:E:168:TYR:HB3	7:E:170:LEU:HD23	1.84	0.59
4:b:969:ARG:NH1	5:c:60:ASP:H	2.00	0.59
3:A:148:CYS:HB2	3:A:171:GLN:NE2	2.15	0.59
4:B:372:SER:OG	4:B:373:ARG:NH1	2.34	0.59
3:a:500:GLU:OE2	4:b:1146:PHE:N	2.35	0.59
3:a:557:ASP:OD1	3:a:559:VAL:N	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:1277:GLU:OE1	3:a:1277:GLU:N	2.33	0.59
3:A:326:ARG:O	3:A:330:LYS:N	2.35	0.59
3:a:366:VAL:HG21	3:a:460:VAL:HG23	1.85	0.59
4:b:397:ASP:OD2	4:b:400:HIS:N	2.36	0.59
4:b:1163:CYS:HB3	4:b:1166:CYS:HB2	1.85	0.59
5:c:182:PRO:HG2	5:c:183:TRP:HD1	1.67	0.59
13:k:85:ASP:O	13:k:89:ASN:ND2	2.29	0.59
3:A:33:ALA:H	3:A:82:GLY:HA2	1.67	0.59
4:B:876:LYS:HB2	4:B:895:ASP:HA	1.83	0.59
5:C:178:PHE:CD1	5:C:230:MET:HE1	2.37	0.59
6:D:56:ARG:NH2	6:D:154:PHE:O	2.31	0.59
10:H:130:ARG:HD3	10:H:130:ARG:H	1.67	0.59
3:a:1079:MET:HE2	3:a:1098:VAL:HG13	1.83	0.59
4:b:308:TRP:CG	11:i:2:THR:HG1	2.21	0.59
4:B:629:ASP:O	4:B:632:ARG:NH2	2.35	0.59
10:H:5:LEU:HD11	10:H:61:SER:HB3	1.83	0.59
4:b:486:TYR:HH	4:b:1096:ARG:HB3	1.68	0.59
9:g:121:PHE:HA	9:g:131:GLN:HE21	1.67	0.59
3:A:589:GLN:HB3	3:A:591:PHE:HE2	1.68	0.59
4:B:1058:LEU:O	4:B:1061:GLU:HG3	2.02	0.59
5:C:66:ARG:NH2	12:J:3:VAL:O	2.35	0.59
9:G:144:ARG:HB2	9:G:169:GLY:H	1.67	0.59
10:H:62:SER:OG	10:H:63:LEU:N	2.36	0.59
4:b:360:PHE:HE2	4:b:374:LYS:HB3	1.68	0.59
3:A:115:LEU:HD21	3:A:145:LYS:HD3	1.83	0.59
3:A:905:ASP:OD1	3:A:906:HIS:N	2.35	0.59
4:B:1082:MET:O	5:C:189:THR:OG1	2.20	0.59
4:b:104:GLU:OE2	14:l:54:ARG:NH2	2.35	0.59
7:e:191:LYS:N	7:e:194:GLU:OE2	2.34	0.59
14:l:28:LYS:HB2	14:l:39:SER:HA	1.84	0.59
3:A:239:LEU:HD12	3:A:240:PRO:HD2	1.85	0.59
3:a:1364:ASN:OD1	3:a:1365:TYR:N	2.36	0.59
4:b:70:ILE:HG22	4:b:89:GLU:HA	1.83	0.59
4:b:342:GLY:H	4:b:344:LYS:HZ3	1.51	0.59
5:c:115:SER:HB2	5:c:141:GLY:HA3	1.83	0.59
3:A:1000:LEU:N	3:A:1011:GLN:OE1	2.36	0.59
5:C:143:LEU:HD21	5:C:146:LYS:HE3	1.84	0.59
5:C:239:PRO:HB2	5:C:242:GLN:HG2	1.85	0.59
9:G:116:PRO:HD2	9:G:119:LEU:HD22	1.83	0.59
3:a:1142:THR:HG23	3:a:1145:SER:H	1.68	0.58
4:b:891:ASP:OD1	4:b:892:LYS:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:770:GLN:O	4:B:770:GLN:NE2	2.35	0.58
4:B:1165:ILE:N	4:B:1190:ASP:OD1	2.30	0.58
10:H:98:TYR:OH	10:H:139:ASN:ND2	2.28	0.58
10:H:135:LEU:HD13	10:H:137:GLN:HB3	1.85	0.58
5:c:248:ILE:HG21	13:k:102:LYS:HB3	1.84	0.58
3:A:147:VAL:HA	3:A:170:THR:HA	1.83	0.58
3:A:1129:GLU:N	3:A:1129:GLU:OE1	2.33	0.58
10:H:99:GLY:HA3	10:H:118:PHE:CD1	2.38	0.58
3:a:9:ALA:O	4:b:1193:GLN:NE2	2.36	0.58
3:a:407:ARG:HB2	3:a:430:TRP:CE2	2.38	0.58
3:a:650:GLN:HA	3:a:653:VAL:HG12	1.84	0.58
3:a:1373:ASP:HA	3:a:1376:THR:HG22	1.86	0.58
3:A:12:ARG:HH21	4:B:1218:THR:HG21	1.68	0.58
4:B:687:GLU:OE1	4:B:687:GLU:N	2.26	0.58
5:C:125:MET:SD	5:C:127:ARG:NE	2.73	0.58
4:b:298:LEU:HA	4:b:301:ILE:HG22	1.85	0.58
3:A:1209:MET:HA	3:A:1212:VAL:HG22	1.85	0.58
4:B:79:THR:HG22	4:B:82:ASP:HA	1.85	0.58
3:a:362:ASP:OD2	3:a:459:ARG:NE	2.33	0.58
4:b:301:ILE:HD11	4:b:382:ILE:HB	1.84	0.58
4:b:847:ASP:HB3	5:c:167:HIS:CE1	2.38	0.58
4:b:1074:ASN:ND2	4:b:1077:THR:H	2.02	0.58
10:h:102:TYR:CZ	10:h:115:TYR:HB3	2.38	0.58
9:G:56:ILE:HG13	9:G:57:GLN:H	1.68	0.58
4:b:548:GLY:N	4:b:612:GLU:OE2	2.33	0.58
4:b:842:ASN:CA	4:b:999:MET:HE1	2.32	0.58
11:i:97:MET:HA	11:i:97:MET:HE3	1.85	0.58
4:b:762:ASN:OD1	4:b:1023:VAL:N	2.35	0.58
4:B:307:ASP:OD1	4:B:308:TRP:N	2.37	0.58
11:I:45:ARG:HE	11:I:46:HIS:N	2.01	0.58
3:a:353:ILE:HG21	3:a:487:MET:CE	2.34	0.58
3:a:959:ASN:OD1	3:a:961:ARG:N	2.34	0.58
3:a:1166:ASP:HA	3:a:1169:ILE:HD13	1.85	0.58
7:e:143:ASN:HB3	7:e:146:HIS:HD2	1.69	0.58
11:i:25:LEU:HG	11:i:38:ALA:HB3	1.86	0.58
3:A:1054:LEU:HB3	8:F:84:TYR:HE1	1.68	0.58
1:N:18:DT:H1'	1:N:19:DG:C8	2.39	0.58
3:a:1059:HIS:HD1	8:f:86:THR:HG1	0.64	0.58
4:b:277:LYS:N	4:b:337:ARG:HH21	2.02	0.58
4:b:1076:HIS:HA	5:c:35:ARG:HH21	1.68	0.58
7:e:195:VAL:HG22	7:e:213:ILE:HG12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:340:LEU:HD21	3:a:1429:ILE:HG23	1.86	0.58
4:b:778:MET:HG2	4:b:796:LEU:HG	1.86	0.58
4:b:798:TYR:OH	5:c:66:ARG:NH2	2.27	0.58
4:b:892:LYS:NZ	4:b:909:ASP:OD2	2.36	0.58
10:h:95:TYR:H	10:h:145:ARG:CZ	2.17	0.58
4:B:48:LEU:O	4:B:52:ASN:ND2	2.27	0.58
2:O:-13:DA:H1'	3:A:835:GLY:HA3	1.86	0.57
3:a:491:VAL:O	4:b:1150:ARG:NH2	2.37	0.57
3:a:918:GLU:OE1	3:a:918:GLU:N	2.34	0.57
3:A:68:GLN:NE2	3:A:70:CYS:SG	2.77	0.57
3:A:1118:VAL:HB	3:A:1306:LEU:HB2	1.86	0.57
9:g:83:LYS:HE2	9:g:150:CYS:H	1.69	0.57
3:A:1444:MET:HE3	8:F:135:ARG:HE	1.69	0.57
8:F:130:ILE:N	8:F:149:GLU:OE2	2.38	0.57
11:i:14:LEU:HB3	11:i:27:PHE:HB3	1.85	0.57
4:B:364:ILE:HG22	4:B:585:VAL:HG23	1.84	0.57
4:B:412:LEU:HB3	4:B:466:TRP:CZ2	2.39	0.57
5:C:55:THR:HB	5:C:152:GLU:H	1.70	0.57
3:a:881:GLN:NE2	3:a:960:ILE:H	2.03	0.57
3:A:243:PRO:HB2	3:A:245:PRO:HD2	1.86	0.57
3:A:490:HIS:HB3	4:B:1150:ARG:HH12	1.69	0.57
3:A:1390:ASN:HD22	3:A:1402:PHE:HD2	1.52	0.57
3:a:1217:LYS:HG2	3:a:1221:LYS:HD3	1.85	0.57
4:b:22:SER:O	4:b:654:ARG:NH1	2.30	0.57
3:A:440:ASP:H	3:A:460:VAL:HG12	1.70	0.57
4:B:70:ILE:HG22	4:B:89:GLU:HA	1.86	0.57
4:B:194:GLU:OE1	4:B:194:GLU:N	2.38	0.57
4:B:918:ILE:HG22	4:B:921:ASP:HB2	1.87	0.57
5:C:208:GLU:OE1	5:C:208:GLU:N	2.37	0.57
1:N:52:DG:H2''	1:N:53:DT:H5'	1.84	0.57
3:a:409:SER:OG	3:a:411:ASP:OD2	2.22	0.57
3:a:961:ARG:HB2	3:a:1025:ARG:HH22	1.70	0.57
4:b:342:GLY:N	4:b:344:LYS:HZ3	2.03	0.57
3:A:372:LYS:NZ	13:K:2:ASN:HB2	2.19	0.57
4:B:75:ALA:O	4:B:76:GLN:HG2	2.03	0.57
4:B:104:GLU:OE2	4:B:110:HIS:CE1	2.58	0.57
10:H:99:GLY:HA3	10:H:118:PHE:HD1	1.68	0.57
3:a:232:GLU:OE1	3:a:232:GLU:N	2.38	0.57
3:a:507:VAL:HG23	3:a:508:PRO:HD3	1.85	0.57
3:a:754:SER:N	3:a:757:ASN:OD1	2.38	0.57
9:g:90:THR:O	9:g:102:GLN:N	2.31	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:738:LYS:NZ	5:C:193:TYR:O	2.37	0.57
3:A:949:ASP:OD1	3:A:950:GLY:N	2.38	0.57
4:B:802:PRO:HB3	4:B:1091:TYR:CG	2.39	0.57
4:B:997:GLU:OE1	4:B:997:GLU:N	2.33	0.57
10:H:128:ASN:OD1	10:H:131:ASN:ND2	2.34	0.57
10:h:115:TYR:OH	10:h:124:ARG:NH1	2.38	0.57
6:D:40:HIS:HB2	9:G:73:LYS:NZ	2.19	0.57
7:E:123:LEU:HD23	7:E:123:LEU:H	1.70	0.57
11:I:27:PHE:O	11:I:36:GLU:N	2.36	0.57
3:a:848:ILE:HG23	3:a:1065:GLY:HA3	1.87	0.57
4:b:175:ARG:NH2	4:b:200:GLY:O	2.32	0.57
4:b:842:ASN:OD1	4:b:844:SER:N	2.38	0.57
11:i:6:PHE:O	11:i:8:ARG:NH1	2.36	0.57
3:A:781:ASP:HB2	3:A:789:LYS:HD2	1.86	0.57
5:c:165:LYS:HB3	13:k:9:LEU:HD13	1.85	0.57
12:j:8:PHE:H	12:j:49:MET:CE	2.17	0.57
3:A:922:ASP:OD1	3:A:923:LEU:N	2.38	0.57
3:A:1116:LEU:HB3	3:A:1329:THR:HG23	1.87	0.57
3:A:1363:VAL:HG23	3:A:1368:MET:HE2	1.87	0.57
3:a:1157:ASP:OD1	3:a:1160:SER:N	2.38	0.56
3:A:434:ARG:HD2	3:A:435:HIS:O	2.05	0.56
3:A:471:ASN:OD1	3:A:472:LEU:N	2.38	0.56
4:B:275:TYR:HB3	4:B:337:ARG:HD2	1.86	0.56
4:B:487:THR:HG22	4:B:489:SER:H	1.70	0.56
5:C:248:ILE:HG21	13:K:102:LYS:HB2	1.87	0.56
3:a:170:THR:HB	3:a:187:LYS:HD2	1.86	0.56
4:b:542:MET:HE2	4:b:636:PRO:HG2	1.87	0.56
5:c:73:GLN:OE1	5:c:75:MET:N	2.37	0.56
5:c:114:TYR:N	5:c:117:ASP:OD2	2.31	0.56
4:B:668:ASP:OD2	17:Q:28:ARG:NH2	2.36	0.56
4:B:1065:GLN:OE1	4:B:1068:GLY:N	2.38	0.56
5:C:43:THR:HG23	5:C:170:TRP:HD1	1.70	0.56
8:F:84:TYR:HE2	8:F:152:ILE:HD11	1.69	0.56
8:F:89:GLU:OE1	8:F:89:GLU:N	2.29	0.56
12:J:3:VAL:HG11	12:J:18:TRP:CD2	2.40	0.56
3:a:146:MET:O	3:a:171:GLN:N	2.37	0.56
3:a:860:LEU:O	7:e:174:GLN:NE2	2.38	0.56
3:a:961:ARG:HG3	3:a:965:GLN:NE2	2.17	0.56
3:a:1153:TYR:HB2	3:a:1192:LEU:HD11	1.87	0.56
4:b:728:ARG:NH2	4:b:1048:THR:O	2.37	0.56
4:b:778:MET:SD	4:b:1094:ARG:HB3	2.46	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:1050:ILE:HD11	4:b:1055:ILE:HD11	1.88	0.56
11:i:7:CYS:HB3	11:i:10:CYS:O	2.05	0.56
12:j:5:VAL:HG12	12:j:6:ARG:HG3	1.87	0.56
3:A:557:ASP:HB3	3:A:559:VAL:HG12	1.86	0.56
3:A:1191:TRP:HZ3	11:I:43:VAL:HG21	1.70	0.56
3:A:1216:ILE:O	3:A:1219:THR:HG22	2.06	0.56
4:B:727:LYS:HB3	4:B:1051:THR:HG21	1.87	0.56
7:E:25:ASP:OD2	7:E:187:TYR:OH	2.19	0.56
8:F:84:TYR:CE2	8:F:152:ILE:HD11	2.40	0.56
3:a:1063:MET:HE3	3:a:1436:ILE:HD13	1.88	0.56
5:c:44:LEU:HB2	5:c:77:ILE:HD13	1.88	0.56
6:d:36:LYS:HG2	6:d:44:GLU:HG3	1.87	0.56
6:d:59:ILE:HD13	6:d:148:LEU:HD11	1.87	0.56
7:e:94:LYS:HA	7:e:97:VAL:HG12	1.88	0.56
8:f:98:ALA:O	8:f:102:SER:HB2	2.06	0.56
11:i:92:ARG:HE	11:i:93:LYS:H	1.51	0.56
12:j:21:TYR:HD2	12:j:22:LEU:HD22	1.71	0.56
3:A:179:LEU:HD12	3:A:297:GLN:HE22	1.70	0.56
4:B:1156:ASP:HB3	4:B:1198:TYR:H	1.71	0.56
9:G:120:THR:OG1	9:G:131:GLN:O	2.22	0.56
3:a:286:HIS:ND1	3:a:286:HIS:O	2.36	0.56
5:c:251:LEU:HD22	13:k:98:LEU:HD21	1.87	0.56
10:h:33:GLN:OE1	10:h:34:ASP:N	2.38	0.56
3:a:490:HIS:HB3	4:b:1150:ARG:HH12	1.69	0.56
3:a:745:GLN:O	3:a:749:ALA:HB2	2.05	0.56
4:b:770:GLN:O	4:b:770:GLN:NE2	2.39	0.56
4:b:827:ILE:HD11	4:b:1014:PRO:HA	1.87	0.56
3:A:806:ARG:O	4:B:728:ARG:NH2	2.38	0.56
4:B:1181:GLU:HG3	4:B:1188:LYS:HE3	1.88	0.56
5:C:76:ASP:OD2	5:C:128:ASN:N	2.38	0.56
3:a:261:ASP:OD2	3:a:323:LYS:N	2.31	0.56
3:a:1169:ILE:HA	3:a:1172:LEU:HD12	1.88	0.56
4:b:287:ARG:HE	4:b:292:ILE:HA	1.71	0.56
4:b:680:THR:H	4:b:683:SER:HB3	1.70	0.56
7:e:182:ASP:OD1	7:e:184:VAL:HG12	2.05	0.56
3:A:1149:ALA:HB1	11:I:45:ARG:HH22	1.70	0.56
4:b:820:GLY:N	4:b:1091:TYR:OH	2.39	0.56
5:c:142:VAL:HG21	12:j:5:VAL:HG22	1.87	0.56
7:e:40:GLU:N	7:e:40:GLU:OE2	2.39	0.56
8:f:86:THR:HG22	8:f:89:GLU:CD	2.31	0.56
13:k:7:PHE:HB2	13:k:11:LEU:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:451:HIS:CD2	3:A:453:MET:HB2	2.41	0.56
3:A:563:PRO:HG3	3:A:570:PRO:HB3	1.87	0.56
3:A:741:ASN:OD1	3:A:742:ASN:N	2.39	0.56
3:A:1329:THR:HB	3:A:1335:ILE:HD11	1.88	0.56
5:C:179:GLU:HB2	5:C:229:TYR:HB2	1.86	0.56
3:a:415:LEU:HA	3:a:418:SER:HB2	1.88	0.56
3:a:1116:LEU:HB3	3:a:1329:THR:HG23	1.88	0.56
3:A:964:ILE:O	3:A:968:GLN:HG3	2.06	0.56
4:B:1166:CYS:SG	4:B:1185:CYS:HB2	2.46	0.56
5:C:114:TYR:N	5:C:117:ASP:OD2	2.35	0.56
3:a:443:LEU:HB2	3:a:490:HIS:HB2	1.88	0.56
3:a:1332:PHE:HA	3:a:1335:ILE:HD13	1.88	0.56
4:b:486:TYR:OH	4:b:1096:ARG:HB3	2.06	0.56
3:A:14:VAL:HG22	4:B:1216:LEU:HD21	1.87	0.56
3:A:737:LEU:HD11	3:A:741:ASN:HD22	1.72	0.56
3:A:1161:THR:HG22	3:A:1163:ILE:N	2.20	0.56
4:B:841:MET:HE1	4:B:980:PHE:CE2	2.36	0.56
5:C:73:GLN:OE1	5:C:75:MET:N	2.36	0.56
3:a:1220:PHE:HZ	3:a:1267:MET:HE1	1.71	0.55
3:a:1325:THR:HA	7:e:147:HIS:HA	1.88	0.55
4:b:466:TRP:CD1	4:b:479:VAL:HG21	2.41	0.55
7:e:85:GLU:HG3	7:e:87:SER:O	2.05	0.55
3:A:761:MET:HE1	4:B:1018:PRO:HA	1.87	0.55
3:A:1192:LEU:HD11	3:A:1239:ARG:HB3	1.87	0.55
4:B:420:LEU:HD21	4:B:456:GLY:HA3	1.86	0.55
4:B:872:GLU:HG2	4:B:917:PRO:HD3	1.88	0.55
5:C:101:LEU:O	5:C:102:GLN:NE2	2.39	0.55
3:a:537:ARG:NH1	3:a:602:ASP:OD2	2.39	0.55
4:B:323:VAL:HG13	4:B:324:ILE:HG13	1.88	0.55
4:B:874:PHE:CE1	4:B:962:LYS:HB3	2.41	0.55
5:C:68:GLY:HA3	14:L:69:ALA:HB1	1.88	0.55
6:D:56:ARG:NH1	6:D:155:ARG:HE	2.03	0.55
2:O:-16:DT:H2"	2:O:-15:DA:C8	2.41	0.55
3:a:563:PRO:HD2	10:h:79:TRP:CD1	2.41	0.55
4:b:1074:ASN:OD1	4:b:1076:HIS:N	2.39	0.55
5:c:179:GLU:N	5:c:229:TYR:O	2.37	0.55
3:A:1335:ILE:HG23	3:A:1339:LEU:HD12	1.88	0.55
5:C:184:ASN:ND2	5:C:189:THR:O	2.37	0.55
18:M:86:ASN:OD1	18:M:90:GLN:NE2	2.40	0.55
3:a:1361:SER:HB2	3:a:1362:TYR:HB3	1.88	0.55
4:b:185:THR:O	4:b:189:LEU:N	2.30	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:866:TYR:HB2	4:b:870:ILE:HG13	1.89	0.55
4:b:978:ASP:N	4:b:989:THR:OG1	2.39	0.55
3:A:173:THR:OG1	3:A:184:SER:OG	2.24	0.55
4:B:82:ASP:N	4:B:83:ASN:HA	2.18	0.55
3:a:768:GLN:NE2	3:a:816:HIS:HA	2.21	0.55
3:a:1446:ASP:OD1	3:a:1447:GLU:N	2.40	0.55
8:f:109:VAL:HG21	8:f:124:GLU:HA	1.87	0.55
5:C:241:ASP:N	5:C:241:ASP:OD1	2.40	0.55
3:a:825:ILE:HD11	4:b:512:ARG:HD3	1.88	0.55
3:a:857:ARG:NH2	7:e:170:LEU:HD21	2.21	0.55
3:a:1136:SER:HB2	3:a:1274:ARG:HH22	1.71	0.55
4:b:98:THR:OG1	4:b:127:GLY:O	2.25	0.55
4:B:824:ILE:HD11	12:J:48:ARG:HD2	1.89	0.55
6:D:191:ALA:HA	6:D:194:LEU:HD12	1.88	0.55
2:O:-45:DA:H2"	3:a:350:ARG:HH12	1.71	0.55
3:a:134:ARG:NH2	3:a:220:THR:O	2.28	0.55
3:a:471:ASN:OD1	3:a:472:LEU:N	2.39	0.55
3:a:1188:GLN:HG3	3:a:1243:VAL:HG23	1.87	0.55
3:a:1427:ASN:O	3:a:1431:GLY:N	2.39	0.55
4:b:286:PHE:CE1	4:b:378:LEU:HD22	2.41	0.55
4:b:842:ASN:ND2	4:b:845:SER:OG	2.39	0.55
6:D:66:ARG:NH1	6:D:67:ARG:HH21	2.04	0.55
3:a:219:PHE:HB3	3:a:224:PHE:HB2	1.88	0.55
3:a:567:LYS:HE2	10:h:47:PHE:HB2	1.88	0.55
4:b:56:ASP:OD1	4:b:57:TYR:N	2.39	0.55
7:e:47:CYS:HA	7:e:52:ARG:O	2.06	0.55
4:B:1155:SER:OG	4:B:1156:ASP:N	2.38	0.55
9:G:13:LEU:HD12	9:G:26:LEU:HD21	1.89	0.55
3:a:253:ASN:ND2	15:r:38:G:N7	2.55	0.55
3:a:881:GLN:HE22	3:a:960:ILE:H	1.54	0.55
3:a:1009:ASN:HD22	3:a:1012:ARG:HH21	1.55	0.55
4:B:510:LYS:HG3	4:B:511:PRO:CD	2.27	0.55
7:E:171:LYS:O	7:E:173:SER:N	2.39	0.55
10:H:130:ARG:HB2	10:H:133:ASN:HB3	1.88	0.55
3:a:98:LYS:HB3	3:a:234:MET:HE1	1.89	0.55
3:a:511:ILE:HG21	3:a:634:THR:HG21	1.87	0.55
4:b:563:MET:HE2	4:b:563:MET:HA	1.89	0.55
4:b:780:VAL:HG21	4:b:817:LEU:HD12	1.88	0.55
6:d:62:ALA:HB1	6:d:66:ARG:NH1	2.22	0.55
7:e:112:TYR:CD1	7:e:116:ILE:HD11	2.42	0.55
3:A:44:THR:N	3:A:45:GLN:HA	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:874:ASP:O	3:A:878:ILE:HD11	2.07	0.55
4:B:35:SER:HG	4:B:811:TYR:HH	1.55	0.55
4:B:247:GLY:HA2	4:B:418:LYS:HE2	1.88	0.55
4:B:277:LYS:HA	4:B:337:ARG:HH21	1.71	0.55
4:B:805:THR:O	4:B:1044:ALA:N	2.40	0.55
5:C:54:ASN:OD1	5:C:55:THR:N	2.39	0.55
3:a:406:ILE:HB	3:a:431:LYS:HB2	1.89	0.54
3:a:1004:ASN:HD21	3:a:1007:ILE:HG12	1.72	0.54
4:b:850:LEU:HG	4:b:851:PHE:HD1	1.72	0.54
4:b:1037:LEU:O	12:j:47:ARG:NH1	2.40	0.54
13:k:93:SER:O	13:k:97:LYS:HG2	2.07	0.54
3:A:848:ILE:HB	3:A:1065:GLY:HA3	1.89	0.54
12:J:32:GLU:OE1	12:J:32:GLU:N	2.33	0.54
13:K:8:GLU:HG2	13:K:37:LYS:HZ3	1.72	0.54
16:R:14:C:O2	16:R:14:C:C2'	2.55	0.54
3:a:549:MET:HE1	3:a:655:PHE:CD2	2.43	0.54
3:A:40:THR:O	3:A:50:ILE:N	2.38	0.54
4:B:185:THR:O	4:B:189:LEU:N	2.25	0.54
4:B:487:THR:OG1	4:B:777:ALA:O	2.25	0.54
7:E:156:LEU:HD21	7:E:197:LYS:HB2	1.89	0.54
13:K:98:LEU:HD12	13:K:99:GLY:N	2.22	0.54
14:L:50:ASP:OD1	14:L:51:CYS:N	2.39	0.54
3:a:482:PHE:N	4:b:836:GLU:OE1	2.40	0.54
3:a:868:TYR:CZ	3:a:1064:VAL:HG21	2.42	0.54
4:b:145:ARG:HB3	4:b:146:GLU:HB2	1.89	0.54
4:b:547:VAL:N	4:b:612:GLU:OE2	2.40	0.54
4:b:604:ARG:NH1	4:b:692:TYR:O	2.41	0.54
11:i:5:ARG:NE	11:i:6:PHE:H	2.04	0.54
3:A:337:ARG:HH21	3:A:839:ARG:CZ	2.20	0.54
3:A:530:GLY:HA3	3:A:657:LEU:HD21	1.89	0.54
3:A:540:PHE:HB3	3:A:571:LEU:HD23	1.89	0.54
4:B:1156:ASP:CB	4:B:1198:TYR:H	2.19	0.54
4:b:758:PHE:CZ	4:b:1044:ALA:HA	2.43	0.54
3:A:439:ASN:N	3:A:460:VAL:O	2.33	0.54
3:A:664:THR:OG1	3:A:668:ASP:OD2	2.16	0.54
7:E:85:GLU:OE2	7:E:89:GLY:N	2.38	0.54
8:F:77:ASP:OD2	8:F:78:GLN:N	2.40	0.54
10:H:145:ARG:O	10:H:146:ARG:HD3	2.08	0.54
3:a:362:ASP:O	3:a:458:HIS:ND1	2.36	0.54
3:a:577:ILE:O	3:a:580:VAL:HG12	2.07	0.54
3:a:741:ASN:HD21	3:a:743:VAL:HG12	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:1192:LEU:HD22	3:a:1239:ARG:HH21	1.73	0.54
4:b:855:PHE:HB3	4:b:970:THR:O	2.06	0.54
10:h:93:TYR:CB	10:h:145:ARG:HE	2.21	0.54
4:B:542:MET:CE	4:B:747:MET:HB3	2.37	0.54
4:B:863:GLU:HG2	4:B:872:GLU:HB2	1.90	0.54
3:a:1293:SER:N	3:a:1297:GLU:O	2.32	0.54
4:b:302:CYS:SG	4:b:303:TYR:N	2.81	0.54
6:d:45:GLU:OE2	9:g:5:LYS:NZ	2.40	0.54
10:h:130:ARG:HG3	10:h:134:ASN:HB2	1.88	0.54
7:E:201:LYS:HA	7:E:206:GLY:O	2.07	0.54
9:G:46:LEU:HD11	9:G:79:PHE:HB2	1.90	0.54
13:K:12:LEU:HA	13:K:37:LYS:HG3	1.88	0.54
3:a:1387:HIS:HB2	3:a:1391:ARG:HE	1.72	0.54
6:d:67:ARG:NH2	6:d:132:GLN:OE1	2.41	0.54
11:i:27:PHE:N	11:i:36:GLU:O	2.34	0.54
7:E:202:SER:O	7:E:206:GLY:N	2.33	0.54
8:F:70:LYS:O	8:F:71:GLU:HG3	2.07	0.54
10:H:135:LEU:O	10:H:137:GLN:N	2.40	0.54
1:N:-5:DA:H2"	1:N:-4:DG:C8	2.42	0.54
3:a:372:LYS:HD3	13:k:1:MET:HG3	1.90	0.54
3:a:654:ASN:OD1	3:a:655:PHE:N	2.41	0.54
4:b:617:ARG:NE	4:b:619:ILE:HG22	2.23	0.54
4:b:951:GLN:HB3	4:b:967:ARG:HE	1.72	0.54
9:g:21:ARG:HH11	9:g:25:TYR:HB2	1.72	0.54
6:D:125:SER:O	6:D:129:LEU:HG	2.07	0.54
3:a:363:GLN:O	3:a:458:HIS:ND1	2.40	0.54
3:a:996:ASN:ND2	3:a:1050:GLU:OE1	2.27	0.54
3:a:1325:THR:O	7:e:147:HIS:ND1	2.41	0.54
4:b:749:LEU:HB3	4:b:753:ALA:HB3	1.89	0.54
4:b:788:ARG:O	4:b:789:MET:HE2	2.07	0.54
7:e:16:PHE:CE2	7:e:20:LYS:HD2	2.42	0.54
3:A:535:THR:HG21	3:A:617:VAL:HG23	1.90	0.54
3:A:946:VAL:HG23	3:A:947:PHE:H	1.71	0.54
5:C:66:ARG:HH22	12:J:5:VAL:HG23	1.73	0.54
13:K:9:LEU:HG	13:K:10:PHE:CD2	2.43	0.54
3:a:33:ALA:HA	3:a:57:ARG:NH2	2.23	0.54
3:a:368:LYS:HE3	13:k:2:ASN:CG	2.33	0.54
3:a:1315:GLU:OE1	3:a:1315:GLU:N	2.41	0.54
3:a:1438:THR:O	8:f:92:ARG:NH1	2.41	0.54
4:b:861:ASP:OD1	4:b:861:ASP:N	2.39	0.54
14:l:38:LEU:HB3	14:l:40:LEU:HD23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1149:ALA:HB3	3:A:1196:GLU:HB3	1.89	0.54
11:I:22:ASN:HB3	11:I:24:ARG:NH1	2.23	0.54
17:Q:377:SER:OG	18:M:67:GLN:O	2.24	0.54
3:a:852:TYR:CD2	8:f:136:ARG:HG3	2.43	0.53
3:a:900:ASP:OD1	3:a:903:ASN:N	2.41	0.53
4:b:1060:ARG:O	4:b:1060:ARG:NH1	2.36	0.53
8:f:140:ASP:OD1	8:f:141:GLY:N	2.41	0.53
13:k:47:ARG:HD3	13:k:60:ALA:HA	1.91	0.53
3:A:114:LEU:C	3:A:164:ARG:HH22	2.16	0.53
3:A:446:ARG:HD2	3:A:480:ALA:HB2	1.89	0.53
4:B:680:THR:H	4:B:683:SER:HB2	1.73	0.53
12:J:48:ARG:O	12:J:52:THR:HG22	2.07	0.53
17:Q:363:GLY:HA2	17:Q:395:PHE:HA	1.89	0.53
18:M:67:GLN:HB2	18:M:219:CYS:SG	2.49	0.53
3:a:438:ASP:HA	3:a:460:VAL:HG13	1.89	0.53
3:a:849:MET:HE3	3:a:1063:MET:HE1	1.89	0.53
4:b:326:ASP:OD1	4:b:329:THR:OG1	2.14	0.53
7:e:54:GLN:O	7:e:57:MET:HG3	2.08	0.53
9:g:45:ILE:HA	9:g:78:VAL:HG13	1.90	0.53
3:A:1052:GLN:HG2	3:A:1055:ARG:HH21	1.73	0.53
9:G:94:CYS:HB2	9:G:127:PRO:HB2	1.89	0.53
10:H:95:TYR:CE2	10:H:97:MET:HG2	2.44	0.53
11:I:88:SER:O	11:I:91:ARG:NH1	2.38	0.53
17:Q:28:ARG:HE	17:Q:32:LEU:HD11	1.73	0.53
18:M:96:ARG:HE	18:M:105:THR:HG22	1.72	0.53
3:a:846:GLU:OE2	3:a:846:GLU:N	2.39	0.53
10:h:63:LEU:HD23	10:h:89:LEU:HG	1.91	0.53
10:h:83:GLN:HB3	10:h:87:ARG:CZ	2.39	0.53
3:A:682:THR:O	3:A:685:GLU:HG3	2.07	0.53
3:A:1445:ILE:HB	9:G:61:ILE:HD11	1.91	0.53
4:B:696:GLU:OE1	4:B:696:GLU:N	2.41	0.53
4:B:705:MET:HA	4:B:705:MET:HE3	1.90	0.53
4:B:743:ILE:HG13	4:B:744:HIS:N	2.22	0.53
18:M:117:PRO:HG3	18:M:233:TYR:HA	1.91	0.53
3:a:512:VAL:HA	3:a:519:PRO:HA	1.90	0.53
3:a:791:ASP:OD2	3:a:792:TYR:N	2.41	0.53
4:b:530:GLY:O	4:b:531:GLN:HG3	2.08	0.53
4:b:917:PRO:HA	4:b:933:SER:O	2.08	0.53
6:d:139:LYS:NZ	6:d:143:ASN:OD1	2.42	0.53
10:h:130:ARG:HB2	10:h:133:ASN:HB2	1.89	0.53
3:A:537:ARG:NH1	3:A:602:ASP:OD2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:833:GLU:O	3:A:837:ILE:HD12	2.07	0.53
3:A:957:PRO:HG2	3:A:1018:PHE:CD1	2.44	0.53
4:B:620:ARG:NH1	11:I:57:GLY:HA3	2.23	0.53
4:B:957:ASN:OD1	4:B:960:GLY:N	2.42	0.53
11:I:26:LEU:HD13	11:I:37:GLU:HA	1.89	0.53
3:a:1053:PHE:O	3:a:1056:SER:OG	2.23	0.53
3:a:1357:ALA:HA	3:a:1361:SER:HB3	1.91	0.53
4:b:146:GLU:HG2	4:b:147:LEU:H	1.73	0.53
4:b:364:ILE:HG13	4:b:365:THR:N	2.23	0.53
5:c:240:VAL:O	5:c:243:VAL:HG22	2.08	0.53
9:g:6:ASP:OD2	9:g:75:ARG:NE	2.41	0.53
12:j:19:GLU:O	12:j:23:ASN:ND2	2.42	0.53
12:j:23:ASN:OD1	12:j:24:LEU:N	2.41	0.53
3:A:346:ASP:CG	4:B:1108:ARG:H	2.17	0.53
3:A:857:ARG:NH1	8:F:139:PRO:HG2	2.24	0.53
3:A:918:GLU:OE1	3:A:918:GLU:N	2.35	0.53
4:B:789:MET:HE2	4:B:789:MET:HA	1.90	0.53
4:B:860:MET:HB2	4:B:963:PHE:HE1	1.73	0.53
4:B:1041:GLU:N	17:Q:23:LYS:HZ1	2.07	0.53
5:C:50:GLU:HB2	5:C:156:THR:HB	1.89	0.53
7:E:48:ASP:OD1	7:E:49:SER:N	2.39	0.53
17:Q:98:TYR:CD1	17:Q:100:GLU:HG2	2.44	0.53
4:b:304:ASP:OD2	4:b:307:ASP:N	2.38	0.53
4:b:570:VAL:HG13	4:b:573:GLN:HB2	1.90	0.53
4:b:842:ASN:CG	4:b:845:SER:H	2.16	0.53
4:b:1203:LEU:HA	4:b:1206:GLU:OE2	2.09	0.53
5:c:46:ILE:HD13	5:c:67:LEU:HB3	1.90	0.53
11:i:10:CYS:O	11:i:12:ASN:N	2.42	0.53
3:A:1319:VAL:HG13	3:A:1322:ILE:HG13	1.89	0.53
4:B:830:TYR:CZ	4:B:1000:PRO:HD3	2.44	0.53
4:B:1031:LEU:HD21	4:B:1042:GLY:HA3	1.89	0.53
5:C:166:GLU:O	13:K:6:ARG:NH2	2.26	0.53
7:E:3:GLN:OE1	7:E:4:GLU:HG3	2.09	0.53
10:H:145:ARG:C	10:H:146:ARG:HD3	2.33	0.53
3:a:156:ASP:OD1	3:a:156:ASP:N	2.42	0.53
3:a:452:LYS:HZ1	4:b:1141:HIS:HA	1.74	0.53
3:a:568:PRO:HD2	3:a:569:LYS:H	1.73	0.53
4:b:611:PRO:HG2	4:b:685:LEU:HD21	1.90	0.53
9:g:94:CYS:HB3	9:g:127:PRO:HG2	1.90	0.53
3:A:225:ASN:O	3:A:229:SER:N	2.35	0.53
3:A:346:ASP:OD1	3:A:347:PHE:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1002:GLY:HA3	3:A:1007:ILE:HG21	1.91	0.53
4:B:355:ILE:O	4:B:359:GLU:HG3	2.09	0.53
4:B:384:ARG:HE	4:B:387:LEU:HD12	1.74	0.53
3:a:176:LYS:HA	3:a:181:LEU:HA	1.90	0.53
4:b:129:PHE:HA	4:b:167:ILE:HG12	1.91	0.53
4:b:371:GLU:OE1	4:b:371:GLU:N	2.36	0.53
4:b:1207:LEU:HD22	4:b:1214:PRO:HG3	1.91	0.53
5:c:162:GLY:HA3	5:c:170:TRP:CZ2	2.44	0.53
5:c:255:VAL:O	5:c:258:ILE:HG22	2.08	0.53
3:A:851:HIS:CD2	8:F:139:PRO:HG3	2.44	0.53
3:A:1359:ASP:N	3:A:1359:ASP:OD1	2.42	0.53
4:B:921:ASP:O	4:B:927:GLN:NE2	2.38	0.53
11:I:100:PHE:HB3	11:I:109:ILE:HD11	1.90	0.53
3:a:1142:THR:O	3:a:1145:SER:OG	2.22	0.53
4:b:574:SER:OG	4:b:591:ARG:NH2	2.42	0.53
5:c:101:LEU:HB3	5:c:155:LEU:HB2	1.91	0.53
3:A:381:THR:HG1	3:A:384:ASN:H	1.57	0.53
3:A:542:GLU:OE1	3:A:544:ASP:N	2.33	0.53
4:B:85:SER:O	4:B:87:LYS:N	2.42	0.53
4:B:1041:GLU:H	17:Q:23:LYS:HZ1	1.56	0.53
9:G:21:ARG:HH12	9:G:25:TYR:H	1.57	0.53
7:e:3:GLN:HE21	7:e:5:ASN:HB3	1.74	0.53
3:A:443:LEU:HB2	3:A:501:LEU:HD11	1.91	0.53
3:A:1111:MET:C	3:A:1113:THR:H	2.17	0.53
9:G:45:ILE:HG13	9:G:78:VAL:HG12	1.90	0.53
3:a:1161:THR:HG22	3:a:1163:ILE:H	1.74	0.52
3:A:315:LEU:HD23	3:A:315:LEU:H	1.73	0.52
3:A:336:ILE:HG22	3:A:341:MET:HE1	1.91	0.52
3:a:766:GLY:H	3:a:800:VAL:HB	1.74	0.52
3:A:851:HIS:CE1	3:A:857:ARG:HB2	2.43	0.52
3:a:457:ALA:N	3:a:505:CYS:O	2.29	0.52
3:a:808:LEU:HB2	4:b:760:ASP:HB2	1.89	0.52
3:a:1297:GLU:OE1	3:a:1297:GLU:N	2.42	0.52
4:b:113:TYR:HB2	4:b:116:GLU:HB3	1.90	0.52
4:b:1153:GLU:N	4:b:1153:GLU:OE1	2.43	0.52
6:d:33:PHE:CZ	9:g:80:LYS:HG2	2.44	0.52
7:e:2:ASP:O	7:e:7:ARG:NH1	2.34	0.52
7:E:100:ILE:HG23	7:E:105:PHE:HB2	1.90	0.52
10:H:118:PHE:O	10:H:120:GLY:N	2.42	0.52
11:I:7:CYS:HB3	11:I:10:CYS:O	2.09	0.52
17:Q:121:PHE:HB2	18:M:131:ASN:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:31:DA:H2''	1:N:32:DA:C8	2.45	0.52
2:O:-37:DT:H1'	2:O:-36:DT:H5'	1.90	0.52
3:a:644:LYS:O	3:a:648:ASN:ND2	2.42	0.52
4:b:58:THR:O	4:b:62:ILE:HG12	2.09	0.52
4:b:1076:HIS:HD2	13:k:40:HIS:CD2	2.27	0.52
9:g:3:PHE:HB2	9:g:80:LYS:NZ	2.25	0.52
3:A:113:LEU:O	3:A:164:ARG:NH2	2.42	0.52
3:A:387:ARG:HH21	3:A:437:MET:HE1	1.75	0.52
3:A:768:GLN:HE21	3:A:800:VAL:HG21	1.75	0.52
3:A:1035:TYR:HB3	3:A:1037:LEU:HD23	1.91	0.52
7:E:180:ARG:N	7:E:215:MET:OXT	2.42	0.52
2:O:-42:DA:OP1	4:b:857:ARG:NH2	2.43	0.52
3:a:60:SER:OG	3:a:64:ASN:O	2.14	0.52
3:a:367:PRO:HB3	3:a:466:SER:HA	1.91	0.52
3:a:877:HIS:CD2	3:a:1056:SER:HA	2.43	0.52
3:A:69:THR:HA	3:A:71:GLN:NE2	2.24	0.52
3:A:566:ILE:HB	10:H:96:VAL:HG23	1.92	0.52
3:A:1166:ASP:HA	3:A:1169:ILE:HD13	1.92	0.52
4:B:29:ASP:HB3	4:B:658:ILE:HD13	1.92	0.52
4:B:102:VAL:H	4:B:112:LEU:HD23	1.74	0.52
4:B:276:ILE:O	4:B:337:ARG:NH2	2.42	0.52
4:B:546:SER:OG	4:B:631:GLY:N	2.43	0.52
5:C:138:GLU:OE1	5:C:138:GLU:N	2.43	0.52
6:D:52:LEU:HD12	6:D:148:LEU:HD23	1.91	0.52
13:K:53:ASP:OD1	13:K:54:ARG:N	2.43	0.52
2:O:-19:DC:H2''	2:O:-18:DA:C8	2.44	0.52
8:f:70:LYS:O	8:f:71:GLU:HG3	2.10	0.52
3:A:386:ASP:N	3:A:386:ASP:OD1	2.39	0.52
3:A:1126:ALA:HA	3:A:1304:TRP:CD1	2.42	0.52
4:B:120:ARG:HG2	4:B:955:THR:HG21	1.92	0.52
4:B:747:MET:HA	4:B:747:MET:HE2	1.92	0.52
4:B:1080:LYS:HG2	5:C:180:TYR:OH	2.10	0.52
7:E:118:PRO:HA	7:E:121:MET:HG3	1.92	0.52
9:G:10:ASN:HA	9:G:71:ASN:HA	1.91	0.52
3:a:868:TYR:HD2	3:a:1058:VAL:HG11	1.73	0.52
3:a:874:ASP:OD1	3:a:875:ALA:N	2.43	0.52
4:b:394:ASP:OD1	4:b:395:GLN:N	2.41	0.52
5:c:76:ASP:OD2	5:c:128:ASN:N	2.43	0.52
5:c:254:LYS:O	5:c:257:SER:OG	2.23	0.52
10:h:135:LEU:O	10:h:137:GLN:N	2.43	0.52
4:B:580:VAL:HG22	4:B:624:LEU:HD23	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:922:GLU:HG2	4:B:926:GLY:HA3	1.92	0.52
9:G:116:PRO:HD3	9:G:163:ILE:HG13	1.91	0.52
1:N:17:DG:H2'	1:N:18:DT:C6	2.45	0.52
3:a:482:PHE:O	4:b:989:THR:HG22	2.10	0.52
4:b:79:THR:HA	4:b:81:SER:H	1.75	0.52
5:c:196:ASP:OD1	5:c:197:SER:N	2.43	0.52
5:c:217:ASP:N	5:c:217:ASP:OD1	2.42	0.52
6:d:40:HIS:CG	9:g:73:LYS:HD2	2.45	0.52
15:r:35:C:H2'	15:r:35:C:P	2.50	0.52
3:A:92:HIS:HB2	3:A:236:LEU:HD23	1.92	0.52
3:A:775:ILE:HD12	3:A:775:ILE:H	1.75	0.52
3:A:821:ARG:NH2	4:B:534:GLY:HA2	2.25	0.52
3:A:852:TYR:CD1	3:A:1060:PRO:HB2	2.45	0.52
4:B:604:ARG:NH2	4:B:613:VAL:O	2.43	0.52
4:B:1000:PRO:HB2	4:B:1072:MET:HE2	1.91	0.52
4:B:1065:GLN:NE2	4:B:1067:ARG:H	2.08	0.52
6:D:59:ILE:HG13	6:D:60:LYS:HD3	1.92	0.52
7:E:182:ASP:OD2	7:E:184:VAL:HG12	2.10	0.52
18:M:73:LEU:HD11	18:M:77:LEU:HD23	1.90	0.52
4:b:260:GLY:O	4:b:267:ARG:NH2	2.36	0.52
4:b:295:GLY:N	11:i:11:ASN:O	2.43	0.52
6:d:126:ILE:HA	6:d:129:LEU:HD13	1.92	0.52
10:h:93:TYR:HB3	10:h:145:ARG:NH2	2.22	0.52
10:h:124:ARG:NE	10:h:126:GLU:OE2	2.29	0.52
4:B:245:GLU:N	4:B:246:LYS:HA	2.24	0.52
4:B:640:VAL:HA	4:B:651:LEU:HA	1.91	0.52
4:B:745:PRO:HB2	4:B:1047:PHE:HD2	1.75	0.52
3:a:531:ILE:O	3:a:535:THR:HG22	2.10	0.52
3:a:871:ASP:OD1	3:a:872:GLY:N	2.43	0.52
3:a:1100:ARG:CZ	3:a:1104:ILE:HD11	2.39	0.52
3:a:1312:ASN:ND2	3:a:1315:GLU:OE2	2.43	0.52
4:b:706:GLN:OE1	4:b:707:PRO:HD2	2.09	0.52
4:b:1006:ILE:HD12	12:j:45:CYS:HB3	1.92	0.52
5:c:230:MET:N	5:c:230:MET:SD	2.83	0.52
3:A:108:MET:SD	3:A:171:GLN:HG3	2.50	0.52
3:A:903:ASN:O	3:A:907:THR:OG1	2.28	0.52
7:E:40:GLU:OE1	7:E:40:GLU:N	2.43	0.52
7:E:170:LEU:HD12	7:E:174:GLN:HB2	1.92	0.52
12:J:20:SER:HA	12:J:23:ASN:HD21	1.74	0.52
17:Q:116:THR:HG22	18:M:136:THR:HG22	1.92	0.52
3:a:14:VAL:HB	3:a:1430:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:285:PRO:HB2	3:a:287:HIS:NE2	2.24	0.51
4:b:78:THR:HG23	4:b:79:THR:H	1.74	0.51
4:b:651:LEU:HD23	4:b:651:LEU:H	1.75	0.51
6:d:206:GLU:O	6:d:209:ARG:HG3	2.09	0.51
10:h:33:GLN:HG3	10:h:35:GLN:H	1.74	0.51
3:A:590:ARG:NH1	3:A:621:THR:OG1	2.43	0.51
4:B:73:GLN:HA	17:Q:330:ARG:NH2	2.25	0.51
4:B:867:GLY:HA3	4:B:868:MET:O	2.10	0.51
6:D:57:LEU:HD13	6:D:157:GLN:HG2	1.91	0.51
3:a:311:GLN:CG	3:a:312:PRO:HD3	2.35	0.51
3:a:1359:ASP:N	3:a:1359:ASP:OD1	2.42	0.51
4:b:1000:PRO:HB2	4:b:1072:MET:HE3	1.92	0.51
10:h:43:ASN:ND2	10:h:46:LEU:HD13	2.25	0.51
3:A:172:PRO:HG3	3:A:185:TRP:CE2	2.46	0.51
3:A:1364:ASN:OD1	3:A:1365:TYR:N	2.43	0.51
4:B:129:PHE:HB3	4:B:166:PHE:HA	1.90	0.51
5:C:255:VAL:O	5:C:258:ILE:HG22	2.10	0.51
2:O:-2:DA:H2''	2:O:-1:DG:C8	2.45	0.51
3:a:169:ASN:OD1	3:a:170:THR:N	2.36	0.51
3:a:424:ILE:HG22	3:a:426:LEU:HD12	1.91	0.51
3:a:529:CYS:SG	3:a:533:LYS:NZ	2.83	0.51
3:a:1031:VAL:HG12	3:a:1032:LEU:HD23	1.91	0.51
3:a:1063:MET:HE2	3:a:1436:ILE:HA	1.92	0.51
4:b:100:PRO:O	4:b:101:MET:HE2	2.10	0.51
4:b:911:ILE:HG21	4:b:966:VAL:HG21	1.92	0.51
12:j:20:SER:HA	12:j:23:ASN:HD21	1.74	0.51
3:A:368:LYS:NZ	13:K:4:PRO:HD3	2.25	0.51
3:A:1074:GLU:HG3	3:A:1075:PRO:HD3	1.91	0.51
3:a:120:GLU:HG3	3:a:123:ARG:NH2	2.25	0.51
3:a:566:ILE:HD13	10:h:96:VAL:HG12	1.91	0.51
3:a:1329:THR:HB	3:a:1335:ILE:HD11	1.92	0.51
4:b:1181:GLU:OE2	4:b:1187:ASN:N	2.43	0.51
4:B:391:ASP:OD2	11:I:90:GLN:NE2	2.44	0.51
8:F:93:ILE:HD11	8:F:132:LEU:HG	1.92	0.51
10:H:33:GLN:OE1	10:H:34:ASP:N	2.43	0.51
13:K:110:ASN:HA	13:K:113:THR:HG23	1.93	0.51
3:a:351:THR:OG1	3:a:352:VAL:N	2.43	0.51
3:a:682:THR:O	3:a:685:GLU:HG3	2.10	0.51
3:a:1373:ASP:O	3:a:1377:THR:HG23	2.10	0.51
4:b:431:TYR:HD2	4:b:445:LYS:HE3	1.76	0.51
4:b:494:HIS:HA	4:b:497:ARG:NH1	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:643:ASP:N	4:b:643:ASP:OD1	2.41	0.51
4:b:867:GLY:HA3	4:b:868:MET:C	2.36	0.51
5:c:238:ILE:HD12	5:c:239:PRO:HD2	1.92	0.51
10:h:128:ASN:ND2	10:h:131:ASN:OD1	2.44	0.51
10:h:130:ARG:HD3	10:h:130:ARG:H	1.75	0.51
3:A:993:LEU:HD21	3:A:1046:LEU:HB3	1.92	0.51
3:A:1373:ASP:HA	3:A:1376:THR:HG22	1.92	0.51
4:B:809:MET:HG3	4:B:814:PHE:HD1	1.76	0.51
5:C:15:LYS:NZ	5:C:135:GLN:OE1	2.36	0.51
5:C:161:LYS:O	5:C:170:TRP:NE1	2.44	0.51
17:Q:129:PRO:HA	17:Q:133:PHE:CD1	2.45	0.51
18:M:73:LEU:HD12	18:M:74:PRO:HD2	1.92	0.51
18:M:96:ARG:NH2	18:M:98:ASN:OD1	2.42	0.51
3:a:726:ARG:NH1	3:a:765:VAL:O	2.41	0.51
4:b:779:GLY:O	4:b:795:ILE:HA	2.11	0.51
4:b:1198:TYR:O	4:b:1201:LYS:HG3	2.09	0.51
10:h:93:TYR:HB3	10:h:145:ARG:HE	1.76	0.51
3:A:106:VAL:HG21	3:A:214:ILE:HD12	1.91	0.51
3:A:567:LYS:HE3	10:H:95:TYR:HD1	1.75	0.51
17:Q:404:LEU:HB3	17:Q:408:GLU:OE2	2.10	0.51
3:a:35:ILE:HD13	3:a:241:VAL:HG21	1.92	0.51
3:a:566:ILE:HB	10:h:96:VAL:HB	1.93	0.51
3:a:631:HIS:NE2	3:a:879:GLU:OE2	2.38	0.51
3:a:852:TYR:HD2	8:f:136:ARG:HG3	1.76	0.51
3:a:1121:GLU:HG3	3:a:1123:GLY:H	1.76	0.51
4:b:328:GLU:OE1	4:b:328:GLU:N	2.35	0.51
4:b:546:SER:OG	4:b:632:ARG:N	2.32	0.51
5:c:22:LEU:HG	5:c:25:VAL:HG21	1.92	0.51
10:h:63:LEU:HD13	10:h:141:TYR:CD2	2.44	0.51
10:h:118:PHE:O	10:h:120:GLY:N	2.44	0.51
3:A:862:ASN:HA	7:E:174:GLN:HB3	1.92	0.51
3:A:942:PHE:HD2	3:A:943:LEU:HD22	1.75	0.51
4:B:62:ILE:HD13	4:B:417:PHE:HD2	1.75	0.51
4:B:189:LEU:HD21	4:B:196:PRO:HA	1.91	0.51
4:B:406:LEU:HB2	4:B:545:ILE:HD11	1.93	0.51
4:B:806:THR:H	4:B:809:MET:HE1	1.75	0.51
3:a:18:GLN:O	4:b:1215:ARG:N	2.44	0.51
4:b:260:GLY:C	4:b:267:ARG:HH22	2.18	0.51
4:b:1093:GLN:OE1	4:b:1093:GLN:N	2.43	0.51
3:A:1215:ARG:O	3:A:1218:GLN:NE2	2.43	0.51
14:L:31:CYS:HB2	14:L:48:CYS:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:1112:GLN:HG3	4:b:1114:LEU:H	1.76	0.51
9:g:111:THR:HG22	9:g:114:LEU:HG	1.92	0.51
10:h:129:TYR:CZ	10:h:130:ARG:HD2	2.46	0.51
11:i:17:ARG:HG3	11:i:28:GLU:HB3	1.92	0.51
3:A:40:THR:HB	3:A:54:ASN:HB2	1.92	0.51
7:E:96:PHE:CZ	7:E:100:ILE:HD11	2.45	0.51
11:I:17:ARG:N	11:I:26:LEU:O	2.37	0.51
17:Q:386:MET:HE3	18:M:87:LEU:HD13	1.93	0.51
3:a:192:GLY:HA3	3:a:196:GLU:HB3	1.93	0.51
3:a:376:TYR:OH	3:a:495:GLU:OE2	2.26	0.51
4:b:38:PHE:CD2	4:b:811:TYR:HB3	2.46	0.51
6:d:14:ARG:O	6:d:17:LYS:HG2	2.12	0.51
8:f:147:SER:O	8:f:150:GLU:HG2	2.11	0.51
13:k:81:TYR:CE2	13:k:86:ALA:HB2	2.45	0.51
3:A:311:GLN:CG	3:A:312:PRO:HD3	2.41	0.51
3:A:348:SER:HB3	4:B:1128:LEU:HD12	1.93	0.51
3:a:335:ARG:HA	3:a:339:ASN:HB2	1.92	0.50
3:a:1063:MET:CE	3:a:1436:ILE:HA	2.41	0.50
10:h:100:THR:O	10:h:117:SER:N	2.32	0.50
3:A:1199:ARG:HD3	3:A:1236:LEU:HD11	1.93	0.50
17:Q:97:GLU:HA	18:M:99:LYS:HE3	1.92	0.50
3:a:1284:MET:C	3:a:1285:MET:HE2	2.36	0.50
4:b:1065:GLN:NE2	4:b:1067:ARG:H	2.09	0.50
5:c:69:LEU:HG	12:j:6:ARG:HD2	1.91	0.50
9:g:45:ILE:HG23	9:g:78:VAL:HG22	1.93	0.50
3:A:653:VAL:O	3:A:657:LEU:HD23	2.10	0.50
3:A:1116:LEU:HD23	3:A:1311:VAL:HA	1.92	0.50
3:A:1173:HIS:CE1	3:A:1227:ILE:HG23	2.47	0.50
4:B:79:THR:CB	4:B:81:SER:H	2.24	0.50
4:B:212:LEU:HD11	4:B:409:ALA:HB2	1.94	0.50
17:Q:390:ASP:OD1	17:Q:391:LYS:N	2.44	0.50
3:a:172:PRO:HG3	3:a:185:TRP:CZ2	2.47	0.50
3:a:385:ILE:O	3:a:389:THR:OG1	2.24	0.50
3:a:1173:HIS:CE1	3:a:1227:ILE:HG23	2.46	0.50
4:b:809:MET:O	4:b:812:LEU:N	2.44	0.50
4:b:878:GLN:N	4:b:878:GLN:OE1	2.43	0.50
3:A:909:ASP:HB3	3:A:912:LEU:HD13	1.92	0.50
4:B:247:GLY:O	4:B:249:ARG:N	2.44	0.50
4:B:1166:CYS:HB3	4:B:1168:LEU:HD23	1.93	0.50
5:C:6:PRO:HG2	13:K:101:LEU:HB2	1.94	0.50
10:H:137:GLN:OE1	10:H:139:ASN:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:266:LEU:O	3:a:269:ILE:HG22	2.12	0.50
3:a:353:ILE:HG21	3:a:487:MET:HE1	1.93	0.50
3:a:912:LEU:O	3:a:979:SER:N	2.43	0.50
3:a:940:ARG:NH2	3:a:944:ARG:HH21	2.06	0.50
4:b:1110:PRO:O	4:b:1111:MET:HE2	2.12	0.50
6:d:56:ARG:NE	6:d:157:GLN:OE1	2.44	0.50
11:i:5:ARG:HE	11:i:6:PHE:H	1.58	0.50
12:j:9:SER:OG	12:j:45:CYS:HB2	2.10	0.50
3:A:1165:GLU:OE1	3:A:1165:GLU:N	2.44	0.50
4:B:25:ILE:HG23	4:B:29:ASP:HB2	1.94	0.50
4:B:195:CYS:HB3	4:B:782:LEU:HD22	1.93	0.50
4:B:648:HIS:CD2	4:B:648:HIS:H	2.29	0.50
7:E:43:LYS:HE3	7:E:47:CYS:HB2	1.93	0.50
3:a:427:GLN:OE1	3:a:427:GLN:N	2.37	0.50
3:a:827:THR:HA	3:a:830:LYS:HG2	1.92	0.50
4:b:803:LEU:HD22	12:j:52:THR:HG21	1.94	0.50
4:b:892:LYS:HZ3	4:b:905:VAL:HA	1.76	0.50
11:i:73:ARG:HH12	11:i:112:SER:HA	1.76	0.50
11:i:103:CYS:SG	11:i:105:SER:OG	2.69	0.50
12:j:36:LEU:HD22	12:j:47:ARG:HG3	1.94	0.50
4:B:216:GLU:HG2	4:B:500:THR:HB	1.92	0.50
4:B:360:PHE:CE2	4:B:374:LYS:HD2	2.46	0.50
3:a:446:ARG:HD2	3:a:447:GLN:O	2.12	0.50
3:a:543:LEU:O	3:a:547:LEU:HG	2.12	0.50
5:c:99:LEU:O	5:c:157:CYS:N	2.30	0.50
6:d:131:GLU:HG3	6:d:136:GLY:H	1.77	0.50
8:f:112:GLU:HG2	8:f:123:LYS:NZ	2.27	0.50
4:B:171:PRO:HG2	4:B:461:LEU:HD12	1.92	0.50
4:B:360:PHE:HE2	4:B:374:LYS:HD2	1.76	0.50
10:H:13:SER:OG	10:H:27:GLU:OE2	2.28	0.50
10:H:37:LYS:H	10:H:126:GLU:HB2	1.76	0.50
16:R:12:A:H2'	16:R:13:U:C6	2.47	0.50
3:a:557:ASP:HA	13:k:26:LYS:HE3	1.94	0.50
3:a:993:LEU:HG	3:a:1046:LEU:HD22	1.92	0.50
4:b:420:LEU:HB3	4:b:453:ILE:HD12	1.93	0.50
5:c:66:ARG:HD2	12:j:2:ILE:HD11	1.94	0.50
9:g:21:ARG:NH1	9:g:25:TYR:HB2	2.26	0.50
10:h:94:ASP:H	10:h:145:ARG:NE	2.10	0.50
3:A:864:ILE:HD12	3:A:1377:THR:HG21	1.94	0.50
5:C:35:ARG:HA	5:C:38:ILE:HG22	1.94	0.50
7:E:141:VAL:HG13	7:E:142:VAL:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:140:ASP:OD1	8:F:141:GLY:N	2.45	0.50
17:Q:17:ASN:HB3	17:Q:20:PRO:HD3	1.93	0.50
3:a:232:GLU:OE2	3:a:233:TRP:NE1	2.45	0.50
3:a:242:PRO:C	3:a:247:ARG:HH12	2.17	0.50
3:a:853:ASP:HB3	3:a:855:THR:HG22	1.93	0.50
4:b:446:LEU:HA	4:b:449:ASN:HD22	1.77	0.50
4:b:1045:SER:O	4:b:1047:PHE:N	2.45	0.50
7:e:109:ILE:HG13	7:e:133:GLU:OE2	2.11	0.50
3:A:66:LYS:HE2	3:A:69:THR:HG23	1.92	0.50
3:A:171:GLN:N	3:A:171:GLN:OE1	2.44	0.50
4:B:526:GLU:OE2	4:B:752:ALA:N	2.45	0.50
4:B:604:ARG:NH2	4:B:614:SER:HA	2.27	0.50
4:B:604:ARG:HH22	4:B:614:SER:HA	1.77	0.50
7:E:87:SER:OG	7:E:88:VAL:N	2.43	0.50
9:G:96:GLN:HA	9:G:128:PRO:HB2	1.93	0.50
3:a:18:GLN:OE1	3:a:19:PHE:N	2.44	0.50
3:a:779:PHE:CZ	4:b:517:THR:HA	2.47	0.50
4:b:653:VAL:HG22	4:b:689:LEU:HD13	1.94	0.50
4:b:708:GLU:HA	4:b:711:GLU:HG2	1.93	0.50
10:h:81:PRO:HB2	13:k:54:ARG:HH22	1.77	0.50
10:h:101:ALA:HB2	10:h:116:TYR:CE1	2.47	0.50
3:A:446:ARG:HB2	3:A:487:MET:SD	2.52	0.50
4:B:980:PHE:CE1	4:B:1094:ARG:HG3	2.46	0.50
7:E:180:ARG:NH2	7:E:192:ARG:HB2	2.27	0.50
10:H:26:ILE:N	10:H:40:LEU:O	2.38	0.50
2:O:-12:DT:OP2	3:A:332:LYS:NZ	2.45	0.49
4:b:773:MET:HE1	4:b:987:LYS:HD3	1.93	0.49
10:h:10:PHE:CE2	10:h:38:LEU:HB2	2.47	0.49
3:A:325:ILE:HG13	4:B:1210:MET:CE	2.42	0.49
3:A:665:GLY:O	3:A:668:ASP:HB2	2.12	0.49
3:A:1157:ASP:OD1	3:A:1160:SER:N	2.45	0.49
4:B:800:GLN:OE1	12:J:53:HIS:HA	2.12	0.49
5:C:66:ARG:NH2	12:J:5:VAL:HG23	2.27	0.49
10:H:95:TYR:HB3	10:H:144:ILE:HB	1.94	0.49
3:a:119:ASN:O	3:a:123:ARG:NH1	2.45	0.49
3:a:647:GLY:O	3:a:651:LYS:HB2	2.12	0.49
3:a:804:TYR:O	4:b:761:HIS:ND1	2.39	0.49
4:b:394:ASP:HB2	11:i:91:ARG:NH2	2.24	0.49
4:b:551:PRO:HB3	4:b:628:THR:HG21	1.93	0.49
4:B:445:LYS:NZ	4:B:449:ASN:OD1	2.38	0.49
4:B:900:ALA:HB1	14:L:61:THR:OG1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:73:GLN:OE1	5:C:74:SER:N	2.45	0.49
5:C:258:ILE:HD11	13:K:35:PHE:CZ	2.47	0.49
7:E:106:GLN:HG2	7:E:107:THR:HG23	1.92	0.49
8:F:97:ARG:O	8:F:101:ILE:HG12	2.12	0.49
10:H:105:GLU:O	10:H:113:ALA:N	2.41	0.49
11:I:113:ASP:OD1	11:I:115:LYS:NZ	2.40	0.49
2:O:2:DC:H2"	2:O:3:DA:C8	2.48	0.49
3:a:43:GLU:HG2	3:a:44:THR:N	2.27	0.49
3:a:91:PHE:N	3:a:297:GLN:HE22	2.10	0.49
3:a:591:PHE:HA	3:a:595:THR:HG21	1.93	0.49
3:a:1004:ASN:ND2	7:e:167:ARG:HD2	2.27	0.49
4:b:351:TYR:CE2	4:b:355:ILE:HD11	2.47	0.49
4:b:428:ILE:O	4:b:432:MET:HE3	2.12	0.49
4:b:766:ARG:NH1	4:b:1020:ARG:HD3	2.28	0.49
5:c:37:MET:HE1	5:c:244:VAL:HA	1.95	0.49
5:c:161:LYS:O	5:c:170:TRP:NE1	2.45	0.49
11:i:75:CYS:SG	11:i:79:HIS:N	2.85	0.49
4:B:123:THR:O	4:B:125:SER:N	2.45	0.49
4:B:582:VAL:HG22	4:B:626:ILE:HB	1.93	0.49
5:C:7:GLN:HA	13:K:104:ASN:ND2	2.27	0.49
2:O:-33:DT:H2"	2:O:-32:DT:C6	2.47	0.49
3:a:546:VAL:HG23	3:a:577:ILE:HD12	1.94	0.49
3:a:567:LYS:CG	3:a:568:PRO:HD3	2.42	0.49
3:a:598:LEU:O	10:h:25:ARG:NH2	2.45	0.49
3:a:991:LYS:HA	3:a:994:GLN:HG2	1.94	0.49
4:b:1112:GLN:HB3	4:b:1117:GLN:H	1.77	0.49
3:A:589:GLN:HB3	3:A:591:PHE:CE2	2.45	0.49
3:A:675:THR:HG21	3:A:736:ASN:HB2	1.95	0.49
4:B:793:ALA:HB3	4:B:856:PHE:HB2	1.94	0.49
6:D:31:GLN:O	6:D:34:GLN:NE2	2.44	0.49
1:N:53:DT:H2"	1:N:54:DG:H8	1.77	0.49
3:a:899:VAL:HG13	3:a:929:LEU:HD23	1.95	0.49
4:b:1033:LYS:HD3	4:b:1059:LEU:HD11	1.94	0.49
5:c:175:ALA:HB3	5:c:233:GLU:HB3	1.95	0.49
5:c:259:LEU:O	5:c:262:LEU:HG	2.12	0.49
8:f:135:ARG:HD2	8:f:143:PHE:CD2	2.47	0.49
3:A:147:VAL:HG23	3:A:170:THR:HG22	1.93	0.49
3:A:232:GLU:OE1	3:A:232:GLU:N	2.43	0.49
3:A:402:ALA:HA	3:A:434:ARG:HA	1.94	0.49
3:A:509:LEU:HD23	3:A:509:LEU:H	1.78	0.49
3:A:668:ASP:OD2	3:A:742:ASN:HB2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:811:GLN:H	3:A:811:GLN:CD	2.19	0.49
3:A:1430:LEU:HB3	3:A:1432:GLN:NE2	2.23	0.49
4:B:373:ARG:NE	4:B:566:LEU:HB2	2.28	0.49
4:B:563:MET:HE2	4:B:563:MET:HA	1.94	0.49
5:C:102:GLN:HE22	5:C:154:LYS:HA	1.78	0.49
6:D:14:ARG:O	6:D:17:LYS:HG3	2.12	0.49
12:J:9:SER:HB2	12:J:45:CYS:HB2	1.94	0.49
3:a:185:TRP:CD1	3:a:187:LYS:HE2	2.46	0.49
3:a:559:VAL:HA	10:h:78:SER:OG	2.13	0.49
6:d:144:THR:O	6:d:148:LEU:N	2.46	0.49
3:A:877:HIS:CD2	3:A:1056:SER:HA	2.46	0.49
3:A:1138:ILE:HD11	3:A:1316:VAL:HG12	1.93	0.49
3:A:1277:GLU:OE1	3:A:1277:GLU:N	2.39	0.49
4:B:217:ARG:NE	4:B:407:ASP:OD2	2.35	0.49
4:B:327:ARG:HG3	4:B:328:GLU:OE1	2.13	0.49
4:B:910:VAL:HA	4:B:940:PRO:HA	1.93	0.49
7:E:21:GLU:OE2	7:E:143:ASN:ND2	2.46	0.49
11:I:76:PRO:O	11:I:77:LYS:HD3	2.12	0.49
1:N:17:DG:H2'	1:N:18:DT:H71	1.95	0.49
3:a:1000:LEU:N	3:a:1011:GLN:OE1	2.44	0.49
3:a:1419:ASP:OD1	3:a:1420:ASP:N	2.46	0.49
5:c:59:ALA:O	5:c:63:ILE:HG12	2.13	0.49
3:A:399:HIS:O	3:A:401:GLY:N	2.45	0.49
3:A:711:ARG:CZ	11:I:97:MET:HE1	2.43	0.49
3:A:808:LEU:O	4:B:728:ARG:NH1	2.46	0.49
4:B:121:ASN:HA	4:B:207:GLY:HA3	1.94	0.49
4:B:325:GLN:O	17:Q:401:TYR:OH	2.30	0.49
4:B:992:ILE:HD11	4:B:994:TYR:CZ	2.47	0.49
5:C:146:LYS:HD2	12:J:57:ILE:HD12	1.95	0.49
6:D:53:SER:O	6:D:57:LEU:HG	2.12	0.49
11:I:44:TYR:OH	11:I:46:HIS:ND1	2.40	0.49
3:a:55:ASP:OD1	3:a:58:LEU:N	2.46	0.49
4:b:954:VAL:HG23	4:b:964:VAL:HG22	1.94	0.49
3:A:35:ILE:H	3:A:35:ILE:HD12	1.78	0.49
3:A:766:GLY:HA2	3:A:799:PHE:HE1	1.78	0.49
4:B:822:ASN:HA	4:B:1091:TYR:HA	1.94	0.49
1:N:65:DA:H61	2:O:-65:DC:H42	0.69	0.49
3:a:871:ASP:CG	3:a:873:MET:H	2.21	0.49
4:b:700:SER:O	4:b:700:SER:OG	2.28	0.49
4:b:797:TYR:O	12:j:1:MET:HE2	2.13	0.49
9:g:147:ILE:HG23	9:g:159:ALA:HB1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:i:5:ARG:HB3	11:i:14:LEU:HB2	1.93	0.49
4:B:260:GLY:O	4:B:267:ARG:NH2	2.38	0.49
3:a:96:ILE:O	3:a:99:ILE:HG22	2.13	0.49
3:a:210:ILE:O	3:a:214:ILE:HD12	2.12	0.49
3:a:632:VAL:HG13	3:a:962:ARG:HD3	1.94	0.49
3:a:949:ASP:OD1	3:a:950:GLY:N	2.45	0.49
4:b:309:GLN:OE1	4:b:392:ARG:NH2	2.43	0.49
4:b:805:THR:OG1	4:b:809:MET:HE3	2.12	0.49
4:b:872:GLU:HG2	4:b:916:THR:HA	1.94	0.49
4:B:336:ARG:HG3	4:B:337:ARG:H	1.78	0.49
5:C:252:GLN:HB3	13:K:98:LEU:HD13	1.95	0.49
6:D:55:ALA:HA	6:D:58:VAL:HG22	1.95	0.49
3:a:46:THR:O	3:a:47:ARG:HG2	2.12	0.48
3:a:149:GLU:O	3:a:165:GLY:HA3	2.12	0.48
3:a:573:SER:HB3	3:a:576:GLN:HB2	1.94	0.48
4:b:759:PRO:HD2	4:b:1046:PRO:HB3	1.95	0.48
4:b:760:ASP:OD1	4:b:761:HIS:N	2.46	0.48
4:b:850:LEU:HG	4:b:851:PHE:CD1	2.48	0.48
4:b:865:LYS:NZ	4:b:869:SER:HB2	2.28	0.48
3:A:65:LEU:O	3:A:71:GLN:HA	2.13	0.48
3:A:594:GLY:HA3	3:A:603:ASN:HD21	1.77	0.48
4:B:20:ASP:OD1	4:B:22:SER:N	2.41	0.48
4:B:1196:ILE:HD12	4:B:1197:PRO:HD2	1.94	0.48
6:D:53:SER:OG	6:D:152:SER:HB3	2.13	0.48
11:I:54:GLU:HB2	11:I:100:PHE:CE2	2.48	0.48
3:a:38:PRO:HA	3:a:270:LEU:HD23	1.95	0.48
3:a:802:ASN:HB3	3:a:806:ARG:HD2	1.95	0.48
4:b:411:PRO:O	4:b:415:GLN:HG2	2.14	0.48
4:b:582:VAL:HA	4:b:626:ILE:HB	1.94	0.48
5:c:34:ARG:HG2	5:c:176:ILE:HD13	1.95	0.48
6:d:69:ALA:HA	6:d:72:ARG:HE	1.78	0.48
10:h:118:PHE:HB2	10:h:121:LEU:HB2	1.94	0.48
3:A:108:MET:C	3:A:110:CYS:H	2.21	0.48
3:A:261:ASP:OD1	3:A:322:VAL:HG23	2.13	0.48
4:B:190:TYR:CE2	4:B:196:PRO:HD3	2.43	0.48
4:B:868:MET:O	4:B:870:ILE:N	2.47	0.48
6:D:216:ASN:OD1	6:D:217:LEU:N	2.46	0.48
10:H:137:GLN:CD	10:H:138:GLU:H	2.20	0.48
3:a:446:ARG:NH2	3:a:478:TYR:O	2.47	0.48
3:a:914:GLU:HG2	3:a:979:SER:O	2.12	0.48
3:a:943:LEU:HA	3:a:946:VAL:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:1094:VAL:HG13	3:a:1113:THR:HG21	1.94	0.48
4:b:806:THR:HB	4:b:1044:ALA:HB3	1.95	0.48
6:d:142:LYS:O	6:d:146:GLN:N	2.35	0.48
7:e:29:PHE:CE2	7:e:65:THR:HA	2.48	0.48
9:g:3:PHE:HB2	9:g:80:LYS:HZ3	1.77	0.48
3:A:5:GLN:HG3	4:B:1175:LEU:HD13	1.95	0.48
3:A:1332:PHE:HA	3:A:1335:ILE:HD13	1.94	0.48
3:A:1426:GLU:OE2	3:A:1426:GLU:N	2.39	0.48
4:B:104:GLU:OE1	4:B:104:GLU:N	2.43	0.48
8:F:97:ARG:HD2	8:F:100:GLN:NE2	2.25	0.48
9:G:125:SER:HB3	9:G:128:PRO:HA	1.95	0.48
3:a:81:PHE:CE1	3:a:243:PRO:HD3	2.48	0.48
3:a:81:PHE:HE1	3:a:243:PRO:HD3	1.78	0.48
3:a:114:LEU:HD11	3:a:171:GLN:NE2	2.27	0.48
3:a:666:ILE:H	3:a:666:ILE:HD12	1.78	0.48
3:a:862:ASN:HA	7:e:174:GLN:HB3	1.94	0.48
4:b:874:PHE:HE1	4:b:914:LYS:HE2	1.79	0.48
4:b:1205:GLN:HA	4:b:1208:MET:SD	2.54	0.48
9:g:110:VAL:HG11	9:g:163:ILE:HD11	1.95	0.48
13:k:12:LEU:HD23	13:k:12:LEU:H	1.77	0.48
3:A:456:MET:HE2	3:A:478:TYR:CZ	2.49	0.48
4:B:247:GLY:C	4:B:249:ARG:H	2.20	0.48
4:B:400:HIS:CE1	4:B:402:GLY:H	2.31	0.48
4:B:1171:VAL:HG11	4:B:1191:ILE:HD13	1.94	0.48
5:C:54:ASN:ND2	5:C:60:ASP:OD1	2.23	0.48
1:N:-6:DT:H2''	1:N:-5:DA:C8	2.48	0.48
1:N:41:DT:H5''	4:b:426:LYS:NZ	2.28	0.48
3:a:185:TRP:HA	3:a:187:LYS:NZ	2.29	0.48
3:a:449:SER:H	4:b:1133:MET:HE2	1.78	0.48
3:a:768:GLN:HE21	3:a:816:HIS:HA	1.77	0.48
3:a:1198:ASP:OD2	3:a:1201:ALA:N	2.46	0.48
4:b:252:SER:HB3	4:b:362:PRO:HG2	1.95	0.48
4:b:546:SER:OG	4:b:631:GLY:N	2.47	0.48
4:b:1106:ARG:NH1	4:b:1109:GLY:H	2.11	0.48
11:i:74:GLU:OE2	11:i:81:ARG:HD3	2.12	0.48
15:r:35:C:H3'	15:r:35:C:OP1	2.13	0.48
3:A:802:ASN:ND2	3:A:806:ARG:HB2	2.17	0.48
4:B:211:VAL:HG21	4:B:483:LEU:HD13	1.95	0.48
6:D:67:ARG:NE	6:D:129:LEU:HD22	2.29	0.48
1:N:47:DT:H2''	1:N:48:DT:C5	2.48	0.48
3:a:219:PHE:O	3:a:223:GLY:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:843:LYS:HD3	3:a:846:GLU:OE1	2.14	0.48
4:b:85:SER:HB3	4:b:139:ALA:N	2.18	0.48
4:b:445:LYS:O	4:b:448:ILE:HG22	2.13	0.48
5:c:55:THR:CG2	5:c:152:GLU:H	2.27	0.48
9:g:46:LEU:HG	9:g:77:VAL:O	2.14	0.48
9:g:129:SER:O	9:g:135:ASP:HB3	2.13	0.48
13:k:21:ILE:HG22	13:k:33:ILE:HD12	1.95	0.48
3:A:619:LYS:NZ	16:R:18:A:OP2	2.42	0.48
4:B:78:THR:HG23	4:B:79:THR:H	1.78	0.48
4:B:522:VAL:HG21	4:B:537:LYS:HB2	1.95	0.48
5:C:99:LEU:HD11	5:C:120:ILE:HD13	1.94	0.48
7:E:20:LYS:HD2	7:E:35:VAL:HA	1.95	0.48
2:O:-14:DT:OP1	2:O:-14:DT:H4'	2.13	0.48
3:a:567:LYS:HG2	3:a:568:PRO:HD3	1.95	0.48
3:a:794:PRO:HB2	3:a:799:PHE:HB3	1.96	0.48
3:a:1041:ALA:O	3:a:1045:VAL:HG13	2.13	0.48
3:a:1288:ASP:HA	3:a:1302:PRO:HA	1.95	0.48
4:b:210:LYS:HZ3	4:b:211:VAL:H	1.60	0.48
4:b:276:ILE:HG23	4:b:335:GLY:HA3	1.96	0.48
4:b:1045:SER:OG	4:b:1048:THR:OG1	2.17	0.48
5:c:166:GLU:HA	13:k:9:LEU:HD21	1.94	0.48
6:d:139:LYS:HG3	6:d:143:ASN:HD21	1.78	0.48
12:j:17:LYS:HB3	12:j:39:LEU:HD11	1.95	0.48
13:k:7:PHE:HB2	13:k:11:LEU:HD12	1.95	0.48
3:A:115:LEU:HA	3:A:164:ARG:HH12	1.78	0.48
3:A:118:HIS:HA	3:A:123:ARG:NH2	2.29	0.48
3:A:1077:THR:OG1	3:A:1078:GLN:OE1	2.29	0.48
3:A:1443:VAL:HG12	9:G:61:ILE:HD13	1.94	0.48
4:B:256:VAL:HG21	4:B:381:MET:HE1	1.95	0.48
4:B:706:GLN:OE1	4:B:707:PRO:HD2	2.14	0.48
9:G:6:ASP:HA	9:G:75:ARG:HA	1.96	0.48
13:K:24:ASP:OD1	13:K:25:THR:N	2.46	0.48
18:M:239:GLN:O	18:M:243:ILE:HG12	2.13	0.48
2:O:-57:DA:H2''	2:O:-56:DA:C8	2.49	0.48
3:a:446:ARG:HB2	3:a:487:MET:HG3	1.96	0.48
3:a:757:ASN:HB3	4:b:1021:MET:HE1	1.94	0.48
3:a:1342:GLU:O	3:a:1345:ARG:HG2	2.14	0.48
4:b:561:TRP:O	4:b:595:ARG:NH1	2.34	0.48
4:b:641:GLU:N	4:b:641:GLU:OE1	2.47	0.48
4:b:901:PRO:HA	4:b:949:VAL:HG12	1.94	0.48
4:b:923:GLU:C	4:b:928:ARG:HH22	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:1171:VAL:HG12	4:b:1182:CYS:HB2	1.95	0.48
5:c:73:GLN:HE22	5:c:75:MET:HE3	1.79	0.48
11:i:13:MET:HE1	11:i:15:TYR:HA	1.96	0.48
3:A:744:LYS:O	3:A:748:MET:HG3	2.13	0.48
3:A:972:HIS:ND1	3:A:972:HIS:O	2.47	0.48
4:B:530:GLY:C	4:B:532:ALA:H	2.22	0.48
4:B:546:SER:OG	4:B:632:ARG:N	2.33	0.48
3:a:525:GLN:HB2	4:b:1015:HIS:CG	2.49	0.48
3:a:1270:ASN:OD1	3:a:1271:ILE:HD12	2.13	0.48
3:a:1373:ASP:O	3:a:1376:THR:N	2.47	0.48
4:b:210:LYS:HD2	4:b:210:LYS:HA	1.51	0.48
4:b:582:VAL:O	4:b:585:VAL:HG12	2.14	0.48
8:f:79:ARG:HD2	8:f:144:GLU:OE2	2.13	0.48
3:A:960:ILE:O	3:A:963:ILE:HG22	2.14	0.48
4:B:308:TRP:O	4:B:311:LEU:N	2.47	0.48
4:B:918:ILE:HA	4:B:919:SER:C	2.39	0.48
13:K:35:PHE:HD2	13:K:71:PHE:CZ	2.32	0.48
3:a:1116:LEU:HG	3:a:1308:THR:HG21	1.96	0.48
4:b:336:ARG:HG3	4:b:338:GLY:H	1.77	0.48
4:b:466:TRP:NE1	4:b:479:VAL:HG11	2.29	0.48
7:e:136:ASN:OD1	7:e:137:GLU:N	2.47	0.48
7:e:180:ARG:HH12	7:e:192:ARG:HB2	1.79	0.48
8:f:74:ILE:HD12	8:f:75:PRO:HD2	1.94	0.48
3:A:172:PRO:HG3	3:A:185:TRP:CZ2	2.49	0.48
3:A:217:LYS:O	3:A:220:THR:OG1	2.28	0.48
4:B:307:ASP:CG	4:B:310:MET:HE1	2.39	0.48
4:B:428:ILE:HA	4:B:445:LYS:HE3	1.96	0.48
4:B:1106:ARG:HH22	4:B:1111:MET:HE2	1.79	0.48
3:a:182:VAL:HG12	3:a:201:VAL:HA	1.96	0.47
3:a:208:LEU:CD2	3:a:212:LYS:HZ2	2.14	0.47
4:b:702:LEU:HD23	4:b:738:PHE:HA	1.95	0.47
3:A:1312:ASN:OD1	3:A:1313:LEU:N	2.47	0.47
3:A:1444:MET:HG3	9:G:58:ARG:HD2	1.96	0.47
5:C:167:HIS:ND1	5:C:169:LYS:HG3	2.28	0.47
6:D:56:ARG:HH12	6:D:155:ARG:HE	1.62	0.47
9:G:111:THR:HB	9:G:114:LEU:HD13	1.96	0.47
3:a:2:VAL:HG13	3:a:410:GLY:HA2	1.96	0.47
3:a:1114:PRO:HB2	3:a:1311:VAL:HB	1.95	0.47
4:b:82:ASP:HB2	4:b:140:ILE:HD11	1.96	0.47
4:b:348:ARG:HG2	4:b:351:TYR:N	2.26	0.47
4:b:396:ASP:OD1	4:b:403:LYS:NZ	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:459:TYR:O	4:b:463:THR:HG22	2.14	0.47
7:e:169:ARG:NH2	8:f:140:ASP:OD2	2.47	0.47
7:e:179:GLN:HG3	7:e:181:ALA:H	1.79	0.47
8:f:130:ILE:HB	8:f:148:VAL:HG11	1.96	0.47
10:h:126:GLU:C	10:h:130:ARG:HH12	2.22	0.47
3:A:120:GLU:O	3:A:123:ARG:HB2	2.13	0.47
3:A:878:ILE:HA	3:A:956:LEU:O	2.13	0.47
3:A:1191:TRP:CZ3	11:I:43:VAL:HG21	2.49	0.47
3:A:1208:THR:H	3:A:1211:GLN:NE2	2.11	0.47
3:A:1254:ALA:N	3:A:1256:GLU:OE2	2.47	0.47
4:B:450:ALA:HA	4:B:453:ILE:HG22	1.96	0.47
8:F:108:PHE:HE1	8:F:131:PRO:HG3	1.79	0.47
9:G:49:LEU:HG	9:G:76:ALA:HA	1.96	0.47
11:I:87:GLN:HE22	11:I:91:ARG:NH1	2.11	0.47
2:O:-45:DA:H4'	3:a:350:ARG:NH2	2.29	0.47
3:a:14:VAL:N	3:a:1432:GLN:HE22	2.07	0.47
3:a:172:PRO:HG3	3:a:185:TRP:CH2	2.48	0.47
3:a:356:ASP:OD1	3:a:358:ASN:N	2.39	0.47
3:a:1390:ASN:HD22	3:a:1402:PHE:HD2	1.61	0.47
4:b:120:ARG:NH2	4:b:956:THR:O	2.46	0.47
4:b:298:LEU:HD12	11:i:6:PHE:CZ	2.50	0.47
4:b:641:GLU:CD	4:b:652:LYS:HB2	2.40	0.47
4:b:744:HIS:CG	4:b:745:PRO:HD2	2.50	0.47
7:e:3:GLN:HG2	7:e:5:ASN:H	1.79	0.47
3:A:451:HIS:CD2	3:A:453:MET:HE2	2.49	0.47
3:A:528:LEU:HD22	3:A:751:SER:HB3	1.95	0.47
3:A:567:LYS:HE2	10:H:95:TYR:HA	1.96	0.47
3:A:1116:LEU:HG	3:A:1308:THR:HG21	1.96	0.47
4:B:35:SER:OG	4:B:811:TYR:OH	2.24	0.47
4:B:277:LYS:HE3	4:B:278:GLN:NE2	2.30	0.47
4:B:444:MET:SD	4:B:445:LYS:N	2.87	0.47
5:C:249:ASP:O	5:C:252:GLN:NE2	2.46	0.47
6:D:139:LYS:HD2	6:D:142:LYS:HD2	1.96	0.47
3:a:474:VAL:O	3:a:477:PRO:HD2	2.15	0.47
3:a:619:LYS:HG3	3:a:620:LYS:N	2.29	0.47
3:a:999:VAL:H	3:a:1011:GLN:NE2	2.12	0.47
3:a:1059:HIS:CE1	8:f:87:LYS:H	2.32	0.47
4:b:1181:GLU:OE1	4:b:1188:LYS:HG2	2.14	0.47
7:e:80:VAL:HG12	7:e:109:ILE:HB	1.96	0.47
7:e:91:LYS:O	7:e:94:LYS:HG2	2.14	0.47
3:A:121:LEU:HD12	3:A:124:GLN:NE2	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1072:MET:HE3	4:B:1073:TYR:H	1.79	0.47
5:C:61:GLU:H	5:C:61:GLU:CD	2.23	0.47
6:D:126:ILE:HD13	6:D:145:MET:HG3	1.96	0.47
3:a:101:LYS:HG2	3:a:139:TRP:CZ2	2.50	0.47
3:a:367:PRO:HA	3:a:463:ILE:O	2.14	0.47
3:a:800:VAL:HA	3:a:812:GLU:OE1	2.15	0.47
3:a:874:ASP:HA	3:a:1058:VAL:HG12	1.96	0.47
3:a:957:PRO:HG2	3:a:1018:PHE:CD1	2.50	0.47
3:a:1408:ILE:HG23	3:a:1409:LEU:HD12	1.96	0.47
4:b:530:GLY:C	4:b:532:ALA:H	2.22	0.47
4:b:1008:PRO:HB3	4:b:1087:PHE:HE1	1.78	0.47
7:e:40:GLU:HA	7:e:43:LYS:HG2	1.95	0.47
7:e:68:SER:O	7:e:72:PHE:N	2.42	0.47
3:A:118:HIS:HA	3:A:123:ARG:HH22	1.78	0.47
3:A:474:VAL:O	3:A:477:PRO:HD2	2.14	0.47
3:A:1156:PRO:HA	3:A:1190:PRO:HB2	1.96	0.47
4:B:183:GLU:OE1	4:B:183:GLU:N	2.48	0.47
4:B:604:ARG:NH2	4:B:615:MET:SD	2.87	0.47
5:C:33:LEU:HB3	5:C:37:MET:HE1	1.96	0.47
6:D:64:VAL:HG23	6:D:68:ARG:NH2	2.26	0.47
10:H:17:PRO:HA	10:H:24:CYS:SG	2.54	0.47
3:a:365:GLY:HA2	3:a:463:ILE:HD13	1.96	0.47
4:b:429:PHE:HD2	4:b:430:ARG:HH12	1.63	0.47
4:b:850:LEU:HD13	12:j:8:PHE:CD2	2.50	0.47
5:c:113:VAL:HG12	5:c:144:ILE:HD13	1.97	0.47
5:c:241:ASP:OD1	5:c:241:ASP:N	2.45	0.47
7:e:121:MET:O	7:e:124:VAL:HG12	2.14	0.47
9:g:137:ILE:HG13	9:g:137:ILE:O	2.14	0.47
10:h:97:MET:SD	10:h:98:TYR:N	2.88	0.47
12:j:12:LYS:O	12:j:14:VAL:HG23	2.14	0.47
3:A:673:GLY:O	3:A:676:MET:HG3	2.14	0.47
3:A:1042:PHE:O	3:A:1045:VAL:HG12	2.14	0.47
4:B:496:ARG:O	4:B:497:ARG:NH1	2.42	0.47
9:G:131:GLN:HB2	9:G:136:VAL:HG22	1.96	0.47
16:R:16:C:H3'	16:R:16:C:H6	1.79	0.47
1:N:48:DT:H2''	1:N:49:DC:OP2	2.14	0.47
3:a:239:LEU:HD12	3:a:240:PRO:HD2	1.96	0.47
3:a:455:MET:N	3:a:455:MET:SD	2.88	0.47
3:a:505:CYS:HG	4:b:1141:HIS:CE1	2.30	0.47
3:a:722:LEU:HD12	3:a:799:PHE:CE2	2.50	0.47
3:a:959:ASN:HD21	3:a:961:ARG:HB3	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:1149:ALA:HB1	11:i:45:ARG:HH21	1.79	0.47
3:a:1192:LEU:HA	3:a:1241:ARG:HG2	1.97	0.47
3:a:1198:ASP:CG	3:a:1201:ALA:H	2.22	0.47
4:b:238:ALA:HB3	4:b:256:VAL:HB	1.95	0.47
4:b:282:ILE:HA	4:b:285:ILE:HD13	1.97	0.47
4:b:638:PHE:CD2	4:b:743:ILE:HD13	2.49	0.47
7:e:32:GLN:O	7:e:35:VAL:HG22	2.15	0.47
10:h:5:LEU:HD11	10:h:61:SER:HB3	1.97	0.47
10:h:58:THR:HG22	10:h:143:LEU:HB2	1.97	0.47
10:h:101:ALA:HB2	10:h:116:TYR:CZ	2.49	0.47
3:A:33:ALA:HA	3:A:57:ARG:HH22	1.79	0.47
3:A:219:PHE:HB3	3:A:224:PHE:HB2	1.96	0.47
3:A:445:ASN:CB	3:A:455:MET:HE1	2.44	0.47
3:A:1102:LYS:O	3:A:1106:ASN:CB	2.63	0.47
3:A:1102:LYS:O	3:A:1106:ASN:HB3	2.13	0.47
4:B:124:TYR:O	4:B:172:ILE:HG22	2.14	0.47
4:B:424:LEU:CD1	4:B:449:ASN:HB3	2.45	0.47
4:B:431:TYR:HD2	4:B:445:LYS:HD2	1.79	0.47
4:B:449:ASN:O	4:B:452:THR:OG1	2.27	0.47
4:B:526:GLU:CB	4:B:538:ASN:HD22	2.28	0.47
4:B:835:GLN:OE1	4:B:835:GLN:N	2.40	0.47
5:C:252:GLN:HB3	13:K:98:LEU:CD1	2.44	0.47
9:G:90:THR:OG1	9:G:141:SER:OG	2.25	0.47
16:R:13:U:H5''	16:R:14:C:C5'	2.43	0.47
16:R:17:A:H8	16:R:17:A:O5'	1.98	0.47
3:a:14:VAL:H	3:a:1432:GLN:NE2	2.10	0.47
3:a:804:TYR:OH	3:a:816:HIS:NE2	2.47	0.47
3:a:1031:VAL:HA	3:a:1035:TYR:HD1	1.79	0.47
5:c:84:ARG:NE	13:k:11:LEU:HD13	2.29	0.47
5:c:148:ARG:O	5:c:150:GLY:N	2.48	0.47
6:d:172:LEU:HD21	6:d:176:GLU:HB2	1.96	0.47
8:f:119:ARG:HG2	8:f:119:ARG:HH21	1.80	0.47
10:h:108:SER:C	10:h:110:ASP:H	2.23	0.47
11:i:21:GLU:HG2	11:i:22:ASN:H	1.80	0.47
3:A:252:PHE:C	3:A:254:GLU:H	2.21	0.47
3:A:590:ARG:HH22	3:A:620:LYS:C	2.22	0.47
3:A:871:ASP:CG	3:A:873:MET:H	2.22	0.47
3:A:923:LEU:O	3:A:927:VAL:HG23	2.15	0.47
4:B:597:MET:HE2	4:B:597:MET:HA	1.96	0.47
17:Q:407:ASP:HB3	17:Q:411:LYS:NZ	2.30	0.47
1:N:-9:DC:H2''	1:N:-8:DA:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:2:DT:H6	1:N:2:DT:H5''	1.80	0.47
2:O:-57:DA:H2''	2:O:-56:DA:H8	1.79	0.47
3:a:242:PRO:O	3:a:247:ARG:NH1	2.33	0.47
3:a:311:GLN:HG2	3:a:312:PRO:CD	2.37	0.47
3:a:1100:ARG:O	3:a:1104:ILE:HD12	2.15	0.47
4:b:123:THR:O	4:b:125:SER:N	2.48	0.47
4:b:364:ILE:HG23	4:b:585:VAL:HG11	1.97	0.47
4:b:629:ASP:OD2	4:b:629:ASP:N	2.48	0.47
4:b:848:ARG:NH1	12:j:8:PHE:O	2.47	0.47
4:b:918:ILE:HA	4:b:919:SER:C	2.39	0.47
6:d:165:GLN:O	6:d:168:LYS:HG2	2.15	0.47
8:f:71:GLU:OE1	8:f:73:ALA:HB3	2.14	0.47
11:i:22:ASN:ND2	11:i:24:ARG:HD3	2.30	0.47
11:i:91:ARG:HA	11:i:95:THR:HG21	1.96	0.47
3:A:843:LYS:NZ	3:A:1401:SER:O	2.44	0.47
4:B:1222:ARG:NE	4:B:1222:ARG:O	2.48	0.47
1:N:22:DA:H2''	1:N:23:DA:OP2	2.14	0.47
1:N:50:DG:C2	1:N:51:DA:C4	3.03	0.47
1:N:50:DG:H4'	1:N:51:DA:OP1	2.15	0.47
3:a:115:LEU:HB3	3:a:122:MET:CE	2.45	0.47
3:a:816:HIS:CD2	4:b:764:SER:H	2.33	0.47
3:a:1035:TYR:HB3	3:a:1037:LEU:HD23	1.96	0.47
3:a:1263:ILE:O	3:a:1267:MET:HG2	2.14	0.47
4:b:865:LYS:HZ3	4:b:869:SER:HB2	1.80	0.47
9:g:146:LYS:HD2	9:g:168:LEU:HD11	1.97	0.47
3:A:346:ASP:OD2	4:B:1108:ARG:N	2.34	0.47
3:A:811:GLN:OE1	3:A:811:GLN:N	2.29	0.47
3:A:1062:GLU:OE1	3:A:1062:GLU:N	2.35	0.47
3:A:1417:GLU:OE1	3:A:1417:GLU:N	2.46	0.47
4:B:593:PRO:HG2	4:B:617:ARG:NH2	2.30	0.47
4:B:874:PHE:HD1	4:B:962:LYS:HD3	1.80	0.47
5:C:56:THR:HG23	5:C:58:LEU:H	1.79	0.47
7:E:32:GLN:O	7:E:35:VAL:HG22	2.15	0.47
11:I:69:PRO:HB2	11:I:85:PHE:CE1	2.50	0.47
1:N:41:DT:H5''	4:b:426:LYS:HZ3	1.80	0.46
3:a:780:VAL:HG22	3:a:781:ASP:CG	2.40	0.46
4:b:144:GLY:HA2	4:b:145:ARG:HA	1.71	0.46
4:b:642:ASP:HA	4:b:649:LYS:HG2	1.97	0.46
4:b:806:THR:O	4:b:809:MET:HE1	2.15	0.46
5:c:104:PHE:HA	5:c:152:GLU:OE1	2.16	0.46
5:c:114:TYR:CD1	5:c:140:ASN:HB3	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:c:210:GLU:OE1	5:c:229:TYR:OH	2.32	0.46
8:f:84:TYR:CZ	8:f:152:ILE:HD11	2.50	0.46
11:i:22:ASN:HB3	11:i:24:ARG:HH11	1.80	0.46
13:k:34:THR:HG22	13:k:72:LYS:HG2	1.96	0.46
3:A:81:PHE:CE2	4:B:1208:MET:HE3	2.50	0.46
3:A:807:GLY:O	4:B:728:ARG:NH1	2.49	0.46
4:B:67:SER:HG	4:B:92:PHE:H	1.58	0.46
2:O:-19:DC:H2''	2:O:-18:DA:OP2	2.16	0.46
2:O:2:DC:H2''	2:O:3:DA:H8	1.79	0.46
3:a:741:ASN:OD1	3:a:743:VAL:N	2.49	0.46
3:a:1042:PHE:O	3:a:1045:VAL:HG22	2.15	0.46
3:a:1407:GLU:HA	3:a:1410:PHE:HD2	1.79	0.46
4:b:916:THR:N	4:b:934:LYS:O	2.48	0.46
7:e:136:ASN:ND2	7:e:138:ALA:HB3	2.30	0.46
3:A:62:ASP:OD1	3:A:62:ASP:N	2.49	0.46
3:A:891:ALA:HA	3:A:894:GLU:OE2	2.15	0.46
4:B:104:GLU:HG3	14:L:54:ARG:HH12	1.79	0.46
4:B:709:ASP:OD1	4:B:710:LEU:N	2.48	0.46
4:B:1100:ASP:OD1	4:B:1101:ASP:N	2.49	0.46
10:H:83:GLN:OE1	13:K:54:ARG:NH2	2.48	0.46
2:O:-54:DC:H2''	2:O:-53:DA:OP2	2.14	0.46
2:O:-15:DA:H5''	3:A:1386:ARG:HD3	1.96	0.46
3:a:101:LYS:HE3	3:a:139:TRP:CZ3	2.50	0.46
3:a:452:LYS:NZ	4:b:1141:HIS:HA	2.30	0.46
4:b:233:PRO:O	4:b:260:GLY:N	2.45	0.46
4:b:425:THR:HA	4:b:428:ILE:HD12	1.97	0.46
6:d:183:LEU:HD13	9:g:144:ARG:HG2	1.95	0.46
10:h:98:TYR:CE1	10:h:139:ASN:HB2	2.51	0.46
12:j:16:ASP:N	12:j:16:ASP:OD1	2.46	0.46
3:A:560:ILE:HD11	10:H:79:TRP:O	2.16	0.46
3:A:839:ARG:NH2	3:A:1403:GLU:OE2	2.35	0.46
3:A:868:TYR:CD1	3:A:1058:VAL:HG21	2.45	0.46
4:B:526:GLU:HB3	4:B:538:ASN:HD22	1.80	0.46
5:C:102:GLN:HE22	5:C:154:LYS:HG2	1.81	0.46
7:E:185:ALA:O	7:E:189:GLY:N	2.47	0.46
18:M:63:ARG:HH22	18:M:66:ARG:NH1	2.13	0.46
18:M:73:LEU:HD23	18:M:78:ALA:HA	1.97	0.46
2:O:-31:DT:H2''	2:O:-30:DT:C6	2.49	0.46
3:a:446:ARG:NH2	3:a:479:ASN:O	2.44	0.46
3:a:552:TRP:CZ3	3:a:651:LYS:HD2	2.50	0.46
4:b:75:ALA:HB1	4:b:80:GLU:CD	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:77:HIS:HB3	4:b:80:GLU:OE1	2.15	0.46
4:b:299:GLU:HB3	4:b:571:PRO:HG3	1.97	0.46
6:d:220:LEU:HG	6:d:221:TYR:H	1.81	0.46
7:e:21:GLU:CD	7:e:146:HIS:HE2	2.23	0.46
13:k:65:HIS:CG	13:k:66:PRO:HD2	2.50	0.46
3:A:95:PHE:O	3:A:99:ILE:HG13	2.16	0.46
4:B:274:PRO:HA	4:B:275:TYR:HA	1.67	0.46
4:B:901:PRO:HA	4:B:949:VAL:HG12	1.97	0.46
12:J:55:ASP:O	12:J:56:LEU:HD23	2.16	0.46
1:N:15:DT:H2''	1:N:16:DA:C8	2.51	0.46
2:O:-45:DA:H3'	2:O:-44:DG:C8	2.51	0.46
3:a:21:LEU:HD21	3:a:95:PHE:HE1	1.81	0.46
3:a:434:ARG:HD2	3:a:435:HIS:O	2.15	0.46
3:a:451:HIS:HA	3:a:1070:GLN:HG2	1.97	0.46
3:a:825:ILE:HD11	4:b:512:ARG:HH11	1.81	0.46
4:b:44:VAL:HG21	4:b:200:GLY:HA2	1.98	0.46
4:b:1025:HIS:O	4:b:1028:GLU:HG3	2.15	0.46
10:h:91:ASP:C	10:h:93:TYR:H	2.24	0.46
11:i:21:GLU:HG2	11:i:22:ASN:N	2.30	0.46
3:A:41:MET:HE3	3:A:47:ARG:HA	1.98	0.46
3:A:722:LEU:HD12	3:A:799:PHE:CE1	2.51	0.46
3:A:928:LEU:O	3:A:931:GLU:HG3	2.16	0.46
3:A:1159:ARG:HH11	3:A:1185:PHE:HB3	1.81	0.46
4:B:279:ASP:N	4:B:279:ASP:OD1	2.46	0.46
4:B:408:LEU:HG	4:B:409:ALA:H	1.80	0.46
6:D:14:ARG:HB2	6:D:17:LYS:HE2	1.98	0.46
7:E:112:TYR:CE2	7:E:136:ASN:HB2	2.51	0.46
13:K:49:GLU:OE1	13:K:90:ALA:HB1	2.15	0.46
3:a:503:GLN:C	3:a:504:LEU:HD12	2.41	0.46
4:b:38:PHE:HD2	4:b:811:TYR:HB3	1.79	0.46
4:b:216:GLU:HB3	4:b:500:THR:HB	1.96	0.46
9:g:85:GLU:O	9:g:147:ILE:N	2.48	0.46
3:A:153:PRO:HB2	3:A:156:ASP:CG	2.41	0.46
5:C:71:PRO:HB2	5:C:133:ILE:HD13	1.97	0.46
17:Q:326:ARG:HD3	17:Q:326:ARG:HA	1.80	0.46
3:a:1208:THR:O	3:a:1211:GLN:HG3	2.15	0.46
3:a:1406:VAL:N	3:a:1407:GLU:OE1	2.47	0.46
4:b:79:THR:HA	4:b:81:SER:N	2.31	0.46
4:b:704:ALA:O	4:b:741:CYS:HA	2.16	0.46
4:b:822:ASN:HD22	12:j:48:ARG:HB2	1.81	0.46
4:b:841:MET:SD	4:b:990:ILE:HG12	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:874:PHE:HA	4:b:913:GLY:O	2.16	0.46
3:A:679:ILE:HD11	3:A:732:LEU:HB3	1.96	0.46
4:B:803:LEU:HG	4:B:822:ASN:HD22	1.81	0.46
5:C:91:HIS:HB2	5:C:96:SER:HB2	1.98	0.46
5:C:134:ILE:HG13	5:C:134:ILE:O	2.15	0.46
7:E:108:GLY:N	7:E:131:THR:O	2.35	0.46
17:Q:109:GLU:H	17:Q:109:GLU:CD	2.24	0.46
3:a:1438:THR:OG1	8:f:92:ARG:NH1	2.42	0.46
4:b:194:GLU:HA	4:b:784:ASN:HD22	1.80	0.46
4:b:341:LEU:HD23	4:b:344:LYS:HG3	1.97	0.46
4:b:486:TYR:CZ	4:b:1096:ARG:HD2	2.50	0.46
9:g:78:VAL:HB	9:g:80:LYS:NZ	2.31	0.46
3:A:18:GLN:O	4:B:1215:ARG:N	2.48	0.46
3:A:457:ALA:HB3	3:A:506:ALA:HA	1.98	0.46
5:C:186:LEU:HB3	5:C:188:HIS:CD2	2.51	0.46
3:a:66:LYS:HG2	3:a:69:THR:H	1.81	0.46
3:a:545:GLN:O	3:a:549:MET:HG2	2.16	0.46
3:a:568:PRO:CD	3:a:569:LYS:H	2.28	0.46
3:a:665:GLY:HA3	4:b:1069:PHE:HE1	1.81	0.46
3:a:966:ASN:OD1	3:a:967:ALA:N	2.49	0.46
4:b:310:MET:HA	4:b:386:LEU:HD21	1.98	0.46
4:b:1084:GLN:OE1	4:b:1084:GLN:N	2.49	0.46
4:b:1099:VAL:O	4:b:1103:ILE:HG12	2.16	0.46
5:c:240:VAL:HA	5:c:243:VAL:HG22	1.98	0.46
10:h:144:ILE:O	10:h:144:ILE:HG13	2.15	0.46
3:A:33:ALA:HB3	3:A:82:GLY:HA3	1.96	0.46
3:A:187:LYS:O	3:A:188:ASP:C	2.59	0.46
4:B:862:GLN:O	4:B:914:LYS:NZ	2.31	0.46
1:N:31:DA:H2''	1:N:32:DA:H8	1.81	0.46
3:a:35:ILE:H	3:a:35:ILE:HD12	1.81	0.46
3:a:399:HIS:NE2	3:a:462:VAL:HG21	2.31	0.46
3:a:788:SER:HB2	11:i:69:PRO:HG3	1.98	0.46
3:a:837:ILE:HD13	3:a:840:ARG:HH12	1.79	0.46
3:a:1224:LEU:HA	3:a:1243:VAL:HG12	1.98	0.46
3:a:1441:PHE:CZ	8:f:89:GLU:HA	2.50	0.46
4:b:1206:GLU:HA	4:b:1209:ALA:HB3	1.98	0.46
10:h:47:PHE:HZ	10:h:146:ARG:HD3	1.81	0.46
13:k:38:GLU:HG2	13:k:42:LEU:HD12	1.98	0.46
3:A:346:ASP:OD1	4:B:1107:ALA:HA	2.15	0.46
4:B:216:GLU:CG	4:B:500:THR:HB	2.46	0.46
4:B:778:MET:HE1	4:B:1094:ARG:HH11	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1010:LEU:HD11	4:B:1092:TYR:CE2	2.49	0.46
5:C:35:ARG:HE	13:K:41:THR:HB	1.81	0.46
5:C:181:ASP:OD2	5:C:184:ASN:N	2.49	0.46
10:H:102:TYR:CZ	10:H:115:TYR:HB3	2.51	0.46
10:H:118:PHE:N	10:H:121:LEU:O	2.39	0.46
3:a:344:ARG:NH2	4:b:1120:GLU:OE1	2.49	0.45
3:a:375:THR:OG1	3:a:376:TYR:N	2.48	0.45
3:a:506:ALA:HB1	3:a:508:PRO:HD2	1.98	0.45
3:a:1168:GLU:O	3:a:1171:GLN:NE2	2.49	0.45
4:b:281:PRO:HD2	4:b:284:ILE:HD13	1.98	0.45
4:b:1160:VAL:HG11	4:b:1169:MET:SD	2.56	0.45
6:d:123:LEU:HD12	6:d:145:MET:HG3	1.98	0.45
7:e:26:ARG:NH2	7:e:187:TYR:O	2.37	0.45
13:k:65:HIS:CD2	13:k:67:PHE:HB2	2.44	0.45
3:A:372:LYS:HD2	13:K:2:ASN:HB3	1.99	0.45
3:A:530:GLY:CA	3:A:657:LEU:HD21	2.45	0.45
5:C:146:LYS:C	5:C:147:LEU:HD12	2.40	0.45
9:G:56:ILE:HG22	9:G:72:VAL:HG22	1.98	0.45
10:H:116:TYR:HB2	10:H:123:MET:SD	2.55	0.45
1:N:53:DT:H4'	3:a:1387:HIS:CE1	2.51	0.45
2:O:-55:DG:H2''	2:O:-54:DC:C6	2.51	0.45
3:a:556:TRP:CD1	3:a:558:GLY:H	2.34	0.45
3:a:1098:VAL:N	3:a:1099:PRO:HD2	2.31	0.45
3:a:1202:MET:HE3	3:a:1209:MET:HB3	1.96	0.45
3:a:1259:MET:O	3:a:1263:ILE:HG12	2.16	0.45
4:b:530:GLY:O	4:b:532:ALA:N	2.50	0.45
4:b:1082:MET:HE2	4:b:1082:MET:HA	1.97	0.45
7:e:5:ASN:ND2	7:e:52:ARG:HH22	2.14	0.45
9:g:108:VAL:HA	9:g:159:ALA:O	2.16	0.45
14:l:49:LYS:HD2	14:l:49:LYS:C	2.41	0.45
3:A:98:LYS:O	3:A:102:VAL:HG23	2.16	0.45
3:A:332:LYS:HD2	3:A:332:LYS:HA	1.79	0.45
3:A:443:LEU:HD12	3:A:444:PHE:H	1.81	0.45
3:A:1239:ARG:HH22	3:A:1241:ARG:HH21	1.63	0.45
3:A:1293:SER:N	3:A:1297:GLU:O	2.31	0.45
4:B:304:ASP:OD2	4:B:307:ASP:N	2.45	0.45
4:B:363:HIS:HD2	4:B:364:ILE:HG23	1.80	0.45
4:B:637:LEU:HD12	4:B:693:ILE:HG13	1.98	0.45
4:B:1043:ASP:OD2	4:B:1045:SER:OG	2.30	0.45
4:B:1065:GLN:HE22	4:B:1067:ARG:HB2	1.82	0.45
5:C:11:ARG:HD3	5:C:19:ASP:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:399:HIS:O	3:a:435:HIS:ND1	2.38	0.45
3:a:958:VAL:HG11	3:a:1052:GLN:HB3	1.97	0.45
3:a:1284:MET:N	3:a:1284:MET:SD	2.90	0.45
4:b:842:ASN:HD21	4:b:844:SER:HB2	1.81	0.45
5:c:44:LEU:HD12	5:c:160:LYS:O	2.17	0.45
5:c:91:HIS:HB2	5:c:96:SER:HB3	1.97	0.45
9:g:39:THR:N	9:g:43:GLY:O	2.49	0.45
10:h:61:SER:HA	10:h:140:ALA:HB1	1.98	0.45
3:A:826:ASP:HA	4:B:508:LEU:HD11	1.99	0.45
6:D:25:ALA:HA	6:D:175:PHE:HE2	1.80	0.45
9:G:3:PHE:HE2	9:G:82:PHE:HE2	1.64	0.45
9:G:165:GLU:O	9:G:168:LEU:HB3	2.15	0.45
3:a:66:LYS:CG	3:a:69:THR:H	2.29	0.45
3:a:344:ARG:HD3	4:b:1129:ARG:HA	1.99	0.45
3:a:368:LYS:HG2	3:a:462:VAL:HG12	1.99	0.45
4:b:842:ASN:ND2	4:b:845:SER:H	2.14	0.45
8:f:133:VAL:HG21	9:g:58:ARG:HH21	1.81	0.45
10:h:10:PHE:HB3	10:h:28:ALA:HB1	1.98	0.45
3:A:50:ILE:HG23	3:A:52:GLY:H	1.81	0.45
3:A:85:ASP:O	3:A:273:ASN:ND2	2.47	0.45
3:A:563:PRO:HD2	10:H:79:TRP:CD1	2.51	0.45
3:A:999:VAL:H	3:A:1011:GLN:CD	2.25	0.45
7:E:180:ARG:HH21	7:E:192:ARG:HB2	1.81	0.45
12:J:19:GLU:OE1	12:J:19:GLU:N	2.40	0.45
1:N:59:DT:H2"	1:N:60:DC:C5	2.52	0.45
3:a:314:ALA:O	3:a:322:VAL:HG12	2.17	0.45
3:a:369:SER:OG	3:a:370:ILE:HD12	2.17	0.45
3:a:569:LYS:NZ	5:c:221:TYR:HB2	2.30	0.45
4:b:48:LEU:HA	4:b:173:MET:HE1	1.98	0.45
4:b:209:GLU:OE1	4:b:485:ARG:NE	2.43	0.45
4:b:486:TYR:CZ	4:b:1096:ARG:HB3	2.52	0.45
4:b:1058:LEU:HD23	4:b:1061:GLU:OE1	2.17	0.45
7:e:90:VAL:HA	7:e:93:MET:HG3	1.99	0.45
12:j:48:ARG:HG3	12:j:49:MET:N	2.31	0.45
3:A:563:PRO:HA	3:A:572:TRP:NE1	2.31	0.45
3:A:727:ASP:OD1	3:A:728:LYS:N	2.50	0.45
3:A:1121:GLU:CD	3:A:1122:PRO:HD2	2.42	0.45
3:A:1143:LEU:O	3:A:1147:THR:N	2.50	0.45
4:B:281:PRO:HD2	4:B:284:ILE:HD12	1.99	0.45
4:B:839:MET:HG2	4:B:1010:LEU:HD12	1.97	0.45
4:B:976:ILE:O	4:B:990:ILE:HB	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:55:ARG:HB2	7:E:84:ASP:OD1	2.16	0.45
10:H:135:LEU:HD22	10:H:137:GLN:HB2	1.99	0.45
17:Q:100:GLU:OE1	18:M:94:LYS:HB3	2.17	0.45
18:M:98:ASN:OD1	18:M:103:LYS:HB3	2.17	0.45
1:N:49:DC:H1'	1:N:50:DG:C8	2.51	0.45
3:a:209:ASN:HA	3:a:212:LYS:NZ	2.29	0.45
3:a:216:VAL:HA	3:a:219:PHE:CE2	2.51	0.45
3:a:843:LYS:HG2	3:a:1402:PHE:HB2	1.97	0.45
4:b:428:ILE:HG22	4:b:432:MET:HE3	1.97	0.45
4:b:737:THR:HB	11:i:66:PRO:HB3	1.99	0.45
6:d:147:TYR:O	6:d:151:PHE:N	2.45	0.45
13:k:9:LEU:HD12	13:k:10:PHE:N	2.31	0.45
3:A:1399:ARG:NH1	3:A:1408:ILE:HD11	2.32	0.45
4:B:278:GLN:OE1	4:B:335:GLY:HA2	2.17	0.45
4:B:345:LYS:N	4:B:348:ARG:HH21	2.14	0.45
4:B:1187:ASN:ND2	4:B:1190:ASP:HB3	2.31	0.45
9:G:21:ARG:NH1	9:G:24:GLN:HB2	2.31	0.45
9:G:62:LEU:HD12	9:G:63:PRO:HD2	1.97	0.45
12:J:16:ASP:OD1	12:J:17:LYS:N	2.50	0.45
14:L:30:ILE:HA	14:L:36:SER:O	2.16	0.45
2:O:-53:DA:H2''	2:O:-52:DC:O5'	2.16	0.45
3:a:23:SER:O	3:a:26:GLU:HG3	2.17	0.45
3:a:365:GLY:N	3:a:469:ARG:O	2.34	0.45
3:a:476:SER:OG	3:a:477:PRO:HD3	2.17	0.45
3:a:783:THR:O	3:a:784:LEU:HD23	2.15	0.45
4:b:1202:LEU:HA	4:b:1205:GLN:OE1	2.16	0.45
5:c:88:CYS:HB3	5:c:92:CYS:SG	2.57	0.45
5:c:148:ARG:HH22	12:j:64:ASN:HA	1.80	0.45
6:d:118:THR:O	6:d:121:LYS:HG3	2.17	0.45
7:e:48:ASP:OD1	7:e:49:SER:N	2.46	0.45
12:j:36:LEU:CD2	12:j:47:ARG:HG3	2.47	0.45
3:A:678:GLU:HA	3:A:681:GLU:HG3	1.99	0.45
3:A:821:ARG:HH21	4:B:534:GLY:HA2	1.81	0.45
3:A:1209:MET:HE1	3:A:1228:TRP:HB2	1.98	0.45
4:B:75:ALA:C	4:B:77:HIS:H	2.25	0.45
4:B:198:ASP:OD2	4:B:202:TYR:OH	2.28	0.45
4:B:629:ASP:OD1	4:B:632:ARG:NE	2.36	0.45
6:D:56:ARG:HD3	6:D:149:THR:HA	1.97	0.45
3:a:424:ILE:H	3:a:424:ILE:HD12	1.81	0.45
3:a:635:ARG:HH22	3:a:876:ALA:C	2.19	0.45
3:a:1155:ASP:CG	3:a:1162:VAL:HG23	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:79:THR:CA	4:b:81:SER:H	2.30	0.45
4:b:357:GLN:O	4:b:366:GLN:HB3	2.17	0.45
3:A:1390:ASN:ND2	3:A:1402:PHE:HB3	2.32	0.45
4:B:810:GLU:HG3	17:Q:24:ARG:HH22	1.82	0.45
7:E:153:HIS:CD2	7:E:184:VAL:HG21	2.52	0.45
7:E:169:ARG:NH2	8:F:140:ASP:OD2	2.50	0.45
10:H:124:ARG:NE	10:H:126:GLU:OE1	2.48	0.45
1:N:16:DA:H2'	1:N:17:DG:C8	2.52	0.45
3:a:524:VAL:HB	3:a:525:GLN:OE1	2.16	0.45
3:a:590:ARG:HB3	3:a:605:MET:H	1.82	0.45
3:a:1111:MET:C	3:a:1113:THR:H	2.24	0.45
3:a:1315:GLU:HG2	3:a:1316:VAL:N	2.31	0.45
3:a:1444:MET:HE2	9:g:58:ARG:HB2	1.98	0.45
4:b:438:GLU:HB3	4:b:439:ALA:HB2	1.99	0.45
4:b:708:GLU:N	4:b:708:GLU:OE1	2.50	0.45
4:b:762:ASN:ND2	4:b:1024:ALA:HB3	2.31	0.45
4:b:952:VAL:HG13	4:b:966:VAL:HG12	1.98	0.45
5:c:18:VAL:HG12	5:c:20:PHE:HD2	1.82	0.45
5:c:60:ASP:O	5:c:63:ILE:N	2.50	0.45
6:d:145:MET:HA	6:d:148:LEU:CB	2.46	0.45
6:d:184:ALA:HB3	9:g:144:ARG:NH2	2.32	0.45
10:h:12:VAL:HG23	10:h:26:ILE:HG23	1.99	0.45
3:A:314:ALA:O	3:A:322:VAL:HG12	2.17	0.45
3:A:1116:LEU:H	3:A:1308:THR:HG22	1.82	0.45
3:A:1198:ASP:HB3	3:A:1201:ALA:HB3	1.99	0.45
3:A:1282:VAL:HG12	3:A:1308:THR:HA	1.98	0.45
4:B:259:TYR:O	4:B:267:ARG:NH2	2.50	0.45
4:B:441:ASP:CG	4:B:444:MET:H	2.24	0.45
4:B:1106:ARG:HH22	4:B:1111:MET:CE	2.30	0.45
4:B:1166:CYS:O	4:B:1215:ARG:HD2	2.17	0.45
13:K:60:ALA:O	13:K:73:LEU:HD12	2.16	0.45
17:Q:118:LEU:HB3	17:Q:392:VAL:HG22	1.99	0.45
3:a:391:LEU:HG	3:a:400:PRO:O	2.16	0.45
3:a:622:VAL:HG23	3:a:629:LEU:HD21	1.98	0.45
3:a:635:ARG:NH2	3:a:877:HIS:HA	2.32	0.45
4:b:402:GLY:O	4:b:405:ARG:NH1	2.50	0.45
4:b:438:GLU:HA	4:b:439:ALA:HA	1.70	0.45
4:b:1005:GLY:HA3	5:c:176:ILE:O	2.17	0.45
8:f:70:LYS:C	8:f:71:GLU:HG3	2.42	0.45
9:g:140:LYS:HA	9:g:140:LYS:HD2	1.77	0.45
5:C:104:PHE:HA	5:C:152:GLU:OE1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:110:VAL:HG11	9:G:163:ILE:HG12	1.98	0.45
12:J:18:TRP:CZ2	12:J:22:LEU:HD21	2.52	0.45
17:Q:120:LYS:HB3	17:Q:394:LYS:HA	1.99	0.45
18:M:81:TRP:N	18:M:81:TRP:CD1	2.84	0.45
3:a:368:LYS:HB3	13:k:2:ASN:HB3	1.99	0.44
3:a:549:MET:HE1	3:a:655:PHE:HD2	1.80	0.44
3:a:878:ILE:HA	3:a:956:LEU:O	2.16	0.44
4:b:74:LEU:HD12	4:b:85:SER:HB2	1.99	0.44
4:b:94:LYS:O	4:b:130:VAL:HG13	2.18	0.44
4:b:809:MET:HB2	4:b:809:MET:HE2	1.75	0.44
13:k:57:LEU:HB2	13:k:77:THR:HA	1.99	0.44
3:A:570:PRO:C	3:A:571:LEU:HD12	2.42	0.44
3:A:770:VAL:HG12	3:A:771:GLU:CD	2.43	0.44
3:A:1306:LEU:HD23	3:A:1306:LEU:HA	1.83	0.44
3:A:1330:ASN:OD1	3:A:1331:SER:N	2.50	0.44
4:B:139:ALA:N	4:B:150:GLU:O	2.50	0.44
4:B:929:THR:HG23	4:B:931:TYR:HB2	1.99	0.44
5:C:6:PRO:HA	5:C:24:ASN:HB2	1.98	0.44
5:C:40:GLU:OE1	5:C:40:GLU:N	2.51	0.44
7:E:23:VAL:HG13	7:E:78:LEU:HD21	1.99	0.44
9:G:14:HIS:CG	9:G:15:PRO:HD2	2.52	0.44
11:I:21:GLU:HG2	11:I:22:ASN:N	2.32	0.44
14:L:31:CYS:HA	14:L:56:LEU:HD23	1.99	0.44
3:a:22:PHE:HB2	4:b:1211:ASN:OD1	2.17	0.44
3:a:877:HIS:O	3:a:957:PRO:HA	2.17	0.44
4:b:79:THR:HG22	4:b:82:ASP:O	2.17	0.44
4:b:130:VAL:HG23	4:b:167:ILE:HG13	1.98	0.44
4:b:579:ARG:HA	4:b:589:VAL:HG22	1.99	0.44
5:c:22:LEU:HB2	5:c:230:MET:HE1	1.99	0.44
7:e:2:ASP:C	7:e:7:ARG:HH12	2.20	0.44
7:e:203:GLU:OE1	7:e:203:GLU:N	2.49	0.44
9:g:29:LYS:O	9:g:33:GLU:OE1	2.34	0.44
10:h:128:ASN:OD1	10:h:131:ASN:ND2	2.39	0.44
13:k:102:LYS:O	13:k:105:PHE:N	2.50	0.44
3:A:890:ASP:O	3:A:893:PHE:HB3	2.18	0.44
3:A:946:VAL:HG23	3:A:947:PHE:N	2.32	0.44
4:B:919:SER:HA	4:B:920:PRO:HA	1.74	0.44
4:B:1073:TYR:CE1	4:B:1080:LYS:HD2	2.52	0.44
5:C:148:ARG:HG3	5:C:148:ARG:O	2.17	0.44
5:C:148:ARG:N	5:C:151:GLN:OE1	2.23	0.44
6:D:54:GLU:HA	6:D:57:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:41:ASP:OD2	10:H:122:LEU:N	2.44	0.44
1:N:24:DA:H2''	1:N:25:DA:C8	2.52	0.44
2:O:-43:DT:H2'	2:O:-42:DA:C8	2.53	0.44
3:a:575:LYS:HE2	10:h:120:GLY:HA2	1.99	0.44
3:a:961:ARG:O	3:a:965:GLN:NE2	2.49	0.44
4:b:173:MET:SD	4:b:201:GLY:HA3	2.58	0.44
4:b:428:ILE:HA	4:b:445:LYS:HD3	1.99	0.44
4:b:435:THR:OG1	4:b:437:GLU:O	2.32	0.44
4:b:898:LEU:HD11	4:b:964:VAL:HG11	2.00	0.44
4:b:908:GLU:N	4:b:908:GLU:OE1	2.51	0.44
5:c:73:GLN:OE1	5:c:75:MET:HG2	2.18	0.44
10:h:6:PHE:CE1	10:h:8:ASP:HB2	2.52	0.44
13:k:103:THR:HA	13:k:106:GLU:OE2	2.17	0.44
3:A:791:ASP:OD1	3:A:792:TYR:N	2.51	0.44
4:B:237:VAL:HG12	4:B:257:LYS:HG2	2.00	0.44
4:B:995:ARG:HB2	4:B:997:GLU:OE2	2.18	0.44
5:C:187:LYS:HB2	5:C:219:PHE:HE1	1.82	0.44
9:G:165:GLU:HB3	9:G:168:LEU:HD23	2.00	0.44
10:H:18:GLY:O	10:H:19:ARG:HG2	2.17	0.44
18:M:200:ARG:HD2	18:M:201:TYR:N	2.32	0.44
1:N:51:DA:H2'	1:N:52:DG:C8	2.53	0.44
2:O:-3:DA:C2	3:A:252:PHE:CD2	3.06	0.44
3:a:1133:LEU:O	3:a:1136:SER:OG	2.33	0.44
6:d:206:GLU:HA	6:d:209:ARG:HG3	1.99	0.44
10:h:135:LEU:HB3	10:h:137:GLN:N	2.32	0.44
3:A:957:PRO:HG2	3:A:1018:PHE:HD1	1.82	0.44
3:A:1329:THR:HG22	3:A:1331:SER:H	1.82	0.44
4:B:51:PHE:CG	4:B:173:MET:HB2	2.53	0.44
4:B:350:GLN:HA	4:B:353:LYS:HG2	1.99	0.44
4:B:862:GLN:HB3	4:B:963:PHE:CD1	2.53	0.44
4:B:953:LEU:HD21	4:B:965:LYS:HB2	1.99	0.44
4:B:1106:ARG:HD2	4:B:1126:GLY:C	2.43	0.44
5:C:148:ARG:HG2	12:J:61:LEU:HG	1.98	0.44
10:H:108:SER:C	10:H:110:ASP:H	2.25	0.44
11:I:28:GLU:HB3	11:I:35:VAL:HG23	1.97	0.44
4:b:428:ILE:HG23	4:b:445:LYS:HD2	1.99	0.44
4:b:641:GLU:HB3	4:b:643:ASP:OD1	2.17	0.44
4:b:833:TYR:O	4:b:838:SER:OG	2.22	0.44
4:b:1080:LYS:HG3	5:c:180:TYR:CE1	2.53	0.44
5:c:99:LEU:HD13	5:c:120:ILE:HA	1.99	0.44
11:i:6:PHE:HA	11:i:12:ASN:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:i:16:PRO:HA	11:i:27:PHE:HD1	1.81	0.44
3:A:33:ALA:C	3:A:34:LYS:HD3	2.42	0.44
3:A:737:LEU:HD11	3:A:741:ASN:ND2	2.31	0.44
4:B:89:GLU:HG3	4:B:159:ASP:OD1	2.17	0.44
4:B:343:ILE:HD12	4:B:343:ILE:H	1.83	0.44
4:B:573:GLN:OE1	4:B:573:GLN:N	2.51	0.44
4:B:843:GLN:NE2	4:B:847:ASP:OD1	2.50	0.44
5:C:142:VAL:HG21	12:J:5:VAL:HG22	1.99	0.44
7:E:72:PHE:HB2	7:E:75:MET:HE1	1.99	0.44
10:H:7:ASP:OD1	10:H:8:ASP:N	2.51	0.44
10:H:109:LYS:O	10:H:109:LYS:HD3	2.17	0.44
1:N:53:DT:H2''	1:N:54:DG:C8	2.53	0.44
3:a:42:ASP:OD1	3:a:47:ARG:NH2	2.51	0.44
3:a:525:GLN:HB2	4:b:1015:HIS:ND1	2.33	0.44
3:a:557:ASP:OD1	3:a:558:GLY:N	2.51	0.44
3:a:1419:ASP:CG	3:a:1421:CYS:H	2.25	0.44
4:b:131:ASP:N	4:b:131:ASP:OD1	2.50	0.44
4:b:205:ILE:O	4:b:208:SER:OG	2.29	0.44
4:b:566:LEU:HD12	4:b:588:GLY:HA2	1.99	0.44
9:g:28:THR:O	9:g:31:LEU:HB2	2.18	0.44
11:i:69:PRO:HB2	11:i:85:PHE:CE1	2.52	0.44
3:A:455:MET:HG3	4:B:1137:CYS:SG	2.58	0.44
4:B:68:THR:HG21	17:Q:334:VAL:HB	2.00	0.44
4:B:1081:LEU:HD23	4:B:1081:LEU:HA	1.86	0.44
6:D:63:LEU:O	6:D:66:ARG:HG3	2.17	0.44
6:D:209:ARG:HA	6:D:212:LYS:NZ	2.33	0.44
7:E:88:VAL:HG11	7:E:116:ILE:HG23	1.99	0.44
1:N:4:DA:H5'	1:N:5:DA:H5'	1.99	0.44
3:a:243:PRO:O	3:a:246:VAL:HG12	2.17	0.44
4:b:699:GLU:OE1	4:b:699:GLU:N	2.43	0.44
4:b:785:TYR:HA	4:b:788:ARG:HB3	2.00	0.44
4:b:998:ASP:O	4:b:1075:GLY:HA3	2.16	0.44
9:g:84:GLY:HA2	9:g:146:LYS:HE2	1.98	0.44
9:g:90:THR:HA	9:g:140:LYS:O	2.17	0.44
9:g:130:TYR:CE1	9:g:136:VAL:HG12	2.53	0.44
13:k:49:GLU:HG2	13:k:94:ILE:HD11	1.99	0.44
14:l:44:ASP:N	14:l:44:ASP:OD1	2.48	0.44
3:A:353:ILE:HG22	3:A:468:PHE:HB2	1.99	0.44
3:A:445:ASN:OD1	3:A:446:ARG:N	2.50	0.44
3:A:545:GLN:O	3:A:549:MET:HG2	2.17	0.44
3:A:1063:MET:SD	3:A:1436:ILE:HD12	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1361:SER:HA	3:A:1362:TYR:HA	1.63	0.44
4:B:102:VAL:HB	4:B:112:LEU:HD21	2.00	0.44
4:B:128:LEU:HD11	4:B:170:LEU:HG	2.00	0.44
6:D:52:LEU:HG	6:D:148:LEU:HA	1.99	0.44
7:E:43:LYS:HA	7:E:43:LYS:HD2	1.67	0.44
7:E:48:ASP:OD1	7:E:52:ARG:HB2	2.18	0.44
7:E:92:THR:O	7:E:95:THR:OG1	2.29	0.44
7:E:126:SER:OG	7:E:127:ILE:N	2.51	0.44
7:E:154:ILE:CG2	7:E:197:LYS:HB3	2.48	0.44
9:G:21:ARG:NH2	9:G:25:TYR:HB2	2.26	0.44
9:G:116:PRO:HA	9:G:164:LYS:NZ	2.32	0.44
3:a:363:GLN:HE21	3:a:459:ARG:HH12	1.66	0.44
3:a:635:ARG:HH22	3:a:877:HIS:HA	1.83	0.44
3:a:1288:ASP:OD1	3:a:1288:ASP:N	2.51	0.44
4:b:103:ASN:HB3	4:b:109:THR:HA	1.99	0.44
4:b:569:TYR:OH	4:b:571:PRO:HA	2.17	0.44
6:d:64:VAL:HG23	6:d:68:ARG:HH12	1.82	0.44
9:g:78:VAL:HB	9:g:80:LYS:HZ1	1.82	0.44
9:g:101:VAL:HG12	9:g:103:VAL:HG13	1.99	0.44
10:h:61:SER:OG	10:h:62:SER:N	2.49	0.44
10:h:138:GLU:OE1	10:h:138:GLU:N	2.51	0.44
3:A:1259:MET:SD	3:A:1260:LEU:N	2.91	0.44
4:B:57:TYR:C	4:B:59:LEU:H	2.24	0.44
4:B:662:MET:HE3	4:B:662:MET:HB3	1.82	0.44
5:C:62:PHE:O	5:C:66:ARG:HG3	2.17	0.44
7:E:13:TRP:CE3	7:E:39:LEU:HD12	2.52	0.44
7:E:22:MET:HE2	7:E:187:TYR:CD1	2.53	0.44
7:E:121:MET:HA	7:E:124:VAL:HG23	1.99	0.44
9:G:7:LEU:HD22	9:G:74:TYR:OH	2.18	0.44
17:Q:119:LEU:HD21	17:Q:121:PHE:CE1	2.52	0.44
1:N:52:DG:H2'	1:N:53:DT:H6	1.76	0.44
3:a:344:ARG:NE	4:b:1129:ARG:HB2	2.33	0.44
3:a:363:GLN:HE21	3:a:459:ARG:NH1	2.16	0.44
3:a:372:LYS:HE2	13:k:1:MET:HE3	1.99	0.44
3:a:604:GLY:O	3:a:605:MET:HE2	2.18	0.44
3:a:843:LYS:NZ	4:b:1135:ARG:HH22	2.16	0.44
3:a:1003:LYS:HD2	3:a:1003:LYS:HA	1.82	0.44
4:b:243:ALA:HB1	4:b:246:LYS:HG3	1.99	0.44
4:b:343:ILE:HB	4:b:348:ARG:NH1	2.32	0.44
4:b:397:ASP:CG	4:b:399:ASP:H	2.25	0.44
4:b:438:GLU:OE1	4:b:438:GLU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:826:ALA:HB3	4:b:1011:ILE:HD12	1.99	0.44
8:f:70:LYS:C	8:f:72:LYS:H	2.26	0.44
9:g:89:GLY:HA3	9:g:103:VAL:HG12	1.99	0.44
10:h:100:THR:N	10:h:117:SER:O	2.45	0.44
12:j:1:MET:O	12:j:53:HIS:HE1	2.01	0.44
3:A:399:HIS:HB3	3:A:400:PRO:HD3	1.99	0.44
3:A:449:SER:O	4:B:1133:MET:HE2	2.18	0.44
3:A:928:LEU:HD13	3:A:987:VAL:HG11	2.00	0.44
4:B:246:LYS:NZ	4:B:415:GLN:OE1	2.31	0.44
4:B:328:GLU:HA	4:B:331:LEU:HD12	1.99	0.44
4:B:1032:SER:OG	4:B:1089:PRO:HG2	2.17	0.44
6:D:72:ARG:HB3	6:D:76:LYS:NZ	2.32	0.44
10:H:12:VAL:HG21	10:H:26:ILE:HD11	1.99	0.44
13:K:8:GLU:HG2	13:K:37:LYS:NZ	2.33	0.44
18:M:233:TYR:C	18:M:235:LYS:H	2.26	0.44
2:O:-46:DT:H2''	3:a:447:GLN:NE2	2.33	0.43
3:a:368:LYS:HE3	13:k:2:ASN:OD1	2.18	0.43
3:a:368:LYS:HB3	13:k:2:ASN:ND2	2.32	0.43
4:b:604:ARG:HD2	4:b:615:MET:HE1	1.99	0.43
4:b:980:PHE:CZ	4:b:1094:ARG:HG3	2.52	0.43
4:b:1031:LEU:HD21	4:b:1043:ASP:H	1.83	0.43
6:d:123:LEU:CD1	6:d:145:MET:HG3	2.47	0.43
6:d:206:GLU:HG2	6:d:209:ARG:HE	1.83	0.43
7:e:82:PHE:HE1	7:e:111:VAL:HG21	1.83	0.43
9:g:168:LEU:HD23	9:g:168:LEU:HA	1.84	0.43
3:A:557:ASP:C	13:K:26:LYS:HE3	2.43	0.43
4:B:43:LEU:O	4:B:496:ARG:NH2	2.51	0.43
4:B:405:ARG:NE	4:B:629:ASP:OD2	2.38	0.43
4:B:595:ARG:O	4:B:598:GLU:HG3	2.18	0.43
5:C:32:SER:O	5:C:36:VAL:HG13	2.18	0.43
9:G:142:ARG:HG3	9:G:171:ILE:HD13	2.00	0.43
2:O:-59:DA:H2''	2:O:-58:DT:H71	2.00	0.43
2:O:-28:DG:H2'	2:O:-27:DT:H71	2.00	0.43
3:a:108:MET:C	3:a:110:CYS:H	2.26	0.43
3:a:187:LYS:HA	3:a:187:LYS:HD3	1.92	0.43
3:a:597:LEU:HB3	10:h:115:TYR:HE2	1.83	0.43
3:a:977:LYS:HA	3:a:977:LYS:HD3	1.73	0.43
4:b:242:SER:O	4:b:252:SER:HB2	2.18	0.43
6:d:65:GLU:OE1	6:d:68:ARG:NH2	2.50	0.43
6:d:67:ARG:HB3	6:d:71:LYS:NZ	2.32	0.43
9:g:1:MET:HA	9:g:79:PHE:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:538:ASP:OD1	10:H:22:LYS:HB2	2.18	0.43
3:A:764:CYS:SG	3:A:765:VAL:N	2.90	0.43
3:A:965:GLN:HA	3:A:968:GLN:OE1	2.17	0.43
3:A:1207:LEU:CD1	3:A:1211:GLN:HE21	2.31	0.43
3:A:1207:LEU:HD21	3:A:1274:ARG:HH21	1.83	0.43
4:B:223:VAL:HG22	4:B:240:ILE:HD11	2.00	0.43
4:B:862:GLN:HB3	4:B:963:PHE:HD1	1.83	0.43
14:L:51:CYS:HB3	14:L:53:HIS:ND1	2.33	0.43
17:Q:105:ALA:O	18:M:89:GLY:HA2	2.17	0.43
18:M:105:THR:HA	18:M:121:ASP:HA	1.99	0.43
1:N:56:DT:H5'	1:N:56:DT:H6	1.83	0.43
3:a:535:THR:HG21	3:a:617:VAL:H	1.83	0.43
3:a:955:PRO:C	3:a:956:LEU:HD22	2.43	0.43
4:b:597:MET:HE2	4:b:617:ARG:HB2	2.00	0.43
5:c:5:GLY:O	5:c:7:GLN:NE2	2.50	0.43
6:d:220:LEU:HG	6:d:221:TYR:N	2.34	0.43
7:e:16:PHE:CZ	7:e:20:LYS:HD2	2.53	0.43
10:h:99:GLY:HA3	10:h:118:PHE:CD1	2.43	0.43
13:k:53:ASP:OD2	13:k:56:VAL:HG13	2.18	0.43
3:A:146:MET:HB3	3:A:171:GLN:O	2.18	0.43
3:A:513:SER:HB3	3:A:520:CYS:HB3	1.99	0.43
3:A:543:LEU:HD21	3:A:570:PRO:HB2	2.00	0.43
3:A:1063:MET:HG3	4:B:1139:ILE:HG22	2.00	0.43
4:B:344:LYS:HA	4:B:348:ARG:HE	1.82	0.43
4:B:499:ASN:OD1	4:B:500:THR:N	2.51	0.43
4:B:996:ARG:HG3	4:B:1007:VAL:HG11	2.00	0.43
18:M:86:ASN:CG	18:M:87:LEU:H	2.25	0.43
18:M:225:MET:SD	18:M:226:PRO:HD2	2.58	0.43
3:a:33:ALA:O	3:a:83:HIS:ND1	2.51	0.43
3:a:209:ASN:CA	3:a:212:LYS:HZ3	2.27	0.43
3:a:353:ILE:HG21	3:a:487:MET:HE2	2.00	0.43
3:a:441:PRO:HG2	3:a:498:ARG:HB2	2.01	0.43
3:a:490:HIS:HB3	4:b:1150:ARG:NH1	2.32	0.43
3:a:821:ARG:HD3	4:b:514:LEU:HB2	1.99	0.43
3:a:871:ASP:OD2	3:a:873:MET:HB2	2.18	0.43
3:a:1100:ARG:HH12	3:a:1111:MET:HE3	1.83	0.43
3:a:1424:VAL:O	3:a:1428:VAL:HG23	2.18	0.43
4:b:67:SER:OG	4:b:68:THR:N	2.51	0.43
4:b:563:MET:SD	4:b:588:GLY:HA3	2.58	0.43
4:b:1034:VAL:HG11	4:b:1055:ILE:HG23	2.00	0.43
9:g:57:GLN:CD	9:g:57:GLN:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:k:19:LEU:HD23	13:k:19:LEU:H	1.84	0.43
3:A:666:ILE:CG1	4:B:1026:LEU:HB3	2.48	0.43
3:A:943:LEU:HA	3:A:946:VAL:HG22	2.00	0.43
4:B:424:LEU:O	4:B:428:ILE:HG13	2.19	0.43
4:B:803:LEU:HG	4:B:822:ASN:ND2	2.33	0.43
6:D:192:LYS:HZ3	6:D:204:ASP:HB2	1.82	0.43
17:Q:128:ASN:HB3	17:Q:131:THR:OG1	2.18	0.43
1:N:25:DA:H2''	1:N:26:DA:H8	1.82	0.43
1:N:41:DT:H1'	1:N:42:DT:H5'	1.98	0.43
4:b:74:LEU:HD21	4:b:83:ASN:H	1.83	0.43
4:b:287:ARG:NE	4:b:292:ILE:HA	2.32	0.43
4:b:363:HIS:HB2	4:b:585:VAL:HG21	2.00	0.43
4:b:800:GLN:OE1	4:b:822:ASN:N	2.23	0.43
4:b:852:ARG:NH1	5:c:65:HIS:HD2	2.16	0.43
4:b:992:ILE:HD11	4:b:994:TYR:CZ	2.53	0.43
7:e:180:ARG:NH1	7:e:192:ARG:HB2	2.33	0.43
3:A:42:ASP:HB3	3:A:45:GLN:C	2.43	0.43
3:A:67:CYS:C	3:A:68:GLN:HG3	2.43	0.43
3:A:115:LEU:N	3:A:164:ARG:HH22	2.15	0.43
3:A:230:ARG:HB3	3:A:232:GLU:OE1	2.19	0.43
3:A:311:GLN:HG2	3:A:312:PRO:CD	2.46	0.43
3:A:476:SER:OG	3:A:477:PRO:HD3	2.19	0.43
3:A:543:LEU:HD22	3:A:572:TRP:HZ3	1.83	0.43
4:B:637:LEU:HD23	4:B:637:LEU:HA	1.84	0.43
5:C:45:ALA:HA	5:C:72:LEU:HD13	2.00	0.43
6:D:123:LEU:HA	6:D:145:MET:CE	2.48	0.43
7:E:47:CYS:C	7:E:54:GLN:HE22	2.26	0.43
12:J:24:LEU:O	12:J:28:ASP:HB2	2.18	0.43
16:R:16:C:C6	16:R:16:C:O5'	2.72	0.43
3:a:195:ASP:OD1	3:a:196:GLU:N	2.50	0.43
3:a:212:LYS:HB2	3:a:212:LYS:HE2	1.79	0.43
3:a:666:ILE:HD11	4:b:1026:LEU:HB3	2.01	0.43
3:a:806:ARG:HD3	4:b:728:ARG:HA	2.00	0.43
3:a:1029:ARG:NH2	3:a:1033:GLN:OE1	2.52	0.43
3:a:1154:TYR:CE1	3:a:1190:PRO:HB2	2.54	0.43
4:b:380:TYR:O	4:b:384:ARG:HG2	2.19	0.43
4:b:680:THR:H	4:b:683:SER:CB	2.31	0.43
6:d:160:VAL:O	6:d:164:ILE:HG13	2.19	0.43
11:i:25:LEU:HD23	11:i:25:LEU:H	1.84	0.43
13:k:102:LYS:HG3	13:k:103:THR:N	2.33	0.43
13:k:107:THR:O	13:k:111:LEU:HD23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:32:VAL:N	3:A:81:PHE:O	2.51	0.43
3:A:360:GLU:OE1	3:A:360:GLU:N	2.40	0.43
3:A:1173:HIS:CD2	3:A:1227:ILE:HG23	2.54	0.43
4:B:213:ILE:O	4:B:215:GLN:NE2	2.52	0.43
4:B:689:LEU:HD23	4:B:689:LEU:HA	1.87	0.43
5:C:162:GLY:HA3	5:C:170:TRP:CD2	2.53	0.43
6:D:55:ALA:O	6:D:59:ILE:HG23	2.18	0.43
13:K:39:ASP:OD1	13:K:41:THR:HG22	2.19	0.43
14:L:63:ARG:NH1	14:L:64:LEU:H	2.17	0.43
3:a:119:ASN:HB3	3:a:122:MET:CE	2.43	0.43
3:a:434:ARG:NH1	3:a:437:MET:HG2	2.33	0.43
3:a:446:ARG:CB	3:a:487:MET:HG3	2.49	0.43
3:a:483:ASP:N	3:a:483:ASP:OD1	2.50	0.43
3:a:1169:ILE:H	3:a:1169:ILE:HD12	1.83	0.43
4:b:169:ARG:H	4:b:454:THR:HG1	1.65	0.43
11:i:19:ASP:HB3	11:i:24:ARG:N	2.24	0.43
3:A:189:ARG:HA	3:A:189:ARG:HD2	1.58	0.43
3:A:337:ARG:HE	3:A:839:ARG:HH22	1.66	0.43
3:A:844:ALA:HB3	3:A:845:LEU:HD12	2.01	0.43
3:A:1263:ILE:O	3:A:1267:MET:HG2	2.19	0.43
4:B:174:LEU:HD23	4:B:174:LEU:HA	1.73	0.43
4:B:395:GLN:OE1	4:B:396:ASP:N	2.52	0.43
4:B:882:THR:HB	4:B:885:MET:HB3	2.00	0.43
5:C:11:ARG:HG2	5:C:11:ARG:HH11	1.84	0.43
6:D:177:VAL:HA	6:D:180:LEU:HB2	2.01	0.43
12:J:17:LYS:HB3	12:J:39:LEU:HD21	2.01	0.43
2:O:-2:DA:H2"	2:O:-1:DG:N7	2.33	0.43
3:a:66:LYS:HG2	3:a:68:GLN:N	2.33	0.43
3:a:108:MET:SD	3:a:171:GLN:HG2	2.59	0.43
3:a:419:LYS:HG3	3:a:420:ARG:HG2	1.99	0.43
3:a:928:LEU:HD23	3:a:987:VAL:HG11	1.99	0.43
3:a:1111:MET:SD	3:a:1331:SER:HA	2.59	0.43
3:a:1269:GLU:OE1	3:a:1269:GLU:N	2.52	0.43
4:b:449:ASN:O	4:b:453:ILE:HG12	2.19	0.43
4:b:788:ARG:NE	4:b:790:ASP:OD2	2.52	0.43
4:b:827:ILE:HD12	4:b:1012:ILE:HG23	2.01	0.43
4:b:867:GLY:HA3	4:b:868:MET:O	2.18	0.43
5:c:123:ASN:OD1	5:c:124:LEU:N	2.51	0.43
3:A:354:SER:OG	3:A:469:ARG:NE	2.52	0.43
3:A:368:LYS:HZ3	13:K:3:ALA:HA	1.82	0.43
4:B:603:LEU:HB3	4:B:609:ILE:CD1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:235:VAL:HG13	5:C:237:SER:H	1.82	0.43
5:C:249:ASP:O	5:C:252:GLN:HG3	2.19	0.43
7:E:4:GLU:HA	7:E:7:ARG:HG2	2.00	0.43
9:G:91:VAL:HG11	9:G:137:ILE:HG12	2.01	0.43
10:H:5:LEU:HB2	10:H:59:ILE:HG21	2.01	0.43
10:H:118:PHE:HB2	10:H:121:LEU:HB2	2.01	0.43
11:I:113:ASP:OD2	11:I:115:LYS:HB2	2.19	0.43
3:a:132:LYS:O	3:a:135:PHE:HB3	2.18	0.43
3:a:403:LYS:HZ1	3:a:416:ARG:HH12	1.67	0.43
3:a:495:GLU:HA	3:a:498:ARG:HG2	2.00	0.43
3:a:1070:GLN:NE2	4:b:1137:CYS:SG	2.76	0.43
4:b:694:ASP:OD1	4:b:695:ALA:N	2.52	0.43
5:c:146:LYS:C	5:c:147:LEU:HD12	2.44	0.43
6:d:38:ILE:HG13	6:d:39:ASN:H	1.84	0.43
6:d:72:ARG:O	6:d:75:LYS:HG3	2.19	0.43
7:e:21:GLU:OE1	7:e:143:ASN:ND2	2.42	0.43
9:g:15:PRO:HD3	9:g:67:SER:HA	2.01	0.43
11:i:19:ASP:O	11:i:23:ASN:HA	2.19	0.43
3:A:842:VAL:O	3:A:846:GLU:HG3	2.19	0.43
3:A:1004:ASN:HD21	3:A:1007:ILE:HG12	1.84	0.43
3:A:1042:PHE:O	3:A:1046:LEU:HG	2.19	0.43
3:A:1171:GLN:O	3:A:1175:SER:OG	2.36	0.43
12:J:4:PRO:HD3	12:J:53:HIS:HD2	1.84	0.43
1:N:63:DT:H2"	1:N:64:DA:N7	2.34	0.43
3:a:99:ILE:HD12	3:a:234:MET:HG2	2.01	0.43
3:a:519:PRO:HD3	3:a:631:HIS:ND1	2.34	0.43
3:a:536:LEU:HD23	3:a:536:LEU:H	1.83	0.43
3:a:1412:ALA:O	3:a:1416:ALA:N	2.52	0.43
4:b:100:PRO:HA	4:b:126:SER:HB3	2.00	0.43
4:b:203:PHE:O	4:b:210:LYS:N	2.52	0.43
4:b:228:LYS:HG3	4:b:229:ALA:H	1.84	0.43
4:b:569:TYR:CZ	4:b:571:PRO:HA	2.54	0.43
7:e:17:ARG:NH1	7:e:35:VAL:O	2.52	0.43
10:h:7:ASP:OD1	10:h:8:ASP:N	2.51	0.43
3:A:81:PHE:CZ	4:B:1208:MET:HE3	2.54	0.43
3:A:88:LYS:HB3	3:A:293:GLU:OE2	2.19	0.43
3:A:807:GLY:HA3	4:B:728:ARG:HH22	1.84	0.43
3:A:849:MET:HG3	3:A:1063:MET:HE1	2.00	0.43
3:A:1295:THR:OG1	3:A:1297:GLU:OE1	2.34	0.43
3:A:1400:CYS:HB2	3:A:1405:THR:HG23	2.00	0.43
4:B:431:TYR:HA	4:B:434:ARG:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:487:THR:HG22	4:B:489:SER:N	2.34	0.43
4:B:651:LEU:HD23	4:B:651:LEU:H	1.84	0.43
4:B:836:GLU:OE1	4:B:836:GLU:N	2.52	0.43
4:B:923:GLU:HG3	4:B:924:GLU:OE1	2.19	0.43
7:E:112:TYR:CD1	7:E:116:ILE:HD11	2.54	0.43
10:H:96:VAL:HG12	10:H:143:LEU:HD22	2.00	0.43
11:I:65:ASP:OD2	11:I:67:THR:OG1	2.33	0.43
2:O:-3:DA:H2	3:A:252:PHE:CD2	2.37	0.42
3:a:960:ILE:HB	3:a:1025:ARG:NH1	2.34	0.42
3:a:1226:VAL:HG23	3:a:1240:CYS:SG	2.58	0.42
4:b:349:ILE:H	4:b:349:ILE:HD12	1.83	0.42
4:b:481:GLN:NE2	15:r:44:C:OP1	2.52	0.42
4:b:494:HIS:CD2	4:b:497:ARG:HH12	2.37	0.42
4:b:757:PRO:HG3	4:b:983:ARG:NH2	2.33	0.42
4:b:758:PHE:CE2	4:b:1044:ALA:HA	2.54	0.42
4:b:918:ILE:HA	4:b:919:SER:O	2.19	0.42
4:b:1074:ASN:HD21	4:b:1076:HIS:HB2	1.84	0.42
4:b:1155:SER:OG	4:b:1156:ASP:N	2.47	0.42
4:b:1185:CYS:HA	6:d:16:LYS:HZ2	1.84	0.42
4:b:1206:GLU:O	4:b:1210:MET:N	2.52	0.42
5:c:56:THR:HG22	5:c:58:LEU:H	1.84	0.42
9:g:28:THR:O	9:g:32:GLU:OE1	2.37	0.42
12:j:7:CYS:SG	12:j:46:CYS:HA	2.59	0.42
3:A:116:ASP:HB3	3:A:164:ARG:CZ	2.49	0.42
3:A:252:PHE:HE1	16:R:4:C:N1	2.17	0.42
3:A:350:ARG:NE	3:A:486:GLU:OE1	2.28	0.42
3:A:1104:ILE:HD12	3:A:1352:VAL:HG22	2.01	0.42
4:B:69:LEU:HD12	4:B:69:LEU:HA	1.84	0.42
4:B:912:ILE:HG13	4:B:939:THR:HB	1.99	0.42
3:a:489:LEU:HA	3:a:489:LEU:HD12	1.80	0.42
3:a:792:TYR:HA	3:a:797:LYS:NZ	2.34	0.42
4:b:1004:GLU:OE2	4:b:1064:TYR:OH	2.25	0.42
5:c:252:GLN:HA	5:c:255:VAL:HG12	2.01	0.42
9:g:83:LYS:HD3	9:g:148:GLU:O	2.19	0.42
10:h:6:PHE:O	10:h:58:THR:HA	2.20	0.42
10:h:47:PHE:CZ	10:h:146:ARG:HD3	2.54	0.42
11:i:73:ARG:H	11:i:83:ASN:HD21	1.67	0.42
3:A:370:ILE:O	3:A:374:LEU:N	2.50	0.42
3:A:390:GLN:NE2	3:A:390:GLN:O	2.51	0.42
3:A:843:LYS:HD3	3:A:846:GLU:CD	2.44	0.42
3:A:857:ARG:HB3	3:A:861:GLY:HA2	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:951:GLU:O	3:A:954:TRP:NE1	2.48	0.42
6:D:126:ILE:HG13	6:D:127:ASP:N	2.34	0.42
12:J:23:ASN:HB2	12:J:27:GLU:OE2	2.19	0.42
3:a:43:GLU:OE2	3:a:46:THR:OG1	2.37	0.42
3:a:744:LYS:O	3:a:748:MET:HG2	2.18	0.42
3:a:1397:LEU:HA	3:a:1400:CYS:SG	2.60	0.42
4:b:744:HIS:CE1	4:b:746:SER:HG	2.31	0.42
4:b:917:PRO:O	4:b:919:SER:OG	2.37	0.42
5:c:62:PHE:CZ	12:j:1:MET:HE1	2.54	0.42
6:d:150:ASN:OD1	6:d:155:ARG:NH2	2.52	0.42
6:d:153:ARG:HH12	6:d:163:VAL:HG11	1.83	0.42
10:h:33:GLN:OE1	10:h:35:GLN:N	2.52	0.42
3:A:302:THR:HA	3:A:305:ASP:O	2.19	0.42
3:A:368:LYS:NZ	13:K:2:ASN:O	2.49	0.42
3:A:385:ILE:O	3:A:389:THR:OG1	2.20	0.42
3:A:778:GLY:HA3	4:B:516:ASN:HB2	2.00	0.42
3:A:1173:HIS:NE2	3:A:1227:ILE:HG23	2.35	0.42
3:A:1326:ARG:HA	7:E:148:GLU:OE2	2.18	0.42
4:B:21:GLU:N	4:B:21:GLU:OE1	2.52	0.42
4:B:828:ALA:O	4:B:834:ASN:ND2	2.53	0.42
5:C:101:LEU:HB3	5:C:155:LEU:HB2	2.00	0.42
5:C:239:PRO:O	5:C:242:GLN:HB2	2.18	0.42
5:C:257:SER:O	5:C:260:LEU:HG	2.19	0.42
8:F:79:ARG:NH1	8:F:150:GLU:OE1	2.38	0.42
3:a:37:PHE:CD2	3:a:50:ILE:HG12	2.55	0.42
3:a:368:LYS:HD2	3:a:464:PRO:HG3	2.01	0.42
3:a:451:HIS:CD2	3:a:453:MET:HE2	2.54	0.42
3:a:574:GLY:O	3:a:577:ILE:HG22	2.19	0.42
3:a:646:PHE:O	3:a:647:GLY:C	2.61	0.42
3:a:672:ASP:OD1	3:a:673:GLY:N	2.53	0.42
3:a:974:ASP:OD2	3:a:977:LYS:HG2	2.19	0.42
3:a:993:LEU:HD21	3:a:1046:LEU:HB3	2.00	0.42
3:a:1426:GLU:O	3:a:1430:LEU:HB2	2.20	0.42
5:c:182:PRO:HG2	5:c:183:TRP:CD1	2.51	0.42
9:g:13:LEU:HD11	9:g:17:PHE:HB2	2.00	0.42
10:h:116:TYR:HB2	10:h:123:MET:HG3	2.02	0.42
3:A:914:GLU:OE1	3:A:978:PRO:HB2	2.20	0.42
3:A:1293:SER:HB3	3:A:1297:GLU:H	1.83	0.42
4:B:251:ILE:H	4:B:251:ILE:HD12	1.84	0.42
4:B:326:ASP:O	4:B:329:THR:OG1	2.35	0.42
4:B:658:ILE:O	4:B:662:MET:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:130:ARG:H	10:H:130:ARG:CD	2.32	0.42
1:N:-3:DT:H2''	1:N:-2:DG:H8	1.84	0.42
2:O:5:DT:H2''	2:O:6:DA:C8	2.54	0.42
3:a:266:LEU:HD23	3:a:266:LEU:HA	1.87	0.42
3:a:570:PRO:C	3:a:571:LEU:HD12	2.44	0.42
3:a:736:ASN:C	3:a:736:ASN:HD22	2.26	0.42
3:a:860:LEU:HD22	3:a:862:ASN:ND2	2.34	0.42
4:b:194:GLU:OE1	4:b:195:CYS:N	2.52	0.42
4:b:566:LEU:HD11	4:b:586:TRP:CD1	2.55	0.42
4:b:616:ILE:HG22	4:b:697:GLU:HA	2.00	0.42
4:b:789:MET:HE1	4:b:967:ARG:CZ	2.50	0.42
4:b:830:TYR:CE1	4:b:1000:PRO:HD3	2.54	0.42
4:b:990:ILE:H	4:b:990:ILE:HD12	1.85	0.42
7:e:175:LEU:HD22	7:e:213:ILE:HG13	2.02	0.42
8:f:81:THR:HG21	8:f:136:ARG:HD3	2.01	0.42
8:f:135:ARG:HD3	8:f:135:ARG:HA	1.84	0.42
10:h:89:LEU:HD23	10:h:90:ALA:C	2.44	0.42
10:h:89:LEU:HD23	10:h:90:ALA:N	2.34	0.42
10:h:99:GLY:HA3	10:h:118:PHE:HA	2.01	0.42
3:A:92:HIS:NE2	3:A:304:MET:HE2	2.35	0.42
3:A:274:ILE:O	3:A:277:GLU:HG3	2.19	0.42
3:A:1202:MET:HE3	3:A:1207:LEU:HB3	2.01	0.42
3:A:1315:GLU:OE1	3:A:1315:GLU:N	2.53	0.42
4:B:203:PHE:N	4:B:210:LYS:O	2.49	0.42
4:B:1152:MET:HA	4:B:1152:MET:HE3	2.01	0.42
5:C:229:TYR:O	5:C:230:MET:HE2	2.19	0.42
13:K:18:LYS:HA	13:K:18:LYS:HD2	1.89	0.42
16:R:16:C:C6	16:R:16:C:C3'	3.03	0.42
3:a:434:ARG:NH1	3:a:437:MET:HE3	2.35	0.42
3:a:1328:TYR:CG	3:a:1329:THR:N	2.88	0.42
4:b:270:LYS:HD3	4:b:279:ASP:HB2	2.02	0.42
4:b:287:ARG:NH2	4:b:294:ASP:OD1	2.47	0.42
4:b:616:ILE:CG2	4:b:697:GLU:HA	2.50	0.42
4:b:862:GLN:HB3	4:b:963:PHE:HD2	1.83	0.42
5:c:16:ASP:OD1	5:c:16:ASP:N	2.48	0.42
6:d:172:LEU:HD23	6:d:173:HIS:O	2.20	0.42
10:h:84:ALA:H	13:k:54:ARG:NH1	2.17	0.42
11:i:5:ARG:C	11:i:14:LEU:HD23	2.44	0.42
12:j:1:MET:N	12:j:57:ILE:HB	2.35	0.42
15:r:42:U:H2'	15:r:43:A:C8	2.55	0.42
3:A:12:ARG:HH21	4:B:1218:THR:CG2	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:756:ILE:H	3:A:756:ILE:HD12	1.85	0.42
3:A:805:LEU:HD12	3:A:805:LEU:HA	1.78	0.42
4:B:760:ASP:OD1	4:B:761:HIS:N	2.53	0.42
4:B:979:LYS:O	4:B:1095:LEU:HB2	2.19	0.42
5:C:54:ASN:OD1	5:C:56:THR:HG22	2.20	0.42
6:D:123:LEU:HA	6:D:145:MET:HE1	1.99	0.42
3:a:43:GLU:HG2	3:a:44:THR:H	1.85	0.42
3:a:139:TRP:CE2	3:a:143:LYS:HE3	2.55	0.42
3:a:300:VAL:O	3:a:304:MET:HG2	2.20	0.42
3:a:965:GLN:HA	3:a:968:GLN:OE1	2.19	0.42
3:a:1425:SER:O	3:a:1428:VAL:N	2.52	0.42
4:b:219:ALA:HB2	4:b:405:ARG:HG2	2.02	0.42
4:b:286:PHE:HE1	4:b:378:LEU:HD22	1.80	0.42
4:b:287:ARG:O	4:b:327:ARG:HB3	2.20	0.42
4:b:956:THR:CG2	4:b:960:GLY:HA2	2.50	0.42
4:b:1196:ILE:HD11	4:b:1201:LYS:HB3	2.02	0.42
5:c:48:SER:OG	5:c:158:VAL:HB	2.19	0.42
5:c:183:TRP:HE1	5:c:207:CYS:HA	1.85	0.42
9:g:15:PRO:HA	9:g:18:PHE:CE1	2.55	0.42
9:g:100:GLU:HB3	9:g:107:LYS:HE2	2.02	0.42
10:h:110:ASP:O	10:h:128:ASN:ND2	2.37	0.42
3:A:205:GLU:OE1	3:A:205:GLU:N	2.34	0.42
3:A:207:ILE:H	3:A:207:ILE:HD12	1.85	0.42
3:A:858:ASN:OD1	3:A:862:ASN:N	2.49	0.42
3:A:1225:PHE:CE2	3:A:1227:ILE:HD11	2.55	0.42
3:A:1384:VAL:O	3:A:1384:VAL:HG23	2.20	0.42
3:A:1444:MET:HE3	8:F:135:ARG:NE	2.33	0.42
4:B:954:VAL:O	14:L:56:LEU:HB2	2.19	0.42
4:B:987:LYS:HZ3	16:R:12:A:P	2.41	0.42
8:F:70:LYS:C	8:F:72:LYS:H	2.28	0.42
10:H:18:GLY:C	10:H:19:ARG:HG2	2.44	0.42
12:J:1:MET:H1	12:J:56:LEU:HB2	1.85	0.42
13:K:81:TYR:CE2	13:K:86:ALA:HB2	2.54	0.42
3:a:128:ILE:O	3:a:134:ARG:HB3	2.20	0.42
3:a:153:PRO:O	3:a:161:LEU:HA	2.19	0.42
3:a:1136:SER:C	3:a:1274:ARG:HH12	2.28	0.42
3:a:1379:GLY:O	7:e:179:GLN:HB2	2.20	0.42
4:b:1185:CYS:HA	6:d:16:LYS:NZ	2.35	0.42
5:c:11:ARG:NH2	5:c:209:TYR:OH	2.53	0.42
6:d:64:VAL:O	6:d:67:ARG:HB2	2.19	0.42
7:e:202:SER:OG	7:e:203:GLU:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:f:101:ILE:HA	8:f:105:ALA:HB3	2.01	0.42
9:g:65:ASP:CG	9:g:67:SER:HG	2.21	0.42
10:h:145:ARG:HA	10:h:145:ARG:HD3	1.61	0.42
14:l:48:CYS:HB3	14:l:51:CYS:O	2.20	0.42
3:A:90:VAL:HG21	3:A:300:VAL:HG11	2.01	0.42
3:A:343:LYS:HE3	4:B:1117:GLN:HE21	1.84	0.42
3:A:415:LEU:HA	3:A:418:SER:HB2	2.00	0.42
3:A:672:ASP:OD2	3:A:674:PRO:HG2	2.20	0.42
3:A:889:SER:HA	3:A:1297:GLU:HG3	2.00	0.42
3:A:902:LEU:HD23	3:A:902:LEU:H	1.85	0.42
3:A:1244:ARG:HA	3:A:1245:PRO:HD3	1.92	0.42
4:B:526:GLU:HG2	4:B:771:SER:OG	2.20	0.42
4:B:839:MET:HE1	4:B:988:GLY:C	2.45	0.42
4:B:954:VAL:HG23	4:B:964:VAL:HG22	2.02	0.42
4:B:1036:ALA:O	12:J:47:ARG:HD3	2.19	0.42
5:C:16:ASP:OD1	5:C:16:ASP:N	2.47	0.42
6:D:14:ARG:HE	6:D:17:LYS:NZ	2.18	0.42
7:E:48:ASP:CG	7:E:52:ARG:HB2	2.44	0.42
9:G:99:PHE:H	9:G:115:MET:HE1	1.84	0.42
14:L:27:LEU:HD11	14:L:62:LYS:NZ	2.35	0.42
3:a:341:MET:HE2	3:a:341:MET:HB2	1.87	0.42
3:a:764:CYS:HA	3:a:802:ASN:O	2.19	0.42
3:a:913:LEU:HD12	3:a:979:SER:O	2.20	0.42
3:a:1434:ALA:O	3:a:1436:ILE:N	2.53	0.42
4:b:126:SER:C	4:b:169:ARG:HG3	2.45	0.42
4:b:147:LEU:C	4:b:148:LYS:HG2	2.45	0.42
4:b:246:LYS:H	4:b:418:LYS:NZ	2.17	0.42
4:b:552:MET:HA	4:b:555:ILE:HD13	2.01	0.42
4:b:936:ASP:OD1	4:b:937:ALA:N	2.53	0.42
4:b:1085:ILE:HG22	4:b:1086:PHE:O	2.20	0.42
4:b:1106:ARG:HH12	4:b:1109:GLY:H	1.66	0.42
4:b:1124:ARG:NH1	15:r:38:G:H5'	2.35	0.42
4:b:1194:ILE:HG22	4:b:1196:ILE:HG23	2.02	0.42
6:d:49:ALA:HB1	9:g:1:MET:HE2	2.02	0.42
14:l:40:LEU:HD12	14:l:44:ASP:HB2	2.01	0.42
3:A:367:PRO:HA	3:A:463:ILE:O	2.19	0.42
3:A:453:MET:C	3:A:455:MET:H	2.27	0.42
3:A:851:HIS:CG	8:F:139:PRO:HG3	2.55	0.42
4:B:282:ILE:HD12	4:B:382:ILE:HD13	2.01	0.42
4:B:412:LEU:HB3	4:B:466:TRP:HZ2	1.83	0.42
4:B:1153:GLU:OE1	4:B:1153:GLU:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:63:LEU:HD13	6:D:126:ILE:HG22	2.01	0.42
7:E:198:ILE:HB	7:E:210:SER:OG	2.20	0.42
9:G:115:MET:HG2	9:G:163:ILE:HD11	2.01	0.42
11:I:19:ASP:CG	11:I:22:ASN:HB2	2.45	0.42
18:M:86:ASN:HA	18:M:88:HIS:CE1	2.55	0.42
1:N:13:DT:H6	1:N:13:DT:H2'	1.68	0.42
1:N:30:DA:H2''	1:N:31:DA:C8	2.55	0.42
3:a:31:SER:HB2	3:a:83:HIS:HB3	2.01	0.42
3:a:1017:LEU:HD12	7:e:204:THR:O	2.19	0.42
4:b:47:GLN:NE2	4:b:173:MET:HG3	2.19	0.42
4:b:168:GLY:HA2	4:b:450:ALA:HB1	2.02	0.42
4:b:562:GLY:O	4:b:590:HIS:ND1	2.52	0.42
4:b:661:LEU:HD23	4:b:661:LEU:HA	1.82	0.42
4:b:1219:ASP:OD1	4:b:1219:ASP:N	2.51	0.42
11:i:8:ARG:NE	11:i:8:ARG:HA	2.34	0.42
3:A:446:ARG:CD	3:A:480:ALA:HB2	2.49	0.42
3:A:589:GLN:HG3	3:A:606:LEU:HD13	2.01	0.42
4:B:297:ILE:H	4:B:297:ILE:HD12	1.84	0.42
4:B:344:LYS:HZ2	4:B:348:ARG:H	1.68	0.42
4:B:403:LYS:HZ2	4:B:403:LYS:HG2	1.65	0.42
4:B:975:GLN:HG2	4:B:976:ILE:H	1.85	0.42
4:B:998:ASP:HB2	4:B:1076:HIS:CD2	2.55	0.42
4:B:1115:THR:HG23	4:B:1117:GLN:H	1.85	0.42
5:C:183:TRP:CE3	5:C:213:PRO:HD3	2.55	0.42
6:D:173:HIS:CD2	6:D:175:PHE:HB3	2.54	0.42
7:E:147:HIS:CE1	7:E:149:LEU:HB2	2.54	0.42
9:G:121:PHE:HB2	9:G:130:TYR:CD2	2.55	0.42
18:M:68:VAL:N	18:M:217:THR:O	2.53	0.42
2:O:-64:DT:H2''	2:O:-63:DA:C8	2.55	0.41
2:O:-45:DA:H3'	2:O:-44:DG:H8	1.85	0.41
2:O:-20:DG:H2''	2:O:-19:DC:C6	2.54	0.41
3:a:668:ASP:OD2	3:a:742:ASN:ND2	2.44	0.41
3:a:1115:SER:OG	3:a:1308:THR:O	2.27	0.41
3:a:1141:THR:OG1	3:a:1273:LEU:HB2	2.20	0.41
4:b:64:CYS:HA	4:b:67:SER:HB3	2.02	0.41
4:b:394:ASP:CB	11:i:91:ARG:HH22	2.25	0.41
4:b:957:ASN:OD1	4:b:960:GLY:N	2.52	0.41
4:b:1001:PHE:HE2	5:c:178:PHE:HB3	1.84	0.41
4:b:1200:ALA:O	4:b:1203:LEU:HB3	2.20	0.41
5:c:99:LEU:HB2	5:c:157:CYS:HB2	2.01	0.41
9:g:22:MET:SD	9:g:23:LYS:N	2.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:h:110:ASP:C	10:h:128:ASN:HD22	2.24	0.41
12:j:7:CYS:O	12:j:11:GLY:N	2.53	0.41
3:A:344:ARG:CZ	4:B:1129:ARG:HB2	2.50	0.41
3:A:364:VAL:HG12	3:A:459:ARG:O	2.21	0.41
3:A:444:PHE:CZ	3:A:487:MET:HG2	2.55	0.41
3:A:1199:ARG:NH1	3:A:1231:ASP:OD1	2.53	0.41
4:B:51:PHE:CD1	4:B:173:MET:HB2	2.55	0.41
4:B:144:GLY:HA2	4:B:145:ARG:HA	1.79	0.41
4:B:638:PHE:CD2	4:B:743:ILE:HG22	2.55	0.41
4:B:847:ASP:HB3	5:C:167:HIS:CE1	2.55	0.41
5:C:10:ILE:HB	13:K:108:GLU:CD	2.45	0.41
5:C:33:LEU:HA	5:C:36:VAL:HG22	2.01	0.41
5:C:39:ALA:O	5:C:164:ALA:HB3	2.21	0.41
5:C:148:ARG:HD3	12:J:61:LEU:O	2.20	0.41
7:E:60:PHE:O	7:E:80:VAL:HG22	2.20	0.41
7:E:171:LYS:O	7:E:171:LYS:HG3	2.20	0.41
7:E:171:LYS:C	7:E:173:SER:H	2.28	0.41
8:F:130:ILE:HB	8:F:148:VAL:HG11	2.01	0.41
18:M:133:TYR:HB3	18:M:214:ILE:HD11	2.01	0.41
2:O:-13:DA:C8	3:A:832:ALA:HA	2.55	0.41
3:a:370:ILE:HD12	3:a:370:ILE:H	1.85	0.41
3:a:399:HIS:HB3	3:a:400:PRO:HD3	2.01	0.41
3:a:407:ARG:HB2	3:a:430:TRP:CZ2	2.54	0.41
3:a:567:LYS:HB3	10:h:95:TYR:HA	2.01	0.41
3:a:648:ASN:O	3:a:652:VAL:HG12	2.19	0.41
3:a:1199:ARG:HH22	3:a:1231:ASP:CG	2.28	0.41
4:b:428:ILE:HG22	4:b:432:MET:CE	2.51	0.41
4:b:583:ASN:N	4:b:626:ILE:O	2.51	0.41
4:b:662:MET:O	4:b:665:GLU:HG3	2.19	0.41
4:b:840:ILE:O	4:b:1010:LEU:HA	2.20	0.41
5:c:18:VAL:HG12	5:c:20:PHE:CD2	2.55	0.41
5:c:52:GLU:HG2	5:c:53:THR:HG23	2.02	0.41
13:k:65:HIS:CD2	13:k:67:PHE:H	2.37	0.41
3:A:41:MET:HA	3:A:49:LYS:HA	2.01	0.41
3:A:50:ILE:HG13	3:A:51:GLY:H	1.85	0.41
3:A:332:LYS:HA	3:A:337:ARG:NH1	2.35	0.41
3:A:1063:MET:CE	3:A:1436:ILE:HG23	2.50	0.41
3:A:1195:LEU:O	3:A:1237:ILE:HA	2.20	0.41
3:A:1438:THR:OG1	8:F:92:ARG:HD3	2.20	0.41
4:B:225:VAL:N	4:B:396:ASP:OD2	2.44	0.41
4:B:737:THR:HG22	11:I:66:PRO:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:192:LYS:HG2	6:D:199:ASN:HA	2.02	0.41
7:E:156:LEU:HB2	7:E:195:VAL:O	2.21	0.41
9:G:56:ILE:C	9:G:57:GLN:OE1	2.63	0.41
10:H:101:ALA:HB2	10:H:116:TYR:CE1	2.55	0.41
11:I:28:GLU:HA	11:I:35:VAL:HA	2.02	0.41
18:M:108:LEU:HB3	18:M:118:HIS:HA	2.00	0.41
1:N:32:DA:H1'	1:N:33:DA:C8	2.54	0.41
3:a:251:SER:OG	3:a:256:GLN:O	2.30	0.41
3:a:338:GLY:HA2	4:b:1129:ARG:HH22	1.85	0.41
3:a:638:GLY:O	3:a:640:GLN:N	2.53	0.41
3:a:860:LEU:O	3:a:860:LEU:HD23	2.20	0.41
4:b:445:LYS:HG3	4:b:446:LEU:HD23	2.01	0.41
4:b:1104:HIS:ND1	4:b:1122:ARG:HG3	2.35	0.41
5:c:88:CYS:HB2	5:c:92:CYS:HB3	2.02	0.41
6:d:184:ALA:HB3	9:g:144:ARG:HH21	1.86	0.41
9:g:91:VAL:HG22	9:g:101:VAL:HG22	2.02	0.41
10:h:142:LEU:HD12	10:h:142:LEU:HA	1.87	0.41
3:A:351:THR:HG22	4:B:1103:ILE:HG13	2.01	0.41
3:A:439:ASN:HA	3:A:460:VAL:H	1.84	0.41
3:A:549:MET:SD	3:A:577:ILE:HD13	2.60	0.41
5:C:148:ARG:NH1	12:J:63:TYR:O	2.53	0.41
7:E:26:ARG:NH1	7:E:189:GLY:HA3	2.36	0.41
9:G:24:GLN:O	9:G:28:THR:HG23	2.20	0.41
10:H:26:ILE:HG22	10:H:40:LEU:HB3	2.02	0.41
10:H:58:THR:HB	10:H:143:LEU:HB2	2.02	0.41
2:O:-17:DC:H2'	2:O:-16:DT:H72	2.02	0.41
3:a:836:TYR:CZ	3:a:840:ARG:HD3	2.55	0.41
3:a:1173:HIS:CD2	3:a:1227:ILE:HG23	2.55	0.41
4:b:586:TRP:HD1	4:b:588:GLY:H	1.67	0.41
4:b:1167:GLY:O	4:b:1215:ARG:HA	2.21	0.41
5:c:138:GLU:OE1	5:c:138:GLU:N	2.53	0.41
5:c:186:LEU:HB3	5:c:188:HIS:NE2	2.36	0.41
7:e:93:MET:SD	7:e:123:LEU:HD23	2.60	0.41
11:i:73:ARG:H	11:i:83:ASN:ND2	2.18	0.41
11:i:92:ARG:HG3	11:i:93:LYS:N	2.35	0.41
13:k:39:ASP:OD1	13:k:41:THR:HG22	2.20	0.41
3:A:57:ARG:O	3:A:68:GLN:HB3	2.20	0.41
3:A:1044:TRP:CD2	3:A:1048:ASN:ND2	2.88	0.41
3:A:1147:THR:HA	3:A:1197:LEU:HD23	2.03	0.41
4:B:438:GLU:HA	4:B:439:ALA:HA	1.68	0.41
5:C:191:TYR:HB3	5:C:201:TRP:NE1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:73:ARG:O	11:I:83:ASN:ND2	2.54	0.41
13:K:84:LYS:O	13:K:87:LEU:HG	2.20	0.41
17:Q:428:LEU:O	17:Q:432:GLY:N	2.52	0.41
3:a:11:LEU:H	3:a:11:LEU:HD23	1.85	0.41
3:a:55:ASP:HA	3:a:58:LEU:CD2	2.42	0.41
3:a:61:ILE:O	3:a:74:MET:HE1	2.19	0.41
3:a:75:ASN:OD1	3:a:76:GLU:N	2.52	0.41
3:a:381:THR:HG23	3:a:384:ASN:ND2	2.35	0.41
3:a:770:VAL:HG23	3:a:822:GLU:HG3	2.02	0.41
3:a:852:TYR:CD1	3:a:1060:PRO:HB2	2.55	0.41
3:a:868:TYR:CE1	3:a:1064:VAL:HG21	2.55	0.41
3:a:1199:ARG:NH2	3:a:1236:LEU:HD21	2.35	0.41
3:a:1212:VAL:O	3:a:1216:ILE:HG12	2.21	0.41
4:b:344:LYS:HD3	4:b:344:LYS:HA	1.78	0.41
4:b:394:ASP:CG	4:b:395:GLN:N	2.78	0.41
4:b:637:LEU:HD23	4:b:637:LEU:HA	1.96	0.41
4:b:1202:LEU:O	4:b:1206:GLU:OE1	2.39	0.41
6:d:57:LEU:HD11	6:d:161:GLY:HA2	2.02	0.41
6:d:190:GLU:HB3	9:g:167:TYR:CE2	2.56	0.41
8:f:89:GLU:HG2	8:f:134:ILE:HD11	2.02	0.41
9:g:116:PRO:HD3	9:g:163:ILE:CG2	2.50	0.41
3:A:956:LEU:HD22	3:A:957:PRO:HD2	2.02	0.41
3:A:1121:GLU:HG3	3:A:1123:GLY:H	1.85	0.41
4:B:880:THR:HA	4:B:931:TYR:N	2.24	0.41
8:F:94:LEU:HD21	8:F:125:LEU:HD22	2.02	0.41
9:G:13:LEU:HD21	9:G:17:PHE:O	2.20	0.41
9:G:138:THR:O	9:G:141:SER:HB3	2.20	0.41
10:H:54:SER:O	10:H:146:ARG:NH1	2.53	0.41
17:Q:104:ARG:H	17:Q:383:SER:HB3	1.86	0.41
18:M:112:ASP:OD1	18:M:118:HIS:NE2	2.54	0.41
2:O:-64:DT:H6	2:O:-64:DT:H2'	1.66	0.41
3:a:1143:LEU:H	3:a:1143:LEU:HD12	1.85	0.41
3:a:1436:ILE:O	3:a:1439:GLY:N	2.38	0.41
5:c:67:LEU:C	5:c:69:LEU:H	2.28	0.41
5:c:148:ARG:O	5:c:148:ARG:HD2	2.19	0.41
9:g:128:PRO:HB2	9:g:131:GLN:HE22	1.85	0.41
10:h:16:ASP:N	10:h:16:ASP:OD1	2.53	0.41
12:j:8:PHE:N	12:j:49:MET:HE1	2.25	0.41
3:A:151:ASP:OD1	3:A:163:SER:HA	2.20	0.41
3:A:362:ASP:OD1	3:A:362:ASP:N	2.53	0.41
3:A:543:LEU:HA	3:A:546:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:929:LEU:O	3:A:932:GLU:HG3	2.20	0.41
3:A:956:LEU:HD23	3:A:956:LEU:HA	1.87	0.41
4:B:441:ASP:OD1	4:B:444:MET:HG3	2.21	0.41
6:D:65:GLU:HA	6:D:68:ARG:CZ	2.51	0.41
7:E:167:ARG:HD3	7:E:167:ARG:HA	1.89	0.41
12:J:3:VAL:HA	12:J:53:HIS:CD2	2.56	0.41
18:M:67:GLN:OE1	18:M:67:GLN:N	2.50	0.41
3:a:62:ASP:C	3:a:64:ASN:H	2.27	0.41
3:a:311:GLN:H	3:a:311:GLN:CD	2.29	0.41
3:a:341:MET:HE1	3:a:1429:ILE:HD11	2.02	0.41
3:a:596:THR:HG23	3:a:598:LEU:H	1.86	0.41
3:a:951:GLU:O	3:a:954:TRP:NE1	2.53	0.41
4:b:175:ARG:HH22	4:b:198:ASP:C	2.16	0.41
4:b:274:PRO:HA	4:b:275:TYR:HA	1.44	0.41
4:b:361:LEU:HB3	4:b:374:LYS:NZ	2.35	0.41
4:b:481:GLN:HG2	15:r:43:A:O2'	2.21	0.41
4:b:826:ALA:HB3	4:b:1011:ILE:CD1	2.50	0.41
5:c:233:GLU:OE1	12:j:43:ARG:NH1	2.26	0.41
6:d:204:ASP:O	6:d:207:LEU:N	2.54	0.41
7:e:171:LYS:C	7:e:173:SER:H	2.29	0.41
8:f:130:ILE:H	8:f:130:ILE:HD12	1.85	0.41
3:A:376:TYR:CD1	3:A:377:PRO:HD2	2.56	0.41
3:A:784:LEU:HD12	3:A:784:LEU:HA	1.95	0.41
3:A:926:GLN:HE21	3:A:930:ASP:CG	2.29	0.41
3:A:1217:LYS:HE3	3:A:1221:LYS:HD2	2.02	0.41
4:B:431:TYR:CD2	4:B:445:LYS:HD2	2.56	0.41
4:B:590:HIS:HD2	4:B:592:ASN:N	2.19	0.41
4:B:1134:GLU:HA	4:B:1137:CYS:SG	2.60	0.41
5:C:101:LEU:HD13	5:C:118:LEU:HB3	2.02	0.41
9:G:38:CYS:HA	9:G:44:TYR:HA	2.02	0.41
13:K:57:LEU:HD23	13:K:57:LEU:HA	1.88	0.41
14:L:31:CYS:SG	14:L:48:CYS:CB	3.08	0.41
3:a:139:TRP:C	3:a:143:LYS:HZ2	2.29	0.41
3:a:265:LYS:HZ3	3:a:303:TYR:N	2.19	0.41
3:a:560:ILE:HD11	13:k:58:PHE:HD1	1.86	0.41
3:a:789:LYS:HE3	11:i:67:THR:HB	2.03	0.41
3:a:816:HIS:HE2	4:b:763:GLN:HB2	1.84	0.41
3:a:858:ASN:C	3:a:860:LEU:H	2.29	0.41
3:a:861:GLY:HA3	7:e:174:GLN:NE2	2.36	0.41
3:a:1112:LYS:HE2	3:a:1112:LYS:HB2	1.82	0.41
7:e:167:ARG:HD3	7:e:167:ARG:HA	1.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:l:34:CYS:O	14:l:36:SER:N	2.53	0.41
14:l:47:ARG:NE	14:l:52:GLY:HA2	2.36	0.41
3:A:129:LYS:O	3:A:129:LYS:HG3	2.21	0.41
3:A:534:LEU:HD13	3:A:656:TRP:CD2	2.55	0.41
3:A:1079:MET:HE2	3:A:1098:VAL:HG23	2.03	0.41
4:B:265:SER:C	4:B:267:ARG:H	2.28	0.41
4:B:295:GLY:O	4:B:299:GLU:HG2	2.21	0.41
4:B:364:ILE:CG2	4:B:585:VAL:HG23	2.48	0.41
11:I:103:CYS:HB3	11:I:106:CYS:SG	2.61	0.41
1:N:-3:DT:OP1	4:B:868:MET:N	2.53	0.41
3:a:455:MET:HE3	3:a:455:MET:HB3	1.95	0.41
3:a:567:LYS:HD3	10:h:95:TYR:CA	2.48	0.41
3:a:857:ARG:HA	3:a:862:ASN:O	2.20	0.41
3:a:890:ASP:CG	3:a:1296:GLY:HA3	2.46	0.41
3:a:1035:TYR:HB3	3:a:1037:LEU:CD2	2.51	0.41
3:a:1106:ASN:OD1	3:a:1385:THR:HG22	2.21	0.41
3:a:1154:TYR:HD1	3:a:1191:TRP:CD2	2.39	0.41
3:a:1157:ASP:HB3	3:a:1160:SER:O	2.21	0.41
3:a:1210:GLY:O	3:a:1214:GLU:HG2	2.21	0.41
3:a:1442:ASP:HB2	8:f:135:ARG:HB3	2.02	0.41
4:b:174:LEU:HD12	4:b:202:TYR:CZ	2.56	0.41
4:b:383:ASN:O	4:b:387:LEU:HD23	2.21	0.41
4:b:555:ILE:H	4:b:555:ILE:HD12	1.85	0.41
4:b:586:TRP:HD1	4:b:587:HIS:N	2.19	0.41
4:b:640:VAL:HB	4:b:739:THR:C	2.45	0.41
4:b:1057:LYS:HG2	4:b:1061:GLU:OE2	2.20	0.41
6:d:23:ASN:O	9:g:83:LYS:HB2	2.20	0.41
6:d:119:ARG:HG3	6:d:149:THR:HG21	2.03	0.41
6:d:186:ASP:CG	6:d:220:LEU:HD22	2.46	0.41
7:e:25:ASP:OD2	7:e:187:TYR:OH	2.30	0.41
7:e:113:GLN:NE2	7:e:137:GLU:OE2	2.54	0.41
7:e:161:LYS:O	7:e:165:LEU:HD23	2.20	0.41
7:e:190:LEU:H	7:e:190:LEU:HD23	1.85	0.41
9:g:42:PHE:O	9:g:80:LYS:HG3	2.21	0.41
9:g:103:VAL:HG23	9:g:106:MET:SD	2.61	0.41
10:h:108:SER:HG	10:h:111:LEU:H	1.68	0.41
13:k:77:THR:OG1	13:k:78:THR:N	2.53	0.41
3:A:13:THR:OG1	3:A:1432:GLN:HG2	2.21	0.41
3:A:67:CYS:O	3:A:68:GLN:HG3	2.20	0.41
3:A:177:ASP:N	3:A:177:ASP:OD1	2.52	0.41
3:A:372:LYS:HZ2	13:K:2:ASN:HB2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:451:HIS:HD2	3:A:453:MET:H	1.69	0.41
3:A:500:GLU:CD	4:B:1145:SER:HG	2.27	0.41
3:A:598:LEU:HD12	3:A:598:LEU:HA	1.83	0.41
3:A:890:ASP:O	3:A:893:PHE:N	2.54	0.41
3:A:1112:LYS:HA	3:A:1112:LYS:HD2	1.85	0.41
3:A:1297:GLU:OE1	3:A:1297:GLU:N	2.54	0.41
4:B:81:SER:HA	4:B:82:ASP:HA	1.94	0.41
4:B:101:MET:HE3	4:B:109:THR:HG22	2.02	0.41
4:B:190:TYR:CE1	12:J:62:ARG:HG3	2.55	0.41
4:B:247:GLY:O	4:B:250:PHE:CD2	2.74	0.41
4:B:289:LEU:HD22	4:B:375:ALA:HB2	2.03	0.41
4:B:772:ALA:HA	4:B:775:LYS:HZ1	1.86	0.41
4:B:829:CYS:C	4:B:831:SER:H	2.29	0.41
4:B:839:MET:N	4:B:989:THR:O	2.52	0.41
4:B:992:ILE:HD11	4:B:994:TYR:CE2	2.56	0.41
4:B:1027:ILE:H	4:B:1027:ILE:HD12	1.85	0.41
5:C:259:LEU:HD13	13:K:91:CYS:HB2	2.03	0.41
6:D:195:ILE:HG13	9:G:86:VAL:HG23	2.02	0.41
12:J:31:ASP:OD1	12:J:34:THR:OG1	2.33	0.41
13:K:40:HIS:CD2	13:K:40:HIS:H	2.38	0.41
14:L:40:LEU:CD1	14:L:44:ASP:HB2	2.51	0.41
17:Q:23:LYS:HD3	17:Q:23:LYS:HA	1.87	0.41
17:Q:376:LEU:HA	17:Q:385:THR:O	2.21	0.41
17:Q:408:GLU:HA	17:Q:411:LYS:HE2	2.03	0.41
18:M:71:VAL:HA	18:M:222:CYS:O	2.21	0.41
18:M:71:VAL:HG22	18:M:222:CYS:SG	2.61	0.41
1:N:16:DA:H3'	1:N:17:DG:H8	1.86	0.41
3:a:407:ARG:HA	3:a:430:TRP:CG	2.56	0.41
3:a:451:HIS:ND1	3:a:1074:GLU:OE2	2.54	0.41
3:a:590:ARG:HG2	3:a:604:GLY:HA2	2.02	0.41
3:a:847:ASP:OD1	3:a:847:ASP:N	2.52	0.41
4:b:116:GLU:O	4:b:120:ARG:HB2	2.21	0.41
4:b:335:GLY:HA2	4:b:337:ARG:HH12	1.86	0.41
4:b:448:ILE:HA	4:b:451:LYS:HG2	2.02	0.41
4:b:1076:HIS:CD2	13:k:40:HIS:CD2	3.08	0.41
4:b:1202:LEU:O	4:b:1205:GLN:N	2.54	0.41
5:c:41:ILE:HD11	5:c:246:ARG:HB3	2.02	0.41
5:c:73:GLN:HB3	5:c:131:HIS:H	1.85	0.41
6:d:139:LYS:HG3	6:d:143:ASN:ND2	2.36	0.41
3:A:697:ALA:HB1	11:I:97:MET:HG3	2.03	0.41
3:A:1435:PRO:HA	3:A:1439:GLY:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:438:GLU:HB3	4:B:439:ALA:HB2	2.03	0.41
4:B:1164:GLY:N	4:B:1190:ASP:OD1	2.54	0.41
9:G:88:ASP:OD1	9:G:88:ASP:N	2.53	0.41
11:I:62:ILE:HD13	11:I:62:ILE:HA	1.96	0.41
13:K:97:LYS:HB3	13:K:97:LYS:HE2	1.86	0.41
3:a:350:ARG:HD2	3:a:486:GLU:CD	2.46	0.40
3:a:1025:ARG:HA	3:a:1030:ARG:NH1	2.36	0.40
3:a:1055:ARG:HD3	8:f:155:LEU:HD11	2.02	0.40
3:a:1427:ASN:HB3	3:a:1432:GLN:O	2.21	0.40
4:b:638:PHE:CE2	4:b:743:ILE:HA	2.56	0.40
4:b:1000:PRO:C	4:b:1072:MET:HE3	2.46	0.40
7:e:22:MET:HB2	7:e:187:TYR:HE1	1.86	0.40
7:e:84:ASP:OD1	7:e:84:ASP:N	2.54	0.40
9:g:21:ARG:O	9:g:21:ARG:HD2	2.21	0.40
11:i:87:GLN:OE1	11:i:88:SER:N	2.54	0.40
3:A:272:ALA:O	3:A:296:LEU:HD11	2.21	0.40
3:A:407:ARG:HG2	3:A:430:TRP:CE2	2.55	0.40
4:B:558:LEU:HD21	4:B:580:VAL:HG11	2.04	0.40
4:B:592:ASN:O	4:B:596:LEU:HD13	2.21	0.40
4:B:821:GLN:NE2	4:B:851:PHE:H	2.19	0.40
4:B:919:SER:H	4:B:923:GLU:HA	1.86	0.40
6:D:39:ASN:HB2	6:D:45:GLU:HB2	2.02	0.40
8:F:72:LYS:HA	8:F:72:LYS:HD3	1.81	0.40
18:M:121:ASP:OD1	18:M:225:MET:HB3	2.21	0.40
2:O:-42:DA:H4'	2:O:-41:DG:OP1	2.21	0.40
3:a:18:GLN:NE2	3:a:1418:LEU:HB3	2.36	0.40
3:a:22:PHE:CZ	4:b:1208:MET:HB2	2.56	0.40
3:a:115:LEU:HB3	3:a:122:MET:HE3	2.03	0.40
3:a:172:PRO:HA	3:a:187:LYS:NZ	2.36	0.40
3:a:434:ARG:CZ	3:a:437:MET:HE3	2.52	0.40
3:a:525:GLN:HG2	3:a:526:ASP:N	2.35	0.40
4:b:81:SER:HA	4:b:82:ASP:HA	1.85	0.40
5:c:125:MET:CE	5:c:127:ARG:HH21	2.33	0.40
6:d:188:ALA:O	6:d:192:LYS:HG2	2.20	0.40
10:h:10:PHE:CZ	10:h:30:SER:HB2	2.56	0.40
11:i:21:GLU:OE1	11:i:21:GLU:N	2.54	0.40
13:k:5:ASP:HB2	13:k:8:GLU:HG3	2.03	0.40
3:A:315:LEU:HB2	3:A:321:PRO:HA	2.04	0.40
3:A:525:GLN:CD	4:B:1013:ASN:HD21	2.28	0.40
3:A:737:LEU:HD21	3:A:741:ASN:HD22	1.85	0.40
3:A:1163:ILE:H	3:A:1163:ILE:HD12	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1229:SER:OG	3:A:1230:GLU:N	2.55	0.40
3:A:1234:GLU:OE1	3:A:1234:GLU:N	2.55	0.40
4:B:758:PHE:CE2	4:B:1044:ALA:HA	2.56	0.40
4:B:963:PHE:CZ	4:B:965:LYS:HD3	2.55	0.40
8:F:134:ILE:N	8:F:146:TRP:O	2.50	0.40
9:G:91:VAL:HB	9:G:141:SER:HB2	2.04	0.40
1:N:22:DA:H2''	1:N:23:DA:C8	2.57	0.40
3:a:630:ILE:HG13	3:a:631:HIS:N	2.35	0.40
3:a:1268:LEU:HB3	3:a:1269:GLU:OE1	2.21	0.40
4:b:57:TYR:C	4:b:59:LEU:H	2.29	0.40
4:b:213:ILE:HD11	4:b:481:GLN:HB2	2.03	0.40
4:b:230:ALA:N	4:b:231:PRO:HD2	2.36	0.40
4:b:485:ARG:NH1	4:b:491:THR:HG21	2.36	0.40
4:b:1065:GLN:CD	4:b:1067:ARG:H	2.29	0.40
5:c:36:VAL:HG11	5:c:251:LEU:HD12	2.03	0.40
8:f:103:MET:HE2	8:f:103:MET:O	2.22	0.40
10:h:126:GLU:O	10:h:130:ARG:NH1	2.53	0.40
3:A:407:ARG:HG2	3:A:430:TRP:CD2	2.56	0.40
3:A:860:LEU:HD23	3:A:860:LEU:HA	1.90	0.40
3:A:1135:ARG:HG3	3:A:1282:VAL:HG23	2.02	0.40
4:B:59:LEU:O	4:B:62:ILE:HG22	2.21	0.40
4:B:848:ARG:NH1	12:J:8:PHE:O	2.38	0.40
4:B:889:THR:C	4:B:891:ASP:H	2.30	0.40
4:B:1202:LEU:HA	4:B:1205:GLN:OE1	2.20	0.40
6:D:23:ASN:H	9:G:83:LYS:HE2	1.86	0.40
17:Q:140:HIS:HB2	17:Q:142:LYS:HZ2	1.87	0.40
18:M:85:ASN:O	18:M:88:HIS:NE2	2.54	0.40
3:a:57:ARG:HA	3:a:66:LYS:NZ	2.35	0.40
3:a:323:LYS:HE2	3:a:328:ARG:HA	2.03	0.40
3:a:434:ARG:HH12	3:a:437:MET:HG2	1.85	0.40
4:b:416:LEU:HD11	4:b:466:TRP:HB3	2.04	0.40
4:b:825:VAL:HG12	4:b:1010:LEU:HD21	2.02	0.40
4:b:884:ARG:NE	15:r:36:U:H4'	2.37	0.40
5:c:43:THR:OG1	5:c:44:LEU:N	2.52	0.40
9:g:47:CYS:O	9:g:77:VAL:N	2.51	0.40
11:i:45:ARG:HB3	11:i:47:GLU:OE1	2.21	0.40
12:j:24:LEU:O	12:j:28:ASP:HB2	2.22	0.40
3:A:72:GLU:HB3	3:A:76:GLU:HB2	2.03	0.40
3:A:800:VAL:HA	3:A:812:GLU:CD	2.46	0.40
3:A:851:HIS:HE1	3:A:857:ARG:HB2	1.85	0.40
3:A:860:LEU:O	7:E:174:GLN:NE2	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1335:ILE:H	3:A:1335:ILE:HD12	1.86	0.40
3:A:1425:SER:O	3:A:1429:ILE:HG12	2.21	0.40
4:B:69:LEU:HB3	4:B:90:ILE:HG13	2.04	0.40
5:C:35:ARG:HH21	13:K:41:THR:HB	1.87	0.40
6:D:215:SER:HA	6:D:218:GLU:HG3	2.04	0.40
18:M:94:LYS:O	18:M:106:LEU:HD12	2.21	0.40
3:a:227:VAL:HG13	3:a:228:PHE:CD1	2.56	0.40
3:a:532:ARG:NH1	3:a:745:GLN:HB2	2.37	0.40
3:a:575:LYS:O	3:a:612:ILE:HD12	2.22	0.40
3:a:1035:TYR:O	3:a:1037:LEU:HD22	2.21	0.40
3:a:1332:PHE:CD2	3:a:1348:LEU:HD12	2.57	0.40
4:b:331:LEU:CD2	4:b:353:LYS:HG3	2.51	0.40
4:b:522:VAL:HG23	4:b:538:ASN:O	2.22	0.40
4:b:527:THR:CG2	4:b:533:CYS:HA	2.52	0.40
4:b:554:ILE:O	4:b:558:LEU:HD23	2.22	0.40
4:b:798:TYR:CE2	12:j:4:PRO:HB3	2.57	0.40
4:b:882:THR:HG22	4:b:934:LYS:CA	2.52	0.40
4:b:959:ASP:OD1	4:b:961:LEU:HG	2.20	0.40
4:b:975:GLN:O	4:b:990:ILE:HD13	2.22	0.40
4:b:1094:ARG:HB3	4:b:1094:ARG:HE	1.68	0.40
4:b:1152:MET:HB3	4:b:1153:GLU:OE1	2.21	0.40
4:b:1174:LYS:O	4:b:1178:ASN:N	2.55	0.40
5:c:73:GLN:CD	5:c:75:MET:HG2	2.46	0.40
5:c:98:VAL:HG12	5:c:121:VAL:HB	2.04	0.40
6:d:156:ASP:O	6:d:160:VAL:HG12	2.22	0.40
3:A:407:ARG:HB2	3:A:411:ASP:HB2	2.04	0.40
3:A:1220:PHE:C	3:A:1222:ASN:H	2.29	0.40
4:B:952:VAL:HG13	4:B:966:VAL:HG12	2.04	0.40
7:E:190:LEU:HD23	7:E:190:LEU:H	1.87	0.40
8:F:85:MET:SD	8:F:89:GLU:HG2	2.61	0.40
18:M:120:TYR:HD2	18:M:226:PRO:HA	1.86	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	
3	A	1417/1733 (82%)	1266 (89%)	148 (10%)	3 (0%)	43	73
3	a	1417/1733 (82%)	1235 (87%)	182 (13%)	0	100	100
4	B	1150/1224 (94%)	1000 (87%)	148 (13%)	2 (0%)	43	73
4	b	1142/1224 (93%)	984 (86%)	158 (14%)	0	100	100
5	C	263/318 (83%)	231 (88%)	32 (12%)	0	100	100
5	c	263/318 (83%)	225 (86%)	38 (14%)	0	100	100
6	D	164/221 (74%)	159 (97%)	5 (3%)	0	100	100
6	d	164/221 (74%)	156 (95%)	8 (5%)	0	100	100
7	E	212/215 (99%)	196 (92%)	16 (8%)	0	100	100
7	e	212/215 (99%)	193 (91%)	18 (8%)	1 (0%)	24	58
8	F	85/155 (55%)	77 (91%)	8 (9%)	0	100	100
8	f	85/155 (55%)	77 (91%)	8 (9%)	0	100	100
9	G	169/171 (99%)	155 (92%)	14 (8%)	0	100	100
9	g	169/171 (99%)	152 (90%)	17 (10%)	0	100	100
10	H	129/146 (88%)	110 (85%)	19 (15%)	0	100	100
10	h	129/146 (88%)	111 (86%)	18 (14%)	0	100	100
11	I	112/122 (92%)	102 (91%)	10 (9%)	0	100	100
11	i	112/122 (92%)	104 (93%)	8 (7%)	0	100	100
12	J	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
12	j	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
13	K	113/120 (94%)	108 (96%)	5 (4%)	0	100	100
13	k	113/120 (94%)	106 (94%)	7 (6%)	0	100	100
14	L	42/70 (60%)	30 (71%)	12 (29%)	0	100	100
14	l	42/70 (60%)	30 (71%)	12 (29%)	0	100	100
17	Q	208/735 (28%)	202 (97%)	6 (3%)	0	100	100
18	M	131/400 (33%)	123 (94%)	8 (6%)	0	100	100
All	All	8171/10265 (80%)	7240 (89%)	925 (11%)	6 (0%)	49	79

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	188	ASP
4	B	364	ILE
3	A	195	ASP
3	A	253	ASN
4	B	363	HIS
7	e	172	GLU

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	
3	A	1235/1520 (81%)	1231 (100%)	4 (0%)	86	83
3	a	1240/1520 (82%)	1239 (100%)	1 (0%)	88	87
4	B	1000/1061 (94%)	1000 (100%)	0	100	100
4	b	999/1061 (94%)	999 (100%)	0	100	100
5	C	233/274 (85%)	233 (100%)	0	100	100
5	c	233/274 (85%)	233 (100%)	0	100	100
6	D	146/200 (73%)	146 (100%)	0	100	100
6	d	146/200 (73%)	146 (100%)	0	100	100
7	E	196/197 (100%)	196 (100%)	0	100	100
7	e	196/197 (100%)	196 (100%)	0	100	100
8	F	77/137 (56%)	77 (100%)	0	100	100
8	f	77/137 (56%)	77 (100%)	0	100	100
9	G	151/152 (99%)	151 (100%)	0	100	100
9	g	152/152 (100%)	152 (100%)	0	100	100
10	H	118/128 (92%)	118 (100%)	0	100	100
10	h	118/128 (92%)	118 (100%)	0	100	100
11	I	108/116 (93%)	108 (100%)	0	100	100
11	i	108/116 (93%)	108 (100%)	0	100	100
12	J	61/65 (94%)	61 (100%)	0	100	100
12	j	61/65 (94%)	61 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	K	99/102 (97%)	99 (100%)	0	100	100
13	k	99/102 (97%)	99 (100%)	0	100	100
14	L	39/57 (68%)	39 (100%)	0	100	100
14	l	39/57 (68%)	39 (100%)	0	100	100
17	Q	147/641 (23%)	147 (100%)	0	100	100
18	M	125/363 (34%)	125 (100%)	0	100	100
All	All	7203/9022 (80%)	7198 (100%)	5 (0%)	87	87

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	a	1211	GLN
3	A	189	ARG
3	A	191	THR
3	A	193	ASP
3	A	195	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
3	a	209	ASN
3	a	313	GLN
3	a	358	ASN
3	a	447	GLN
3	a	548	ASN
3	a	576	GLN
3	a	768	GLN
3	a	881	GLN
3	a	965	GLN
3	a	1171	GLN
3	a	1211	GLN
3	a	1432	GLN
4	b	47	GLN
4	b	278	GLN
4	b	325	GLN
4	b	357	GLN
4	b	383	ASN
4	b	395	GLN
4	b	449	ASN

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Mol	Chain	Res	Type
4	b	770	GLN
4	b	794	ASN
4	b	821	GLN
4	b	822	ASN
4	b	834	ASN
4	b	1062	HIS
4	b	1076	HIS
4	b	1187	ASN
5	c	65	HIS
5	c	242	GLN
5	c	267	GLN
6	d	23	ASN
7	e	5	ASN
7	e	63	ASN
7	e	106	GLN
9	g	113	HIS
10	h	52	GLN
11	i	79	HIS
13	k	65	HIS
13	k	76	GLN
3	A	71	GLN
3	A	399	HIS
3	A	451	HIS
3	A	458	HIS
3	A	545	GLN
3	A	576	GLN
3	A	757	ASN
3	A	768	GLN
3	A	802	ASN
3	A	851	HIS
3	A	935	GLN
3	A	1009	ASN
3	A	1427	ASN
4	B	73	GLN
4	B	110	HIS
4	B	538	ASN
4	B	572	HIS
4	B	834	ASN
4	B	842	ASN
4	B	881	ASN
5	C	102	GLN
5	C	203	GLN

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Mol	Chain	Res	Type
6	D	39	ASN
6	D	41	GLN
6	D	74	GLN
6	D	150	ASN
7	E	114	ASN
8	F	100	GLN
9	G	24	GLN
9	G	117	GLN
10	H	52	GLN
11	I	22	ASN
11	I	87	GLN
11	I	89	GLN
13	K	40	HIS
17	Q	30	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	r	15/16 (93%)	9 (60%)	0
16	R	14/15 (93%)	8 (57%)	0
All	All	29/31 (93%)	17 (58%)	0

All (17) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	r	35	C
15	r	36	U
15	r	38	G
15	r	41	C
15	r	42	U
15	r	43	A
15	r	45	U
15	r	47	U
15	r	48	C
16	R	5	C
16	R	8	A
16	R	9	C
16	R	10	A
16	R	11	A
16	R	13	U
16	R	15	C

Continued on next page...

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Mol	Chain	Res	Type
16	R	18	A

There are no RNA pucker outliers to report.

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 20 ligands modelled in this entry, 20 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

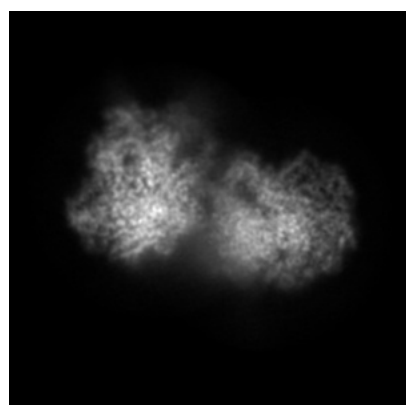
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23789. These allow visual inspection of the internal detail of the map and identification of artifacts.

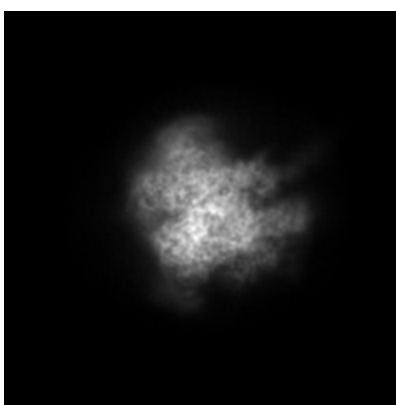
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

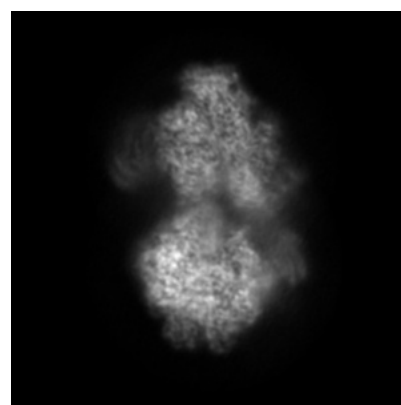
6.1.1 Primary map



X



Y

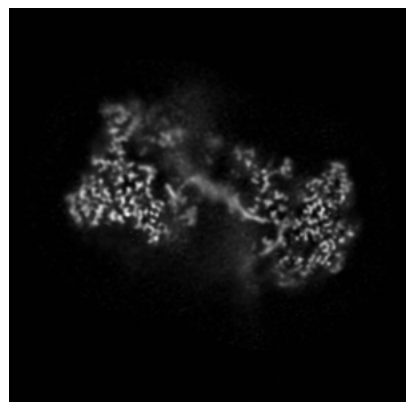


Z

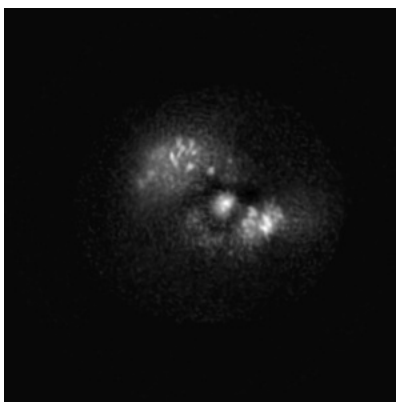
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

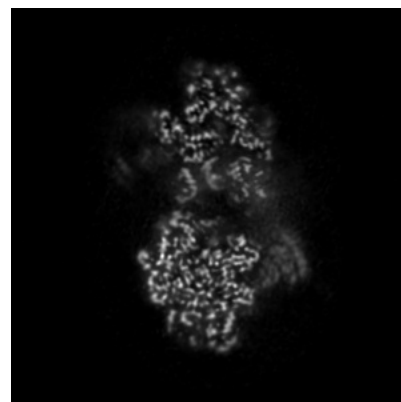
6.2.1 Primary map



X Index: 170



Y Index: 170

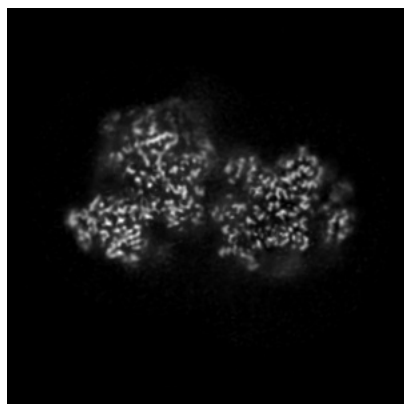


Z Index: 170

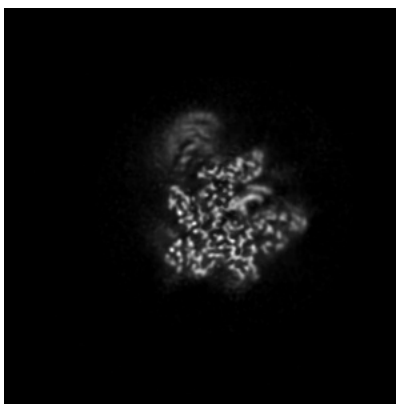
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

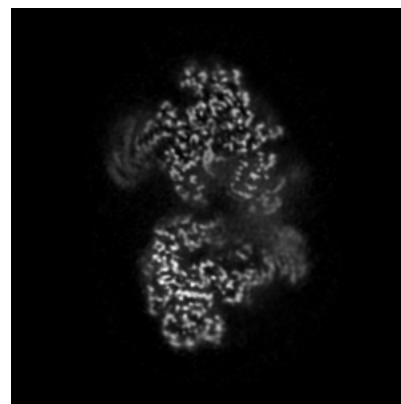
6.3.1 Primary map



X Index: 150



Y Index: 119

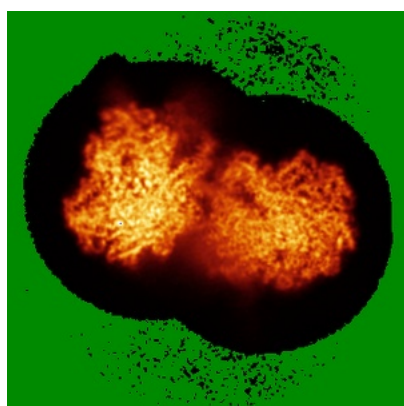


Z Index: 159

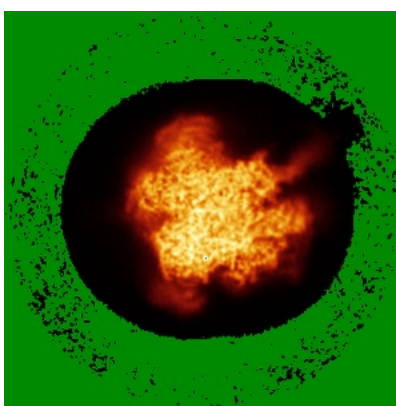
The images above show the largest variance slices of the map in three orthogonal directions.

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

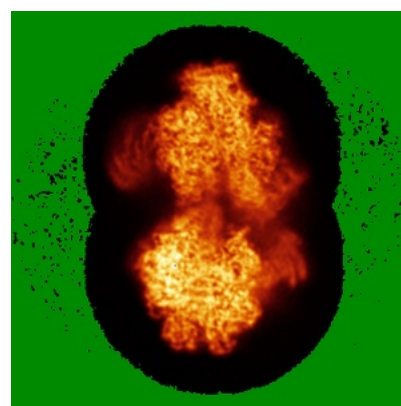
6.4.1 Primary map



X



Y

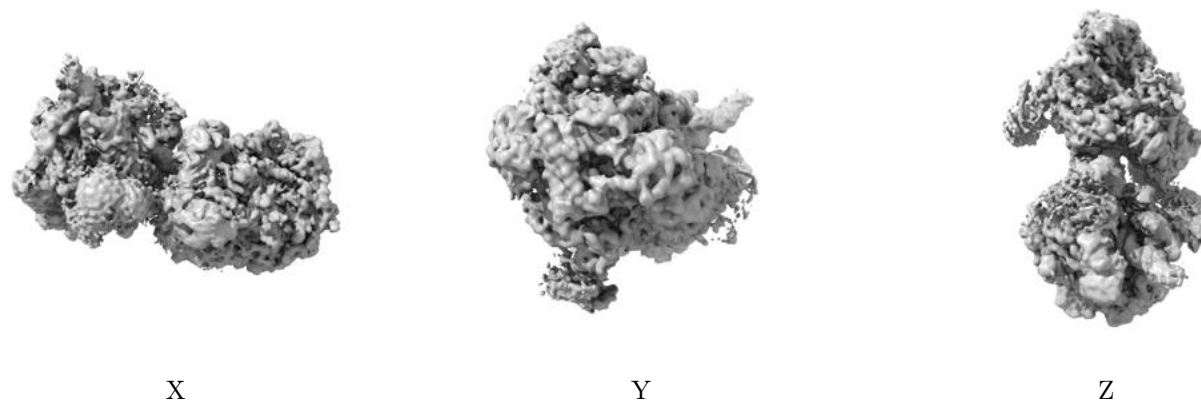


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0088. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

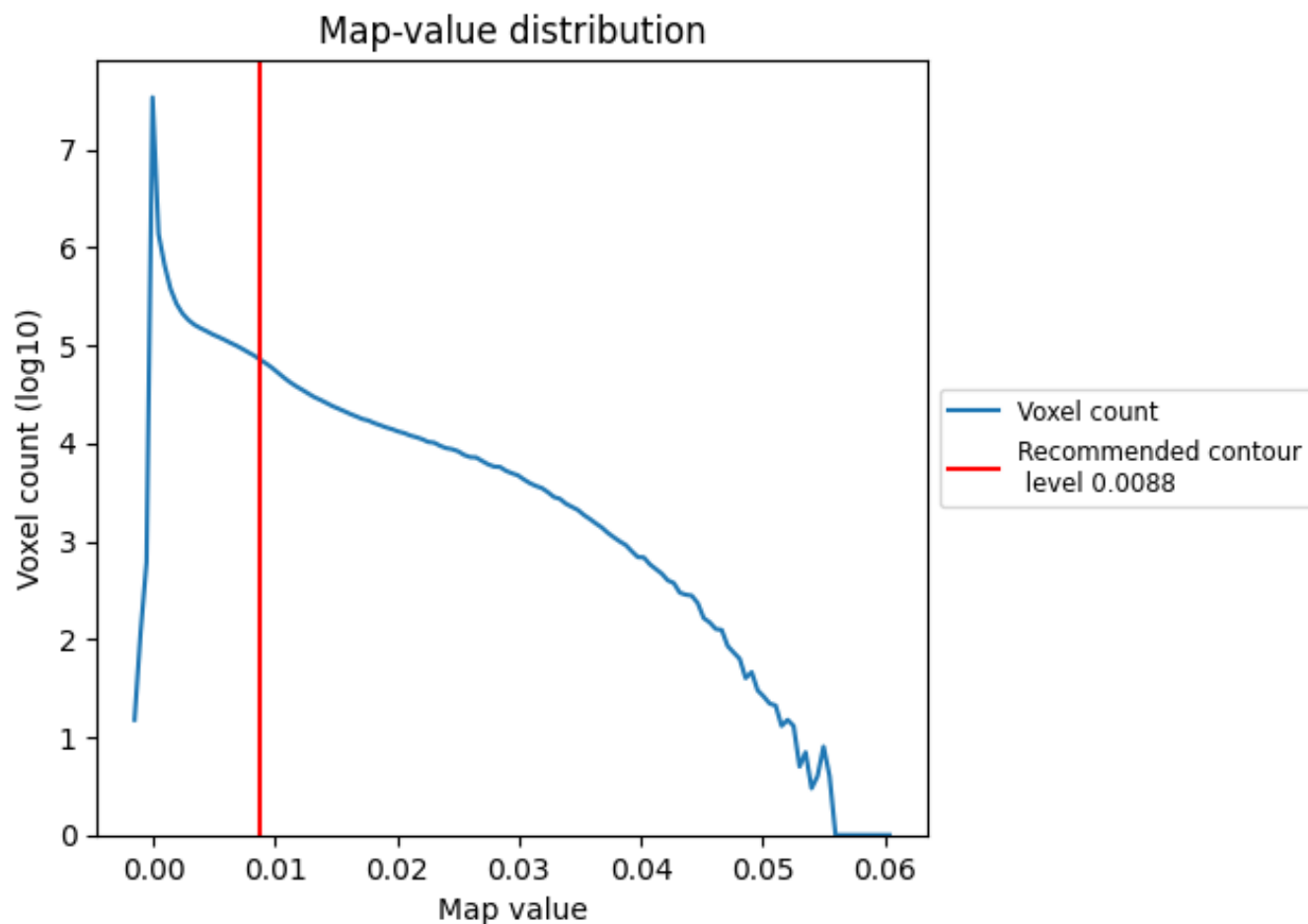
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

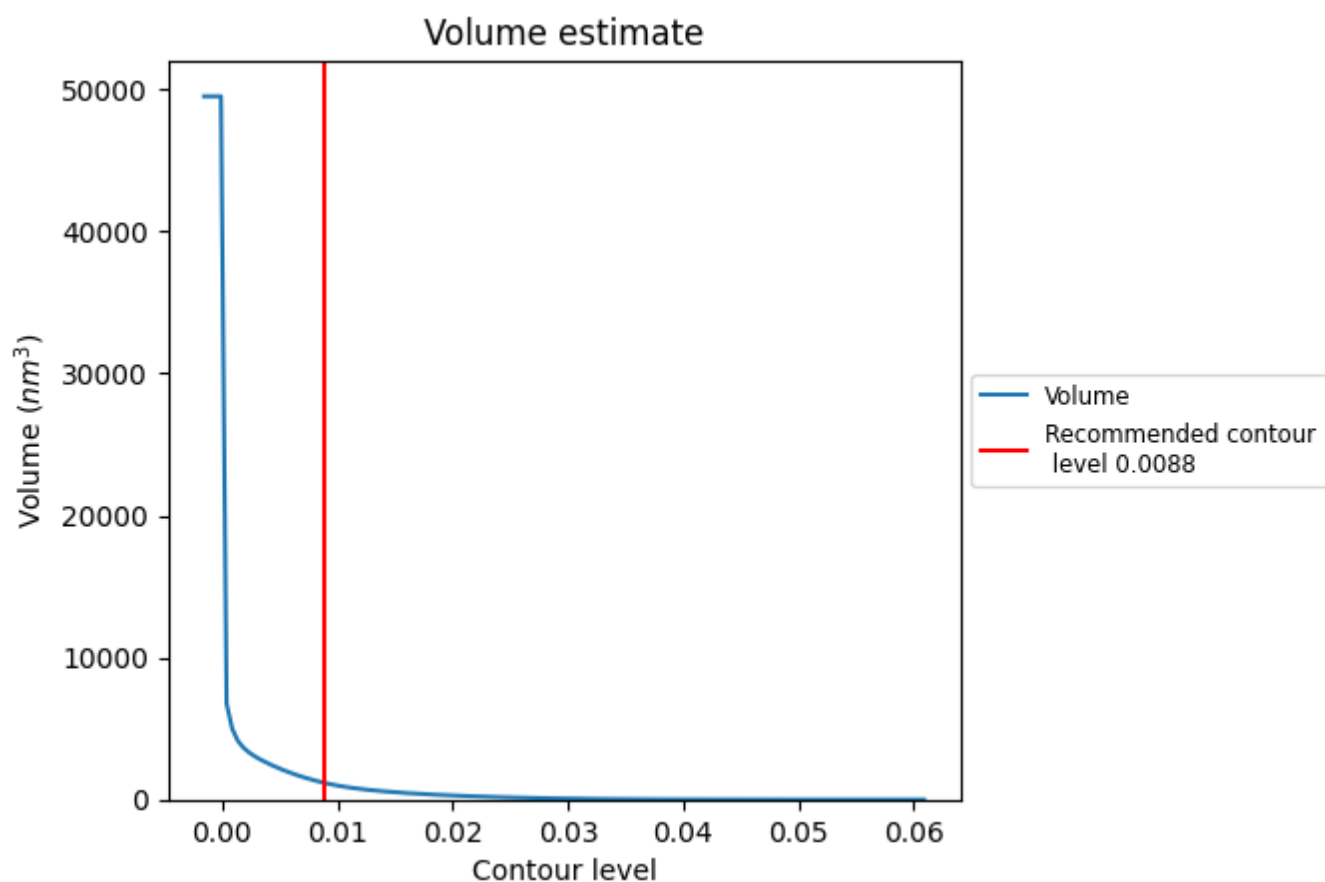
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

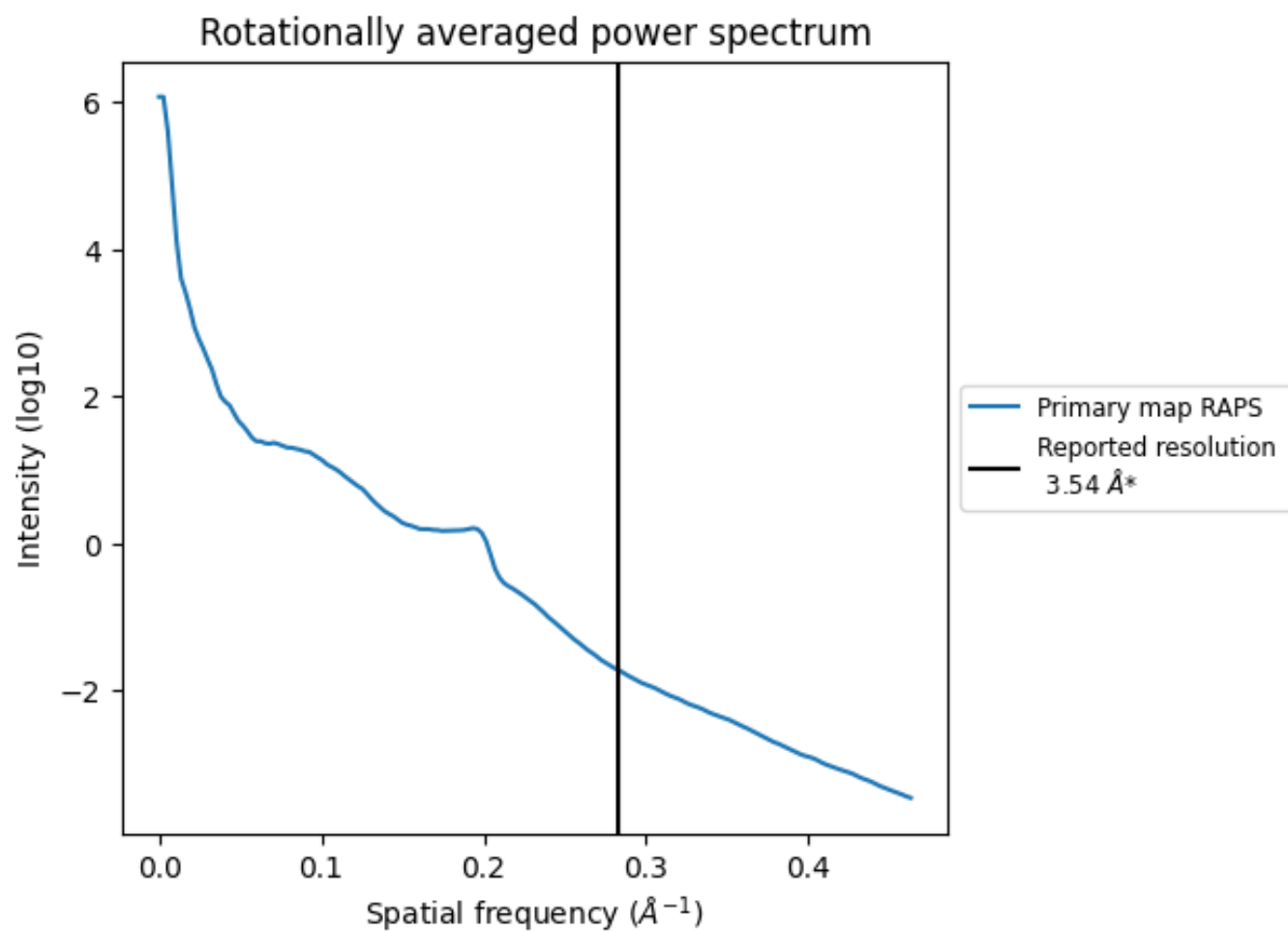
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1192 nm³; this corresponds to an approximate mass of 1077 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 0.282 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

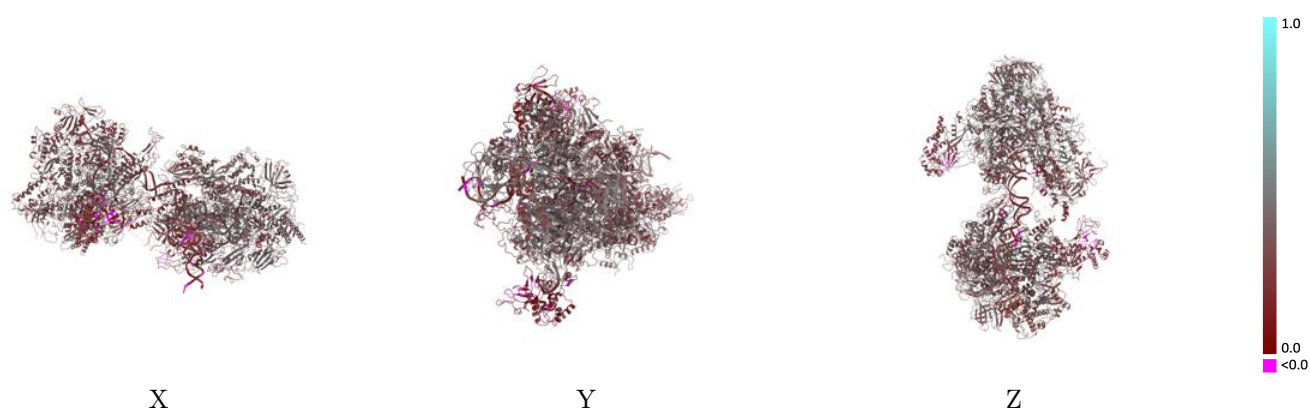
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23789 and PDB model 7MEI. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

This section was not generated.

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

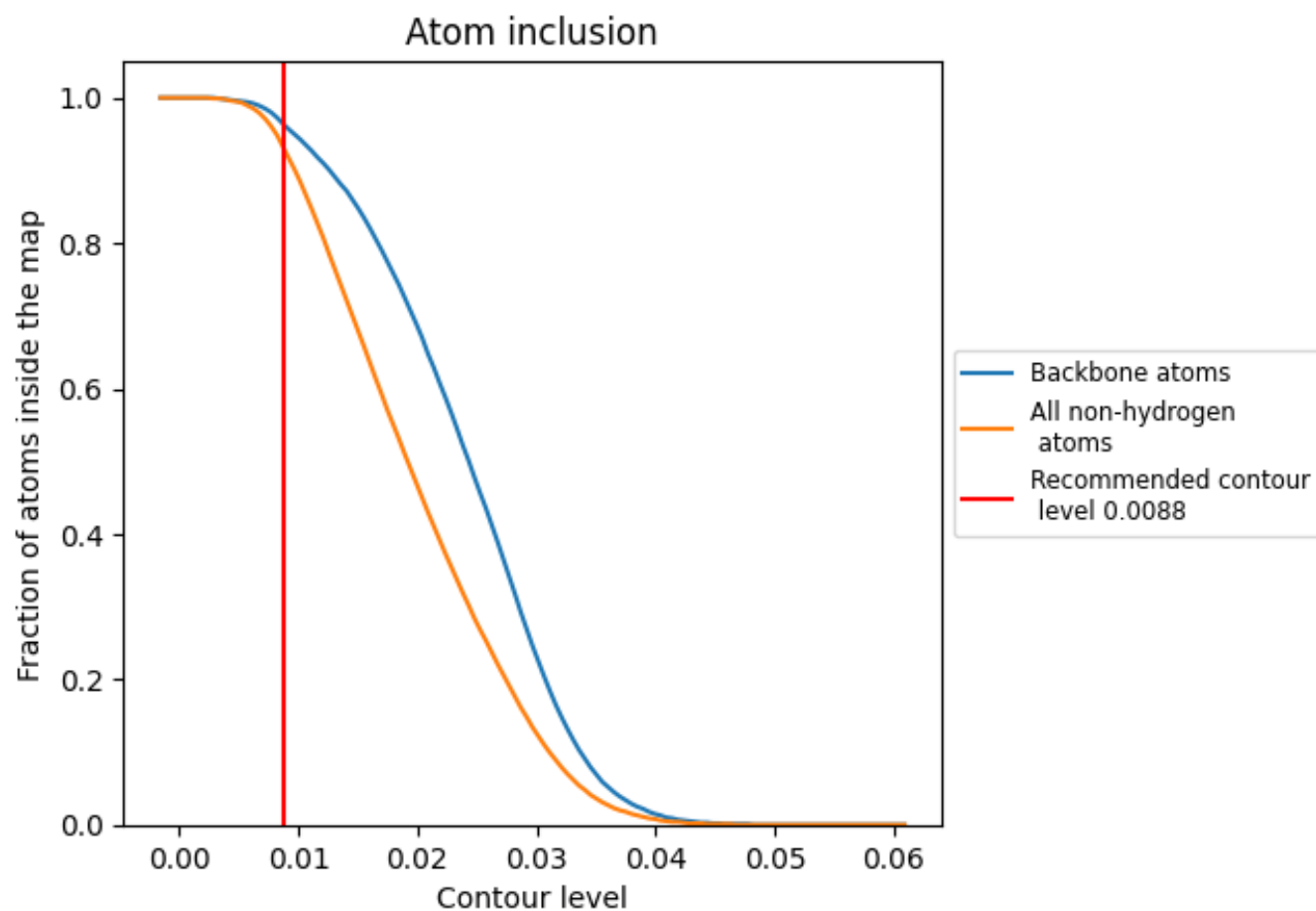


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.0088) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.3350
A	 0.9470	 0.3680
B	 0.9210	 0.3680
C	 0.9610	 0.3920
D	 0.4650	 0.1990
E	 0.9600	 0.3480
F	 0.9550	 0.3820
G	 0.5370	 0.2010
H	 0.9680	 0.3690
I	 0.9320	 0.3360
J	 0.9830	 0.3960
K	 0.8880	 0.3340
L	 0.9560	 0.3390
M	 0.8410	 0.2300
N	 0.7730	 0.1950
O	 0.8920	 0.2700
Q	 0.8350	 0.2660
R	 0.7860	 0.2650
a	 0.9860	 0.3450
b	 0.9740	 0.3520
c	 0.9910	 0.3650
d	 0.9300	 0.1650
e	 0.9940	 0.3490
f	 0.9850	 0.3520
g	 0.9500	 0.2100
h	 0.9850	 0.3470
i	 0.9690	 0.3160
j	 0.9960	 0.3620
k	 0.9180	 0.3320
l	 0.9790	 0.3520
r	 0.9370	 0.2630

