



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:28 PM UTC

PDB ID : 7EGA / pdb_00007ega
EMDB ID : EMD-31110
Title : TFIID-based intermediate PIC on PUMA promoter
Authors : Chen, X.; Wu, Z.; Hou, H.; Qi, Y.; Wang, X.; Li, J.; Xu, Y.
Deposited on : 2021-03-24
Resolution : 4.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

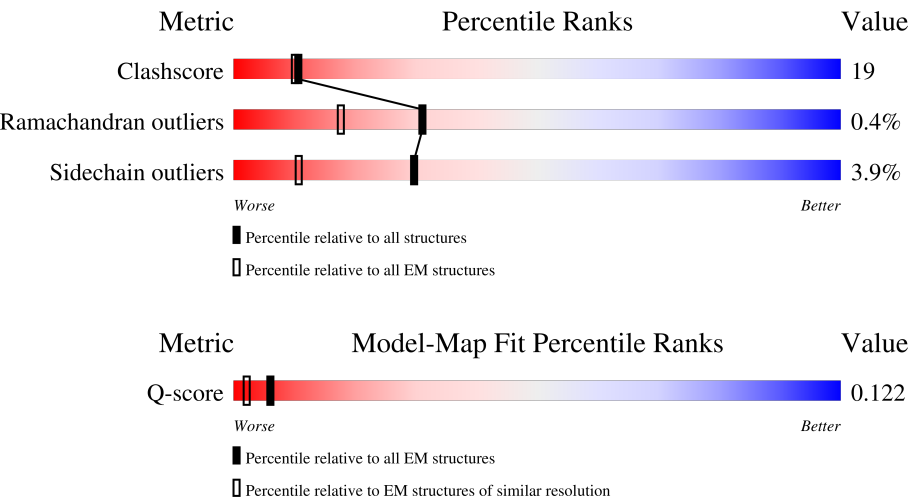
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	A	1872	12% 23% 8% 68%
2	B	1199	14% 66% 13% 20%
3	D	1085	9% 5% 85%
3	d	1085	15% 13% 85%

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Mol	Chain	Length	Quality of chain
4	E	800	
4	e	800	
5	F	677	
5	f	677	
6	G	349	
7	H	310	
8	I	264	
8	i	264	
9	J	218	
9	j	218	
10	L	161	
10	l	161	
11	O	109	
12	P	339	
13	Q	376	
14	R	316	
15	S	517	
16	T	249	
17	U	439	
18	V	291	
19	c	929	
20	k	211	
21	m	124	
22	o	1487	
23	p	1174	

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Mol	Chain	Length	Quality of chain
24	q	273	
25	r	142	
26	s	210	
27	t	127	
28	v	150	
29	w	125	
30	x	64	
31	y	117	
32	z	58	
33	X	85	
34	Y	85	
35	u	172	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 85697 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	602	Total	C	N	O	S	0	0
			4927	3142	858	899	28		

- Molecule 2 is a protein called Transcription initiation factor TFIID subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	963	Total	C	N	O	S	0	0
			7796	5011	1315	1412	58		

- Molecule 3 is a protein called Transcription initiation factor TFIID subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	164	Total	C	N	O	S	0	0
			1366	851	256	255	4		
3	d	158	Total	C	N	O	S	0	0
			1307	814	238	252	3		

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	546	Total	C	N	O	S	0	0
			4364	2766	757	820	21		
4	e	539	Total	C	N	O	S	0	0
			4327	2746	748	814	19		

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	404	Total	C	N	O	S	0	0
			3081	1954	537	572	18		
5	f	403	Total	C	N	O	S	0	0
			3081	1954	533	576	18		

- Molecule 6 is a protein called Transcription initiation factor TFIID subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	145	Total	C	N	O	S	0	0
			1180	748	217	211	4		

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	209	Total	C	N	O	S	0	0
			1633	1034	283	311	5		

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	120	Total	C	N	O	S	0	0
			959	610	166	177	6		
8	i	121	Total	C	N	O	S	0	0
			967	615	167	178	7		

- Molecule 9 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	89	Total	C	N	O	S	0	0
			709	457	114	134	4		
9	j	95	Total	C	N	O	S	0	0
			759	488	124	143	4		

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	76	Total	C	N	O	S	0	0
			622	388	109	122	3		
10	l	107	Total	C	N	O	S	0	0
			876	547	158	166	5		

- Molecule 11 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	97	Total	C	N	O	S	0	0
			771	491	133	145	2		

- Molecule 12 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	177	Total	C	N	O	S	0	0
			1412	918	249	238	7		

- Molecule 13 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	122	Total	C	N	O	S	0	0
			996	623	162	207	4		

- Molecule 14 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	251	Total	C	N	O	S	0	0
			1939	1214	344	364	17		

- Molecule 15 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	108	Total	C	N	O	S	0	0
			872	558	153	159	2		

- Molecule 16 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	222	Total	C	N	O	S	0	0
			1788	1127	320	338	3		

- Molecule 17 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	179	Total	C	N	O	S	0	0
			1476	932	261	272	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	172	Total	C	N	O	S	0	0
			1404	893	243	264	4		

- Molecule 19 is a protein called Transcription initiation factor TFIID subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	127	Total	C	N	O	S	0	0
			1011	638	174	193	6		

- Molecule 20 is a protein called Transcription initiation factor TFIID subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	k	98	Total	C	N	O	S	0	0
			785	499	142	139	5		

- Molecule 21 is a protein called Transcription initiation factor TFIID subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	m	87	Total	C	N	O	S	0	0
			724	456	131	131	6		

- Molecule 22 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	o	1427	Total	C	N	O	S	0	0
			11308	7114	2023	2099	72		

- Molecule 23 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	1134	Total	C	N	O	S	0	0
			9062	5732	1595	1671	64		

- Molecule 24 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	q	257	Total	C	N	O	S	0	0
			2059	1294	351	408	6		

- Molecule 25 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	128	Total	C	N	O	S	0	0
			1005	632	172	197	4		

- Molecule 26 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	209	Total	C	N	O	S	0	0
			1720	1089	300	323	8		

- Molecule 27 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	79	Total	C	N	O	S	0	0
			635	406	108	116	5		

- Molecule 28 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	v	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 29 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	114	Total	C	N	O	S	0	0
			927	571	166	179	11		

- Molecule 30 is a protein called RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	x	64	Total	C	N	O	S	0	0
			507	328	86	87	6		

- Molecule 31 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	117	Total	C	N	O	S	0	0
			937	604	154	177	2		

- Molecule 32 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	z	44	Total	C	N	O	S	0	0
			372	231	72	63	6		

- Molecule 33 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	X	85	Total	C	N	O	P	0	0
			1751	829	329	508	85		

- Molecule 34 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Y	85	Total	C	N	O	P	0	0
			1734	824	313	512	85		

- Molecule 35 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	u	171	Total	C	N	O	S	0	0
			1351	875	219	249	8		

- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

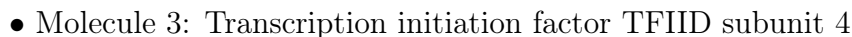
Mol	Chain	Residues	Atoms		AltConf
36	R	1	Total	Zn	0
			1	1	
36	U	1	Total	Zn	0
			1	1	
36	o	2	Total	Zn	0
			2	2	
36	p	1	Total	Zn	0
			1	1	
36	q	1	Total	Zn	0
			1	1	
36	w	2	Total	Zn	0
			2	2	
36	x	1	Total	Zn	0
			1	1	
36	z	1	Total	Zn	0
			1	1	

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

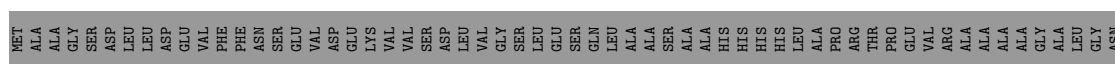
Mol	Chain	Residues	Atoms		AltConf
37	o	1	Total	Mg	0
			1	1	



Chain B:



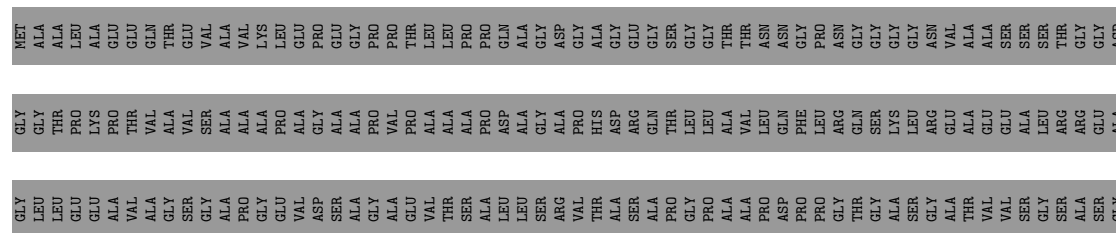
Chain D:

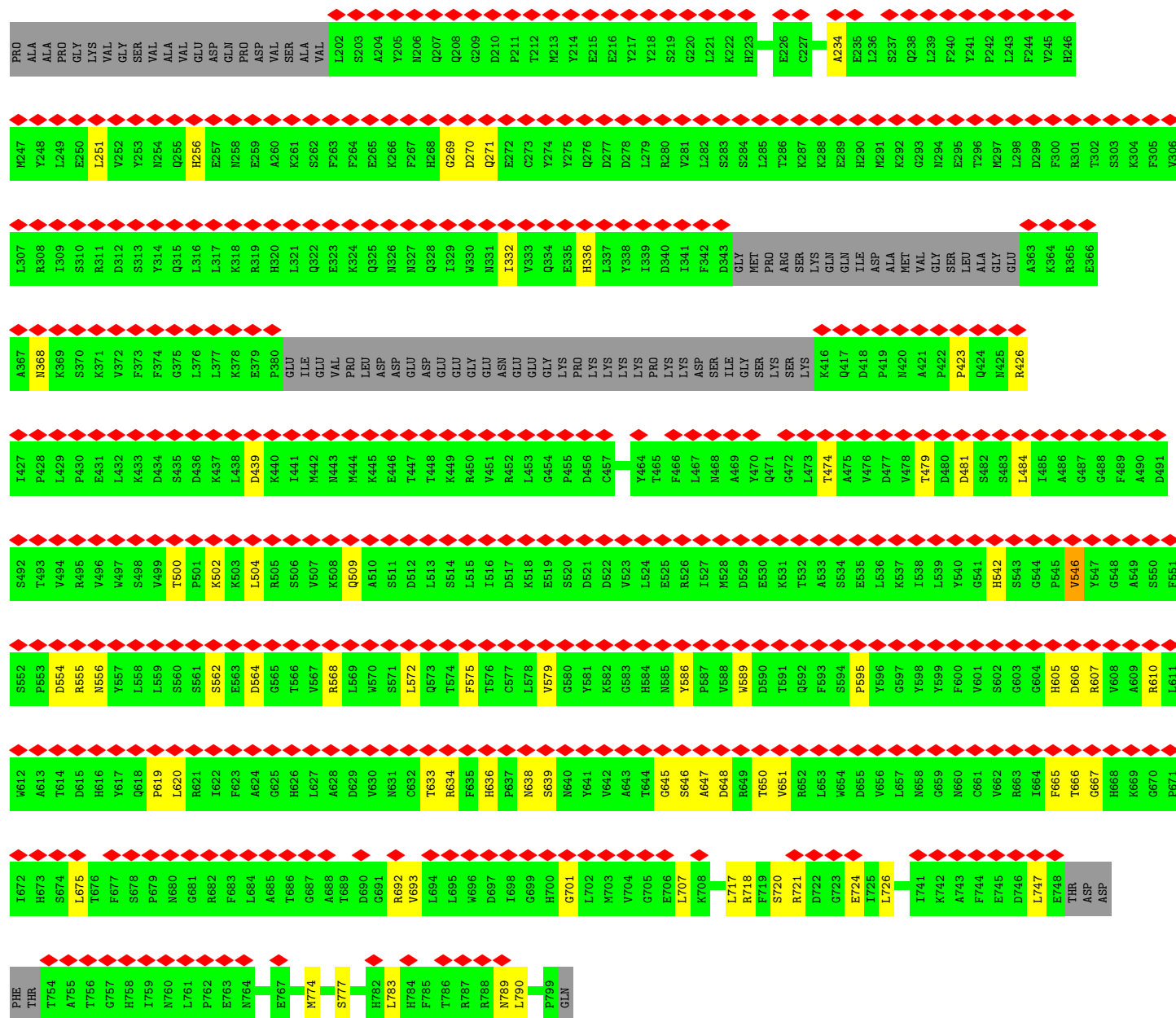


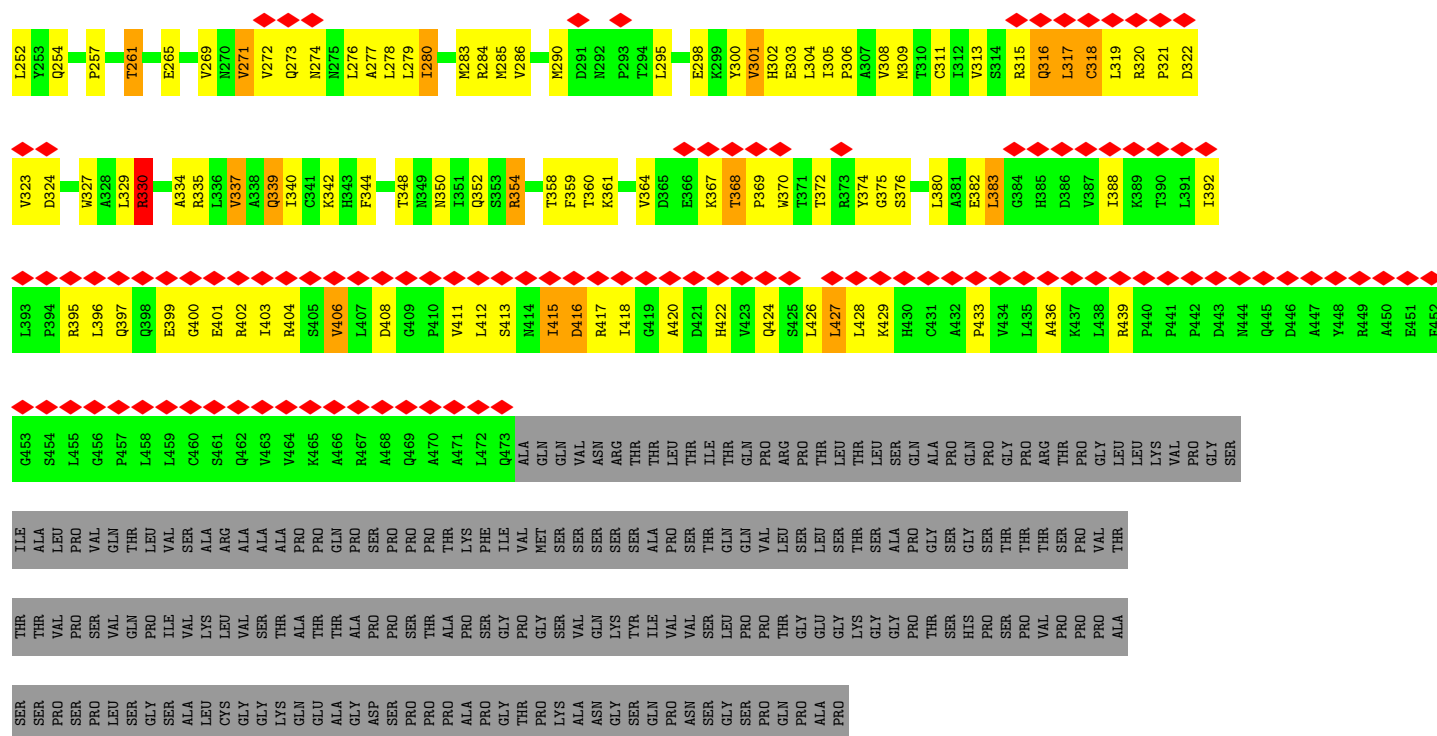
- Molecule 3: Transcription initiation factor TFIID subunit 4



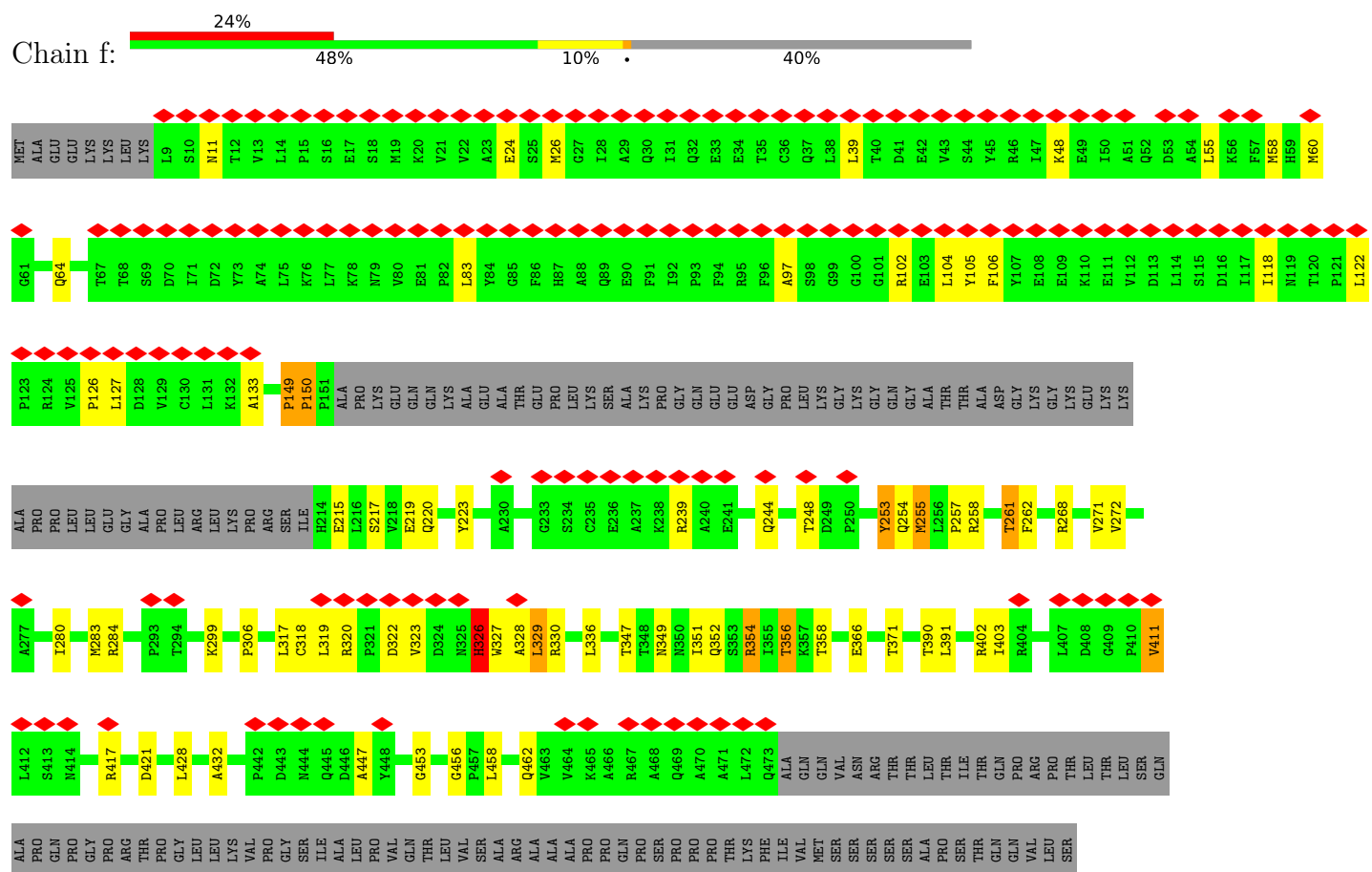


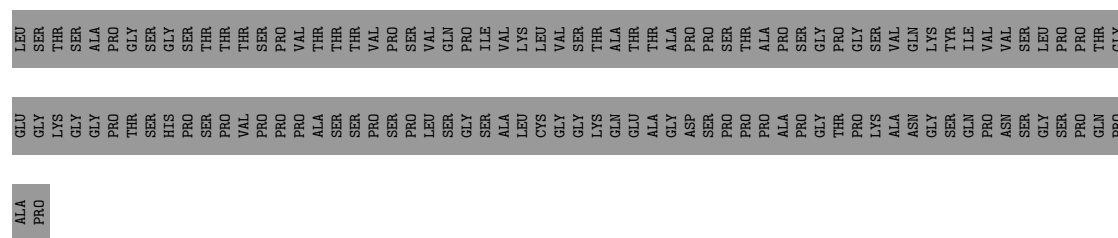




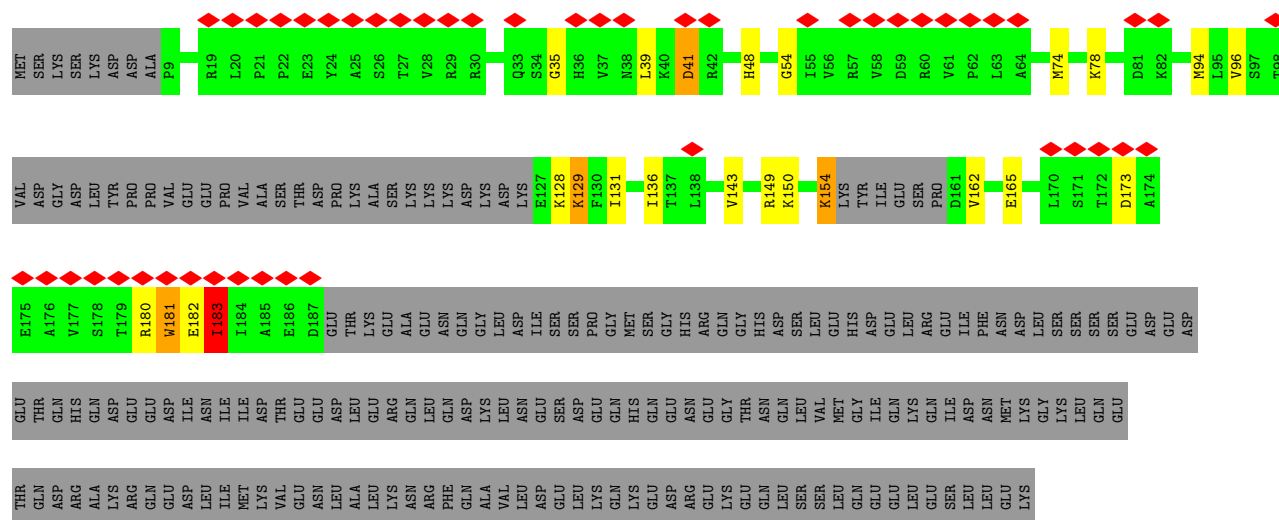
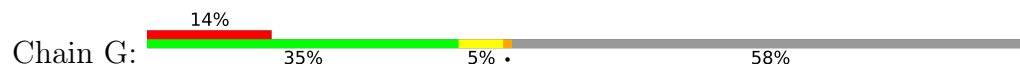


• Molecule 5: Transcription initiation factor TFIID subunit 6

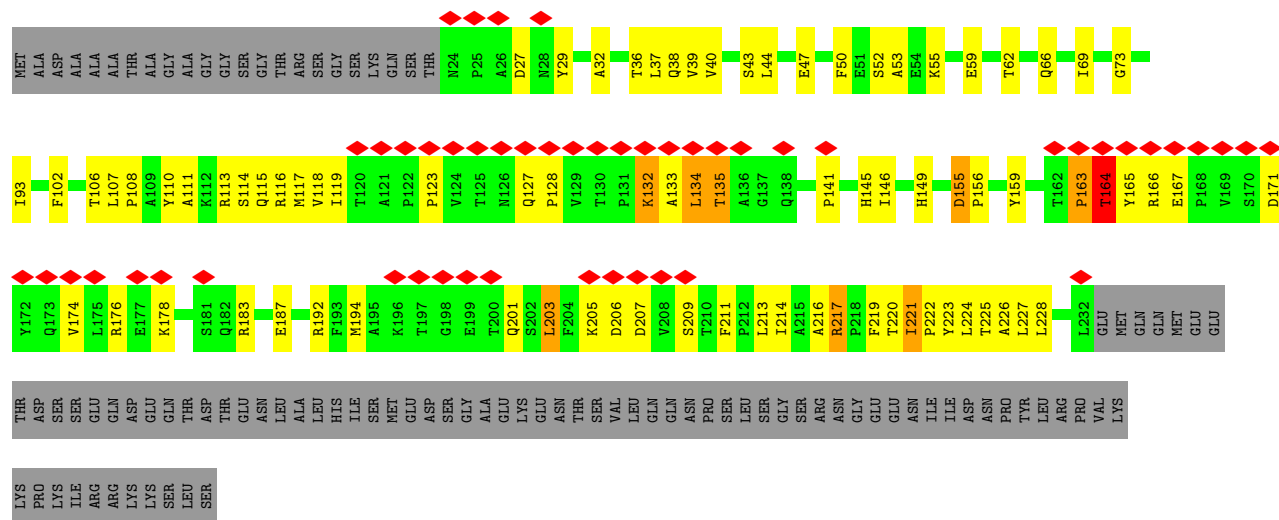
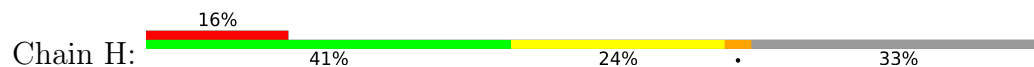




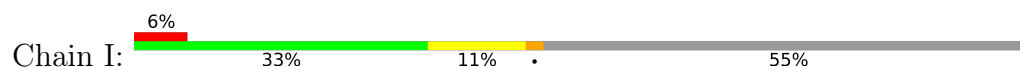
• Molecule 6: Transcription initiation factor TFIID subunit 7

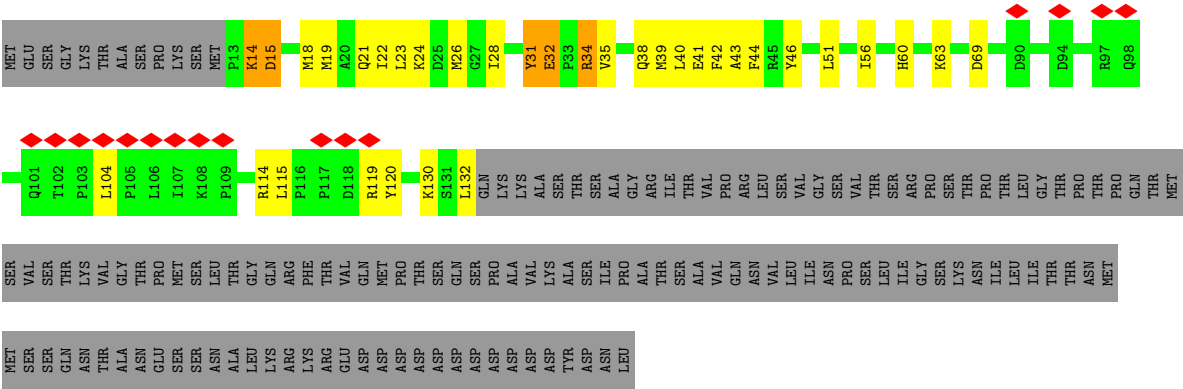


• Molecule 7: Transcription initiation factor TFIID subunit 8

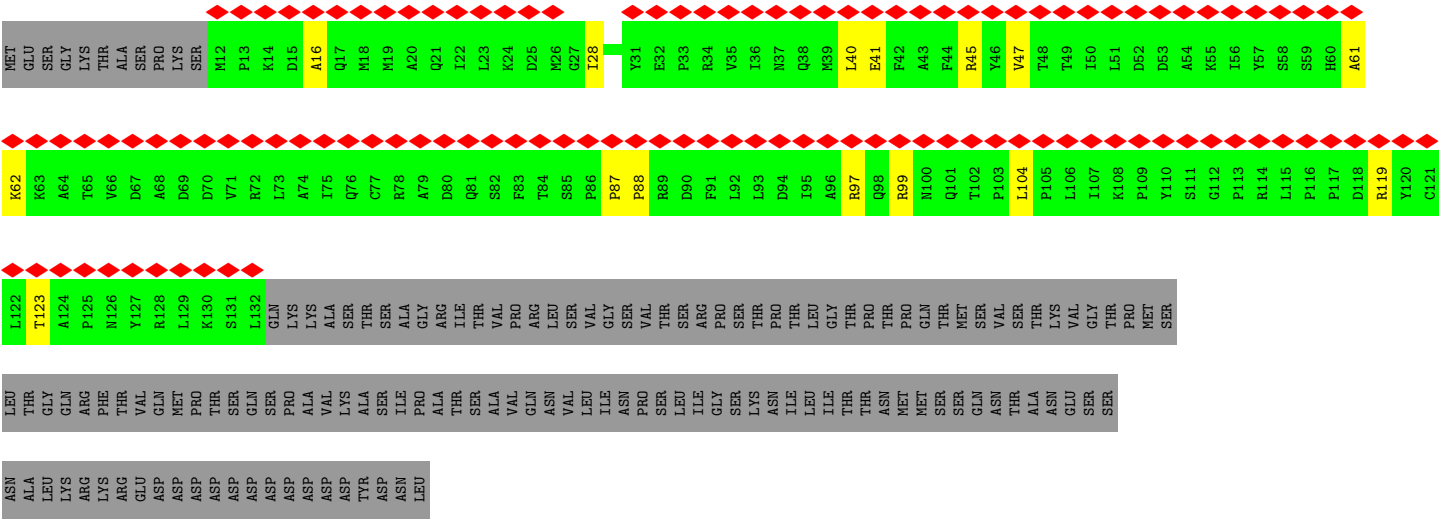
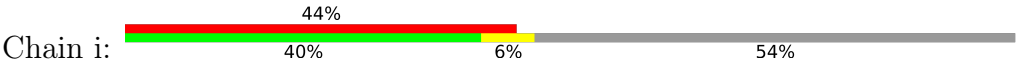


• Molecule 8: Transcription initiation factor TFIID subunit 9

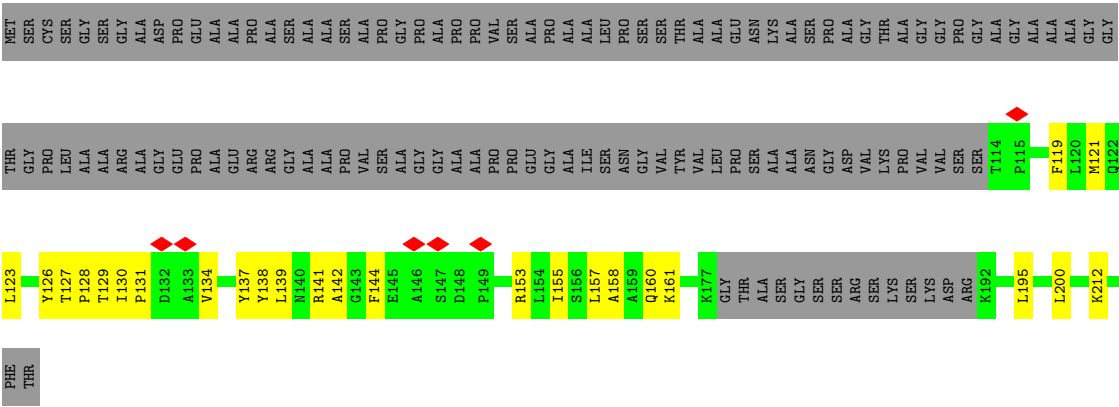




• Molecule 8: Transcription initiation factor TFIID subunit 9

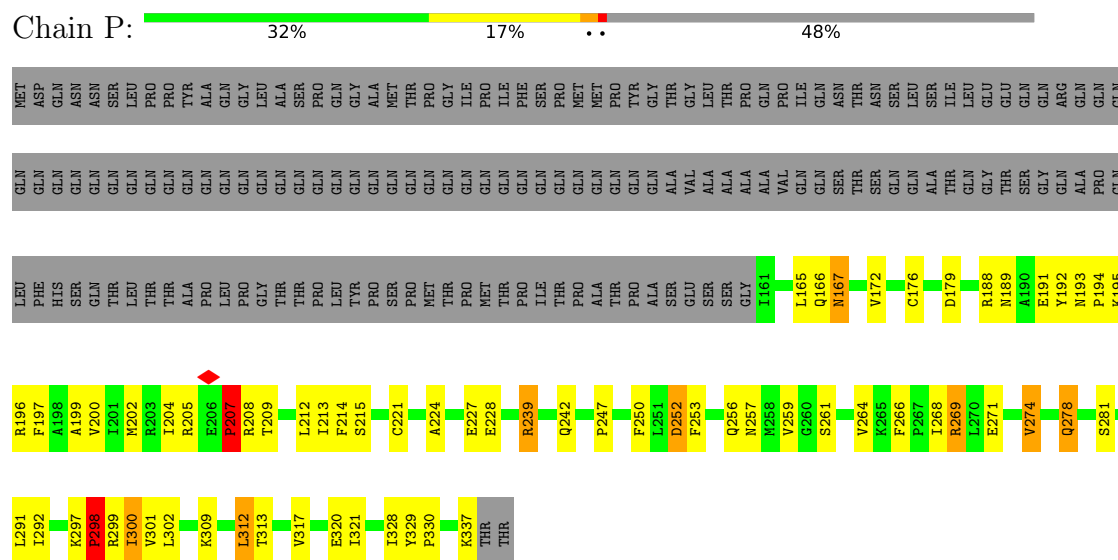


• Molecule 9: Transcription initiation factor TFIID subunit 10

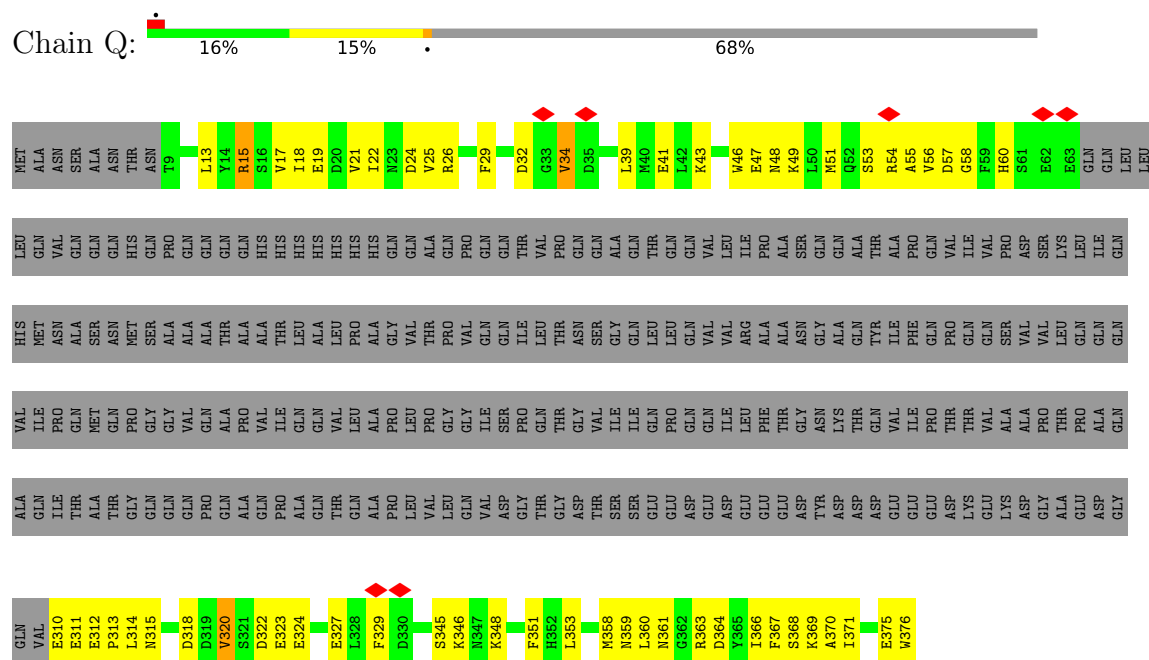


• Molecule 9: Transcription initiation factor TFIID subunit 10

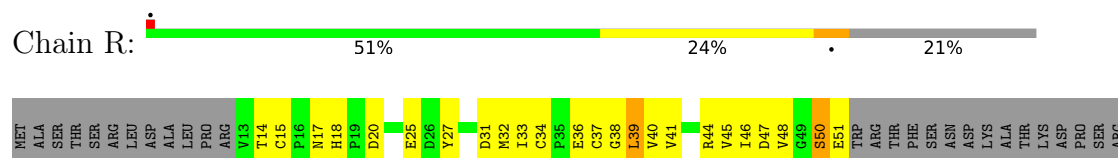
- Molecule 12: TATA-box-binding protein

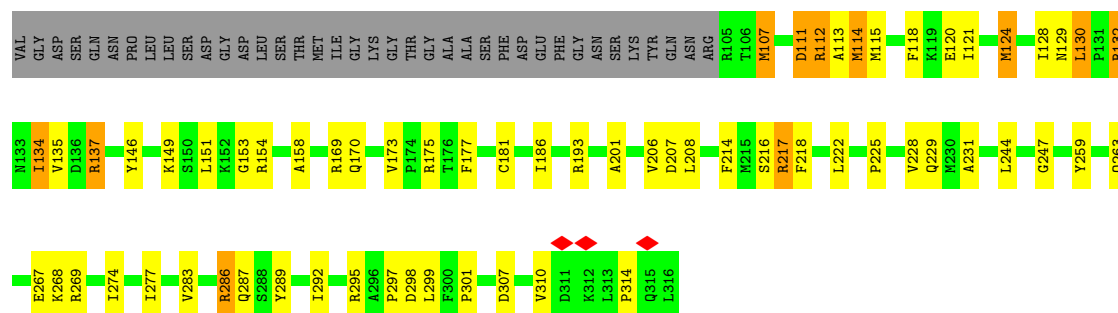


- Molecule 13: Transcription initiation factor IIA subunit 1

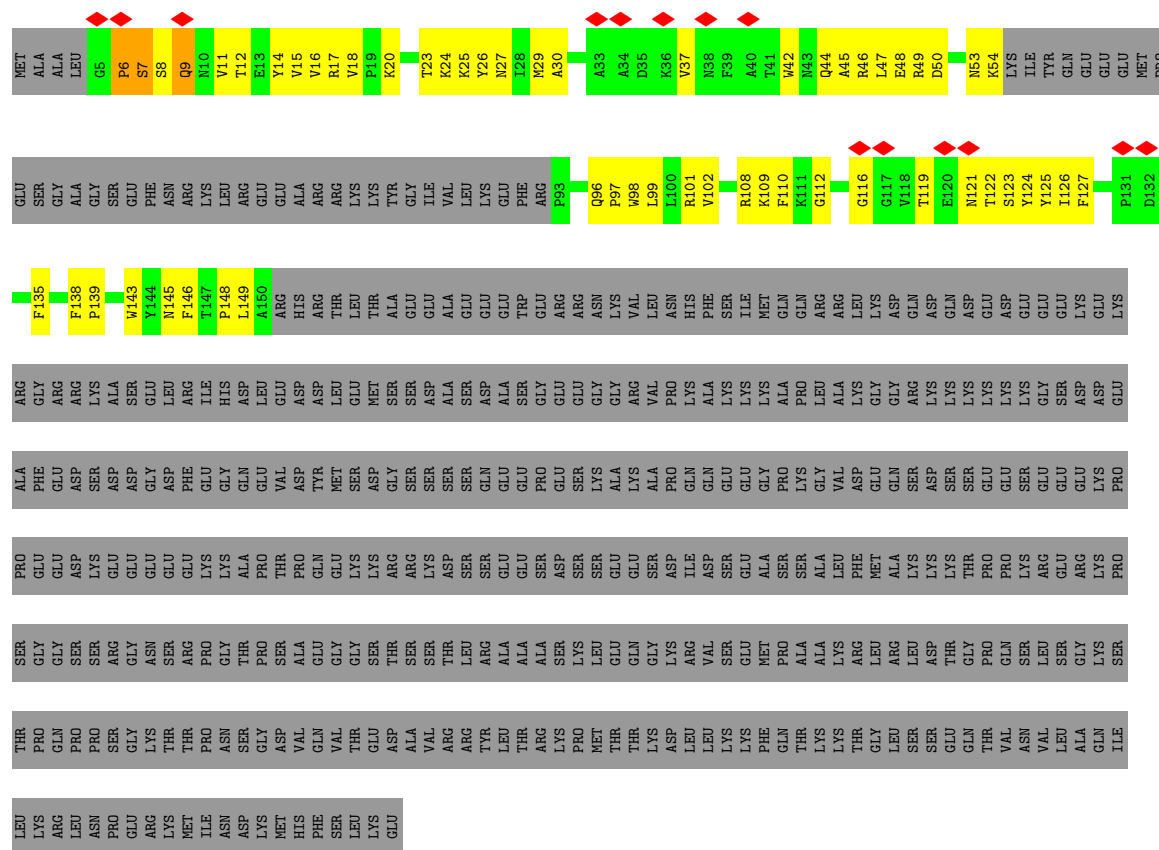


- Molecule 14: Transcription initiation factor IIB

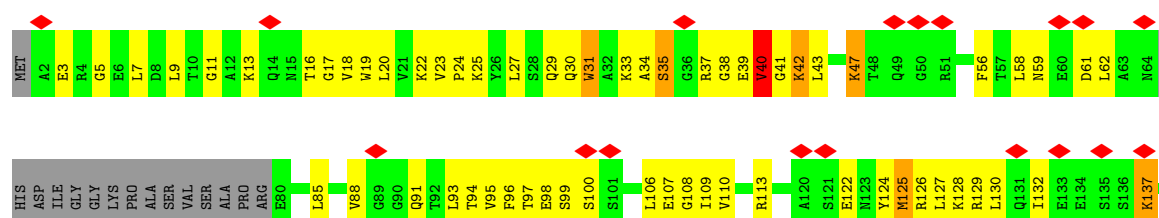




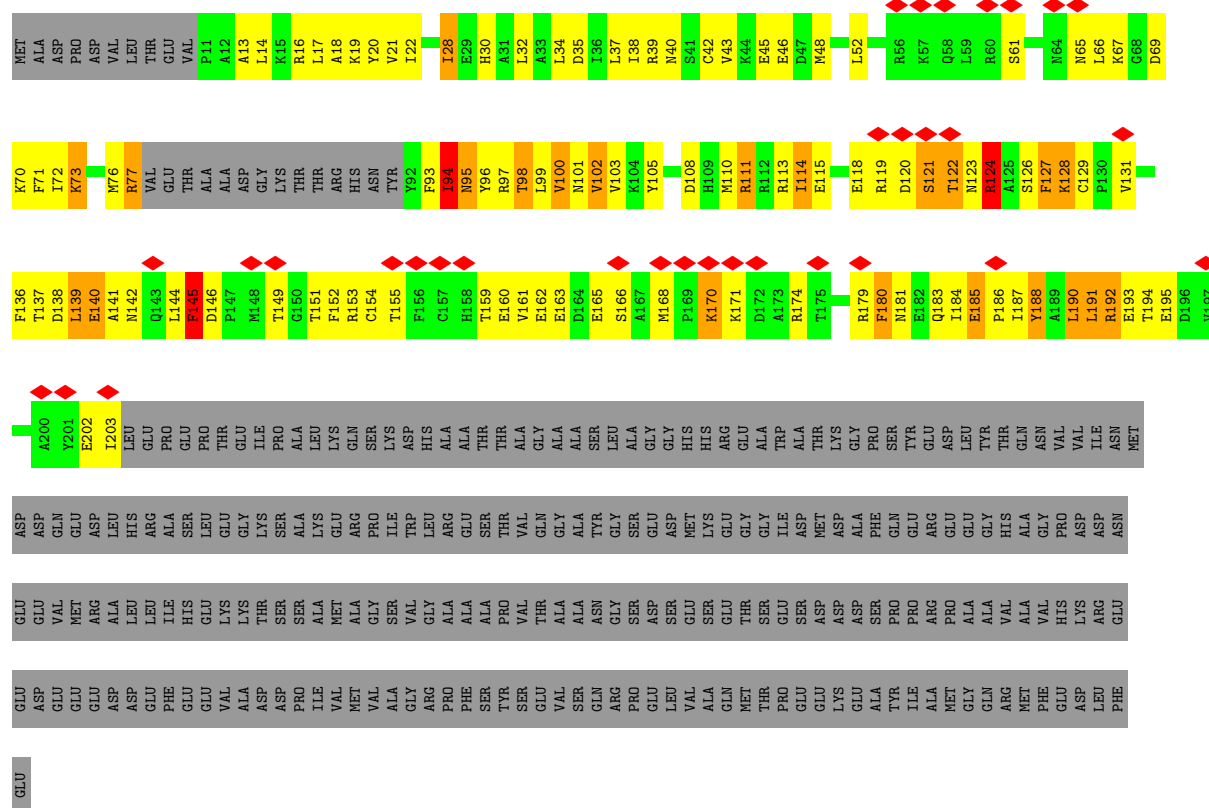
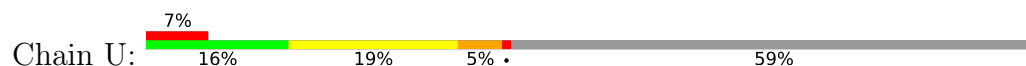
• Molecule 15: General transcription factor IIF subunit 1



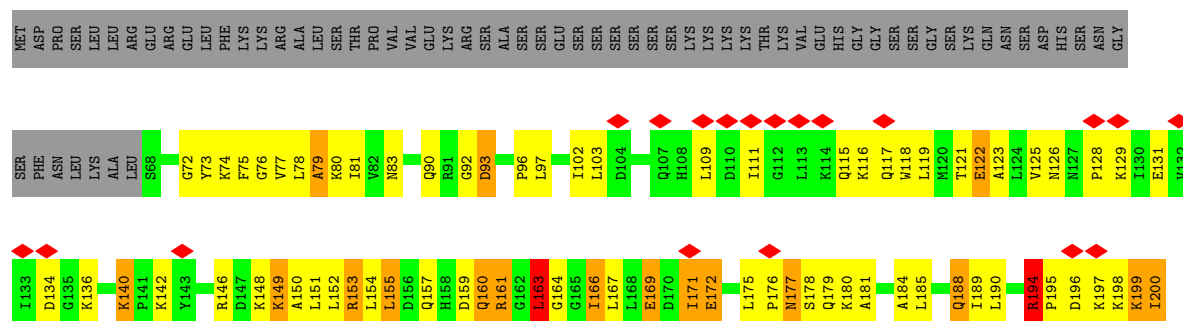
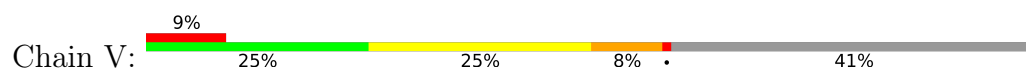
• Molecule 16: General transcription factor IIF subunit 2

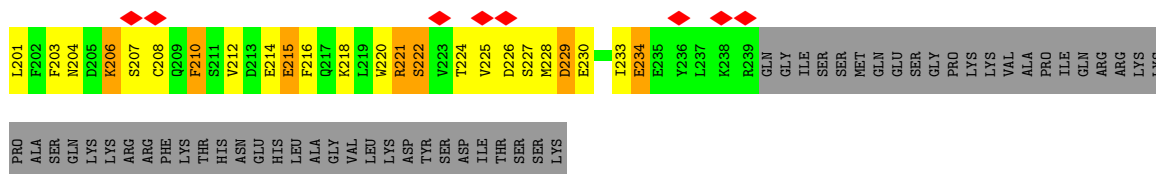


- Molecule 17: General transcription factor IIE subunit 1

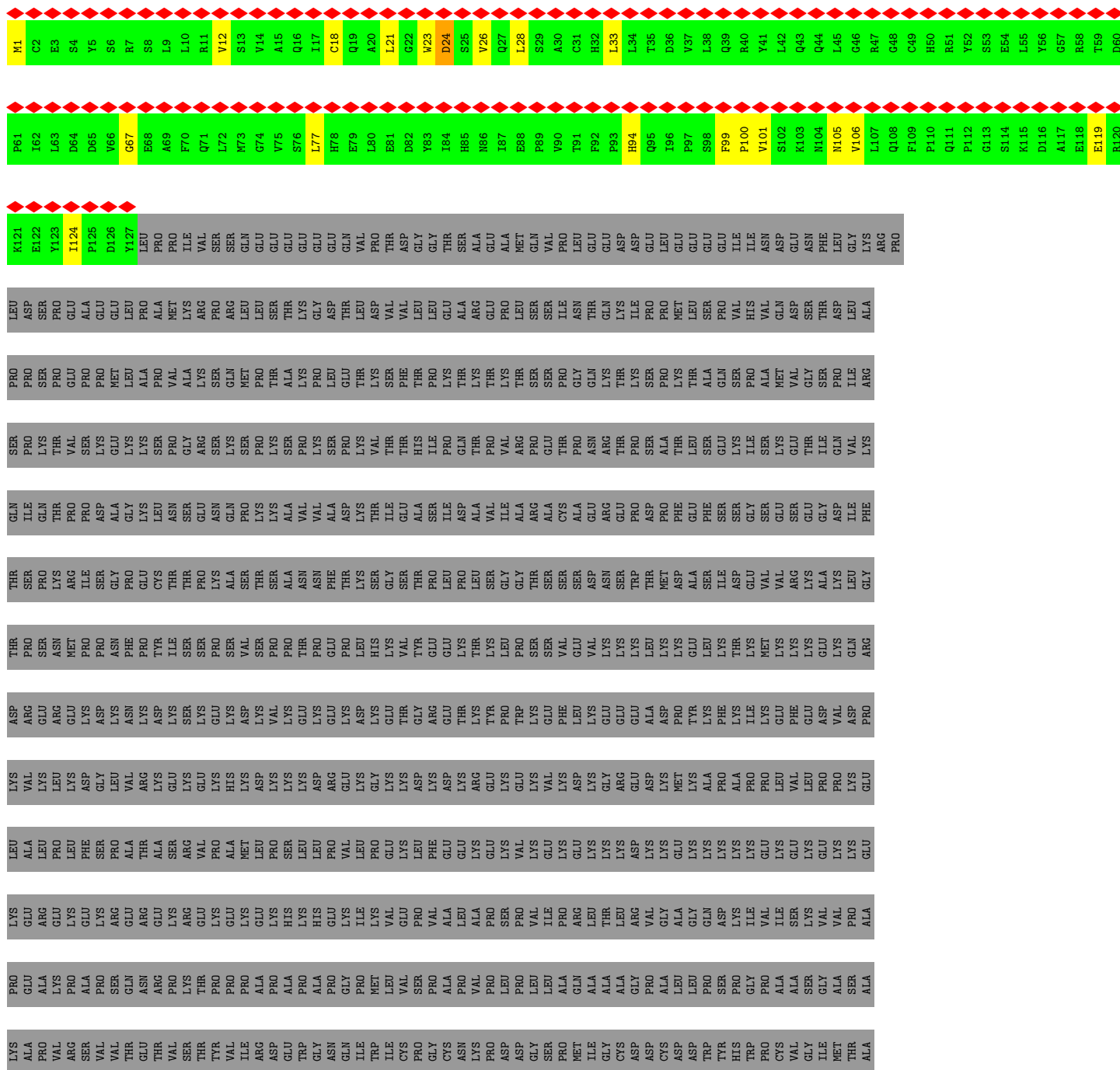


- Molecule 18: Transcription initiation factor IIE subunit beta





● Molecule 19: Transcription initiation factor TFIID subunit 3



PRO PRO
GLU GLU
MET MET
GLN GLN
TTP TTP
PHE PHE
CYS CYS
LYS LYS
CYS CYS
ALA ALA
ASN ASN
LYS LYS
LYS LYS
LYS LYS
LYS LYS
LYS LYS
ARG ARG
LYS LYS
HIS HIS
ARG ARG
ALA ALA
HIS HIS

• Molecule 20: Transcription initiation factor TFIID subunit 11

Chain k: 46%
43% 54%

MET ASP
ASP ASP
ALA ALA
HIS HIS
GLU GLU
SER SER
PRO PRO
CYS CYS
LYS LYS
GLY GLY
GLY GLY
GLU GLU
THR THR
LYS LYS
GLU GLU
SER SER
ASN ASN
ASP ASP
LYS LYS
THR THR
ALA ALA
LYS LYS
VAL VAL
PRO PRO
GLY GLY
ASP ASP
PRO PRO
GLY GLY
THR THR
LYS LYS
ALA ALA
THR THR
ASP ASP
GLY GLY
ILE ILE
PRO PRO
GLU GLU
GLU GLU
THR THR
ASP ASP
GLY GLY
ASP ASP
ILE ILE
ALA ALA
ASP ASP
VAL VAL
ASP ASP
LEU LEU
LYS LYS
GLU GLU
ALA ALA
SER SER
PHE PHE

GLN VAL
SER SER
LEU LEU
THR THR
THR THR
VAL VAL
ARG ARG
GLY GLY
ASP ASP
SER SER
SER SER
LEU LEU
GLU GLU
ASN ASN
PRO PRO
ALA ALA
ALA ALA
LYS LYS
LYS LYS
VAL VAL
LEU LEU
LYS LYS
ILE ILE
THR THR
ASP ASP
THR THR
LYS LYS
GLU GLU
GLY GLY
LYS LYS
GLN GLN
PRO PRO
VAL VAL
ASP ASP
GLU GLU
THR THR
ASP ASP
GLY GLY
ASP ASP
ILE ILE
GLN GLN
LYS LYS
MET MET
GLN GLN
ILE ILE
LEU LEU
VAL VAL
SER SER
PHE PHE
S114
E115
E116
Q117
L118
N119
R120

Y121 E122 M123 Y124 R125 R126 S127 A128 F129 P130 K131 A132 A133 I134 K135 R136 L137 L138 Q139 S140 I141 T142 G143 T144 S145 S146 S147 Q148 L149 V150 V151 I152 A153 M154 S155 G156 I157 S158 K159 V160 F161 V162 G163 E164 V165 V166 E167 E168 A169 L170 D171 V172 C173 E174 K175 W176 G177 E178 M179 P180

F181 L182 Q183 P184 H186 M187 R188 E189 A190 V191 R192 R193 L194 K195 S196 K197 G198 Q199 I200 P201 N202 S203 K204 H205 K206 K207 L208 I209 F210 F211

• Molecule 21: Transcription initiation factor TFIID subunit 13

Chain m: 70%
60% 10% 30%

MET ALA
ASP ASP
GLU GLU
GLU GLU
ASP ASP
PRO PRO
PHE PHE
GLU GLU
GLU GLU
ASN ASN
GLU GLU
GLU GLU
ILE ILE
GLY GLY
GLY GLY
ALA ALA
GLU GLU
GLY GLY
GLN GLN
GLY GLY
LYS LYS
R28 K29 R30 L31 F32 S33 K34 E35 L36 R37 C38 M39 M40 Y41 G42 F43 G44 D45 D46 Q47 N48 P49 Y50 T51 E52 S53 V54 D55 I56 L57 E58 D59 L60

V61 I62 E63 F64 I65 T66 E67 M68 S69 H70 K71 A72 T73 M74 I75 T76 G77 R78 G79 R80 V81 Q82 V83 E84 D85 I86 V87 F88 L89 I90 R91 K92 D93 P94 R95 K96 F97 A98 R99 V100 K101 D102 L103 L104 T105 M106 N107 E108 E109 K110 K111 R112 A113 R114 LYS ALA PHE ASP GLU ALA

ASN
TYR
GLY
SER

• Molecule 22: DNA-directed RNA polymerase subunit

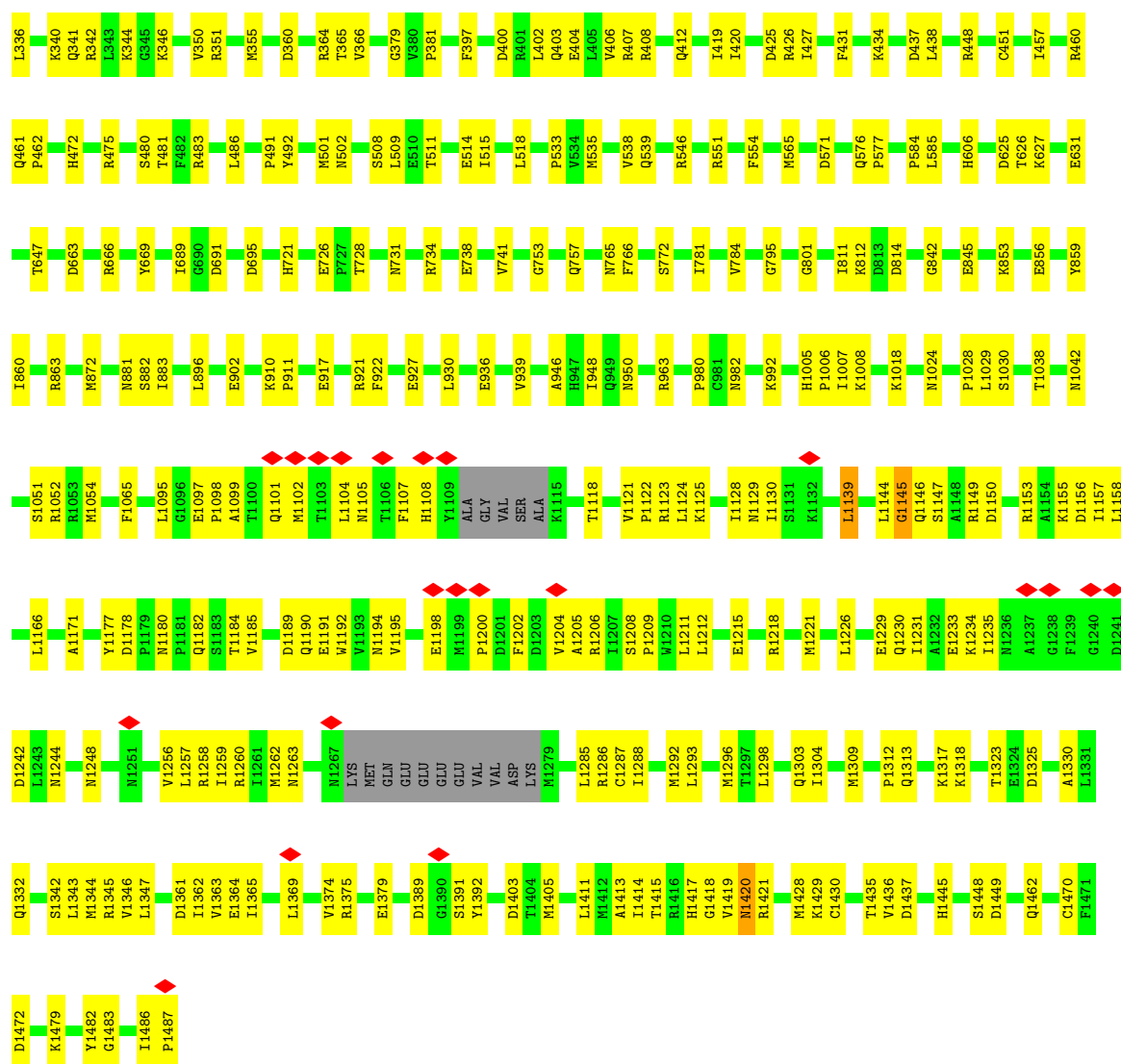
Chain o: 69% 27%

MET HIS
GLY GLY
GLY GLY
PRO PRO
PRO PRO
SER SER
ASP ASP
S11 A12 L15 R16 T17 I18 L26 S27 P28 R192 R193 L198 Y199 W202 E294 H298 Q299 A298 A300 H301 V302 K212 K213 L214 L215 L216 S217 P218 E219 R220 V221 I224 R227 I228 D229 D230 E231 E232 V235 L236 V260

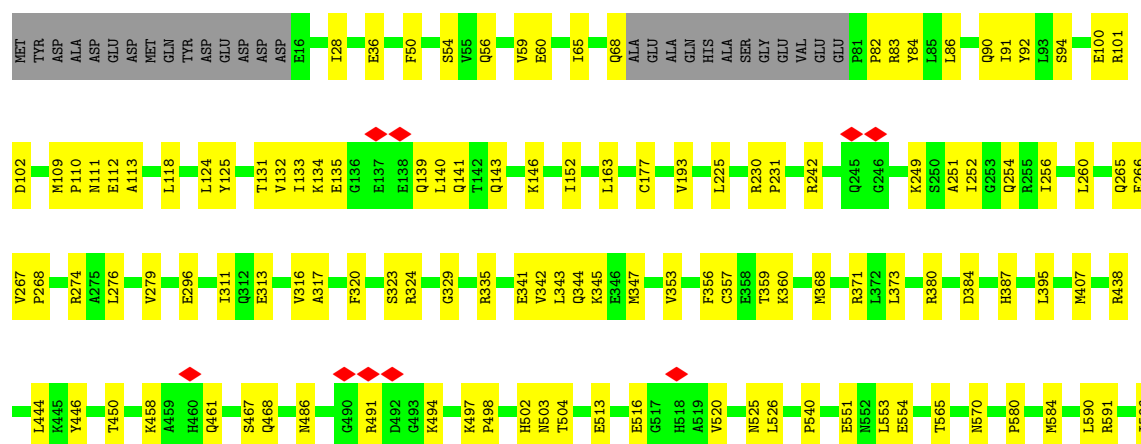
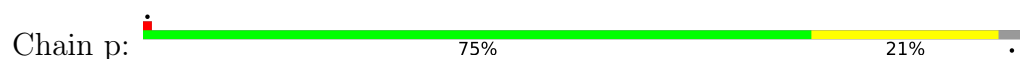
H67 K92 P93 V94 F95 H96 V97 L100 V101 K102 T103 M104 V106 L107 R108 C111 C114 K125 T129 L130 A131 K132 S133 K134 G135 Q136 K139 R140 L141 T142 K149 G150 K151 N152 T153 C154 E155 GLY GLY GLU GLU MET ASN ASN LYS PHE GLY VAL GLN

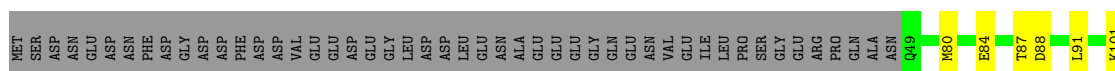
PRO GLU
ASP ASP
GLU GLU
LEU LEU
THR THR
GLY GLY
GLY GLY
H181 C184 Q188 P189 R190 I191 R192 R193 L198 Y199 W202 E294 H298 Q299 A298 A300 H301 V302 K212 K213 L214 L215 L216 S217 P218 E219 R220 V221 I224 R227 I228 D229 D230 E231 E232 V235 L236 V260

R261 Q267 Q273 D274 D275 L276 T277 H278 K279 L280 A281 D282 L283 T286 N287 N288 Q289 L290 R291 R292 N293 E294 Q295 N296 Q297 A298 A299 A300 H301 V302 K212 K213 L214 L215 L216 S217 P218 E219 R220 V221 I224 R227 I228 D229 D230 E231 E232 V235 L236 V260 R327 Q330 K331 R334 P335

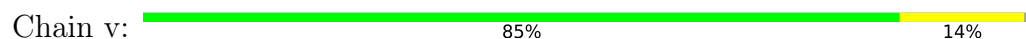


• Molecule 23: DNA-directed RNA polymerase subunit beta





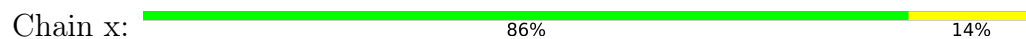
- Molecule 28: DNA-directed RNA polymerases I, II, and III subunit RPABC3



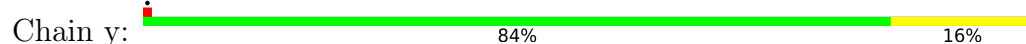
- Molecule 29: DNA-directed RNA polymerase II subunit RPB9



- Molecule 30: RPB10



- Molecule 31: RNA_pol_L_2 domain-containing protein

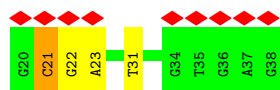


- Molecule 32: RPB12

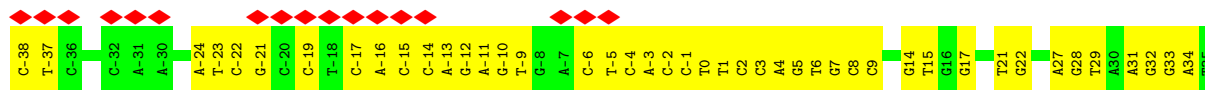


- Molecule 33: DNA (85-MER)

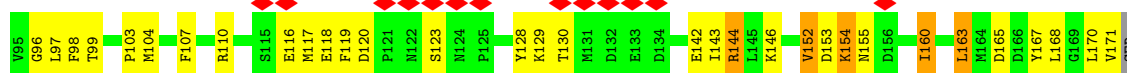




• Molecule 34: DNA (85-MER)



• Molecule 35: DNA-directed RNA polymerase II subunit RPB7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21692	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 ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.114	Depositor
Minimum map value	-0.069	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0085	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	A	0.68	0/5046	0.95	6/6810 (0.1%)
2	B	0.48	1/7993 (0.0%)	0.70	8/10836 (0.1%)
3	D	0.65	0/1379	0.95	3/1843 (0.2%)
3	d	0.22	0/1321	0.44	0/1772
4	E	0.34	0/4469	0.58	1/6050 (0.0%)
4	e	0.29	0/4433	0.53	0/6004
5	F	0.71	1/3139 (0.0%)	1.08	11/4264 (0.3%)
5	f	0.46	0/3140	0.79	6/4268 (0.1%)
6	G	0.69	0/1199	0.96	1/1612 (0.1%)
7	H	0.55	0/1673	0.79	2/2285 (0.1%)
8	I	0.31	0/981	0.50	0/1332
8	i	0.23	0/989	0.41	0/1343
9	J	0.28	0/724	0.51	0/982
9	j	0.22	0/775	0.45	0/1049
10	L	0.40	0/630	0.73	0/852
10	l	0.48	0/888	0.77	0/1194
11	O	0.78	0/781	1.25	8/1061 (0.8%)
12	P	0.95	0/1438	1.22	3/1935 (0.2%)
13	Q	0.63	0/1013	1.03	2/1366 (0.1%)
14	R	0.51	0/1967	1.02	7/2656 (0.3%)
15	S	0.45	0/896	0.83	0/1213
16	T	0.82	1/1817 (0.1%)	1.18	5/2445 (0.2%)
17	U	0.76	2/1499 (0.1%)	1.31	15/2012 (0.7%)
18	V	0.73	0/1428	1.16	4/1917 (0.2%)
19	c	0.48	0/1035	0.67	0/1406
20	k	0.29	0/799	0.53	1/1070 (0.1%)
21	m	0.31	0/733	0.55	0/977
22	o	0.31	0/11516	0.53	2/15548 (0.0%)
23	p	0.33	0/9243	0.48	0/12475
24	q	0.32	0/2102	0.44	0/2857
25	r	0.18	0/1019	0.45	0/1374
26	s	0.23	0/1751	0.47	0/2366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	t	0.29	0/645	0.48	0/871
28	v	0.29	0/1207	0.47	0/1628
29	w	0.23	0/948	0.44	0/1284
30	x	0.36	0/516	0.44	0/696
31	y	0.31	0/956	0.47	0/1294
32	z	0.28	0/377	0.44	0/500
33	X	0.40	0/1966	0.72	4/3034 (0.1%)
34	Y	0.38	0/1942	0.68	2/2993 (0.1%)
35	u	0.43	0/1382	0.82	3/1874 (0.2%)
All	All	0.47	5/87755 (0.0%)	0.73	94/119348 (0.1%)

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
15	S	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	U	123	ASN	C-N	9.49	1.47	1.33
17	U	124	ARG	C-N	6.88	1.42	1.33
16	T	132	ILE	C-O	-6.40	1.16	1.24
2	B	61	ASN	C-O	-6.23	1.18	1.24
5	F	395	ARG	C-O	5.69	1.32	1.24

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	U	101	ASN	N-CA-C	-10.64	97.82	112.30
2	B	491	HIS	N-CA-C	-9.48	100.95	111.28
5	f	149	PRO	O-C-N	9.36	125.61	121.31
17	U	127	PHE	CB-CA-C	9.28	126.62	109.54
11	O	58	PHE	N-CA-C	9.13	120.29	108.24
3	D	993	GLN	N-CA-C	8.45	120.49	111.28
3	D	881	ARG	CB-CA-C	-8.43	97.99	110.96
17	U	138	ASP	N-CA-C	-8.31	102.22	111.28
17	U	127	PHE	N-CA-C	-8.02	99.19	110.50
1	A	356	PRO	N-CA-C	7.91	124.81	114.68
5	F	382	GLU	CB-CA-C	-7.68	100.59	112.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	U	123	ASN	O-C-N	7.62	132.29	122.39
7	H	163	PRO	N-CA-C	7.38	124.02	113.47
11	O	62	LEU	N-CA-C	7.34	120.46	110.55
2	B	495	GLN	N-CA-C	-7.24	104.45	113.28
1	A	715	PRO	N-CA-C	-7.19	99.95	111.03
17	U	140	GLU	CB-CA-C	-7.15	99.66	110.88
5	F	271	VAL	N-CA-C	-7.06	106.13	112.90
22	o	1144	LEU	N-CA-C	6.92	118.61	111.14
5	F	330	ARG	CB-CA-C	-6.86	100.10	110.88
5	f	326	HIS	N-CA-C	-6.72	104.19	112.38
20	k	180	PRO	N-CA-C	6.70	118.88	110.70
17	U	180	PHE	N-CA-C	6.68	118.64	111.36
18	V	126	ASN	N-CA-C	-6.65	105.03	113.01
1	A	396	LEU	N-CA-C	-6.63	104.94	113.16
3	D	994	GLN	N-CA-C	6.62	118.49	111.28
5	F	383	LEU	N-CA-C	-6.58	104.39	112.88
5	f	319	LEU	N-CA-C	-6.54	103.98	112.68
7	H	114	SER	N-CA-C	-6.46	105.44	113.38
17	U	103	VAL	N-CA-C	-6.41	104.08	110.62
14	R	34	CYS	CA-C-N	6.26	126.00	119.05
14	R	34	CYS	C-N-CA	6.26	126.00	119.05
35	u	152	VAL	N-CA-C	6.26	117.75	107.24
1	A	1205	PHE	CA-CB-CG	-6.22	107.58	113.80
17	U	98	THR	N-CA-C	6.21	119.37	110.24
17	U	14	LEU	N-CA-C	-6.13	104.15	111.69
14	R	217	ARG	N-CA-C	6.10	117.93	111.28
14	R	50	SER	CB-CA-C	-6.09	109.56	116.63
33	X	19	DG	C2'-C3'-O3'	-6.08	102.37	111.50
2	B	181	GLY	CA-C-O	-6.07	117.94	122.37
33	X	21	DC	C2'-C3'-O3'	-5.96	102.56	111.50
5	f	255	MET	N-CA-C	-5.94	104.88	114.09
16	T	188	PHE	N-CA-C	-5.86	104.97	111.36
5	F	316	GLN	CB-CA-C	5.75	120.16	110.79
18	V	122	GLU	N-CA-C	5.69	120.25	112.68
17	U	188	TYR	N-CA-C	-5.66	106.42	113.38
12	P	298	PRO	N-CA-C	-5.66	100.81	112.47
33	X	-30	DT	C2'-C3'-O3'	-5.63	103.06	111.50
2	B	583	GLU	CB-CA-C	-5.62	101.45	110.79
2	B	264	GLU	N-CA-C	-5.58	106.13	113.17
18	V	150	ALA	N-CA-C	5.57	119.38	111.92
14	R	307	ASP	N-CA-C	-5.56	106.85	113.97
5	f	150	PRO	N-CA-C	5.53	117.45	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	T	157	ALA	N-CA-C	-5.51	100.19	109.07
11	O	6	TYR	N-CA-C	5.50	119.09	112.93
14	R	112	ARG	N-CA-C	-5.44	105.69	112.93
13	Q	368	SER	N-CA-C	-5.42	106.83	113.50
17	U	94	ILE	N-CA-C	5.42	116.99	109.29
22	o	1145	GLY	CA-C-O	-5.42	116.86	122.28
5	f	329	LEU	N-CA-C	-5.41	106.38	112.87
16	T	183	VAL	O-C-N	5.40	127.50	121.94
12	P	207	PRO	N-CA-C	-5.40	101.35	112.47
6	G	183	ILE	N-CA-C	-5.39	102.57	109.30
5	F	382	GLU	N-CA-CB	5.39	117.10	110.53
5	F	272	VAL	N-CA-C	-5.38	105.13	110.62
18	V	163	LEU	N-CA-C	5.38	119.00	111.74
17	U	128	LYS	N-CA-CB	5.36	119.61	110.71
11	O	57	ASN	CA-C-O	-5.33	115.03	120.99
16	T	31	TRP	N-CA-C	5.30	117.80	111.71
2	B	491	HIS	CB-CA-C	5.28	119.55	110.79
5	F	149	PRO	N-CA-C	5.27	117.13	110.70
12	P	205	ARG	CB-CA-C	-5.22	101.14	110.70
14	R	113	ALA	N-CA-C	-5.22	105.76	111.82
16	T	185	ASP	N-CA-C	-5.19	105.52	111.07
11	O	27	GLN	CA-C-N	-5.14	114.09	122.57
11	O	27	GLN	C-N-CA	-5.14	114.09	122.57
35	u	160	ILE	N-CA-C	5.13	115.86	108.48
5	F	219	GLU	N-CA-C	-5.12	105.78	111.36
13	Q	15	ARG	N-CA-C	-5.10	105.61	111.07
11	O	9	THR	N-CA-C	-5.10	101.66	109.41
33	X	-40	DC	C2'-C3'-O3'	-5.10	103.85	111.50
11	O	58	PHE	CB-CA-C	-5.09	101.69	112.78
34	Y	43	DT	C2'-C3'-O3'	-5.09	103.87	111.50
1	A	498	PRO	N-CA-CB	5.08	108.59	103.25
4	E	795	GLY	N-CA-C	5.08	125.22	113.18
35	u	96	GLY	N-CA-C	5.08	117.70	110.74
5	F	330	ARG	CG-CD-NE	-5.08	100.82	112.00
34	Y	36	DG	C2'-C3'-O3'	-5.08	103.89	111.50
17	U	98	THR	CA-C-N	-5.07	114.27	122.24
17	U	98	THR	C-N-CA	-5.07	114.27	122.24
1	A	999	SER	CA-C-O	-5.05	116.41	122.27
2	B	541	ARG	CB-CA-C	-5.04	101.68	110.09
2	B	984	PRO	N-CA-C	-5.01	103.31	111.03
5	F	416	ASP	CB-CA-C	5.01	119.10	110.79

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	S	6	PRO	Mainchain

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	A	4927	0	4871	261	0
2	B	7796	0	7751	215	0
3	D	1366	0	1390	193	0
3	d	1307	0	1318	15	0
4	E	4364	0	4244	100	0
4	e	4327	0	4197	46	0
5	F	3081	0	3018	353	0
5	f	3081	0	3012	88	0
6	G	1180	0	1235	38	0
7	H	1633	0	1621	218	0
8	I	959	0	969	130	0
8	i	967	0	977	13	0
9	J	709	0	710	89	0
9	j	759	0	759	18	0
10	L	622	0	620	118	0
10	l	876	0	893	13	0
11	O	771	0	764	182	0
12	P	1412	0	1506	93	0
13	Q	996	0	926	135	0
14	R	1939	0	1980	173	0
15	S	872	0	848	126	0
16	T	1788	0	1819	239	0
17	U	1476	0	1487	161	0
18	V	1404	0	1424	159	0
19	c	1011	0	975	27	0
20	k	785	0	818	8	0
21	m	724	0	744	12	0
22	o	11308	0	11428	339	0
23	p	9062	0	9107	233	0
24	q	2059	0	2008	32	0
25	r	1005	0	964	111	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	s	1720	0	1737	46	0
27	t	635	0	665	5	0
28	v	1186	0	1147	12	0
29	w	927	0	859	18	0
30	x	507	0	523	8	0
31	y	937	0	959	15	0
32	z	372	0	379	11	0
33	X	1751	0	954	76	0
34	Y	1734	0	956	66	0
35	u	1351	0	1358	150	0
36	R	1	0	0	0	0
36	U	1	0	0	0	0
36	o	2	0	0	0	0
36	p	1	0	0	0	0
36	q	1	0	0	0	0
36	w	2	0	0	0	0
36	x	1	0	0	0	0
36	z	1	0	0	0	0
37	o	1	0	0	0	0
All	All	85697	0	83920	3169	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (3169) 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)
5:F:47:ILE:HG21	8:I:19:MET:SD	1.09	1.64
3:D:871:THR:CG2	10:L:66:LEU:HD22	1.31	1.61
14:R:33:ILE:HG21	22:o:431:PHE:CD2	1.22	1.59
14:R:33:ILE:CD1	22:o:431:PHE:HE2	1.10	1.58
14:R:27:TYR:CD1	14:R:48:VAL:CG2	1.86	1.58
5:F:48:LYS:CG	8:I:22:ILE:HG23	1.17	1.57
5:F:320:ARG:CB	5:F:415:ILE:HD12	1.23	1.57
5:F:48:LYS:HG3	8:I:22:ILE:CG2	1.11	1.57
11:O:88:ILE:HG21	13:Q:360:LEU:CB	1.27	1.56
8:I:60:HIS:CE1	10:L:118:LEU:CD2	1.84	1.56
5:F:47:ILE:CD1	8:I:19:MET:HE1	1.11	1.56
1:A:468:PHE:HZ	5:F:224:TYR:CD2	1.18	1.55
5:F:320:ARG:HB2	5:F:415:ILE:CD1	1.28	1.55
8:I:60:HIS:CE1	10:L:118:LEU:HD22	1.36	1.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:320:ARG:HD3	5:F:415:ILE:CB	1.36	1.51
5:F:47:ILE:HD13	8:I:19:MET:CE	1.04	1.50
14:R:33:ILE:HD13	22:o:431:PHE:CE2	1.45	1.50
14:R:33:ILE:CG2	22:o:431:PHE:HD2	1.22	1.50
25:r:103:LEU:HD23	35:u:144:ARG:NH1	1.18	1.50
11:O:22:LEU:CB	11:O:28:ILE:HG12	1.35	1.49
5:F:211:ARG:HG2	7:H:165:TYR:CD2	1.51	1.46
5:F:47:ILE:CG2	8:I:19:MET:SD	2.03	1.46
2:B:883:PHE:HE1	7:H:223:TYR:CB	1.26	1.45
25:r:103:LEU:CD2	35:u:144:ARG:HH11	1.27	1.45
1:A:468:PHE:CZ	5:F:224:TYR:CD2	2.05	1.44
5:F:412:LEU:CD1	5:F:417:ARG:HD2	1.47	1.44
14:R:27:TYR:CD1	14:R:48:VAL:HG21	0.92	1.44
5:F:320:ARG:CD	5:F:415:ILE:HB	1.48	1.43
5:F:211:ARG:CG	7:H:165:TYR:HD2	1.29	1.42
3:D:871:THR:CA	10:L:66:LEU:HD13	1.49	1.42
12:P:197:PHE:CE1	33:X:-24:DG:N2	1.88	1.42
3:D:963:ARG:NH1	3:D:964:GLU:HA	1.34	1.41
10:L:106:ARG:HH11	10:L:114:LYS:NZ	1.00	1.41
11:O:44:ILE:CD1	13:Q:17:VAL:HG11	1.48	1.40
10:L:106:ARG:HH12	10:L:114:LYS:CD	1.35	1.40
2:B:883:PHE:CE1	7:H:223:TYR:HA	1.56	1.40
25:r:103:LEU:HA	35:u:144:ARG:NH1	1.24	1.40
14:R:27:TYR:HD1	14:R:48:VAL:CG2	1.23	1.39
1:A:638:PRO:CG	6:G:39:LEU:HD23	1.48	1.39
3:D:871:THR:CG2	10:L:66:LEU:CD2	1.99	1.39
14:R:27:TYR:CG	23:p:841:ARG:CZ	2.04	1.39
14:R:33:ILE:CG2	22:o:431:PHE:CD2	2.00	1.39
13:Q:47:GLU:OE2	13:Q:60:HIS:CE1	1.75	1.38
35:u:40:GLY:HA2	35:u:152:VAL:CG2	1.54	1.38
11:O:88:ILE:CG2	13:Q:360:LEU:HB3	1.55	1.37
5:F:71:ILE:HB	8:I:38:GLN:NE2	1.39	1.36
10:L:106:ARG:NH1	10:L:114:LYS:HZ3	1.18	1.36
14:R:33:ILE:CD1	22:o:431:PHE:CE2	2.02	1.35
14:R:27:TYR:CG	23:p:841:ARG:NH1	1.95	1.34
2:B:883:PHE:CE1	7:H:223:TYR:CB	2.11	1.34
5:F:43:VAL:CG2	8:I:43:ALA:HB1	1.55	1.34
5:F:308:VAL:HG11	5:F:337:VAL:CG2	1.58	1.34
14:R:33:ILE:CG1	22:o:431:PHE:CE2	2.08	1.34
11:O:79:VAL:O	11:O:90:VAL:CG1	1.76	1.33
2:B:883:PHE:CD1	7:H:223:TYR:HA	1.61	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:883:PHE:CE1	7:H:223:TYR:CA	2.12	1.32
5:F:211:ARG:CG	7:H:165:TYR:CD2	2.09	1.31
5:F:412:LEU:HD13	5:F:417:ARG:CD	1.60	1.31
12:P:274:VAL:CG1	14:R:208:LEU:HD11	1.58	1.31
11:O:22:LEU:CB	11:O:28:ILE:CG1	2.09	1.31
25:r:60:VAL:HG11	35:u:44:PHE:CZ	1.67	1.29
25:r:16:ASP:CG	35:u:81:LYS:HZ2	1.37	1.29
17:U:70:LYS:O	17:U:99:LEU:HB3	1.24	1.28
11:O:22:LEU:HB2	11:O:28:ILE:CD1	1.62	1.27
10:L:101:GLN:O	10:L:105:HIS:CD2	1.88	1.27
3:D:963:ARG:NH1	3:D:964:GLU:CA	1.97	1.26
11:O:32:LEU:HD13	13:Q:32:ASP:OD2	1.28	1.26
10:L:106:ARG:NH1	10:L:114:LYS:HD2	1.47	1.26
3:D:891:ILE:CG2	10:L:111:LEU:HB2	1.66	1.26
14:R:48:VAL:CG2	23:p:841:ARG:HH12	1.46	1.26
1:A:1014:GLU:OE2	22:o:1204:VAL:HG11	1.33	1.26
16:T:140:ARG:O	23:p:56:GLN:HG2	1.15	1.25
4:E:694:LEU:HD13	4:E:703:MET:CE	1.64	1.25
3:D:963:ARG:HH11	3:D:964:GLU:CA	1.46	1.25
5:F:87:HIS:HB3	9:J:212:LYS:NZ	1.49	1.25
16:T:124:TYR:CE2	23:p:590:LEU:HD21	1.71	1.25
17:U:126:SER:CB	17:U:136:PHE:O	1.84	1.25
2:B:883:PHE:CD1	7:H:223:TYR:CA	2.18	1.25
1:A:405:VAL:CA	5:F:302:HIS:HB3	1.65	1.24
11:O:88:ILE:CD1	13:Q:360:LEU:HB2	1.67	1.24
14:R:27:TYR:HB2	23:p:841:ARG:NH1	1.50	1.24
5:F:219:GLU:CG	7:H:156:PRO:HB2	1.68	1.23
1:A:488:ALA:HB1	5:f:271:VAL:CG2	1.65	1.23
1:A:468:PHE:CE1	5:F:224:TYR:CE2	2.25	1.23
2:B:883:PHE:CE1	7:H:223:TYR:HB3	1.74	1.23
14:R:27:TYR:CB	23:p:841:ARG:NH1	2.00	1.23
18:V:181:ALA:O	18:V:185:LEU:N	1.72	1.23
1:A:468:PHE:CZ	5:F:224:TYR:CE2	2.26	1.22
10:L:106:ARG:NH1	10:L:114:LYS:CD	1.98	1.22
11:O:22:LEU:HB2	11:O:28:ILE:CG1	1.65	1.22
14:R:33:ILE:CG1	22:o:431:PHE:HE2	1.46	1.22
11:O:88:ILE:HG23	13:Q:361:ASN:ND2	1.54	1.22
13:Q:310:GLU:O	13:Q:313:PRO:HD2	1.35	1.22
17:U:145:PHE:CZ	35:u:98:PHE:HE2	1.57	1.22
1:A:405:VAL:CB	5:F:302:HIS:HB3	1.70	1.22
3:D:964:GLU:O	3:D:967:MET:SD	1.97	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1005:ASN:O	3:D:1009:LEU:HD13	1.36	1.22
4:E:615:ASP:OD1	8:I:114:ARG:HB3	1.34	1.20
5:F:213:ILE:HB	7:H:163:PRO:O	1.38	1.20
25:r:103:LEU:CA	35:u:144:ARG:HH12	1.53	1.20
12:P:188:ARG:NH1	13:Q:322:ASP:CG	1.98	1.20
17:U:37:LEU:HD13	17:U:71:PHE:CE1	1.75	1.20
5:F:290:MET:SD	5:F:340:ILE:HG21	1.81	1.20
3:D:871:THR:N	10:L:66:LEU:CD1	2.03	1.19
18:V:121:THR:O	18:V:125:VAL:HG21	1.39	1.19
4:E:694:LEU:CD1	4:E:703:MET:HE1	1.71	1.19
25:r:103:LEU:HA	35:u:144:ARG:CZ	1.73	1.18
3:D:889:HIS:HA	10:L:104:ARG:NH2	1.57	1.18
3:D:889:HIS:C	10:L:104:ARG:HH21	1.51	1.18
17:U:121:SER:OG	17:U:124:ARG:NH1	1.77	1.18
25:r:16:ASP:CG	35:u:81:LYS:NZ	2.01	1.17
5:F:320:ARG:HD2	5:F:321:PRO:HD3	1.19	1.17
12:P:188:ARG:NH2	13:Q:323:GLU:O	1.75	1.17
11:O:79:VAL:O	11:O:90:VAL:HG12	1.33	1.16
1:A:564:PRO:HG2	2:B:744:PHE:CE2	1.78	1.16
4:E:704:VAL:HG11	4:E:747:LEU:HG	1.23	1.16
25:r:16:ASP:OD2	35:u:81:LYS:NZ	1.79	1.16
35:u:38:CYS:SG	35:u:44:PHE:HA	1.86	1.15
2:B:768:PRO:HG2	2:B:771:VAL:CG2	1.76	1.15
14:R:27:TYR:CD1	23:p:841:ARG:NH1	2.15	1.15
5:F:213:ILE:HG21	7:H:163:PRO:CB	1.75	1.15
5:F:290:MET:HE1	5:F:337:VAL:HA	1.17	1.15
15:S:135:PHE:CE2	16:T:43:LEU:HD23	1.80	1.15
3:D:963:ARG:HD3	3:D:964:GLU:N	1.61	1.14
14:R:33:ILE:HG12	22:o:431:PHE:CD2	1.82	1.14
11:O:65:TYR:HE1	12:P:191:GLU:CG	1.60	1.14
5:F:71:ILE:CB	8:I:38:GLN:HE21	1.59	1.14
11:O:65:TYR:CE1	12:P:191:GLU:HG2	1.81	1.14
3:D:871:THR:HG22	10:L:66:LEU:CD2	1.70	1.13
15:S:122:THR:HG22	16:T:24:PRO:HA	1.29	1.13
14:R:33:ILE:HG12	22:o:431:PHE:CE2	1.82	1.13
25:r:60:VAL:CG1	35:u:44:PHE:HZ	1.60	1.13
5:F:43:VAL:CG2	8:I:43:ALA:CB	2.27	1.13
10:L:106:ARG:NH1	10:L:114:LYS:CE	2.11	1.13
11:O:22:LEU:HB3	11:O:28:ILE:HG12	1.21	1.13
35:u:44:PHE:CE2	35:u:46:ILE:HG13	1.82	1.13
4:E:696:TRP:CE3	4:E:703:MET:HB3	1.83	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:244:GLN:OE1	7:H:133:ALA:HB3	1.48	1.12
25:r:103:LEU:CA	35:u:144:ARG:NH1	2.07	1.12
2:B:834:THR:HG23	7:H:213:LEU:HD23	1.25	1.12
15:S:135:PHE:HE2	16:T:43:LEU:HD23	1.02	1.12
3:D:1006:LEU:HD11	11:O:68:CYS:HB3	1.27	1.12
5:F:51:ALA:CB	8:I:23:LEU:CD2	2.28	1.12
11:O:88:ILE:HD13	13:Q:360:LEU:HB2	1.13	1.12
1:A:488:ALA:HB1	5:f:271:VAL:HG23	1.24	1.12
3:D:891:ILE:HG21	10:L:111:LEU:HD22	1.31	1.12
35:u:40:GLY:CA	35:u:152:VAL:HG21	1.78	1.12
2:B:883:PHE:HE1	7:H:223:TYR:HB3	0.97	1.11
11:O:7:ARG:NE	11:O:41:ASP:OD2	1.82	1.11
11:O:88:ILE:CG2	13:Q:360:LEU:CB	2.17	1.11
14:R:44:ARG:NH2	23:p:1067:ILE:HG23	1.63	1.11
1:A:405:VAL:HB	5:F:302:HIS:HB3	1.23	1.11
12:P:274:VAL:HG11	14:R:208:LEU:HD11	1.22	1.11
17:U:32:LEU:HD22	18:V:161:ARG:NH2	1.64	1.11
15:S:125:TYR:CE2	16:T:31:TRP:CE3	2.39	1.11
18:V:224:THR:CG2	18:V:227:SER:HB2	1.80	1.11
1:A:657:SER:O	2:B:475:LYS:NZ	1.84	1.10
3:D:963:ARG:HD3	3:D:964:GLU:H	1.10	1.10
5:F:51:ALA:HB1	8:I:23:LEU:HD22	1.33	1.10
14:R:48:VAL:HG23	23:p:841:ARG:HH12	1.12	1.10
16:T:189:SER:HA	18:V:75:PHE:HB2	1.22	1.10
14:R:44:ARG:HH21	23:p:1067:ILE:CG2	1.64	1.10
2:B:882:HIS:O	7:H:222:PRO:CG	1.97	1.10
3:D:1083:PHE:HE2	4:E:585:ASN:ND2	1.47	1.10
14:R:44:ARG:HH21	23:p:1067:ILE:HG23	0.94	1.10
1:A:1190:VAL:HG22	6:G:162:VAL:HG13	1.24	1.10
11:O:39:GLN:NE2	13:Q:24:ASP:HB3	1.65	1.10
35:u:44:PHE:CD2	35:u:46:ILE:HG13	1.85	1.10
5:F:213:ILE:HG21	7:H:163:PRO:HB3	1.15	1.10
5:F:219:GLU:HG2	7:H:156:PRO:CB	1.82	1.09
11:O:88:ILE:HD12	13:Q:360:LEU:HD12	1.30	1.09
17:U:145:PHE:CZ	35:u:98:PHE:CE2	2.40	1.09
11:O:65:TYR:CE1	12:P:191:GLU:CG	2.34	1.09
11:O:88:ILE:HG21	13:Q:360:LEU:HB2	1.26	1.09
15:S:44:GLN:C	16:T:9:LEU:HD11	1.77	1.09
18:V:121:THR:O	18:V:125:VAL:CG2	1.99	1.09
5:F:43:VAL:HG21	8:I:43:ALA:HB1	1.21	1.09
11:O:17:GLU:HB2	13:Q:49:LYS:HZ3	1.06	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:Q:47:GLU:OE2	13:Q:60:HIS:ND1	1.85	1.09
14:R:27:TYR:CB	23:p:841:ARG:HH11	1.60	1.09
1:A:1014:GLU:CG	22:o:1204:VAL:HG12	1.82	1.08
5:F:320:ARG:HD3	5:F:415:ILE:CG1	1.82	1.08
7:H:116:ARG:HD3	9:J:126:TYR:HE1	1.09	1.08
12:P:197:PHE:CD1	33:X:-24:DG:N2	2.21	1.08
17:U:46:GLU:OE2	17:U:93:PHE:HE2	1.33	1.08
1:A:575:PRO:HD3	2:B:608:ASN:HD22	0.98	1.08
11:O:79:VAL:O	11:O:90:VAL:HG13	1.54	1.07
3:D:871:THR:HG23	10:L:66:LEU:CD2	1.77	1.07
14:R:33:ILE:HG21	22:o:431:PHE:CG	1.88	1.07
1:A:639:LEU:CD1	1:A:643:ILE:HD11	1.85	1.07
5:F:316:GLN:NE2	5:F:319:LEU:O	1.86	1.07
3:D:871:THR:HA	10:L:66:LEU:HD13	1.17	1.07
11:O:22:LEU:HB3	11:O:28:ILE:CG1	1.80	1.07
14:R:33:ILE:CG1	22:o:431:PHE:CD2	2.37	1.07
3:D:963:ARG:HD3	3:D:964:GLU:HG3	1.30	1.06
25:r:16:ASP:HB2	35:u:81:LYS:CE	1.85	1.06
14:R:27:TYR:CE1	14:R:48:VAL:HG21	1.90	1.06
19:c:67:GLY:HA3	9:j:116:LEU:CD1	1.85	1.06
2:B:883:PHE:HD1	7:H:223:TYR:N	1.51	1.06
3:D:917:ILE:CD1	3:D:1058:VAL:HG21	1.84	1.06
1:A:1014:GLU:OE2	22:o:1204:VAL:CG1	2.04	1.06
4:E:697:ASP:O	4:E:701:GLY:HA2	1.54	1.06
14:R:27:TYR:CD2	23:p:841:ARG:CZ	2.38	1.06
14:R:33:ILE:CB	22:o:431:PHE:CD2	2.39	1.06
1:A:486:TRP:HH2	5:f:358:THR:HB	1.17	1.05
1:A:573:TYR:HA	2:B:657:ARG:HD3	1.34	1.05
17:U:126:SER:HB2	17:U:136:PHE:O	0.89	1.05
7:H:116:ARG:HD3	9:J:126:TYR:CE1	1.91	1.05
11:O:17:GLU:CB	13:Q:49:LYS:HZ3	1.68	1.05
5:F:313:VAL:HG12	5:F:375:GLY:C	1.80	1.05
5:F:320:ARG:CD	5:F:321:PRO:HD3	1.87	1.05
2:B:768:PRO:HG2	2:B:771:VAL:HG23	1.38	1.05
18:V:181:ALA:HA	18:V:184:ALA:HB3	1.08	1.05
7:H:111:ALA:O	9:J:126:TYR:CZ	2.10	1.04
5:F:313:VAL:HG12	5:F:376:SER:N	1.72	1.04
11:O:23:ILE:HA	11:O:28:ILE:O	1.56	1.04
16:T:140:ARG:CG	23:p:60:GLU:OE2	2.06	1.04
25:r:110:GLU:HG3	35:u:167:TYR:CB	1.87	1.04
3:D:889:HIS:CA	10:L:104:ARG:NH2	2.21	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:87:HIS:HB3	9:J:212:LYS:HZ1	1.05	1.04
1:A:638:PRO:HG3	6:G:39:LEU:HD23	1.07	1.03
11:O:65:TYR:HE1	12:P:191:GLU:HG2	1.15	1.03
15:S:125:TYR:CD2	16:T:31:TRP:HZ3	1.74	1.03
25:r:110:GLU:HG3	35:u:167:TYR:HB2	1.34	1.03
1:A:638:PRO:HG3	6:G:39:LEU:CD2	1.88	1.03
12:P:188:ARG:NH1	13:Q:322:ASP:OD1	1.90	1.03
17:U:70:LYS:O	17:U:99:LEU:CB	2.06	1.03
1:A:638:PRO:CB	6:G:39:LEU:HD23	1.86	1.03
5:F:43:VAL:HG22	8:I:43:ALA:HB1	1.35	1.03
14:R:27:TYR:CB	23:p:841:ARG:HD3	1.87	1.03
15:S:45:ALA:CB	16:T:9:LEU:HD21	1.88	1.03
3:D:871:THR:CA	10:L:66:LEU:CD1	2.35	1.03
3:D:964:GLU:O	3:D:968:ARG:HG2	1.59	1.03
11:O:22:LEU:HB2	11:O:28:ILE:HG12	1.23	1.03
17:U:70:LYS:HB3	17:U:99:LEU:HD23	1.06	1.03
11:O:44:ILE:HD13	13:Q:17:VAL:HG11	1.04	1.03
18:V:77:VAL:HG21	18:V:111:ILE:HD11	1.41	1.03
5:F:290:MET:SD	5:F:340:ILE:CG2	2.46	1.02
14:R:27:TYR:HB3	23:p:841:ARG:HD3	1.06	1.02
5:F:308:VAL:CG1	5:F:337:VAL:HG21	1.89	1.02
1:A:575:PRO:HD3	2:B:608:ASN:ND2	1.73	1.02
4:E:615:ASP:OD1	8:I:114:ARG:CB	2.08	1.02
14:R:27:TYR:HB2	23:p:841:ARG:HH11	0.86	1.02
14:R:44:ARG:NH2	23:p:1067:ILE:CG2	2.21	1.02
1:A:1014:GLU:CD	22:o:1204:VAL:CG1	2.33	1.01
15:S:121:ASN:HA	16:T:25:LYS:HE2	1.42	1.01
15:S:124:TYR:HE1	16:T:22:LYS:HG3	1.24	1.01
17:U:32:LEU:HD22	18:V:161:ARG:CZ	1.89	1.01
1:A:1165:LEU:HB2	1:A:1191:ILE:CG2	1.90	1.01
16:T:147:LYS:HG3	16:T:148:VAL:H	1.24	1.01
17:U:32:LEU:HD22	18:V:161:ARG:HH21	1.22	1.01
18:V:181:ALA:CA	18:V:184:ALA:HB3	1.89	1.01
25:r:16:ASP:CB	35:u:81:LYS:NZ	2.23	1.01
2:B:883:PHE:CD1	7:H:223:TYR:N	2.27	1.01
25:r:16:ASP:HB2	35:u:81:LYS:NZ	1.75	1.01
15:S:125:TYR:CE2	16:T:31:TRP:CZ3	2.48	1.00
18:V:181:ALA:HA	18:V:184:ALA:CB	1.91	1.00
1:A:575:PRO:HG3	2:B:610:GLU:HG2	1.41	1.00
3:D:917:ILE:HD12	3:D:1058:VAL:HG21	1.42	1.00
25:r:103:LEU:CD2	35:u:144:ARG:NH1	1.97	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:735:ILE:CG2	7:H:176:ARG:NH1	2.24	1.00
4:E:696:TRP:HA	4:E:703:MET:HA	1.44	1.00
1:A:486:TRP:CH2	5:f:358:THR:HB	1.97	1.00
11:O:17:GLU:HB2	13:Q:49:LYS:NZ	1.77	1.00
15:S:124:TYR:CE1	16:T:22:LYS:HG3	1.97	1.00
10:L:106:ARG:HH11	10:L:114:LYS:CE	1.69	0.99
14:R:154:ARG:NH1	34:Y:22:DG:H5''	1.76	0.99
15:S:45:ALA:HB3	16:T:9:LEU:HD21	1.42	0.99
16:T:140:ARG:O	23:p:56:GLN:CG	2.10	0.99
14:R:27:TYR:CD1	23:p:841:ARG:CZ	2.43	0.99
16:T:140:ARG:HG2	23:p:60:GLU:OE2	1.62	0.99
16:T:214:LYS:NZ	34:Y:17:DG:OP1	1.94	0.99
16:T:124:TYR:HE2	23:p:590:LEU:CD2	1.76	0.99
11:O:44:ILE:CD1	13:Q:17:VAL:CG1	2.41	0.98
1:A:405:VAL:HB	5:F:302:HIS:CB	1.93	0.98
7:H:119:ILE:O	9:J:131:PRO:HG3	1.63	0.98
1:A:1185:VAL:O	1:A:1191:ILE:HD11	1.63	0.98
5:F:327:TRP:HA	5:F:330:ARG:HG3	1.45	0.98
33:X:-46:DA:N1	34:Y:46:DT:N3	2.11	0.98
1:A:405:VAL:HA	5:F:302:HIS:CB	1.92	0.98
3:D:917:ILE:HD12	3:D:1058:VAL:HG11	1.46	0.98
25:r:60:VAL:CG1	35:u:44:PHE:CZ	2.39	0.98
3:D:1005:ASN:O	3:D:1009:LEU:CD1	2.12	0.98
17:U:32:LEU:HD22	18:V:161:ARG:NE	1.78	0.98
5:F:211:ARG:HB3	7:H:165:TYR:HE2	1.26	0.98
14:R:27:TYR:CE1	14:R:48:VAL:CG2	2.47	0.98
1:A:725:CYS:SG	1:A:725:CYS:O	2.22	0.97
16:T:124:TYR:HE2	23:p:590:LEU:HD21	0.81	0.97
19:c:77:LEU:CD1	9:j:116:LEU:HD23	1.94	0.97
5:F:48:LYS:HG3	8:I:22:ILE:HG21	1.44	0.97
2:B:781:TYR:HB3	7:H:176:ARG:NH2	1.80	0.97
5:F:308:VAL:HG11	5:F:337:VAL:HG21	0.97	0.97
12:P:257:ASN:HB2	33:X:-27:DT:H5''	1.45	0.97
11:O:44:ILE:HD12	13:Q:17:VAL:HG11	1.47	0.97
35:u:40:GLY:CA	35:u:152:VAL:CG2	2.39	0.97
2:B:735:ILE:CG2	7:H:176:ARG:CZ	2.43	0.97
13:Q:47:GLU:CD	13:Q:60:HIS:ND1	2.23	0.97
17:U:46:GLU:OE2	17:U:93:PHE:CE2	2.16	0.97
3:D:891:ILE:HG13	10:L:100:CYS:SG	2.05	0.97
3:D:871:THR:HG22	10:L:66:LEU:HD22	0.99	0.96
1:A:564:PRO:HG2	2:B:744:PHE:CD2	2.00	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:834:THR:HG23	7:H:213:LEU:CD2	1.95	0.96
15:S:44:GLN:HA	16:T:9:LEU:HD12	1.47	0.96
1:A:1187:LYS:O	1:A:1191:ILE:HG13	1.65	0.96
8:I:60:HIS:CE1	10:L:118:LEU:HD21	1.98	0.96
35:u:38:CYS:N	35:u:155:ASN:OD1	1.98	0.96
3:D:871:THR:HG21	10:L:66:LEU:HD22	1.46	0.96
3:D:963:ARG:NE	3:D:964:GLU:HG2	1.81	0.96
5:F:43:VAL:HG22	8:I:43:ALA:CB	1.91	0.96
12:P:188:ARG:HH11	13:Q:322:ASP:CG	1.68	0.96
18:V:175:LEU:HD23	18:V:175:LEU:H	1.29	0.96
1:A:405:VAL:CA	5:F:302:HIS:CB	2.43	0.96
3:D:1005:ASN:OD1	3:D:1009:LEU:HD11	1.65	0.96
5:F:211:ARG:HG3	7:H:165:TYR:CD2	1.96	0.96
3:D:889:HIS:O	10:L:104:ARG:NH2	1.97	0.96
10:L:106:ARG:HH12	10:L:114:LYS:HD2	0.81	0.95
14:R:48:VAL:CG2	23:p:841:ARG:NH1	2.28	0.95
15:S:24:LYS:HA	16:T:98:GLU:O	1.66	0.95
16:T:137:LYS:HB2	16:T:137:LYS:HZ2	1.28	0.95
7:H:106:THR:OG1	9:J:161:LYS:NZ	1.98	0.95
11:O:39:GLN:HG2	13:Q:25:VAL:HG12	1.45	0.95
4:E:615:ASP:CG	8:I:114:ARG:HB3	1.90	0.95
18:V:175:LEU:HB3	18:V:179:GLN:OE1	1.67	0.95
4:E:598:TYR:CE1	8:I:114:ARG:HD3	2.02	0.95
5:F:71:ILE:HB	8:I:38:GLN:HE21	0.82	0.95
16:T:125:MET:HA	23:p:596:ILE:HD11	1.47	0.95
1:A:349:TRP:CZ2	5:f:262:PHE:CE1	2.55	0.95
3:D:891:ILE:HG22	10:L:111:LEU:HB2	1.48	0.95
25:r:103:LEU:HD23	35:u:144:ARG:CZ	1.96	0.95
18:V:229:ASP:CB	22:o:227:ARG:HH22	1.79	0.95
18:V:175:LEU:HB2	18:V:179:GLN:HB3	1.46	0.94
3:D:901:TYR:CE1	10:L:128:ILE:O	2.21	0.94
3:D:963:ARG:HD3	3:D:964:GLU:CG	1.97	0.94
8:I:60:HIS:CE1	10:L:118:LEU:HD23	1.99	0.94
12:P:188:ARG:NH1	13:Q:322:ASP:OD2	2.01	0.94
1:A:638:PRO:HB3	6:G:39:LEU:CD2	1.97	0.94
17:U:20:TYR:HB3	17:U:191:LEU:HD22	1.50	0.94
3:D:901:TYR:CE1	10:L:128:ILE:HB	2.01	0.94
15:S:44:GLN:C	16:T:9:LEU:CD1	2.39	0.94
25:r:60:VAL:HG11	35:u:44:PHE:CE1	2.03	0.94
5:F:52:GLN:HE21	8:I:26:MET:HB3	1.32	0.94
14:R:33:ILE:HD13	22:o:431:PHE:CZ	2.01	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:151:THR:HB	17:U:160:GLU:OE2	1.68	0.94
25:r:73:ARG:HH12	35:u:144:ARG:NH2	1.64	0.94
5:F:319:LEU:H	5:F:319:LEU:HD23	1.31	0.94
15:S:6:PRO:C	15:S:8:SER:H	1.72	0.94
11:O:60:GLY:HA2	11:O:79:VAL:HG13	1.51	0.93
19:c:67:GLY:HA3	9:j:116:LEU:HD11	1.48	0.93
2:B:310:ASP:CG	7:H:223:TYR:HE2	1.75	0.93
5:F:322:ASP:C	5:F:324:ASP:H	1.71	0.93
14:R:48:VAL:HG21	23:p:841:ARG:HH12	1.32	0.93
1:A:488:ALA:CB	5:f:271:VAL:HG23	1.98	0.93
3:D:871:THR:CG2	10:L:66:LEU:HD13	1.98	0.93
4:E:621:ARG:NH2	8:I:104:LEU:HG	1.82	0.93
5:F:211:ARG:HG2	7:H:165:TYR:HD2	0.80	0.93
5:F:320:ARG:HD2	5:F:321:PRO:CD	1.97	0.93
1:A:1014:GLU:HG3	22:o:1204:VAL:HG12	1.48	0.93
3:D:901:TYR:HE1	10:L:128:ILE:O	1.49	0.93
5:F:213:ILE:HA	7:H:164:THR:O	1.67	0.93
11:O:17:GLU:CB	13:Q:49:LYS:NZ	2.32	0.93
11:O:44:ILE:HD13	13:Q:17:VAL:CG1	1.97	0.93
3:D:1005:ASN:OD1	3:D:1009:LEU:CD1	2.17	0.92
11:O:32:LEU:CD1	13:Q:32:ASP:OD2	2.17	0.92
1:A:468:PHE:HE1	5:F:224:TYR:CE2	1.77	0.92
14:R:27:TYR:HB3	23:p:841:ARG:CD	1.96	0.92
1:A:784:GLN:H	1:A:1073:GLN:HE22	1.16	0.92
2:B:780:LYS:O	7:H:183:ARG:NH1	2.01	0.92
11:O:22:LEU:HB3	11:O:28:ILE:CG2	1.99	0.92
12:P:197:PHE:HE1	33:X:-24:DG:N2	1.47	0.92
3:D:871:THR:CG2	10:L:66:LEU:CD1	2.47	0.92
15:S:125:TYR:CD2	16:T:31:TRP:CZ3	2.58	0.92
3:D:1004:ALA:HB2	11:O:4:GLN:HB2	1.52	0.92
25:r:16:ASP:HB2	35:u:81:LYS:HE3	1.48	0.91
5:F:219:GLU:HG2	7:H:156:PRO:HB2	0.91	0.91
7:H:110:TYR:OH	9:J:160:GLN:HB3	1.70	0.91
11:O:22:LEU:CA	11:O:28:ILE:HG12	2.00	0.91
11:O:58:PHE:HZ	13:Q:358:MET:HE1	1.36	0.91
35:u:40:GLY:HA2	35:u:152:VAL:HG21	0.91	0.91
1:A:468:PHE:CE2	5:F:221:GLN:HG3	2.05	0.91
11:O:22:LEU:HD12	11:O:28:ILE:HD13	1.52	0.91
1:A:657:SER:O	2:B:475:LYS:CE	2.18	0.91
3:D:917:ILE:HD12	3:D:1058:VAL:CG2	2.00	0.91
4:E:598:TYR:HE1	8:I:114:ARG:HD3	1.32	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:u:38:CYS:SG	35:u:43:GLY:O	2.28	0.91
7:H:118:VAL:HG21	9:J:127:THR:CG2	2.00	0.91
11:O:88:ILE:HG21	13:Q:360:LEU:HB3	0.92	0.91
13:Q:310:GLU:O	13:Q:313:PRO:CD	2.18	0.91
14:R:50:SER:HA	23:p:841:ARG:NH2	1.83	0.91
11:O:76:LEU:HB3	11:O:79:VAL:HG21	1.51	0.91
17:U:70:LYS:CB	17:U:99:LEU:HD23	1.97	0.91
2:B:735:ILE:HG22	7:H:176:ARG:NH1	1.86	0.90
3:D:917:ILE:CD1	3:D:1058:VAL:HG11	2.00	0.90
3:D:963:ARG:NH1	3:D:964:GLU:CB	2.33	0.90
3:D:917:ILE:HD12	3:D:1058:VAL:CB	2.01	0.90
5:F:51:ALA:HB1	8:I:23:LEU:CD2	1.95	0.90
25:r:103:LEU:CG	35:u:144:ARG:NH1	2.34	0.90
12:P:250:PHE:HB2	13:Q:314:LEU:HD21	1.51	0.90
15:S:44:GLN:CA	16:T:9:LEU:HD12	2.00	0.90
12:P:197:PHE:CE1	33:X:-24:DG:C2	2.59	0.90
14:R:27:TYR:CE1	14:R:50:SER:HB3	2.06	0.90
1:A:495:LEU:HD13	5:f:268:ARG:NH2	1.86	0.90
5:F:320:ARG:CG	5:F:415:ILE:HD12	2.02	0.90
3:D:917:ILE:HD12	3:D:1058:VAL:CG1	2.02	0.90
7:H:37:LEU:HD11	9:J:138:TYR:CE2	2.07	0.90
10:L:102:LEU:HA	10:L:105:HIS:HD2	1.36	0.90
11:O:22:LEU:HB3	11:O:28:ILE:HG23	1.50	0.90
14:R:27:TYR:CD2	23:p:841:ARG:NE	2.40	0.90
3:D:898:VAL:HG22	10:L:113:VAL:HG23	1.50	0.89
5:F:211:ARG:HG3	7:H:165:TYR:HD2	1.31	0.89
11:O:39:GLN:HE21	13:Q:24:ASP:HB3	1.30	0.89
17:U:179:ARG:O	17:U:183:GLN:HB2	1.70	0.89
25:r:16:ASP:CB	35:u:81:LYS:HZ1	1.85	0.89
5:F:48:LYS:HG2	8:I:22:ILE:HG23	1.51	0.89
5:F:211:ARG:HB3	7:H:165:TYR:CE2	2.08	0.89
3:D:917:ILE:HB	3:D:1058:VAL:CG1	2.03	0.89
12:P:274:VAL:HG11	14:R:208:LEU:CD1	2.03	0.89
15:S:23:THR:O	16:T:99:SER:HA	1.71	0.89
5:F:48:LYS:CG	8:I:22:ILE:CG2	2.01	0.89
13:Q:55:ALA:O	13:Q:56:VAL:HG23	1.71	0.89
15:S:125:TYR:CE2	16:T:31:TRP:HE3	1.86	0.89
17:U:30:HIS:NE2	17:U:65:ASN:OD1	2.05	0.89
3:D:871:THR:N	10:L:66:LEU:HD11	1.85	0.89
3:D:963:ARG:CD	3:D:964:GLU:HG3	2.03	0.88
11:O:88:ILE:CG2	13:Q:361:ASN:ND2	2.36	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:ALA:HB1	5:f:271:VAL:HG21	1.52	0.88
15:S:24:LYS:HD3	16:T:97:THR:CB	2.03	0.88
1:A:639:LEU:HD13	1:A:643:ILE:HD11	1.52	0.88
3:D:871:THR:HA	10:L:66:LEU:CD1	2.02	0.88
3:D:914:VAL:HG12	10:L:70:VAL:HG11	1.55	0.88
13:Q:47:GLU:CD	13:Q:60:HIS:CG	2.51	0.88
17:U:71:PHE:O	17:U:98:THR:HA	1.74	0.88
2:B:310:ASP:CG	7:H:223:TYR:CE2	2.50	0.88
16:T:16:THR:HG21	16:T:107:GLU:O	1.73	0.88
17:U:32:LEU:CD2	18:V:161:ARG:HH21	1.87	0.88
5:F:66:LEU:HB3	8:I:31:TYR:HA	1.56	0.88
5:F:71:ILE:HD11	8:I:35:VAL:HG13	1.52	0.88
1:A:466:SER:OG	5:F:221:GLN:NE2	2.06	0.88
12:P:274:VAL:HG12	14:R:208:LEU:HD11	1.56	0.88
15:S:135:PHE:CE2	16:T:43:LEU:CD2	2.57	0.88
3:D:889:HIS:C	10:L:104:ARG:NH2	2.31	0.87
5:F:48:LYS:HE3	8:I:22:ILE:HG12	1.56	0.87
5:F:71:ILE:HD11	8:I:35:VAL:HG22	1.57	0.87
1:A:638:PRO:CG	6:G:39:LEU:CD2	2.44	0.87
8:I:60:HIS:ND1	10:L:118:LEU:CD2	2.37	0.87
1:A:1165:LEU:HB2	1:A:1191:ILE:HG21	1.54	0.87
11:O:43:ALA:HB3	13:Q:21:VAL:HG22	1.54	0.87
25:r:103:LEU:HA	35:u:144:ARG:NH2	1.90	0.87
1:A:468:PHE:HZ	5:F:224:TYR:HD2	0.89	0.87
14:R:27:TYR:CG	14:R:48:VAL:HG21	2.02	0.87
25:r:114:LEU:HD21	35:u:167:TYR:HD2	1.36	0.87
3:D:871:THR:N	10:L:66:LEU:HD13	1.74	0.87
3:D:871:THR:HG23	10:L:66:LEU:HD21	1.57	0.87
14:R:33:ILE:CB	22:o:431:PHE:CE2	2.55	0.87
35:u:44:PHE:CE2	35:u:46:ILE:CG1	2.57	0.87
3:D:889:HIS:HA	10:L:104:ARG:HH22	1.36	0.87
2:B:835:ARG:CD	7:H:187:GLU:OE2	2.23	0.87
17:U:32:LEU:HD22	18:V:161:ARG:HE	1.37	0.87
1:A:639:LEU:CD1	1:A:643:ILE:CD1	2.52	0.86
18:V:117:GLN:HE21	18:V:121:THR:HG23	1.39	0.86
18:V:176:PRO:O	18:V:178:SER:N	2.07	0.86
1:A:468:PHE:HE2	5:F:221:GLN:HG3	1.37	0.86
1:A:753:TYR:CE2	1:A:1077:LEU:HD13	2.11	0.86
3:D:963:ARG:HH12	3:D:964:GLU:HA	1.36	0.86
3:D:963:ARG:HH11	3:D:964:GLU:N	1.73	0.86
1:A:511:LEU:H	1:A:511:LEU:HD22	1.37	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:TYR:HE2	1:A:1077:LEU:HD13	1.38	0.86
5:F:51:ALA:O	8:I:28:ILE:HD11	1.74	0.86
14:R:48:VAL:HG21	23:p:841:ARG:NH1	1.89	0.86
5:F:51:ALA:HB2	8:I:23:LEU:HD21	1.58	0.86
11:O:22:LEU:CB	11:O:28:ILE:CD1	2.42	0.86
14:R:46:ILE:HA	22:o:67:ARG:HH21	1.40	0.86
5:F:313:VAL:CG1	5:F:375:GLY:C	2.49	0.86
5:F:322:ASP:O	5:F:324:ASP:N	2.08	0.86
11:O:58:PHE:CZ	13:Q:358:MET:HE1	2.10	0.86
2:B:835:ARG:HD3	7:H:187:GLU:HG3	1.58	0.85
5:F:313:VAL:CG1	5:F:376:SER:N	2.40	0.85
5:F:87:HIS:CB	9:J:212:LYS:NZ	2.38	0.85
11:O:22:LEU:CD1	11:O:28:ILE:HD13	2.06	0.85
35:u:86:ASP:OD2	35:u:171:VAL:HG21	1.75	0.85
1:A:486:TRP:HH2	5:f:358:THR:CB	1.89	0.85
7:H:111:ALA:HB1	9:J:126:TYR:CE2	2.11	0.85
1:A:1185:VAL:CG1	1:A:1191:ILE:HG12	2.06	0.85
5:F:298:GLU:O	5:F:301:VAL:HG12	1.77	0.85
18:V:229:ASP:HB2	22:o:227:ARG:HH22	1.39	0.85
5:F:71:ILE:CD1	8:I:35:VAL:HA	2.07	0.85
2:B:768:PRO:HG2	2:B:771:VAL:HG21	1.57	0.85
3:D:871:THR:HG23	10:L:66:LEU:CD1	2.07	0.85
1:A:1165:LEU:HB2	1:A:1191:ILE:HG23	1.58	0.85
15:S:102:VAL:HB	15:S:108:ARG:HB3	1.59	0.85
3:D:963:ARG:CD	3:D:964:GLU:CG	2.54	0.85
12:P:188:ARG:HH12	13:Q:322:ASP:CG	1.81	0.84
5:F:412:LEU:HD12	5:F:417:ARG:HD2	1.60	0.84
18:V:117:GLN:HE21	18:V:121:THR:CG2	1.90	0.84
4:E:704:VAL:HG11	4:E:747:LEU:CG	2.06	0.84
11:O:88:ILE:HG23	13:Q:361:ASN:HD22	1.37	0.84
18:V:224:THR:HG22	18:V:227:SER:HB2	1.57	0.84
3:D:871:THR:CB	10:L:66:LEU:HD13	2.08	0.84
8:I:60:HIS:ND1	10:L:118:LEU:HD21	1.93	0.84
11:O:22:LEU:O	11:O:28:ILE:N	2.10	0.84
2:B:882:HIS:O	7:H:222:PRO:HG3	1.01	0.84
15:S:125:TYR:HE2	16:T:31:TRP:CE3	1.96	0.84
1:A:572:TYR:CD2	2:B:689:GLN:HB2	2.13	0.84
3:D:889:HIS:CA	10:L:104:ARG:HH21	1.87	0.84
7:H:111:ALA:O	9:J:126:TYR:CE1	2.31	0.83
5:F:48:LYS:CD	8:I:22:ILE:HG23	2.08	0.83
7:H:73:GLY:HA3	9:J:142:ALA:HB3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:917:ILE:HB	3:D:1058:VAL:HG13	1.59	0.83
5:F:214:HIS:H	7:H:164:THR:HG22	1.43	0.83
14:R:25:GLU:OE1	14:R:46:ILE:HD11	1.76	0.83
17:U:145:PHE:CE2	35:u:98:PHE:CZ	2.65	0.83
12:P:259:VAL:HG21	34:Y:28:DG:N2	1.93	0.83
17:U:37:LEU:HD13	17:U:71:PHE:HE1	1.42	0.83
15:S:18:VAL:HG23	16:T:40:VAL:HG11	1.59	0.83
16:T:140:ARG:HG3	23:p:60:GLU:OE2	1.75	0.83
17:U:121:SER:HG	17:U:124:ARG:NH1	1.75	0.83
18:V:77:VAL:HG11	18:V:119:LEU:CD1	2.07	0.83
33:X:-13:DA:OP2	33:X:-13:DA:H3'	1.75	0.83
11:O:22:LEU:C	11:O:28:ILE:HG12	2.03	0.83
15:S:6:PRO:C	15:S:8:SER:N	2.29	0.83
3:D:881:ARG:HB2	10:L:57:VAL:HG11	1.58	0.83
3:D:891:ILE:HG23	10:L:111:LEU:HB2	1.57	0.83
3:D:901:TYR:HE1	10:L:128:ILE:C	1.86	0.83
5:F:244:GLN:OE1	7:H:133:ALA:CB	2.26	0.83
4:E:747:LEU:HD22	4:E:747:LEU:H	1.44	0.83
5:F:320:ARG:HB2	5:F:415:ILE:HD11	1.58	0.83
17:U:32:LEU:HD13	18:V:161:ARG:NH2	1.94	0.83
3:D:871:THR:HG22	10:L:66:LEU:CG	2.08	0.82
5:F:313:VAL:O	5:F:372:THR:HA	1.78	0.82
10:L:101:GLN:C	10:L:105:HIS:CD2	2.57	0.82
1:A:569:ASN:CG	2:B:689:GLN:HA	2.04	0.82
11:O:22:LEU:HD13	11:O:28:ILE:HG21	1.59	0.82
19:c:77:LEU:HD13	9:j:116:LEU:HD23	1.61	0.82
1:A:1185:VAL:CG1	1:A:1191:ILE:CG1	2.58	0.82
2:B:310:ASP:OD1	7:H:223:TYR:CE2	2.31	0.82
5:F:211:ARG:CG	7:H:165:TYR:CE2	2.61	0.82
5:F:412:LEU:HD13	5:F:417:ARG:HD2	0.83	0.82
5:f:447:ALA:HA	5:f:456:GLY:HA3	1.61	0.82
1:A:564:PRO:CG	2:B:744:PHE:CE2	2.62	0.82
2:B:735:ILE:HG21	7:H:176:ARG:NH1	1.92	0.82
3:D:901:TYR:CE1	10:L:128:ILE:CB	2.62	0.81
1:A:1014:GLU:CD	22:o:1204:VAL:HG12	2.03	0.81
3:D:905:ALA:O	10:L:126:MET:HE1	1.80	0.81
11:O:39:GLN:CG	13:Q:25:VAL:HG12	2.09	0.81
3:D:891:ILE:CG2	10:L:111:LEU:CB	2.54	0.81
7:H:111:ALA:HB2	9:J:157:LEU:CD1	2.09	0.81
11:O:62:LEU:HA	11:O:76:LEU:HD13	1.62	0.81
11:O:88:ILE:HD13	13:Q:360:LEU:CB	2.05	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:27:TYR:HD1	14:R:48:VAL:CB	1.93	0.81
14:R:51:GLU:O	23:p:893:SER:O	1.96	0.81
18:V:206:LYS:HA	18:V:206:LYS:NZ	1.94	0.81
25:r:110:GLU:CG	35:u:167:TYR:HB2	2.10	0.81
25:r:114:LEU:HD11	35:u:167:TYR:CD2	2.15	0.81
11:O:27:GLN:NE2	13:Q:41:GLU:OE1	2.14	0.81
11:O:65:TYR:HE1	12:P:191:GLU:HG3	1.43	0.81
18:V:73:TYR:HB2	18:V:115:GLN:HG2	1.61	0.81
5:F:274:ASN:O	5:F:318:CYS:SG	2.37	0.81
1:A:468:PHE:CE1	5:F:224:TYR:HE2	1.98	0.81
15:S:121:ASN:CA	16:T:25:LYS:HE2	2.10	0.81
15:S:16:VAL:HB	16:T:56:PHE:HE1	1.46	0.81
1:A:405:VAL:HA	5:F:302:HIS:HB2	1.60	0.81
8:I:132:LEU:HG	9:J:121:MET:HE2	1.61	0.81
19:c:67:GLY:HA3	9:j:116:LEU:HD13	1.60	0.81
1:A:639:LEU:HD13	1:A:643:ILE:CD1	2.08	0.81
3:D:960:GLU:O	3:D:964:GLU:HG3	1.81	0.81
12:P:197:PHE:HE1	33:X:-24:DG:C2	1.96	0.81
1:A:1190:VAL:HG22	6:G:162:VAL:CG1	2.10	0.80
3:D:891:ILE:HG21	10:L:111:LEU:CD2	2.11	0.80
11:O:15:LEU:HD22	11:O:40:PHE:CD1	2.16	0.80
1:A:1185:VAL:HG11	1:A:1191:ILE:HG12	1.62	0.80
2:B:781:TYR:HB3	7:H:176:ARG:HH21	1.46	0.80
16:T:147:LYS:HG3	16:T:148:VAL:N	1.96	0.80
14:R:27:TYR:CE1	23:p:841:ARG:NH2	2.49	0.80
16:T:140:ARG:HB3	23:p:56:GLN:NE2	1.96	0.80
2:B:735:ILE:HG22	7:H:176:ARG:HH12	1.46	0.80
3:D:914:VAL:HG11	10:L:70:VAL:HG21	1.62	0.80
5:F:290:MET:CE	5:F:337:VAL:HA	2.05	0.80
18:V:175:LEU:HD12	18:V:180:LYS:N	1.97	0.80
23:p:68:GLN:HB3	23:p:83:ARG:HB3	1.64	0.80
11:O:22:LEU:HB2	11:O:28:ILE:HD11	1.62	0.80
1:A:1185:VAL:HG12	1:A:1191:ILE:CG1	2.10	0.80
14:R:51:GLU:C	23:p:893:SER:O	2.25	0.80
15:S:24:LYS:HB3	16:T:99:SER:HA	1.64	0.80
8:I:132:LEU:HG	9:J:121:MET:CE	2.12	0.80
14:R:46:ILE:CA	22:o:67:ARG:HH21	1.94	0.80
2:B:883:PHE:HE1	7:H:223:TYR:HB2	1.39	0.80
17:U:70:LYS:HB3	17:U:99:LEU:CD2	2.01	0.80
18:V:117:GLN:NE2	18:V:121:THR:HG23	1.96	0.80
3:D:1006:LEU:HD12	11:O:69:ASP:HB2	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:35:SER:HB3	16:T:61:ASP:HB3	1.63	0.79
16:T:137:LYS:HB2	16:T:137:LYS:NZ	1.97	0.79
18:V:77:VAL:HG11	18:V:119:LEU:HD11	1.64	0.79
3:D:891:ILE:CG2	10:L:111:LEU:HD22	2.12	0.79
11:O:43:ALA:CB	13:Q:21:VAL:HG22	2.13	0.79
15:S:121:ASN:O	16:T:25:LYS:HG3	1.82	0.79
3:D:963:ARG:CD	3:D:964:GLU:N	2.44	0.79
15:S:124:TYR:HE1	16:T:22:LYS:CG	1.95	0.79
16:T:177:ARG:H	16:T:177:ARG:HD3	1.48	0.79
18:V:229:ASP:HB3	22:o:227:ARG:NH2	1.97	0.79
1:A:405:VAL:HG11	5:F:301:VAL:HG13	1.64	0.79
1:A:639:LEU:HD12	1:A:639:LEU:O	1.82	0.79
11:O:7:ARG:CZ	11:O:41:ASP:OD2	2.30	0.79
33:X:22:DG:N2	34:Y:-22:DC:O2	2.14	0.79
11:O:88:ILE:HD12	13:Q:360:LEU:CD1	2.10	0.79
17:U:128:LYS:O	17:U:162:GLU:N	2.16	0.79
5:F:47:ILE:CD1	8:I:19:MET:CE	1.97	0.78
5:F:308:VAL:HG11	5:F:337:VAL:HG22	1.62	0.78
10:L:106:ARG:NH1	10:L:114:LYS:NZ	1.81	0.78
16:T:145:LEU:HG	23:p:92:TYR:HB3	1.65	0.78
4:e:747:LEU:HD23	4:e:747:LEU:H	1.47	0.78
5:F:273:GLN:NE2	5:F:273:GLN:H	1.81	0.78
5:F:316:GLN:NE2	5:F:319:LEU:C	2.41	0.78
15:S:45:ALA:N	16:T:9:LEU:HD11	1.97	0.78
15:S:124:TYR:OH	16:T:22:LYS:HE2	1.83	0.78
3:D:963:ARG:CZ	3:D:964:GLU:HG2	2.11	0.78
5:F:71:ILE:HD11	8:I:35:VAL:CG1	2.13	0.78
5:F:80:VAL:HG11	8:I:42:PHE:CE1	2.18	0.78
22:o:461:GLN:HB2	22:o:462:PRO:HD3	1.65	0.78
3:D:1003:ASP:OD2	11:O:3:TYR:CE1	2.36	0.78
5:F:274:ASN:ND2	5:F:316:GLN:HA	1.99	0.78
11:O:18:SER:N	13:Q:49:LYS:HZ2	1.81	0.78
16:T:16:THR:O	16:T:109:ILE:HD12	1.83	0.78
16:T:18:VAL:HG21	16:T:95:VAL:HG23	1.65	0.78
1:A:638:PRO:CB	6:G:39:LEU:CD2	2.56	0.78
5:F:286:VAL:HG11	5:F:337:VAL:HG21	1.63	0.78
5:F:368:THR:HG22	5:F:369:PRO:HD2	1.64	0.78
14:R:44:ARG:HD3	23:p:1067:ILE:HD13	1.65	0.78
17:U:40:ASN:HD21	17:U:97:ARG:HB3	1.46	0.78
5:F:47:ILE:HD13	8:I:19:MET:SD	2.24	0.78
2:B:835:ARG:HD2	7:H:187:GLU:OE2	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:m:31:LEU:HD23	21:m:31:LEU:H	1.47	0.78
14:R:48:VAL:HG23	23:p:841:ARG:NH1	1.95	0.78
1:A:950:VAL:HG11	1:A:1066:CYS:SG	2.24	0.77
1:A:1185:VAL:O	1:A:1191:ILE:CD1	2.31	0.77
1:A:1194:TYR:OH	6:G:173:ASP:OD2	2.02	0.77
3:D:901:TYR:CD1	10:L:128:ILE:HG22	2.19	0.77
7:H:36:THR:HG21	9:J:134:VAL:HG21	1.66	0.77
25:r:115:ILE:HG22	25:r:117:SER:H	1.48	0.77
15:S:50:ASP:HB3	15:S:97:PRO:HG2	1.66	0.77
18:V:190:LEU:HB2	18:V:203:PHE:O	1.85	0.77
2:B:883:PHE:CD1	7:H:222:PRO:C	2.61	0.77
14:R:44:ARG:NH2	23:p:1065:GLY:O	2.18	0.77
1:A:1185:VAL:HG12	1:A:1191:ILE:HD11	1.65	0.77
14:R:27:TYR:CD1	23:p:841:ARG:NH2	2.52	0.77
14:R:154:ARG:HH12	34:Y:22:DG:H5"	1.45	0.77
33:X:-22:DC:O2	34:Y:22:DG:N2	2.18	0.77
35:u:44:PHE:CD2	35:u:46:ILE:CG1	2.65	0.77
17:U:108:ASP:OD2	18:V:234:GLU:HG2	1.85	0.77
3:D:871:THR:CG2	10:L:66:LEU:CG	2.61	0.77
18:V:96:PRO:HB2	18:V:136:LYS:HD3	1.67	0.77
18:V:229:ASP:HB3	22:o:227:ARG:HH22	1.50	0.77
7:H:117:MET:O	9:J:129:THR:HA	1.84	0.77
3:D:1006:LEU:HD11	11:O:68:CYS:CB	2.12	0.77
5:F:71:ILE:HD11	8:I:35:VAL:CB	2.15	0.77
5:F:429:LYS:O	5:F:433:PRO:HD2	1.85	0.77
16:T:40:VAL:HG22	16:T:62:LEU:HD22	1.65	0.77
17:U:145:PHE:CE2	35:u:98:PHE:HZ	2.02	0.77
18:V:229:ASP:CB	22:o:227:ARG:NH2	2.48	0.76
35:u:86:ASP:CG	35:u:171:VAL:HG21	2.10	0.76
5:F:51:ALA:CB	8:I:23:LEU:HD21	2.14	0.76
13:Q:43:LYS:O	13:Q:47:GLU:HG3	1.85	0.76
5:F:87:HIS:HB3	9:J:212:LYS:HZ3	1.43	0.76
18:V:226:ASP:HB3	22:o:220:ARG:HH12	1.48	0.76
2:B:361:ARG:HD2	2:B:367:GLU:HB2	1.67	0.76
5:F:213:ILE:HD13	7:H:163:PRO:HB3	1.68	0.76
25:r:73:ARG:NH1	35:u:144:ARG:NH2	2.32	0.76
18:V:212:VAL:HB	18:V:215:GLU:HB3	1.66	0.76
22:o:108:ARG:HH12	22:o:191:ILE:HB	1.50	0.76
15:S:24:LYS:HD3	16:T:97:THR:OG1	1.86	0.76
1:A:638:PRO:CD	6:G:39:LEU:HD23	2.16	0.76
14:R:18:HIS:HE1	14:R:37:CYS:SG	2.08	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:322:ASP:C	5:F:324:ASP:N	2.43	0.76
7:H:102:PHE:CZ	9:J:158:ALA:HA	2.20	0.76
11:O:22:LEU:HB3	11:O:28:ILE:CB	2.14	0.76
15:S:24:LYS:HD3	16:T:97:THR:HB	1.65	0.76
11:O:7:ARG:NH2	11:O:41:ASP:OD2	2.18	0.76
11:O:82:ARG:HE	11:O:87:LEU:HB2	1.49	0.76
15:S:121:ASN:HA	16:T:25:LYS:CE	2.16	0.76
16:T:225:VAL:C	16:T:227:GLY:H	1.94	0.76
23:p:83:ARG:HG3	23:p:133:ILE:HG23	1.68	0.76
16:T:181:GLN:HE21	16:T:181:GLN:HA	1.52	0.75
18:V:175:LEU:HB2	18:V:179:GLN:CB	2.16	0.75
1:A:484:ILE:HA	5:f:306:PRO:HB3	1.68	0.75
5:F:359:PHE:HB3	5:F:380:LEU:HG	1.68	0.75
17:U:32:LEU:CD2	18:V:161:ARG:HE	1.99	0.75
22:o:319:ASP:HB2	22:o:340:LYS:HD3	1.68	0.75
15:S:23:THR:O	16:T:100:SER:N	2.19	0.75
1:A:784:GLN:H	1:A:1073:GLN:NE2	1.83	0.75
5:F:71:ILE:HD11	8:I:35:VAL:CG2	2.16	0.75
11:O:5:LEU:HD22	11:O:98:CYS:SG	2.27	0.75
1:A:405:VAL:HB	5:F:302:HIS:CA	2.16	0.75
5:F:211:ARG:CB	7:H:165:TYR:CE2	2.69	0.75
11:O:7:ARG:CZ	11:O:37:LEU:HB3	2.17	0.75
11:O:39:GLN:HE21	13:Q:24:ASP:CB	2.00	0.75
17:U:32:LEU:CD2	18:V:161:ARG:NH2	2.44	0.75
17:U:108:ASP:OD2	18:V:234:GLU:CG	2.33	0.75
5:F:308:VAL:CG1	5:F:337:VAL:CG2	2.53	0.75
5:F:311:CYS:HB3	5:F:330:ARG:HH22	1.51	0.75
10:L:106:ARG:HH12	10:L:114:LYS:CG	1.99	0.75
1:A:1019:LYS:HB2	1:A:1019:LYS:NZ	2.01	0.75
11:O:47:ALA:CB	13:Q:17:VAL:HG22	2.17	0.75
14:R:33:ILE:HD13	22:o:431:PHE:HE2	0.80	0.75
16:T:180:LYS:NZ	16:T:180:LYS:HB2	2.02	0.75
23:p:953:ASP:OD1	24:q:36:ARG:NH2	2.19	0.75
11:O:65:TYR:CE1	12:P:191:GLU:HG3	2.15	0.75
12:P:257:ASN:HB2	33:X:-27:DT:C5'	2.16	0.75
15:S:125:TYR:HD2	16:T:23:VAL:HG21	1.52	0.75
22:o:606:HIS:HB3	22:o:626:THR:HG23	1.69	0.74
22:o:1125:LYS:HA	22:o:1128:ILE:HB	1.69	0.74
3:D:901:TYR:CE1	10:L:128:ILE:HG22	2.22	0.74
5:F:211:ARG:CB	7:H:165:TYR:HE2	1.99	0.74
5:F:283:MET:HE1	5:F:308:VAL:HA	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:118:VAL:HG21	9:J:127:THR:HG23	1.67	0.74
5:F:71:ILE:CD1	8:I:35:VAL:HG13	2.15	0.74
12:P:259:VAL:CG2	34:Y:28:DG:N2	2.49	0.74
14:R:146:TYR:O	14:R:149:LYS:HG3	1.86	0.74
16:T:189:SER:HA	18:V:75:PHE:CB	2.13	0.74
11:O:88:ILE:CG2	13:Q:360:LEU:HB2	2.03	0.74
25:r:103:LEU:HD23	35:u:144:ARG:CD	2.17	0.74
11:O:7:ARG:HE	11:O:41:ASP:CG	1.96	0.74
12:P:271:GLU:OE1	14:R:208:LEU:HD13	1.88	0.74
10:L:102:LEU:HA	10:L:105:HIS:CD2	2.22	0.74
29:w:30:LYS:HA	29:w:33:ARG:HH21	1.53	0.74
2:B:276:LEU:HD11	7:H:228:LEU:HD23	1.69	0.74
12:P:197:PHE:HZ	33:X:-25:DA:C2	2.05	0.74
2:B:835:ARG:HD3	7:H:187:GLU:CG	2.16	0.74
17:U:145:PHE:CE2	35:u:98:PHE:CE2	2.76	0.74
17:U:127:PHE:HB3	17:U:161:VAL:HB	1.69	0.74
14:R:44:ARG:HH11	23:p:1064:ARG:HG3	1.51	0.74
2:B:276:LEU:HD11	7:H:228:LEU:CD2	2.18	0.73
2:B:883:PHE:HD1	7:H:222:PRO:C	1.94	0.73
4:E:359:LEU:HD12	4:E:359:LEU:O	1.87	0.73
5:F:316:GLN:HE21	5:F:319:LEU:C	1.96	0.73
14:R:51:GLU:O	23:p:894:THR:HA	1.88	0.73
17:U:127:PHE:HB3	17:U:161:VAL:CB	2.18	0.73
5:F:213:ILE:HG22	7:H:164:THR:O	1.88	0.73
11:O:15:LEU:HD22	11:O:40:PHE:CE1	2.23	0.73
11:O:15:LEU:CD2	11:O:40:PHE:CD1	2.71	0.73
1:A:1165:LEU:CB	1:A:1191:ILE:HG23	2.18	0.73
5:F:213:ILE:CB	7:H:163:PRO:O	2.30	0.73
15:S:14:TYR:O	16:T:43:LEU:N	2.21	0.73
18:V:175:LEU:CB	18:V:179:GLN:HB3	2.18	0.73
4:E:694:LEU:HD13	4:E:703:MET:HE1	0.81	0.73
11:O:88:ILE:HG21	13:Q:360:LEU:CA	2.16	0.73
23:p:274:ARG:HG2	23:p:279:VAL:HA	1.70	0.73
25:r:103:LEU:CD2	35:u:144:ARG:HD3	2.18	0.73
35:u:40:GLY:HA2	35:u:152:VAL:HG22	1.66	0.73
5:F:320:ARG:CD	5:F:415:ILE:CG1	2.62	0.73
11:O:44:ILE:HD12	13:Q:17:VAL:CG1	2.12	0.73
17:U:35:ASP:O	17:U:38:ILE:HG12	1.88	0.73
18:V:175:LEU:HD12	18:V:179:GLN:HB3	1.69	0.73
19:c:77:LEU:HD12	9:j:116:LEU:HD23	1.69	0.73
1:A:567:LEU:HD22	2:B:745:GLN:CG	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:TYR:CE2	1:A:1077:LEU:CD1	2.72	0.72
5:F:114:LEU:HD13	7:H:53:ALA:HB3	1.70	0.72
13:Q:29:PHE:HD2	13:Q:34:VAL:HG11	1.54	0.72
14:R:32:MET:SD	14:R:46:ILE:HG21	2.29	0.72
15:S:126:ILE:HB	15:S:138:PHE:HB2	1.70	0.72
3:D:965:ILE:O	3:D:968:ARG:HG3	1.88	0.72
1:A:573:TYR:CD2	2:B:657:ARG:HA	2.24	0.72
1:A:639:LEU:HD11	1:A:774:ARG:HG2	1.69	0.72
15:S:24:LYS:CA	16:T:98:GLU:O	2.37	0.72
22:o:1189:ASP:OD2	22:o:1258:ARG:NH1	2.22	0.72
29:w:81:THR:HG22	29:w:83:ASP:H	1.55	0.72
4:E:694:LEU:HB3	4:E:703:MET:HE3	1.72	0.72
3:D:1083:PHE:CE2	4:E:585:ASN:ND2	2.37	0.72
11:O:88:ILE:HB	13:Q:360:LEU:HD13	1.70	0.72
25:r:103:LEU:CB	35:u:144:ARG:NH1	2.51	0.72
3:D:901:TYR:CE1	10:L:128:ILE:CG2	2.73	0.72
23:p:344:GLN:NE2	23:p:353:VAL:O	2.22	0.72
18:V:163:LEU:O	18:V:163:LEU:HD13	1.90	0.72
11:O:58:PHE:HB3	11:O:81:PHE:CE2	2.25	0.71
22:o:60:PRO:HA	22:o:65:ILE:HD11	1.71	0.71
22:o:406:VAL:HG21	22:o:419:ILE:HD11	1.72	0.71
25:r:110:GLU:CG	35:u:167:TYR:CB	2.67	0.71
5:F:213:ILE:CG2	7:H:163:PRO:CB	2.64	0.71
12:P:256:GLN:HG3	33:X:-26:DC:H5"	1.72	0.71
16:T:16:THR:CG2	16:T:107:GLU:O	2.37	0.71
35:u:44:PHE:HE2	35:u:46:ILE:CG1	2.03	0.71
5:F:43:VAL:HG21	8:I:43:ALA:CB	2.03	0.71
5:F:418:ILE:H	5:F:418:ILE:HD12	1.54	0.71
8:I:132:LEU:HD21	9:J:121:MET:HE1	1.72	0.71
13:Q:55:ALA:O	13:Q:56:VAL:CG2	2.38	0.71
15:S:23:THR:O	16:T:99:SER:CA	2.38	0.71
17:U:17:LEU:HD12	17:U:191:LEU:HB2	1.71	0.71
22:o:538:VAL:HG22	22:o:539:GLN:H	1.54	0.71
14:R:153:GLY:HA3	34:Y:21:DT:H5"	1.72	0.71
17:U:102:VAL:HB	17:U:105:TYR:HB3	1.73	0.71
18:V:175:LEU:H	18:V:175:LEU:CD2	2.04	0.71
3:D:917:ILE:CB	3:D:1058:VAL:HG11	2.21	0.71
4:E:704:VAL:HG12	4:E:759:ILE:HD13	1.72	0.71
11:O:88:ILE:CD1	13:Q:360:LEU:CB	2.60	0.71
14:R:154:ARG:NH2	34:Y:22:DG:OP1	2.24	0.71
1:A:465:TYR:CG	7:H:167:GLU:OE1	2.43	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:TYR:HE2	1:A:1077:LEU:CD1	2.03	0.71
25:r:73:ARG:NH1	35:u:144:ARG:HH22	1.87	0.71
7:H:66:GLN:HG3	9:J:138:TYR:CE1	2.25	0.71
13:Q:18:ILE:HG12	13:Q:46:TRP:CH2	2.26	0.71
23:p:133:ILE:HA	23:p:139:GLN:HE22	1.55	0.71
25:r:16:ASP:HB2	35:u:81:LYS:HZ1	1.44	0.71
25:r:108:ALA:HB2	25:r:128:GLN:HB2	1.71	0.71
1:A:572:TYR:CE2	2:B:689:GLN:HB2	2.25	0.71
2:B:877:TYR:CE2	7:H:216:ALA:HB2	2.26	0.71
16:T:128:LYS:HE3	23:p:540:PRO:HB2	1.73	0.71
25:r:87:LEU:HD22	25:r:97:LEU:HB2	1.71	0.71
1:A:1187:LYS:O	1:A:1191:ILE:CG1	2.39	0.71
14:R:32:MET:HE1	14:R:46:ILE:HD12	1.71	0.71
5:F:361:LYS:HA	5:F:364:VAL:HG22	1.73	0.71
7:H:110:TYR:CZ	9:J:160:GLN:HB3	2.26	0.71
14:R:297:PRO:HB3	14:R:310:VAL:HG21	1.73	0.71
3:D:917:ILE:CG1	3:D:1058:VAL:HG21	2.21	0.70
22:o:334:ARG:NH1	22:o:335:PRO:O	2.20	0.70
15:S:45:ALA:HB2	16:T:9:LEU:HD21	1.70	0.70
15:S:121:ASN:O	16:T:25:LYS:HE2	1.91	0.70
17:U:127:PHE:CD2	17:U:161:VAL:HG21	2.25	0.70
35:u:38:CYS:SG	35:u:44:PHE:CA	2.75	0.70
1:A:657:SER:O	2:B:475:LYS:CD	2.38	0.70
1:A:1185:VAL:HG12	1:A:1191:ILE:CD1	2.21	0.70
2:B:241:PRO:HG2	2:B:496:MET:HE1	1.72	0.70
15:S:45:ALA:HB3	16:T:9:LEU:CD2	2.20	0.70
15:S:125:TYR:HD2	16:T:31:TRP:HZ3	1.37	0.70
35:u:110:ARG:NH2	35:u:118:GLU:OE2	2.24	0.70
3:D:1006:LEU:CD1	11:O:68:CYS:HB3	2.15	0.70
7:H:111:ALA:HB2	9:J:157:LEU:HD11	1.72	0.70
5:F:320:ARG:NE	5:F:415:ILE:HB	2.07	0.70
7:H:119:ILE:HD13	9:J:129:THR:O	1.91	0.70
12:P:300:ILE:HD11	12:P:320:GLU:HB3	1.73	0.70
20:k:191:VAL:HG13	20:k:200:ILE:HD13	1.74	0.70
2:B:735:ILE:HG21	7:H:176:ARG:CZ	2.18	0.70
7:H:93:ILE:HD13	9:J:155:ILE:HD11	1.72	0.70
13:Q:47:GLU:OE2	13:Q:60:HIS:CG	2.45	0.70
1:A:657:SER:O	2:B:475:LYS:HD3	1.91	0.70
1:A:640:LEU:HD23	6:G:35:GLY:HA3	1.71	0.70
1:A:657:SER:OG	2:B:475:LYS:NZ	2.24	0.70
5:F:81:GLU:C	5:F:83:LEU:H	1.99	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:25:SER:C	11:O:27:GLN:H	1.98	0.70
3:D:898:VAL:CG2	10:L:113:VAL:HG23	2.22	0.70
5:F:211:ARG:HG2	7:H:165:TYR:CE2	2.25	0.70
17:U:124:ARG:HH22	17:U:170:LYS:HE2	1.57	0.70
25:r:103:LEU:HD23	35:u:144:ARG:HD3	1.72	0.70
5:F:51:ALA:HB2	8:I:23:LEU:CD2	2.11	0.69
5:F:313:VAL:HG12	5:F:375:GLY:CA	2.21	0.69
2:B:792:ASN:HB3	2:B:845:SER:HB2	1.74	0.69
5:F:52:GLN:HG2	8:I:26:MET:HG3	1.74	0.69
14:R:39:LEU:HD21	22:o:425:ASP:CG	2.16	0.69
16:T:137:LYS:HZ2	16:T:137:LYS:CB	2.03	0.69
22:o:1102:MET:HE1	22:o:1124:LEU:HD13	1.73	0.69
22:o:1166:LEU:HB3	22:o:1293:LEU:HA	1.73	0.69
3:D:966:LEU:C	3:D:966:LEU:HD23	2.17	0.69
3:D:1009:LEU:HD12	3:D:1009:LEU:N	2.07	0.69
22:o:811:ILE:HD12	29:w:79:PRO:HB3	1.74	0.69
14:R:146:TYR:O	14:R:149:LYS:CG	2.39	0.69
15:S:16:VAL:HB	16:T:56:PHE:CE1	2.28	0.69
1:A:405:VAL:N	5:F:302:HIS:HB3	2.07	0.69
11:O:18:SER:N	13:Q:49:LYS:NZ	2.40	0.69
8:I:60:HIS:HE1	10:L:118:LEU:HD22	0.92	0.69
5:F:274:ASN:HB2	5:F:317:LEU:H	1.58	0.69
25:r:103:LEU:HD23	35:u:144:ARG:HH11	0.61	0.69
2:B:835:ARG:HD3	7:H:187:GLU:OE2	1.92	0.69
3:D:917:ILE:HB	3:D:1058:VAL:HG11	1.75	0.69
5:F:71:ILE:HD12	8:I:35:VAL:HA	1.73	0.69
5:F:213:ILE:HB	7:H:163:PRO:C	2.15	0.69
11:O:88:ILE:HG22	13:Q:360:LEU:HB3	1.68	0.69
15:S:44:GLN:CA	16:T:9:LEU:CD1	2.71	0.69
25:r:60:VAL:HG12	35:u:44:PHE:HZ	1.51	0.69
5:F:412:LEU:CD1	5:F:417:ARG:CD	2.38	0.69
16:T:177:ARG:HD3	16:T:177:ARG:N	2.07	0.69
26:s:172:ARG:NH2	26:s:210:GLN:O	2.25	0.69
34:Y:-19:DC:OP2	34:Y:-19:DC:H6	1.75	0.69
1:A:568:SER:HB2	2:B:389:ASN:HB2	1.74	0.69
6:G:129:LYS:O	6:G:129:LYS:NZ	2.23	0.69
7:H:36:THR:CG2	9:J:134:VAL:HG21	2.22	0.69
14:R:27:TYR:CZ	23:p:841:ARG:NH2	2.61	0.69
35:u:93:ASN:OD1	35:u:94:LYS:N	2.26	0.69
11:O:47:ALA:HB1	13:Q:17:VAL:HG22	1.74	0.68
15:S:135:PHE:HE2	16:T:43:LEU:CD2	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:180:LYS:HB2	16:T:180:LYS:HZ2	1.56	0.68
5:f:447:ALA:CA	5:f:456:GLY:HA3	2.23	0.68
25:r:26:PHE:HE2	35:u:80:PHE:HZ	1.42	0.68
25:r:103:LEU:HA	35:u:144:ARG:HH12	0.86	0.68
25:r:103:LEU:O	35:u:144:ARG:NH2	2.27	0.68
35:u:38:CYS:O	35:u:155:ASN:OD1	2.12	0.68
1:A:1185:VAL:C	1:A:1191:ILE:HD11	2.18	0.68
16:T:196:TYR:HB2	16:T:232:THR:CG2	2.22	0.68
25:r:29:ALA:O	25:r:94:LYS:NZ	2.18	0.68
3:D:965:ILE:HA	3:D:968:ARG:HH11	1.58	0.68
5:F:213:ILE:HG21	7:H:163:PRO:HB2	1.75	0.68
4:E:615:ASP:OD1	8:I:114:ARG:CA	2.41	0.68
11:O:58:PHE:CD1	11:O:81:PHE:HD2	2.11	0.68
12:P:167:ASN:ND2	12:P:259:VAL:H	1.92	0.68
13:Q:358:MET:HE2	13:Q:367:PHE:HD2	1.57	0.68
35:u:38:CYS:O	35:u:155:ASN:HA	1.93	0.68
5:F:298:GLU:C	5:F:301:VAL:HG12	2.18	0.68
11:O:22:LEU:HB2	11:O:28:ILE:HD13	1.67	0.68
14:R:45:VAL:C	22:o:67:ARG:NH2	2.51	0.68
4:e:645:GLY:H	4:e:675:LEU:HD11	1.59	0.68
23:p:320:PHE:O	23:p:324:ARG:NH1	2.27	0.68
2:B:310:ASP:OD2	7:H:223:TYR:HE2	1.77	0.68
16:T:18:VAL:HG21	16:T:95:VAL:CG2	2.23	0.68
22:o:1156:ASP:OD1	22:o:1157:ILE:N	2.27	0.68
35:u:153:ASP:O	35:u:155:ASN:N	2.27	0.68
3:D:914:VAL:CG1	10:L:70:VAL:HG21	2.24	0.68
7:H:111:ALA:HB2	9:J:157:LEU:HD13	1.76	0.68
12:P:274:VAL:CG1	14:R:208:LEU:CD1	2.53	0.68
14:R:27:TYR:CG	23:p:841:ARG:NE	2.59	0.68
29:w:105:GLU:HG2	29:w:106:ASP:H	1.58	0.68
11:O:22:LEU:CB	11:O:28:ILE:HD13	2.23	0.68
15:S:49:ARG:NH1	15:S:96:GLN:O	2.25	0.68
22:o:95:PHE:HB2	22:o:311:GLN:HE22	1.59	0.68
2:B:877:TYR:CZ	7:H:216:ALA:HB2	2.29	0.67
25:r:26:PHE:CE2	35:u:80:PHE:HZ	2.11	0.67
14:R:283:VAL:HA	14:R:286:ARG:HE	1.59	0.67
1:A:411:GLU:HG2	5:F:358:THR:HG21	1.75	0.67
25:r:114:LEU:HD21	35:u:167:TYR:CD2	2.25	0.67
3:D:891:ILE:HG22	10:L:111:LEU:CB	2.19	0.67
16:T:149:VAL:HG11	23:p:146:LYS:CD	2.25	0.67
22:o:1344:MET:HE2	26:s:134:GLU:HA	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:80:ILE:HA	25:r:83:VAL:HG12	1.75	0.67
28:v:104:THR:HG22	28:v:105:SER:H	1.57	0.67
1:A:349:TRP:HE1	5:f:262:PHE:HA	1.60	0.67
2:B:848:HIS:CD2	2:B:886:ILE:HD11	2.30	0.67
5:F:22:VAL:HG13	8:I:44:PHE:HE1	1.56	0.67
5:F:46:ARG:HB3	8:I:42:PHE:HE2	1.60	0.67
5:F:51:ALA:O	8:I:28:ILE:CD1	2.42	0.67
16:T:16:THR:O	16:T:109:ILE:N	2.24	0.67
18:V:96:PRO:HB2	18:V:136:LYS:CD	2.25	0.67
3:D:962:GLU:O	3:D:965:ILE:HG22	1.95	0.67
12:P:189:ASN:CG	13:Q:376:TRP:HZ2	2.01	0.67
8:i:61:ALA:HA	10:l:106:ARG:HG2	1.76	0.67
23:p:249:LYS:HG2	23:p:252:ILE:HD11	1.77	0.67
29:w:109:ARG:NH2	29:w:125:GLU:O	2.28	0.67
4:E:359:LEU:HD13	4:E:627:LEU:HD12	1.76	0.67
17:U:32:LEU:CD2	18:V:161:ARG:NE	2.55	0.67
5:f:239:ARG:HD3	5:f:284:ARG:HH11	1.60	0.67
1:A:495:LEU:HD13	5:f:268:ARG:CZ	2.24	0.67
7:H:108:PRO:HG3	9:J:119:PHE:CD2	2.30	0.67
18:V:78:LEU:C	18:V:80:LYS:H	2.02	0.67
18:V:203:PHE:O	18:V:203:PHE:CG	2.48	0.67
22:o:626:THR:HG22	22:o:627:LYS:H	1.60	0.67
25:r:73:ARG:HH12	35:u:144:ARG:HH21	1.41	0.67
4:E:426:ARG:HH11	4:E:640:ASN:HD22	1.42	0.67
7:H:108:PRO:HG3	9:J:119:PHE:CG	2.30	0.67
11:O:57:ASN:O	11:O:57:ASN:ND2	2.28	0.67
1:A:567:LEU:HD22	2:B:745:GLN:HG2	1.76	0.67
16:T:128:LYS:CE	23:p:540:PRO:HB3	2.25	0.67
22:o:1005:HIS:HD2	22:o:1007:ILE:HG12	1.59	0.67
5:F:320:ARG:HD3	5:F:415:ILE:HB	0.70	0.66
15:S:27:ASN:HB2	16:T:96:PHE:CE1	2.30	0.66
2:B:402:ILE:HD12	2:B:455:LEU:HD12	1.77	0.66
3:D:1009:LEU:HD12	3:D:1009:LEU:H	1.60	0.66
3:D:955:LYS:O	3:D:955:LYS:NZ	2.23	0.66
10:L:102:LEU:CA	10:L:105:HIS:HD2	2.09	0.66
35:u:99:THR:HG21	35:u:143:ILE:HD11	1.76	0.66
5:F:47:ILE:HD13	8:I:19:MET:HE3	1.57	0.66
5:F:219:GLU:CB	7:H:156:PRO:HB2	2.26	0.66
5:F:257:PRO:HD3	5:F:300:TYR:OH	1.95	0.66
18:V:190:LEU:HD12	18:V:204:ASN:HA	1.77	0.66
22:o:1345:ARG:HG2	26:s:133:GLN:NE2	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:910:LEU:HB2	10:L:66:LEU:HD21	1.77	0.66
12:P:204:ILE:HG13	12:P:207:PRO:HD2	1.78	0.66
16:T:128:LYS:CE	23:p:540:PRO:CB	2.73	0.66
25:r:103:LEU:CA	35:u:144:ARG:NH2	2.59	0.66
2:B:792:ASN:ND2	2:B:846:TYR:HB3	2.10	0.66
7:H:111:ALA:HA	9:J:126:TYR:OH	1.95	0.66
11:O:19:LEU:HA	11:O:28:ILE:HD11	1.78	0.66
23:p:854:ILE:HD12	23:p:866:ILE:HG22	1.77	0.66
25:r:110:GLU:CG	35:u:167:TYR:CG	2.77	0.66
35:u:167:TYR:CD2	35:u:167:TYR:O	2.48	0.66
7:H:111:ALA:CB	9:J:157:LEU:HD11	2.26	0.66
7:H:118:VAL:CG2	9:J:127:THR:HG23	2.25	0.66
5:F:80:VAL:HG11	8:I:42:PHE:HE1	1.58	0.66
5:F:113:ASP:HA	7:H:52:SER:HA	1.77	0.66
13:Q:26:ARG:HH21	13:Q:39:LEU:HD23	1.61	0.66
16:T:137:LYS:O	16:T:137:LYS:HD3	1.95	0.66
23:p:690:CYS:SG	23:p:691:SER:N	2.69	0.66
2:B:490:SER:HA	2:B:493:TRP:HB2	1.77	0.66
11:O:80:GLU:HG2	11:O:89:LYS:HA	1.77	0.66
12:P:278:GLN:CD	12:P:278:GLN:H	2.04	0.66
25:r:103:LEU:CG	35:u:144:ARG:HH11	2.00	0.66
3:D:1005:ASN:OD1	3:D:1009:LEU:HD13	1.94	0.66
4:E:697:ASP:O	4:E:701:GLY:CA	2.38	0.66
15:S:121:ASN:C	16:T:25:LYS:HE2	2.20	0.66
15:S:124:TYR:CE1	16:T:22:LYS:HE2	2.31	0.66
23:p:1022:LEU:HD12	23:p:1023:ARG:HG2	1.78	0.66
3:D:963:ARG:CD	3:D:964:GLU:HG2	2.23	0.65
3:D:1011:ALA:HB2	11:O:94:LYS:HE2	1.77	0.65
12:P:188:ARG:HH21	13:Q:324:GLU:HA	1.60	0.65
35:u:32:THR:OG1	35:u:33:GLU:OE1	2.14	0.65
4:E:614:THR:O	8:I:114:ARG:O	2.14	0.65
4:E:694:LEU:HB3	4:E:703:MET:CE	2.26	0.65
5:F:43:VAL:CG2	8:I:43:ALA:CA	2.73	0.65
7:H:102:PHE:CE1	9:J:158:ALA:O	2.49	0.65
24:q:154:ARG:HD3	30:x:64:PRO:HD3	1.78	0.65
25:r:87:LEU:HD13	25:r:97:LEU:HD22	1.77	0.65
2:B:431:LEU:HD22	2:B:431:LEU:H	1.62	0.65
4:E:615:ASP:OD2	8:I:114:ARG:HG2	1.96	0.65
5:F:213:ILE:CG2	7:H:163:PRO:HB3	2.10	0.65
11:O:25:SER:OG	11:O:27:GLN:HB2	1.96	0.65
18:V:206:LYS:HA	18:V:206:LYS:HZ2	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:s:51:GLY:O	26:s:54:ARG:NH2	2.29	0.65
17:U:179:ARG:O	17:U:183:GLN:CB	2.41	0.65
5:F:48:LYS:HE3	8:I:22:ILE:HA	1.77	0.65
14:R:27:TYR:CZ	14:R:50:SER:HB3	2.30	0.65
16:T:148:VAL:HG13	23:p:125:TYR:OH	1.96	0.65
18:V:121:THR:O	18:V:125:VAL:HG23	1.91	0.65
23:p:1120:ASN:HD22	23:p:1145:GLN:HB2	1.60	0.65
25:r:16:ASP:OD1	35:u:81:LYS:O	2.14	0.65
5:F:320:ARG:N	5:F:321:PRO:HD2	2.11	0.65
8:I:60:HIS:NE2	10:L:118:LEU:CD2	2.54	0.65
19:c:67:GLY:CA	9:j:116:LEU:HD11	2.25	0.65
1:A:575:PRO:HG3	2:B:610:GLU:CG	2.21	0.65
5:F:320:ARG:CB	5:F:415:ILE:CD1	2.17	0.65
7:H:69:ILE:HG21	9:J:138:TYR:HB2	1.79	0.65
16:T:31:TRP:HD1	16:T:62:LEU:HD21	1.62	0.65
22:o:533:PRO:O	22:o:647:THR:OG1	2.15	0.65
22:o:922:PHE:H	22:o:1052:ARG:HH11	1.43	0.65
24:q:19:VAL:HG23	24:q:241:PRO:HB2	1.79	0.65
4:E:696:TRP:CE3	4:E:703:MET:CB	2.70	0.65
6:G:154:LYS:HZ3	6:G:154:LYS:HB3	1.62	0.65
11:O:15:LEU:CD2	11:O:40:PHE:CG	2.80	0.65
17:U:141:ALA:HB1	17:U:152:PHE:HB3	1.79	0.65
3:D:963:ARG:NH1	3:D:964:GLU:HB3	2.12	0.65
13:Q:47:GLU:OE2	13:Q:60:HIS:NE2	2.27	0.65
17:U:46:GLU:CD	17:U:93:PHE:HE2	2.05	0.65
18:V:224:THR:HG23	18:V:227:SER:HB2	1.73	0.65
22:o:1323:THR:OG1	22:o:1325:ASP:OD1	2.15	0.65
15:S:125:TYR:CD2	16:T:23:VAL:HG21	2.32	0.65
15:S:135:PHE:CD2	16:T:43:LEU:CD2	2.80	0.64
16:T:196:TYR:HB2	16:T:232:THR:HG22	1.80	0.64
26:s:17:ILE:HD11	26:s:135:LEU:HD13	1.78	0.64
35:u:91:GLN:HB2	35:u:98:PHE:HD2	1.62	0.64
4:E:615:ASP:OD1	8:I:114:ARG:C	2.41	0.64
15:S:47:LEU:HB2	16:T:7:LEU:HD22	1.79	0.64
18:V:117:GLN:NE2	18:V:121:THR:CG2	2.55	0.64
22:o:1146:GLN:HB3	22:o:1149:ARG:HH21	1.62	0.64
7:H:107:LEU:HD11	9:J:157:LEU:C	2.21	0.64
22:o:232:GLU:HA	22:o:235:VAL:HG12	1.80	0.64
1:A:468:PHE:HD2	5:F:221:GLN:NE2	1.93	0.64
3:D:967:MET:SD	3:D:968:ARG:HG2	2.38	0.64
17:U:185:GLU:N	17:U:186:PRO:CD	2.60	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:Q:312:GLU:H	13:Q:313:PRO:HD3	1.61	0.64
35:u:40:GLY:CA	35:u:152:VAL:HG22	2.22	0.64
2:B:827:ARG:NE	7:H:211:PHE:HZ	1.95	0.64
4:E:788:ARG:O	7:H:145:HIS:HB2	1.96	0.64
24:q:15:THR:HG22	24:q:16:ASP:H	1.61	0.64
13:Q:47:GLU:OE1	13:Q:60:HIS:ND1	2.30	0.64
18:V:77:VAL:HG11	18:V:119:LEU:HD13	1.79	0.64
2:B:583:GLU:CD	2:B:583:GLU:H	2.06	0.64
3:D:901:TYR:CD1	10:L:128:ILE:CG2	2.80	0.64
13:Q:48:ASN:HA	13:Q:51:MET:HE2	1.78	0.64
14:R:111:ASP:HA	14:R:114:MET:HB2	1.80	0.64
5:f:320:ARG:NH1	5:f:320:ARG:HB3	2.12	0.64
23:p:313:GLU:HG3	23:p:316:VAL:HG12	1.80	0.64
3:D:963:ARG:HH11	3:D:964:GLU:HA	1.05	0.64
4:E:745:GLU:OE1	4:E:745:GLU:HA	1.98	0.64
5:F:87:HIS:CB	9:J:212:LYS:HZ3	2.05	0.64
14:R:27:TYR:CE1	14:R:48:VAL:HG22	2.32	0.64
14:R:45:VAL:O	22:o:67:ARG:NH2	2.31	0.64
22:o:508:SER:OG	22:o:509:LEU:N	2.31	0.64
1:A:355:VAL:O	1:A:355:VAL:HG23	1.97	0.64
3:D:962:GLU:HA	3:D:965:ILE:HB	1.79	0.64
12:P:197:PHE:CZ	33:X:-25:DA:C2	2.86	0.64
3:D:936:GLN:HE21	3:D:936:GLN:H	1.47	0.63
7:H:132:LYS:HE2	7:H:134:LEU:H	1.62	0.63
11:O:3:TYR:C	11:O:5:LEU:H	2.04	0.63
22:o:327:ARG:NH2	22:o:336:LEU:O	2.29	0.63
1:A:575:PRO:CD	2:B:608:ASN:HB2	2.28	0.63
10:L:106:ARG:CZ	10:L:114:LYS:HZ3	2.03	0.63
17:U:120:ASP:HB2	17:U:170:LYS:HD2	1.80	0.63
23:p:677:MET:H	23:p:682:LEU:HD12	1.62	0.63
2:B:159:LEU:HD23	2:B:159:LEU:H	1.62	0.63
14:R:33:ILE:CB	22:o:431:PHE:HD2	1.87	0.63
14:R:173:VAL:HB	14:R:175:ARG:HH12	1.64	0.63
1:A:405:VAL:HG11	5:F:301:VAL:CG1	2.28	0.63
15:S:126:ILE:N	15:S:138:PHE:O	2.23	0.63
18:V:171:ILE:HG12	18:V:177:ASN:HB2	1.79	0.63
25:r:62:MET:HA	25:r:65:LEU:HB3	1.79	0.63
25:r:103:LEU:CD2	35:u:144:ARG:CD	2.76	0.63
1:A:1019:LYS:HB2	1:A:1019:LYS:HZ2	1.61	0.63
12:P:239:ARG:HG3	13:Q:315:ASN:HA	1.80	0.63
1:A:639:LEU:HD11	1:A:643:ILE:HD11	1.75	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:881:ARG:HB2	10:L:57:VAL:CG1	2.27	0.63
5:F:87:HIS:CB	9:J:212:LYS:HZ1	1.97	0.63
5:F:283:MET:HE1	5:F:308:VAL:HG12	1.81	0.63
17:U:114:ILE:HG21	17:U:181:ASN:HD22	1.62	0.63
23:p:311:ILE:HD11	23:p:317:ALA:HA	1.81	0.63
1:A:349:TRP:NE1	5:f:262:PHE:CD1	2.66	0.63
3:D:963:ARG:NE	3:D:964:GLU:CG	2.57	0.63
7:H:108:PRO:HA	9:J:119:PHE:CE1	2.34	0.63
19:c:67:GLY:CA	9:j:116:LEU:CD1	2.71	0.63
17:U:105:TYR:HA	18:V:234:GLU:OE2	1.99	0.63
4:E:359:LEU:HD11	4:E:648:ASP:HB2	1.80	0.63
17:U:105:TYR:HA	18:V:234:GLU:CD	2.24	0.63
11:O:39:GLN:NE2	13:Q:24:ASP:CB	2.52	0.62
16:T:225:VAL:C	16:T:227:GLY:N	2.56	0.62
2:B:735:ILE:CG2	7:H:176:ARG:NH2	2.62	0.62
16:T:149:VAL:HG11	23:p:146:LYS:HD3	1.81	0.62
16:T:183:VAL:HG12	16:T:187:LEU:HG	1.81	0.62
2:B:158:GLY:HA2	2:B:188:PHE:HB3	1.81	0.62
12:P:259:VAL:CG2	34:Y:28:DG:H21	2.11	0.62
33:X:-9:DG:N2	34:Y:9:DC:C2	2.68	0.62
5:F:114:LEU:HD13	7:H:53:ALA:CB	2.29	0.62
5:F:320:ARG:HD3	5:F:415:ILE:HG13	1.80	0.62
11:O:58:PHE:CG	11:O:81:PHE:HD2	2.16	0.62
12:P:188:ARG:NH2	13:Q:323:GLU:C	2.56	0.62
14:R:33:ILE:HG21	22:o:431:PHE:CB	2.28	0.62
17:U:32:LEU:HD21	18:V:203:PHE:CD2	2.34	0.62
18:V:77:VAL:HG21	18:V:111:ILE:CD1	2.24	0.62
23:p:407:MET:HE1	23:p:444:LEU:HG	1.81	0.62
3:D:964:GLU:O	3:D:968:ARG:CG	2.41	0.62
17:U:187:ILE:HG21	18:V:210:PHE:HB3	1.81	0.62
33:X:-12:DC:H2"	33:X:-11:DT:H71	1.81	0.62
13:Q:15:ARG:HH21	13:Q:58:GLY:HA2	1.65	0.62
15:S:24:LYS:HB3	16:T:99:SER:CA	2.29	0.62
3:D:893:GLU:OE2	10:L:110:THR:OG1	2.18	0.62
3:D:963:ARG:CZ	3:D:964:GLU:CG	2.78	0.62
7:H:118:VAL:HG21	9:J:127:THR:HG21	1.82	0.62
16:T:137:LYS:HD3	16:T:137:LYS:C	2.24	0.62
3:d:884:GLU:HA	3:d:887:LYS:HE3	1.82	0.62
22:o:97:VAL:HA	22:o:100:LEU:HD23	1.81	0.62
5:F:84:TYR:HB3	8:I:41:GLU:OE1	1.98	0.62
5:F:279:LEU:HB3	5:F:330:ARG:NH1	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:297:PRO:HA	14:R:310:VAL:HG11	1.82	0.62
16:T:188:PHE:HB3	18:V:76:GLY:CA	2.29	0.62
1:A:1016:GLU:HA	1:A:1019:LYS:HE3	1.82	0.62
3:D:871:THR:HG22	10:L:66:LEU:CD1	2.30	0.62
5:F:309:MET:SD	5:F:359:PHE:HZ	2.22	0.62
17:U:193:GLU:OE1	17:U:193:GLU:HA	1.98	0.62
4:E:613:ALA:HB2	4:E:620:LEU:HD11	1.81	0.62
4:E:696:TRP:CZ3	4:E:703:MET:HB3	2.31	0.61
14:R:44:ARG:HH11	23:p:1064:ARG:CG	2.13	0.61
16:T:128:LYS:HE3	23:p:540:PRO:CB	2.30	0.61
16:T:147:LYS:CG	16:T:148:VAL:H	2.04	0.61
5:F:15:PRO:HG3	8:I:14:LYS:HB3	1.80	0.61
7:H:192:ARG:NH1	7:H:209:SER:O	2.34	0.61
12:P:274:VAL:HG11	14:R:208:LEU:HD21	1.82	0.61
5:F:66:LEU:HD23	8:I:31:TYR:HB3	1.81	0.61
17:U:127:PHE:HB3	17:U:161:VAL:CG2	2.31	0.61
18:V:175:LEU:CD1	18:V:179:GLN:HB3	2.30	0.61
22:o:217:SER:OG	22:o:219:GLU:OE1	2.18	0.61
24:q:193:ARG:HD3	24:q:220:TYR:HD1	1.65	0.61
1:A:564:PRO:CG	2:B:744:PHE:CD2	2.82	0.61
2:B:873:LEU:HD12	7:H:201:GLN:HE22	1.64	0.61
16:T:183:VAL:O	16:T:187:LEU:N	2.29	0.61
8:I:60:HIS:NE2	10:L:118:LEU:HD23	2.16	0.61
25:r:16:ASP:CB	35:u:81:LYS:CE	2.68	0.61
29:w:35:LEU:HD12	29:w:51:SER:HA	1.83	0.61
2:B:203:LYS:HD3	2:B:237:MET:HE3	1.83	0.61
2:B:431:LEU:C	2:B:431:LEU:HD23	2.26	0.61
33:X:-21:DA:H61	34:Y:21:DT:H3	1.49	0.61
35:u:24:ASN:HA	35:u:27:LYS:HG3	1.82	0.61
3:D:914:VAL:HG11	10:L:70:VAL:CG2	2.30	0.61
23:p:82:PRO:HB3	23:p:134:LYS:HB3	1.81	0.61
23:p:111:ASN:HD21	23:p:742:VAL:HG11	1.65	0.61
2:B:328:ASN:HA	7:H:227:LEU:CD1	2.31	0.61
16:T:40:VAL:C	16:T:59:ASN:HB2	2.25	0.61
16:T:181:GLN:HA	16:T:181:GLN:NE2	2.15	0.61
19:c:18:CYS:O	19:c:23:TRP:HB2	2.00	0.61
4:E:703:MET:O	4:E:703:MET:HG3	2.00	0.61
11:O:22:LEU:HD13	11:O:28:ILE:CG2	2.28	0.61
15:S:127:PHE:O	16:T:19:TRP:HB2	2.01	0.61
16:T:228:ILE:HG13	16:T:228:ILE:O	2.01	0.61
17:U:188:TYR:HA	17:U:191:LEU:HD21	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:916:LYS:HE2	3:D:1066:CYS:SG	2.41	0.61
12:P:259:VAL:HG23	34:Y:28:DG:H21	1.65	0.61
22:o:136:GLN:HG3	22:o:139:LYS:HB3	1.83	0.61
25:r:16:ASP:CB	35:u:81:LYS:HE3	2.26	0.61
5:F:319:LEU:HD23	5:F:319:LEU:N	2.09	0.60
11:O:88:ILE:HD12	13:Q:360:LEU:HB2	1.77	0.60
22:o:1430:CYS:O	22:o:1435:THR:HG22	2.01	0.60
1:A:657:SER:CB	2:B:475:LYS:NZ	2.65	0.60
4:E:746:ASP:OD1	4:E:746:ASP:N	2.29	0.60
11:O:58:PHE:CG	11:O:81:PHE:CD2	2.89	0.60
12:P:250:PHE:O	13:Q:311:GLU:HB3	2.00	0.60
17:U:52:LEU:HD23	18:V:161:ARG:NH1	2.16	0.60
21:m:31:LEU:HD23	21:m:31:LEU:N	2.16	0.60
22:o:125:LYS:O	22:o:129:ILE:HG12	2.01	0.60
23:p:565:THR:HG21	23:p:580:PRO:HG3	1.83	0.60
1:A:639:LEU:HD13	1:A:643:ILE:CG1	2.30	0.60
2:B:873:LEU:HD12	7:H:201:GLN:NE2	2.16	0.60
18:V:175:LEU:CB	18:V:179:GLN:OE1	2.46	0.60
3:D:1080:TYR:CD1	4:E:585:ASN:OD1	2.55	0.60
5:F:213:ILE:CD1	7:H:163:PRO:HB3	2.30	0.60
12:P:189:ASN:ND2	13:Q:376:TRP:HZ2	1.99	0.60
16:T:223:GLN:H	16:T:223:GLN:CD	2.09	0.60
12:P:194:PRO:HB3	16:T:176:ALA:HB2	1.84	0.60
15:S:24:LYS:CB	16:T:99:SER:HA	2.31	0.60
15:S:116:GLY:HA2	23:p:356:PHE:CD1	2.37	0.60
15:S:124:TYR:HE1	16:T:22:LYS:CE	2.15	0.60
22:o:1030:SER:HB2	26:s:162:ARG:HE	1.67	0.60
12:P:196:ARG:NH2	16:T:169:LYS:O	2.35	0.60
14:R:27:TYR:OH	23:p:1078:ARG:HB2	2.00	0.60
15:S:102:VAL:O	15:S:108:ARG:N	2.35	0.60
17:U:136:PHE:HB3	17:U:140:GLU:CB	2.31	0.60
24:q:36:ARG:HH12	31:y:40:HIS:HB2	1.66	0.60
3:D:1009:LEU:CD1	3:D:1009:LEU:H	2.14	0.60
5:F:330:ARG:HB3	5:F:330:ARG:CZ	2.31	0.60
7:H:40:VAL:HG11	9:J:130:ILE:HG12	1.84	0.60
7:H:93:ILE:HD11	9:J:144:PHE:HZ	1.65	0.60
7:H:93:ILE:HD11	9:J:144:PHE:CZ	2.36	0.60
13:Q:56:VAL:HG12	13:Q:57:ASP:N	2.16	0.60
18:V:175:LEU:HD23	18:V:175:LEU:N	2.10	0.60
3:D:958:LYS:O	3:D:958:LYS:HE2	2.02	0.60
5:F:412:LEU:HD13	5:F:417:ARG:HD3	1.76	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:25:SER:C	11:O:27:GLN:N	2.59	0.60
17:U:32:LEU:CD1	18:V:161:ARG:NH2	2.65	0.60
33:X:-24:DG:OP2	33:X:-24:DG:H8	1.85	0.60
1:A:485:ILE:CD1	5:f:268:ARG:HG2	2.32	0.60
13:Q:15:ARG:HH21	13:Q:58:GLY:CA	2.15	0.60
13:Q:26:ARG:NH2	13:Q:39:LEU:CD2	2.65	0.60
13:Q:312:GLU:N	13:Q:313:PRO:HD3	2.17	0.60
14:R:289:TYR:OH	14:R:314:PRO:O	2.17	0.60
19:c:99:PHE:HB2	19:c:100:PRO:HD3	1.83	0.60
5:f:330:ARG:HH22	5:f:371:THR:HB	1.66	0.60
1:A:950:VAL:HG21	1:A:1065:GLU:HG3	1.84	0.60
5:F:279:LEU:HB3	5:F:330:ARG:CZ	2.31	0.60
11:O:58:PHE:HB2	13:Q:371:ILE:O	2.02	0.60
15:S:25:LYS:N	16:T:98:GLU:O	2.34	0.60
15:S:46:ARG:NH2	16:T:3:GLU:OE1	2.32	0.60
16:T:209:PRO:HG2	16:T:212:TYR:HB3	1.84	0.60
17:U:43:VAL:O	17:U:43:VAL:HG12	2.02	0.60
22:o:330:GLN:HE22	22:o:336:LEU:HD11	1.65	0.60
4:E:474:THR:OG1	4:E:546:VAL:O	2.19	0.59
11:O:39:GLN:HE22	13:Q:24:ASP:HB3	1.58	0.59
16:T:188:PHE:HB3	18:V:76:GLY:HA3	1.84	0.59
22:o:67:ARG:HH12	23:p:1069:ILE:HD12	1.66	0.59
23:p:584:MET:HE3	23:p:605:ARG:HB2	1.83	0.59
25:r:103:LEU:HA	35:u:144:ARG:HH22	1.67	0.59
11:O:5:LEU:HD13	11:O:98:CYS:SG	2.42	0.59
14:R:32:MET:CE	14:R:46:ILE:HD12	2.32	0.59
16:T:220:ILE:C	16:T:220:ILE:HD12	2.26	0.59
22:o:1005:HIS:CD2	22:o:1007:ILE:HG12	2.36	0.59
35:u:38:CYS:HG	35:u:44:PHE:HA	1.63	0.59
4:E:501:PRO:HD3	7:H:149:HIS:HB3	1.83	0.59
8:I:132:LEU:CG	9:J:121:MET:CE	2.79	0.59
17:U:71:PHE:HD1	17:U:72:ILE:HG23	1.68	0.59
25:r:16:ASP:HB3	25:r:19:GLN:HG2	1.83	0.59
25:r:132:ASP:HA	25:r:135:GLN:HG2	1.84	0.59
1:A:1157:ASN:O	1:A:1159:SER:N	2.35	0.59
2:B:883:PHE:CE1	7:H:223:TYR:HB2	2.23	0.59
5:F:48:LYS:CE	8:I:22:ILE:HG12	2.30	0.59
8:I:56:ILE:HG21	10:L:122:ARG:HH21	1.68	0.59
13:Q:324:GLU:CD	13:Q:324:GLU:H	2.09	0.59
15:S:26:TYR:CD1	16:T:97:THR:HG22	2.38	0.59
17:U:127:PHE:HB3	17:U:161:VAL:HG21	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:o:341:GLN:HA	22:o:344:LYS:HE3	1.83	0.59
5:F:52:GLN:HG2	8:I:26:MET:CG	2.32	0.59
15:S:18:VAL:HB	16:T:40:VAL:HG21	1.84	0.59
16:T:184:LEU:C	16:T:184:LEU:HD23	2.27	0.59
1:A:1187:LYS:NZ	6:G:165:GLU:OE2	2.36	0.59
11:O:75:VAL:HG21	13:Q:327:GLU:HG3	1.84	0.59
22:o:1257:LEU:HD12	22:o:1259:ILE:HD11	1.85	0.59
23:p:387:HIS:NE2	23:p:671:GLU:OE2	2.35	0.59
3:D:871:THR:HG22	10:L:66:LEU:HD13	1.85	0.59
5:F:71:ILE:CG2	8:I:38:GLN:HE21	2.15	0.59
22:o:1177:TYR:OH	29:w:28:GLU:OE2	2.19	0.59
23:p:591:ARG:NH1	23:p:601:VAL:O	2.36	0.59
17:U:184:ILE:HD12	18:V:212:VAL:HG13	1.85	0.59
18:V:118:TRP:NE1	18:V:122:GLU:OE1	2.35	0.59
18:V:167:LEU:HB3	18:V:200:ILE:HD13	1.85	0.59
18:V:226:ASP:HB3	22:o:220:ARG:NH1	2.17	0.59
22:o:930:LEU:HG	22:o:939:VAL:HG23	1.83	0.59
5:F:214:HIS:N	7:H:164:THR:HG22	2.17	0.59
11:O:25:SER:O	11:O:27:GLN:N	2.36	0.59
11:O:89:LYS:N	13:Q:361:ASN:HD21	2.00	0.59
15:S:15:VAL:HA	16:T:42:LYS:HA	1.85	0.59
17:U:136:PHE:HB3	17:U:140:GLU:HB2	1.85	0.59
24:q:44:ILE:HD12	24:q:178:PRO:HB3	1.84	0.59
35:u:167:TYR:CG	35:u:167:TYR:O	2.54	0.59
1:A:405:VAL:HB	5:F:302:HIS:N	2.18	0.58
5:F:71:ILE:CD1	8:I:35:VAL:HG22	2.30	0.58
5:F:114:LEU:HB2	7:H:52:SER:N	2.18	0.58
11:O:22:LEU:O	11:O:28:ILE:O	2.21	0.58
13:Q:312:GLU:N	13:Q:313:PRO:CD	2.66	0.58
15:S:16:VAL:CG2	16:T:43:LEU:HB2	2.32	0.58
18:V:181:ALA:C	18:V:184:ALA:HB3	2.27	0.58
4:e:562:SER:OG	4:e:564:ASP:OD1	2.21	0.58
22:o:27:SER:N	22:o:30:GLU:OE1	2.33	0.58
23:p:124:LEU:HD22	23:p:152:ILE:HD11	1.85	0.58
23:p:988:LYS:O	23:p:992:ASN:ND2	2.31	0.58
33:X:7:DT:H2"	33:X:8:DC:C6	2.38	0.58
4:E:742:LYS:HA	4:E:745:GLU:HG2	1.85	0.58
5:F:43:VAL:HG22	8:I:43:ALA:HB2	1.83	0.58
7:H:102:PHE:HZ	9:J:158:ALA:HA	1.65	0.58
14:R:39:LEU:HD21	22:o:425:ASP:OD2	2.03	0.58
16:T:20:LEU:O	16:T:113:ARG:HA	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:188:PHE:N	16:T:188:PHE:HD1	2.00	0.58
18:V:226:ASP:O	18:V:227:SER:C	2.43	0.58
22:o:17:THR:HG22	22:o:18:ILE:H	1.68	0.58
5:F:44:SER:HB3	8:I:22:ILE:HD11	1.85	0.58
5:F:319:LEU:H	5:F:319:LEU:CD2	2.09	0.58
5:f:349:ASN:HB3	5:f:351:ILE:HG13	1.84	0.58
23:p:820:LYS:HE3	23:p:826:GLU:HB2	1.85	0.58
2:B:769:LYS:O	2:B:769:LYS:HG3	2.03	0.58
3:D:1003:ASP:OD2	11:O:3:TYR:HE1	1.84	0.58
4:E:621:ARG:HH22	8:I:104:LEU:HG	1.68	0.58
5:F:47:ILE:CD1	8:I:19:MET:HE3	2.22	0.58
22:o:1129:ASN:ND2	22:o:1415:THR:HB	2.18	0.58
25:r:132:ASP:O	25:r:136:THR:OG1	2.14	0.58
1:A:405:VAL:CB	5:F:302:HIS:CB	2.56	0.58
2:B:489:GLN:OE1	2:B:489:GLN:N	2.34	0.58
5:F:309:MET:SD	5:F:359:PHE:CZ	2.96	0.58
14:R:50:SER:CA	23:p:841:ARG:NH2	2.61	0.58
16:T:140:ARG:CB	23:p:56:GLN:NE2	2.65	0.58
17:U:124:ARG:HH22	17:U:170:LYS:CE	2.15	0.58
4:e:484:LEU:HD21	4:e:504:LEU:HD21	1.86	0.58
5:F:320:ARG:HB3	5:F:415:ILE:HD12	1.63	0.58
15:S:18:VAL:CG2	16:T:40:VAL:HG11	2.33	0.58
18:V:206:LYS:HA	18:V:206:LYS:HZ3	1.67	0.58
14:R:295:ARG:HG2	14:R:299:LEU:HG	1.86	0.58
25:r:103:LEU:C	35:u:144:ARG:NH2	2.62	0.58
1:A:1165:LEU:HG	1:A:1191:ILE:HG23	1.85	0.58
3:D:963:ARG:CZ	3:D:964:GLU:CB	2.82	0.58
5:F:207:ARG:HD2	5:F:207:ARG:N	2.18	0.58
5:F:290:MET:HE2	5:F:337:VAL:HB	1.86	0.58
5:F:303:GLU:OE1	5:f:347:THR:OG1	2.22	0.58
17:U:131:VAL:HG21	17:U:159:THR:HG21	1.85	0.58
22:o:331:LYS:O	22:o:334:ARG:N	2.35	0.58
22:o:1230:GLN:HA	22:o:1233:GLU:CD	2.28	0.58
15:S:124:TYR:CZ	16:T:22:LYS:HE2	2.39	0.58
17:U:28:ILE:H	17:U:28:ILE:HD13	1.69	0.58
17:U:127:PHE:CD2	17:U:161:VAL:CG2	2.87	0.58
17:U:184:ILE:O	17:U:184:ILE:HG22	2.02	0.58
19:c:21:LEU:HD12	19:c:21:LEU:C	2.29	0.58
2:B:781:TYR:HB3	7:H:176:ARG:HH22	1.67	0.57
2:B:834:THR:CG2	7:H:213:LEU:HD23	2.17	0.57
2:B:877:TYR:CZ	7:H:216:ALA:CB	2.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:36:VAL:O	11:O:40:PHE:N	2.24	0.57
17:U:136:PHE:HA	17:U:140:GLU:HG3	1.86	0.57
18:V:78:LEU:C	18:V:80:LYS:N	2.62	0.57
22:o:460:ARG:HG2	22:o:461:GLN:H	1.69	0.57
25:r:78:GLU:HA	25:r:81:ALA:HB3	1.86	0.57
11:O:23:ILE:CA	11:O:28:ILE:O	2.43	0.57
17:U:124:ARG:HG2	17:U:124:ARG:O	2.05	0.57
22:o:1184:THR:HG21	22:o:1190:GLN:HB2	1.85	0.57
25:r:130:ILE:HA	25:r:133:ASP:HB2	1.86	0.57
1:A:468:PHE:CZ	5:F:224:TYR:HD2	1.78	0.57
14:R:46:ILE:HG23	14:R:46:ILE:O	2.04	0.57
15:S:126:ILE:O	15:S:138:PHE:N	2.34	0.57
1:A:844:LYS:HZ3	33:X:31:DT:H71	1.69	0.57
7:H:73:GLY:HA3	9:J:142:ALA:CB	2.31	0.57
11:O:76:LEU:HB3	11:O:79:VAL:CG2	2.30	0.57
22:o:18:ILE:HB	22:o:1462:GLN:HE22	1.68	0.57
22:o:554:PHE:HB3	22:o:585:LEU:HD23	1.85	0.57
23:p:1046:THR:HG22	23:p:1047:TYR:H	1.70	0.57
23:p:1078:ARG:C	23:p:1080:ARG:H	2.12	0.57
29:w:105:GLU:HG2	29:w:106:ASP:N	2.19	0.57
33:X:-17:DC:N3	34:Y:17:DG:O6	2.37	0.57
3:D:905:ALA:O	10:L:126:MET:CE	2.51	0.57
14:R:25:GLU:CD	14:R:46:ILE:CD1	2.77	0.57
15:S:124:TYR:CE1	16:T:22:LYS:CE	2.87	0.57
19:c:12:VAL:HG23	5:f:118:ILE:HA	1.85	0.57
24:q:9:VAL:HG11	31:y:105:PHE:HD1	1.69	0.57
1:A:740:LEU:HD22	1:A:1070:PHE:HZ	1.70	0.57
2:B:560:TYR:CD2	2:B:581:ILE:HD11	2.39	0.57
4:E:586:TYR:HB3	4:E:605:HIS:HB3	1.85	0.57
5:F:324:ASP:OD2	5:F:422:HIS:NE2	2.37	0.57
7:H:118:VAL:CG2	9:J:127:THR:CG2	2.80	0.57
16:T:31:TRP:CD1	16:T:62:LEU:HD21	2.39	0.57
18:V:212:VAL:HG12	18:V:215:GLU:H	1.70	0.57
23:p:685:LYS:NZ	23:p:686:GLU:O	2.38	0.57
35:u:38:CYS:CA	35:u:155:ASN:OD1	2.52	0.57
1:A:472:ASN:N	5:f:299:LYS:HZ3	2.03	0.57
2:B:431:LEU:H	2:B:431:LEU:CD2	2.17	0.57
3:D:965:ILE:HG22	3:D:966:LEU:N	2.20	0.57
5:F:51:ALA:CB	8:I:23:LEU:HD23	2.30	0.57
10:L:119:HIS:NE2	10:L:123:GLN:OE1	2.38	0.57
14:R:169:ARG:NH1	14:R:207:ASP:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:188:PHE:CB	18:V:76:GLY:HA3	2.35	0.57
17:U:52:LEU:HD23	18:V:161:ARG:HH12	1.70	0.57
5:f:320:ARG:CB	5:f:320:ARG:HH11	2.17	0.57
4:E:464:TYR:CE2	5:F:133:ALA:HB2	2.39	0.57
7:H:69:ILE:CG2	9:J:138:TYR:HB2	2.35	0.57
12:P:227:GLU:OE1	12:P:227:GLU:N	2.37	0.57
17:U:144:LEU:HB3	17:U:153:ARG:O	2.05	0.57
18:V:180:LYS:O	18:V:184:ALA:N	2.36	0.57
19:c:67:GLY:CA	9:j:116:LEU:HD13	2.33	0.57
1:A:486:TRP:HH2	5:f:358:THR:CG2	2.18	0.57
4:E:694:LEU:CD1	4:E:703:MET:CE	2.54	0.57
11:O:88:ILE:HB	13:Q:360:LEU:CD1	2.35	0.57
14:R:214:PHE:HB3	14:R:218:PHE:CE2	2.40	0.57
15:S:112:GLY:HA2	15:S:145:ASN:O	2.04	0.57
18:V:171:ILE:HG22	18:V:171:ILE:O	2.04	0.57
3:d:917:ILE:HD11	3:d:1063:LEU:HD13	1.87	0.57
22:o:1242:ASP:HA	22:o:1262:MET:HE2	1.86	0.57
4:E:695:LEU:O	4:E:703:MET:HA	2.05	0.57
8:I:15:ASP:O	8:I:40:LEU:HD21	2.05	0.57
12:P:188:ARG:NH2	13:Q:324:GLU:HA	2.20	0.57
13:Q:55:ALA:C	13:Q:56:VAL:HG23	2.30	0.57
14:R:27:TYR:CD1	14:R:48:VAL:CB	2.76	0.57
16:T:122:GLU:HG3	16:T:127:LEU:HB2	1.86	0.57
18:V:76:GLY:O	18:V:80:LYS:CB	2.53	0.57
22:o:1389:ASP:OD1	22:o:1389:ASP:N	2.38	0.57
26:s:11:TRP:NE1	26:s:35:GLN:O	2.33	0.57
33:X:-6:DA:C2	34:Y:7:DG:N2	2.72	0.57
35:u:55:GLY:HA3	35:u:69:PRO:HG2	1.86	0.57
1:A:401:ASN:H	1:A:401:ASN:HD22	1.53	0.56
1:A:575:PRO:HD2	2:B:608:ASN:HB2	1.87	0.56
15:S:29:MET:HG3	15:S:146:PHE:CE1	2.40	0.56
15:S:47:LEU:HB3	16:T:7:LEU:HB2	1.87	0.56
18:V:226:ASP:CB	22:o:220:ARG:NH1	2.68	0.56
22:o:1435:THR:OG1	22:o:1436:VAL:N	2.38	0.56
25:r:128:GLN:O	25:r:132:ASP:N	2.34	0.56
33:X:-40:DC:OP2	33:X:-40:DC:H2'	2.05	0.56
7:H:108:PRO:HA	9:J:119:PHE:CZ	2.40	0.56
7:H:171:ASP:HB3	7:H:174:VAL:HG12	1.86	0.56
11:O:32:LEU:O	11:O:36:VAL:HG23	2.05	0.56
15:S:135:PHE:CD2	16:T:43:LEU:HD22	2.40	0.56
16:T:18:VAL:N	16:T:109:ILE:O	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:280:ILE:O	5:f:284:ARG:HG3	2.05	0.56
23:p:666:ASP:OD1	23:p:667:THR:N	2.36	0.56
1:A:950:VAL:HG21	1:A:1065:GLU:CG	2.35	0.56
5:F:311:CYS:HB3	5:F:330:ARG:NH2	2.18	0.56
8:I:132:LEU:HG	9:J:121:MET:SD	2.45	0.56
11:O:17:GLU:C	13:Q:49:LYS:NZ	2.63	0.56
14:R:50:SER:HA	23:p:841:ARG:HH22	1.65	0.56
14:R:173:VAL:O	14:R:175:ARG:NH1	2.39	0.56
17:U:17:LEU:HD22	17:U:195:GLU:HB2	1.88	0.56
22:o:856:GLU:OE2	23:p:494:LYS:NZ	2.39	0.56
1:A:564:PRO:HB2	2:B:744:PHE:CE2	2.41	0.56
1:A:851:ASP:OD1	1:A:851:ASP:N	2.37	0.56
6:G:154:LYS:HB3	6:G:154:LYS:NZ	2.20	0.56
18:V:78:LEU:O	18:V:80:LYS:N	2.38	0.56
28:v:27:ARG:HD2	28:v:40:ILE:HG23	1.86	0.56
34:Y:1:DT:H2"	34:Y:2:DC:C6	2.40	0.56
1:A:349:TRP:CE2	5:f:262:PHE:CD1	2.94	0.56
3:D:917:ILE:HG13	3:D:1058:VAL:HG21	1.86	0.56
4:E:345:MET:HE3	4:E:346:PRO:HD2	1.87	0.56
5:f:223:TYR:HD2	5:f:255:MET:HE1	1.70	0.56
22:o:1150:ASP:OD2	22:o:1153:ARG:NH1	2.39	0.56
1:A:472:ASN:N	5:f:299:LYS:NZ	2.53	0.56
1:A:485:ILE:HD12	5:f:268:ARG:HG2	1.87	0.56
2:B:310:ASP:OD1	7:H:223:TYR:CD2	2.58	0.56
5:F:48:LYS:HE3	8:I:22:ILE:CG1	2.31	0.56
12:P:192:TYR:HB2	12:P:200:VAL:HG22	1.87	0.56
15:S:42:TRP:O	16:T:13:LYS:HD3	2.06	0.56
5:f:219:GLU:OE1	5:f:219:GLU:N	2.26	0.56
22:o:691:ASP:OD2	22:o:765:ASN:ND2	2.32	0.56
1:A:929:THR:HG22	1:A:954:ALA:HA	1.86	0.56
3:D:871:THR:HG23	10:L:66:LEU:CG	2.32	0.56
16:T:30:GLN:HG2	16:T:62:LEU:HG	1.87	0.56
4:e:636:HIS:HD2	4:e:638:ASN:H	1.53	0.56
22:o:457:ILE:HD11	22:o:515:ILE:HD12	1.86	0.56
26:s:100:THR:HG23	26:s:125:TYR:H	1.69	0.56
1:A:402:PHE:HA	1:A:407:GLN:NE2	2.20	0.56
2:B:259:ASP:HB3	2:B:262:MET:O	2.06	0.56
4:E:519:GLU:HG3	4:E:519:GLU:O	2.06	0.56
4:E:790:LEU:HD13	7:H:146:ILE:HG12	1.87	0.56
12:P:196:ARG:NH1	16:T:172:ASP:HB2	2.21	0.56
22:o:1139:LEU:HD12	22:o:1139:LEU:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:17:LEU:CD1	17:U:191:LEU:HB2	2.36	0.56
17:U:152:PHE:O	17:U:160:GLU:OE1	2.23	0.56
18:V:76:GLY:O	18:V:80:LYS:HB3	2.06	0.56
23:p:625:LEU:HD13	23:p:675:LEU:HD21	1.88	0.56
26:s:56:THR:HG22	26:s:57:ASP:H	1.71	0.56
2:B:735:ILE:HG23	7:H:176:ARG:NH2	2.20	0.56
4:E:561:SER:HB2	4:E:588:VAL:HB	1.88	0.55
5:F:283:MET:HE2	5:F:334:ALA:CB	2.36	0.55
14:R:27:TYR:CB	23:p:841:ARG:CD	2.68	0.55
16:T:188:PHE:N	16:T:188:PHE:CD1	2.71	0.55
17:U:67:LYS:HG3	17:U:72:ILE:HD11	1.88	0.55
22:o:46:THR:HG22	22:o:57:LEU:HB2	1.87	0.55
1:A:1014:GLU:CD	22:o:1204:VAL:CB	2.79	0.55
5:F:290:MET:HE1	5:F:337:VAL:CA	2.11	0.55
10:L:101:GLN:O	10:L:105:HIS:CG	2.52	0.55
15:S:119:THR:HG22	15:S:123:SER:HA	1.89	0.55
15:S:125:TYR:HE2	16:T:31:TRP:CZ3	2.11	0.55
5:f:253:TYR:O	5:f:254:GLN:HB3	2.06	0.55
1:A:575:PRO:CD	2:B:608:ASN:HD22	1.92	0.55
5:F:265:GLU:OE2	5:F:265:GLU:HA	2.06	0.55
12:P:176:CYS:SG	12:P:247:PRO:O	2.60	0.55
16:T:225:VAL:O	16:T:227:GLY:N	2.38	0.55
18:V:72:GLY:HA3	18:V:115:GLN:HG3	1.89	0.55
22:o:1101:GLN:NE2	22:o:1389:ASP:OD2	2.39	0.55
3:D:1083:PHE:HE2	4:E:585:ASN:HD21	0.72	0.55
11:O:39:GLN:CG	13:Q:25:VAL:CG1	2.82	0.55
11:O:90:VAL:HG22	11:O:92:LYS:H	1.71	0.55
12:P:165:LEU:HD21	12:P:321:ILE:HG13	1.88	0.55
14:R:214:PHE:O	14:R:218:PHE:HD2	1.89	0.55
24:q:31:ALA:O	24:q:231:TYR:OH	2.23	0.55
1:A:1153:VAL:HG11	6:G:150:LYS:HE3	1.89	0.55
5:F:286:VAL:HG11	5:F:308:VAL:CG1	2.37	0.55
7:H:47:GLU:OE1	7:H:113:ARG:NH2	2.40	0.55
11:O:82:ARG:HB2	11:O:87:LEU:HD13	1.88	0.55
16:T:184:LEU:HG	16:T:188:PHE:CZ	2.42	0.55
18:V:216:PHE:CE1	22:o:296:ASN:HA	2.41	0.55
22:o:139:LYS:HA	22:o:142:THR:HG22	1.89	0.55
23:p:357:CYS:HB2	23:p:360:LYS:HE2	1.89	0.55
2:B:61:ASN:O	2:B:130:VAL:HG23	2.06	0.55
2:B:768:PRO:CG	2:B:771:VAL:HG23	2.26	0.55
5:F:114:LEU:HB2	7:H:52:SER:H	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:111:ALA:HA	9:J:157:LEU:HD21	1.88	0.55
12:P:253:PHE:CD2	12:P:253:PHE:O	2.59	0.55
15:S:45:ALA:N	16:T:9:LEU:CD1	2.64	0.55
17:U:34:LEU:HA	17:U:37:LEU:HD12	1.89	0.55
22:o:853:LYS:NZ	22:o:1102:MET:O	2.30	0.55
3:D:1003:ASP:OD2	11:O:3:TYR:CD1	2.59	0.55
7:H:110:TYR:CE2	9:J:160:GLN:HB3	2.41	0.55
11:O:22:LEU:C	11:O:28:ILE:H	2.09	0.55
1:A:349:TRP:CZ2	5:f:262:PHE:CD1	2.95	0.55
2:B:248:SER:OG	2:B:322:MET:SD	2.65	0.55
2:B:768:PRO:C	2:B:770:GLU:H	2.14	0.55
5:F:342:LYS:NZ	5:F:352:GLN:NE2	2.55	0.55
11:O:88:ILE:CB	13:Q:360:LEU:CB	2.84	0.55
14:R:50:SER:CA	23:p:841:ARG:HH22	2.19	0.55
3:D:965:ILE:CA	3:D:968:ARG:HH11	2.19	0.55
5:F:406:VAL:HG11	5:F:420:ALA:HB2	1.88	0.55
7:H:50:PHE:CZ	9:J:195:LEU:HB2	2.42	0.55
22:o:1130:ILE:HD11	22:o:1405:MET:HE2	1.89	0.55
22:o:1218:ARG:HA	22:o:1221:MET:HB2	1.89	0.55
23:p:629:GLU:OE1	23:p:630:LYS:N	2.40	0.55
24:q:2:PRO:HB3	31:y:54:PRO:HD2	1.87	0.55
34:Y:31:DA:H8	34:Y:31:DA:H5"	1.72	0.55
1:A:349:TRP:CZ2	5:f:262:PHE:CZ	2.95	0.55
2:B:838:ASN:CG	7:H:214:ILE:HG13	2.33	0.55
4:E:645:GLY:H	4:E:675:LEU:HD11	1.72	0.55
5:F:298:GLU:O	5:F:301:VAL:CG1	2.54	0.55
1:A:355:VAL:O	1:A:355:VAL:CG2	2.54	0.54
1:A:638:PRO:HG3	6:G:39:LEU:HB3	1.88	0.54
2:B:544:LEU:HD23	2:B:590:ILE:HD11	1.88	0.54
5:F:43:VAL:HG23	8:I:43:ALA:HA	1.88	0.54
5:F:47:ILE:HG23	8:I:39:MET:SD	2.47	0.54
14:R:33:ILE:HB	22:o:431:PHE:CE2	2.41	0.54
23:p:313:GLU:OE2	23:p:316:VAL:N	2.35	0.54
1:A:405:VAL:CG1	5:F:301:VAL:HG13	2.36	0.54
5:F:55:LEU:HD13	8:I:28:ILE:HG23	1.88	0.54
15:S:24:LYS:CA	16:T:99:SER:HA	2.37	0.54
18:V:175:LEU:HD11	18:V:180:LYS:HB2	1.88	0.54
33:X:9:DG:N2	34:Y:9:DC:O2	2.39	0.54
2:B:827:ARG:NE	7:H:211:PHE:CZ	2.75	0.54
4:E:278:ASP:OD2	4:E:649:ARG:NH2	2.41	0.54
12:P:167:ASN:HA	12:P:224:ALA:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:277:ILE:O	16:T:154:LYS:HE3	2.07	0.54
15:S:48:GLU:OE2	16:T:5:GLY:HA3	2.07	0.54
22:o:1124:LEU:O	22:o:1128:ILE:N	2.36	0.54
22:o:1365:ILE:HG23	22:o:1369:LEU:HD12	1.89	0.54
1:A:488:ALA:CB	5:f:271:VAL:CG2	2.59	0.54
2:B:571:LEU:HD21	2:B:619:MET:HE1	1.89	0.54
3:D:914:VAL:CG1	10:L:70:VAL:HG11	2.35	0.54
5:F:71:ILE:HD11	8:I:35:VAL:CA	2.37	0.54
5:F:71:ILE:HD11	8:I:35:VAL:HA	1.86	0.54
17:U:18:ALA:HA	17:U:21:VAL:HG22	1.90	0.54
4:e:646:SER:OG	4:e:647:ALA:N	2.40	0.54
22:o:360:ASP:HB3	23:p:1062:ARG:HE	1.72	0.54
23:p:570:ASN:ND2	23:p:616:THR:OG1	2.39	0.54
23:p:627:ILE:HD11	23:p:663:GLU:HB2	1.88	0.54
23:p:910:THR:OG1	32:z:42:ARG:O	2.24	0.54
33:X:2:DG:H2"	33:X:3:DT:C6	2.43	0.54
35:u:51:ILE:HG22	35:u:72:TYR:HB3	1.90	0.54
1:A:1165:LEU:CG	1:A:1191:ILE:HG23	2.36	0.54
3:D:965:ILE:CG2	3:D:966:LEU:N	2.70	0.54
13:Q:43:LYS:NZ	13:Q:60:HIS:HE1	2.06	0.54
4:e:610:ARG:HD3	4:e:619:PRO:HG3	1.89	0.54
22:o:364:ARG:NH1	22:o:502:ASN:OD1	2.40	0.54
22:o:1118:THR:HG22	22:o:1123:ARG:HB2	1.90	0.54
25:r:33:LEU:HD13	25:r:101:ALA:HB1	1.87	0.54
26:s:189:GLN:O	26:s:209:VAL:HG12	2.07	0.54
1:A:1007:LEU:HD22	1:A:1012:VAL:HG21	1.89	0.54
3:D:958:LYS:HE2	3:D:958:LYS:C	2.31	0.54
5:F:340:ILE:HG23	5:F:344:PHE:HD2	1.71	0.54
3:d:911:GLN:NE2	10:l:69:GLU:OE2	2.40	0.54
7:H:37:LEU:CD1	9:J:138:TYR:CE2	2.87	0.54
7:H:40:VAL:HG21	9:J:130:ILE:HG23	1.88	0.54
7:H:116:ARG:NH1	9:J:126:TYR:CE1	2.76	0.54
16:T:126:ARG:HA	16:T:129:ARG:HB3	1.89	0.54
18:V:203:PHE:O	18:V:203:PHE:CD2	2.60	0.54
34:Y:27:DA:H2'	34:Y:27:DA:OP2	2.08	0.54
35:u:67:LEU:HD12	35:u:67:LEU:O	2.07	0.54
1:A:675:ASP:OD1	6:G:78:LYS:NZ	2.37	0.54
2:B:345:CYS:HA	2:B:348:GLN:HE21	1.73	0.54
2:B:629:ARG:NH1	2:B:658:ASP:OD2	2.37	0.54
3:D:964:GLU:C	3:D:967:MET:SD	2.86	0.54
17:U:137:THR:H	17:U:140:GLU:HG3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:352:GLN:O	5:f:356:THR:OG1	2.25	0.54
23:p:830:GLU:OE2	23:p:870:THR:OG1	2.23	0.54
3:D:1004:ALA:CB	11:O:4:GLN:HB2	2.32	0.54
5:F:433:PRO:HA	5:F:436:ALA:HB3	1.90	0.54
7:H:36:THR:HG21	9:J:134:VAL:CG2	2.37	0.54
14:R:267:GLU:OE1	14:R:269:ARG:NH2	2.41	0.54
15:S:110:PHE:CD1	15:S:148:PRO:HA	2.42	0.54
18:V:103:LEU:HB3	18:V:109:LEU:HA	1.90	0.54
22:o:381:PRO:HB3	22:o:480:SER:HA	1.90	0.54
22:o:1287:CYS:HA	23:p:251:ALA:HB2	1.90	0.54
22:o:1375:ARG:NE	22:o:1403:ASP:OD1	2.40	0.54
22:o:1437:ASP:OD1	22:o:1437:ASP:N	2.41	0.54
23:p:1078:ARG:C	23:p:1080:ARG:N	2.64	0.54
33:X:22:DG:N2	34:Y:-21:DG:C2	2.75	0.54
1:A:564:PRO:HG2	2:B:744:PHE:CZ	2.40	0.54
5:F:313:VAL:HG12	5:F:375:GLY:HA3	1.90	0.54
5:F:342:LYS:HZ1	5:F:352:GLN:NE2	2.06	0.54
14:R:27:TYR:CE2	23:p:841:ARG:NH2	2.76	0.54
17:U:129:CYS:SG	17:U:159:THR:OG1	2.62	0.54
4:e:251:LEU:O	4:e:256:HIS:HB2	2.07	0.54
22:o:1212:LEU:HB2	22:o:1285:LEU:HD21	1.90	0.54
25:r:42:GLU:O	25:r:46:GLN:N	2.40	0.54
25:r:125:GLU:HA	25:r:128:GLN:HB3	1.90	0.54
28:v:8:ASP:OD1	28:v:9:ILE:N	2.39	0.54
4:E:563:GLU:HG2	4:E:587:PRO:HG3	1.90	0.53
5:F:14:LEU:HD23	8:I:18:MET:HB3	1.91	0.53
7:H:118:VAL:CG2	9:J:127:THR:OG1	2.56	0.53
11:O:19:LEU:O	11:O:28:ILE:HD11	2.08	0.53
17:U:203:ILE:HG22	17:U:203:ILE:O	2.08	0.53
22:o:728:THR:OG1	22:o:731:ASN:OD1	2.25	0.53
22:o:1205:ALA:O	22:o:1206:ARG:NE	2.38	0.53
23:p:1136:GLU:HG2	23:p:1143:LYS:HE3	1.89	0.53
25:r:103:LEU:CA	35:u:144:ARG:HH22	2.18	0.53
1:A:472:ASN:HB2	5:f:299:LYS:HD3	1.90	0.53
2:B:66:ASN:HD21	2:B:119:PRO:HB3	1.73	0.53
2:B:628:ILE:O	2:B:644:GLN:NE2	2.41	0.53
7:H:73:GLY:C	9:J:142:ALA:HB1	2.32	0.53
7:H:102:PHE:CZ	9:J:158:ALA:CA	2.91	0.53
12:P:256:GLN:CG	33:X:-26:DC:H5"	2.38	0.53
23:p:242:ARG:HB2	23:p:254:GLN:HE21	1.73	0.53
5:F:55:LEU:HD13	8:I:28:ILE:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:25:GLU:CD	14:R:46:ILE:HD11	2.34	0.53
16:T:173:GLY:O	16:T:175:ARG:N	2.41	0.53
17:U:146:ASP:HB3	17:U:149:THR:HG22	1.90	0.53
23:p:113:ALA:HA	23:p:118:LEU:HB2	1.89	0.53
13:Q:15:ARG:NH2	13:Q:58:GLY:HA3	2.22	0.53
15:S:46:ARG:HB2	15:S:101:ARG:HB2	1.91	0.53
16:T:94:THR:HG22	16:T:109:ILE:HG23	1.90	0.53
18:V:117:GLN:HE21	18:V:121:THR:HG21	1.72	0.53
4:e:368:ASN:ND2	4:e:701:GLY:HA3	2.23	0.53
22:o:101:VAL:O	22:o:104:MET:HG3	2.08	0.53
22:o:535:MET:O	22:o:669:TYR:OH	2.21	0.53
5:F:81:GLU:C	5:F:83:LEU:N	2.63	0.53
15:S:16:VAL:HG23	16:T:43:LEU:N	2.23	0.53
15:S:24:LYS:HE2	16:T:99:SER:OG	2.07	0.53
16:T:149:VAL:HG11	23:p:146:LYS:HD2	1.90	0.53
17:U:16:ARG:HB3	17:U:194:THR:HG21	1.91	0.53
5:f:390:THR:HG23	5:f:391:LEU:HD22	1.90	0.53
22:o:76:GLY:HA2	22:o:80:GLU:HG2	1.90	0.53
35:u:59:ILE:HG12	35:u:66:VAL:HG22	1.90	0.53
1:A:844:LYS:HZ3	33:X:31:DT:C7	2.21	0.53
2:B:835:ARG:HD3	7:H:187:GLU:CD	2.34	0.53
4:E:704:VAL:HA	4:E:759:ILE:HD11	1.90	0.53
14:R:47:ASP:H	22:o:67:ARG:NH2	2.07	0.53
18:V:226:ASP:CB	22:o:220:ARG:HH12	2.18	0.53
19:c:33:LEU:HD13	9:j:197:MET:HE1	1.91	0.53
5:f:318:CYS:SG	5:f:326:HIS:HB3	2.49	0.53
22:o:77:ASN:ND2	22:o:80:GLU:OE2	2.41	0.53
25:r:115:ILE:HD12	25:r:118:LEU:HD12	1.91	0.53
4:E:653:LEU:HB2	4:E:663:ARG:HB2	1.91	0.53
5:F:22:VAL:CG1	8:I:44:PHE:HE1	2.21	0.53
5:F:76:LYS:HG3	5:F:96:PHE:HB3	1.91	0.53
5:F:257:PRO:O	5:F:261:THR:OG1	2.26	0.53
7:H:107:LEU:HD11	9:J:157:LEU:O	2.09	0.53
12:P:167:ASN:OD1	12:P:259:VAL:HB	2.08	0.53
12:P:302:LEU:HD12	12:P:302:LEU:N	2.24	0.53
18:V:160:GLN:OE1	18:V:163:LEU:HD23	2.08	0.53
4:e:423:PRO:HG2	4:e:426:ARG:HB2	1.91	0.53
22:o:1101:GLN:HE22	22:o:1391:SER:HB2	1.73	0.53
22:o:1374:VAL:HG11	22:o:1411:LEU:HD21	1.90	0.53
25:r:103:LEU:HD21	35:u:84:VAL:CG1	2.39	0.53
25:r:110:GLU:O	25:r:114:LEU:N	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:123:GLU:HG2	25:r:126:GLU:HB2	1.90	0.53
1:A:395:ASP:OD1	1:A:395:ASP:N	2.41	0.53
1:A:406:THR:C	5:F:354:ARG:HH22	2.17	0.53
1:A:567:LEU:HD22	2:B:745:GLN:NE2	2.23	0.53
1:A:572:TYR:CE1	2:B:689:GLN:OE1	2.62	0.53
2:B:202:TRP:HB2	2:B:238:LEU:HB3	1.91	0.53
16:T:27:LEU:HD11	16:T:58:LEU:HD21	1.91	0.53
22:o:576:GLN:HA	28:v:75:TYR:HB2	1.91	0.53
22:o:911:PRO:O	22:o:963:ARG:NH2	2.42	0.53
25:r:100:LEU:HA	25:r:103:LEU:HB2	1.89	0.53
25:r:132:ASP:OD1	25:r:135:GLN:NE2	2.41	0.53
9:J:130:ILE:HG13	9:J:160:GLN:HE21	1.74	0.53
11:O:78:ASP:HA	11:O:91:ASP:HA	1.91	0.53
14:R:45:VAL:C	22:o:67:ARG:HH21	2.16	0.53
16:T:192:GLU:HB3	18:V:75:PHE:CD2	2.44	0.53
17:U:102:VAL:HA	17:U:105:TYR:HB3	1.91	0.53
4:e:595:PRO:HD2	4:e:639:SER:HB3	1.91	0.53
22:o:93:PRO:HG2	22:o:219:GLU:HG3	1.90	0.53
35:u:119:PHE:HB2	35:u:128:TYR:CE1	2.44	0.53
1:A:349:TRP:HZ2	5:f:262:PHE:CE1	2.24	0.53
1:A:1014:GLU:CD	22:o:1204:VAL:HB	2.34	0.53
5:F:403:ILE:O	5:F:406:VAL:HG22	2.08	0.53
14:R:27:TYR:CZ	14:R:50:SER:CB	2.92	0.53
14:R:263:GLN:HA	14:R:268:LYS:HG2	1.91	0.53
22:o:631:GLU:HG3	22:o:992:LYS:HE3	1.91	0.53
22:o:1177:TYR:CE1	22:o:1209:PRO:HB2	2.44	0.53
22:o:1343:LEU:HB3	22:o:1364:GLU:OE2	2.09	0.53
32:z:36:CYS:SG	32:z:37:ARG:N	2.82	0.53
11:O:57:ASN:HD22	11:O:57:ASN:N	2.07	0.52
13:Q:26:ARG:NH2	13:Q:39:LEU:HD21	2.24	0.52
1:A:950:VAL:CG2	1:A:1065:GLU:CG	2.87	0.52
5:F:340:ILE:HG23	5:F:344:PHE:CD2	2.44	0.52
5:F:412:LEU:O	5:F:412:LEU:HG	2.09	0.52
9:J:137:TYR:OH	9:J:141:ARG:NH2	2.43	0.52
17:U:141:ALA:O	17:U:145:PHE:N	2.36	0.52
5:f:283:MET:HG3	5:f:329:LEU:HD11	1.91	0.52
22:o:902:GLU:OE2	22:o:982:ASN:HB2	2.08	0.52
5:F:418:ILE:HD12	5:F:418:ILE:N	2.20	0.52
7:H:107:LEU:HD11	9:J:157:LEU:HB3	1.90	0.52
15:S:47:LEU:CB	16:T:7:LEU:HB2	2.39	0.52
17:U:100:VAL:HG12	17:U:102:VAL:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:s:94:MET:HE2	26:s:125:TYR:HD2	1.75	0.52
33:X:11:DT:H2"	33:X:12:DC:C6	2.44	0.52
1:A:828:GLU:HA	1:A:831:LYS:HB2	1.92	0.52
4:E:601:VAL:HG21	4:E:642:VAL:HG11	1.92	0.52
5:F:52:GLN:NE2	8:I:26:MET:O	2.43	0.52
5:F:320:ARG:HB2	5:F:415:ILE:HD12	0.54	0.52
13:Q:26:ARG:NH2	13:Q:39:LEU:HD23	2.23	0.52
17:U:108:ASP:OD2	18:V:234:GLU:CB	2.57	0.52
4:e:607:ARG:NH1	8:i:87:PRO:O	2.43	0.52
22:o:1192:TRP:HA	22:o:1195:VAL:HG22	1.91	0.52
22:o:1345:ARG:HG2	26:s:133:GLN:HE22	1.74	0.52
33:X:12:DC:H2"	33:X:13:DT:C6	2.44	0.52
34:Y:37:DT:H2"	34:Y:38:DC:H5"	1.91	0.52
35:u:119:PHE:HB2	35:u:128:TYR:HE1	1.73	0.52
1:A:564:PRO:CB	2:B:744:PHE:CE2	2.92	0.52
2:B:768:PRO:CG	2:B:771:VAL:CG2	2.70	0.52
3:D:931:ASP:HB3	8:I:130:LYS:HD2	1.92	0.52
4:E:696:TRP:CZ3	4:E:703:MET:SD	3.02	0.52
5:F:368:THR:HG22	5:F:369:PRO:CD	2.36	0.52
6:G:154:LYS:NZ	6:G:154:LYS:CB	2.73	0.52
17:U:127:PHE:HD2	17:U:161:VAL:CG2	2.22	0.52
3:d:943:GLN:NE2	4:e:509:GLN:O	2.41	0.52
1:A:569:ASN:ND2	2:B:689:GLN:HA	2.24	0.52
5:F:276:LEU:HD21	5:F:327:TRP:HB2	1.90	0.52
11:O:89:LYS:H	13:Q:361:ASN:HD21	1.58	0.52
5:f:320:ARG:NH1	5:f:320:ARG:CB	2.73	0.52
22:o:364:ARG:HH22	22:o:461:GLN:CD	2.17	0.52
22:o:364:ARG:HH22	22:o:461:GLN:NE2	2.08	0.52
25:r:114:LEU:HD11	35:u:167:TYR:CE2	2.44	0.52
1:A:844:LYS:NZ	33:X:31:DT:C7	2.73	0.52
3:D:871:THR:HG23	10:L:66:LEU:HD11	1.89	0.52
6:G:181:TRP:CE3	6:G:181:TRP:O	2.63	0.52
13:Q:18:ILE:HG23	13:Q:46:TRP:CZ3	2.44	0.52
14:R:151:LEU:HD11	14:R:201:ALA:HB2	1.90	0.52
15:S:48:GLU:O	15:S:99:LEU:N	2.38	0.52
16:T:141:LEU:O	23:p:90:GLN:NE2	2.42	0.52
17:U:144:LEU:HD21	17:U:155:THR:HG22	1.92	0.52
3:d:963:ARG:NH2	3:d:964:GLU:OE2	2.42	0.52
5:f:215:GLU:H	5:f:215:GLU:CD	2.17	0.52
22:o:365:THR:OG1	22:o:366:VAL:N	2.40	0.52
26:s:26:TYR:HD1	26:s:64:HIS:HA	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:LEU:HD13	1:A:643:ILE:HG13	1.91	0.52
1:A:1163:ARG:HB3	6:G:183:ILE:HG22	1.91	0.52
2:B:328:ASN:HA	7:H:227:LEU:HD11	1.90	0.52
3:D:960:GLU:O	3:D:963:ARG:CD	2.57	0.52
11:O:17:GLU:HB3	13:Q:49:LYS:NZ	2.18	0.52
12:P:259:VAL:HG11	34:Y:29:DT:C2	2.45	0.52
14:R:154:ARG:CZ	34:Y:22:DG:H5''	2.36	0.52
14:R:225:PRO:HG2	14:R:228:VAL:HG23	1.90	0.52
17:U:20:TYR:CB	17:U:191:LEU:HB3	2.40	0.52
17:U:102:VAL:HG23	17:U:102:VAL:O	2.10	0.52
18:V:103:LEU:HD12	18:V:116:LYS:HE3	1.92	0.52
22:o:1155:LYS:HA	22:o:1309:MET:HE1	1.92	0.52
22:o:1229:GLU:OE1	22:o:1229:GLU:N	2.38	0.52
22:o:1288:ILE:O	22:o:1292:MET:HG2	2.10	0.52
29:w:96:PHE:HD2	29:w:110:LEU:HD11	1.75	0.52
33:X:-5:DC:H2''	33:X:-4:DT:C6	2.45	0.52
2:B:66:ASN:OD1	2:B:187:ARG:NH1	2.43	0.52
2:B:152:LEU:HD23	2:B:155:PRO:HB3	1.91	0.52
2:B:827:ARG:CG	7:H:211:PHE:HZ	2.23	0.52
2:B:937:THR:HG23	2:B:939:ASN:H	1.74	0.52
3:D:967:MET:SD	3:D:968:ARG:N	2.82	0.52
4:E:304:LYS:NZ	4:E:335:GLU:O	2.42	0.52
4:E:690:ASP:OD1	4:E:690:ASP:N	2.43	0.52
5:F:51:ALA:HB1	8:I:28:ILE:HD12	1.91	0.52
11:O:88:ILE:CB	13:Q:360:LEU:HB2	2.39	0.52
17:U:48:MET:HG2	17:U:52:LEU:HD12	1.90	0.52
17:U:102:VAL:CA	17:U:105:TYR:HB3	2.40	0.52
17:U:137:THR:H	17:U:140:GLU:CG	2.23	0.52
17:U:179:ARG:O	17:U:183:GLN:CG	2.58	0.52
22:o:34:MET:HA	23:p:1138:ARG:HB3	1.92	0.52
22:o:282:ASP:OD1	22:o:283:ILE:N	2.43	0.52
25:r:103:LEU:CA	35:u:144:ARG:CZ	2.63	0.52
33:X:-28:DC:OP2	33:X:-28:DC:H2'	2.10	0.52
2:B:735:ILE:HG23	7:H:176:ARG:CZ	2.38	0.52
5:F:290:MET:SD	5:F:340:ILE:HG22	2.46	0.52
5:F:324:ASP:OD2	5:F:422:HIS:CD2	2.63	0.52
14:R:27:TYR:CE1	14:R:48:VAL:CG1	2.93	0.52
18:V:218:LYS:O	18:V:222:SER:OG	2.28	0.52
4:e:747:LEU:HG	4:e:747:LEU:O	2.09	0.52
5:f:447:ALA:O	5:f:453:GLY:HA2	2.09	0.52
34:Y:-6:DC:H2''	34:Y:-5:DT:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:90:THR:O	2:B:968:ARG:NH2	2.43	0.51
5:F:118:ILE:HA	7:H:39:VAL:HG13	1.91	0.51
18:V:210:PHE:N	18:V:210:PHE:CD1	2.78	0.51
22:o:1313:GLN:HA	22:o:1332:GLN:HE21	1.74	0.51
33:X:15:DG:H2''	33:X:16:DT:C6	2.45	0.51
34:Y:5:DG:H2''	34:Y:6:DT:C6	2.44	0.51
35:u:54:ILE:HG13	35:u:70:VAL:HG23	1.93	0.51
2:B:159:LEU:HD23	2:B:159:LEU:N	2.25	0.51
2:B:983:ARG:NH1	2:B:983:ARG:HG3	2.25	0.51
4:E:423:PRO:HG2	4:E:426:ARG:HB2	1.92	0.51
4:E:562:SER:OG	4:E:564:ASP:OD1	2.28	0.51
5:F:273:GLN:H	5:F:273:GLN:CD	2.17	0.51
13:Q:15:ARG:NH2	13:Q:58:GLY:CA	2.74	0.51
15:S:125:TYR:CZ	16:T:31:TRP:HE3	2.27	0.51
18:V:176:PRO:C	18:V:178:SER:N	2.68	0.51
22:o:734:ARG:NH1	29:w:107:ALA:O	2.39	0.51
26:s:64:HIS:HD2	26:s:66:ASP:H	1.58	0.51
1:A:1014:GLU:CG	22:o:1204:VAL:CG1	2.65	0.51
4:E:754:THR:OG1	4:E:755:ALA:N	2.43	0.51
11:O:17:GLU:C	13:Q:49:LYS:HZ1	2.18	0.51
11:O:88:ILE:HG21	13:Q:360:LEU:C	2.35	0.51
13:Q:353:LEU:HB2	13:Q:370:ALA:HB3	1.90	0.51
16:T:147:LYS:CG	16:T:148:VAL:N	2.66	0.51
17:U:61:SER:OG	22:o:301:HIS:HE1	1.93	0.51
23:p:134:LYS:O	23:p:135:GLU:HG3	2.10	0.51
25:r:125:GLU:O	25:r:129:GLN:N	2.39	0.51
4:E:747:LEU:HD22	4:E:747:LEU:N	2.20	0.51
9:J:128:PRO:HB2	9:J:160:GLN:HE22	1.75	0.51
9:J:139:LEU:HB3	9:J:144:PHE:HB3	1.92	0.51
10:L:106:ARG:CD	10:L:114:LYS:HZ3	2.24	0.51
16:T:216:ILE:O	16:T:220:ILE:HG13	2.10	0.51
18:V:77:VAL:O	18:V:81:ILE:HG13	2.09	0.51
18:V:81:ILE:HG23	18:V:102:ILE:HG21	1.92	0.51
22:o:304:ALA:O	22:o:307:VAL:HG12	2.10	0.51
23:p:888:THR:HG23	23:p:889:LYS:H	1.76	0.51
26:s:46:ASP:OD1	26:s:52:ARG:NH2	2.44	0.51
33:X:-13:DA:H3'	33:X:-13:DA:P	2.49	0.51
1:A:472:ASN:HD22	5:f:299:LYS:HA	1.75	0.51
2:B:808:PRO:HA	2:B:864:ASN:HB3	1.90	0.51
3:D:897:ASP:OD2	10:L:130:GLY:O	2.29	0.51
5:F:55:LEU:CD1	8:I:28:ILE:HG23	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:17:GLU:HB3	13:Q:49:LYS:HZ3	1.66	0.51
33:X:-11:DT:H2'	33:X:-11:DT:OP2	2.10	0.51
1:A:468:PHE:HE1	5:F:224:TYR:CZ	2.26	0.51
2:B:276:LEU:HD11	7:H:228:LEU:HD21	1.92	0.51
5:F:114:LEU:H	7:H:52:SER:HA	1.76	0.51
5:F:320:ARG:CD	5:F:415:ILE:HG13	2.38	0.51
11:O:5:LEU:HD23	11:O:6:TYR:CZ	2.45	0.51
11:O:88:ILE:CD1	13:Q:360:LEU:HD12	2.21	0.51
16:T:30:GLN:NE2	16:T:62:LEU:O	2.27	0.51
16:T:126:ARG:O	16:T:126:ARG:HD3	2.11	0.51
16:T:180:LYS:NZ	16:T:180:LYS:CB	2.73	0.51
16:T:230:LYS:O	16:T:231:ASN:C	2.53	0.51
4:e:500:THR:HG22	4:e:502:LYS:H	1.76	0.51
35:u:44:PHE:HD2	35:u:46:ILE:HG13	1.62	0.51
2:B:847:ARG:HG3	2:B:885:ASP:OD2	2.11	0.51
4:E:324:LYS:HG2	4:E:327:ASN:HD22	1.74	0.51
4:E:324:LYS:O	4:E:327:ASN:ND2	2.44	0.51
5:F:71:ILE:CD1	8:I:35:VAL:CA	2.83	0.51
14:R:50:SER:HA	23:p:841:ARG:HH21	1.72	0.51
14:R:146:TYR:O	14:R:149:LYS:HG2	2.10	0.51
14:R:231:ALA:HA	14:R:301:PRO:HG3	1.93	0.51
4:e:269:GLY:O	8:i:97:ARG:NH2	2.43	0.51
22:o:66:GLU:HG2	22:o:69:GLY:H	1.76	0.51
22:o:400:ASP:N	22:o:400:ASP:OD1	2.41	0.51
23:p:892:CYS:SG	23:p:893:SER:N	2.82	0.51
23:p:933:ASP:OD2	23:p:1050:ARG:NH2	2.41	0.51
1:A:468:PHE:CD2	5:F:221:GLN:HG3	2.44	0.51
2:B:529:VAL:HG11	2:B:560:TYR:HB2	1.91	0.51
13:Q:18:ILE:O	13:Q:22:ILE:HG12	2.10	0.51
17:U:124:ARG:HH12	17:U:170:LYS:HZ2	1.58	0.51
17:U:127:PHE:CE2	17:U:152:PHE:CD2	2.99	0.51
5:f:24:GLU:HG2	10:l:145:THR:HG21	1.93	0.51
22:o:220:ARG:O	22:o:224:ILE:HG13	2.10	0.51
26:s:55:ARG:HH22	26:s:107:GLN:HG3	1.74	0.51
33:X:-43:DA:H2''	33:X:-42:DG:C8	2.45	0.51
34:Y:38:DC:H2''	34:Y:39:DA:H5'	1.93	0.51
1:A:468:PHE:CE2	5:F:221:GLN:CG	2.89	0.51
1:A:564:PRO:HB2	2:B:744:PHE:HE2	1.76	0.51
2:B:877:TYR:CE2	7:H:216:ALA:CB	2.93	0.51
6:G:181:TRP:CD2	6:G:181:TRP:C	2.87	0.51
8:I:132:LEU:CD2	9:J:121:MET:CE	2.89	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:88:ILE:CG1	13:Q:360:LEU:HB2	2.37	0.51
15:S:24:LYS:CD	16:T:97:THR:HB	2.37	0.51
28:v:65:TYR:O	28:v:66:GLU:HG2	2.11	0.51
32:z:16:ILE:HD11	32:z:25:GLU:HB3	1.93	0.51
33:X:22:DG:C2	34:Y:-21:DG:N1	2.79	0.51
1:A:640:LEU:CD2	6:G:35:GLY:HA3	2.40	0.51
3:D:898:VAL:HG22	10:L:113:VAL:CG2	2.33	0.51
4:E:501:PRO:HD3	7:H:149:HIS:CB	2.40	0.51
19:c:1:MET:HG3	5:f:126:PRO:HB3	1.93	0.51
19:c:21:LEU:HD12	19:c:21:LEU:O	2.11	0.51
19:c:77:LEU:HD23	19:c:77:LEU:O	2.11	0.51
21:m:69:THR:HG23	21:m:80:ARG:HE	1.76	0.51
22:o:104:MET:HA	22:o:107:LEU:HG	1.93	0.51
23:p:311:ILE:HG13	23:p:316:VAL:HG13	1.93	0.51
25:r:103:LEU:CG	35:u:144:ARG:HH12	2.18	0.51
2:B:656:GLU:HG2	2:B:661:ALA:HB3	1.93	0.50
13:Q:29:PHE:CD2	13:Q:34:VAL:HG11	2.40	0.50
14:R:218:PHE:HD1	14:R:277:ILE:HG22	1.74	0.50
3:d:1080:TYR:OH	4:e:606:ASP:OD2	2.26	0.50
2:B:274:LEU:HG	2:B:278:LYS:HE2	1.93	0.50
5:F:42:GLU:OE2	8:I:46:TYR:HE2	1.94	0.50
14:R:27:TYR:CG	23:p:841:ARG:NH2	2.69	0.50
21:m:28:ARG:HH21	21:m:31:LEU:HD21	1.75	0.50
35:u:86:ASP:OD2	35:u:171:VAL:CG2	2.55	0.50
35:u:86:ASP:OD1	35:u:143:ILE:O	2.28	0.50
1:A:1185:VAL:HG12	1:A:1191:ILE:HG13	1.93	0.50
2:B:983:ARG:HG3	2:B:983:ARG:HH11	1.75	0.50
5:F:290:MET:CE	5:F:337:VAL:HB	2.41	0.50
7:H:110:TYR:HD2	9:J:157:LEU:HD22	1.75	0.50
7:H:116:ARG:NH1	9:J:126:TYR:CD1	2.79	0.50
12:P:312:LEU:HD13	12:P:321:ILE:HG23	1.94	0.50
14:R:17:ASN:OD1	14:R:18:HIS:ND1	2.39	0.50
22:o:64:VAL:HG22	22:o:71:CYS:HB2	1.93	0.50
22:o:1242:ASP:O	22:o:1262:MET:N	2.41	0.50
23:p:341:GLU:O	23:p:345:LYS:N	2.41	0.50
23:p:647:GLU:H	23:p:647:GLU:CD	2.20	0.50
1:A:406:THR:HG22	5:F:350:ASN:HD22	1.76	0.50
1:A:927:VAL:O	1:A:933:ASN:ND2	2.44	0.50
7:H:110:TYR:CE2	9:J:160:GLN:CB	2.95	0.50
14:R:47:ASP:N	22:o:67:ARG:NH2	2.59	0.50
16:T:16:THR:HB	16:T:108:GLY:HA2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:o:546:ARG:HD3	22:o:772:SER:HB3	1.93	0.50
23:p:230:ARG:HB2	23:p:231:PRO:HD3	1.92	0.50
25:r:105:PRO:HG2	25:r:131:LEU:HD11	1.92	0.50
28:v:14:ASP:OD1	28:v:15:ILE:N	2.43	0.50
33:X:-42:DG:OP2	33:X:-42:DG:H2'	2.10	0.50
35:u:44:PHE:HD2	35:u:46:ILE:CG1	2.19	0.50
5:F:243:LEU:HD21	5:F:284:ARG:HB3	1.92	0.50
14:R:214:PHE:HB3	14:R:218:PHE:HE2	1.75	0.50
17:U:144:LEU:O	17:U:145:PHE:C	2.55	0.50
1:A:510:ILE:HB	1:A:511:LEU:HD13	1.92	0.50
3:D:1009:LEU:CD1	3:D:1009:LEU:N	2.73	0.50
5:F:71:ILE:HB	8:I:38:GLN:HE22	1.59	0.50
5:F:273:GLN:CD	5:F:273:GLN:N	2.70	0.50
12:P:195:LYS:HA	16:T:174:LYS:O	2.11	0.50
16:T:17:GLY:HA2	16:T:109:ILE:O	2.10	0.50
25:r:129:GLN:O	25:r:133:ASP:N	2.38	0.50
2:B:739:ASN:ND2	2:B:782:ASN:OD1	2.44	0.50
3:D:901:TYR:HE1	10:L:128:ILE:CB	2.17	0.50
12:P:271:GLU:OE1	14:R:208:LEU:CD1	2.58	0.50
16:T:184:LEU:HD21	18:V:80:LYS:HD2	1.93	0.50
23:p:132:VAL:HG22	23:p:140:LEU:HB3	1.93	0.50
25:r:36:GLU:HG3	25:r:39:MET:HE2	1.92	0.50
1:A:567:LEU:HD22	2:B:745:GLN:HE21	1.76	0.50
3:D:946:PHE:CD1	3:D:946:PHE:C	2.90	0.50
4:E:693:VAL:HB	4:E:707:LEU:HB2	1.94	0.50
5:F:71:ILE:CB	8:I:38:GLN:NE2	2.32	0.50
5:F:211:ARG:O	7:H:165:TYR:CE2	2.65	0.50
5:F:213:ILE:CA	7:H:164:THR:O	2.51	0.50
17:U:32:LEU:HD13	18:V:161:ARG:HH22	1.73	0.50
17:U:34:LEU:HD23	17:U:37:LEU:HD12	1.92	0.50
17:U:122:THR:C	17:U:124:ARG:N	2.70	0.50
2:B:598:ARG:HH11	2:B:619:MET:HE3	1.77	0.50
2:B:844:PRO:HB2	7:H:225:THR:O	2.12	0.50
5:F:367:LYS:O	5:F:367:LYS:HG2	2.12	0.50
14:R:27:TYR:CE1	14:R:48:VAL:HG11	2.46	0.50
14:R:169:ARG:HD3	14:R:207:ASP:H	1.77	0.50
15:S:121:ASN:C	16:T:25:LYS:HG3	2.36	0.50
16:T:177:ARG:N	16:T:177:ARG:CD	2.73	0.50
18:V:73:TYR:CD2	18:V:74:LYS:HG2	2.47	0.50
23:p:851:ASP:H	32:z:15:MET:HE1	1.77	0.50
2:B:217:ASN:ND2	2:B:320:ALA:O	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:481:ASP:HB3	4:E:787:ARG:HH22	1.77	0.49
5:F:47:ILE:HG23	8:I:19:MET:SD	2.37	0.49
7:H:50:PHE:CE1	9:J:195:LEU:HB2	2.47	0.49
12:P:167:ASN:HB3	34:Y:28:DG:H1'	1.93	0.49
17:U:152:PHE:O	17:U:160:GLU:CD	2.54	0.49
4:e:586:TYR:HB3	4:e:605:HIS:HB3	1.94	0.49
4:e:650:THR:HG22	4:e:666:THR:HG22	1.93	0.49
23:p:1119:CYS:SG	23:p:1120:ASN:N	2.85	0.49
5:F:52:GLN:NE2	8:I:26:MET:HB3	2.15	0.49
5:F:124:ARG:HA	7:H:123:PRO:O	2.12	0.49
5:F:342:LYS:HE2	5:F:383:LEU:O	2.12	0.49
14:R:27:TYR:CB	23:p:841:ARG:CZ	2.64	0.49
22:o:1318:LYS:HD3	22:o:1330:ALA:HB1	1.94	0.49
25:r:26:PHE:HE2	35:u:80:PHE:CZ	2.27	0.49
2:B:847:ARG:HB3	2:B:849:THR:HG23	1.94	0.49
3:D:898:VAL:HG23	10:L:113:VAL:HB	1.94	0.49
5:F:51:ALA:C	8:I:28:ILE:HD11	2.37	0.49
9:J:126:TYR:HE2	9:J:157:LEU:HD11	1.77	0.49
17:U:13:ALA:HA	17:U:16:ARG:HB2	1.95	0.49
17:U:145:PHE:C	17:U:145:PHE:CD1	2.89	0.49
4:e:234:ALA:HB2	4:e:648:ASP:HB2	1.94	0.49
22:o:141:LEU:HB2	22:o:236:LEU:O	2.11	0.49
22:o:340:LYS:HG2	22:o:1436:VAL:HG11	1.93	0.49
23:p:497:LYS:HG3	23:p:498:PRO:HD3	1.95	0.49
23:p:1144:THR:HG21	35:u:41:LYS:HB2	1.93	0.49
24:q:190:ASN:O	24:q:193:ARG:NH1	2.42	0.49
2:B:328:ASN:HA	7:H:227:LEU:HD13	1.94	0.49
4:E:466:PHE:HB2	4:E:796:ALA:HA	1.94	0.49
11:O:59:ARG:O	11:O:59:ARG:HG2	2.12	0.49
14:R:130:LEU:HD13	14:R:134:ILE:HD12	1.95	0.49
14:R:295:ARG:NH2	14:R:298:ASP:OD2	2.46	0.49
15:S:26:TYR:HD1	16:T:97:THR:HG22	1.75	0.49
16:T:18:VAL:HG23	16:T:110:VAL:HG22	1.94	0.49
16:T:228:ILE:O	16:T:229:HIS:C	2.56	0.49
22:o:860:ILE:HD12	22:o:1124:LEU:HD23	1.93	0.49
22:o:1391:SER:OG	22:o:1392:TYR:N	2.46	0.49
33:X:-11:DT:OP2	33:X:-11:DT:H6	1.95	0.49
5:F:215:GLU:O	5:F:254:GLN:NE2	2.39	0.49
5:F:320:ARG:CD	5:F:415:ILE:CB	2.31	0.49
12:P:207:PRO:HD2	12:P:207:PRO:O	2.11	0.49
16:T:184:LEU:HG	16:T:188:PHE:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:137:THR:N	17:U:140:GLU:HB2	2.27	0.49
22:o:795:GLY:HA3	22:o:1107:PHE:HD2	1.78	0.49
22:o:1417:HIS:HA	22:o:1420:ASN:HB2	1.93	0.49
24:q:189:ASP:O	24:q:191:ALA:N	2.41	0.49
26:s:103:LEU:HG	26:s:128:GLU:HB2	1.95	0.49
1:A:1168:TYR:HB2	6:G:180:ARG:HB3	1.95	0.49
8:I:56:ILE:HG21	10:L:122:ARG:NH2	2.27	0.49
12:P:192:TYR:O	12:P:192:TYR:CG	2.65	0.49
13:Q:47:GLU:OE2	13:Q:60:HIS:CD2	2.65	0.49
14:R:27:TYR:CD2	23:p:841:ARG:NH2	2.78	0.49
22:o:1347:LEU:HB3	26:s:137:ILE:HD13	1.94	0.49
29:w:68:ILE:HG13	29:w:122:ARG:HD2	1.95	0.49
1:A:1185:VAL:HG11	1:A:1191:ILE:CG1	2.32	0.49
3:D:891:ILE:CG2	10:L:111:LEU:CD2	2.82	0.49
11:O:57:ASN:HD22	11:O:57:ASN:H	1.59	0.49
18:V:212:VAL:HB	18:V:215:GLU:CB	2.41	0.49
1:A:998:LEU:HB2	1:A:1003:ALA:HB2	1.94	0.49
3:D:932:ASP:O	3:D:933:ARG:C	2.56	0.49
7:H:43:SER:CB	7:H:119:ILE:HD11	2.43	0.49
11:O:58:PHE:HB3	11:O:81:PHE:HE2	1.77	0.49
13:Q:348:LYS:HZ2	13:Q:375:GLU:CD	2.20	0.49
22:o:132:LYS:HD2	22:o:133:SER:HB3	1.93	0.49
22:o:753:GLY:O	22:o:757:GLN:HG2	2.13	0.49
23:p:359:THR:HG21	23:p:554:GLU:HG3	1.94	0.49
26:s:188:GLY:N	26:s:210:GLN:OE1	2.45	0.49
4:E:634:ARG:HG3	4:E:675:LEU:HB2	1.95	0.49
5:F:214:HIS:H	7:H:164:THR:CG2	2.20	0.49
7:H:32:ALA:O	7:H:36:THR:OG1	2.29	0.49
12:P:297:LYS:HB3	12:P:298:PRO:HD3	1.94	0.49
13:Q:43:LYS:HE2	13:Q:47:GLU:OE2	2.13	0.49
4:e:693:VAL:HB	4:e:707:LEU:HB2	1.94	0.49
4:e:724:GLU:OE1	4:e:789:ASN:ND2	2.46	0.49
5:F:286:VAL:CG1	5:F:337:VAL:HG21	2.37	0.49
6:G:48:HIS:HD2	6:G:54:GLY:HA2	1.78	0.49
11:O:15:LEU:HD21	11:O:40:PHE:CG	2.48	0.49
12:P:269:ARG:HG3	12:P:337:LYS:HE2	1.94	0.49
15:S:24:LYS:CD	16:T:97:THR:CB	2.86	0.49
4:e:720:SER:OG	4:e:721:ARG:N	2.46	0.49
22:o:111:CYS:SG	22:o:114:CYS:HB3	2.53	0.49
5:F:283:MET:HE1	5:F:308:VAL:CA	2.37	0.48
14:R:44:ARG:HB3	23:p:1067:ILE:CD1	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:S:20:LYS:HE3	16:T:34:ALA:HB3	1.94	0.48
16:T:18:VAL:O	16:T:110:VAL:HA	2.12	0.48
20:k:191:VAL:HG13	20:k:200:ILE:CD1	2.41	0.48
22:o:812:LYS:HG3	29:w:77:THR:O	2.12	0.48
23:p:513:GLU:CD	23:p:525:ASN:HD22	2.20	0.48
23:p:1137:CYS:HB3	23:p:1142:ASN:HB3	1.95	0.48
24:q:183:ALA:HB3	24:q:232:ASN:HB3	1.95	0.48
25:r:64:THR:OG1	35:u:103:PRO:HD3	2.13	0.48
33:X:-10:DA:H2''	33:X:-9:DG:C8	2.48	0.48
1:A:840:SER:HA	1:A:843:ARG:HE	1.77	0.48
4:E:651:VAL:HB	4:E:665:PHE:HB2	1.94	0.48
7:H:135:THR:HG22	7:H:135:THR:O	2.12	0.48
12:P:167:ASN:HD21	12:P:259:VAL:H	1.61	0.48
13:Q:18:ILE:HG12	13:Q:46:TRP:CZ2	2.48	0.48
18:V:194:ARG:HB3	18:V:195:PRO:HD3	1.94	0.48
22:o:551:ARG:NH2	22:o:625:ASP:OD1	2.46	0.48
22:o:795:GLY:HA2	22:o:1108:HIS:NE2	2.28	0.48
1:A:968:ILE:HG13	1:A:969:PRO:HD2	1.95	0.48
11:O:39:GLN:HG2	13:Q:25:VAL:CG1	2.29	0.48
14:R:27:TYR:CD1	14:R:48:VAL:CG1	2.96	0.48
14:R:27:TYR:OH	14:R:50:SER:CB	2.61	0.48
14:R:222:LEU:HD22	14:R:269:ARG:HG3	1.94	0.48
22:o:766:PHE:HB3	22:o:781:ILE:HD12	1.95	0.48
24:q:77:ASP:OD1	24:q:77:ASP:N	2.46	0.48
28:v:32:SER:HB3	28:v:37:MET:H	1.78	0.48
30:x:3:ILE:HD12	30:x:4:PRO:HD2	1.95	0.48
1:A:997:ARG:H	1:A:997:ARG:HG2	1.43	0.48
2:B:329:LEU:HB3	2:B:342:THR:HG23	1.96	0.48
5:F:342:LYS:HD2	5:F:383:LEU:HD22	1.95	0.48
8:I:132:LEU:CD2	9:J:121:MET:HE1	2.41	0.48
17:U:187:ILE:HD13	18:V:210:PHE:HB3	1.96	0.48
5:f:97:ALA:HB2	5:f:106:PHE:HE1	1.77	0.48
22:o:1296:MET:CG	22:o:1298:LEU:HG	2.43	0.48
23:p:845:TYR:CD1	23:p:865:VAL:HG11	2.48	0.48
26:s:56:THR:O	26:s:57:ASP:HB3	2.13	0.48
28:v:64:LEU:HB3	28:v:84:ARG:HB2	1.96	0.48
1:A:481:GLU:HA	1:A:484:ILE:HG13	1.96	0.48
1:A:575:PRO:HD3	2:B:608:ASN:HB2	1.95	0.48
2:B:636:VAL:HG23	2:B:638:ARG:HB3	1.96	0.48
3:D:1005:ASN:C	3:D:1009:LEU:HD13	2.30	0.48
5:F:39:LEU:HD11	8:I:51:LEU:HD11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:214:HIS:CB	7:H:164:THR:CG2	2.92	0.48
6:G:94:MET:HE3	6:G:96:VAL:HG22	1.94	0.48
12:P:199:ALA:HB2	12:P:214:PHE:CD2	2.48	0.48
12:P:259:VAL:HG21	34:Y:28:DG:C2	2.48	0.48
13:Q:358:MET:HE2	13:Q:367:PHE:CD2	2.45	0.48
15:S:24:LYS:HA	16:T:99:SER:HA	1.96	0.48
18:V:220:TRP:O	18:V:220:TRP:CG	2.66	0.48
4:e:651:VAL:HG13	4:e:665:PHE:HB2	1.95	0.48
20:k:173:CYS:SG	20:k:179:MET:O	2.72	0.48
22:o:278:HIS:CD2	22:o:330:GLN:HE21	2.32	0.48
22:o:1202:PHE:HZ	22:o:1262:MET:HG3	1.78	0.48
26:s:102:ALA:HB3	26:s:127:LEU:HG	1.95	0.48
26:s:120:ASP:OD1	26:s:120:ASP:N	2.44	0.48
33:X:-21:DA:H2"	33:X:-20:DG:C8	2.49	0.48
1:A:953:VAL:O	6:G:149:ARG:NH2	2.47	0.48
3:D:964:GLU:HA	3:D:967:MET:HB3	1.95	0.48
3:D:1006:LEU:CD1	11:O:68:CYS:O	2.61	0.48
15:S:29:MET:HB3	16:T:94:THR:OG1	2.14	0.48
22:o:1312:PRO:HG3	22:o:1317:LYS:HB2	1.96	0.48
25:r:22:PHE:HD1	35:u:80:PHE:CE2	2.32	0.48
26:s:18:MET:HE2	26:s:32:GLU:HG2	1.95	0.48
26:s:64:HIS:CD2	26:s:66:ASP:H	2.31	0.48
29:w:27:LYS:HD2	29:w:38:ALA:HB2	1.95	0.48
1:A:468:PHE:HE2	5:F:221:GLN:CG	2.19	0.48
5:F:317:LEU:N	5:F:317:LEU:HD23	2.29	0.48
7:H:40:VAL:CG1	9:J:130:ILE:HG12	2.43	0.48
8:I:63:LYS:NZ	8:I:69:ASP:OD1	2.47	0.48
13:Q:56:VAL:CG1	13:Q:57:ASP:N	2.76	0.48
14:R:27:TYR:CD1	14:R:48:VAL:HG11	2.47	0.48
16:T:188:PHE:O	16:T:189:SER:C	2.57	0.48
18:V:78:LEU:HD13	18:V:123:ALA:HB1	1.95	0.48
18:V:164:GLY:HA2	18:V:201:LEU:HG	1.96	0.48
22:o:267:GLN:HB3	23:p:890:ARG:HH22	1.79	0.48
22:o:946:ALA:O	22:o:950:ASN:ND2	2.47	0.48
22:o:1028:PRO:C	22:o:1030:SER:H	2.21	0.48
24:q:9:VAL:HG11	31:y:105:PHE:CD1	2.48	0.48
24:q:197:TYR:HD2	24:q:217:GLN:HE21	1.62	0.48
35:u:97:LEU:HD13	35:u:128:TYR:CD2	2.49	0.48
2:B:27:LYS:HE3	2:B:490:SER:HB3	1.95	0.48
3:D:901:TYR:CZ	10:L:128:ILE:HB	2.44	0.48
5:F:320:ARG:NE	5:F:321:PRO:HD3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:S:49:ARG:HB3	15:S:96:GLN:HB3	1.95	0.48
17:U:32:LEU:HB3	18:V:161:ARG:CZ	2.43	0.48
19:c:119:GLU:HG3	4:e:790:LEU:HD11	1.96	0.48
22:o:565:MET:HE1	31:y:74:ARG:HB2	1.96	0.48
25:r:104:CYS:O	35:u:167:TYR:OH	2.29	0.48
25:r:128:GLN:HA	25:r:131:LEU:HB2	1.95	0.48
1:A:349:TRP:CE2	5:f:262:PHE:CE1	3.01	0.48
1:A:950:VAL:CG2	1:A:1065:GLU:HG3	2.42	0.48
2:B:953:LEU:HD12	2:B:979:PHE:HE2	1.79	0.48
3:D:933:ARG:HB2	8:I:132:LEU:HD22	1.94	0.48
3:D:943:GLN:HG3	4:E:510:ALA:O	2.13	0.48
3:D:962:GLU:HG2	3:D:963:ARG:N	2.25	0.48
11:O:7:ARG:NH1	11:O:37:LEU:HD13	2.27	0.48
16:T:147:LYS:O	23:p:94:SER:HB2	2.14	0.48
16:T:210:VAL:O	16:T:214:LYS:N	2.36	0.48
17:U:124:ARG:HH12	17:U:170:LYS:HD3	1.77	0.48
18:V:181:ALA:O	18:V:184:ALA:C	2.50	0.48
5:f:39:LEU:HD22	8:i:47:VAL:HG13	1.94	0.48
22:o:59:ASP:HB3	22:o:62:GLN:HB2	1.95	0.48
22:o:278:HIS:HD2	22:o:330:GLN:HE21	1.61	0.48
34:Y:-11:DA:H2"	34:Y:-10:DG:C8	2.49	0.48
1:A:1014:GLU:O	1:A:1018:LYS:HB2	2.13	0.48
1:A:1187:LYS:HZ2	6:G:165:GLU:CD	2.21	0.48
4:E:696:TRP:CH2	4:E:703:MET:SD	3.06	0.48
11:O:20:ASP:HA	11:O:23:ILE:HD12	1.95	0.48
17:U:32:LEU:CG	18:V:161:ARG:NH2	2.75	0.48
4:e:556:ASN:HA	4:e:572:LEU:HB2	1.96	0.48
23:p:856:PRO:HG2	32:z:48:ARG:HA	1.96	0.48
33:X:-22:DC:N3	34:Y:22:DG:N2	2.59	0.48
2:B:135:TRP:HA	2:B:138:VAL:HG12	1.95	0.47
5:F:43:VAL:CG2	8:I:43:ALA:HA	2.44	0.47
5:F:58:MET:HG3	5:F:66:LEU:H	1.79	0.47
5:F:370:TRP:CH2	5:F:402:ARG:HB3	2.49	0.47
12:P:299:ARG:C	12:P:300:ILE:HG12	2.39	0.47
13:Q:359:ASN:HA	13:Q:363:ARG:O	2.14	0.47
4:e:474:THR:OG1	4:e:546:VAL:O	2.28	0.47
4:e:589:TRP:HB3	5:f:60:MET:HE3	1.96	0.47
5:f:254:GLN:O	5:f:258:ARG:NH2	2.47	0.47
22:o:408:ARG:HH21	22:o:412:GLN:HB3	1.79	0.47
22:o:1192:TRP:CZ2	22:o:1258:ARG:HD3	2.49	0.47
22:o:1206:ARG:O	22:o:1263:ASN:ND2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:s:61:LEU:HD12	26:s:73:PHE:HD2	1.79	0.47
2:B:570:GLU:HA	2:B:625:LEU:HA	1.95	0.47
5:F:315:ARG:CZ	5:F:369:PRO:HB3	2.44	0.47
5:F:319:LEU:N	5:F:319:LEU:CD2	2.73	0.47
13:Q:17:VAL:O	13:Q:21:VAL:HG23	2.14	0.47
16:T:186:MET:O	16:T:189:SER:HB2	2.14	0.47
17:U:127:PHE:CZ	17:U:152:PHE:CE2	3.01	0.47
17:U:152:PHE:HB2	17:U:161:VAL:CG2	2.44	0.47
18:V:181:ALA:O	18:V:184:ALA:HB3	2.14	0.47
18:V:188:GLN:H	18:V:188:GLN:HG2	1.42	0.47
23:p:380:ARG:HG2	23:p:608:ARG:HH22	1.78	0.47
26:s:107:GLN:HG2	26:s:108:GLN:OE1	2.14	0.47
27:t:88:ASP:HB3	27:t:91:LEU:HB2	1.96	0.47
2:B:848:HIS:CG	2:B:886:ILE:HD11	2.48	0.47
5:F:317:LEU:N	5:F:317:LEU:CD2	2.77	0.47
14:R:27:TYR:OH	14:R:50:SER:HB2	2.14	0.47
15:S:124:TYR:HD1	16:T:22:LYS:HA	1.77	0.47
17:U:102:VAL:CB	17:U:105:TYR:HB3	2.41	0.47
5:f:102:ARG:HD3	10:l:151:ARG:HG3	1.96	0.47
5:f:257:PRO:O	5:f:261:THR:OG1	2.32	0.47
22:o:1030:SER:HB2	26:s:162:ARG:NE	2.28	0.47
23:p:773:PRO:HG3	30:x:53:VAL:HG11	1.96	0.47
24:q:193:ARG:HD3	24:q:220:TYR:CD1	2.47	0.47
25:r:124:ASP:OD1	25:r:125:GLU:N	2.47	0.47
1:A:472:ASN:H	5:f:299:LYS:HZ3	1.60	0.47
1:A:569:ASN:HB3	1:A:572:TYR:HD2	1.78	0.47
5:F:283:MET:HE2	5:F:334:ALA:HB1	1.96	0.47
11:O:22:LEU:CB	11:O:28:ILE:CG2	2.83	0.47
16:T:148:VAL:CG1	23:p:125:TYR:OH	2.61	0.47
16:T:188:PHE:HB3	18:V:76:GLY:HA2	1.95	0.47
22:o:881:ASN:OD1	22:o:882:SER:N	2.41	0.47
22:o:1129:ASN:HD22	22:o:1413:ALA:HB1	1.80	0.47
25:r:110:GLU:HG3	35:u:167:TYR:CG	2.40	0.47
1:A:824:ARG:HB3	1:A:863:VAL:HG12	1.95	0.47
3:D:955:LYS:HA	3:D:955:LYS:HD2	1.56	0.47
3:D:960:GLU:O	3:D:963:ARG:HD3	2.15	0.47
5:F:415:ILE:O	5:F:415:ILE:HG12	2.14	0.47
6:G:41:ASP:OD1	6:G:41:ASP:N	2.48	0.47
11:O:92:LYS:NZ	13:Q:329:PHE:HB2	2.28	0.47
17:U:127:PHE:HD2	17:U:161:VAL:HG23	1.80	0.47
4:e:439:ASP:OD1	4:e:555:ARG:NH2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:326:HIS:O	5:f:330:ARG:HG2	2.15	0.47
22:o:154:CYS:SG	22:o:184:CYS:HB3	2.55	0.47
22:o:738:GLU:HA	22:o:741:VAL:HG12	1.95	0.47
22:o:896:LEU:HD13	22:o:980:PRO:HG3	1.95	0.47
22:o:1184:THR:OG1	22:o:1189:ASP:OD1	2.31	0.47
23:p:131:THR:HA	23:p:141:GLN:HA	1.95	0.47
33:X:16:DT:H2"	33:X:17:DG:C8	2.49	0.47
1:A:658:GLY:HA3	2:B:475:LYS:HG2	1.96	0.47
4:E:788:ARG:HB3	7:H:145:HIS:HA	1.96	0.47
5:F:81:GLU:HB3	5:F:83:LEU:HD13	1.96	0.47
5:F:298:GLU:HA	5:F:301:VAL:CG1	2.45	0.47
11:O:79:VAL:N	11:O:90:VAL:O	2.48	0.47
15:S:46:ARG:N	15:S:101:ARG:O	2.39	0.47
3:d:922:GLN:NE2	10:l:71:ASP:OD2	2.47	0.47
23:p:809:VAL:HG22	23:p:810:PHE:H	1.80	0.47
25:r:16:ASP:HA	35:u:81:LYS:HB3	1.96	0.47
26:s:85:LYS:HD2	26:s:88:LYS:HD2	1.96	0.47
30:x:24:LEU:HB3	30:x:29:TYR:HD2	1.79	0.47
31:y:5:PRO:HG2	31:y:8:GLU:HG3	1.96	0.47
35:u:97:LEU:HD13	35:u:128:TYR:HD2	1.79	0.47
1:A:573:TYR:HD2	2:B:657:ARG:C	2.23	0.47
1:A:657:SER:CB	2:B:475:LYS:HZ3	2.27	0.47
3:D:960:GLU:O	3:D:963:ARG:HD2	2.14	0.47
5:F:47:ILE:CG1	8:I:19:MET:CE	2.86	0.47
5:F:418:ILE:H	5:F:418:ILE:CD1	2.27	0.47
7:H:110:TYR:HD2	9:J:157:LEU:CD2	2.28	0.47
7:H:221:ILE:HG13	7:H:224:LEU:HD12	1.97	0.47
8:I:14:LYS:HD2	8:I:14:LYS:HA	1.42	0.47
14:R:107:MET:HE2	14:R:107:MET:HB3	1.73	0.47
15:S:121:ASN:O	16:T:25:LYS:CE	2.61	0.47
17:U:73:LYS:HE2	17:U:73:LYS:HB2	1.57	0.47
17:U:142:ASN:O	17:U:145:PHE:HB3	2.14	0.47
17:U:154:CYS:SG	17:U:155:THR:N	2.88	0.47
17:U:184:ILE:CD1	18:V:212:VAL:HG13	2.45	0.47
18:V:93:ASP:OD1	18:V:93:ASP:N	2.47	0.47
18:V:146:ARG:HH22	18:V:172:GLU:HG3	1.80	0.47
19:c:26:VAL:HG23	9:j:195:LEU:HB3	1.96	0.47
3:d:910:LEU:HD11	10:l:88:ALA:HB2	1.97	0.47
22:o:37:THR:O	22:o:87:HIS:HE1	1.98	0.47
23:p:371:ARG:NH1	23:p:609:GLU:OE1	2.47	0.47
23:p:384:ASP:HB3	23:p:387:HIS:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:v:96:VAL:HG22	28:v:116:VAL:HG22	1.96	0.47
1:A:638:PRO:HA	1:A:773:ILE:HG23	1.96	0.47
1:A:657:SER:C	2:B:475:LYS:NZ	2.67	0.47
4:E:324:LYS:HA	4:E:327:ASN:HB3	1.97	0.47
5:F:112:VAL:O	7:H:53:ALA:O	2.33	0.47
11:O:39:GLN:OE1	11:O:39:GLN:HA	2.15	0.47
16:T:181:GLN:O	16:T:184:LEU:HB3	2.14	0.47
3:d:1061:ARG:NH1	8:i:119:ARG:O	2.48	0.47
22:o:229:SER:N	22:o:232:GLU:OE2	2.48	0.47
22:o:291:ARG:O	22:o:295:GLN:HB2	2.15	0.47
22:o:327:ARG:CZ	22:o:335:PRO:HB2	2.45	0.47
1:A:463:PRO:C	1:A:465:TYR:N	2.73	0.47
1:A:1068:ARG:HD2	1:A:1068:ARG:C	2.40	0.47
2:B:792:ASN:CB	2:B:845:SER:HB2	2.43	0.47
3:D:936:GLN:HE21	3:D:936:GLN:N	2.11	0.47
11:O:15:LEU:CD2	11:O:40:PHE:CE1	2.94	0.47
12:P:274:VAL:HG11	14:R:208:LEU:CD2	2.44	0.47
15:S:45:ALA:HB2	16:T:9:LEU:HD11	1.97	0.47
22:o:1104:LEU:HG	22:o:1105:ASN:OD1	2.14	0.47
23:p:84:TYR:CD2	23:p:132:VAL:HG12	2.50	0.47
1:A:471:ASP:HB3	1:A:476:VAL:HG21	1.97	0.47
2:B:27:LYS:CE	2:B:490:SER:HB3	2.45	0.47
3:D:898:VAL:CG2	10:L:113:VAL:HA	2.45	0.47
5:F:48:LYS:CE	8:I:22:ILE:HG23	2.45	0.47
5:F:320:ARG:N	5:F:321:PRO:CD	2.76	0.47
11:O:76:LEU:CB	11:O:79:VAL:HG21	2.35	0.47
14:R:244:LEU:HD11	14:R:295:ARG:HD3	1.95	0.47
16:T:177:ARG:HG2	16:T:177:ARG:O	2.15	0.47
18:V:175:LEU:CD2	18:V:175:LEU:N	2.74	0.47
22:o:107:LEU:HD13	22:o:191:ILE:HD12	1.97	0.47
22:o:842:GLY:O	22:o:845:GLU:HG3	2.14	0.47
22:o:1128:ILE:HG23	22:o:1414:ILE:HD11	1.97	0.47
22:o:1479:LYS:HE2	22:o:1482:TYR:HE1	1.80	0.47
23:p:265:GLN:HG2	23:p:266:GLU:N	2.29	0.47
23:p:934:LYS:HZ1	23:p:942:LYS:HD2	1.80	0.47
33:X:17:DG:H2"	33:X:18:DA:C8	2.50	0.47
7:H:118:VAL:HG22	9:J:127:THR:OG1	2.15	0.46
8:I:119:ARG:NH1	8:I:120:TYR:OH	2.48	0.46
14:R:25:GLU:CD	14:R:46:ILE:HD12	2.40	0.46
16:T:23:VAL:HG21	16:T:31:TRP:CZ3	2.50	0.46
18:V:77:VAL:HG13	18:V:81:ILE:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:916:LYS:NZ	3:d:1070:GLU:OE2	2.42	0.46
22:o:52:PRO:HA	22:o:58:MET:HE1	1.96	0.46
22:o:152:ASN:O	22:o:188:GLN:HG2	2.15	0.46
23:p:28:ILE:HD11	23:p:644:LYS:HB3	1.97	0.46
33:X:23:DA:OP2	33:X:23:DA:H8	1.98	0.46
15:S:17:ARG:HG2	16:T:39:GLU:HA	1.97	0.46
4:e:479:THR:OG1	4:e:481:ASP:O	2.32	0.46
5:f:326:HIS:ND1	5:f:326:HIS:N	2.63	0.46
22:o:215:LEU:HD23	22:o:215:LEU:H	1.79	0.46
22:o:286:ILE:HG13	22:o:289:GLN:HE21	1.79	0.46
22:o:922:PHE:HB2	22:o:1052:ARG:HB2	1.97	0.46
22:o:1097:GLU:CG	22:o:1098:PRO:HD3	2.45	0.46
22:o:1483:GLY:HA3	27:t:80:MET:HG2	1.97	0.46
23:p:59:VAL:HG11	23:p:91:ILE:HD11	1.97	0.46
23:p:853:LEU:HB2	32:z:46:LYS:NZ	2.30	0.46
23:p:1035:ARG:NH1	23:p:1036:LYS:O	2.48	0.46
24:q:123:ASN:OD1	24:q:124:SER:N	2.49	0.46
33:X:3:DT:H2"	33:X:4:DG:C8	2.50	0.46
2:B:184:ASN:N	2:B:184:ASN:ND2	2.62	0.46
4:E:646:SER:OG	4:E:647:ALA:N	2.49	0.46
5:F:298:GLU:HA	5:F:301:VAL:HB	1.98	0.46
17:U:32:LEU:HD21	18:V:203:PHE:CG	2.50	0.46
22:o:305:GLU:O	22:o:309:LEU:HD23	2.16	0.46
22:o:460:ARG:HB2	22:o:501:MET:HE3	1.96	0.46
22:o:859:TYR:CZ	22:o:863:ARG:HD2	2.50	0.46
22:o:1095:LEU:C	22:o:1098:PRO:HD2	2.39	0.46
25:r:103:LEU:CB	35:u:144:ARG:HH12	2.15	0.46
34:Y:-23:DT:H2"	34:Y:-22:DC:C6	2.50	0.46
34:Y:-2:DC:H2"	34:Y:-1:DC:C6	2.51	0.46
1:A:469:PRO:HA	7:H:166:ARG:NH1	2.29	0.46
7:H:73:GLY:CA	9:J:142:ALA:HB3	2.39	0.46
8:I:38:GLN:HA	8:I:41:GLU:HB2	1.98	0.46
12:P:194:PRO:O	16:T:174:LYS:O	2.33	0.46
14:R:44:ARG:NH1	23:p:1064:ARG:HA	2.30	0.46
14:R:48:VAL:O	14:R:48:VAL:HG13	2.14	0.46
15:S:24:LYS:CB	16:T:98:GLU:C	2.89	0.46
16:T:30:GLN:O	16:T:62:LEU:HD11	2.15	0.46
16:T:95:VAL:O	16:T:106:LEU:HD12	2.15	0.46
4:e:718:ARG:HA	4:e:718:ARG:HD3	1.77	0.46
4:e:747:LEU:H	4:e:747:LEU:CD2	2.22	0.46
5:f:328:ALA:C	5:f:330:ARG:N	2.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:176:MET:HE1	21:m:75:ILE:HD11	1.98	0.46
1:A:857:MET:HE3	1:A:858:ASP:H	1.81	0.46
12:P:228:GLU:OE1	12:P:228:GLU:HA	2.16	0.46
12:P:252:ASP:OD1	12:P:252:ASP:N	2.49	0.46
16:T:33:LYS:O	16:T:34:ALA:C	2.58	0.46
17:U:18:ALA:O	17:U:22:ILE:HG23	2.15	0.46
17:U:69:ASP:OD2	17:U:100:VAL:HG22	2.15	0.46
5:f:327:TRP:O	5:f:330:ARG:HB2	2.15	0.46
24:q:91:GLU:HG3	24:q:92:GLU:H	1.80	0.46
26:s:75:PHE:HB2	26:s:104:ILE:HG22	1.96	0.46
28:v:136:GLU:OE1	28:v:136:GLU:N	2.48	0.46
1:A:1153:VAL:HG11	6:G:150:LYS:CE	2.45	0.46
2:B:564:LEU:HB2	2:B:581:ILE:HD13	1.97	0.46
3:D:917:ILE:CG1	3:D:1058:VAL:HG11	2.45	0.46
3:D:1080:TYR:HD1	4:E:585:ASN:OD1	1.97	0.46
5:F:44:SER:O	8:I:22:ILE:HD13	2.15	0.46
7:H:111:ALA:CB	9:J:126:TYR:CE2	2.93	0.46
14:R:15:CYS:HB2	14:R:18:HIS:O	2.15	0.46
14:R:175:ARG:HH22	23:p:102:ASP:HA	1.80	0.46
17:U:72:ILE:HA	17:U:97:ARG:O	2.15	0.46
24:q:193:ARG:NH2	24:q:217:GLN:OE1	2.48	0.46
35:u:84:VAL:HG12	35:u:144:ARG:HD3	1.98	0.46
1:A:473:GLU:CD	5:F:212:SER:HB2	2.41	0.46
1:A:730:PHE:CD1	1:A:730:PHE:N	2.82	0.46
2:B:431:LEU:CD2	2:B:431:LEU:N	2.76	0.46
2:B:560:TYR:HD2	2:B:581:ILE:HD11	1.78	0.46
17:U:46:GLU:CD	17:U:93:PHE:CE2	2.88	0.46
17:U:118:GLU:HG2	17:U:174:ARG:HA	1.98	0.46
5:f:317:LEU:HD12	5:f:329:LEU:HD23	1.98	0.46
22:o:221:VAL:HA	22:o:224:ILE:HD12	1.97	0.46
23:p:446:TYR:O	23:p:450:THR:HG22	2.16	0.46
29:w:124:THR:OG1	29:w:125:GLU:N	2.49	0.46
33:X:13:DT:H2"	33:X:14:DG:C8	2.50	0.46
17:U:137:THR:H	17:U:140:GLU:HB2	1.81	0.46
23:p:323:SER:OG	23:p:324:ARG:NH1	2.48	0.46
7:H:221:ILE:H	7:H:221:ILE:HG12	1.57	0.46
15:S:24:LYS:HB2	16:T:97:THR:HB	1.96	0.46
15:S:26:TYR:HB2	15:S:139:PRO:O	2.16	0.46
15:S:42:TRP:CD1	15:S:102:VAL:HG11	2.50	0.46
16:T:128:LYS:NZ	23:p:540:PRO:HB3	2.31	0.46
16:T:220:ILE:HG22	18:V:83:ASN:ND2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:111:ARG:HA	17:U:111:ARG:HD3	1.52	0.46
17:U:185:GLU:N	17:U:186:PRO:HD2	2.31	0.46
18:V:149:LYS:HE2	18:V:149:LYS:HB2	1.55	0.46
3:d:860:VAL:HA	21:m:47:GLN:HG2	1.98	0.46
5:f:330:ARG:NH1	5:f:371:THR:O	2.48	0.46
20:k:182:LEU:HD23	20:k:182:LEU:HA	1.84	0.46
22:o:111:CYS:SG	22:o:154:CYS:HB2	2.56	0.46
22:o:472:HIS:NE2	22:o:492:TYR:OH	2.47	0.46
23:p:329:GLY:HA3	23:p:335:ARG:HG3	1.98	0.46
23:p:1119:CYS:HA	23:p:1146:ILE:HD13	1.98	0.46
33:X:-29:DA:H1'	33:X:-28:DC:C5	2.51	0.46
33:X:14:DG:H2''	33:X:15:DG:C8	2.50	0.46
35:u:165:ASP:HB2	35:u:168:LEU:HD11	1.98	0.46
1:A:349:TRP:HE1	5:f:262:PHE:CA	2.28	0.46
1:A:465:TYR:CD1	7:H:167:GLU:OE1	2.69	0.46
1:A:511:LEU:HD22	1:A:511:LEU:N	2.10	0.46
1:A:567:LEU:HA	2:B:745:GLN:NE2	2.30	0.46
1:A:1026:ILE:HA	1:A:1029:VAL:HG12	1.98	0.46
3:D:871:THR:HG21	3:D:910:LEU:HD12	1.98	0.46
3:D:881:ARG:CB	10:L:57:VAL:HG11	2.39	0.46
5:F:427:LEU:HD12	5:F:427:LEU:HA	1.71	0.46
11:O:22:LEU:C	11:O:28:ILE:CG1	2.82	0.46
22:o:79:THR:OG1	22:o:80:GLU:OE1	2.34	0.46
23:p:625:LEU:HD12	23:p:665:ILE:HG13	1.97	0.46
23:p:794:VAL:HG12	23:p:967:ILE:HG22	1.98	0.46
35:u:38:CYS:HB2	35:u:44:PHE:CD1	2.51	0.46
1:A:844:LYS:NZ	33:X:31:DT:H71	2.31	0.45
2:B:338:GLU:HG2	2:B:846:TYR:OH	2.16	0.45
5:F:112:VAL:HG11	7:H:55:LYS:HD3	1.97	0.45
5:F:214:HIS:HB3	7:H:164:THR:HG21	1.98	0.45
5:F:319:LEU:O	5:F:319:LEU:HG	2.16	0.45
12:P:261:SER:HB3	34:Y:29:DT:H4'	1.98	0.45
14:R:44:ARG:HH12	23:p:1064:ARG:HA	1.80	0.45
4:e:717:LEU:HD22	4:e:726:LEU:HD11	1.97	0.45
22:o:294:GLU:OE2	22:o:303:ILE:HG21	2.16	0.45
22:o:511:THR:HG22	23:p:1101:GLN:HB3	1.98	0.45
22:o:584:PRO:O	22:o:585:LEU:HD12	2.16	0.45
23:p:50:PHE:HA	23:p:54:SER:HB3	1.97	0.45
26:s:70:ASP:OD1	26:s:70:ASP:N	2.49	0.45
34:Y:-24:DA:H2''	34:Y:-23:DT:H72	1.97	0.45
34:Y:8:DC:H2''	34:Y:9:DC:C5	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:S:109:LYS:HD2	15:S:149:LEU:HD23	1.97	0.45
3:d:941:ARG:NH2	8:i:123:THR:O	2.48	0.45
5:f:83:LEU:HD22	8:i:41:GLU:HG2	1.99	0.45
22:o:1230:GLN:O	22:o:1234:LYS:HG2	2.17	0.45
23:p:65:ILE:HD11	23:p:86:LEU:HD12	1.98	0.45
24:q:190:ASN:HD21	24:q:195:THR:HG23	1.81	0.45
26:s:11:TRP:HB2	26:s:40:PHE:CD2	2.51	0.45
2:B:492:MET:HE3	2:B:492:MET:HB2	1.85	0.45
3:D:936:GLN:HB2	3:D:937:ALA:H	1.66	0.45
4:E:321:LEU:HB3	4:E:330:TRP:HB2	1.97	0.45
5:F:114:LEU:N	7:H:52:SER:HA	2.31	0.45
5:F:424:GLN:O	5:F:428:LEU:HG	2.15	0.45
15:S:45:ALA:CB	16:T:9:LEU:HD11	2.46	0.45
16:T:11:GLY:HA3	16:T:106:LEU:O	2.17	0.45
16:T:154:LYS:N	16:T:155:PRO:HD3	2.32	0.45
17:U:127:PHE:CD1	17:U:141:ALA:HB3	2.50	0.45
17:U:141:ALA:HA	17:U:144:LEU:HD12	1.98	0.45
22:o:801:GLY:HA3	23:p:503:ASN:HB2	1.97	0.45
22:o:872:MET:HE1	22:o:1470:CYS:SG	2.55	0.45
22:o:1342:SER:O	22:o:1346:VAL:HG23	2.16	0.45
23:p:260:LEU:HD22	23:p:347:MET:HE1	1.97	0.45
23:p:1141:ARG:HE	23:p:1143:LYS:HZ1	1.64	0.45
26:s:47:LYS:O	26:s:51:GLY:HA3	2.16	0.45
26:s:55:ARG:HA	26:s:58:LEU:HD12	1.98	0.45
33:X:-14:DC:H2''	33:X:-13:DA:H5'	1.98	0.45
1:A:572:TYR:CD1	2:B:689:GLN:CD	2.95	0.45
2:B:367:GLU:OE2	2:B:371:LYS:NZ	2.39	0.45
5:F:103:GLU:HB3	7:H:59:GLU:HG2	1.97	0.45
22:o:1121:VAL:N	22:o:1122:PRO:HD2	2.31	0.45
22:o:1166:LEU:HB2	22:o:1296:MET:HB2	1.98	0.45
23:p:591:ARG:NH2	23:p:663:GLU:OE2	2.50	0.45
26:s:94:MET:HE2	26:s:125:TYR:CD2	2.52	0.45
35:u:43:GLY:HA2	35:u:78:ARG:HD3	1.98	0.45
1:A:1063:LYS:HD3	1:A:1063:LYS:C	2.41	0.45
1:A:1167:ILE:HD13	6:G:181:TRP:HB2	1.97	0.45
2:B:568:VAL:HG22	2:B:628:ILE:HG23	1.98	0.45
2:B:883:PHE:CD1	7:H:223:TYR:HB3	2.42	0.45
4:E:747:LEU:H	4:E:747:LEU:CD2	2.21	0.45
18:V:72:GLY:CA	18:V:115:GLN:HG3	2.46	0.45
18:V:155:LEU:HD12	18:V:155:LEU:HA	1.85	0.45
4:e:270:ASP:OD1	4:e:271:GLN:NE2	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:o:198:LEU:HG	22:o:216:LEU:HB2	1.98	0.45
22:o:571:ASP:OD1	22:o:571:ASP:N	2.46	0.45
22:o:1286:ARG:NH2	23:p:251:ALA:O	2.50	0.45
27:t:84:GLU:O	27:t:84:GLU:HG2	2.16	0.45
30:x:10:CYS:SG	30:x:42:ARG:NE	2.86	0.45
34:Y:14:DG:H1'	34:Y:15:DT:H5'	1.98	0.45
2:B:71:ARG:HD3	2:B:73:TYR:CE1	2.51	0.45
2:B:847:ARG:H	7:H:227:LEU:HA	1.80	0.45
15:S:44:GLN:O	16:T:9:LEU:HD11	2.11	0.45
17:U:32:LEU:CD1	18:V:161:ARG:HH21	2.29	0.45
18:V:90:GLN:C	18:V:92:GLY:H	2.23	0.45
23:p:276:LEU:HG	23:p:343:LEU:HD21	1.97	0.45
1:A:502:LEU:HD22	1:A:502:LEU:HA	1.79	0.45
5:F:233:GLY:HA2	5:F:239:ARG:HE	1.82	0.45
5:F:280:ILE:CD1	5:F:330:ARG:HG2	2.46	0.45
12:P:281:SER:HB2	12:P:291:LEU:HD21	1.98	0.45
22:o:26:LEU:HD23	22:o:26:LEU:H	1.82	0.45
22:o:346:LYS:HB2	22:o:351:ARG:HH21	1.82	0.45
22:o:1190:GLN:NE2	22:o:1194:ASN:HB2	2.32	0.45
23:p:371:ARG:HH22	23:p:380:ARG:HH22	1.63	0.45
23:p:908:MET:HE3	23:p:910:THR:HG22	1.97	0.45
23:p:961:ILE:HD11	30:x:42:ARG:HD2	1.98	0.45
25:r:103:LEU:HD21	35:u:84:VAL:HG12	1.99	0.45
34:Y:-3:DA:H2''	34:Y:-2:DC:C6	2.52	0.45
34:Y:2:DC:H2''	34:Y:3:DC:C6	2.52	0.45
1:A:401:ASN:HD22	1:A:401:ASN:N	2.14	0.45
2:B:366:ASP:OD1	2:B:500:THR:OG1	2.34	0.45
4:E:650:THR:HG22	4:E:666:THR:HG22	1.99	0.45
14:R:32:MET:SD	14:R:46:ILE:CG2	3.01	0.45
16:T:178:ALA:O	16:T:179:ASP:HB2	2.15	0.45
17:U:127:PHE:CG	17:U:161:VAL:HG21	2.52	0.45
22:o:1177:TYR:HE1	22:o:1209:PRO:HB2	1.80	0.45
22:o:1178:ASP:OD1	22:o:1185:VAL:HG23	2.17	0.45
34:Y:-1:DC:H2''	34:Y:0:DT:C6	2.52	0.45
35:u:107:PHE:O	35:u:160:ILE:HG13	2.17	0.45
1:A:1019:LYS:NZ	1:A:1019:LYS:CB	2.73	0.45
2:B:768:PRO:C	2:B:770:GLU:N	2.73	0.45
5:F:279:LEU:HD23	5:F:311:CYS:SG	2.57	0.45
7:H:27:ASP:OD1	7:H:27:ASP:N	2.46	0.45
7:H:44:LEU:HD11	9:J:160:GLN:HG2	1.99	0.45
7:H:127:GLN:N	7:H:128:PRO:HD2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:177:PHE:O	14:R:181:CYS:N	2.38	0.45
16:T:181:GLN:NE2	16:T:181:GLN:CA	2.78	0.45
16:T:188:PHE:HE2	18:V:79:ALA:O	2.00	0.45
5:f:149:PRO:HA	5:f:150:PRO:HD3	1.83	0.45
24:q:116:THR:HB	24:q:147:ASP:HB3	1.99	0.45
25:r:18:SER:OG	35:u:82:GLY:HA3	2.17	0.45
26:s:88:LYS:HA	26:s:91:CYS:HB2	1.99	0.45
26:s:154:GLU:O	26:s:157:THR:HG22	2.17	0.45
33:X:23:DA:N6	34:Y:-24:DA:N6	2.65	0.45
12:P:188:ARG:HH21	13:Q:324:GLU:CA	2.29	0.45
13:Q:310:GLU:C	13:Q:313:PRO:CD	2.89	0.45
17:U:37:LEU:HD11	17:U:66:LEU:HD13	1.99	0.45
18:V:198:LYS:HB3	18:V:198:LYS:HE2	1.65	0.45
3:d:1084:LEU:HB3	8:i:99:ARG:HH21	1.81	0.45
4:e:777:SER:O	4:e:777:SER:OG	2.34	0.45
22:o:189:PRO:HA	22:o:202:TRP:HA	1.98	0.45
22:o:1248:ASN:ND2	22:o:1256:VAL:H	2.15	0.45
35:u:24:ASN:OD1	35:u:25:THR:N	2.50	0.45
1:A:690:LEU:HD22	1:A:747:LEU:HD22	1.99	0.44
2:B:559:LYS:HB2	2:B:559:LYS:NZ	2.31	0.44
3:D:965:ILE:HA	3:D:968:ARG:HD2	1.98	0.44
4:E:784:HIS:HB3	4:E:792:LEU:HB2	1.99	0.44
14:R:132:ARG:HA	14:R:132:ARG:HD2	1.63	0.44
5:f:217:SER:H	5:f:220:GLN:HE21	1.65	0.44
20:k:150:VAL:HG22	21:m:82:GLN:HB3	1.98	0.44
22:o:695:ASP:OD1	22:o:695:ASP:N	2.43	0.44
22:o:1038:THR:O	22:o:1042:ASN:ND2	2.46	0.44
26:s:4:GLU:HA	26:s:7:THR:HG22	1.98	0.44
28:v:71:ASP:O	28:v:72:ASP:HB3	2.17	0.44
35:u:6:SER:HB3	35:u:71:LYS:NZ	2.31	0.44
5:F:411:VAL:HG22	5:F:413:SER:H	1.82	0.44
5:F:426:LEU:C	5:F:426:LEU:HD23	2.42	0.44
7:H:59:GLU:HA	7:H:62:THR:HG22	1.99	0.44
7:H:116:ARG:HG3	7:H:116:ARG:O	2.16	0.44
11:O:18:SER:H	13:Q:49:LYS:HZ2	1.61	0.44
15:S:124:TYR:OH	16:T:22:LYS:CE	2.60	0.44
18:V:169:GLU:H	18:V:169:GLU:HG2	1.48	0.44
23:p:787:GLY:HA2	23:p:790:GLN:HE21	1.82	0.44
35:u:40:GLY:O	35:u:152:VAL:HG11	2.17	0.44
35:u:60:GLN:NE2	35:u:65:PHE:HB2	2.32	0.44
1:A:489:GLN:H	1:A:489:GLN:CD	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1185:VAL:CG1	1:A:1191:ILE:CD1	2.93	0.44
3:D:905:ALA:CB	10:L:120:LEU:HD21	2.46	0.44
3:D:917:ILE:CG2	3:D:1058:VAL:HG11	2.47	0.44
4:E:464:TYR:CD2	5:F:133:ALA:HB2	2.52	0.44
5:F:313:VAL:HG11	5:F:376:SER:CA	2.47	0.44
7:H:43:SER:HB2	7:H:119:ILE:HD11	1.98	0.44
9:J:123:LEU:O	9:J:153:ARG:NH1	2.50	0.44
11:O:61:SER:H	11:O:79:VAL:HG22	1.83	0.44
12:P:207:PRO:O	12:P:207:PRO:CD	2.65	0.44
14:R:169:ARG:HD3	14:R:206:VAL:HB	1.99	0.44
15:S:25:LYS:O	16:T:97:THR:HA	2.18	0.44
5:f:11:ASN:OD1	5:f:48:LYS:NZ	2.51	0.44
22:o:726:GLU:OE1	22:o:726:GLU:N	2.51	0.44
22:o:1030:SER:CB	26:s:162:ARG:HE	2.30	0.44
23:p:626:LEU:HD23	23:p:662:VAL:HG12	1.98	0.44
29:w:103:ARG:O	29:w:103:ARG:HD3	2.17	0.44
32:z:19:CYS:SG	32:z:20:GLY:N	2.91	0.44
33:X:18:DA:H2''	33:X:19:DG:C8	2.53	0.44
33:X:21:DC:H2'	33:X:21:DC:OP2	2.17	0.44
34:Y:-15:DC:H2''	34:Y:-14:DC:C6	2.52	0.44
34:Y:-10:DG:H2''	34:Y:-9:DT:C6	2.52	0.44
2:B:431:LEU:HD23	2:B:431:LEU:O	2.17	0.44
2:B:883:PHE:HB2	7:H:222:PRO:O	2.17	0.44
3:D:1007:THR:HG21	11:O:5:LEU:HD12	1.99	0.44
4:E:369:LYS:HA	4:E:369:LYS:HD3	1.74	0.44
12:P:256:GLN:HA	12:P:256:GLN:OE1	2.16	0.44
12:P:278:GLN:OE1	12:P:278:GLN:N	2.48	0.44
15:S:143:TRP:C	15:S:143:TRP:CD1	2.95	0.44
16:T:226:LYS:HA	16:T:226:LYS:HD3	1.82	0.44
19:c:24:ASP:CB	9:j:192:LYS:HD2	2.48	0.44
10:l:113:VAL:O	10:l:113:VAL:HG22	2.18	0.44
22:o:1028:PRO:O	22:o:1029:LEU:HB3	2.18	0.44
22:o:1198:GLU:C	22:o:1200:PRO:HD3	2.43	0.44
23:p:486:ASN:OD1	23:p:491:ARG:NH2	2.50	0.44
23:p:628:VAL:HG22	23:p:633:LEU:HD23	2.00	0.44
23:p:849:ASP:HB3	32:z:15:MET:HE3	2.00	0.44
24:q:266:GLU:HG2	31:y:21:ILE:HG12	1.98	0.44
32:z:52:LEU:HD23	32:z:52:LEU:HA	1.79	0.44
1:A:405:VAL:N	5:F:302:HIS:CB	2.76	0.44
1:A:489:GLN:H	1:A:489:GLN:NE2	2.15	0.44
2:B:69:GLN:NE2	2:B:156:LYS:O	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:839:MET:HE1	2:B:843:LEU:HD13	2.00	0.44
2:B:859:ARG:HA	2:B:859:ARG:HD2	1.80	0.44
3:D:1006:LEU:HD12	11:O:68:CYS:O	2.17	0.44
5:F:316:GLN:NE2	5:F:320:ARG:HA	2.32	0.44
7:H:194:MET:HE2	7:H:194:MET:HB2	1.85	0.44
18:V:216:PHE:HE1	22:o:296:ASN:HA	1.81	0.44
19:c:101:VAL:HG22	5:f:127:LEU:HA	2.00	0.44
22:o:514:GLU:O	22:o:518:LEU:HB2	2.18	0.44
22:o:663:ASP:OD1	22:o:666:ARG:NH1	2.51	0.44
22:o:910:LYS:N	22:o:911:PRO:HD2	2.33	0.44
23:p:256:ILE:HD11	23:p:373:LEU:HD21	2.00	0.44
25:r:50:SER:OG	25:r:51:ALA:N	2.50	0.44
31:y:37:LYS:HD3	31:y:37:LYS:HA	1.69	0.44
33:X:-6:DA:H2"	33:X:-5:DC:C6	2.53	0.44
34:Y:40:DG:H2"	34:Y:41:DA:C8	2.53	0.44
35:u:116:GLU:O	35:u:130:THR:HA	2.17	0.44
1:A:345:PRO:HG3	1:A:500:LEU:HG	1.99	0.44
1:A:573:TYR:CD1	2:B:657:ARG:NH1	2.86	0.44
2:B:414:LEU:HB2	2:B:523:VAL:HG13	1.99	0.44
13:Q:348:LYS:NZ	13:Q:375:GLU:CD	2.76	0.44
15:S:7:SER:HA	16:T:47:LYS:HD3	1.99	0.44
4:e:774:MET:HE2	4:e:774:MET:HB2	1.91	0.44
22:o:17:THR:HG22	22:o:18:ILE:N	2.31	0.44
22:o:261:ARG:HB3	22:o:276:LEU:HD11	1.99	0.44
22:o:402:LEU:HD23	22:o:402:LEU:HA	1.87	0.44
24:q:101:PHE:CE1	24:q:122:SER:HB3	2.53	0.44
25:r:94:LYS:O	25:r:97:LEU:HG	2.17	0.44
33:X:5:DA:H2"	33:X:6:DG:C8	2.53	0.44
35:u:120:ASP:OD2	35:u:129:LYS:NZ	2.42	0.44
1:A:469:PRO:HA	7:H:166:ARG:HH12	1.82	0.44
3:D:889:HIS:O	10:L:104:ARG:CZ	2.61	0.44
3:D:950:LEU:HD23	3:D:950:LEU:HA	1.87	0.44
3:D:983:ARG:H	3:D:983:ARG:HG2	1.50	0.44
5:F:48:LYS:HE3	8:I:22:ILE:CB	2.48	0.44
5:F:305:ILE:N	5:F:306:PRO:HD2	2.33	0.44
7:H:178:LYS:HA	7:H:178:LYS:HD3	1.81	0.44
11:O:15:LEU:HD23	11:O:40:PHE:CD2	2.53	0.44
15:S:54:LYS:HE2	15:S:54:LYS:HB2	1.84	0.44
16:T:223:GLN:OE1	16:T:223:GLN:N	2.47	0.44
8:i:16:ALA:HB2	8:i:40:LEU:HD11	2.00	0.44
25:r:109:GLU:O	25:r:113:ALA:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:X:-15:DA:H2"	33:X:-14:DC:C6	2.53	0.44
1:A:352:MET:HE3	1:A:352:MET:HB3	1.82	0.44
1:A:567:LEU:CD2	2:B:745:GLN:HE21	2.30	0.44
1:A:575:PRO:HD3	2:B:608:ASN:CB	2.48	0.44
4:E:250:GLU:O	4:E:254:ASN:ND2	2.50	0.44
5:F:298:GLU:CA	5:F:301:VAL:HG12	2.47	0.44
16:T:145:LEU:HD21	23:p:92:TYR:CD2	2.53	0.44
5:f:58:MET:HE3	5:f:64:GLN:HA	1.98	0.44
22:o:42:LYS:O	22:o:288:ASN:ND2	2.44	0.44
22:o:481:THR:O	22:o:483:ARG:NE	2.50	0.44
22:o:917:GLU:O	22:o:921:ARG:HB2	2.17	0.44
24:q:103:LEU:HD12	24:q:120:LEU:HD22	2.00	0.44
25:r:32:LEU:CD2	35:u:2:PHE:HB3	2.48	0.44
31:y:42:LEU:O	31:y:45:ILE:HG22	2.17	0.44
31:y:63:VAL:HG22	31:y:71:ILE:HG22	2.00	0.44
31:y:114:GLU:OE1	31:y:114:GLU:N	2.40	0.44
33:X:-1:DA:H2"	33:X:0:DA:C8	2.53	0.44
34:Y:-14:DC:H2"	34:Y:-13:DA:C8	2.53	0.44
35:u:86:ASP:OD1	35:u:87:ALA:N	2.51	0.44
1:A:1060:GLU:HA	1:A:1060:GLU:OE1	2.18	0.44
2:B:867:VAL:HG13	7:H:203:LEU:HB3	1.99	0.44
3:D:901:TYR:CE2	10:L:120:LEU:HD22	2.52	0.44
3:D:963:ARG:CG	3:D:964:GLU:N	2.81	0.44
16:T:153:TYR:C	16:T:155:PRO:HD3	2.42	0.44
18:V:220:TRP:O	18:V:220:TRP:CD1	2.71	0.44
5:f:317:LEU:HG	5:f:330:ARG:HE	1.83	0.44
22:o:784:VAL:HG22	23:p:978:ILE:HD11	1.99	0.44
22:o:1171:ALA:HB3	22:o:1215:GLU:HG3	2.00	0.44
23:p:526:LEU:H	23:p:526:LEU:HD23	1.83	0.44
23:p:1046:THR:HG22	23:p:1047:TYR:N	2.32	0.44
33:X:1:DG:H2"	33:X:2:DG:C8	2.53	0.44
34:Y:-12:DG:H2"	34:Y:-11:DA:C8	2.53	0.44
7:H:111:ALA:O	9:J:126:TYR:OH	2.33	0.43
14:R:38:GLY:O	22:o:427:ILE:HG22	2.17	0.43
14:R:154:ARG:CZ	34:Y:22:DG:OP1	2.66	0.43
15:S:30:ALA:O	15:S:146:PHE:HB2	2.18	0.43
17:U:37:LEU:HD13	17:U:71:PHE:CD1	2.42	0.43
17:U:163:GLU:C	17:U:165:GLU:N	2.74	0.43
4:e:542:HIS:CE1	4:e:568:ARG:HG3	2.53	0.43
10:l:101:GLN:HA	10:l:104:ARG:HG2	2.00	0.43
23:p:177:CYS:SG	23:p:738:THR:OG1	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:p:371:ARG:NH2	23:p:380:ARG:HH22	2.16	0.43
23:p:551:GLU:OE1	23:p:551:GLU:N	2.45	0.43
23:p:628:VAL:HG12	23:p:629:GLU:O	2.18	0.43
29:w:75:ASP:HB3	29:w:78:LEU:HD12	1.99	0.43
1:A:925:ASP:OD1	1:A:925:ASP:N	2.52	0.43
2:B:780:LYS:HA	7:H:183:ARG:HH12	1.83	0.43
2:B:827:ARG:CG	7:H:211:PHE:CZ	3.00	0.43
10:L:106:ARG:HH11	10:L:114:LYS:HZ3	0.46	0.43
10:L:106:ARG:HD2	10:L:114:LYS:NZ	2.33	0.43
11:O:22:LEU:CB	11:O:28:ILE:HG23	2.36	0.43
15:S:47:LEU:HG	15:S:98:TRP:CE3	2.53	0.43
24:q:240:ARG:HB2	24:q:243:THR:HG22	1.99	0.43
35:u:94:LYS:O	35:u:110:ARG:HD2	2.18	0.43
2:B:639:LYS:NZ	2:B:641:GLU:OE2	2.42	0.43
3:D:1006:LEU:HD11	11:O:68:CYS:C	2.43	0.43
4:E:613:ALA:HB3	4:E:616:HIS:HD2	1.83	0.43
5:F:311:CYS:CB	5:F:330:ARG:HH12	2.31	0.43
11:O:58:PHE:CD1	11:O:81:PHE:CD2	3.00	0.43
14:R:27:TYR:HE1	14:R:50:SER:HB3	1.75	0.43
16:T:23:VAL:HG13	16:T:27:LEU:HD23	2.01	0.43
17:U:77:ARG:HB2	17:U:93:PHE:H	1.84	0.43
17:U:105:TYR:HE1	18:V:222:SER:HB2	1.84	0.43
19:c:21:LEU:HD11	19:c:23:TRP:CD1	2.54	0.43
19:c:77:LEU:HD12	9:j:116:LEU:CD2	2.45	0.43
5:f:411:VAL:O	5:f:417:ARG:NH2	2.51	0.43
5:f:447:ALA:CB	5:f:456:GLY:HA3	2.48	0.43
10:l:139:TYR:HD2	21:m:73:MET:HE3	1.84	0.43
21:m:103:LEU:O	21:m:107:ASN:ND2	2.51	0.43
22:o:260:VAL:O	22:o:342:ARG:NH2	2.50	0.43
22:o:1211:LEU:HD11	22:o:1258:ARG:NE	2.33	0.43
23:p:110:PRO:HG2	23:p:163:LEU:HD11	2.00	0.43
23:p:502:HIS:ND1	23:p:504:THR:OG1	2.33	0.43
25:r:103:LEU:HD23	35:u:144:ARG:NE	2.30	0.43
33:X:-40:DC:O2	34:Y:40:DG:C2	2.71	0.43
1:A:400:GLU:HG3	1:A:401:ASN:N	2.32	0.43
2:B:594:SER:OG	2:B:595:LYS:N	2.51	0.43
4:E:564:ASP:OD1	4:E:564:ASP:N	2.51	0.43
5:F:400:GLY:O	5:F:404:ARG:HG2	2.18	0.43
15:S:11:VAL:O	15:S:12:THR:HG23	2.18	0.43
16:T:140:ARG:CB	23:p:56:GLN:HE21	2.30	0.43
16:T:182:HIS:O	16:T:185:ASP:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:210:VAL:HA	16:T:213:LEU:HB3	2.00	0.43
18:V:175:LEU:HD12	18:V:179:GLN:C	2.42	0.43
5:f:105:TYR:O	9:j:217:PHE:N	2.51	0.43
22:o:1097:GLU:HG2	22:o:1098:PRO:HD3	2.00	0.43
22:o:1312:PRO:O	22:o:1332:GLN:NE2	2.51	0.43
22:o:1482:TYR:HE2	27:t:101:LYS:HZ2	1.65	0.43
23:p:458:LYS:NZ	23:p:461:GLN:HB3	2.33	0.43
25:r:82:SER:O	25:r:86:LEU:N	2.52	0.43
33:X:22:DG:N2	34:Y:-21:DG:N1	2.66	0.43
3:D:871:THR:HG22	10:L:66:LEU:CB	2.47	0.43
5:F:283:MET:CE	5:F:308:VAL:HA	2.43	0.43
5:F:286:VAL:HG12	5:F:337:VAL:HB	2.01	0.43
10:L:83:MET:HE3	10:L:83:MET:HB3	1.93	0.43
16:T:220:ILE:C	16:T:220:ILE:CD1	2.91	0.43
16:T:229:HIS:ND1	34:Y:14:DG:N2	2.67	0.43
17:U:32:LEU:CD2	18:V:161:ARG:CZ	2.80	0.43
18:V:175:LEU:HD12	18:V:179:GLN:CB	2.45	0.43
10:l:59:THR:O	10:l:59:THR:OG1	2.36	0.43
22:o:277:THR:HA	22:o:280:LEU:HD12	1.99	0.43
22:o:434:LYS:NZ	22:o:437:ASP:HB3	2.34	0.43
22:o:863:ARG:HH21	22:o:1415:THR:HA	1.84	0.43
22:o:936:GLU:HA	22:o:939:VAL:HG12	1.99	0.43
23:p:225:LEU:H	23:p:225:LEU:HD23	1.84	0.43
23:p:1108:PHE:HZ	23:p:1150:ARG:HG2	1.82	0.43
1:A:740:LEU:CD2	1:A:1070:PHE:HZ	2.30	0.43
2:B:653:LEU:HG	2:B:684:ILE:HG13	2.00	0.43
5:F:92:ILE:H	5:F:92:ILE:HG13	1.60	0.43
5:F:361:LYS:HA	5:F:364:VAL:CG2	2.45	0.43
6:G:129:LYS:HA	6:G:129:LYS:HD2	1.77	0.43
8:I:132:LEU:CD1	9:J:121:MET:SD	3.06	0.43
10:L:84:LEU:HD23	10:L:84:LEU:HA	1.77	0.43
15:S:27:ASN:HB2	16:T:96:PHE:CZ	2.53	0.43
18:V:76:GLY:O	18:V:80:LYS:HB2	2.18	0.43
5:f:26:MET:HE3	5:f:26:MET:HB3	1.77	0.43
22:o:322:LEU:HD12	22:o:323:PRO:HD2	2.00	0.43
23:p:840:MET:HB3	23:p:891:ASP:OD2	2.18	0.43
26:s:49:SER:C	26:s:50:GLU:HG3	2.44	0.43
34:Y:4:DA:H2"	34:Y:5:DG:C8	2.53	0.43
1:A:500:LEU:HD23	1:A:500:LEU:HA	1.81	0.43
2:B:339:THR:HB	2:B:340:PRO:HD3	2.01	0.43
11:O:5:LEU:CD2	11:O:98:CYS:SG	3.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:32:LEU:HD13	13:Q:32:ASP:CG	2.27	0.43
14:R:18:HIS:NE2	14:R:36:GLU:OE2	2.52	0.43
17:U:19:LYS:O	17:U:22:ILE:HG13	2.19	0.43
22:o:273:GLN:OE1	22:o:278:HIS:N	2.52	0.43
22:o:274:ASP:OD1	22:o:277:THR:N	2.29	0.43
23:p:799:SER:HB2	24:q:174:ALA:HB2	2.00	0.43
23:p:821:LYS:HE3	23:p:821:LYS:HB3	1.70	0.43
33:X:-3:DG:H2"	33:X:-2:DG:C8	2.53	0.43
1:A:727:THR:HG23	1:A:727:THR:O	2.19	0.43
5:F:48:LYS:HG2	8:I:22:ILE:CG2	2.24	0.43
5:F:274:ASN:HB2	5:F:317:LEU:N	2.30	0.43
7:H:217:ARG:H	7:H:217:ARG:HG3	1.66	0.43
15:S:23:THR:O	16:T:99:SER:C	2.62	0.43
15:S:24:LYS:HB2	16:T:98:GLU:C	2.44	0.43
17:U:73:LYS:H	17:U:97:ARG:H	1.66	0.43
22:o:403:GLN:O	22:o:406:VAL:HG12	2.19	0.43
22:o:1024:ASN:OD1	22:o:1024:ASN:N	2.52	0.43
25:r:95:PHE:CE1	35:u:1:MET:HE3	2.54	0.43
33:X:6:DG:H2"	33:X:7:DT:C6	2.54	0.43
34:Y:-13:DA:H2"	34:Y:-12:DG:C8	2.53	0.43
3:D:891:ILE:HG21	10:L:111:LEU:HB2	1.80	0.43
15:S:53:ASN:HB2	15:S:96:GLN:OE1	2.19	0.43
22:o:48:GLU:OE1	22:o:48:GLU:N	2.52	0.43
22:o:1418:GLY:HA2	22:o:1421:ARG:HE	1.84	0.43
24:q:15:THR:HG22	24:q:16:ASP:N	2.32	0.43
25:r:76:ASN:O	25:r:80:ILE:HD12	2.19	0.43
26:s:85:LYS:O	26:s:89:VAL:N	2.46	0.43
26:s:173:ILE:O	26:s:209:VAL:HA	2.18	0.43
1:A:349:TRP:HZ2	5:f:262:PHE:CZ	2.36	0.43
2:B:216:SER:OG	2:B:217:ASN:N	2.52	0.43
3:D:910:LEU:HB2	10:L:66:LEU:CD2	2.46	0.43
3:D:917:ILE:HG21	3:D:1058:VAL:HG11	2.00	0.43
3:D:963:ARG:CZ	3:D:964:GLU:HB3	2.48	0.43
4:E:476:VAL:HB	4:E:782:HIS:HB2	2.01	0.43
5:F:402:ARG:O	5:F:406:VAL:HG13	2.19	0.43
10:L:101:GLN:C	10:L:105:HIS:HD2	2.17	0.43
11:O:63:ASN:HB3	11:O:75:VAL:O	2.19	0.43
14:R:158:ALA:HA	14:R:186:ILE:HG13	2.01	0.43
14:R:214:PHE:HA	14:R:217:ARG:NH1	2.34	0.43
16:T:18:VAL:HG13	16:T:108:GLY:HA3	2.00	0.43
16:T:236:LYS:C	16:T:238:GLU:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:o:28:PRO:HA	22:o:31:LEU:HB2	2.01	0.43
22:o:379:GLY:HA2	22:o:475:ARG:O	2.19	0.43
22:o:403:GLN:HA	22:o:406:VAL:HG12	2.01	0.43
22:o:420:ILE:HD11	22:o:426:ARG:HH21	1.83	0.43
22:o:1226:LEU:HA	22:o:1230:GLN:NE2	2.34	0.43
24:q:69:GLY:HA3	32:z:57:ALA:HB1	2.01	0.43
26:s:185:ILE:HG22	26:s:209:VAL:HG11	2.01	0.43
33:X:-36:DC:H2''	33:X:-35:DA:H5'	2.00	0.43
33:X:4:DG:H2''	33:X:5:DA:C8	2.54	0.43
34:Y:6:DT:H2''	34:Y:7:DG:C8	2.53	0.43
1:A:592:SER:OG	1:A:695:GLY:O	2.31	0.42
1:A:1158:SER:HA	1:A:1188:PRO:CG	2.48	0.42
5:F:283:MET:HE1	5:F:308:VAL:CG1	2.48	0.42
5:F:401:GLU:C	5:F:401:GLU:CD	2.88	0.42
7:H:110:TYR:CD2	9:J:157:LEU:CD2	3.01	0.42
8:I:23:LEU:HD22	8:I:28:ILE:HD12	2.00	0.42
11:O:77:ASN:O	11:O:79:VAL:HG23	2.19	0.42
11:O:88:ILE:HG23	13:Q:361:ASN:CG	2.33	0.42
13:Q:351:PHE:CD1	13:Q:351:PHE:N	2.87	0.42
18:V:175:LEU:CD1	18:V:180:LYS:N	2.77	0.42
19:c:94:HIS:CD2	5:f:122:LEU:HD22	2.54	0.42
19:c:124:ILE:HD11	5:f:133:ALA:HB1	2.00	0.42
22:o:102:LYS:HZ2	22:o:1445:HIS:CE1	2.37	0.42
22:o:460:ARG:HG2	22:o:461:GLN:N	2.33	0.42
22:o:1303:GLN:OE1	22:o:1303:GLN:N	2.50	0.42
23:p:143:GLN:N	23:p:143:GLN:OE1	2.52	0.42
23:p:937:SER:OG	23:p:938:ARG:N	2.51	0.42
7:H:134:LEU:HD12	7:H:134:LEU:HA	1.94	0.42
8:I:21:GLN:HE22	8:I:24:LYS:HE2	1.84	0.42
16:T:224:ASN:HB3	16:T:226:LYS:HE2	2.01	0.42
18:V:221:ARG:HE	18:V:221:ARG:HB3	1.70	0.42
4:e:332:ILE:HA	4:e:336:HIS:HD2	1.84	0.42
22:o:202:TRP:HB2	22:o:212:LYS:HD3	1.99	0.42
22:o:320:ASN:HB3	22:o:327:ARG:NE	2.34	0.42
22:o:1244:ASN:O	22:o:1259:ILE:HA	2.19	0.42
35:u:120:ASP:OD2	35:u:123:SER:OG	2.28	0.42
1:A:486:TRP:CH2	5:f:358:THR:CG2	3.01	0.42
2:B:490:SER:O	2:B:491:HIS:C	2.63	0.42
2:B:957:MET:O	2:B:968:ARG:NH1	2.53	0.42
3:D:957:ARG:HA	3:D:957:ARG:HD3	1.55	0.42
3:D:961:GLN:O	3:D:965:ILE:HB	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:128:LYS:HE2	23:p:540:PRO:HB3	2.00	0.42
16:T:183:VAL:HA	16:T:186:MET:HE2	2.00	0.42
5:f:354:ARG:HE	5:f:354:ARG:HB2	1.75	0.42
8:i:87:PRO:HA	8:i:88:PRO:HD3	1.90	0.42
22:o:111:CYS:SG	22:o:188:GLN:NE2	2.92	0.42
22:o:721:HIS:HE1	29:w:98:GLN:HE21	1.67	0.42
23:p:296:GLU:CD	23:p:296:GLU:H	2.27	0.42
23:p:629:GLU:O	23:p:630:LYS:C	2.62	0.42
33:X:-2:DG:H2"	33:X:-1:DA:C8	2.54	0.42
33:X:0:DA:H2"	33:X:1:DG:C8	2.54	0.42
1:A:419:GLU:H	1:A:419:GLU:HG3	1.48	0.42
1:A:468:PHE:CD2	5:F:221:GLN:NE2	2.81	0.42
1:A:657:SER:HB2	2:B:475:LYS:NZ	2.35	0.42
1:A:968:ILE:HD12	1:A:968:ILE:HA	1.94	0.42
3:D:905:ALA:HB2	10:L:120:LEU:HD21	2.00	0.42
4:E:257:GLU:OE2	4:E:287:LYS:NZ	2.48	0.42
4:E:377:LEU:HD21	4:E:422:PRO:HG2	2.00	0.42
4:E:615:ASP:OD2	8:I:114:ARG:CG	2.66	0.42
5:F:50:ILE:O	5:F:54:ALA:N	2.47	0.42
5:F:219:GLU:CD	5:F:219:GLU:C	2.86	0.42
5:F:298:GLU:HA	5:F:301:VAL:HG12	2.01	0.42
5:F:350:ASN:OD1	5:F:350:ASN:N	2.50	0.42
7:H:155:ASP:OD1	7:H:155:ASP:N	2.51	0.42
17:U:95:ASN:HD22	17:U:96:TYR:N	2.17	0.42
17:U:136:PHE:HD1	17:U:140:GLU:CD	2.28	0.42
17:U:145:PHE:HD1	17:U:145:PHE:O	2.03	0.42
17:U:192:ARG:HE	17:U:192:ARG:HB3	1.48	0.42
18:V:228:MET:HE3	18:V:228:MET:HB2	1.83	0.42
5:f:432:ALA:HB1	5:f:462:GLN:CB	2.50	0.42
22:o:491:PRO:HG2	22:o:535:MET:HE2	2.01	0.42
22:o:1191:GLU:O	22:o:1195:VAL:HG13	2.19	0.42
22:o:1248:ASN:HD21	22:o:1256:VAL:HB	1.84	0.42
22:o:1296:MET:HG2	22:o:1298:LEU:HG	2.01	0.42
25:r:110:GLU:OE2	35:u:167:TYR:CE2	2.52	0.42
35:u:2:PHE:CE1	35:u:77:PHE:HB2	2.54	0.42
1:A:1022:ARG:HD3	1:A:1022:ARG:HA	1.86	0.42
4:E:299:ASP:OD2	4:E:607:ARG:NH2	2.38	0.42
6:G:181:TRP:O	6:G:181:TRP:CD2	2.72	0.42
10:L:120:LEU:O	10:L:125:ASN:N	2.52	0.42
16:T:214:LYS:NZ	34:Y:17:DG:P	2.91	0.42
17:U:43:VAL:O	17:U:95:ASN:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:100:VAL:CG1	17:U:102:VAL:HG22	2.50	0.42
20:k:179:MET:HB3	20:k:180:PRO:CD	2.50	0.42
22:o:397:PHE:HB3	27:t:87:THR:HG23	2.02	0.42
22:o:404:GLU:HG3	22:o:407:ARG:NH2	2.34	0.42
28:v:32:SER:OG	28:v:33:GLU:N	2.52	0.42
35:u:117:MET:HE1	35:u:163:LEU:HD22	2.02	0.42
1:A:753:TYR:CE2	1:A:1077:LEU:HD12	2.53	0.42
2:B:562:GLY:O	2:B:581:ILE:HG12	2.19	0.42
2:B:925:LYS:HD3	2:B:925:LYS:HA	1.78	0.42
5:F:283:MET:HE1	5:F:308:VAL:CB	2.50	0.42
13:Q:53:SER:O	13:Q:54:ARG:HB2	2.20	0.42
4:e:667:GLY:O	4:e:692:ARG:NH2	2.52	0.42
33:X:-40:DC:O2	34:Y:40:DG:N1	2.53	0.42
2:B:371:LYS:HD3	2:B:371:LYS:HA	1.87	0.42
2:B:831:GLU:OE1	2:B:835:ARG:NH2	2.52	0.42
3:D:966:LEU:C	3:D:966:LEU:CD2	2.89	0.42
4:E:579:VAL:CG2	8:I:115:LEU:HD22	2.49	0.42
11:O:27:GLN:HE22	13:Q:41:GLU:CD	2.28	0.42
14:R:216:SER:HA	14:R:229:GLN:NE2	2.35	0.42
16:T:158:ASN:HD22	16:T:158:ASN:N	2.18	0.42
4:e:504:LEU:HD22	4:e:575:PHE:HZ	1.85	0.42
4:e:636:HIS:CD2	4:e:638:ASN:H	2.37	0.42
5:f:223:TYR:CD2	5:f:255:MET:HE1	2.52	0.42
20:k:130:PRO:HD3	21:m:35:GLU:HG2	2.02	0.42
10:l:129:PRO:HB2	21:m:56:ILE:HG23	2.01	0.42
22:o:1180:ASN:HB3	22:o:1182:GLN:OE1	2.18	0.42
22:o:1208:SER:O	22:o:1260:ARG:NH2	2.44	0.42
22:o:1448:SER:OG	22:o:1449:ASP:N	2.52	0.42
23:p:36:GLU:OE1	23:p:653:TRP:HB3	2.20	0.42
25:r:36:GLU:OE1	25:r:36:GLU:N	2.53	0.42
1:A:657:SER:HB2	2:B:475:LYS:HZ3	1.85	0.42
2:B:846:TYR:CE1	2:B:847:ARG:HD3	2.55	0.42
11:O:7:ARG:NH1	11:O:37:LEU:HB3	2.35	0.42
12:P:278:GLN:CD	12:P:278:GLN:N	2.76	0.42
13:Q:19:GLU:HA	13:Q:19:GLU:OE1	2.19	0.42
16:T:217:LEU:HD13	16:T:233:TRP:CD1	2.55	0.42
18:V:119:LEU:O	18:V:123:ALA:HB3	2.20	0.42
22:o:350:VAL:HG13	22:o:351:ARG:HG3	2.01	0.42
23:p:840:MET:HE2	23:p:891:ASP:OD2	2.20	0.42
23:p:1021:HIS:HD2	23:p:1025:ASN:HB2	1.85	0.42
24:q:44:ILE:HD11	24:q:238:SER:CB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:87:LEU:H	25:r:87:LEU:HG	1.64	0.42
31:y:26:LYS:HG3	31:y:27:VAL:HG22	2.00	0.42
35:u:78:ARG:HG3	35:u:80:PHE:CE1	2.54	0.42
2:B:219:ASP:OD1	2:B:219:ASP:N	2.52	0.42
5:F:213:ILE:CG2	7:H:163:PRO:C	2.93	0.42
12:P:167:ASN:HD22	12:P:167:ASN:C	2.28	0.42
16:T:181:GLN:HE22	16:T:184:LEU:HD13	1.84	0.42
5:f:320:ARG:HH11	5:f:320:ARG:HB2	1.83	0.42
22:o:1005:HIS:O	22:o:1008:LYS:HB2	2.20	0.42
22:o:1230:GLN:HB2	22:o:1234:LYS:NZ	2.34	0.42
22:o:1361:ASP:OD1	22:o:1363:VAL:HG22	2.20	0.42
24:q:11:ILE:HD11	31:y:109:ILE:HG22	2.02	0.42
31:y:82:SER:OG	31:y:84:GLN:OE1	2.38	0.42
4:E:747:LEU:N	4:E:747:LEU:HD13	2.34	0.42
5:F:62:LYS:HZ3	5:F:62:LYS:HG3	1.75	0.42
11:O:7:ARG:NH2	11:O:37:LEU:HB3	2.33	0.42
14:R:46:ILE:N	22:o:67:ARG:HH21	2.18	0.42
14:R:124:MET:HE2	14:R:124:MET:HB2	1.82	0.42
17:U:190:LEU:HD13	17:U:190:LEU:HA	1.85	0.42
4:e:633:THR:O	4:e:634:ARG:NH2	2.45	0.42
5:f:244:GLN:O	5:f:248:THR:OG1	2.34	0.42
20:k:179:MET:HB3	20:k:180:PRO:HD2	2.01	0.42
22:o:140:ARG:HH12	22:o:235:VAL:HA	1.85	0.42
25:r:29:ALA:HB1	35:u:3:TYR:CG	2.55	0.42
33:X:-26:DC:H3'	33:X:-26:DC:P	2.60	0.42
1:A:645:LYS:HA	1:A:645:LYS:HD2	1.76	0.41
1:A:825:ILE:HD12	1:A:830:ILE:HD11	2.02	0.41
1:A:954:ALA:HA	6:G:149:ARG:HH22	1.85	0.41
2:B:848:HIS:CD2	7:H:226:ALA:HB2	2.55	0.41
3:D:898:VAL:CG2	10:L:113:VAL:CG2	2.96	0.41
7:H:106:THR:CB	9:J:161:LYS:NZ	2.83	0.41
12:P:196:ARG:NH1	16:T:172:ASP:CB	2.83	0.41
14:R:14:THR:N	14:R:20:ASP:HB3	2.34	0.41
14:R:38:GLY:O	22:o:427:ILE:CG2	2.67	0.41
14:R:154:ARG:NH2	34:Y:22:DG:P	2.93	0.41
17:U:108:ASP:HB2	18:V:234:GLU:HG3	2.02	0.41
4:e:504:LEU:HD23	4:e:504:LEU:HA	1.90	0.41
21:m:68:MET:HE3	21:m:68:MET:HB3	1.95	0.41
22:o:15:LEU:HA	23:p:1148:LEU:O	2.20	0.41
22:o:1145:GLY:C	22:o:1147:SER:N	2.78	0.41
25:r:36:GLU:HA	25:r:39:MET:HE2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Y:-4:DC:H2"	34:Y:-3:DA:C8	2.55	0.41
35:u:38:CYS:C	35:u:155:ASN:OD1	2.62	0.41
1:A:639:LEU:HD12	1:A:643:ILE:CD1	2.46	0.41
3:D:1006:LEU:CD1	11:O:68:CYS:C	2.93	0.41
5:F:360:THR:O	5:F:364:VAL:HG22	2.21	0.41
7:H:166:ARG:HD2	7:H:166:ARG:HA	1.87	0.41
11:O:19:LEU:O	11:O:23:ILE:HG13	2.20	0.41
12:P:329:TYR:N	12:P:330:PRO:HD2	2.35	0.41
14:R:137:ARG:HH11	14:R:170:GLN:HB3	1.85	0.41
17:U:202:GLU:OE1	17:U:202:GLU:HA	2.20	0.41
4:e:554:ASP:OD1	4:e:554:ASP:N	2.45	0.41
5:f:428:LEU:HD13	5:f:458:LEU:CB	2.49	0.41
8:i:45:ARG:HG3	9:j:212:LYS:HB3	2.01	0.41
10:l:105:HIS:C	10:l:107:LYS:H	2.28	0.41
22:o:330:GLN:O	22:o:331:LYS:HE2	2.19	0.41
22:o:437:ASP:OD1	22:o:438:LEU:N	2.53	0.41
22:o:1098:PRO:O	22:o:1101:GLN:HG2	2.20	0.41
22:o:1430:CYS:HA	22:o:1435:THR:HA	2.03	0.41
23:p:267:VAL:HG12	23:p:268:PRO:O	2.20	0.41
23:p:341:GLU:HG2	23:p:342:VAL:N	2.35	0.41
23:p:728:MET:HE2	23:p:942:LYS:HD3	2.02	0.41
23:p:1088:GLU:OE1	23:p:1091:ARG:NH1	2.53	0.41
35:u:79:PRO:HG3	35:u:104:MET:SD	2.60	0.41
3:D:898:VAL:HG22	10:L:113:VAL:HA	2.02	0.41
4:E:508:LYS:HB3	4:E:512:ASP:HB2	2.02	0.41
11:O:15:LEU:HD23	11:O:40:PHE:CE2	2.55	0.41
11:O:65:TYR:CD1	12:P:191:GLU:HG2	2.46	0.41
12:P:250:PHE:O	13:Q:311:GLU:CG	2.68	0.41
14:R:289:TYR:HA	14:R:292:ILE:HG12	2.03	0.41
15:S:37:VAL:HG11	15:S:42:TRP:CZ2	2.55	0.41
16:T:126:ARG:NH2	16:T:130:LEU:HD11	2.35	0.41
18:V:229:ASP:HB2	22:o:227:ARG:NH2	2.16	0.41
22:o:1146:GLN:HA	22:o:1149:ARG:HE	1.85	0.41
23:p:691:SER:O	23:p:691:SER:OG	2.38	0.41
23:p:718:GLN:HG2	23:p:720:PRO:HD2	2.01	0.41
33:X:-4:DT:H2"	33:X:-3:DG:C8	2.56	0.41
34:Y:33:DG:H2'	34:Y:34:DA:C8	2.55	0.41
1:A:1195:VAL:HG13	1:A:1198:ARG:NH2	2.35	0.41
2:B:487:LYS:O	2:B:487:LYS:CG	2.67	0.41
3:D:891:ILE:HG21	10:L:111:LEU:CG	2.50	0.41
6:G:74:MET:HE1	6:G:136:ILE:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:154:LYS:O	6:G:154:LYS:HG2	2.20	0.41
10:L:106:ARG:HD2	10:L:114:LYS:HZ3	1.85	0.41
11:O:88:ILE:HD12	13:Q:360:LEU:CG	2.50	0.41
16:T:169:LYS:HA	16:T:169:LYS:HE3	2.02	0.41
18:V:153:ARG:HD3	18:V:153:ARG:HA	1.77	0.41
9:j:149:PRO:O	9:j:153:ARG:NH1	2.46	0.41
22:o:927:GLU:HG3	22:o:927:GLU:O	2.18	0.41
22:o:1006:PRO:HB3	22:o:1051:SER:OG	2.20	0.41
22:o:1054:MET:HE1	22:o:1065:PHE:CE1	2.56	0.41
1:A:604:PRO:O	1:A:889:TYR:OH	2.34	0.41
2:B:176:HIS:HE1	2:B:310:ASP:H	1.67	0.41
2:B:835:ARG:HE	2:B:835:ARG:HB2	1.73	0.41
3:D:965:ILE:HG22	3:D:966:LEU:H	1.84	0.41
11:O:39:GLN:HG3	13:Q:25:VAL:CG1	2.50	0.41
12:P:167:ASN:HD21	12:P:259:VAL:N	2.19	0.41
16:T:160:GLN:H	16:T:160:GLN:HG3	1.66	0.41
17:U:145:PHE:CD1	17:U:145:PHE:O	2.74	0.41
5:f:215:GLU:CD	5:f:215:GLU:N	2.78	0.41
5:f:402:ARG:HH22	5:f:403:ILE:HD12	1.85	0.41
22:o:355:MET:N	22:o:355:MET:SD	2.94	0.41
22:o:1129:ASN:HD21	22:o:1415:THR:HB	1.85	0.41
22:o:1158:LEU:HD22	22:o:1309:MET:HE3	2.02	0.41
32:z:29:LYS:HE2	32:z:29:LYS:HB2	1.94	0.41
1:A:847:LYS:HE2	1:A:847:LYS:HB3	1.77	0.41
1:A:950:VAL:CG2	1:A:1065:GLU:HG2	2.50	0.41
2:B:55:PRO:HB3	2:B:60:LEU:HD22	2.02	0.41
2:B:937:THR:HG22	2:B:940:MET:HG3	2.03	0.41
4:E:359:LEU:HD12	4:E:359:LEU:C	2.46	0.41
5:F:249:ASP:HB3	5:F:252:LEU:HB2	2.02	0.41
11:O:82:ARG:HA	11:O:87:LEU:HA	2.03	0.41
12:P:179:ASP:OD1	12:P:179:ASP:C	2.62	0.41
12:P:264:VAL:HG23	12:P:266:PHE:H	1.84	0.41
14:R:118:PHE:HA	14:R:121:ILE:HB	2.02	0.41
17:U:139:LEU:H	17:U:139:LEU:HG	1.46	0.41
18:V:77:VAL:HG13	18:V:81:ILE:CD1	2.50	0.41
18:V:81:ILE:HG23	18:V:102:ILE:HD13	2.03	0.41
3:d:871:THR:O	10:l:62:LYS:NZ	2.42	0.41
5:f:55:LEU:HD13	8:i:28:ILE:HG12	2.01	0.41
22:o:1156:ASP:OD1	22:o:1156:ASP:C	2.64	0.41
22:o:1304:ILE:O	22:o:1304:ILE:HG13	2.21	0.41
35:u:142:GLU:O	35:u:170:LEU:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:964:GLU:H	3:D:964:GLU:HG3	1.40	0.41
5:F:213:ILE:CG2	7:H:164:THR:O	2.63	0.41
5:F:311:CYS:HB3	5:F:330:ARG:HH12	1.86	0.41
5:F:313:VAL:HG11	5:F:376:SER:N	2.33	0.41
5:F:374:TYR:CE1	5:F:422:HIS:HB3	2.56	0.41
18:V:140:LYS:H	18:V:140:LYS:HG3	1.79	0.41
5:f:336:LEU:HD12	5:f:336:LEU:HA	1.89	0.41
22:o:76:GLY:HA3	22:o:81:CYS:HB2	2.03	0.41
22:o:1429:LYS:HE2	22:o:1429:LYS:HA	2.01	0.41
23:p:395:LEU:HD23	23:p:395:LEU:HA	1.93	0.41
23:p:468:GLN:H	23:p:468:GLN:HG2	1.72	0.41
34:Y:3:DC:H2''	34:Y:4:DA:C8	2.55	0.41
34:Y:36:DG:H2''	34:Y:37:DT:C6	2.56	0.41
2:B:544:LEU:HD22	2:B:625:LEU:HD22	2.03	0.41
3:D:933:ARG:HG2	8:I:132:LEU:HB3	2.03	0.41
4:E:239:LEU:HB3	4:E:307:LEU:HD21	2.03	0.41
5:F:213:ILE:CB	7:H:163:PRO:C	2.90	0.41
5:F:277:ALA:O	5:F:278:LEU:C	2.64	0.41
16:T:208:GLN:HB2	16:T:209:PRO:HD2	2.03	0.41
17:U:163:GLU:C	17:U:165:GLU:H	2.28	0.41
17:U:180:PHE:CE1	18:V:214:GLU:HG2	2.56	0.41
18:V:175:LEU:HD12	18:V:180:LYS:H	1.81	0.41
23:p:957:THR:HG22	23:p:1028:LEU:CD2	2.51	0.41
25:r:29:ALA:HA	35:u:5:ILE:HG22	2.03	0.41
33:X:-27:DT:H3'	33:X:-27:DT:OP2	2.20	0.41
33:X:-22:DC:H2''	33:X:-21:DA:C8	2.56	0.41
1:A:511:LEU:HD13	1:A:511:LEU:N	2.36	0.41
1:A:899:LYS:HB2	1:A:899:LYS:HE3	1.81	0.41
2:B:77:ILE:HG12	2:B:146:ILE:HG23	2.03	0.41
2:B:560:TYR:CE2	2:B:581:ILE:HD11	2.56	0.41
2:B:984:PRO:HG2	2:B:987:LEU:HD22	2.03	0.41
5:F:15:PRO:HB2	5:F:17:GLU:HG2	2.02	0.41
5:F:231:CYS:HB3	5:F:285:MET:HE2	2.02	0.41
5:F:286:VAL:HG11	5:F:308:VAL:HG11	2.01	0.41
5:F:396:LEU:HA	5:F:399:GLU:CD	2.46	0.41
7:H:73:GLY:C	9:J:142:ALA:CB	2.94	0.41
10:L:106:ARG:CD	10:L:114:LYS:NZ	2.83	0.41
14:R:259:TYR:HD1	14:R:274:ILE:HD12	1.86	0.41
17:U:105:TYR:CE1	18:V:222:SER:HB2	2.56	0.41
17:U:188:TYR:HD1	17:U:192:ARG:HB2	1.86	0.41
5:f:104:LEU:HD22	9:j:216:TYR:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:o:229:SER:OG	22:o:230:ASP:N	2.54	0.41
22:o:448:ARG:NH1	22:o:451:CYS:SG	2.94	0.41
22:o:576:GLN:HG3	22:o:577:PRO:HD2	2.03	0.41
22:o:1428:MET:SD	22:o:1429:LYS:HG2	2.61	0.41
23:p:634:LEU:HD23	23:p:634:LEU:HA	1.86	0.41
23:p:639:HIS:O	23:p:643:LEU:HB2	2.21	0.41
25:r:110:GLU:HG3	35:u:167:TYR:HB3	1.91	0.41
26:s:43:GLN:NE2	26:s:44:PHE:CZ	2.89	0.41
33:X:-44:DA:H2''	33:X:-43:DA:C8	2.56	0.41
34:Y:-17:DC:H2''	34:Y:-16:DA:C8	2.56	0.41
34:Y:27:DA:H2''	34:Y:28:DG:H5''	2.03	0.41
35:u:146:LYS:HD3	35:u:165:ASP:OD2	2.21	0.41
35:u:154:LYS:HG3	35:u:155:ASN:H	1.86	0.41
2:B:713:TRP:NE1	2:B:716:PRO:O	2.50	0.41
4:E:440:LYS:HE2	4:E:440:LYS:HB3	1.93	0.41
12:P:193:ASN:HD22	12:P:194:PRO:HD2	1.86	0.41
14:R:18:HIS:CE1	14:R:37:CYS:SG	3.00	0.41
22:o:12:ALA:HB3	23:p:1135:TYR:HE2	1.85	0.41
22:o:92:LYS:HE2	22:o:290:LEU:HD21	2.03	0.41
22:o:191:ILE:HA	22:o:199:TYR:O	2.21	0.41
22:o:1029:LEU:HD11	26:s:159:LEU:HD23	2.02	0.41
22:o:1375:ARG:NH1	22:o:1379:GLU:OE1	2.54	0.41
22:o:1472:ASP:OD1	22:o:1472:ASP:N	2.53	0.41
23:p:90:GLN:HG3	23:p:91:ILE:N	2.34	0.41
23:p:109:MET:HB2	23:p:112:GLU:OE1	2.20	0.41
23:p:193:VAL:O	23:p:467:SER:HA	2.20	0.41
23:p:968:ASN:OD1	23:p:969:PRO:HD2	2.21	0.41
25:r:110:GLU:CD	35:u:167:TYR:HB2	2.46	0.41
26:s:55:ARG:O	26:s:76:PHE:HB2	2.21	0.41
29:w:60:HIS:O	29:w:60:HIS:ND1	2.54	0.41
35:u:89:VAL:HA	35:u:99:THR:HA	2.03	0.41
2:B:295:LEU:HD13	2:B:477:LEU:HD11	2.03	0.40
2:B:848:HIS:NE2	7:H:225:THR:HG23	2.36	0.40
3:D:962:GLU:CA	3:D:965:ILE:HB	2.49	0.40
4:E:651:VAL:HG21	4:E:686:THR:HG21	2.01	0.40
5:F:388:ILE:HA	5:F:392:ILE:HG12	2.02	0.40
5:F:396:LEU:HA	5:F:399:GLU:OE1	2.20	0.40
5:F:426:LEU:O	5:F:429:LYS:HG2	2.21	0.40
8:I:132:LEU:CG	9:J:121:MET:HE2	2.38	0.40
12:P:202:MET:HE3	12:P:202:MET:HB2	1.85	0.40
12:P:274:VAL:HG11	14:R:208:LEU:CG	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:283:VAL:O	14:R:287:GLN:HG2	2.20	0.40
16:T:25:LYS:O	16:T:29:GLN:N	2.45	0.40
18:V:181:ALA:O	18:V:184:ALA:CA	2.69	0.40
18:V:199:LYS:HE3	18:V:199:LYS:HB2	1.77	0.40
22:o:318:VAL:HG23	22:o:319:ASP:N	2.37	0.40
22:o:814:ASP:OD2	23:p:689:TYR:OH	2.17	0.40
22:o:859:TYR:CE2	22:o:863:ARG:HD2	2.56	0.40
22:o:1018:LYS:HE3	22:o:1018:LYS:HB2	1.90	0.40
22:o:1204:VAL:HG23	22:o:1205:ALA:H	1.85	0.40
22:o:1231:ILE:O	22:o:1235:ILE:HG12	2.20	0.40
23:p:100:GLU:HG3	23:p:101:ARG:H	1.85	0.40
23:p:516:GLU:HA	23:p:520:VAL:HG22	2.02	0.40
23:p:794:VAL:HG22	23:p:944:THR:O	2.20	0.40
25:r:44:ARG:HA	25:r:44:ARG:HD2	1.90	0.40
1:A:725:CYS:SG	1:A:734:LEU:HD12	2.61	0.40
2:B:218:GLY:HA2	2:B:238:LEU:HD13	2.03	0.40
5:F:68:THR:HG23	8:I:34:ARG:HB2	2.03	0.40
5:F:126:PRO:CD	7:H:29:TYR:HA	2.51	0.40
5:F:233:GLY:CA	5:F:239:ARG:HE	2.34	0.40
5:F:335:ARG:O	5:F:339:GLN:HB3	2.22	0.40
5:F:350:ASN:O	5:F:354:ARG:HB2	2.21	0.40
11:O:22:LEU:CD1	11:O:28:ILE:HG21	2.41	0.40
13:Q:43:LYS:HE2	13:Q:60:HIS:CE1	2.56	0.40
14:R:47:ASP:HB2	23:p:1069:ILE:HD11	2.02	0.40
16:T:184:LEU:O	16:T:185:ASP:C	2.64	0.40
17:U:160:GLU:OE1	17:U:160:GLU:HA	2.20	0.40
17:U:180:PHE:O	17:U:184:ILE:HG13	2.21	0.40
18:V:152:LEU:HD12	18:V:152:LEU:HA	1.89	0.40
19:c:105:ASN:OD1	19:c:105:ASN:N	2.55	0.40
3:d:892:THR:OG1	3:d:893:GLU:OE1	2.33	0.40
22:o:286:ILE:HA	22:o:289:GLN:HG3	2.03	0.40
22:o:486:LEU:HD22	23:p:790:GLN:OE1	2.22	0.40
22:o:689:ILE:CD1	23:p:985:LEU:HD22	2.51	0.40
22:o:948:ILE:HG12	22:o:1007:ILE:HG21	2.02	0.40
22:o:1099:ALA:HA	22:o:1102:MET:HG3	2.03	0.40
23:p:1119:CYS:SG	23:p:1121:LEU:HD23	2.61	0.40
1:A:620:LEU:HD11	1:A:766:ARG:HD3	2.02	0.40
5:F:350:ASN:O	5:F:354:ARG:NH1	2.54	0.40
6:G:128:LYS:HE3	6:G:128:LYS:HB3	1.99	0.40
7:H:38:GLN:NE2	7:H:59:GLU:OE2	2.54	0.40
18:V:155:LEU:HD21	18:V:189:ILE:HG12	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:c:28:LEU:HD23	19:c:28:LEU:HA	1.89	0.40
22:o:1130:ILE:HG23	22:o:1362:ILE:HD11	2.02	0.40
22:o:1486:ILE:HB	22:o:1487:PRO:HD3	2.03	0.40
23:p:606:ASP:OD1	23:p:606:ASP:N	2.44	0.40
23:p:961:ILE:CG1	30:x:42:ARG:HD2	2.52	0.40
23:p:980:HIS:O	23:p:980:HIS:ND1	2.54	0.40
23:p:991:ALA:O	30:x:46:ARG:NE	2.52	0.40
24:q:225:LYS:HG3	24:q:226:PRO:HD2	2.03	0.40
35:u:44:PHE:CE2	35:u:46:ILE:HG12	2.52	0.40
1:A:345:PRO:O	1:A:346:ALA:HB3	2.21	0.40
1:A:1065:GLU:OE1	1:A:1065:GLU:HA	2.21	0.40
1:A:1200:THR:O	1:A:1204:GLU:HG2	2.22	0.40
2:B:203:LYS:HZ3	2:B:235:HIS:HB3	1.86	0.40
4:E:306:VAL:HG21	4:E:363:ALA:HA	2.04	0.40
4:E:466:PHE:HE1	4:E:794:ALA:HB1	1.86	0.40
11:O:60:GLY:HA2	11:O:79:VAL:CG1	2.35	0.40
12:P:292:ILE:HG23	12:P:301:VAL:HG13	2.03	0.40
17:U:94:ILE:HG22	17:U:95:ASN:H	1.86	0.40
18:V:166:ILE:H	18:V:166:ILE:HG12	1.55	0.40
4:e:620:LEU:HD13	8:i:104:LEU:HD22	2.04	0.40
4:e:783:LEU:HD23	4:e:783:LEU:HA	1.93	0.40
22:o:102:LYS:O	22:o:106:VAL:HG13	2.22	0.40
23:p:368:MET:HE3	23:p:368:MET:HB2	1.85	0.40
26:s:81:LYS:HA	26:s:109:GLY:O	2.21	0.40
33:X:-23:DC:H2"	33:X:-22:DC:C6	2.57	0.40
34:Y:-38:DC:H2"	34:Y:-37:DT:C6	2.57	0.40
2:B:180:CYS:HB2	2:B:313:TYR:HB2	2.04	0.40
5:F:67:THR:HA	8:I:32:GLU:HG3	2.04	0.40
9:J:200:LEU:HD23	9:J:200:LEU:HA	1.95	0.40
15:S:15:VAL:HG13	16:T:41:GLY:O	2.20	0.40
15:S:25:LYS:CE	16:T:98:GLU:OE1	2.70	0.40
17:U:129:CYS:HB2	17:U:154:CYS:HB2	2.02	0.40
17:U:136:PHE:HB3	17:U:140:GLU:HB3	2.03	0.40
23:p:553:LEU:HD23	23:p:553:LEU:HA	1.87	0.40
23:p:837:CYS:HA	23:p:889:LYS:O	2.21	0.40
31:y:11:LEU:HD12	31:y:11:LEU:HA	1.93	0.40
33:X:-32:DC:H42	34:Y:32:DG:H1	1.69	0.40
35:u:27:LYS:HD3	35:u:51:ILE:HD11	2.02	0.40
35:u:163:LEU:HD23	35:u:163:LEU:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	584/1872 (31%)	552 (94%)	30 (5%)	2 (0%)	36	70
2	B	959/1199 (80%)	914 (95%)	45 (5%)	0	100	100
3	D	158/1085 (15%)	142 (90%)	15 (10%)	1 (1%)	21	58
3	d	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
4	E	540/800 (68%)	507 (94%)	30 (6%)	3 (1%)	21	58
4	e	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
5	F	400/677 (59%)	375 (94%)	21 (5%)	4 (1%)	12	46
5	f	399/677 (59%)	380 (95%)	19 (5%)	0	100	100
6	G	139/349 (40%)	137 (99%)	2 (1%)	0	100	100
7	H	207/310 (67%)	186 (90%)	18 (9%)	3 (1%)	9	39
8	I	118/264 (45%)	115 (98%)	3 (2%)	0	100	100
8	i	119/264 (45%)	115 (97%)	4 (3%)	0	100	100
9	J	85/218 (39%)	82 (96%)	3 (4%)	0	100	100
9	j	91/218 (42%)	89 (98%)	2 (2%)	0	100	100
10	L	74/161 (46%)	67 (90%)	7 (10%)	0	100	100
10	l	105/161 (65%)	100 (95%)	5 (5%)	0	100	100
11	O	95/109 (87%)	83 (87%)	9 (10%)	3 (3%)	3	24
12	P	175/339 (52%)	166 (95%)	7 (4%)	2 (1%)	11	44
13	Q	118/376 (31%)	107 (91%)	10 (8%)	1 (1%)	16	52
14	R	247/316 (78%)	237 (96%)	9 (4%)	1 (0%)	30	65
15	S	104/517 (20%)	99 (95%)	3 (3%)	2 (2%)	6	34
16	T	218/249 (88%)	197 (90%)	15 (7%)	6 (3%)	4	27
17	U	175/439 (40%)	154 (88%)	18 (10%)	3 (2%)	7	36
18	V	170/291 (58%)	131 (77%)	29 (17%)	10 (6%)	1	16
19	c	125/929 (14%)	116 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	k	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
21	m	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
22	o	1417/1487 (95%)	1304 (92%)	113 (8%)	0	100	100
23	p	1128/1174 (96%)	1050 (93%)	77 (7%)	1 (0%)	48	81
24	q	253/273 (93%)	226 (89%)	27 (11%)	0	100	100
25	r	126/142 (89%)	119 (94%)	7 (6%)	0	100	100
26	s	207/210 (99%)	196 (95%)	11 (5%)	0	100	100
27	t	77/127 (61%)	74 (96%)	3 (4%)	0	100	100
28	v	146/150 (97%)	133 (91%)	13 (9%)	0	100	100
29	w	112/125 (90%)	103 (92%)	9 (8%)	0	100	100
30	x	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
31	y	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
32	z	42/58 (72%)	38 (90%)	4 (10%)	0	100	100
35	u	169/172 (98%)	156 (92%)	12 (7%)	1 (1%)	21	58
All	All	10125/18139 (56%)	9423 (93%)	659 (6%)	43 (0%)	31	65

All (43) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1158	SER
5	F	323	VAL
7	H	141	PRO
11	O	52	VAL
15	S	9	GLN
16	T	140	ARG
16	T	174	LYS
17	U	124	ARG
18	V	177	ASN
35	u	154	LYS
4	E	522	ASP
4	E	704	VAL
11	O	26	GLN
18	V	79	ALA
18	V	128	PRO
18	V	171	ILE
18	V	208	CYS
3	D	934	TYR

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Mol	Chain	Res	Type
5	F	64	GLN
12	P	207	PRO
16	T	231	ASN
18	V	134	ASP
18	V	196	ASP
18	V	207	SER
5	F	439	ARG
11	O	84	VAL
13	Q	320	VAL
15	S	7	SER
16	T	226	LYS
17	U	121	SER
17	U	145	PHE
18	V	194	ARG
18	V	225	VAL
5	F	318	CYS
7	H	134	LEU
7	H	164	THR
16	T	38	GLY
23	p	912	ASN
12	P	298	PRO
14	R	247	GLY
4	E	523	VAL
16	T	40	VAL
1	A	498	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	536/1665 (32%)	480 (90%)	56 (10%)	7	24
2	B	876/1083 (81%)	855 (98%)	21 (2%)	43	63
3	D	147/815 (18%)	113 (77%)	34 (23%)	1	6
3	d	146/815 (18%)	146 (100%)	0	100	100
4	E	478/657 (73%)	475 (99%)	3 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	e	475/657 (72%)	473 (100%)	2 (0%)	84	83
5	F	320/574 (56%)	292 (91%)	28 (9%)	9	31
5	f	322/574 (56%)	311 (97%)	11 (3%)	32	55
6	G	133/322 (41%)	125 (94%)	8 (6%)	17	42
7	H	181/270 (67%)	167 (92%)	14 (8%)	12	34
8	I	106/235 (45%)	101 (95%)	5 (5%)	23	47
8	i	107/235 (46%)	106 (99%)	1 (1%)	70	76
9	J	78/154 (51%)	78 (100%)	0	100	100
9	j	83/154 (54%)	83 (100%)	0	100	100
10	L	71/141 (50%)	69 (97%)	2 (3%)	38	59
10	l	98/141 (70%)	94 (96%)	4 (4%)	27	50
11	O	84/98 (86%)	75 (89%)	9 (11%)	6	23
12	P	153/293 (52%)	131 (86%)	22 (14%)	3	16
13	Q	111/324 (34%)	102 (92%)	9 (8%)	11	33
14	R	214/268 (80%)	194 (91%)	20 (9%)	8	28
15	S	93/448 (21%)	92 (99%)	1 (1%)	65	74
16	T	196/218 (90%)	177 (90%)	19 (10%)	8	27
17	U	163/373 (44%)	135 (83%)	28 (17%)	2	12
18	V	155/261 (59%)	121 (78%)	34 (22%)	1	6
19	c	113/833 (14%)	111 (98%)	2 (2%)	51	67
20	k	87/182 (48%)	87 (100%)	0	100	100
21	m	80/106 (76%)	79 (99%)	1 (1%)	61	72
22	o	1257/1306 (96%)	1247 (99%)	10 (1%)	73	77
23	p	993/1027 (97%)	987 (99%)	6 (1%)	78	80
24	q	234/250 (94%)	234 (100%)	0	100	100
25	r	106/126 (84%)	106 (100%)	0	100	100
26	s	191/192 (100%)	191 (100%)	0	100	100
27	t	69/111 (62%)	69 (100%)	0	100	100
28	v	129/131 (98%)	129 (100%)	0	100	100
29	w	103/112 (92%)	103 (100%)	0	100	100
30	x	53/53 (100%)	53 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	y	106/106 (100%)	106 (100%)	0	100	100
32	z	41/55 (74%)	41 (100%)	0	100	100
35	u	152/153 (99%)	150 (99%)	2 (1%)	61	72
All	All	9040/15518 (58%)	8688 (96%)	352 (4%)	30	51

All (352) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	348	LEU
1	A	353	LEU
1	A	395	ASP
1	A	397	LEU
1	A	400	GLU
1	A	401	ASN
1	A	403	LEU
1	A	404	MET
1	A	408	LEU
1	A	410	TRP
1	A	411	GLU
1	A	415	ILE
1	A	419	GLU
1	A	475	LEU
1	A	481	GLU
1	A	483	ASN
1	A	484	ILE
1	A	491	MET
1	A	499	VAL
1	A	500	LEU
1	A	501	THR
1	A	502	LEU
1	A	505	ASN
1	A	511	LEU
1	A	661	GLU
1	A	667	THR
1	A	711	ASP
1	A	727	THR
1	A	730	PHE
1	A	797	LYS
1	A	798	ARG
1	A	804	ARG
1	A	828	GLU

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Mol	Chain	Res	Type
1	A	853	LYS
1	A	925	ASP
1	A	943	LYS
1	A	970	ASN
1	A	971	LYS
1	A	996	ARG
1	A	997	ARG
1	A	998	LEU
1	A	1001	LYS
1	A	1004	LYS
1	A	1007	LEU
1	A	1008	ARG
1	A	1019	LYS
1	A	1021	SER
1	A	1022	ARG
1	A	1025	VAL
1	A	1052	ARG
1	A	1055	VAL
1	A	1150	THR
1	A	1165	LEU
1	A	1181	ARG
1	A	1182	CYS
1	A	1203	GLU
2	B	21	GLU
2	B	71	ARG
2	B	140	GLU
2	B	184	ASN
2	B	262	MET
2	B	266	THR
2	B	293	GLU
2	B	431	LEU
2	B	559	LYS
2	B	603	LYS
2	B	640	VAL
2	B	746	SER
2	B	760	LEU
2	B	771	VAL
2	B	816	VAL
2	B	820	ASP
2	B	844	PRO
2	B	847	ARG
2	B	848	HIS

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Mol	Chain	Res	Type
2	B	849	THR
2	B	987	LEU
3	D	929	LYS
3	D	932	ASP
3	D	935	GLU
3	D	936	GLN
3	D	938	SER
3	D	939	ASP
3	D	941	ARG
3	D	944	LEU
3	D	945	LYS
3	D	946	PHE
3	D	947	PHE
3	D	948	GLU
3	D	949	GLN
3	D	950	LEU
3	D	951	ASP
3	D	952	GLN
3	D	953	ILE
3	D	955	LYS
3	D	957	ARG
3	D	958	LYS
3	D	959	ASP
3	D	960	GLU
3	D	962	GLU
3	D	963	ARG
3	D	964	GLU
3	D	965	ILE
3	D	966	LEU
3	D	967	MET
3	D	968	ARG
3	D	983	ARG
3	D	1054	ARG
3	D	1055	ILE
3	D	1056	THR
3	D	1057	ARG
4	E	745	GLU
4	E	746	ASP
4	E	747	LEU
5	F	17	GLU
5	F	19	MET
5	F	62	LYS

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Mol	Chain	Res	Type
5	F	89	GLN
5	F	90	GLU
5	F	92	ILE
5	F	136	LEU
5	F	261	THR
5	F	269	VAL
5	F	271	VAL
5	F	280	ILE
5	F	295	LEU
5	F	301	VAL
5	F	304	LEU
5	F	317	LEU
5	F	329	LEU
5	F	330	ARG
5	F	337	VAL
5	F	339	GLN
5	F	348	THR
5	F	354	ARG
5	F	368	THR
5	F	397	GLN
5	F	406	VAL
5	F	408	ASP
5	F	415	ILE
5	F	416	ASP
5	F	427	LEU
6	G	41	ASP
6	G	129	LYS
6	G	131	ILE
6	G	143	VAL
6	G	154	LYS
6	G	181	TRP
6	G	182	GLU
6	G	183	ILE
7	H	115	GLN
7	H	132	LYS
7	H	135	THR
7	H	155	ASP
7	H	159	TYR
7	H	164	THR
7	H	203	LEU
7	H	205	LYS
7	H	206	ASP

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Mol	Chain	Res	Type
7	H	207	ASP
7	H	217	ARG
7	H	219	PHE
7	H	220	THR
7	H	221	ILE
8	I	14	LYS
8	I	15	ASP
8	I	31	TYR
8	I	32	GLU
8	I	34	ARG
10	L	85	LEU
10	L	87	ILE
11	O	24	GLN
11	O	52	VAL
11	O	54	ASN
11	O	55	ARG
11	O	56	VAL
11	O	57	ASN
11	O	59	ARG
11	O	76	LEU
11	O	84	VAL
12	P	166	GLN
12	P	167	ASN
12	P	172	VAL
12	P	208	ARG
12	P	209	THR
12	P	212	LEU
12	P	213	ILE
12	P	215	SER
12	P	221	CYS
12	P	239	ARG
12	P	242	GLN
12	P	252	ASP
12	P	268	ILE
12	P	269	ARG
12	P	274	VAL
12	P	278	GLN
12	P	300	ILE
12	P	309	LYS
12	P	312	LEU
12	P	313	THR
12	P	317	VAL

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Mol	Chain	Res	Type
12	P	328	ILE
13	Q	13	LEU
13	Q	34	VAL
13	Q	318	ASP
13	Q	320	VAL
13	Q	345	SER
13	Q	346	LYS
13	Q	364	ASP
13	Q	366	ILE
13	Q	369	LYS
14	R	31	ASP
14	R	39	LEU
14	R	40	VAL
14	R	41	VAL
14	R	107	MET
14	R	111	ASP
14	R	112	ARG
14	R	114	MET
14	R	115	MET
14	R	120	GLU
14	R	124	MET
14	R	128	ILE
14	R	129	ASN
14	R	130	LEU
14	R	132	ARG
14	R	134	ILE
14	R	135	VAL
14	R	137	ARG
14	R	193	ARG
14	R	286	ARG
15	S	9	GLN
16	T	35	SER
16	T	37	ARG
16	T	40	VAL
16	T	42	LYS
16	T	47	LYS
16	T	85	LEU
16	T	88	VAL
16	T	91	GLN
16	T	93	LEU
16	T	125	MET
16	T	137	LYS

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Mol	Chain	Res	Type
16	T	141	LEU
16	T	158	ASN
16	T	160	GLN
16	T	177	ARG
16	T	180	LYS
16	T	184	LEU
16	T	200	LYS
16	T	211	VAL
17	U	28	ILE
17	U	39	ARG
17	U	42	CYS
17	U	45	GLU
17	U	73	LYS
17	U	76	MET
17	U	77	ARG
17	U	94	ILE
17	U	95	ASN
17	U	100	VAL
17	U	102	VAL
17	U	110	MET
17	U	111	ARG
17	U	113	ARG
17	U	114	ILE
17	U	115	GLU
17	U	119	ARG
17	U	122	THR
17	U	139	LEU
17	U	145	PHE
17	U	166	SER
17	U	168	MET
17	U	170	LYS
17	U	171	LYS
17	U	185	GLU
17	U	190	LEU
17	U	191	LEU
17	U	192	ARG
18	V	93	ASP
18	V	97	LEU
18	V	129	LYS
18	V	131	GLU
18	V	140	LYS
18	V	142	LYS

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Mol	Chain	Res	Type
18	V	148	LYS
18	V	149	LYS
18	V	151	LEU
18	V	153	ARG
18	V	154	LEU
18	V	155	LEU
18	V	157	GLN
18	V	159	ASP
18	V	160	GLN
18	V	161	ARG
18	V	163	LEU
18	V	166	ILE
18	V	169	GLU
18	V	172	GLU
18	V	188	GLN
18	V	194	ARG
18	V	197	LYS
18	V	199	LYS
18	V	200	ILE
18	V	206	LYS
18	V	210	PHE
18	V	215	GLU
18	V	221	ARG
18	V	222	SER
18	V	229	ASP
18	V	230	GLU
18	V	233	ILE
18	V	234	GLU
19	c	24	ASP
19	c	106	VAL
4	e	546	VAL
4	e	579	VAL
5	f	253	TYR
5	f	261	THR
5	f	272	VAL
5	f	322	ASP
5	f	323	VAL
5	f	326	HIS
5	f	354	ARG
5	f	356	THR
5	f	366	GLU
5	f	411	VAL

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Mol	Chain	Res	Type
5	f	421	ASP
8	i	62	LYS
10	l	83	MET
10	l	84	LEU
10	l	104	ARG
10	l	106	ARG
21	m	31	LEU
22	o	191	ILE
22	o	192	ARG
22	o	193	ARG
22	o	212	LYS
22	o	213	LYS
22	o	214	ILE
22	o	883	ILE
22	o	1139	LEU
22	o	1419	VAL
22	o	1420	ASN
23	p	438	ARG
23	p	821	LYS
23	p	824	ASP
23	p	864	ASP
23	p	914	GLU
23	p	1076	GLU
35	u	144	ARG
35	u	163	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (173) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	401	ASN
1	A	409	HIS
1	A	489	GLN
1	A	569	ASN
1	A	630	GLN
1	A	637	GLN
1	A	693	GLN
1	A	702	ASN
1	A	860	ASN
1	A	896	GLN
1	A	970	ASN
1	A	1073	GLN
2	B	30	HIS

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Mol	Chain	Res	Type
2	B	36	ASN
2	B	123	ASN
2	B	160	HIS
2	B	176	HIS
2	B	183	GLN
2	B	235	HIS
2	B	348	GLN
2	B	439	HIS
2	B	450	GLN
2	B	471	GLN
2	B	509	ASN
2	B	521	GLN
2	B	577	HIS
2	B	644	GLN
2	B	652	GLN
2	B	745	GLN
2	B	750	GLN
2	B	765	ASN
2	B	813	ASN
2	B	864	ASN
2	B	908	GLN
2	B	912	ASN
2	B	963	HIS
3	D	875	GLN
3	D	912	ASN
3	D	925	ASN
3	D	936	GLN
4	E	254	ASN
4	E	268	HIS
4	E	326	ASN
4	E	327	ASN
4	E	351	GLN
4	E	616	HIS
4	E	640	ASN
4	E	733	ASN
5	F	37	GLN
5	F	52	GLN
5	F	59	HIS
5	F	79	ASN
5	F	119	ASN
5	F	221	GLN
5	F	270	ASN

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Mol	Chain	Res	Type
5	F	273	GLN
5	F	274	ASN
5	F	275	ASN
5	F	316	GLN
5	F	352	GLN
6	G	10	HIS
6	G	48	HIS
6	G	142	ASN
7	H	66	GLN
7	H	145	HIS
7	H	201	GLN
8	I	21	GLN
8	I	38	GLN
8	I	60	HIS
8	I	98	GLN
9	J	160	GLN
9	J	173	HIS
10	L	105	HIS
10	L	117	GLN
11	O	8	ASN
11	O	13	ASN
11	O	27	GLN
11	O	31	GLN
11	O	57	ASN
11	O	70	ASN
12	P	189	ASN
13	Q	60	HIS
13	Q	343	HIS
13	Q	352	HIS
13	Q	361	ASN
14	R	229	GLN
15	S	10	ASN
16	T	14	GLN
16	T	86	GLN
16	T	91	GLN
16	T	158	ASN
16	T	181	GLN
17	U	95	ASN
17	U	109	HIS
17	U	123	ASN
17	U	181	ASN
18	V	83	ASN

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Mol	Chain	Res	Type
18	V	95	HIS
18	V	117	GLN
18	V	126	ASN
19	c	27	GLN
19	c	50	HIS
3	d	912	ASN
4	e	223	HIS
4	e	256	HIS
4	e	320	HIS
4	e	336	HIS
4	e	368	ASN
4	e	424	GLN
4	e	640	ASN
4	e	660	ASN
5	f	30	GLN
5	f	119	ASN
5	f	134	HIS
5	f	325	ASN
8	i	38	GLN
20	k	186	HIS
20	k	205	HIS
10	l	73	ASN
10	l	105	HIS
21	m	107	ASN
22	o	62	GLN
22	o	123	ASN
22	o	278	HIS
22	o	289	GLN
22	o	296	ASN
22	o	301	HIS
22	o	311	GLN
22	o	330	GLN
22	o	372	ASN
22	o	507	GLN
22	o	590	GLN
22	o	620	HIS
22	o	721	HIS
22	o	731	ASN
22	o	739	ASN
22	o	913	ASN
22	o	1005	HIS
22	o	1129	ASN

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Mol	Chain	Res	Type
22	o	1230	GLN
22	o	1248	ASN
22	o	1332	GLN
22	o	1420	ASN
22	o	1445	HIS
22	o	1462	GLN
23	p	56	GLN
23	p	68	GLN
23	p	111	ASN
23	p	254	GLN
23	p	287	HIS
23	p	370	HIS
23	p	525	ASN
23	p	537	GLN
23	p	570	ASN
23	p	741	HIS
23	p	755	GLN
23	p	777	ASN
23	p	1021	HIS
23	p	1094	GLN
23	p	1117	HIS
23	p	1120	ASN
23	p	1160	GLN
25	r	19	GLN
25	r	129	GLN
26	s	22	HIS
26	s	132	GLN
26	s	133	GLN
28	v	130	ASN
28	v	131	ASN
29	w	45	GLN
31	y	29	ASN
31	y	89	ASN
35	u	60	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 11 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.

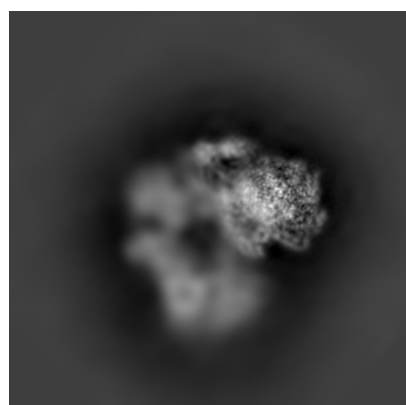
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31110. These allow visual inspection of the internal detail of the map and identification of artifacts.

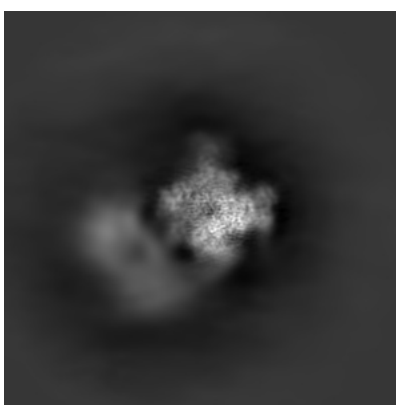
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

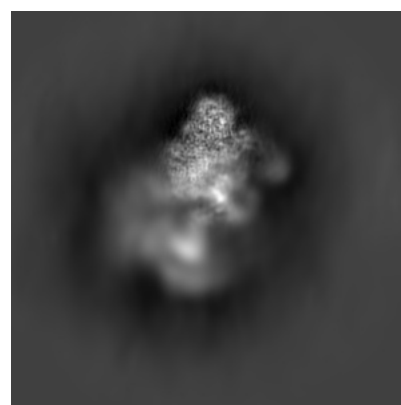
6.1.1 Primary map



X



Y

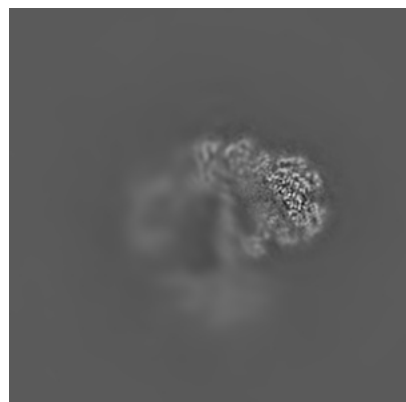


Z

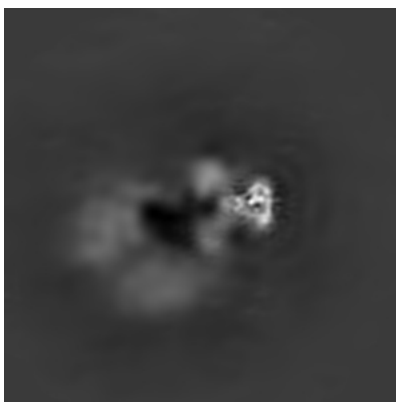
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

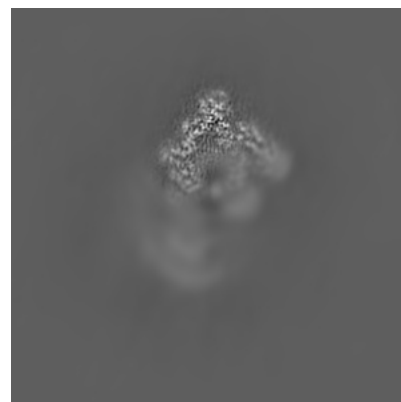
6.2.1 Primary map



X Index: 240



Y Index: 240

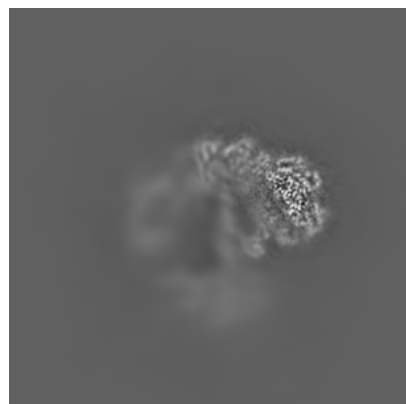


Z Index: 240

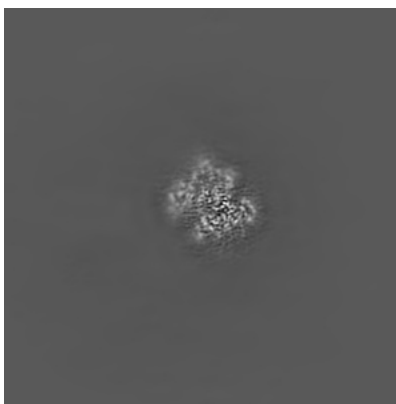
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

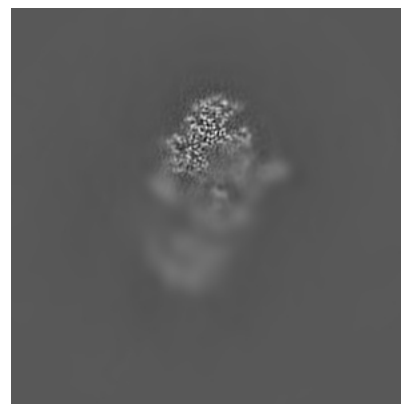
6.3.1 Primary map



X Index: 239



Y Index: 330

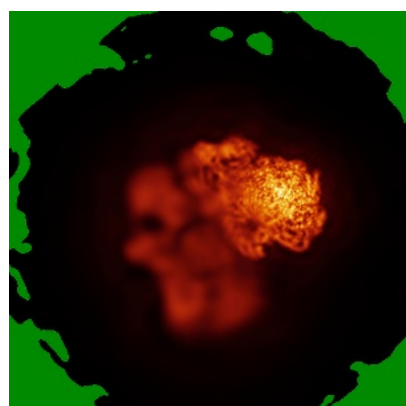


Z Index: 264

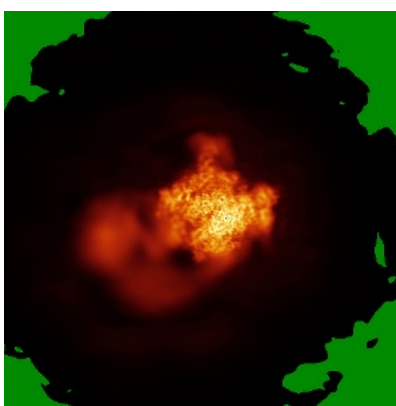
The images above show the largest variance slices of the map in three orthogonal directions.

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

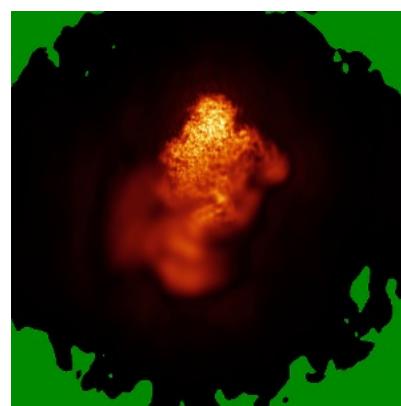
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

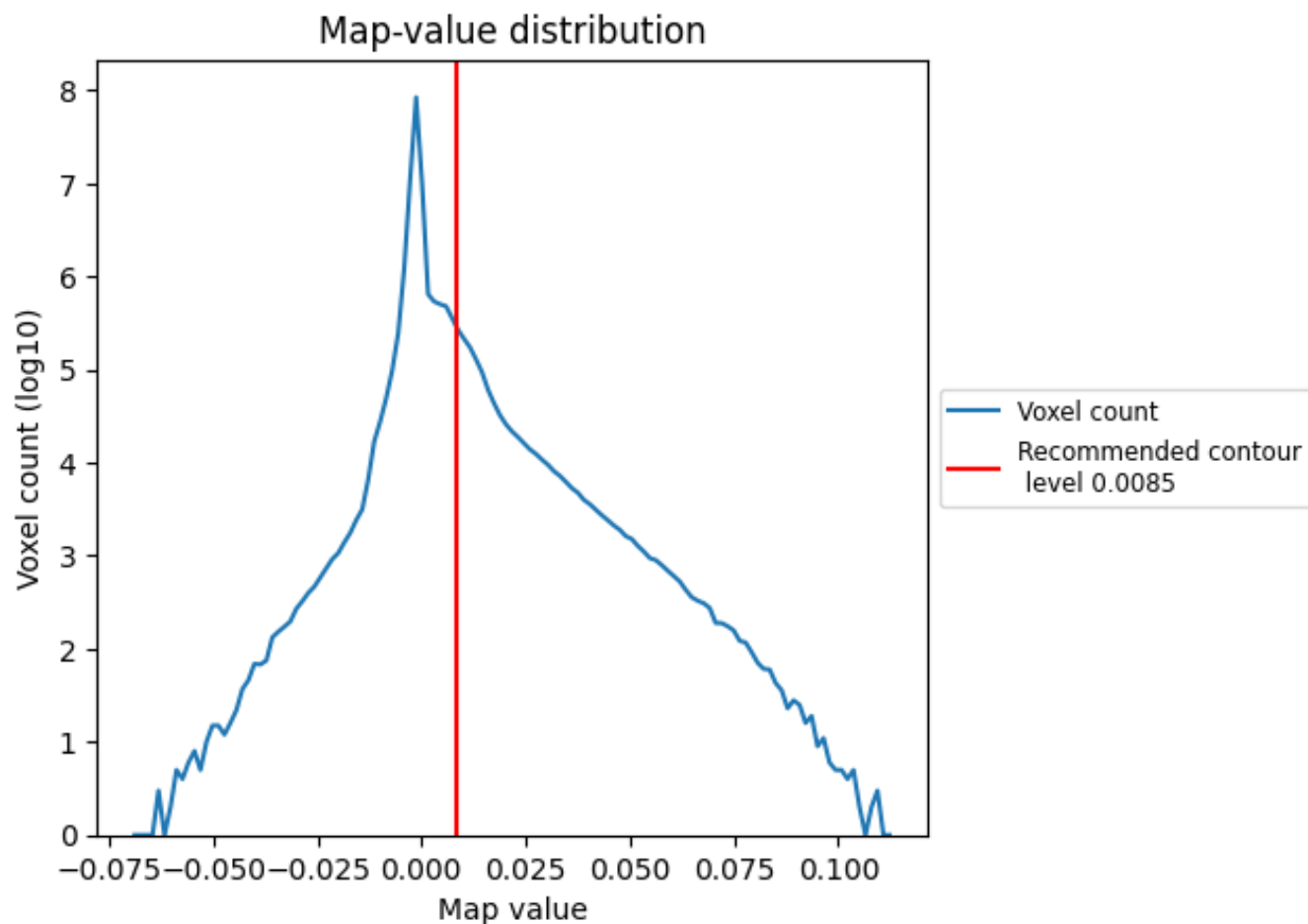
6.6 Mask visualisation

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

7 Map analysis [i](#)

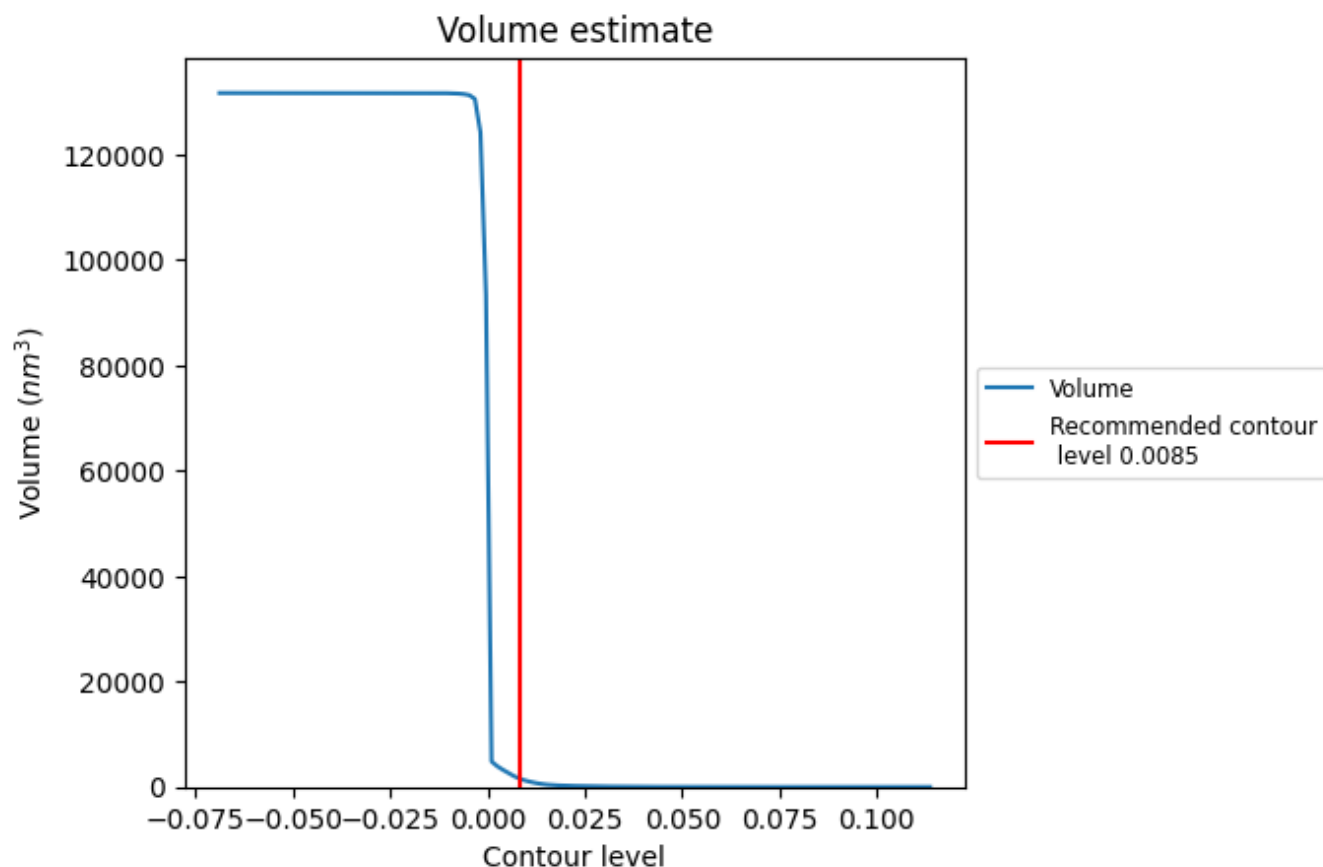
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

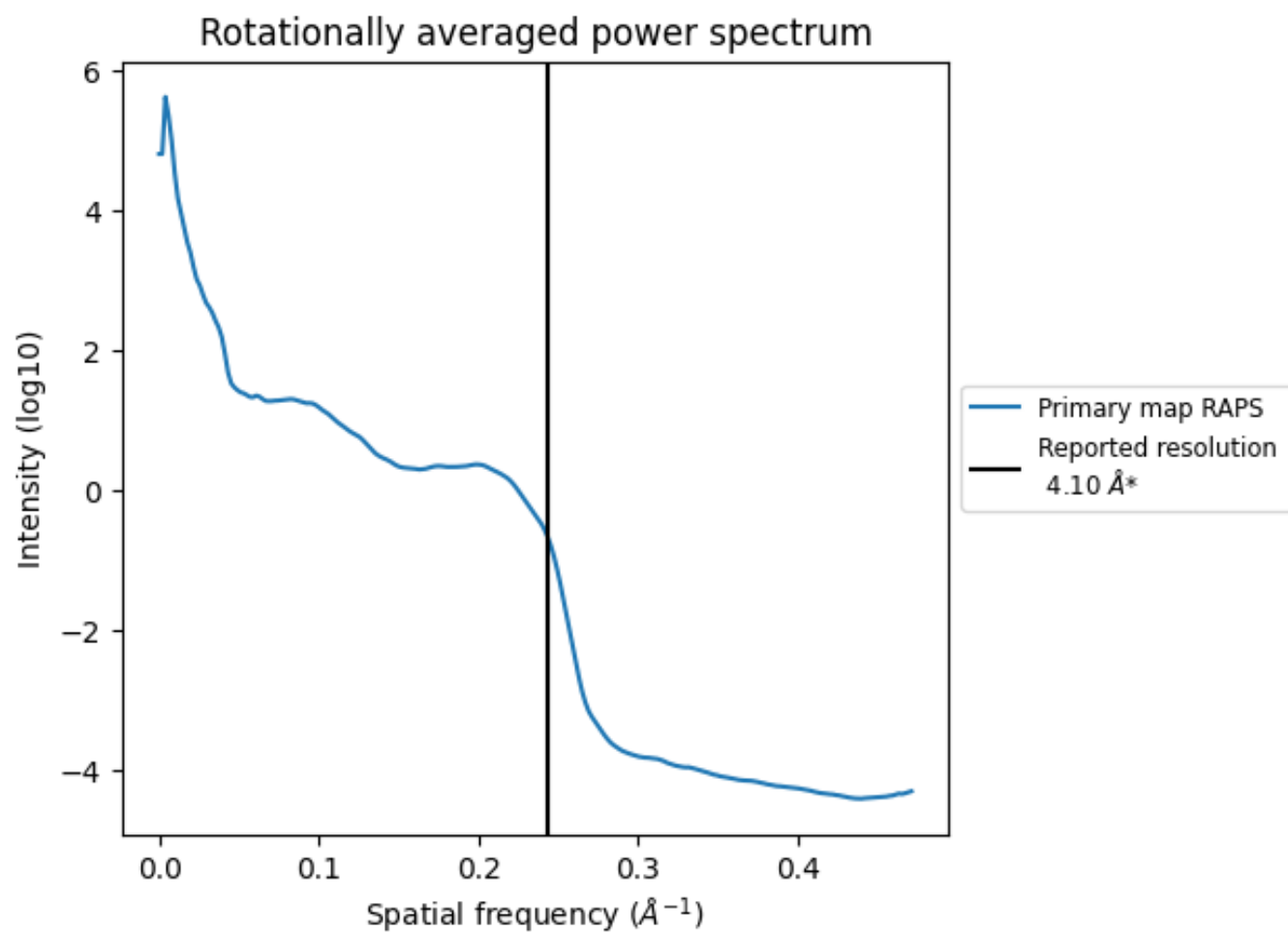
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1522 nm^3 ; this corresponds to an approximate mass of 1374 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 0.244 Å⁻¹

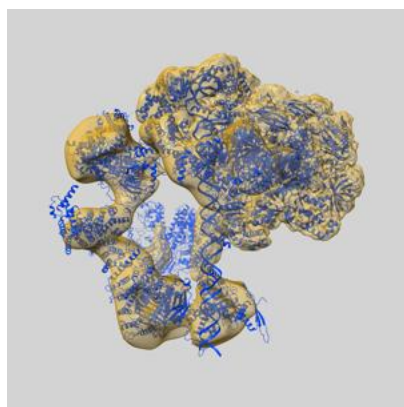
8 Fourier-Shell correlation

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

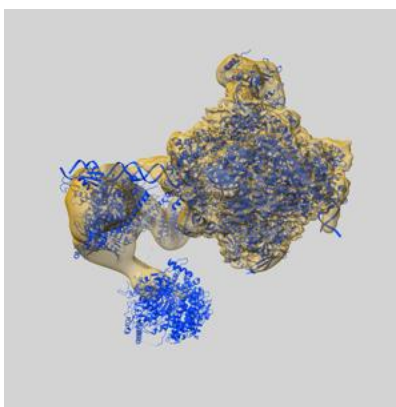
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31110 and PDB model 7EGA. Per-residue inclusion information can be found in section [3](#) on page [11](#).

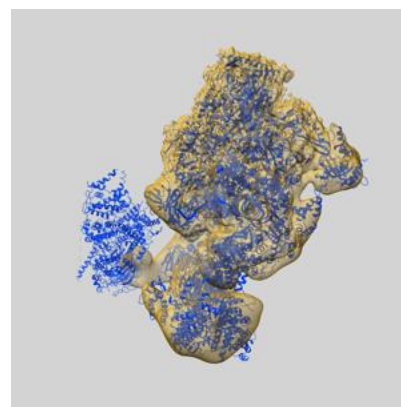
9.1 Map-model overlay [i](#)



X



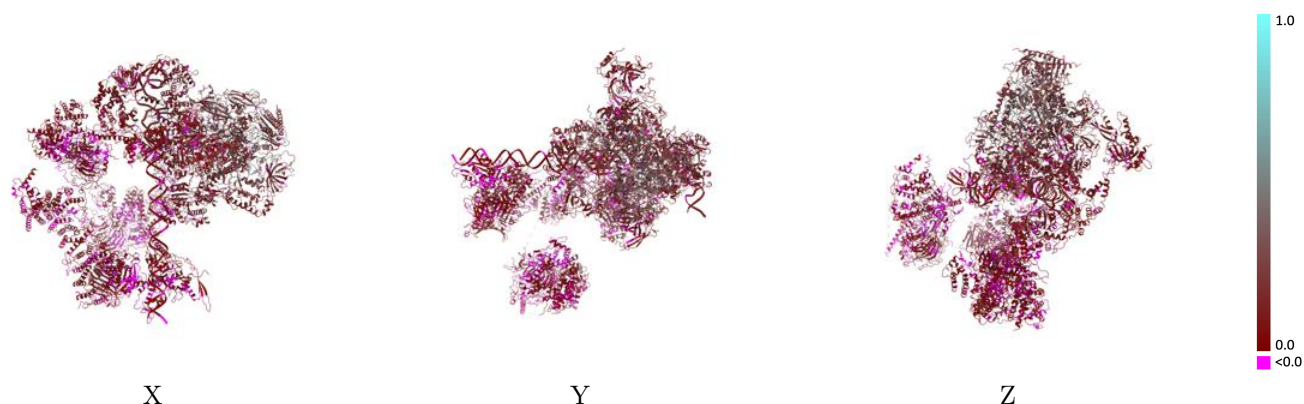
Y



Z

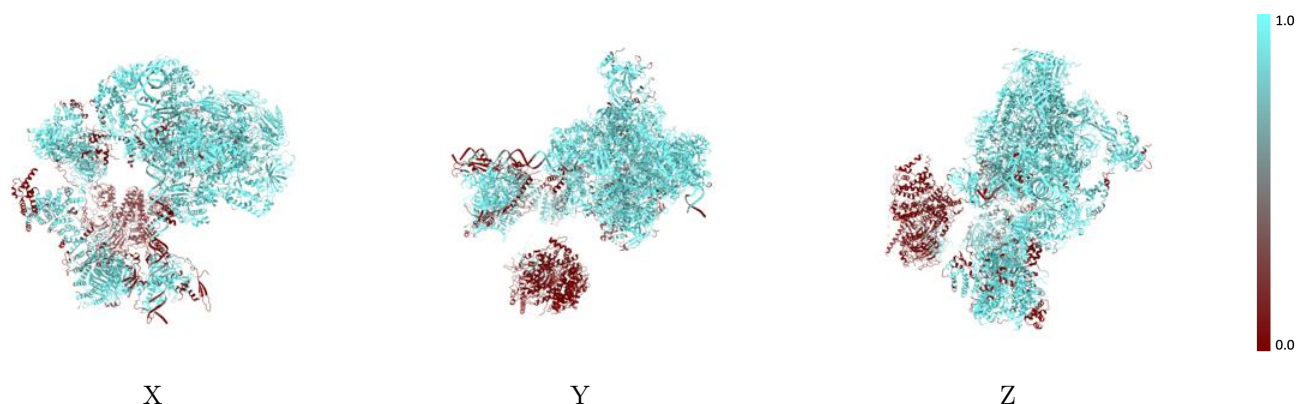
The images above show the 3D surface view of the map at the recommended contour level 0.0085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



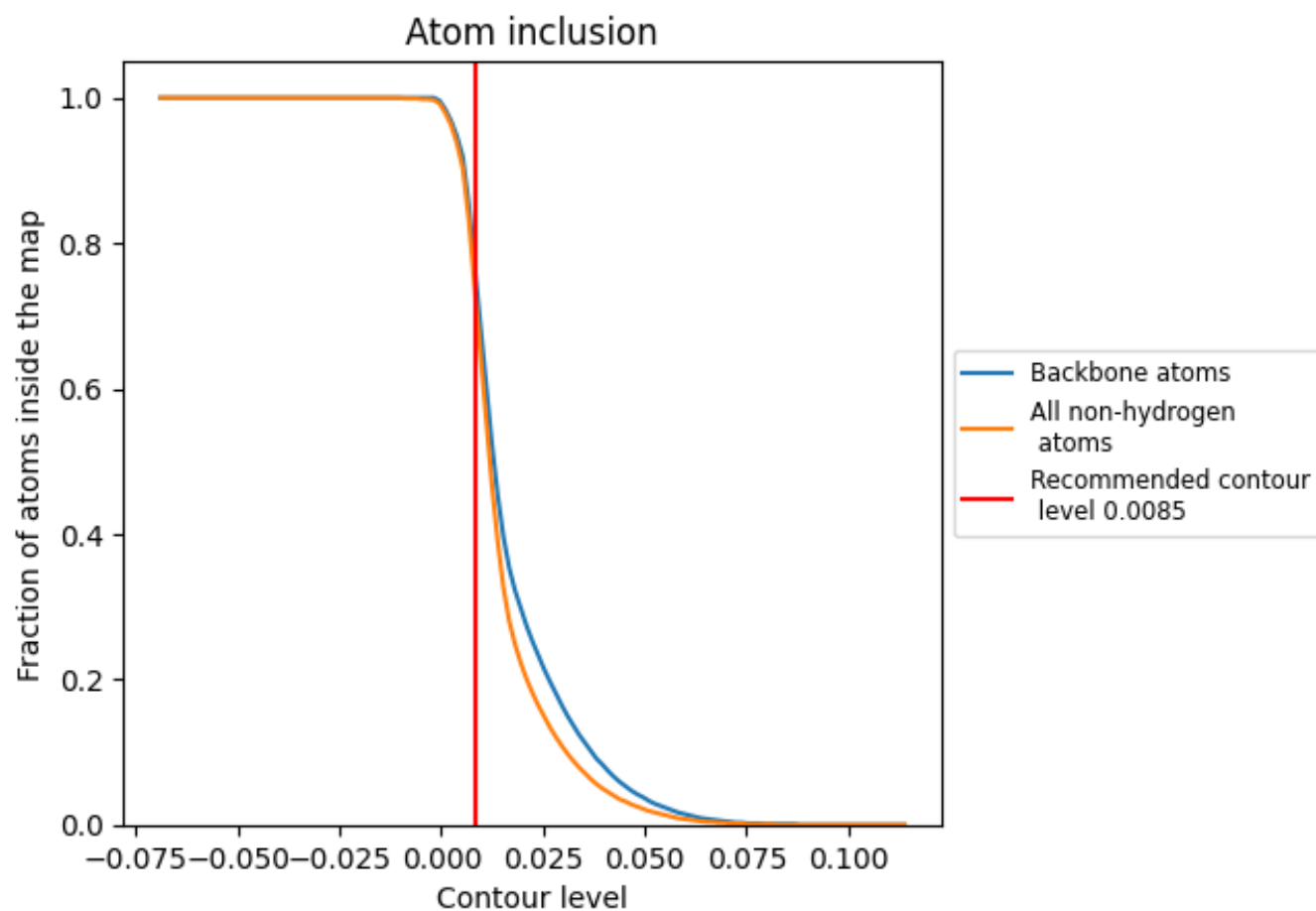
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0085).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 72% 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 (0.0085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7220	 0.1220
A	 0.6010	 0.0360
B	 0.8160	 0.0470
D	 0.7180	 0.0730
E	 0.7490	 0.0490
F	 0.6920	 0.0420
G	 0.6330	 0.0590
H	 0.7350	 0.0450
I	 0.8450	 0.0430
J	 0.9280	 0.0530
L	 0.6420	 0.0560
O	 0.9380	 0.1050
P	 0.9640	 0.1320
Q	 0.9080	 0.1150
R	 0.9270	 0.1760
S	 0.8710	 0.0910
T	 0.8620	 0.1020
U	 0.7800	 0.0840
V	 0.8180	 0.0700
X	 0.7270	 0.1100
Y	 0.7150	 0.1110
c	 0.0000	 0.0100
d	 0.0000	 0.0160
e	 0.1300	 0.0380
f	 0.5800	 0.0480
i	 0.0340	 0.0210
j	 0.0000	 0.0050
k	 0.0000	 0.0400
l	 0.0000	 0.0300
m	 0.0000	 0.0290
o	 0.8980	 0.2140
p	 0.9000	 0.2790
q	 0.9380	 0.2910
r	 0.8490	 0.1080
s	 0.9330	 0.1680



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Chain	Atom inclusion	Q-score
t	 0.9290	 0.2370
u	 0.8870	 0.1280
v	 0.9420	 0.2110
w	 0.8780	 0.1930
x	 0.9210	 0.3030
y	 0.9200	 0.2620
z	 0.9130	 0.2670