



Full wwPDB EM Validation Report ⓘ

Jul 22, 2026 – 04:39 PM JST

PDB ID : 9UG9 / pdb_00009ug9
EMDB ID : EMD-64133
Title : The cryo-EM structure of 26S proteasome-Midnolin complex MB state
Authors : Wang, H.Y.; Xu, W.Q.
Deposited on : 2025-04-11
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

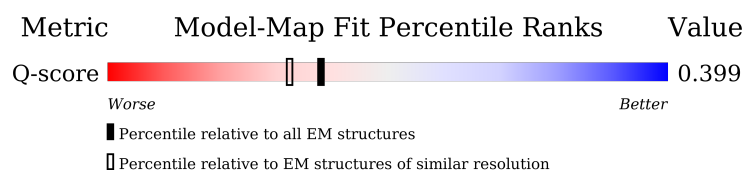
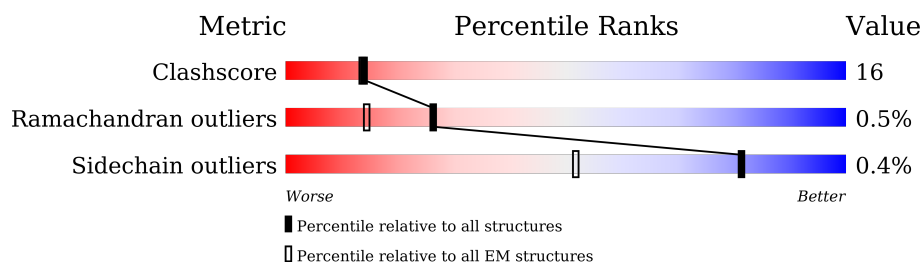
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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



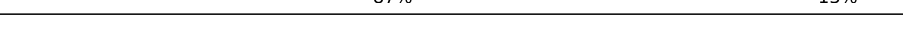
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	u	491	
2	d	350	
3	M	255	
3	m	255	

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Mol	Chain	Length	Quality of chain
4	R	263	
4	r	263	
5	N	239	
5	n	239	
6	E	389	
7	B	440	
8	e	70	
9	O	277	
9	o	277	
10	S	241	
10	s	241	
11	D	418	
12	F	439	
13	P	205	
13	p	205	
14	U	953	
15	C	406	
16	G	246	
16	g	246	
17	Q	201	
17	q	201	
18	A	433	
19	V	534	
20	T	264	
20	t	264	

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Mol	Chain	Length	Quality of chain
21	v	15	
22	W	456	
23	H	234	
23	h	234	
24	f	908	
25	X	422	
26	I	261	
26	i	261	
27	Y	389	
28	J	248	
28	j	248	
29	Z	324	
30	K	241	
30	k	241	
31	a	376	
32	L	263	
32	l	263	
33	b	377	
34	c	310	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	ADP	B	501	-	-	X	-

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 103692 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 Midnolin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	u	114	Total	C	N	O	S	0	0
			908	558	185	163	2		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	0	MET	-	initiating methionine	UNP Q504T8
u	469	GLY	-	expression tag	UNP Q504T8
u	470	SER	-	expression tag	UNP Q504T8
u	471	ASP	-	expression tag	UNP Q504T8
u	472	TYR	-	expression tag	UNP Q504T8
u	473	LYS	-	expression tag	UNP Q504T8
u	474	ASP	-	expression tag	UNP Q504T8
u	475	ASP	-	expression tag	UNP Q504T8
u	476	ASP	-	expression tag	UNP Q504T8
u	477	ASP	-	expression tag	UNP Q504T8
u	478	LYS	-	expression tag	UNP Q504T8
u	479	GLY	-	expression tag	UNP Q504T8
u	480	SER	-	expression tag	UNP Q504T8
u	481	HIS	-	expression tag	UNP Q504T8
u	482	HIS	-	expression tag	UNP Q504T8
u	483	HIS	-	expression tag	UNP Q504T8
u	484	HIS	-	expression tag	UNP Q504T8
u	485	HIS	-	expression tag	UNP Q504T8
u	486	HIS	-	expression tag	UNP Q504T8
u	487	HIS	-	expression tag	UNP Q504T8
u	488	HIS	-	expression tag	UNP Q504T8
u	489	HIS	-	expression tag	UNP Q504T8
u	490	HIS	-	expression tag	UNP Q504T8

- Molecule 2 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	d	260	Total	C	N	O	S	0	0
			2091	1345	348	389	9		

- Molecule 3 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	m	239	Total	C	N	O	S	0	0
			1849	1174	313	351	11		
3	M	240	Total	C	N	O	S	0	0
			1839	1163	313	352	11		

- Molecule 4 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	206	Total	C	N	O	S	0	0
			1571	987	280	295	9		
4	r	201	Total	C	N	O	S	0	0
			1541	968	273	291	9		

- Molecule 5 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	n	201	Total	C	N	O	S	0	0
			1492	932	255	293	12		
5	N	199	Total	C	N	O	S	0	0
			1488	930	255	291	12		

- Molecule 6 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	354	Total	C	N	O	S	0	0
			2782	1751	493	522	16		

- Molecule 7 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	395	Total	C	N	O	S	0	0
			3034	1916	506	597	15		

- Molecule 8 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	e	31	Total	C	N	O	0	0
			180	105	32	43		

- Molecule 9 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	o	220	Total	C	N	O	S	0	0
			1643	1033	280	318	12		
9	O	220	Total	C	N	O	S	0	0
			1643	1033	280	318	12		

- Molecule 10 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	S	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		
10	s	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		

- Molecule 11 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	380	Total	C	N	O	S	0	0
			2997	1894	514	577	12		

- Molecule 12 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	369	Total	C	N	O	S	0	0
			2867	1802	494	556	15		

- Molecule 13 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	p	204	Total	C	N	O	S	0	0
			1585	1010	262	294	19		
13	P	204	Total	C	N	O	S	0	0
			1585	1010	262	294	19		

- Molecule 14 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	U	814	Total	C	N	O	S	0	0
			6298	3995	1069	1190	44		

- Molecule 15 is a protein called 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	C	374	Total	C	N	O	S	0	0
			2877	1810	518	535	14		

- Molecule 16 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	240	Total	C	N	O	S	0	0
			1820	1154	305	348	13		
16	g	239	Total	C	N	O	S	0	0
			1798	1142	300	344	12		

- Molecule 17 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	198	Total	C	N	O	S	0	0
			1565	1003	264	289	9		
17	Q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		

- Molecule 18 is a protein called 26S proteasome regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	A	393	Total	C	N	O	S	0	0
			3059	1925	537	580	17		

- Molecule 19 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	V	472	Total	C	N	O	S	0	0
			3761	2385	668	694	14		

- Molecule 20 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	215	Total	C	N	O	S	0	0
			1662	1049	284	317	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	215	Total	C	N	O	S	0	0
			1662	1049	284	317	12		

- Molecule 21 is a protein called Substrate.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	v	15	Total	C	N	O	0	0
			75	45	15	15		

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	456	Total	C	N	O	S	0	0
			3663	2309	631	700	23		

- Molecule 23 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	H	231	Total	C	N	O	S	0	0
			1702	1078	288	331	5		
23	h	229	Total	C	N	O	S	0	0
			1671	1058	282	326	5		

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	f	889	Total	C	N	O	S	0	0
			6636	4146	1135	1313	42		

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	380	Total	C	N	O	S	0	0
			3004	1915	507	570	12		

- Molecule 26 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	I	256	Total	C	N	O	S	0	0
			1966	1237	339	382	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	i	250	Total	C	N	O	S	0	0
			1900	1192	329	371	8		

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	378	Total	C	N	O	S	0	0
			2995	1901	514	564	16		

- Molecule 28 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	J	239	Total	C	N	O	S	0	0
			1700	1054	307	334	5		
28	j	238	Total	C	N	O	S	0	0
			1684	1040	306	333	5		

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	286	Total	C	N	O	S	0	0
			2260	1441	389	425	5		

- Molecule 30 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	K	234	Total	C	N	O	S	0	0
			1742	1087	288	356	11		
30	k	234	Total	C	N	O	S	0	0
			1743	1092	288	352	11		

- Molecule 31 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	373	Total	C	N	O	S	0	0
			2989	1907	510	557	15		

- Molecule 32 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L	239	Total	C	N	O	S	0	0
			1844	1156	330	347	11		
32	l	237	Total	C	N	O	S	0	0
			1838	1150	333	344	11		

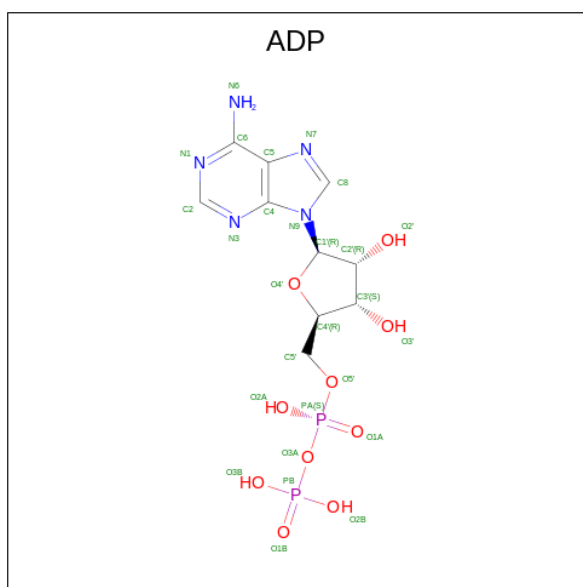
- Molecule 33 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	190	Total	C	N	O	S	0	0
			1444	901	259	277	7		

- Molecule 34 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	287	Total	C	N	O	S	0	0
			2239	1411	388	422	18		

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
35	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	B	1	Total	C	N	O	P	0
			27	10	5	10	2	

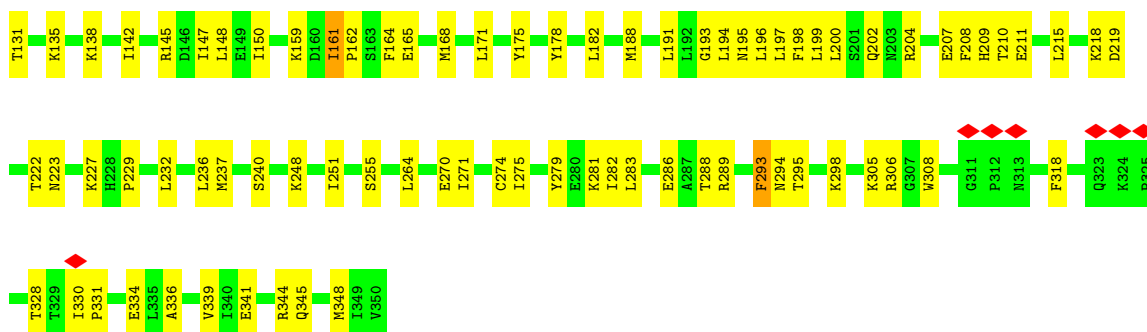
- Molecule 36 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$)

ATP

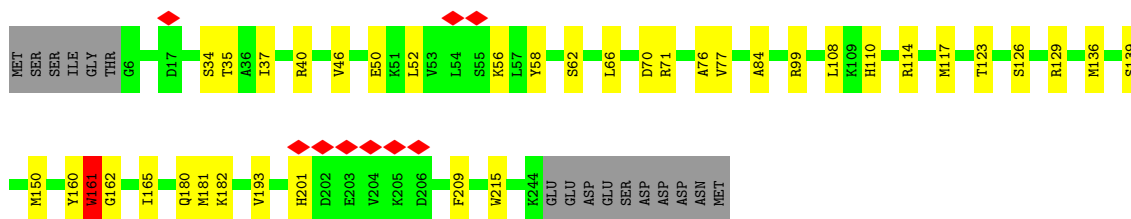
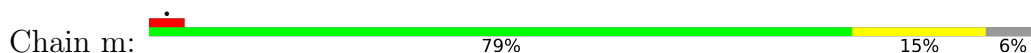
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).



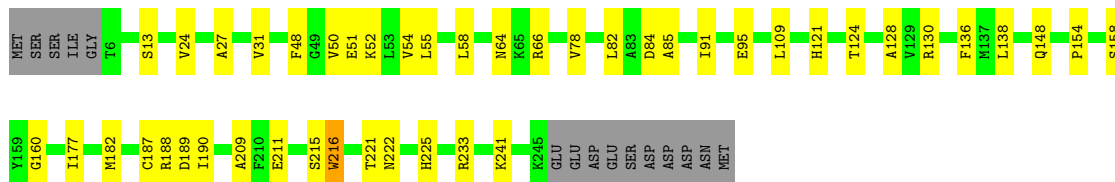
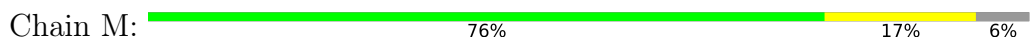
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PDB
PROTEIN DATA BANK



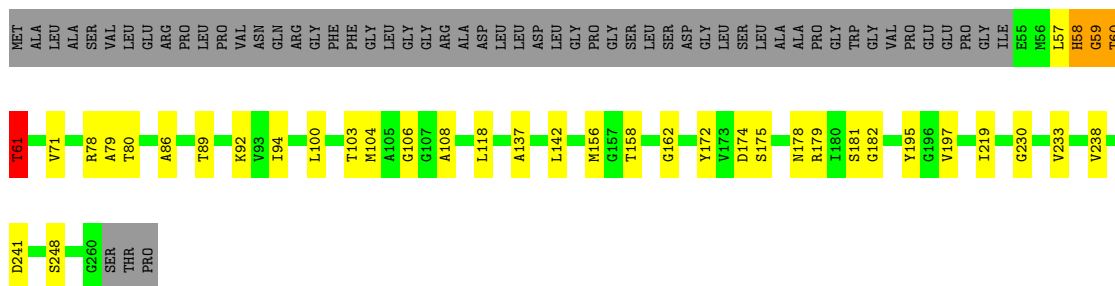
• Molecule 3: Proteasome subunit alpha type-3



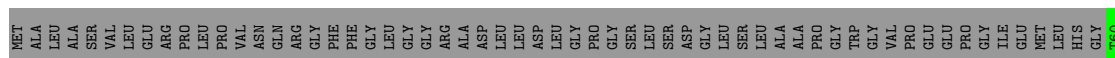
• Molecule 3: Proteasome subunit alpha type-3



• Molecule 4: Proteasome subunit beta type-5



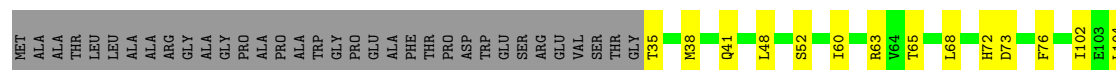
• Molecule 4: Proteasome subunit beta type-5





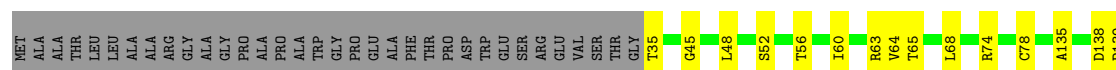
• Molecule 5: Proteasome subunit beta type-6

Chain n: 67% 17% 16%



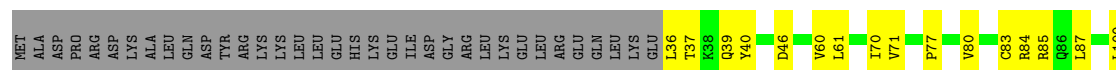
• Molecule 5: Proteasome subunit beta type-6

Chain N: 72% 11% 17%



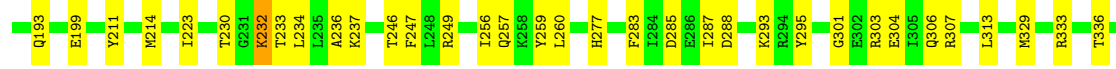
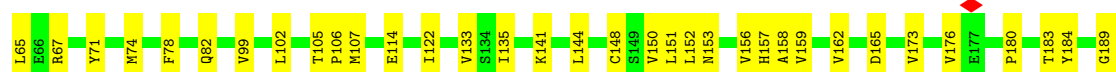
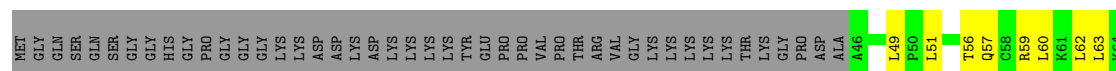
• Molecule 6: 26S proteasome regulatory subunit 10B

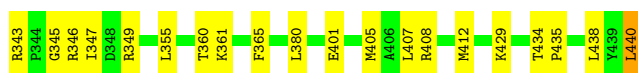
Chain E: 71% 20% 9%



• Molecule 7: 26S proteasome regulatory subunit 4

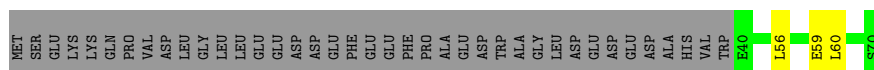
Chain B: 68% 22% 10%





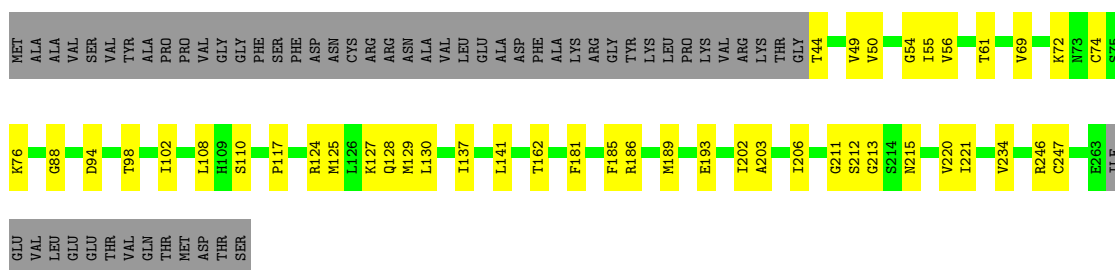
• Molecule 8: 26S proteasome complex subunit SEM1

Chain e: 40% 56%



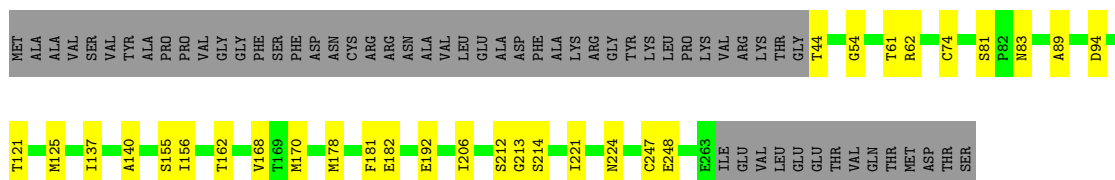
• Molecule 9: Proteasome subunit beta type-7

Chain o: 64% 16% 21%



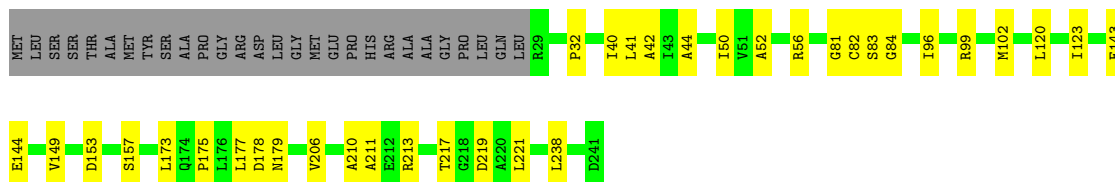
• Molecule 9: Proteasome subunit beta type-7

Chain O: 69% 11% 21%



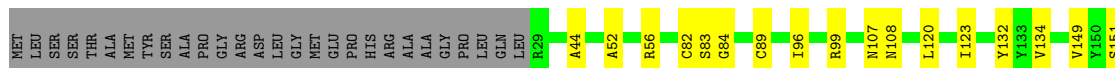
• Molecule 10: Proteasome subunit beta type-1

Chain S: 74% 15% 12%



• Molecule 10: Proteasome subunit beta type-1

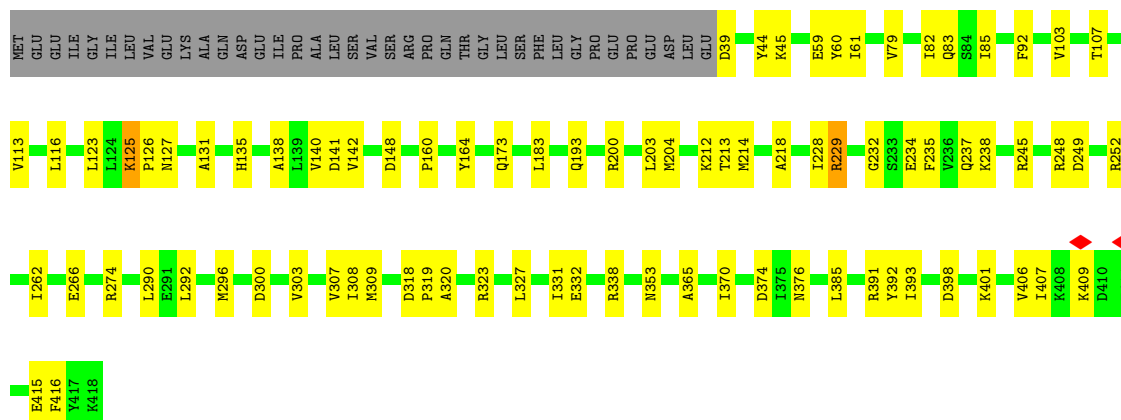
Chain s: 74% 15% 12%





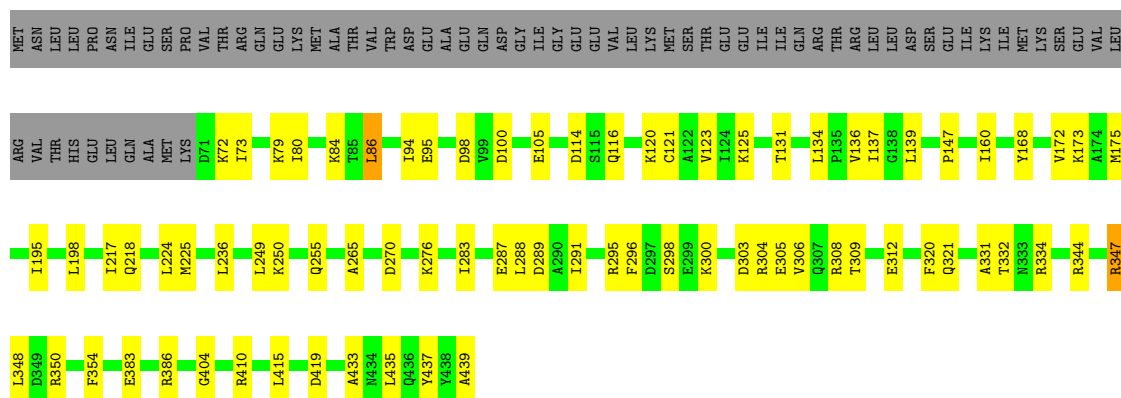
- Molecule 11: 26S proteasome regulatory subunit 6B

Chain D: 71% 20% 9%



- Molecule 12: 26S proteasome regulatory subunit 6A

Chain F: 67% 17% 16%



- Molecule 13: Proteasome subunit beta type-3

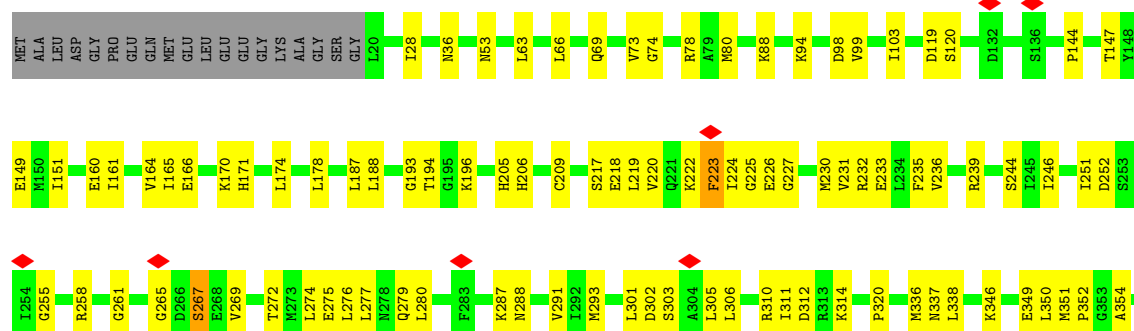
Chain p: 87% 13%

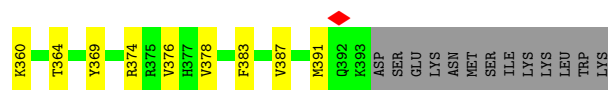


- Molecule 13: Proteasome subunit beta type-3

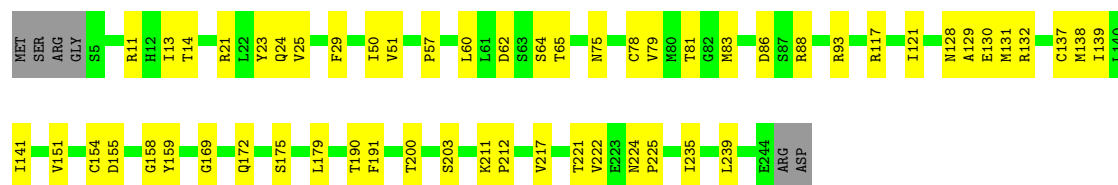
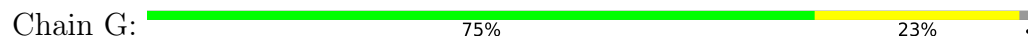
Chain P: 78% 22%



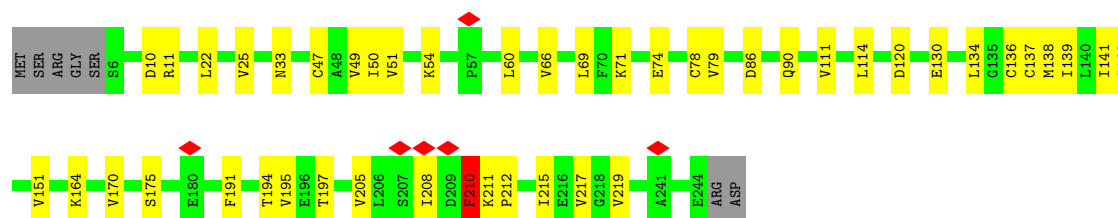
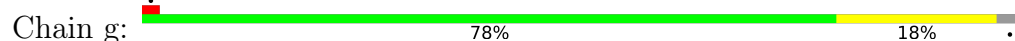




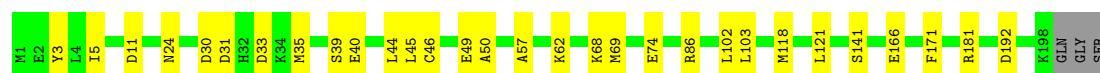
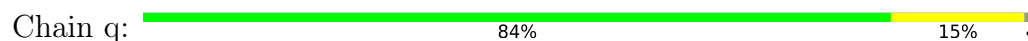
- Molecule 16: Proteasome subunit alpha type-6



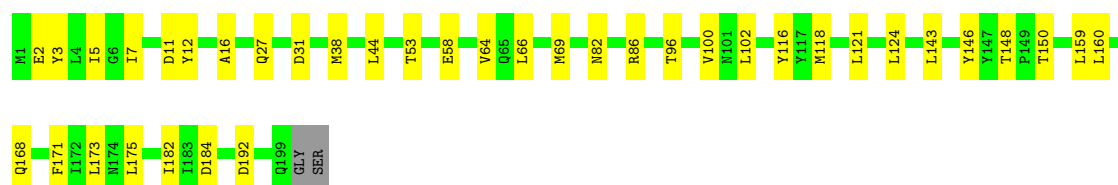
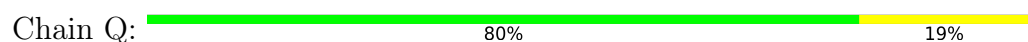
- Molecule 16: Proteasome subunit alpha type-6



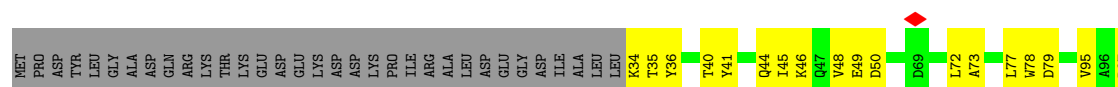
- Molecule 17: Proteasome subunit beta type-2

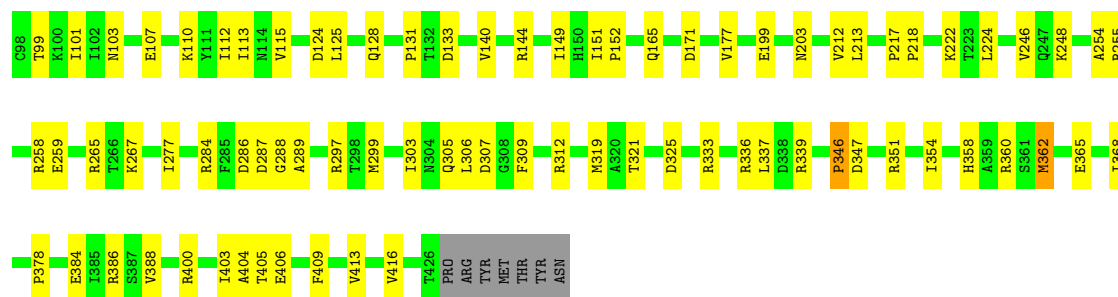


- Molecule 17: Proteasome subunit beta type-2

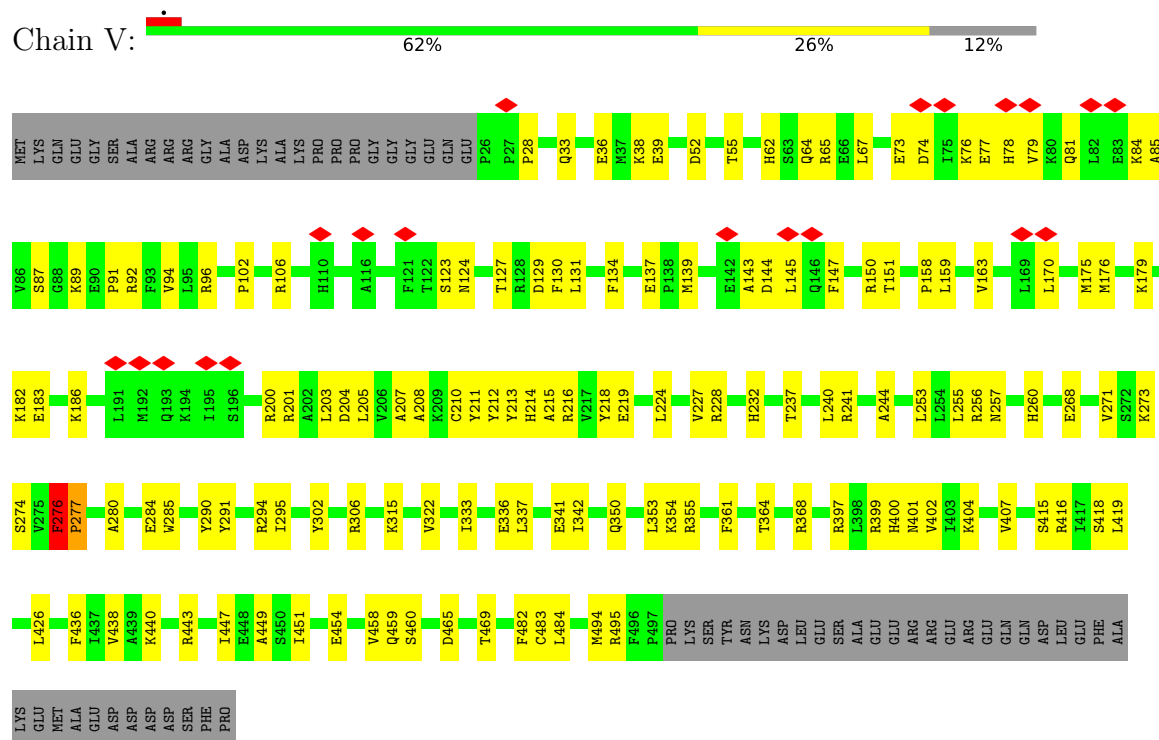


- Molecule 18: 26S proteasome regulatory subunit 7

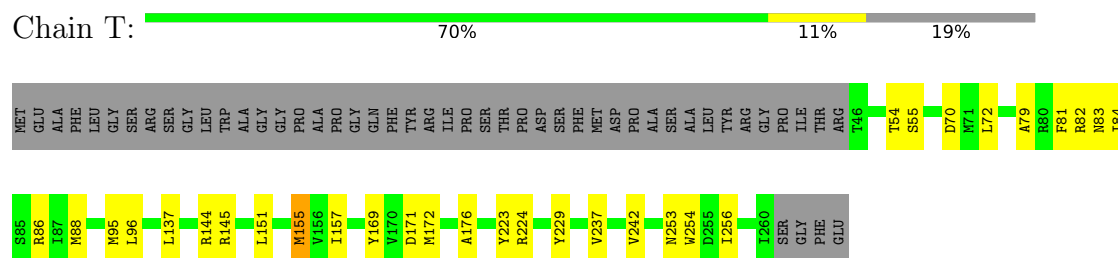




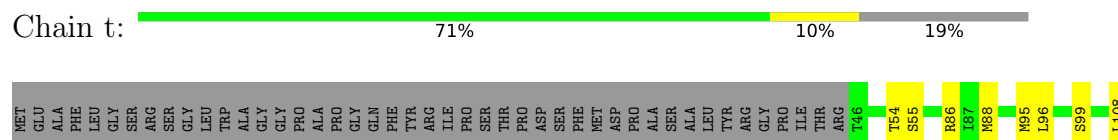
• Molecule 19: 26S proteasome non-ATPase regulatory subunit 3



• Molecule 20: Proteasome subunit beta type-4

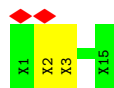
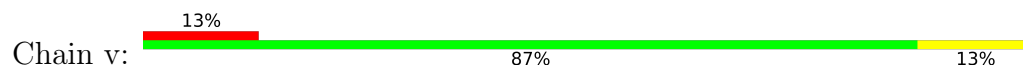


• Molecule 20: Proteasome subunit beta type-4

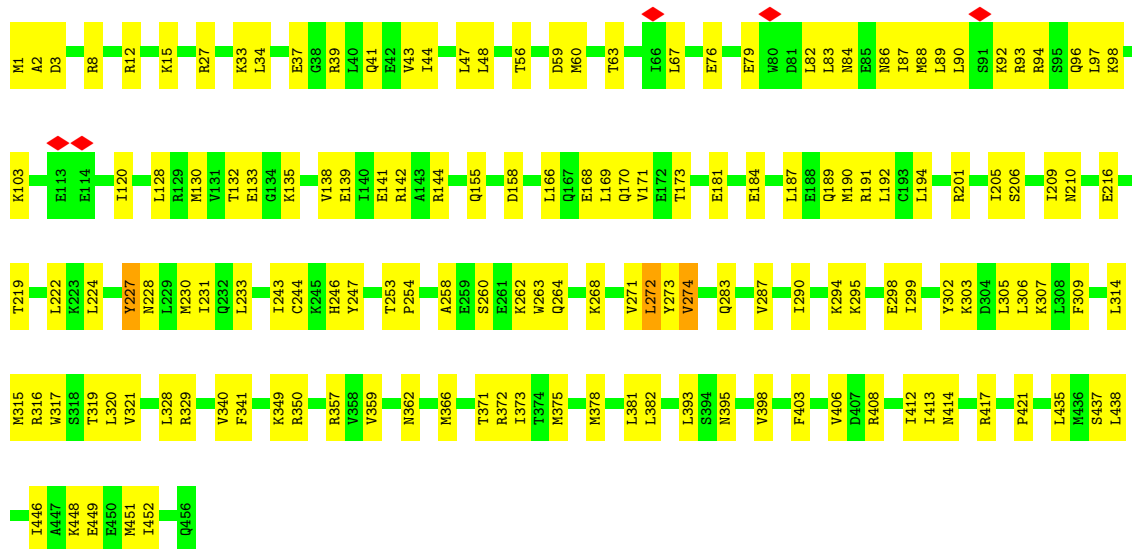




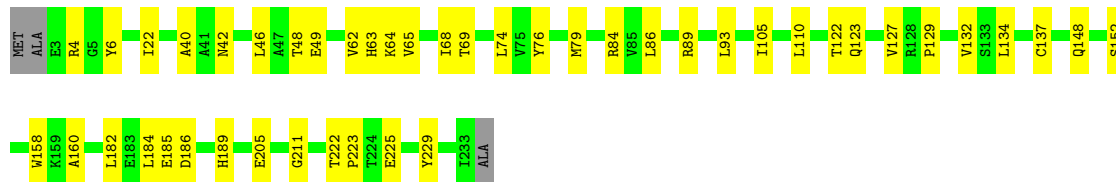
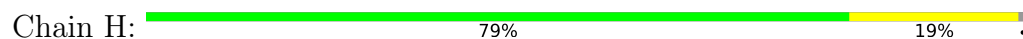
- Molecule 21: Substrate



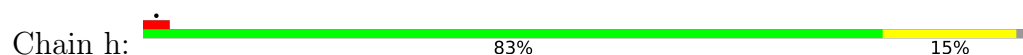
- Molecule 22: 26S proteasome non-ATPase regulatory subunit 12

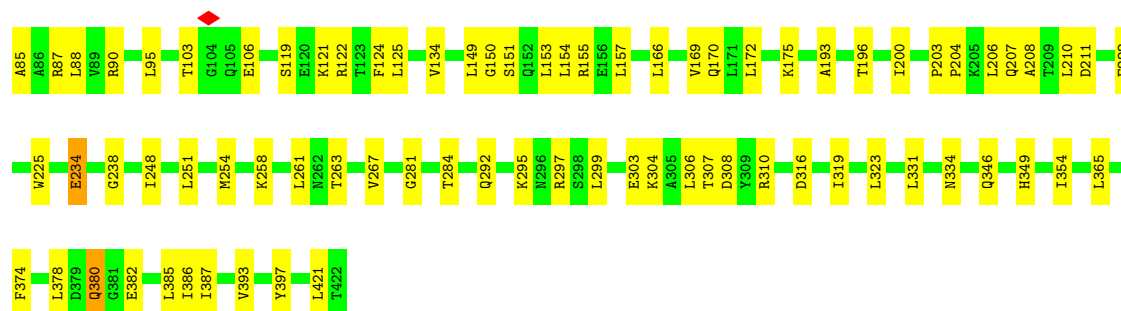


- Molecule 23: Proteasome subunit alpha type-2



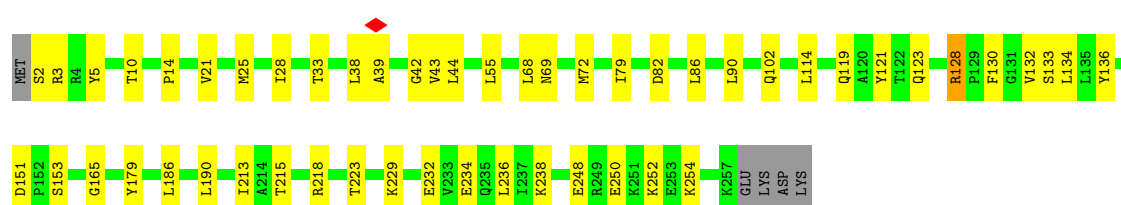
- Molecule 23: Proteasome subunit alpha type-2





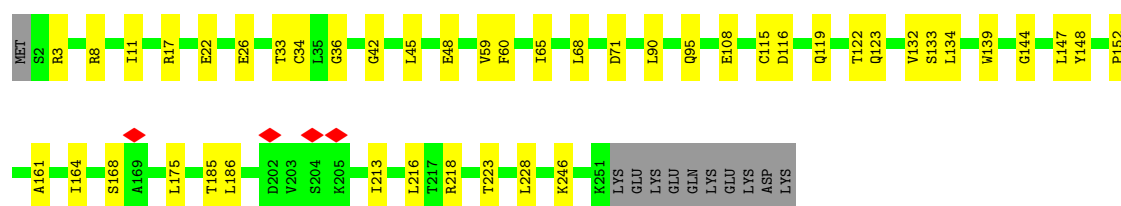
- Molecule 26: Proteasome subunit alpha type-4

Chain I: 78% 20% .



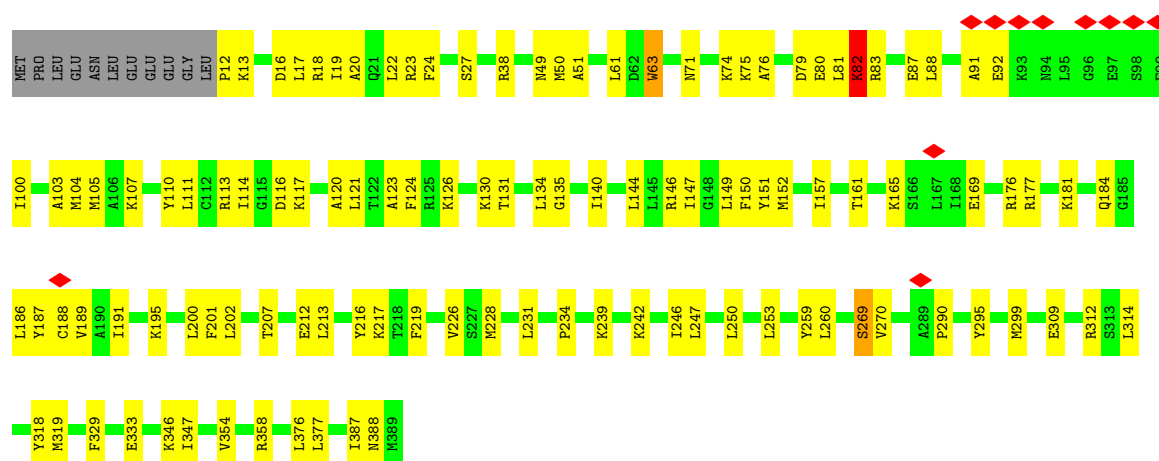
- Molecule 26: Proteasome subunit alpha type-4

Chain i: 79% 17% .



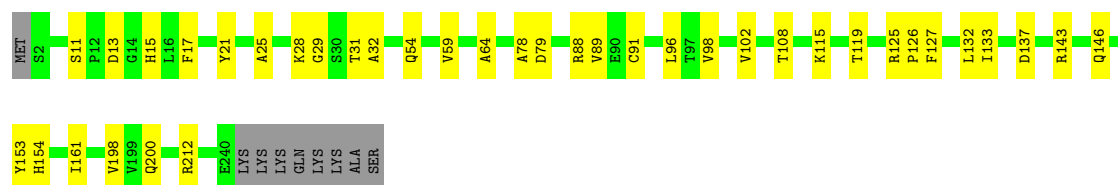
- Molecule 27: 26S proteasome non-ATPase regulatory subunit 6

Chain Y: 68% 28% . .



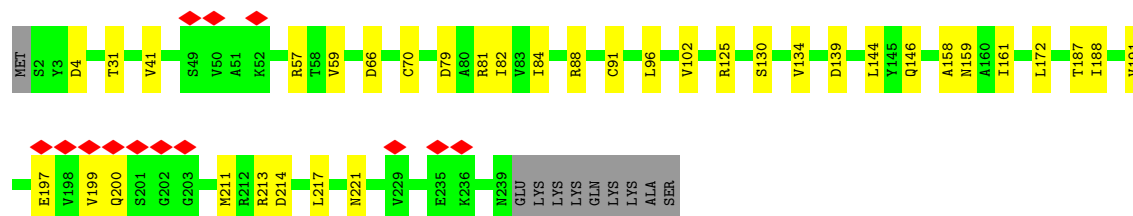
- Molecule 28: Proteasome subunit alpha type-7

Chain J:  81% 15% .



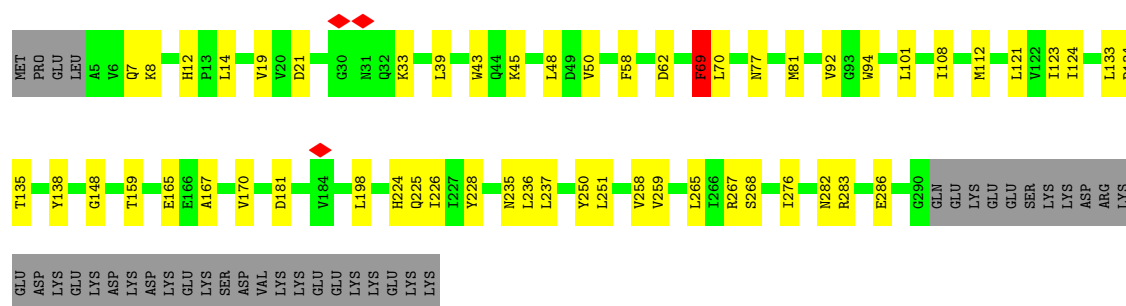
- Molecule 28: Proteasome subunit alpha type-7

Chain j:  5% 81% 15% .



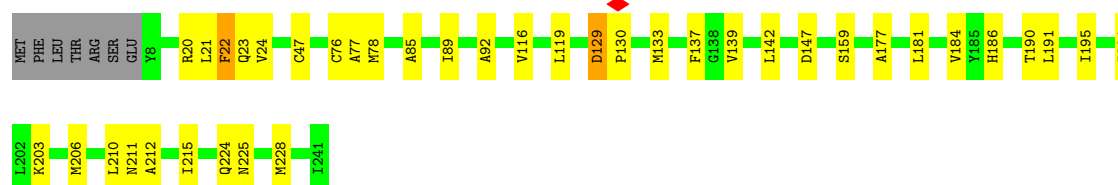
- Molecule 29: 26S proteasome non-ATPase regulatory subunit 7

Chain Z:  71% 17% 12%



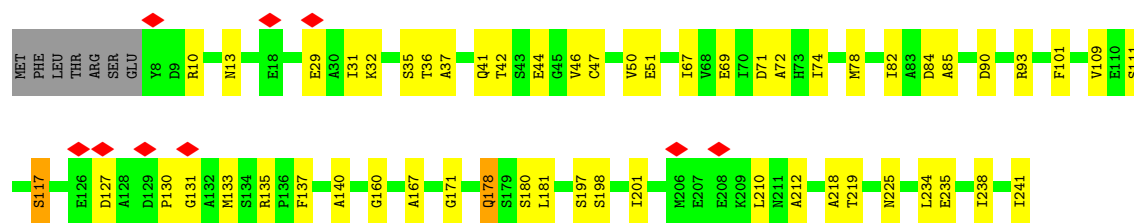
- Molecule 30: Proteasome subunit alpha type-5

Chain K:  81% 15% . .



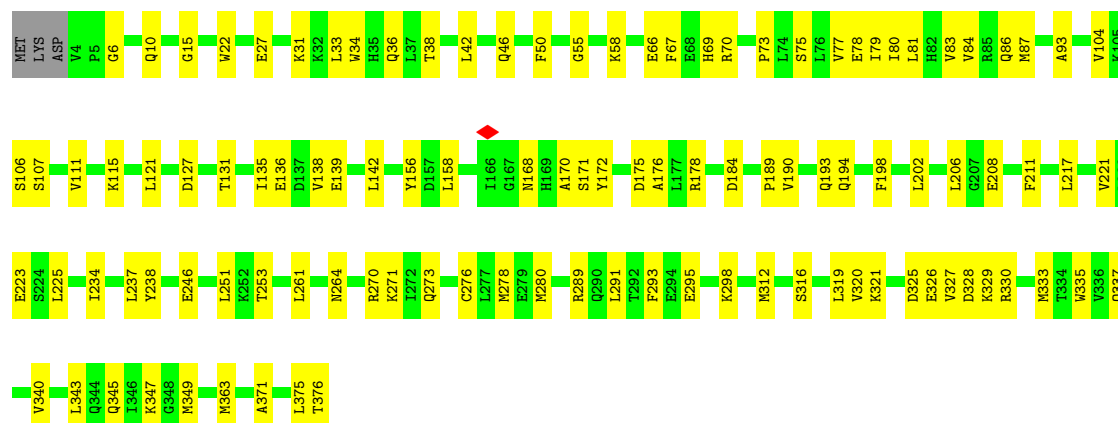
- Molecule 30: Proteasome subunit alpha type-5

Chain k:  74% 22% . .



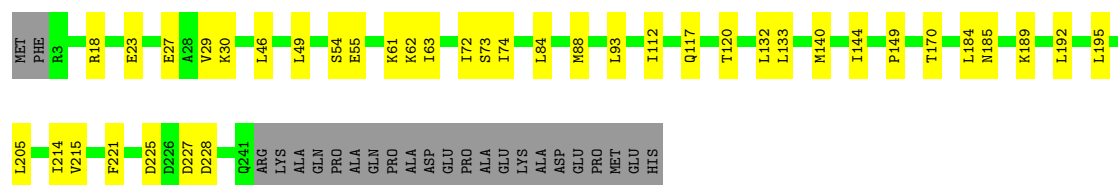
• Molecule 31: 26S proteasome non-ATPase regulatory subunit 13

Chain a: 70% 29% .



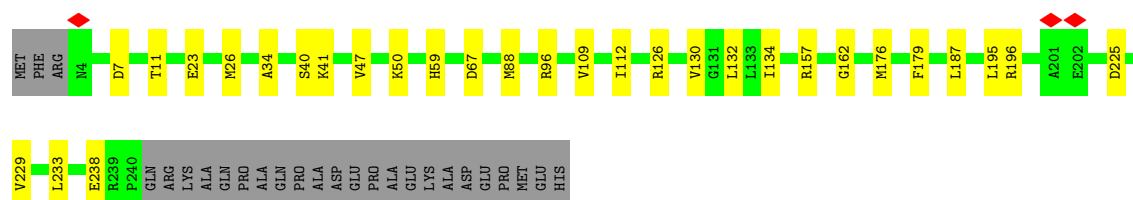
• Molecule 32: Proteasome subunit alpha type-1

Chain L: 76% 15% 9%



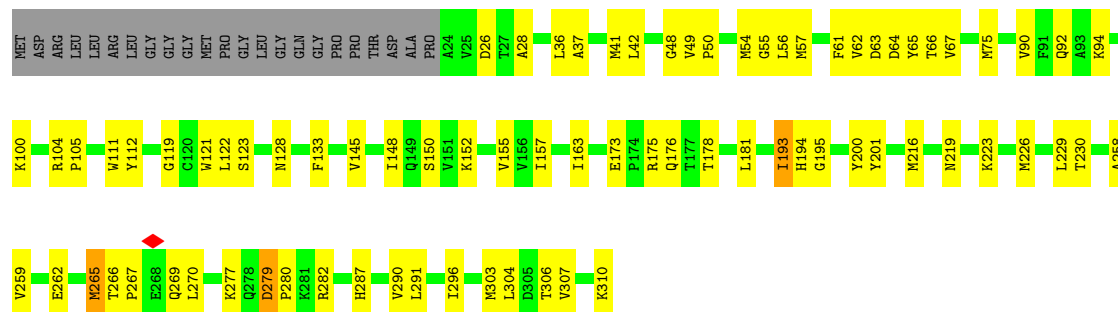
• Molecule 32: Proteasome subunit alpha type-1

Chain I: 79% 11% 10%



• Molecule 33: 26S proteasome non-ATPase regulatory subunit 4

Chain b: 35% 15% 50%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	108120	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.946	Depositor
Minimum map value	-0.195	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.09	Depositor
Map size ($\text{\AA}$)	445.19998, 445.19998, 445.19998	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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: ATP, ZN, ADP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	u	0.54	0/915	1.03	0/1222
2	d	0.37	1/2133 (0.0%)	0.81	3/2882 (0.1%)
3	M	0.25	0/1872	0.55	0/2528
3	m	0.24	0/1884	0.55	2/2542 (0.1%)
4	R	0.31	0/1602	0.63	5/2165 (0.2%)
4	r	0.23	0/1571	0.47	0/2123
5	N	0.34	0/1513	0.55	2/2048 (0.1%)
5	n	0.33	0/1517	0.60	1/2056 (0.0%)
6	E	0.25	0/2827	0.58	0/3814
7	B	0.27	0/3078	0.65	2/4163 (0.0%)
8	e	0.23	0/179	0.72	0/246
9	O	0.22	0/1670	0.45	0/2265
9	o	0.23	0/1670	0.50	0/2265
10	S	0.24	0/1671	0.50	0/2253
10	s	0.24	0/1671	0.44	0/2253
11	D	0.28	0/3045	0.59	1/4116 (0.0%)
12	F	0.28	0/2907	0.59	0/3923
13	P	0.22	0/1614	0.48	0/2177
13	p	0.26	0/1614	0.54	0/2177
14	U	0.25	0/6406	0.64	0/8672
15	C	0.27	0/2914	0.66	2/3927 (0.1%)
16	G	0.26	0/1852	0.54	1/2514 (0.0%)
16	g	0.24	0/1831	0.51	1/2492 (0.0%)
17	Q	0.23	0/1603	0.46	0/2174
17	q	0.28	0/1598	0.53	0/2167
18	A	0.29	0/3109	0.65	3/4198 (0.1%)
19	V	0.28	0/3835	0.70	4/5185 (0.1%)
20	T	0.23	0/1695	0.50	0/2298
20	t	0.25	0/1695	0.52	0/2298
22	W	0.29	0/3709	0.73	1/4990 (0.0%)
23	H	0.21	0/1737	0.49	0/2365
23	h	0.21	0/1705	0.50	0/2324

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
24	f	0.42	0/6737	0.86	0/9132
25	X	0.26	0/3047	0.60	0/4107
26	I	0.25	0/1996	0.54	0/2697
26	i	0.24	0/1928	0.59	2/2610 (0.1%)
27	Y	0.27	0/3045	0.70	1/4108 (0.0%)
28	J	0.20	0/1724	0.52	0/2353
28	j	0.18	0/1706	0.52	1/2329 (0.0%)
29	Z	0.26	0/2303	0.58	1/3123 (0.0%)
30	K	0.27	0/1766	0.52	0/2393
30	k	0.27	0/1769	0.62	1/2397 (0.0%)
31	a	0.26	0/3047	0.66	3/4125 (0.1%)
32	L	0.24	0/1878	0.56	0/2544
32	l	0.19	0/1872	0.47	0/2534
33	b	0.22	0/1464	0.62	0/1984
34	c	0.32	0/2280	0.65	2/3083 (0.1%)
All	All	0.28	1/105204 (0.0%)	0.62	39/142341 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	d	161	ILE	C-N	5.27	1.40	1.34

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	j	59	VAL	N-CA-C	-8.67	105.48	113.71
27	Y	82	LYS	N-CA-C	-7.86	102.65	111.14
18	A	346	PRO	CA-C-N	6.72	134.38	121.54
18	A	346	PRO	C-N-CA	6.72	134.38	121.54
4	R	60	THR	CA-C-N	6.57	134.09	121.54
4	R	60	THR	C-N-CA	6.57	134.09	121.54
5	n	232	ALA	N-CA-C	-6.08	107.68	114.62
3	m	161	TRP	N-CA-C	-6.07	105.19	112.59
15	C	223	PHE	CB-CA-C	5.98	119.12	111.40
5	N	226	ASP	CB-CA-C	-5.96	98.56	110.42
30	k	117	SER	N-CA-C	-5.90	105.92	113.23
4	R	61	THR	CA-C-N	-5.82	114.69	122.72
4	R	61	THR	C-N-CA	-5.82	114.69	122.72
16	G	211	LYS	CB-CG-CD	5.79	124.63	111.30
3	m	180	GLN	N-CA-C	-5.76	101.32	109.96
29	Z	69	PHE	CA-CB-CG	5.74	119.54	113.80
31	a	246	GLU	CA-CB-CG	5.66	125.42	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	W	274	VAL	CA-C-O	-5.64	115.19	121.17
18	A	346	PRO	N-CA-C	5.63	124.07	112.47
11	D	274	ARG	CB-CA-C	-5.48	109.27	115.79
19	V	276	PHE	CA-C-N	5.44	126.64	119.84
19	V	276	PHE	C-N-CA	5.44	126.64	119.84
2	d	105	LYS	CA-C-N	5.43	127.53	120.26
2	d	105	LYS	C-N-CA	5.43	127.53	120.26
34	c	48	GLY	CA-C-N	5.42	125.63	120.43
34	c	48	GLY	C-N-CA	5.42	125.63	120.43
19	V	454	GLU	N-CA-C	-5.41	107.69	114.56
2	d	298	LYS	O-C-N	5.39	130.36	122.39
31	a	276	CYS	CA-C-N	5.38	131.91	121.63
31	a	276	CYS	C-N-CA	5.38	131.91	121.63
16	g	210	PHE	N-CA-C	5.34	117.75	110.55
26	i	59	VAL	CA-C-N	5.31	131.69	121.54
26	i	59	VAL	C-N-CA	5.31	131.69	121.54
7	B	232	LYS	CA-C-N	5.25	129.55	120.58
7	B	232	LYS	C-N-CA	5.25	129.55	120.58
15	C	223	PHE	CA-CB-CG	5.24	119.04	113.80
4	R	80	THR	CB-CA-C	-5.24	101.16	109.80
5	N	227	GLN	N-CA-C	5.19	117.02	110.33
19	V	28	PRO	N-CA-C	5.08	116.90	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	u	908	0	973	66	0
2	d	2091	0	2097	126	0
3	M	1839	0	1791	42	0
3	m	1849	0	1809	38	0
4	R	1571	0	1509	47	0
4	r	1541	0	1489	15	0
5	N	1488	0	1454	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	n	1492	0	1449	55	0
6	E	2782	0	2827	82	0
7	B	3034	0	3037	120	0
8	e	180	0	108	10	0
9	O	1643	0	1641	18	0
9	o	1643	0	1641	37	0
10	S	1641	0	1615	25	0
10	s	1641	0	1615	24	0
11	D	2997	0	3001	102	0
12	F	2867	0	2905	93	0
13	P	1585	0	1598	46	0
13	p	1585	0	1598	30	0
14	U	6298	0	6309	223	0
15	C	2877	0	2937	117	0
16	G	1820	0	1789	68	0
16	g	1798	0	1738	56	0
17	Q	1570	0	1547	32	0
17	q	1565	0	1545	38	0
18	A	3059	0	3083	107	0
19	V	3761	0	3772	148	0
20	T	1662	0	1614	35	0
20	t	1662	0	1614	29	0
21	v	75	0	22	3	0
22	W	3663	0	3750	215	0
23	H	1702	0	1589	41	0
23	h	1671	0	1552	33	0
24	f	6636	0	6461	514	0
25	X	3004	0	3108	87	0
26	I	1966	0	1910	59	0
26	i	1900	0	1837	44	0
27	Y	2995	0	2927	157	0
28	J	1700	0	1511	29	0
28	j	1684	0	1497	34	0
29	Z	2260	0	2263	87	0
30	K	1742	0	1688	49	0
30	k	1743	0	1692	55	0
31	a	2989	0	3001	107	0
32	L	1844	0	1808	40	0
32	l	1838	0	1813	24	0
33	b	1444	0	1477	54	0
34	c	2239	0	2226	96	0
35	B	27	0	12	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	E	27	0	12	2	0
36	A	31	0	12	2	0
36	D	31	0	12	4	0
36	F	31	0	12	0	0
37	c	1	0	0	0	0
All	All	103692	0	102297	3237	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 16.

All (3237) 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)
12:F:435:LEU:HD13	30:K:20:ARG:CD	1.28	1.53
12:F:435:LEU:CD1	30:K:20:ARG:HD3	1.28	1.53
14:U:695:MET:HE1	14:U:709:PHE:CD2	1.44	1.51
30:k:133:MET:HE1	30:k:137:PHE:CE2	1.56	1.40
30:K:21:LEU:CD2	30:K:24:VAL:HG23	1.51	1.40
24:f:399:LEU:HD22	24:f:440:ILE:CD1	1.51	1.39
22:W:438:LEU:HD23	34:c:226:MET:SD	1.64	1.35
14:U:265:ILE:HG22	14:U:269:ARG:CD	1.54	1.34
14:U:725:MET:SD	34:c:181:LEU:HD13	1.67	1.32
2:d:94:MET:SD	2:d:118:ARG:HG2	1.70	1.31
24:f:399:LEU:CD1	24:f:400:TYR:CD1	2.13	1.30
27:Y:12:PRO:HG2	27:Y:113:ARG:CD	1.59	1.29
20:t:137:LEU:HD21	20:t:155:MET:SD	1.72	1.28
24:f:399:LEU:CB	24:f:440:ILE:HD11	1.63	1.28
11:D:125:LYS:CB	11:D:126:PRO:HD3	1.64	1.27
24:f:399:LEU:HD11	24:f:400:TYR:CE2	1.68	1.27
22:W:359:VAL:CG2	22:W:382:LEU:HD23	1.63	1.26
11:D:82:ILE:HD13	15:C:66:LEU:CD2	1.64	1.26
24:f:404:ASP:HB3	24:f:439:TYR:CZ	1.68	1.26
24:f:408:LEU:CD1	24:f:439:TYR:HD1	1.49	1.25
24:f:413:SER:O	24:f:417:ILE:HG13	1.31	1.25
9:o:124:ARG:HG3	9:o:128:GLN:NE2	1.50	1.25
20:t:108:LEU:HD13	20:t:155:MET:CE	1.65	1.25
19:V:176:MET:HE1	19:V:214:HIS:CE1	1.73	1.24
24:f:761:MET:HA	24:f:858:LYS:NZ	1.53	1.24
24:f:92:VAL:CG1	24:f:93:PRO:HD3	1.65	1.23
24:f:408:LEU:HD13	24:f:439:TYR:CD1	1.72	1.23
26:I:44:LEU:HD11	26:I:213:ILE:CG2	1.66	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:228:ILE:CG2	5:N:229:PRO:HD2	1.68	1.22
14:U:2:ILE:CG2	14:U:34:PHE:HE2	1.52	1.22
24:f:539:LEU:O	24:f:543:MET:HG2	1.35	1.22
14:U:695:MET:CE	14:U:709:PHE:CD2	2.22	1.21
11:D:125:LYS:HB3	11:D:126:PRO:CD	1.69	1.21
24:f:761:MET:HG2	24:f:809:ILE:CB	1.70	1.20
14:U:695:MET:HE1	14:U:709:PHE:CE2	1.77	1.20
14:U:265:ILE:CG2	14:U:269:ARG:HD2	1.72	1.20
24:f:376:PHE:CZ	24:f:380:PHE:CE2	2.30	1.20
6:E:46:ASP:OD1	12:F:139:LEU:HD21	1.39	1.19
14:U:265:ILE:HG22	14:U:269:ARG:HD3	1.20	1.19
29:Z:224:HIS:HE1	31:a:340:VAL:HG12	1.03	1.19
12:F:86:LEU:CD2	18:A:124:ASP:HB2	1.70	1.18
12:F:86:LEU:HD21	18:A:124:ASP:CB	1.72	1.18
14:U:486:MET:SD	14:U:518:LEU:HD22	1.83	1.18
19:V:176:MET:CE	19:V:214:HIS:CE1	2.27	1.18
24:f:399:LEU:HD11	24:f:400:TYR:CD2	1.77	1.18
24:f:399:LEU:CD1	24:f:400:TYR:CE1	2.26	1.18
3:m:150:MET:CE	3:m:165:ILE:HD11	1.75	1.17
16:g:22:LEU:HD11	16:g:25:VAL:HB	1.22	1.17
33:b:121:GLU:HG2	33:b:152:LYS:HG3	1.17	1.17
29:Z:224:HIS:CE1	31:a:340:VAL:HG12	1.79	1.17
25:X:153:LEU:HD23	25:X:169:VAL:HG11	1.19	1.17
24:f:399:LEU:HD12	24:f:400:TYR:CG	1.80	1.16
24:f:396:ASN:O	24:f:399:LEU:HG	1.45	1.16
24:f:399:LEU:CD1	24:f:400:TYR:CG	2.29	1.16
22:W:317:TRP:CZ3	22:W:321:VAL:HG21	1.80	1.16
12:F:383:GLU:HG2	32:L:170:THR:HG21	1.22	1.15
14:U:2:ILE:HG21	14:U:34:PHE:CE2	1.79	1.15
33:b:121:GLU:HG2	33:b:152:LYS:CG	1.75	1.15
24:f:399:LEU:CG	24:f:440:ILE:HD11	1.75	1.15
25:X:306:LEU:HD11	25:X:323:LEU:CD1	1.76	1.15
26:I:44:LEU:CD2	26:I:190:LEU:HD23	1.76	1.15
2:d:94:MET:CE	2:d:118:ARG:HG2	1.75	1.15
34:c:121:TRP:CZ3	34:c:123:SER:HA	1.83	1.14
24:f:760:PHE:CZ	24:f:857:GLY:HA2	1.81	1.14
7:B:287:ILE:HD13	7:B:329:MET:SD	1.88	1.13
22:W:375:MET:HE2	22:W:406:VAL:HG13	1.25	1.13
13:P:126:LEU:HD12	13:P:127:ILE:HG13	1.27	1.13
19:V:176:MET:HE1	19:V:214:HIS:ND1	1.64	1.12
25:X:149:LEU:HD11	25:X:153:LEU:HD22	1.26	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:402:LYS:HB3	1:u:406:ARG:NH2	1.62	1.12
25:X:306:LEU:HD11	25:X:323:LEU:HD13	1.22	1.12
1:u:410:ARG:CZ	24:f:326:LEU:HG	1.78	1.12
6:E:39:GLN:C	12:F:73:ILE:HD11	1.73	1.12
6:E:135:ILE:HD11	6:E:182:LEU:HD23	1.31	1.12
7:B:234:LEU:HD22	35:B:501:ADP:H2'	1.23	1.12
31:a:280:MET:HE2	31:a:291:LEU:HD23	1.25	1.12
30:K:21:LEU:CD2	30:K:24:VAL:CG2	2.26	1.11
14:U:695:MET:CE	14:U:709:PHE:HD2	1.57	1.11
24:f:376:PHE:CZ	24:f:380:PHE:HE2	1.67	1.11
24:f:399:LEU:HD13	24:f:400:TYR:CE1	1.84	1.11
30:K:21:LEU:HD21	30:K:24:VAL:HG23	1.18	1.11
14:U:657:GLY:O	14:U:693:LEU:HD22	1.48	1.11
22:W:438:LEU:CD2	34:c:226:MET:SD	2.37	1.11
25:X:149:LEU:CD1	25:X:153:LEU:HD22	1.81	1.11
29:Z:224:HIS:HE1	31:a:340:VAL:CG1	1.64	1.11
24:f:545:LYS:HE2	24:f:588:ARG:HD3	1.29	1.10
24:f:760:PHE:HZ	24:f:857:GLY:HA2	0.97	1.10
2:d:339:VAL:HG22	34:c:296:ILE:HG23	1.31	1.10
9:o:206:ILE:HG23	9:o:213:GLY:HA2	1.28	1.10
27:Y:184:GLN:CB	27:Y:201:PHE:CE1	2.35	1.10
2:d:175:TYR:CE2	2:d:188:MET:HG3	1.86	1.10
16:G:13:ILE:CG2	16:G:129:ALA:HB1	1.82	1.10
16:g:22:LEU:CD1	16:g:25:VAL:HB	1.79	1.10
27:Y:184:GLN:CB	27:Y:201:PHE:HE1	1.65	1.10
2:d:94:MET:HE1	2:d:118:ARG:HA	1.12	1.10
17:q:46:CYS:SG	17:q:57:ALA:HB2	1.90	1.10
26:I:44:LEU:HD22	26:I:190:LEU:CD2	1.81	1.10
4:R:59:GLY:HA3	4:R:92:LYS:NZ	1.66	1.09
24:f:94:LYS:HG3	24:f:133:MET:HE3	1.12	1.09
24:f:399:LEU:HD11	24:f:400:TYR:CZ	1.86	1.09
24:f:399:LEU:HD12	24:f:400:TYR:CD1	1.79	1.09
32:L:215:VAL:HG23	32:L:221:PHE:HD1	1.17	1.09
27:Y:12:PRO:HG2	27:Y:113:ARG:HD3	1.21	1.09
16:G:21:ARG:HD2	16:G:23:TYR:CZ	1.87	1.09
24:f:399:LEU:CD2	24:f:440:ILE:CD1	2.30	1.09
22:W:82:LEU:CD2	22:W:90:LEU:HD22	1.81	1.09
23:H:46:LEU:HD11	23:H:137:CYS:SG	1.93	1.08
31:a:293:PHE:CD2	31:a:329:LYS:HG3	1.86	1.08
22:W:274:VAL:HG12	22:W:283:GLN:HE22	1.09	1.08
24:f:582:VAL:HG22	24:f:588:ARG:NH2	1.68	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Z:101:LEU:HD23	29:Z:123:ILE:HD11	1.15	1.08
30:k:133:MET:CE	30:k:137:PHE:CE2	2.36	1.08
2:d:94:MET:HE1	2:d:118:ARG:CA	1.83	1.08
15:C:187:LEU:HB2	15:C:314:LYS:HG2	1.17	1.08
24:f:400:TYR:CE1	24:f:437:GLU:HG2	1.87	1.08
24:f:92:VAL:HG12	24:f:93:PRO:HD3	1.09	1.08
25:X:90:ARG:HD2	25:X:125:LEU:HD11	1.31	1.07
5:n:233:VAL:HG22	20:T:82:ARG:HH21	1.18	1.07
14:U:2:ILE:CG2	14:U:34:PHE:CE2	2.37	1.07
1:u:77:ASP:OD2	34:c:94:LYS:HE2	1.51	1.06
22:W:79:GLU:HG3	22:W:130:MET:HE1	1.29	1.06
24:f:92:VAL:HG12	24:f:93:PRO:CD	1.85	1.06
11:D:82:ILE:HD13	15:C:66:LEU:HD23	1.35	1.06
24:f:94:LYS:HG3	24:f:133:MET:CE	1.84	1.06
3:m:150:MET:HE1	3:m:165:ILE:CG1	1.84	1.06
24:f:399:LEU:CD2	24:f:440:ILE:HD11	1.85	1.06
5:n:63:ARG:NH1	20:T:223:TYR:CD1	2.23	1.06
17:q:35:MET:HG3	17:q:181:ARG:HE	1.09	1.06
24:f:719:PRO:HB3	24:f:754:LYS:HG2	1.27	1.06
22:W:169:LEU:HD22	22:W:189:GLN:NE2	1.71	1.05
24:f:399:LEU:HB2	24:f:440:ILE:HD11	1.34	1.05
5:N:228:ILE:HG23	5:N:229:PRO:HD2	1.08	1.05
4:R:60:THR:N	4:R:92:LYS:HZ3	1.52	1.05
19:V:176:MET:CE	19:V:214:HIS:HE1	1.67	1.05
24:f:545:LYS:HE2	24:f:588:ARG:CD	1.85	1.05
24:f:594:LEU:HG	24:f:631:LYS:CE	1.84	1.05
16:g:191:PHE:HE1	16:g:195:VAL:HG21	1.21	1.05
24:f:582:VAL:HG22	24:f:588:ARG:HH22	0.88	1.05
14:U:265:ILE:CG2	14:U:269:ARG:CD	2.32	1.04
20:t:108:LEU:HD13	20:t:155:MET:HE1	1.06	1.04
24:f:399:LEU:HD22	24:f:440:ILE:HD13	1.10	1.04
24:f:408:LEU:CD1	24:f:439:TYR:CD1	2.36	1.04
3:m:150:MET:HE3	3:m:165:ILE:HD11	1.38	1.04
24:f:128:VAL:HG22	24:f:129:LEU:H	1.22	1.03
11:D:296:MET:HE1	11:D:307:VAL:HG21	1.39	1.03
30:K:133:MET:SD	30:K:137:PHE:CE2	2.52	1.03
13:P:51:ILE:HD11	13:P:87:LEU:HD21	1.39	1.03
19:V:131:LEU:HD22	19:V:158:PRO:HB3	1.40	1.03
24:f:294:MET:HA	24:f:321:MET:HA	1.07	1.03
24:f:400:TYR:CD1	24:f:437:GLU:HG3	1.94	1.03
27:Y:50:MET:HG2	27:Y:51:ALA:H	1.18	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:110:TYR:CD1	27:Y:114:ILE:HD12	1.93	1.03
30:K:133:MET:SD	30:K:137:PHE:CZ	2.52	1.02
4:R:58:HIS:HE1	4:R:104:MET:SD	1.80	1.02
26:I:44:LEU:HD22	26:I:190:LEU:HD23	1.09	1.02
1:u:413:ARG:HD2	24:f:818:LEU:HD13	1.39	1.02
24:f:594:LEU:CG	24:f:631:LYS:HE2	1.88	1.02
29:Z:8:LYS:HG2	29:Z:159:THR:HB	1.41	1.02
7:B:234:LEU:CD2	35:B:501:ADP:H2'	1.90	1.02
24:f:400:TYR:HE1	24:f:437:GLU:HG2	1.18	1.02
22:W:82:LEU:HD22	22:W:90:LEU:HD22	1.05	1.01
11:D:82:ILE:CD1	15:C:66:LEU:HD23	1.90	1.01
14:U:265:ILE:HG22	14:U:269:ARG:HD2	1.34	1.01
24:f:9:ALA:CB	24:f:59:LEU:CD1	2.38	1.01
25:X:80:ILE:HD12	25:X:84:LYS:HB3	1.42	1.01
20:t:54:THR:HG22	20:t:55:SER:H	1.26	1.01
24:f:370:MET:HE3	24:f:747:GLN:HE22	1.22	1.01
24:f:400:TYR:CE1	24:f:437:GLU:CG	2.44	1.01
30:k:133:MET:SD	30:k:137:PHE:CZ	2.54	1.01
1:u:402:LYS:O	1:u:406:ARG:HG2	1.59	1.01
29:Z:101:LEU:CD2	29:Z:123:ILE:HD11	1.90	1.01
2:d:271:ILE:HA	2:d:274:CYS:SG	2.00	1.01
24:f:761:MET:HA	24:f:858:LYS:HZ3	1.25	1.01
11:D:82:ILE:CD1	15:C:66:LEU:CD2	2.39	1.00
25:X:261:LEU:HD12	25:X:263:THR:HG23	1.39	1.00
14:U:725:MET:HE1	34:c:178:THR:HB	1.39	1.00
27:Y:12:PRO:CG	27:Y:113:ARG:HD3	1.90	1.00
11:D:82:ILE:HD13	15:C:66:LEU:HD21	1.44	1.00
24:f:94:LYS:CG	24:f:133:MET:HE3	1.90	1.00
24:f:404:ASP:CB	24:f:439:TYR:CZ	2.44	0.99
6:E:70:ILE:HG12	6:E:80:VAL:HG12	1.45	0.99
24:f:294:MET:HA	24:f:321:MET:CA	1.92	0.99
6:E:46:ASP:CG	12:F:139:LEU:HD21	1.87	0.99
14:U:725:MET:SD	34:c:181:LEU:CD1	2.50	0.99
24:f:558:LEU:HD12	24:f:559:PRO:CD	1.90	0.99
20:t:254:TRP:HB2	5:N:224:LEU:HD13	1.45	0.99
16:G:13:ILE:HG23	16:G:129:ALA:HB1	1.45	0.99
24:f:370:MET:HE3	24:f:747:GLN:NE2	1.78	0.99
22:W:274:VAL:HG12	22:W:283:GLN:NE2	1.76	0.98
24:f:9:ALA:CB	24:f:59:LEU:HD13	1.92	0.98
26:I:44:LEU:HD11	26:I:213:ILE:HG23	1.01	0.98
14:U:682:TYR:O	14:U:685:GLN:HG2	1.62	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:V:224:LEU:HD12	19:V:224:LEU:O	1.63	0.98
22:W:268:LYS:HG2	22:W:299:ILE:CD1	1.93	0.98
16:G:128:ASN:OD1	23:H:127:VAL:HG12	1.63	0.98
16:g:22:LEU:HD11	16:g:25:VAL:CB	1.94	0.98
13:P:126:LEU:CD1	13:P:127:ILE:HG13	1.93	0.98
16:g:22:LEU:HD12	16:g:22:LEU:O	1.62	0.98
27:Y:12:PRO:CG	27:Y:113:ARG:CD	2.41	0.98
22:W:359:VAL:HG23	22:W:382:LEU:CD2	1.92	0.98
11:D:327:LEU:HD12	11:D:327:LEU:O	1.62	0.98
13:p:164:PHE:HB2	13:p:189:ILE:CD1	1.94	0.98
24:f:408:LEU:HD13	24:f:439:TYR:HD1	0.83	0.98
26:I:44:LEU:HD13	26:I:215:THR:HG22	1.42	0.98
24:f:594:LEU:HG	24:f:631:LYS:HE2	1.00	0.98
5:n:191:ALA:HB3	5:n:228:ILE:HD12	1.43	0.98
27:Y:104:MET:HE1	27:Y:111:LEU:CD2	1.94	0.98
2:d:341:GLU:OE2	2:d:345:GLN:HG2	1.64	0.97
4:R:60:THR:H	4:R:92:LYS:HZ3	1.04	0.97
2:d:339:VAL:CG2	34:c:296:ILE:HG23	1.93	0.97
4:R:59:GLY:HA3	4:R:92:LYS:HZ1	1.22	0.97
30:k:180:SER:OG	30:k:201:ILE:HD11	1.64	0.97
32:L:215:VAL:HG23	32:L:221:PHE:CD1	1.98	0.97
27:Y:104:MET:HE1	27:Y:111:LEU:HG	1.44	0.97
2:d:94:MET:CE	2:d:118:ARG:HA	1.95	0.97
26:I:134:LEU:HD11	26:I:136:TYR:CZ	2.00	0.96
4:R:94:ILE:HD13	4:R:104:MET:HE2	1.48	0.96
24:f:294:MET:CA	24:f:321:MET:HA	1.96	0.96
22:W:378:MET:CE	22:W:413:ILE:HD11	1.96	0.96
33:b:121:GLU:CG	33:b:152:LYS:HG3	1.94	0.96
22:W:166:LEU:HD21	22:W:201:ARG:CD	1.96	0.96
22:W:79:GLU:CG	22:W:130:MET:HE1	1.94	0.96
24:f:187:LEU:O	24:f:191:ILE:HD13	1.65	0.96
7:B:135:ILE:HD12	7:B:141:LYS:HE2	1.46	0.95
8:e:60:LEU:HD11	27:Y:329:PHE:CD1	2.01	0.95
22:W:166:LEU:HD21	22:W:201:ARG:HD2	1.47	0.95
20:t:108:LEU:CD1	20:t:155:MET:CE	2.44	0.95
24:f:100:ARG:CB	24:f:101:PRO:HD3	1.95	0.95
5:N:207:VAL:HG12	5:N:224:LEU:CD2	1.95	0.95
24:f:788:MET:HG2	24:f:789:SER:H	1.28	0.95
14:U:697:GLN:HG3	14:U:745:THR:HG22	1.47	0.95
17:q:35:MET:HG3	17:q:181:ARG:NE	1.82	0.95
27:Y:144:LEU:HA	27:Y:147:ILE:HG22	1.46	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:188:ARG:NH1	3:M:233:ARG:HH21	1.63	0.95
9:o:124:ARG:HG3	9:o:128:GLN:HE22	1.26	0.95
25:X:153:LEU:CD2	25:X:169:VAL:HG11	1.96	0.95
19:V:273:LYS:O	19:V:276:PHE:CE1	2.20	0.94
32:l:130:VAL:HG22	32:l:132:LEU:HD12	1.48	0.94
12:F:291:ILE:HD11	12:F:309:THR:OG1	1.67	0.94
14:U:571:CYS:SG	14:U:583:MET:HE1	2.06	0.94
15:C:147:THR:HG21	15:C:151:ILE:HD11	1.49	0.94
22:W:268:LYS:CG	22:W:299:ILE:HD13	1.97	0.94
24:f:100:ARG:HB3	24:f:101:PRO:HD3	1.48	0.94
23:h:72:ILE:HG12	23:h:107:THR:HG22	1.48	0.94
16:g:191:PHE:HE1	16:g:195:VAL:CG2	1.81	0.94
24:f:387:GLN:OE1	24:f:418:LEU:HD11	1.68	0.94
34:c:121:TRP:HZ3	34:c:123:SER:HA	1.22	0.94
22:W:359:VAL:HG23	22:W:382:LEU:HD23	0.96	0.94
16:g:191:PHE:CE1	16:g:195:VAL:HG21	2.02	0.93
24:f:376:PHE:HZ	24:f:380:PHE:HE2	1.04	0.93
19:V:214:HIS:CE1	19:V:218:TYR:HE2	1.86	0.93
30:k:133:MET:HE1	30:k:137:PHE:CZ	2.02	0.93
7:B:152:LEU:CD2	7:B:159:VAL:HG12	1.99	0.93
24:f:418:LEU:HD11	24:f:428:GLN:OE1	1.69	0.93
27:Y:12:PRO:HD2	27:Y:113:ARG:HE	1.33	0.93
22:W:169:LEU:HD22	22:W:189:GLN:CD	1.93	0.93
15:C:187:LEU:CD1	15:C:314:LYS:HD3	1.98	0.92
19:V:131:LEU:HD22	19:V:158:PRO:CB	1.99	0.92
24:f:376:PHE:CZ	24:f:380:PHE:CD2	2.58	0.92
27:Y:12:PRO:HG2	27:Y:113:ARG:HD2	1.50	0.92
26:I:38:LEU:HB3	26:I:43:VAL:HG23	1.51	0.92
5:n:223:LEU:HD13	5:n:227:GLN:CB	1.99	0.92
24:f:88:SER:O	24:f:92:VAL:HB	1.70	0.92
30:k:78:MET:HE3	30:k:85:ALA:CB	2.00	0.92
19:V:131:LEU:HD13	19:V:158:PRO:HB3	1.49	0.92
2:d:237:MET:HE3	19:V:400:HIS:CE1	2.04	0.91
15:C:187:LEU:HD23	15:C:293:MET:HB2	1.52	0.91
27:Y:157:ILE:CB	27:Y:186:LEU:HD11	1.99	0.91
34:c:56:LEU:CD1	34:c:92:GLN:NE2	2.34	0.91
27:Y:309:GLU:HA	27:Y:358:ARG:HH22	1.35	0.91
9:o:44:THR:N	9:o:212:SER:HG	1.68	0.91
33:b:3:LEU:HD12	33:b:105:HIS:HA	1.52	0.91
19:V:131:LEU:CD2	19:V:158:PRO:HB3	2.01	0.91
19:V:224:LEU:HD13	19:V:227:VAL:HB	1.52	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:231:ILE:HD11	22:W:243:ILE:HG21	1.51	0.91
24:f:370:MET:CE	24:f:747:GLN:HE22	1.81	0.91
22:W:406:VAL:HA	22:W:413:ILE:HG22	1.53	0.91
24:f:558:LEU:CD1	24:f:559:PRO:HD3	2.00	0.91
4:R:59:GLY:CA	4:R:92:LYS:NZ	2.33	0.91
14:U:269:ARG:NH1	14:U:329:LEU:HD11	1.85	0.91
24:f:326:LEU:HD22	24:f:326:LEU:H	1.32	0.91
5:n:227:GLN:O	5:n:228:ILE:HG13	1.71	0.91
24:f:400:TYR:CD1	24:f:437:GLU:CG	2.54	0.91
31:a:190:VAL:HG13	31:a:225:LEU:HD11	1.53	0.91
2:d:199:LEU:HD22	2:d:211:GLU:OE1	1.70	0.90
2:d:232:LEU:O	2:d:236:LEU:HG	1.69	0.90
20:T:155:MET:HE2	20:T:155:MET:HA	1.51	0.90
16:G:21:ARG:HD2	16:G:23:TYR:CE1	2.05	0.90
24:f:761:MET:CG	24:f:809:ILE:CB	2.48	0.90
17:Q:5:ILE:HD13	17:Q:160:LEU:HD11	1.50	0.90
5:n:233:VAL:HG22	20:T:82:ARG:NH2	1.86	0.90
24:f:570:GLY:O	24:f:600:TYR:HD2	1.54	0.90
27:Y:157:ILE:HB	27:Y:186:LEU:HD11	1.54	0.90
24:f:404:ASP:HB3	24:f:439:TYR:CE1	2.05	0.90
13:P:120:PHE:HE2	13:P:122:CYS:HG	1.03	0.90
22:W:375:MET:HE2	22:W:406:VAL:CG1	2.01	0.90
8:e:60:LEU:CD1	27:Y:329:PHE:CD1	2.55	0.90
6:E:135:ILE:CD1	6:E:182:LEU:HD23	2.02	0.89
13:P:146:MET:SD	13:P:174:ALA:HB3	2.12	0.89
24:f:850:VAL:CG1	24:f:852:VAL:HG22	2.02	0.89
30:k:78:MET:HE3	30:k:85:ALA:HB3	1.53	0.89
24:f:92:VAL:CB	24:f:93:PRO:HD3	2.03	0.89
16:g:50:ILE:HD12	16:g:79:VAL:HG23	1.55	0.89
15:C:187:LEU:HD12	15:C:314:LYS:HD3	1.53	0.89
22:W:437:SER:HB2	34:c:226:MET:HG2	1.53	0.89
24:f:399:LEU:CD1	24:f:400:TYR:CZ	2.50	0.89
24:f:399:LEU:CD1	24:f:400:TYR:CD2	2.52	0.89
19:V:484:LEU:CD1	29:Z:267:ARG:HH12	1.86	0.89
12:F:217:ILE:HG13	12:F:218:GLN:H	1.38	0.89
14:U:486:MET:SD	14:U:518:LEU:CD2	2.61	0.89
14:U:695:MET:CE	14:U:709:PHE:CE2	2.47	0.89
30:k:133:MET:SD	30:k:137:PHE:HZ	1.93	0.89
5:n:191:ALA:CB	5:n:228:ILE:HD12	2.03	0.89
24:f:20:ALA:HB2	24:f:75:LEU:HD23	1.54	0.89
14:U:725:MET:HE1	34:c:178:THR:CB	2.03	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:725:MET:CE	34:c:178:THR:HB	2.03	0.88
15:C:351:MET:HE3	15:C:391:MET:SD	2.13	0.88
32:L:215:VAL:CG2	32:L:221:PHE:HD1	1.85	0.88
19:V:451:ILE:HG12	19:V:458:VAL:HG22	1.52	0.88
24:f:825:MET:HE2	24:f:862:ILE:CG2	2.03	0.88
29:Z:224:HIS:O	29:Z:228:TYR:CE2	2.26	0.88
24:f:761:MET:HA	24:f:858:LYS:HZ1	1.29	0.88
24:f:9:ALA:HB1	24:f:59:LEU:CD1	2.02	0.88
22:W:76:GLU:HB3	22:W:130:MET:SD	2.12	0.88
25:X:261:LEU:CD1	25:X:263:THR:HG23	2.04	0.88
1:u:410:ARG:NH2	24:f:326:LEU:HG	1.89	0.88
14:U:2:ILE:HG21	14:U:34:PHE:CZ	2.08	0.88
24:f:49:ASP:OD2	24:f:128:VAL:HG21	1.73	0.88
24:f:850:VAL:CG1	24:f:852:VAL:CG2	2.52	0.88
28:j:91:CYS:SG	28:j:102:VAL:HG21	2.13	0.88
11:D:416:PHE:CZ	16:G:25:VAL:HG21	2.07	0.88
16:g:50:ILE:HD12	16:g:79:VAL:CG2	2.04	0.88
32:L:215:VAL:HG22	32:L:221:PHE:HB2	1.55	0.88
30:k:238:ILE:HD12	30:k:241:ILE:HD12	1.56	0.88
2:d:94:MET:SD	2:d:118:ARG:CG	2.59	0.87
15:C:187:LEU:HB2	15:C:314:LYS:CG	2.04	0.87
25:X:306:LEU:HD23	25:X:310:ARG:HH12	1.36	0.87
30:K:21:LEU:HD23	30:K:24:VAL:HG23	1.56	0.87
6:E:135:ILE:CG1	6:E:182:LEU:CD2	2.53	0.87
7:B:135:ILE:HD12	7:B:141:LYS:CE	2.04	0.87
18:A:360:ARG:NH1	24:f:839:PRO:HB2	1.89	0.87
22:W:378:MET:HE1	22:W:413:ILE:HD11	1.56	0.87
7:B:107:MET:HE3	7:B:151:LEU:CD1	2.05	0.87
32:L:215:VAL:CG2	32:L:221:PHE:CD1	2.57	0.87
24:f:418:LEU:HD21	24:f:428:GLN:OE1	1.75	0.87
5:n:35:THR:N	5:n:204:SER:HG	1.73	0.87
27:Y:376:LEU:CD2	29:Z:265:LEU:HD21	2.05	0.87
1:u:33:LEU:HD21	1:u:90:VAL:CG1	2.04	0.87
22:W:317:TRP:CH2	22:W:321:VAL:HG21	2.09	0.87
16:g:208:ILE:HD11	16:g:210:PHE:HD2	1.40	0.87
26:I:68:LEU:HD12	26:I:69:ASN:HB2	1.55	0.87
14:U:802:TYR:CE2	14:U:893:THR:OG1	2.27	0.86
22:W:268:LYS:HG2	22:W:299:ILE:HD13	1.56	0.86
24:f:9:ALA:HB3	24:f:59:LEU:HD13	1.55	0.86
24:f:399:LEU:HD11	24:f:400:TYR:CG	2.04	0.86
30:k:133:MET:CE	30:k:137:PHE:CZ	2.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:803:LYS:HG2	14:U:892:LEU:CD2	2.04	0.86
8:e:60:LEU:CD1	27:Y:329:PHE:CG	2.59	0.86
15:C:235:PHE:CD2	15:C:239:ARG:NH1	2.43	0.86
24:f:558:LEU:HG	24:f:559:PRO:HD3	1.56	0.86
24:f:755:ASP:CB	24:f:756:PRO:HD3	2.06	0.86
27:Y:157:ILE:CG2	27:Y:186:LEU:HD11	2.05	0.86
24:f:788:MET:HG2	24:f:789:SER:N	1.89	0.86
7:B:150:VAL:HG12	7:B:162:VAL:HG22	1.57	0.86
24:f:89:MET:HA	24:f:93:PRO:HD2	1.55	0.86
24:f:399:LEU:HB2	24:f:440:ILE:CD1	2.06	0.86
29:Z:101:LEU:HD23	29:Z:123:ILE:CD1	2.04	0.86
28:j:66:ASP:OD2	28:j:91:CYS:SG	2.33	0.86
27:Y:309:GLU:HA	27:Y:358:ARG:NH2	1.91	0.86
30:k:235:GLU:O	30:k:238:ILE:HG22	1.76	0.86
19:V:484:LEU:CD1	29:Z:267:ARG:NH1	2.38	0.86
27:Y:104:MET:HE1	27:Y:111:LEU:CG	2.05	0.86
29:Z:69:PHE:CD2	33:b:96:ALA:HA	2.10	0.86
30:K:21:LEU:HD23	30:K:24:VAL:CB	2.06	0.85
16:G:75:ASN:O	16:G:75:ASN:OD1	1.93	0.85
24:f:400:TYR:HE1	24:f:437:GLU:CG	1.86	0.85
11:D:116:LEU:HD21	15:C:66:LEU:HD22	1.57	0.85
30:k:235:GLU:HA	30:k:238:ILE:HG22	1.59	0.85
6:E:39:GLN:C	12:F:73:ILE:CD1	2.49	0.85
7:B:287:ILE:CD1	7:B:329:MET:SD	2.64	0.85
14:U:451:ALA:HB2	14:U:781:LEU:HD11	1.59	0.85
24:f:396:ASN:HA	24:f:399:LEU:HD23	1.57	0.85
14:U:570:LEU:HD21	14:U:578:LEU:O	1.76	0.85
18:A:101:ILE:HD13	18:A:113:ILE:HG13	1.59	0.85
22:W:264:GLN:NE2	22:W:299:ILE:CG1	2.40	0.85
16:g:191:PHE:CE1	16:g:195:VAL:CG2	2.60	0.85
4:R:94:ILE:CD1	4:R:104:MET:HE2	2.06	0.85
16:G:81:THR:HG21	16:G:169:GLY:HA2	1.57	0.85
24:f:9:ALA:HB1	24:f:59:LEU:HD13	1.59	0.85
5:N:228:ILE:CG2	5:N:229:PRO:CD	2.53	0.85
3:m:150:MET:HE1	3:m:165:ILE:CD1	2.06	0.84
14:U:181:LEU:HD13	14:U:201:LEU:HD13	1.59	0.84
14:U:269:ARG:HG2	14:U:325:MET:HG3	1.57	0.84
16:G:13:ILE:HD11	26:I:5:TYR:CE2	2.12	0.84
24:f:400:TYR:HD1	24:f:437:GLU:HG3	1.42	0.84
3:m:150:MET:CE	3:m:165:ILE:CD1	2.54	0.84
7:B:234:LEU:HD22	35:B:501:ADP:C2'	2.05	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:V:131:LEU:CD1	19:V:158:PRO:HB3	2.06	0.84
5:N:207:VAL:CG1	5:N:224:LEU:HD21	2.07	0.84
1:u:385:ASN:ND2	24:f:434:TYR:CD1	2.46	0.84
12:F:296:PHE:CE1	12:F:298:SER:HB3	2.12	0.84
13:p:126:LEU:HD12	13:p:127:ILE:HG23	1.59	0.84
22:W:317:TRP:CH2	22:W:321:VAL:CG2	2.60	0.84
19:V:273:LYS:C	19:V:276:PHE:HE1	1.85	0.84
22:W:79:GLU:HG3	22:W:130:MET:CE	2.07	0.84
6:E:113:ARG:HH12	6:E:220:ASN:HB3	1.42	0.84
2:d:175:TYR:HE2	2:d:188:MET:HG3	1.38	0.84
11:D:290:LEU:HD13	15:C:222:LYS:HB2	1.57	0.84
18:A:362:MET:HE3	18:A:362:MET:HA	1.60	0.84
24:f:558:LEU:CG	24:f:559:PRO:HD3	2.08	0.84
26:I:44:LEU:CD1	26:I:213:ILE:HG23	1.98	0.84
10:s:82:CYS:HB2	10:s:89:CYS:SG	2.18	0.84
24:f:306:GLU:CB	24:f:314:TYR:CZ	2.61	0.83
11:D:125:LYS:HB3	11:D:126:PRO:HD3	0.85	0.83
15:C:187:LEU:HD23	15:C:293:MET:CB	2.07	0.83
29:Z:101:LEU:HD21	29:Z:138:TYR:CE2	2.13	0.83
1:u:77:ASP:CG	34:c:94:LYS:HE2	2.01	0.83
18:A:362:MET:HA	18:A:362:MET:CE	2.08	0.83
24:f:49:ASP:OD2	24:f:128:VAL:HG11	1.78	0.83
24:f:57:GLU:OE1	24:f:58:MET:HG2	1.79	0.83
17:Q:5:ILE:HD13	17:Q:160:LEU:CD1	2.07	0.83
24:f:719:PRO:CB	24:f:754:LYS:HG2	2.07	0.83
7:B:107:MET:HE3	7:B:151:LEU:HD11	1.60	0.83
24:f:471:LEU:HD21	24:f:504:VAL:HG23	1.58	0.83
27:Y:247:LEU:HD23	27:Y:250:LEU:HD12	1.59	0.83
24:f:592:ASN:O	24:f:596:ASP:HB2	1.78	0.83
24:f:699:VAL:HG12	24:f:703:ARG:HG2	1.59	0.83
6:E:39:GLN:O	12:F:73:ILE:HD11	1.78	0.83
22:W:317:TRP:CZ3	22:W:321:VAL:CG2	2.61	0.83
27:Y:144:LEU:HA	27:Y:147:ILE:CG2	2.08	0.83
5:n:221:GLN:HE21	5:n:223:LEU:HD21	1.43	0.82
7:B:233:THR:O	7:B:236:ALA:HB3	1.78	0.82
24:f:396:ASN:OD1	24:f:399:LEU:HD21	1.78	0.82
27:Y:12:PRO:HD2	27:Y:113:ARG:NE	1.91	0.82
12:F:125:LYS:HB2	12:F:131:THR:HG22	1.61	0.82
9:o:124:ARG:HG3	9:o:128:GLN:HE21	1.41	0.82
14:U:681:ASN:HB3	14:U:723:ASP:OD2	1.78	0.82
22:W:97:LEU:HD21	22:W:135:LYS:HE3	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:f:411:ALA:HB3	24:f:443:GLY:HA3	1.59	0.82
2:d:270:GLU:O	2:d:274:CYS:SG	2.37	0.82
20:t:137:LEU:CD2	20:t:155:MET:SD	2.64	0.82
24:f:19:ALA:HB2	24:f:34:ARG:HD3	1.62	0.82
24:f:462:ALA:HB3	24:f:489:TYR:OH	1.79	0.82
4:R:58:HIS:CE1	4:R:104:MET:SD	2.70	0.82
24:f:404:ASP:CG	24:f:439:TYR:CE2	2.58	0.82
24:f:788:MET:CG	24:f:789:SER:H	1.92	0.82
27:Y:130:LYS:HG2	27:Y:131:THR:H	1.45	0.82
3:M:188:ARG:CZ	3:M:233:ARG:HH21	1.91	0.82
12:F:439:ALA:HB1	32:L:62:LYS:HE2	1.61	0.82
16:G:93:ARG:HE	16:G:121:ILE:CD1	1.92	0.82
24:f:850:VAL:HG13	24:f:852:VAL:HG22	1.60	0.82
18:A:299:MET:O	18:A:303:ILE:HG12	1.80	0.82
15:C:306:LEU:HD23	15:C:311:ILE:CD1	2.10	0.81
19:V:277:PRO:HB2	19:V:285:TRP:HZ3	1.44	0.81
22:W:82:LEU:HD22	22:W:90:LEU:CD2	2.00	0.81
24:f:9:ALA:HB3	24:f:59:LEU:CD1	2.08	0.81
27:Y:82:LYS:HB3	27:Y:82:LYS:NZ	1.95	0.81
9:o:124:ARG:CG	9:o:128:GLN:NE2	2.41	0.81
17:q:35:MET:CG	17:q:181:ARG:HH21	1.92	0.81
8:e:60:LEU:HD13	27:Y:329:PHE:HB2	1.62	0.81
14:U:486:MET:CG	14:U:518:LEU:HD22	2.09	0.81
14:U:695:MET:HE1	14:U:709:PHE:HD2	1.08	0.81
20:T:81:PHE:CB	20:T:84:ILE:HD11	2.10	0.81
20:t:254:TRP:HB2	5:N:224:LEU:CD1	2.09	0.81
24:f:418:LEU:CD1	24:f:428:GLN:OE1	2.28	0.81
4:R:60:THR:N	4:R:92:LYS:NZ	2.28	0.81
7:B:293:LYS:HG3	7:B:295:TYR:HD2	1.46	0.81
7:B:214:MET:O	18:A:362:MET:HE1	1.79	0.81
11:D:320:ALA:HA	11:D:323:ARG:HD2	1.62	0.81
22:W:375:MET:CE	22:W:406:VAL:HG13	2.10	0.81
7:B:156:VAL:O	18:A:95:VAL:HG22	1.80	0.81
14:U:725:MET:HE1	34:c:178:THR:CG2	2.10	0.81
18:A:299:MET:SD	18:A:303:ILE:HG13	2.21	0.81
19:V:52:ASP:OD2	19:V:147:PHE:CE1	2.34	0.81
19:V:438:VAL:HG11	19:V:451:ILE:HD11	1.63	0.81
4:R:59:GLY:CA	4:R:92:LYS:HZ3	1.92	0.81
22:W:303:LYS:HZ1	22:W:309:PHE:HZ	1.26	0.81
30:K:21:LEU:HG	30:K:22:PHE:H	1.46	0.81
31:a:234:ILE:CG2	31:a:238:TYR:CE2	2.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:70:ILE:HG12	6:E:80:VAL:CG1	2.11	0.80
24:f:558:LEU:HD12	24:f:559:PRO:N	1.96	0.80
16:G:60:LEU:HD21	3:M:182:MET:HE1	1.62	0.80
24:f:652:VAL:HG11	24:f:686:LEU:HD21	1.64	0.80
30:K:177:ALA:O	30:K:181:LEU:HG	1.81	0.80
2:d:94:MET:CE	2:d:118:ARG:CG	2.59	0.80
6:E:135:ILE:HG12	6:E:182:LEU:CD2	2.10	0.80
27:Y:259:TYR:OH	27:Y:299:MET:HE2	1.80	0.80
1:u:413:ARG:HD2	24:f:818:LEU:CD1	2.10	0.80
5:n:38:MET:SD	5:n:161:ILE:HG22	2.22	0.80
22:W:76:GLU:CB	22:W:130:MET:SD	2.69	0.80
22:W:366:MET:CE	22:W:378:MET:HE2	2.10	0.80
24:f:582:VAL:CG2	24:f:588:ARG:HH22	1.84	0.80
5:N:207:VAL:HG12	5:N:224:LEU:HD21	1.60	0.80
1:u:39:THR:HG23	1:u:40:GLY:N	1.96	0.80
24:f:760:PHE:HZ	24:f:857:GLY:CA	1.88	0.80
2:d:208:PHE:HD2	2:d:209:HIS:CD2	1.99	0.80
24:f:558:LEU:CD1	24:f:559:PRO:CD	2.57	0.80
30:K:21:LEU:HG	30:K:22:PHE:N	1.97	0.80
19:V:484:LEU:HD12	29:Z:267:ARG:HH12	1.45	0.80
11:D:319:PRO:O	11:D:323:ARG:HG3	1.82	0.80
15:C:336:MET:HB3	15:C:338:LEU:HD13	1.63	0.80
12:F:291:ILE:HG13	12:F:306:VAL:HG13	1.64	0.80
16:G:93:ARG:HE	16:G:121:ILE:HD13	1.47	0.80
18:A:368:ILE:CD1	18:A:409:PHE:CE2	2.65	0.80
24:f:100:ARG:CB	24:f:101:PRO:CD	2.59	0.80
24:f:188:VAL:HA	24:f:191:ILE:HD11	1.63	0.80
3:M:124:THR:O	3:M:124:THR:HG22	1.81	0.80
32:l:130:VAL:HG22	32:l:132:LEU:CD1	2.11	0.80
15:C:301:LEU:HG	15:C:302:ASP:H	1.47	0.80
24:f:111:GLU:HG3	24:f:141:LYS:NZ	1.97	0.80
24:f:555:ALA:HB1	24:f:590:PHE:CD2	2.16	0.80
24:f:555:ALA:HB1	24:f:590:PHE:HD2	1.47	0.80
12:F:198:LEU:HD13	12:F:236:LEU:HD13	1.62	0.79
24:f:399:LEU:CG	24:f:440:ILE:CD1	2.58	0.79
9:O:62:ARG:HB2	9:O:214:SER:OG	1.81	0.79
2:d:195:ASN:O	2:d:199:LEU:HD13	1.82	0.79
11:D:125:LYS:HG2	34:c:277:LYS:HG2	1.64	0.79
24:f:305:LEU:HD23	24:f:314:TYR:HD1	1.47	0.79
31:a:293:PHE:CD2	31:a:329:LYS:CG	2.63	0.79
11:D:415:GLU:HG2	16:G:159:TYR:CE2	2.18	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:300:LYS:HD3	21:v:3:UNK:HA	1.65	0.79
5:n:63:ARG:NH1	20:T:223:TYR:CE1	2.49	0.79
7:B:438:LEU:HD22	26:I:153:SER:OG	1.82	0.79
18:A:368:ILE:HD11	18:A:409:PHE:HE2	1.47	0.79
1:u:385:ASN:HB3	24:f:434:TYR:HD1	1.47	0.79
16:g:211:LYS:HB3	16:g:212:PRO:HD2	1.64	0.79
18:A:165:GLN:HE22	18:A:267:LYS:NZ	1.79	0.79
1:u:410:ARG:NH1	24:f:326:LEU:CD2	2.46	0.79
24:f:408:LEU:CD1	24:f:439:TYR:HA	2.12	0.79
24:f:418:LEU:CD2	24:f:428:GLN:OE1	2.30	0.79
24:f:404:ASP:CG	24:f:439:TYR:CZ	2.61	0.79
28:J:96:LEU:CD1	17:Q:58:GLU:HB3	2.13	0.79
30:K:21:LEU:HD23	30:K:24:VAL:CG2	2.06	0.79
7:B:345:GLY:HA2	18:A:386:ARG:HH22	1.47	0.79
5:n:68:LEU:HD13	5:n:76:PHE:CD2	2.18	0.78
24:f:761:MET:CA	24:f:858:LYS:NZ	2.41	0.78
3:M:27:ALA:O	3:M:31:VAL:HG23	1.84	0.78
29:Z:69:PHE:HD2	33:b:96:ALA:HA	1.48	0.78
2:d:175:TYR:CZ	2:d:188:MET:HG3	2.17	0.78
24:f:128:VAL:HG22	24:f:129:LEU:N	1.98	0.78
30:k:78:MET:CE	30:k:85:ALA:HB3	2.13	0.78
16:g:208:ILE:HD11	16:g:210:PHE:CD2	2.17	0.78
2:d:94:MET:HE1	2:d:118:ARG:HG2	1.61	0.78
1:u:403:ARG:HA	1:u:406:ARG:HD2	1.65	0.78
12:F:386:ARG:HH22	32:L:170:THR:HG23	1.48	0.78
18:A:165:GLN:HE22	18:A:267:LYS:HZ1	1.31	0.78
19:V:277:PRO:HB2	19:V:285:TRP:CZ3	2.18	0.78
34:c:259:VAL:O	34:c:262:GLU:HG2	1.83	0.78
16:G:13:ILE:HG21	16:G:129:ALA:HB1	1.63	0.78
18:A:79:ASP:OD1	24:f:692:LEU:HB3	1.82	0.78
20:T:81:PHE:HB3	20:T:84:ILE:HD11	1.64	0.78
24:f:396:ASN:O	24:f:399:LEU:CG	2.29	0.78
24:f:471:LEU:CD2	24:f:504:VAL:HG23	2.13	0.78
11:D:406:VAL:HG12	11:D:407:ILE:HG12	1.63	0.78
24:f:825:MET:HE2	24:f:862:ILE:HG21	1.65	0.78
3:m:150:MET:HE1	3:m:165:ILE:HD11	1.62	0.78
24:f:616:CYS:HB2	24:f:629:LYS:HE3	1.66	0.78
27:Y:144:LEU:CA	27:Y:147:ILE:HG22	2.13	0.78
29:Z:121:LEU:HD11	29:Z:138:TYR:HD2	1.47	0.78
2:d:175:TYR:HE2	2:d:188:MET:CG	1.97	0.78
4:R:59:GLY:C	4:R:92:LYS:HZ3	1.91	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:n:223:LEU:HB3	5:n:227:GLN:CB	2.12	0.77
22:W:268:LYS:HD3	22:W:299:ILE:HG21	1.63	0.77
24:f:9:ALA:CB	24:f:59:LEU:HD12	2.13	0.77
24:f:371:ASN:OD1	24:f:372:LEU:N	2.17	0.77
4:R:60:THR:H	4:R:92:LYS:NZ	1.80	0.77
32:l:229:VAL:O	32:l:233:LEU:HD13	1.83	0.77
26:I:44:LEU:CD2	26:I:190:LEU:CD2	2.52	0.77
27:Y:104:MET:CE	27:Y:111:LEU:HG	2.14	0.77
7:B:293:LYS:HG2	7:B:295:TYR:CE2	2.20	0.77
2:d:147:ILE:HA	2:d:150:ILE:HG22	1.67	0.77
16:G:13:ILE:CG2	16:G:129:ALA:CB	2.63	0.77
24:f:373:ALA:HB2	24:f:744:MET:HG2	1.66	0.77
34:c:56:LEU:HD13	34:c:92:GLN:NE2	1.98	0.77
12:F:386:ARG:HH22	32:L:170:THR:CG2	1.97	0.77
18:A:128:GLN:NE2	24:f:358:PHE:CE1	2.52	0.77
19:V:163:VAL:CG2	19:V:175:MET:HG2	2.14	0.77
1:u:75:HIS:HD1	1:u:88:PHE:HE2	1.31	0.77
24:f:555:ALA:CB	24:f:590:PHE:HD2	1.98	0.77
24:f:542:ILE:HG22	24:f:542:ILE:O	1.84	0.77
31:a:371:ALA:O	31:a:375:LEU:CD2	2.32	0.77
1:u:77:ASP:CG	34:c:94:LYS:CE	2.58	0.77
3:m:40:ARG:HD3	3:m:161:TRP:CD1	2.20	0.77
23:h:107:THR:HG21	23:h:138:GLY:HA3	1.67	0.77
29:Z:101:LEU:HD11	29:Z:138:TYR:CE2	2.20	0.77
19:V:131:LEU:HD22	19:V:158:PRO:CG	2.16	0.76
22:W:231:ILE:CD1	22:W:243:ILE:CG2	2.62	0.76
26:I:68:LEU:HD22	26:I:90:LEU:HD13	1.65	0.76
2:d:293:PHE:CD2	2:d:294:ASN:N	2.47	0.76
24:f:404:ASP:HB3	24:f:439:TYR:OH	1.85	0.76
26:i:68:LEU:HD13	26:i:90:LEU:HD21	1.64	0.76
7:B:293:LYS:CG	7:B:295:TYR:HD2	1.98	0.76
14:U:451:ALA:CB	14:U:781:LEU:HD11	2.16	0.76
29:Z:224:HIS:O	29:Z:228:TYR:HE2	1.66	0.76
24:f:555:ALA:O	24:f:590:PHE:HE2	1.68	0.76
3:M:52:LYS:HD3	3:M:64:ASN:OD1	1.85	0.76
2:d:94:MET:HE1	2:d:118:ARG:CG	2.16	0.76
19:V:129:ASP:OD2	19:V:130:PHE:CE1	2.39	0.76
19:V:322:VAL:O	19:V:322:VAL:HG12	1.85	0.76
3:M:24:VAL:HG11	3:M:124:THR:HG21	1.68	0.76
26:i:36:GLY:O	26:i:147:LEU:CD1	2.34	0.76
18:A:405:THR:HG22	18:A:406:GLU:N	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:231:ILE:HG13	22:W:243:ILE:HG12	1.68	0.76
29:Z:101:LEU:CD2	29:Z:123:ILE:CD1	2.62	0.76
1:u:410:ARG:CZ	24:f:326:LEU:CG	2.62	0.75
13:P:120:PHE:CE2	13:P:122:CYS:SG	2.78	0.75
22:W:359:VAL:CG2	22:W:382:LEU:CD2	2.57	0.75
29:Z:224:HIS:CE1	31:a:340:VAL:CG1	2.52	0.75
1:u:413:ARG:HG2	24:f:818:LEU:HD22	1.68	0.75
14:U:346:ASN:OD1	14:U:348:THR:HG23	1.87	0.75
24:f:555:ALA:CB	24:f:590:PHE:CD2	2.70	0.75
27:Y:201:PHE:HD2	27:Y:226:VAL:HG11	1.49	0.75
33:b:65:THR:HG21	33:b:70:ARG:NH2	2.00	0.75
30:k:78:MET:HE2	30:k:82:ILE:HD12	1.67	0.75
14:U:71:LEU:HD12	14:U:71:LEU:O	1.86	0.75
19:V:129:ASP:OD2	19:V:130:PHE:CD1	2.40	0.75
19:V:176:MET:HE3	19:V:214:HIS:HE1	1.52	0.75
24:f:400:TYR:CE1	24:f:437:GLU:HG3	2.17	0.75
32:L:140:MET:O	32:L:140:MET:HG3	1.86	0.75
3:m:150:MET:HE1	3:m:165:ILE:HG12	1.69	0.75
27:Y:104:MET:HE1	27:Y:111:LEU:HD23	1.67	0.75
2:d:199:LEU:CD2	2:d:211:GLU:OE1	2.35	0.75
7:B:293:LYS:CG	7:B:295:TYR:CD2	2.70	0.75
29:Z:43:TRP:HD1	29:Z:48:LEU:HD12	1.52	0.75
11:D:318:ASP:OD1	11:D:319:PRO:HD2	1.87	0.75
18:A:299:MET:SD	18:A:303:ILE:CG1	2.75	0.75
22:W:82:LEU:CD2	22:W:90:LEU:CD2	2.63	0.75
22:W:274:VAL:CG1	22:W:283:GLN:NE2	2.48	0.75
27:Y:376:LEU:HD23	29:Z:265:LEU:HD21	1.68	0.75
31:a:278:MET:SD	31:a:319:LEU:HD23	2.27	0.75
24:f:616:CYS:C	24:f:629:LYS:HE3	2.12	0.74
30:K:21:LEU:HD23	30:K:24:VAL:H	1.51	0.74
12:F:86:LEU:HD21	18:A:124:ASP:HB2	0.82	0.74
16:G:21:ARG:CD	16:G:23:TYR:CE1	2.70	0.74
30:K:129:ASP:HB3	30:K:130:PRO:CD	2.17	0.74
13:P:22:ILE:HG21	13:P:110:ALA:HB3	1.69	0.74
14:U:2:ILE:HG23	14:U:34:PHE:HE2	1.50	0.74
24:f:612:LEU:O	24:f:613:LEU:HD12	1.87	0.74
27:Y:157:ILE:HG21	27:Y:186:LEU:HD11	1.68	0.74
5:n:187:LEU:HD12	5:n:210:LEU:HD13	1.70	0.74
7:B:293:LYS:HG2	7:B:295:TYR:CD2	2.22	0.74
12:F:383:GLU:HG2	32:L:170:THR:CG2	2.11	0.74
22:W:437:SER:CB	34:c:226:MET:HG2	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:I:44:LEU:CD1	26:I:213:ILE:CG2	2.57	0.74
28:J:96:LEU:HD13	17:Q:58:GLU:HB3	1.69	0.74
1:u:402:LYS:HB3	1:u:406:ARG:CZ	2.17	0.74
24:f:399:LEU:HD11	24:f:400:TYR:CE1	2.10	0.74
30:K:228:MET:HA	30:K:228:MET:CE	2.17	0.74
33:b:184:ILE:O	33:b:184:ILE:HG22	1.86	0.74
6:E:148:VAL:HG11	6:E:170:CYS:SG	2.27	0.74
11:D:300:ASP:CG	11:D:303:VAL:HG23	2.13	0.74
16:G:62:ASP:OD1	16:G:64:SER:N	2.21	0.74
24:f:376:PHE:HZ	24:f:380:PHE:CE2	1.88	0.74
7:B:214:MET:O	18:A:362:MET:CE	2.34	0.74
14:U:682:TYR:O	14:U:685:GLN:CG	2.35	0.74
15:C:269:VAL:O	15:C:272:THR:HB	1.86	0.74
31:a:371:ALA:O	31:a:375:LEU:HD23	1.87	0.74
7:B:135:ILE:HD12	7:B:141:LYS:NZ	2.02	0.74
18:A:46:LYS:O	18:A:50:ASP:HB2	1.87	0.74
19:V:306:ARG:HD2	19:V:341:GLU:OE2	1.88	0.74
24:f:558:LEU:HD12	24:f:559:PRO:CG	2.18	0.74
5:n:187:LEU:CD1	5:n:210:LEU:HD13	2.17	0.74
18:A:368:ILE:HD13	18:A:409:PHE:CD2	2.22	0.74
24:f:413:SER:O	24:f:417:ILE:CG1	2.26	0.74
19:V:179:LYS:HE3	19:V:214:HIS:ND1	2.03	0.74
22:W:272:LEU:C	22:W:272:LEU:HD12	2.13	0.74
30:K:228:MET:HA	30:K:228:MET:HE3	1.70	0.74
2:d:175:TYR:CE2	2:d:188:MET:CG	2.68	0.73
4:R:79:ALA:O	4:R:86:ALA:HB3	1.88	0.73
24:f:761:MET:CA	24:f:858:LYS:HZ1	1.99	0.73
27:Y:124:PHE:HE2	27:Y:147:ILE:CD1	2.01	0.73
15:C:306:LEU:HD23	15:C:311:ILE:HD12	1.69	0.73
19:V:36:GLU:OE2	19:V:77:GLU:HG2	1.88	0.73
19:V:214:HIS:CE1	19:V:218:TYR:CE2	2.76	0.73
31:a:280:MET:HE2	31:a:291:LEU:CD2	2.14	0.73
22:W:169:LEU:CD2	22:W:189:GLN:NE2	2.50	0.73
1:u:39:THR:HG23	1:u:40:GLY:H	1.53	0.73
24:f:305:LEU:HD23	24:f:314:TYR:CD1	2.23	0.73
24:f:762:VAL:N	24:f:858:LYS:HZ1	1.87	0.73
33:b:3:LEU:CD1	33:b:105:HIS:HA	2.18	0.73
14:U:269:ARG:CG	14:U:325:MET:SD	2.77	0.73
14:U:539:THR:CG2	14:U:541:HIS:HD2	2.02	0.73
14:U:802:TYR:HE2	14:U:893:THR:OG1	1.69	0.73
32:L:215:VAL:HG22	32:L:221:PHE:CB	2.17	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:264:GLN:NE2	22:W:299:ILE:HD11	2.04	0.73
19:V:484:LEU:HD12	29:Z:267:ARG:NH1	2.02	0.73
24:f:652:VAL:CG1	24:f:686:LEU:HD21	2.18	0.73
11:D:204:MET:HE2	11:D:308:ILE:HD11	1.69	0.73
6:E:70:ILE:CG1	6:E:80:VAL:HG12	2.19	0.72
11:D:416:PHE:HZ	16:G:25:VAL:HG21	1.53	0.72
14:U:451:ALA:O	14:U:453:HIS:CD2	2.43	0.72
1:u:385:ASN:HB3	24:f:434:TYR:CD1	2.24	0.72
1:u:410:ARG:NH1	24:f:326:LEU:HD23	2.03	0.72
24:f:545:LYS:HE2	24:f:588:ARG:HD2	1.71	0.72
30:k:235:GLU:C	30:k:238:ILE:HG22	2.14	0.72
24:f:306:GLU:CB	24:f:314:TYR:CE1	2.71	0.72
27:Y:246:ILE:O	27:Y:250:LEU:HG	1.89	0.72
7:B:438:LEU:CD2	26:I:153:SER:OG	2.38	0.72
18:A:405:THR:HG22	18:A:406:GLU:H	1.52	0.72
22:W:169:LEU:CD2	22:W:189:GLN:CD	2.63	0.72
18:A:125:LEU:HD21	18:A:131:PRO:HB3	1.71	0.72
16:G:60:LEU:CD2	3:M:182:MET:HE1	2.18	0.72
24:f:382:ASN:O	24:f:417:ILE:HG23	1.90	0.72
31:a:234:ILE:HG23	31:a:238:TYR:CE2	2.23	0.72
19:V:131:LEU:HD13	19:V:158:PRO:CB	2.19	0.72
3:m:50:GLU:OE2	3:m:209:PHE:HB2	1.89	0.72
4:R:61:THR:HG22	4:R:219:ILE:HD13	1.71	0.72
15:C:235:PHE:CE2	15:C:239:ARG:NH1	2.57	0.72
22:W:260:SER:O	22:W:264:GLN:HB2	1.90	0.72
22:W:274:VAL:CG1	22:W:283:GLN:HE22	1.95	0.72
24:f:697:ILE:O	24:f:706:ILE:HG13	1.89	0.72
27:Y:12:PRO:CD	27:Y:113:ARG:HD3	2.19	0.72
14:U:657:GLY:O	14:U:693:LEU:CD2	2.35	0.71
24:f:570:GLY:O	24:f:600:TYR:CD2	2.42	0.71
11:D:232:GLY:N	11:D:266:GLU:OE2	2.22	0.71
30:K:21:LEU:CD2	30:K:24:VAL:H	2.03	0.71
30:K:92:ALA:HB2	30:K:116:VAL:HG21	1.71	0.71
14:U:269:ARG:HG2	14:U:325:MET:CG	2.21	0.71
7:B:365:PHE:HB3	7:B:380:LEU:HD22	1.71	0.71
22:W:231:ILE:CD1	22:W:243:ILE:HG21	2.19	0.71
28:j:70:CYS:SG	28:j:217:LEU:CD2	2.79	0.71
6:E:40:TYR:N	12:F:73:ILE:HD12	2.05	0.71
22:W:393:LEU:HD22	22:W:406:VAL:HG21	1.70	0.71
30:k:235:GLU:CA	30:k:238:ILE:HG22	2.20	0.71
7:B:438:LEU:HD22	26:I:153:SER:CB	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:K:21:LEU:HD23	30:K:24:VAL:HB	1.70	0.71
16:G:75:ASN:ND2	16:G:225:PRO:HB3	2.04	0.71
19:V:276:PHE:HD1	19:V:276:PHE:H	1.39	0.71
24:f:49:ASP:OD2	24:f:128:VAL:CG2	2.38	0.71
5:N:228:ILE:HG22	5:N:229:PRO:HD2	1.70	0.71
22:W:381:LEU:O	22:W:382:LEU:HD12	1.90	0.71
24:f:92:VAL:HB	24:f:93:PRO:HD3	1.72	0.71
1:u:403:ARG:O	1:u:406:ARG:HG3	1.90	0.71
1:u:39:THR:CG2	1:u:40:GLY:H	2.04	0.71
16:G:141:ILE:HG22	16:G:151:VAL:HG22	1.73	0.71
26:I:44:LEU:HD13	26:I:215:THR:CG2	2.19	0.71
14:U:129:ARG:O	14:U:130:LEU:HG	1.90	0.70
6:E:40:TYR:CA	12:F:73:ILE:HD12	2.21	0.70
19:V:354:LYS:HD3	19:V:355:ARG:HG3	1.72	0.70
22:W:359:VAL:HG22	22:W:382:LEU:HD23	1.72	0.70
27:Y:387:ILE:HD12	29:Z:276:ILE:HG22	1.74	0.70
34:c:121:TRP:CZ3	34:c:123:SER:CA	2.69	0.70
32:l:130:VAL:CG2	32:l:132:LEU:CD1	2.68	0.70
2:d:175:TYR:CD2	2:d:188:MET:HE2	2.26	0.70
2:d:339:VAL:HG22	34:c:296:ILE:CG2	2.16	0.70
24:f:306:GLU:CB	24:f:314:TYR:OH	2.39	0.70
31:a:280:MET:CE	31:a:291:LEU:HD23	2.14	0.70
24:f:49:ASP:OD2	24:f:128:VAL:CB	2.40	0.70
22:W:231:ILE:HD11	22:W:243:ILE:CG2	2.20	0.70
24:f:376:PHE:CE2	24:f:380:PHE:CD2	2.79	0.70
2:d:271:ILE:CA	2:d:274:CYS:SG	2.79	0.70
2:d:293:PHE:CG	2:d:294:ASN:N	2.60	0.70
26:i:3:ARG:NH2	30:k:10:ARG:O	2.24	0.70
30:k:235:GLU:HA	30:k:238:ILE:CG2	2.20	0.70
19:V:131:LEU:HD22	19:V:158:PRO:HG3	1.72	0.70
24:f:825:MET:HE2	24:f:862:ILE:HG22	1.72	0.70
27:Y:24:PHE:CZ	27:Y:152:MET:HG2	2.27	0.70
19:V:127:THR:HG23	19:V:127:THR:O	1.90	0.70
23:H:222:THR:OG1	23:H:225:GLU:HG3	1.92	0.70
14:U:682:TYR:C	14:U:685:GLN:HG2	2.16	0.70
24:f:408:LEU:HD11	24:f:439:TYR:HA	1.72	0.70
11:D:125:LYS:CG	11:D:126:PRO:HD3	2.21	0.69
16:G:29:PHE:HZ	16:G:155:ASP:OD2	1.75	0.69
32:l:130:VAL:CG2	32:l:132:LEU:HD12	2.21	0.69
13:P:126:LEU:HD12	13:P:127:ILE:CG1	2.17	0.69
19:V:62:HIS:O	19:V:65:ARG:HB2	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:93:ARG:NH1	22:W:97:LEU:HD23	2.08	0.69
2:d:178:TYR:OH	14:U:2:ILE:HG12	1.92	0.69
6:E:46:ASP:OD2	12:F:80:ILE:HG13	1.92	0.69
19:V:306:ARG:CD	19:V:341:GLU:OE2	2.40	0.69
22:W:76:GLU:CG	22:W:130:MET:SD	2.81	0.69
1:u:60:LEU:O	1:u:64:LEU:HB2	1.93	0.69
24:f:399:LEU:HD13	24:f:400:TYR:CD1	2.11	0.69
3:m:150:MET:HE1	3:m:165:ILE:HG13	1.72	0.69
15:C:187:LEU:HD13	15:C:314:LYS:HD3	1.74	0.69
20:T:96:LEU:HD11	20:T:155:MET:HB3	1.74	0.69
23:H:46:LEU:CD1	23:H:137:CYS:SG	2.77	0.69
31:a:293:PHE:CE2	31:a:329:LYS:HB3	2.27	0.69
12:F:217:ILE:HG13	12:F:218:GLN:N	2.08	0.69
14:U:803:LYS:HG2	14:U:892:LEU:HD21	1.74	0.69
19:V:302:TYR:OH	19:V:397:ARG:NE	2.25	0.69
17:Q:5:ILE:CD1	17:Q:160:LEU:HD11	2.22	0.69
24:f:100:ARG:HB2	24:f:101:PRO:CD	2.23	0.69
27:Y:186:LEU:HG	27:Y:187:TYR:H	1.58	0.69
26:i:68:LEU:HD13	26:i:90:LEU:CD2	2.22	0.69
31:a:198:PHE:CZ	31:a:202:LEU:HD11	2.27	0.69
23:H:189:HIS:CD2	25:X:124:PHE:CD2	2.81	0.68
24:f:92:VAL:CB	24:f:93:PRO:CD	2.70	0.68
24:f:258:LYS:NZ	24:f:261:ARG:HD2	2.09	0.68
6:E:40:TYR:N	12:F:73:ILE:CD1	2.55	0.68
9:o:108:LEU:O	9:o:108:LEU:HD23	1.92	0.68
16:g:22:LEU:HD11	16:g:25:VAL:CG2	2.23	0.68
1:u:403:ARG:HA	1:u:406:ARG:HG3	1.75	0.68
7:B:440:LEU:C	28:J:25:ALA:O	2.37	0.68
12:F:386:ARG:NH2	32:L:170:THR:HG23	2.08	0.68
2:d:344:ARG:HG3	2:d:348:MET:HE3	1.75	0.68
10:S:40:ILE:HD13	10:S:81:GLY:C	2.18	0.68
15:C:235:PHE:HD2	15:C:279:GLN:HE21	1.40	0.68
18:A:40:THR:HG22	18:A:41:TYR:N	2.06	0.68
31:a:289:ARG:HG2	31:a:333:MET:HB3	1.74	0.68
5:n:41:GLN:HG2	5:n:158:SER:O	1.92	0.68
14:U:269:ARG:HG3	14:U:325:MET:SD	2.34	0.68
26:I:68:LEU:HD22	26:I:90:LEU:CD1	2.24	0.68
5:N:207:VAL:CG1	5:N:224:LEU:CD2	2.69	0.68
11:D:83:GLN:NE2	11:D:140:VAL:HG12	2.08	0.68
24:f:420:TRP:CZ2	24:f:806:VAL:HG23	2.28	0.68
5:N:48:LEU:HB3	5:N:68:LEU:HD21	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:320:ALA:HA	11:D:323:ARG:CD	2.22	0.68
19:V:205:LEU:O	19:V:208:ALA:HB3	1.94	0.68
24:f:258:LYS:HZ3	24:f:261:ARG:HD2	1.58	0.68
27:Y:231:LEU:HD22	27:Y:234:PRO:HG2	1.76	0.68
28:j:91:CYS:SG	28:j:102:VAL:CG2	2.81	0.68
17:Q:3:TYR:HE2	17:Q:5:ILE:HD11	1.57	0.68
2:d:142:ILE:HD11	2:d:182:LEU:HB2	1.75	0.68
13:p:20:VAL:CG2	13:p:119:PRO:HB2	2.24	0.68
24:f:92:VAL:HB	24:f:93:PRO:CD	2.23	0.68
23:h:21:GLN:HA	23:h:21:GLN:HE21	1.57	0.68
27:Y:50:MET:CG	27:Y:51:ALA:H	1.96	0.68
7:B:345:GLY:HA2	18:A:386:ARG:NH2	2.08	0.68
9:o:202:ILE:O	9:o:206:ILE:HG13	1.93	0.68
14:U:789:ILE:HG22	14:U:790:GLY:N	2.07	0.68
2:d:147:ILE:O	2:d:150:ILE:HG22	1.92	0.68
19:V:224:LEU:O	19:V:224:LEU:CD1	2.42	0.68
1:u:403:ARG:HA	1:u:406:ARG:CG	2.23	0.67
4:R:57:LEU:C	4:R:57:LEU:HD13	2.19	0.67
5:n:63:ARG:NH1	20:T:223:TYR:CG	2.61	0.67
7:B:107:MET:CE	7:B:151:LEU:HD11	2.24	0.67
33:b:127:LEU:HD23	33:b:130:ARG:HH12	1.60	0.67
24:f:755:ASP:CB	24:f:756:PRO:CD	2.72	0.67
25:X:306:LEU:HD11	25:X:323:LEU:HD11	1.70	0.67
2:d:200:LEU:HD11	2:d:236:LEU:CD1	2.24	0.67
16:G:154:CYS:SG	16:G:155:ASP:N	2.67	0.67
19:V:273:LYS:C	19:V:276:PHE:CE1	2.67	0.67
1:u:403:ARG:HA	1:u:406:ARG:CD	2.23	0.67
2:d:175:TYR:CE2	2:d:188:MET:HE2	2.30	0.67
4:R:197:VAL:HG23	17:q:141:SER:OG	1.95	0.67
12:F:134:LEU:HD12	12:F:134:LEU:O	1.94	0.67
12:F:134:LEU:HD13	12:F:136:VAL:O	1.95	0.67
12:F:300:LYS:CD	21:v:3:UNK:HA	2.23	0.67
24:f:49:ASP:OD2	24:f:128:VAL:CG1	2.42	0.67
23:h:21:GLN:HA	23:h:21:GLN:NE2	2.09	0.67
31:a:289:ARG:HG2	31:a:333:MET:CB	2.23	0.67
19:V:224:LEU:HD12	19:V:228:ARG:HG2	1.76	0.67
31:a:33:LEU:HD13	31:a:36:GLN:HB2	1.77	0.67
13:P:171:MET:O	13:P:175:VAL:HG23	1.94	0.67
14:U:570:LEU:HD23	14:U:570:LEU:C	2.19	0.67
15:C:351:MET:CE	15:C:391:MET:SD	2.82	0.67
24:f:404:ASP:CB	24:f:439:TYR:OH	2.41	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:i:71:ASP:OD1	26:i:223:THR:HB	1.93	0.67
31:a:70:ARG:HE	33:b:17:ARG:HE	1.43	0.67
13:P:146:MET:SD	13:P:174:ALA:CB	2.82	0.67
1:u:74:LEU:HD22	34:c:90:VAL:HG22	1.76	0.67
18:A:277:ILE:HG12	18:A:321:THR:HB	1.77	0.67
19:V:176:MET:HE3	19:V:214:HIS:CE1	2.24	0.67
23:H:6:TYR:HH	26:I:2:SER:N	1.93	0.67
1:u:402:LYS:HB3	1:u:406:ARG:HH21	1.57	0.67
20:t:108:LEU:CD1	20:t:155:MET:HE3	2.24	0.67
29:Z:101:LEU:HD21	29:Z:138:TYR:CD2	2.29	0.67
14:U:2:ILE:O	14:U:2:ILE:HG22	1.93	0.67
14:U:206:MET:HE3	14:U:216:VAL:HG21	1.77	0.67
19:V:159:LEU:HD22	19:V:163:VAL:CG2	2.25	0.67
27:Y:110:TYR:HD1	27:Y:114:ILE:HD12	1.59	0.67
27:Y:186:LEU:HG	27:Y:187:TYR:N	2.10	0.67
24:f:100:ARG:HB2	24:f:101:PRO:HD3	1.76	0.67
1:u:402:LYS:CB	1:u:406:ARG:NH2	2.51	0.66
4:R:197:VAL:HG23	17:q:141:SER:CB	2.24	0.66
5:n:68:LEU:HD13	5:n:76:PHE:CE2	2.29	0.66
6:E:216:ARG:NH2	11:D:234:GLU:HB2	2.10	0.66
22:W:271:VAL:HG22	22:W:290:ILE:HD12	1.77	0.66
24:f:414:LEU:HD21	24:f:428:GLN:HB3	1.77	0.66
24:f:691:PRO:HA	24:f:694:LEU:HB3	1.75	0.66
30:k:212:ALA:HA	30:k:234:LEU:HD11	1.77	0.66
9:o:108:LEU:HD23	9:o:108:LEU:C	2.20	0.66
24:f:9:ALA:HB1	24:f:59:LEU:HD12	1.74	0.66
24:f:848:GLN:O	24:f:850:VAL:HG23	1.95	0.66
24:f:850:VAL:CG1	24:f:852:VAL:HG23	2.23	0.66
27:Y:12:PRO:CD	27:Y:113:ARG:NE	2.58	0.66
17:q:35:MET:HG2	17:q:181:ARG:HH21	1.59	0.66
22:W:408:ARG:NH2	25:X:349:HIS:HB3	2.10	0.66
23:H:68:ILE:HG22	23:H:69:THR:HG23	1.77	0.66
12:F:125:LYS:CB	12:F:131:THR:HG22	2.26	0.66
24:f:227:ALA:H	24:f:232:TYR:HE1	1.44	0.66
30:K:133:MET:SD	30:K:137:PHE:HZ	2.18	0.66
7:B:173:VAL:HG22	15:C:274:LEU:HG	1.77	0.66
14:U:137:MET:HA	14:U:140:ARG:HB2	1.77	0.66
6:E:135:ILE:HG12	6:E:182:LEU:HD22	1.77	0.66
12:F:287:GLU:OE1	12:F:287:GLU:HA	1.94	0.66
14:U:269:ARG:HG2	14:U:325:MET:SD	2.36	0.66
20:T:70:ASP:O	20:T:86:ARG:NH1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:f:643:PRO:HB2	24:f:646:MET:HB2	1.78	0.66
31:a:198:PHE:CE2	31:a:202:LEU:HD11	2.31	0.66
4:R:61:THR:HG22	4:R:219:ILE:CD1	2.25	0.66
15:C:78:ARG:NH1	15:C:80:MET:SD	2.69	0.66
22:W:194:LEU:HD21	22:W:233:LEU:HD23	1.77	0.66
24:f:697:ILE:O	24:f:706:ILE:CG1	2.43	0.66
22:W:366:MET:HE1	22:W:378:MET:HE2	1.78	0.66
16:g:22:LEU:CD1	16:g:25:VAL:CB	2.62	0.66
26:I:39:ALA:HB2	26:I:179:TYR:OH	1.96	0.66
6:E:113:ARG:NH2	6:E:224:ASP:OD1	2.29	0.65
20:T:81:PHE:CB	20:T:84:ILE:CD1	2.74	0.65
30:k:133:MET:CE	30:k:137:PHE:HE2	2.06	0.65
2:d:251:ILE:HD11	2:d:255:SER:HA	1.77	0.65
11:D:116:LEU:CD2	15:C:66:LEU:HD22	2.26	0.65
15:C:387:VAL:O	15:C:391:MET:HG2	1.97	0.65
24:f:836:GLU:HB2	24:f:840:LEU:HD11	1.77	0.65
13:p:164:PHE:HB2	13:p:189:ILE:HD13	1.78	0.65
15:C:351:MET:HE1	15:C:354:ALA:CB	2.26	0.65
10:s:219:ASP:OD1	10:s:220:ALA:N	2.29	0.65
22:W:408:ARG:NH2	25:X:349:HIS:CB	2.59	0.65
34:c:178:THR:HA	34:c:181:LEU:HD12	1.79	0.65
18:A:405:THR:CG2	18:A:406:GLU:H	2.10	0.65
22:W:166:LEU:CD2	22:W:201:ARG:NE	2.60	0.65
25:X:149:LEU:HD12	25:X:153:LEU:HD22	1.76	0.65
1:u:39:THR:CG2	1:u:40:GLY:N	2.58	0.65
6:E:113:ARG:NH1	6:E:220:ASN:HB3	2.12	0.65
11:D:83:GLN:CD	11:D:140:VAL:HG12	2.22	0.65
14:U:509:GLY:HA3	14:U:544:ILE:HA	1.79	0.65
18:A:40:THR:HG22	18:A:41:TYR:H	1.62	0.65
23:H:189:HIS:HD2	25:X:124:PHE:CD2	2.13	0.65
24:f:46:SER:HB2	24:f:92:VAL:CG1	2.26	0.65
27:Y:130:LYS:CG	27:Y:131:THR:H	2.09	0.65
13:P:51:ILE:HD11	13:P:87:LEU:CD2	2.23	0.65
24:f:19:ALA:CB	24:f:34:ARG:HD3	2.26	0.65
24:f:178:LYS:HG2	24:f:181:ARG:HB2	1.79	0.65
24:f:408:LEU:HD12	24:f:439:TYR:CA	2.26	0.65
24:f:408:LEU:HD12	24:f:439:TYR:CB	2.27	0.65
24:f:762:VAL:H	24:f:858:LYS:HZ1	1.45	0.65
25:X:261:LEU:CD1	25:X:263:THR:CG2	2.73	0.65
30:K:21:LEU:HD22	30:K:24:VAL:CG2	2.24	0.65
34:c:56:LEU:HD11	34:c:92:GLN:NE2	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:107:MET:HE3	7:B:151:LEU:HD13	1.78	0.65
14:U:486:MET:HG2	14:U:518:LEU:HD22	1.78	0.65
16:g:208:ILE:CD1	16:g:210:PHE:HD2	2.09	0.65
33:b:148:VAL:O	33:b:148:VAL:HG12	1.97	0.65
19:V:276:PHE:N	19:V:277:PRO:HD2	2.12	0.65
24:f:326:LEU:HA	24:f:330:PHE:HB2	1.78	0.65
24:f:705:ASN:OD1	24:f:706:ILE:HG12	1.96	0.65
2:d:237:MET:HE3	19:V:400:HIS:ND1	2.10	0.65
20:T:81:PHE:HB2	20:T:84:ILE:CD1	2.27	0.65
22:W:189:GLN:HG3	22:W:205:ILE:HD13	1.79	0.65
22:W:231:ILE:CD1	22:W:243:ILE:HG23	2.26	0.65
16:g:90:GLN:HG3	16:g:136:CYS:SG	2.37	0.65
5:n:227:GLN:C	5:n:228:ILE:HG13	2.23	0.64
35:E:401:ADP:O1A	12:F:347:ARG:NH2	2.30	0.64
14:U:23:ALA:O	14:U:27:LEU:HB2	1.98	0.64
24:f:399:LEU:HD12	24:f:400:TYR:N	2.12	0.64
27:Y:124:PHE:CE2	27:Y:147:ILE:HD13	2.32	0.64
27:Y:329:PHE:O	27:Y:333:GLU:HG2	1.97	0.64
15:C:306:LEU:HD23	15:C:311:ILE:HD11	1.78	0.64
19:V:494:MET:HE3	19:V:495:ARG:H	1.63	0.64
27:Y:124:PHE:HE2	27:Y:147:ILE:HD13	1.61	0.64
30:K:129:ASP:HB3	30:K:130:PRO:HD3	1.79	0.64
1:u:77:ASP:OD2	34:c:94:LYS:CE	2.38	0.64
24:f:476:THR:O	24:f:479:LEU:N	2.29	0.64
27:Y:144:LEU:C	27:Y:147:ILE:HG22	2.21	0.64
18:A:101:ILE:HG12	18:A:140:VAL:CG2	2.27	0.64
22:W:372:ARG:HB3	22:W:412:ILE:HD11	1.79	0.64
22:W:375:MET:CE	22:W:406:VAL:CG1	2.71	0.64
24:f:470:VAL:HG11	24:f:501:LEU:HD23	1.80	0.64
24:f:558:LEU:HD12	24:f:559:PRO:HG3	1.79	0.64
28:j:84:ILE:HD12	28:j:88:ARG:HH21	1.62	0.64
8:e:60:LEU:HD13	27:Y:329:PHE:CB	2.26	0.64
24:f:329:ASN:ND2	24:f:421:ASP:HA	2.12	0.64
26:I:44:LEU:CD1	26:I:215:THR:HG22	2.26	0.64
27:Y:18:ARG:HE	27:Y:22:LEU:HD23	1.63	0.64
2:d:237:MET:CE	19:V:400:HIS:CE1	2.79	0.64
11:D:318:ASP:OD1	11:D:319:PRO:CD	2.45	0.64
15:C:336:MET:HB3	15:C:338:LEU:CD1	2.27	0.64
18:A:40:THR:HG22	18:A:41:TYR:CD2	2.33	0.64
24:f:471:LEU:CD2	24:f:504:VAL:CG2	2.76	0.64
31:a:280:MET:HE1	31:a:295:GLU:HG3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:33:LEU:HD11	1:u:90:VAL:HG11	1.80	0.64
16:G:75:ASN:HD21	16:G:225:PRO:HB3	1.62	0.64
22:W:264:GLN:HE22	22:W:299:ILE:HG12	1.61	0.64
24:f:46:SER:HB2	24:f:92:VAL:HG13	1.79	0.64
5:N:68:LEU:HG	5:N:78:CYS:SG	2.38	0.64
30:k:197:SER:O	30:k:201:ILE:HG22	1.96	0.64
1:u:75:HIS:ND1	1:u:88:PHE:HE2	1.95	0.64
1:u:413:ARG:CG	24:f:818:LEU:HD22	2.28	0.64
3:m:35:THR:HB	3:m:201:HIS:CE1	2.33	0.64
7:B:438:LEU:CD2	26:I:153:SER:CB	2.75	0.64
24:f:329:ASN:OD1	24:f:329:ASN:N	2.24	0.64
26:i:119:GLN:HE22	28:j:82:ILE:HG13	1.62	0.64
13:P:120:PHE:HE2	13:P:122:CYS:SG	2.16	0.64
1:u:413:ARG:CD	24:f:818:LEU:HD13	2.22	0.64
11:D:83:GLN:NE2	11:D:140:VAL:CG1	2.61	0.64
22:W:408:ARG:HH22	25:X:346:GLN:HB2	1.62	0.64
20:t:54:THR:CG2	20:t:55:SER:H	2.08	0.64
24:f:475:ASN:O	24:f:478:ARG:CB	2.44	0.64
23:h:5:GLY:HA3	23:h:126:GLY:HA3	1.79	0.64
30:K:133:MET:SD	30:K:137:PHE:HE2	2.17	0.64
1:u:33:LEU:HD21	1:u:90:VAL:HG13	1.80	0.64
12:F:198:LEU:HD13	12:F:236:LEU:CD1	2.27	0.64
12:F:435:LEU:HD13	30:K:20:ARG:NE	2.07	0.64
24:f:261:ARG:HG3	24:f:269:ALA:HB1	1.79	0.64
27:Y:50:MET:HG2	27:Y:51:ALA:N	2.02	0.64
28:J:91:CYS:SG	28:J:102:VAL:HG21	2.38	0.64
26:i:147:LEU:C	26:i:147:LEU:HD23	2.22	0.64
31:a:190:VAL:CG1	31:a:225:LEU:HD11	2.25	0.64
12:F:175:MET:O	12:F:250:LYS:HG2	1.97	0.63
14:U:793:LYS:H	14:U:796:LYS:HB3	1.62	0.63
19:V:200:ARG:HA	19:V:203:LEU:HB2	1.80	0.63
24:f:376:PHE:O	24:f:380:PHE:HB2	1.98	0.63
2:d:328:THR:HG22	29:Z:250:TYR:CE2	2.33	0.63
29:Z:39:LEU:HD23	29:Z:50:VAL:HG11	1.80	0.63
13:P:155:GLU:HG3	13:P:156:PRO:HD2	1.80	0.63
18:A:34:LYS:N	24:f:96:LEU:O	2.32	0.63
22:W:144:ARG:HH21	22:W:168:GLU:CD	2.07	0.63
23:h:110:LEU:CD2	23:h:136:ILE:HD11	2.28	0.63
27:Y:130:LYS:HG2	27:Y:131:THR:N	2.14	0.63
5:N:228:ILE:HG22	5:N:229:PRO:CD	2.26	0.63
34:c:121:TRP:CE3	34:c:194:HIS:HB3	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:o:50:VAL:HG12	9:o:55:ILE:HG12	1.81	0.63
11:D:82:ILE:HD12	15:C:66:LEU:HD23	1.77	0.63
9:O:44:THR:N	9:O:212:SER:HG	1.95	0.63
34:c:42:LEU:HD11	34:c:155:VAL:HG21	1.79	0.63
7:B:313:LEU:O	7:B:346:ARG:NH1	2.32	0.63
12:F:86:LEU:CD2	18:A:124:ASP:CB	2.52	0.63
14:U:682:TYR:HA	14:U:685:GLN:HG2	1.80	0.63
24:f:660:ILE:HD13	24:f:672:LEU:HD11	1.81	0.63
7:B:176:VAL:HG12	7:B:176:VAL:O	1.98	0.63
11:D:82:ILE:CD1	15:C:66:LEU:HG	2.29	0.63
16:G:51:VAL:HG22	16:G:217:VAL:HG22	1.80	0.63
24:f:4:GLY:HA2	24:f:10:PRO:HG2	1.81	0.63
24:f:36:ALA:HA	24:f:39:LYS:HB3	1.80	0.63
5:n:191:ALA:HB3	5:n:228:ILE:CD1	2.26	0.63
16:G:137:CYS:SG	16:G:138:MET:N	2.71	0.63
2:d:102:TRP:CD1	2:d:150:ILE:CD1	2.82	0.63
7:B:107:MET:CE	7:B:151:LEU:CD1	2.75	0.63
14:U:789:ILE:CG2	14:U:790:GLY:N	2.62	0.63
24:f:290:VAL:CG2	24:f:321:MET:SD	2.87	0.63
5:N:138:ASP:OD1	5:N:139:PRO:HD2	1.99	0.63
13:p:20:VAL:CG2	13:p:119:PRO:CB	2.76	0.62
22:W:264:GLN:NE2	22:W:299:ILE:CD1	2.61	0.62
24:f:290:VAL:HG22	24:f:321:MET:CG	2.29	0.62
1:u:410:ARG:NH2	24:f:326:LEU:CG	2.62	0.62
2:d:199:LEU:HD22	2:d:211:GLU:CD	2.24	0.62
22:W:1:MET:SD	22:W:39:ARG:NH2	2.71	0.62
24:f:72:ARG:HA	24:f:75:LEU:HG	1.81	0.62
24:f:873:LEU:HG	24:f:875:ALA:H	1.64	0.62
26:I:44:LEU:HD11	26:I:213:ILE:HG22	1.76	0.62
31:a:78:GLU:HA	31:a:81:LEU:HD12	1.80	0.62
6:E:267:PHE:CZ	11:D:160:PRO:HG3	2.34	0.62
11:D:116:LEU:HD21	15:C:66:LEU:CD2	2.27	0.62
15:C:311:ILE:HG22	15:C:312:ASP:N	2.14	0.62
22:W:264:GLN:HE22	22:W:299:ILE:CG1	2.11	0.62
31:a:375:LEU:C	31:a:375:LEU:HD12	2.24	0.62
17:Q:148:THR:HG22	17:Q:150:THR:H	1.63	0.62
2:d:175:TYR:HE2	2:d:188:MET:SD	2.21	0.62
13:p:20:VAL:HG21	13:p:119:PRO:HB2	1.81	0.62
15:C:338:LEU:HG	15:C:378:VAL:HB	1.81	0.62
20:t:54:THR:HG22	20:t:55:SER:N	2.05	0.62
25:X:258:LYS:HG2	25:X:267:VAL:HG22	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:110:TYR:CE1	27:Y:114:ILE:HD12	2.33	0.62
29:Z:224:HIS:O	29:Z:228:TYR:CD2	2.52	0.62
14:U:181:LEU:HD13	14:U:201:LEU:CD1	2.29	0.62
22:W:274:VAL:HG13	22:W:283:GLN:OE1	1.99	0.62
24:f:399:LEU:HD13	24:f:440:ILE:HD12	1.81	0.62
24:f:414:LEU:HD13	24:f:432:TYR:HE2	1.64	0.62
31:a:375:LEU:HD12	31:a:376:THR:OXT	1.99	0.62
19:V:79:VAL:HG13	19:V:81:GLN:H	1.64	0.62
24:f:324:VAL:HA	24:f:455:VAL:HG13	1.81	0.62
13:P:123:SER:HB3	13:P:137:VAL:HG11	1.82	0.62
16:g:22:LEU:HD12	16:g:25:VAL:HB	1.77	0.62
15:C:303:SER:HA	15:C:306:LEU:HB2	1.82	0.62
18:A:403:ILE:HD11	18:A:405:THR:OG1	1.99	0.62
24:f:652:VAL:CB	24:f:686:LEU:HD21	2.30	0.62
5:n:52:SER:HB2	5:n:65:THR:H	1.65	0.62
22:W:362:ASN:HB3	22:W:382:LEU:HD11	1.81	0.62
24:f:404:ASP:CG	24:f:439:TYR:OH	2.42	0.62
24:f:694:LEU:HD12	24:f:706:ILE:CG2	2.30	0.61
24:f:779:CYS:O	24:f:783:SER:HB3	1.99	0.61
27:Y:314:LEU:HD21	27:Y:319:MET:HB2	1.82	0.61
26:i:71:ASP:OD1	26:i:223:THR:CB	2.48	0.61
2:d:207:GLU:O	2:d:211:GLU:HB3	2.00	0.61
13:p:20:VAL:HG23	13:p:119:PRO:HB3	1.81	0.61
13:p:190:ILE:HG22	13:p:195:ILE:HG23	1.82	0.61
18:A:360:ARG:HH11	24:f:839:PRO:HB2	1.62	0.61
22:W:169:LEU:HD11	22:W:170:GLN:NE2	2.15	0.61
22:W:231:ILE:HG13	22:W:243:ILE:CG1	2.30	0.61
22:W:268:LYS:HG2	22:W:299:ILE:HD12	1.80	0.61
24:f:287:ASP:OD1	24:f:320:ILE:CD1	2.48	0.61
26:I:82:ASP:OD2	26:I:128:ARG:NH2	2.33	0.61
29:Z:225:GLN:HG2	29:Z:226:ILE:H	1.64	0.61
30:K:21:LEU:CG	30:K:22:PHE:H	2.13	0.61
5:n:192:ASN:OD1	5:n:228:ILE:HG21	2.00	0.61
12:F:175:MET:SD	12:F:255:GLN:OE1	2.58	0.61
19:V:237:THR:CG2	19:V:241:ARG:NH1	2.63	0.61
24:f:111:GLU:HG3	24:f:141:LYS:HZ2	1.62	0.61
27:Y:12:PRO:CD	27:Y:113:ARG:CD	2.78	0.61
27:Y:82:LYS:HB3	27:Y:82:LYS:HZ1	1.65	0.61
27:Y:387:ILE:CD1	29:Z:276:ILE:HG22	2.30	0.61
29:Z:101:LEU:HD21	29:Z:138:TYR:HE2	1.62	0.61
23:H:160:ALA:O	26:I:55:LEU:HD13	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:319:LEU:HG	31:a:337:GLN:HG2	1.82	0.61
18:A:286:ASP:HA	18:A:289:ALA:HB2	1.83	0.61
23:H:229:TYR:CE1	25:X:83:ALA:HB2	2.36	0.61
24:f:408:LEU:HD12	24:f:439:TYR:HA	1.78	0.61
26:I:68:LEU:HD12	26:I:68:LEU:C	2.26	0.61
2:d:341:GLU:OE2	2:d:345:GLN:CG	2.46	0.61
17:q:44:LEU:HD23	17:q:45:LEU:O	1.99	0.61
22:W:378:MET:SD	22:W:413:ILE:HD11	2.40	0.61
34:c:279:ASP:OD1	34:c:280:PRO:CD	2.48	0.61
13:p:21:ALA:HB2	13:p:189:ILE:HG12	1.83	0.61
14:U:128:GLN:OE1	14:U:129:ARG:HG3	2.01	0.61
19:V:211:TYR:HA	19:V:214:HIS:HB3	1.83	0.61
24:f:387:GLN:HE22	24:f:414:LEU:HG	1.65	0.61
27:Y:387:ILE:HD12	29:Z:276:ILE:CG2	2.30	0.61
26:i:133:SER:HB2	26:i:152:PRO:HD3	1.83	0.61
31:a:55:GLY:HA2	31:a:58:LYS:HE2	1.81	0.61
22:W:393:LEU:HD22	22:W:406:VAL:CG2	2.31	0.61
31:a:66:GLU:HG3	31:a:67:PHE:CD2	2.36	0.61
12:F:94:ILE:HD12	12:F:123:VAL:HG22	1.82	0.61
19:V:170:LEU:O	19:V:170:LEU:HD23	2.00	0.61
22:W:421:PRO:HG3	29:Z:251:LEU:CD2	2.30	0.61
23:H:189:HIS:CD2	25:X:124:PHE:CB	2.83	0.61
31:a:293:PHE:HD2	31:a:329:LYS:O	1.84	0.61
19:V:438:VAL:CG1	19:V:451:ILE:HD11	2.31	0.61
29:Z:69:PHE:CE2	33:b:96:ALA:HA	2.35	0.61
6:E:135:ILE:CG1	6:E:182:LEU:HD23	2.27	0.60
14:U:524:LYS:HG3	14:U:556:MET:HE1	1.83	0.60
20:T:155:MET:HE2	20:T:155:MET:CA	2.24	0.60
24:f:101:PRO:O	24:f:104:GLY:N	2.33	0.60
27:Y:110:TYR:CE1	27:Y:114:ILE:CD1	2.84	0.60
31:a:234:ILE:CG2	31:a:238:TYR:HE2	2.14	0.60
13:P:111:GLY:HA2	13:P:190:ILE:HD11	1.83	0.60
1:u:389:ARG:NE	1:u:393:GLU:OE1	2.30	0.60
2:d:305:LYS:HG2	2:d:306:ARG:HG3	1.83	0.60
16:G:75:ASN:ND2	16:G:225:PRO:CB	2.64	0.60
27:Y:144:LEU:O	27:Y:147:ILE:HG22	2.01	0.60
4:R:59:GLY:C	4:R:92:LYS:NZ	2.55	0.60
15:C:235:PHE:CD2	15:C:279:GLN:NE2	2.63	0.60
22:W:272:LEU:HD12	22:W:272:LEU:O	2.00	0.60
22:W:303:LYS:NZ	22:W:309:PHE:HZ	1.98	0.60
22:W:437:SER:HB2	34:c:226:MET:CG	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:K:206:MET:HE1	30:K:210:LEU:HD13	1.82	0.60
9:o:215:ASN:OD1	9:o:234:VAL:HG23	2.02	0.60
24:f:75:LEU:HD13	24:f:82:ILE:HD11	1.83	0.60
24:f:520:LEU:HG	24:f:557:TRP:HB3	1.83	0.60
29:Z:121:LEU:HD11	29:Z:138:TYR:CD2	2.33	0.60
9:O:247:CYS:SG	9:O:248:GLU:N	2.72	0.60
11:D:125:LYS:CB	11:D:126:PRO:CD	2.44	0.60
19:V:447:ILE:HG13	19:V:449:ALA:H	1.66	0.60
22:W:438:LEU:HD21	34:c:226:MET:SD	2.38	0.60
16:g:54:LYS:HD2	16:g:66:VAL:HG13	1.83	0.60
32:l:40:SER:HB3	32:l:187:LEU:HD11	1.84	0.60
22:W:408:ARG:NH2	25:X:346:GLN:HB2	2.17	0.60
24:f:583:VAL:O	24:f:583:VAL:HG12	2.02	0.60
24:f:845:ARG:NH1	24:f:860:LYS:NZ	2.49	0.60
32:L:29:VAL:HG21	32:L:149:PRO:CG	2.32	0.60
2:d:283:LEU:H	2:d:286:GLU:HB2	1.67	0.60
4:R:197:VAL:HG23	17:q:141:SER:HB2	1.82	0.60
15:C:187:LEU:HD12	15:C:314:LYS:CD	2.29	0.60
15:C:301:LEU:CG	15:C:302:ASP:H	2.14	0.60
18:A:101:ILE:HG12	18:A:140:VAL:HG22	1.83	0.60
16:g:210:PHE:CZ	16:g:215:ILE:HG21	2.35	0.60
26:I:14:PRO:HA	28:J:21:TYR:HE1	1.67	0.60
27:Y:17:LEU:HD22	27:Y:146:ARG:HD3	1.84	0.60
29:Z:224:HIS:HE1	31:a:340:VAL:HG11	1.65	0.60
34:c:26:ASP:HB2	34:c:173:GLU:HG2	1.83	0.60
2:d:345:GLN:HB2	19:V:484:LEU:HD21	1.83	0.60
4:R:78:ARG:O	4:R:78:ARG:HG2	2.02	0.60
6:E:247:THR:HG22	6:E:249:ALA:H	1.66	0.60
18:A:128:GLN:NE2	24:f:358:PHE:CZ	2.70	0.60
19:V:237:THR:HG23	19:V:241:ARG:CZ	2.32	0.60
9:O:61:THR:HB	9:O:74:CYS:H	1.66	0.60
6:E:230:ILE:HB	6:E:275:MET:HG2	1.84	0.60
14:U:539:THR:HG23	14:U:541:HIS:HD2	1.66	0.60
26:i:8:ARG:HH21	26:i:11:ILE:HD11	1.67	0.60
14:U:695:MET:CE	14:U:709:PHE:HE2	2.12	0.59
18:A:199:GLU:O	18:A:203:ASN:ND2	2.35	0.59
24:f:542:ILE:O	24:f:542:ILE:CG2	2.50	0.59
24:f:884:THR:OG1	24:f:885:GLU:N	2.34	0.59
31:a:280:MET:O	31:a:291:LEU:HD21	2.02	0.59
11:D:292:LEU:O	11:D:296:MET:HG2	2.01	0.59
11:D:300:ASP:OD2	11:D:303:VAL:HG23	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:V:401:ASN:HA	19:V:404:LYS:HB3	1.84	0.59
24:f:558:LEU:CD1	24:f:559:PRO:HG3	2.32	0.59
6:E:83:CYS:HA	6:E:107:ILE:HB	1.84	0.59
7:B:333:ARG:HD3	7:B:336:THR:OG1	2.01	0.59
1:u:52:THR:OG1	1:u:53:VAL:N	2.32	0.59
14:U:160:LEU:HD11	14:U:196:LYS:HG2	1.84	0.59
18:A:405:THR:CG2	18:A:406:GLU:N	2.65	0.59
10:s:96:ILE:HD11	10:s:120:LEU:HD13	1.84	0.59
22:W:378:MET:HE1	22:W:413:ILE:CD1	2.32	0.59
24:f:400:TYR:HD1	24:f:437:GLU:CG	2.07	0.59
24:f:540:GLN:O	24:f:544:GLU:OE1	2.20	0.59
26:I:134:LEU:CD1	26:I:136:TYR:CZ	2.82	0.59
27:Y:12:PRO:HD2	27:Y:113:ARG:CD	2.32	0.59
30:k:29:GLU:HA	30:k:32:LYS:HE3	1.83	0.59
5:n:63:ARG:HH21	20:T:256:ILE:HD11	1.67	0.59
24:f:91:SER:OG	24:f:125:ILE:HG23	2.03	0.59
30:K:21:LEU:HG	30:K:23:GLN:H	1.66	0.59
30:K:181:LEU:HD23	30:K:201:ILE:HG13	1.84	0.59
31:a:38:THR:O	31:a:42:LEU:HG	2.03	0.59
31:a:234:ILE:HG22	31:a:238:TYR:CE2	2.36	0.59
2:d:328:THR:HG22	29:Z:250:TYR:HE2	1.68	0.59
16:G:29:PHE:CZ	16:G:155:ASP:OD2	2.55	0.59
22:W:142:ARG:NH1	22:W:181:GLU:OE1	2.35	0.59
24:f:471:LEU:HD23	24:f:504:VAL:CG2	2.32	0.59
9:o:49:VAL:HG13	9:o:185:PHE:HE1	1.67	0.59
11:D:45:LYS:HG2	14:U:187:LEU:HD13	1.85	0.59
11:D:82:ILE:CD1	15:C:66:LEU:CG	2.80	0.59
24:f:275:MET:HA	24:f:278:VAL:HG22	1.83	0.59
24:f:473:ASN:HD22	24:f:473:ASN:N	1.99	0.59
17:Q:5:ILE:HG21	17:Q:160:LEU:HD13	1.84	0.59
34:c:100:LYS:HG3	34:c:105:PRO:HB3	1.84	0.59
2:d:102:TRP:CD1	2:d:150:ILE:HD11	2.38	0.59
12:F:250:LYS:HD3	18:A:309:PHE:HE2	1.67	0.59
14:U:695:MET:SD	14:U:709:PHE:HD2	2.25	0.59
17:q:35:MET:HG3	17:q:181:ARG:CZ	2.32	0.59
19:V:182:LYS:NZ	19:V:210:CYS:SG	2.75	0.59
19:V:337:LEU:O	19:V:401:ASN:ND2	2.35	0.59
20:t:108:LEU:CD1	20:t:155:MET:HE1	2.01	0.59
24:f:845:ARG:NH1	24:f:848:GLN:HE21	2.01	0.59
28:j:134:VAL:HG13	28:j:144:LEU:HB3	1.85	0.59
30:k:235:GLU:O	30:k:238:ILE:CG2	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:44:TYR:HD1	15:C:28:ILE:HG22	1.68	0.59
18:A:212:VAL:HG22	18:A:339:ARG:HB2	1.84	0.59
24:f:385:PHE:CZ	24:f:421:ASP:CG	2.81	0.59
23:h:74:LEU:HD21	23:h:134:LEU:HG	1.85	0.59
23:h:110:LEU:HD23	23:h:136:ILE:HD11	1.85	0.59
31:a:371:ALA:O	31:a:375:LEU:HD21	2.02	0.59
6:E:333:LYS:HG3	16:G:57:PRO:HA	1.84	0.58
7:B:135:ILE:CD1	7:B:141:LYS:HE2	2.28	0.58
11:D:245:ARG:HE	11:D:248:ARG:HH21	1.48	0.58
14:U:799:LYS:HB3	14:U:801:GLN:HE22	1.68	0.58
23:H:189:HIS:HD2	25:X:124:PHE:HB2	1.68	0.58
24:f:702:PRO:O	24:f:705:ASN:ND2	2.32	0.58
17:Q:44:LEU:HD11	17:Q:102:LEU:HD12	1.85	0.58
5:n:196:LEU:HG	5:n:230:LYS:CB	2.33	0.58
15:C:311:ILE:HG22	15:C:312:ASP:H	1.68	0.58
16:G:60:LEU:CD2	3:M:182:MET:CE	2.80	0.58
19:V:131:LEU:CG	19:V:158:PRO:HB3	2.32	0.58
19:V:255:LEU:HD21	19:V:295:ILE:HD11	1.85	0.58
22:W:94:ARG:HA	22:W:98:LYS:HE3	1.85	0.58
16:g:211:LYS:HB3	16:g:212:PRO:CD	2.31	0.58
23:h:112:GLN:OE1	23:h:112:GLN:HA	2.03	0.58
30:K:92:ALA:HB2	30:K:116:VAL:CG2	2.32	0.58
2:d:94:MET:HE3	2:d:121:LEU:HD12	1.83	0.58
14:U:373:ASN:OD1	14:U:377:HIS:CE1	2.56	0.58
20:T:237:VAL:HG22	20:T:242:VAL:HG22	1.85	0.58
24:f:415:GLY:HA3	24:f:447:ALA:HB1	1.85	0.58
24:f:612:LEU:C	24:f:613:LEU:HD12	2.28	0.58
27:Y:157:ILE:HB	27:Y:186:LEU:CD1	2.32	0.58
30:k:36:THR:HA	30:k:171:GLY:HA3	1.86	0.58
4:R:61:THR:HG22	4:R:61:THR:O	2.04	0.58
8:e:60:LEU:HD13	27:Y:329:PHE:CG	2.37	0.58
15:C:223:PHE:HD2	15:C:226:GLU:HB2	1.68	0.58
24:f:420:TRP:HZ2	24:f:806:VAL:HG23	1.68	0.58
24:f:845:ARG:HG2	24:f:848:GLN:HE22	1.67	0.58
5:N:35:THR:N	5:N:204:SER:HG	2.01	0.58
14:U:381:THR:HG22	14:U:412:HIS:HA	1.85	0.58
14:U:746:ILE:HG13	14:U:783:TYR:CE1	2.39	0.58
22:W:166:LEU:HD21	22:W:201:ARG:NE	2.18	0.58
22:W:264:GLN:NE2	22:W:299:ILE:HG13	2.18	0.58
28:j:211:MET:HE2	28:j:217:LEU:HB3	1.83	0.58
9:O:121:THR:O	9:O:125:MET:HG3	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:415:GLU:CG	16:G:159:TYR:CE2	2.87	0.58
14:U:214:ILE:HD11	14:U:903:PHE:CE2	2.39	0.58
4:r:148:GLN:OE1	4:r:148:GLN:HA	2.01	0.58
24:f:475:ASN:O	24:f:478:ARG:N	2.36	0.58
24:f:496:ASP:OD1	24:f:497:VAL:N	2.36	0.58
23:h:108:ALA:O	23:h:112:GLN:HG2	2.03	0.58
14:U:128:GLN:CD	14:U:129:ARG:HG3	2.28	0.58
14:U:175:GLY:HA2	14:U:178:ALA:HB3	1.85	0.58
24:f:765:ALA:HB1	24:f:769:THR:HA	1.85	0.58
32:l:88:MET:HE2	32:l:112:ILE:HG13	1.85	0.58
2:d:175:TYR:OH	2:d:188:MET:HG3	2.04	0.58
3:m:35:THR:HB	3:m:201:HIS:NE2	2.19	0.58
11:D:232:GLY:CA	11:D:266:GLU:OE2	2.52	0.58
24:f:240:VAL:HG22	24:f:257:ARG:HD2	1.84	0.58
32:L:84:LEU:HD22	32:L:112:ILE:HD11	1.85	0.58
19:V:224:LEU:CD1	19:V:227:VAL:HB	2.29	0.58
22:W:448:LYS:HA	22:W:451:MET:HE3	1.86	0.58
24:f:349:TYR:O	24:f:352:HIS:HE1	1.86	0.58
24:f:408:LEU:HD12	24:f:439:TYR:HB3	1.85	0.58
25:X:234:GLU:HA	25:X:234:GLU:OE2	2.04	0.58
16:g:141:ILE:HG22	16:g:151:VAL:HG12	1.85	0.58
13:P:155:GLU:CG	13:P:156:PRO:HD2	2.34	0.58
2:d:289:ARG:HA	2:d:293:PHE:O	2.03	0.58
14:U:789:ILE:CG2	14:U:790:GLY:H	2.16	0.58
14:U:900:TYR:HB2	14:U:914:LEU:HB3	1.85	0.58
22:W:144:ARG:NH2	22:W:168:GLU:CD	2.62	0.58
23:H:189:HIS:CD2	25:X:124:PHE:HB2	2.39	0.58
24:f:761:MET:CA	24:f:858:LYS:HZ3	2.06	0.58
28:j:31:THR:HG23	28:j:161:ILE:O	2.03	0.58
30:k:178:GLN:NE2	30:k:178:GLN:HA	2.17	0.58
5:n:73:ASP:OD1	5:n:73:ASP:N	2.36	0.57
24:f:349:TYR:O	24:f:352:HIS:CE1	2.57	0.57
24:f:434:TYR:CG	24:f:434:TYR:O	2.56	0.57
24:f:569:LYS:HG2	24:f:569:LYS:O	2.04	0.57
2:d:165:GLU:CD	2:d:198:PHE:HZ	2.11	0.57
2:d:94:MET:HE1	2:d:118:ARG:CB	2.33	0.57
13:p:21:ALA:CB	13:p:189:ILE:HG12	2.34	0.57
14:U:401:LYS:HB3	14:U:438:GLN:NE2	2.19	0.57
24:f:741:LEU:CD1	24:f:788:MET:SD	2.92	0.57
25:X:421:LEU:O	29:Z:283:ARG:NH2	2.37	0.57
24:f:600:TYR:HE1	24:f:603:SER:CB	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:i:116:ASP:OD1	28:j:81:ARG:NH1	2.37	0.57
29:Z:21:ASP:OD2	34:c:36:LEU:HD22	2.04	0.57
4:R:137:ALA:HB2	28:J:98:VAL:HG23	1.87	0.57
7:B:176:VAL:CG2	7:B:249:ARG:HB2	2.34	0.57
15:C:98:ASP:OD1	15:C:98:ASP:N	2.37	0.57
17:q:103:LEU:C	17:q:103:LEU:HD12	2.30	0.57
24:f:94:LYS:CD	24:f:133:MET:HE3	2.34	0.57
24:f:131:MET:HG2	24:f:181:ARG:HH12	1.69	0.57
24:f:169:GLU:HA	24:f:172:GLU:HB3	1.86	0.57
24:f:334:ALA:O	24:f:335:ARG:NH1	2.38	0.57
27:Y:88:LEU:HD13	27:Y:100:ILE:HG22	1.86	0.57
19:V:144:ASP:O	19:V:150:ARG:NH2	2.38	0.57
22:W:56:THR:O	22:W:60:MET:HG2	2.05	0.57
23:h:21:GLN:HE21	23:h:21:GLN:CA	2.13	0.57
31:a:80:ILE:HA	31:a:83:VAL:HB	1.87	0.57
33:b:104:ASN:O	33:b:106:LYS:NZ	2.37	0.57
7:B:223:ILE:HG21	7:B:347:ILE:HD12	1.86	0.57
18:A:101:ILE:CG1	18:A:140:VAL:HG21	2.34	0.57
19:V:484:LEU:HD11	29:Z:267:ARG:HH12	1.69	0.57
20:T:81:PHE:HB2	20:T:84:ILE:HD12	1.85	0.57
27:Y:110:TYR:CD1	27:Y:114:ILE:CD1	2.80	0.57
29:Z:69:PHE:C	29:Z:69:PHE:HD1	2.12	0.57
30:K:228:MET:HE3	30:K:228:MET:CA	2.32	0.57
9:O:54:GLY:HA3	9:O:221:ILE:O	2.04	0.57
1:u:33:LEU:HD21	1:u:90:VAL:HG11	1.83	0.57
7:B:233:THR:O	7:B:236:ALA:CB	2.50	0.57
11:D:300:ASP:OD1	11:D:303:VAL:HG23	2.04	0.57
12:F:439:ALA:HB1	32:L:62:LYS:CE	2.33	0.57
17:q:46:CYS:SG	17:q:57:ALA:CB	2.82	0.57
24:f:450:ILE:HD11	24:f:801:VAL:HG21	1.87	0.57
7:B:233:THR:O	7:B:236:ALA:N	2.37	0.57
17:q:35:MET:HG3	17:q:181:ARG:HH21	1.69	0.57
18:A:165:GLN:NE2	18:A:267:LYS:NZ	2.52	0.57
19:V:36:GLU:HG2	19:V:36:GLU:O	2.05	0.57
9:o:56:VAL:HG22	9:o:220:VAL:HG22	1.86	0.57
12:F:334:ARG:HD3	18:A:284:ARG:HH21	1.69	0.57
20:T:155:MET:HA	20:T:155:MET:CE	2.29	0.57
22:W:264:GLN:NE2	22:W:299:ILE:HG12	2.14	0.57
26:I:119:GLN:NE2	28:J:79:ASP:OD1	2.37	0.57
3:m:181:MET:HE1	16:g:60:LEU:HD13	1.86	0.56
12:F:98:ASP:OD1	12:F:98:ASP:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:139:GLU:HB3	22:W:142:ARG:HB2	1.87	0.56
23:H:22:ILE:HD12	23:H:152:SER:HA	1.86	0.56
24:f:850:VAL:HG11	24:f:852:VAL:HG23	1.85	0.56
25:X:316:ASP:HB3	25:X:319:ILE:HB	1.86	0.56
27:Y:231:LEU:HB3	27:Y:234:PRO:HD2	1.86	0.56
29:Z:77:ASN:O	29:Z:81:MET:HG2	2.05	0.56
31:a:66:GLU:CG	31:a:67:PHE:CD2	2.88	0.56
13:P:22:ILE:HG21	13:P:110:ALA:CB	2.35	0.56
24:f:354:GLU:HG2	24:f:354:GLU:O	2.04	0.56
24:f:399:LEU:HD13	24:f:440:ILE:CD1	2.35	0.56
24:f:415:GLY:CA	24:f:447:ALA:HB1	2.35	0.56
24:f:764:LEU:HD11	24:f:774:GLY:HA3	1.85	0.56
25:X:151:SER:OG	25:X:155:ARG:NH2	2.37	0.56
30:k:35:SER:HB2	30:k:51:GLU:HB3	1.87	0.56
11:D:416:PHE:HZ	16:G:25:VAL:CG2	2.18	0.56
12:F:288:LEU:HB3	12:F:332:THR:CG2	2.35	0.56
12:F:404:GLY:HA2	12:F:415:LEU:HD21	1.87	0.56
14:U:559:ARG:HB3	14:U:562:GLU:HB2	1.86	0.56
14:U:803:LYS:HA	14:U:892:LEU:HD22	1.88	0.56
15:C:305:LEU:HG	15:C:310:ARG:HH22	1.69	0.56
18:A:171:ASP:OD1	18:A:171:ASP:N	2.38	0.56
19:V:237:THR:HG23	19:V:241:ARG:NH1	2.20	0.56
24:f:371:ASN:ND2	24:f:398:TRP:HE1	2.03	0.56
16:g:50:ILE:HD12	16:g:79:VAL:HG21	1.86	0.56
27:Y:228:MET:HE1	27:Y:260:LEU:HD13	1.87	0.56
2:d:345:GLN:CB	19:V:484:LEU:HD21	2.35	0.56
12:F:305:GLU:OE1	12:F:308:ARG:NH1	2.39	0.56
12:F:433:ALA:O	30:K:20:ARG:NH2	2.39	0.56
24:f:58:MET:O	24:f:62:ARG:HD3	2.05	0.56
24:f:719:PRO:HB3	24:f:754:LYS:CG	2.19	0.56
27:Y:12:PRO:CG	27:Y:113:ARG:NE	2.68	0.56
7:B:293:LYS:HG3	7:B:295:TYR:CD2	2.32	0.56
15:C:351:MET:HE1	15:C:354:ALA:HB2	1.86	0.56
19:V:255:LEU:HD22	19:V:291:TYR:HB3	1.87	0.56
25:X:306:LEU:CD2	25:X:310:ARG:HH12	2.13	0.56
3:M:188:ARG:NH1	3:M:233:ARG:NH2	2.45	0.56
29:Z:148:GLY:HA2	31:a:178:ARG:HA	1.88	0.56
22:W:166:LEU:HD22	22:W:201:ARG:NE	2.19	0.56
24:f:54:ASP:HB3	24:f:57:GLU:HB2	1.87	0.56
25:X:306:LEU:CD1	25:X:323:LEU:CD1	2.68	0.56
28:j:211:MET:HG2	28:j:213:ARG:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:P:11:VAL:HG11	13:P:52:GLY:HA3	1.88	0.56
33:b:161:ASN:HD22	33:b:168:SER:H	1.53	0.56
1:u:33:LEU:CD2	1:u:90:VAL:CG1	2.82	0.56
2:d:336:ALA:HB2	34:c:303:MET:HE2	1.88	0.56
6:E:216:ARG:NH2	11:D:234:GLU:CB	2.69	0.56
11:D:353:ASN:ND2	11:D:392:TYR:O	2.39	0.56
15:C:232:ARG:NH2	15:C:275:GLU:OE1	2.39	0.56
15:C:301:LEU:HG	15:C:302:ASP:N	2.20	0.56
19:V:257:ASN:HA	19:V:260:HIS:HB2	1.87	0.56
22:W:44:ILE:HD13	22:W:47:LEU:HD12	1.87	0.56
26:I:2:SER:OG	26:I:3:ARG:N	2.38	0.56
17:Q:168:GLN:NE2	17:Q:175:LEU:O	2.38	0.56
10:S:40:ILE:CD1	10:S:81:GLY:C	2.79	0.56
14:U:51:ASP:HB3	14:U:54:PHE:HB2	1.88	0.56
14:U:58:GLN:NE2	14:U:86:ASP:OD2	2.39	0.56
24:f:128:VAL:CG2	24:f:129:LEU:H	2.01	0.56
24:f:290:VAL:HG11	24:f:317:LEU:HD22	1.87	0.56
26:i:36:GLY:HA3	26:i:147:LEU:HD11	1.88	0.56
28:j:4:ASP:CB	30:k:127:ASP:OD1	2.54	0.56
13:P:159:ASP:N	13:P:159:ASP:OD1	2.39	0.56
3:m:56:LYS:HE2	32:l:176:MET:CE	2.36	0.56
5:n:192:ASN:ND2	5:n:228:ILE:HD13	2.21	0.56
4:r:174:ASP:HB2	4:r:178:ASN:HB2	1.87	0.56
23:H:65:VAL:HG11	23:H:211:GLY:HA3	1.87	0.56
24:f:27:LYS:HE3	24:f:30:GLY:HA3	1.88	0.56
24:f:294:MET:O	24:f:321:MET:O	2.23	0.56
24:f:687:ARG:NH1	24:f:722:SER:OG	2.39	0.56
26:i:36:GLY:O	26:i:147:LEU:HD13	2.06	0.56
34:c:75:MET:SD	34:c:75:MET:N	2.79	0.56
9:o:124:ARG:CG	9:o:128:GLN:HE22	2.10	0.56
18:A:368:ILE:HD13	18:A:409:PHE:HD2	1.71	0.56
22:W:144:ARG:NH2	22:W:168:GLU:OE1	2.39	0.56
22:W:168:GLU:O	22:W:171:VAL:HB	2.06	0.56
1:u:410:ARG:HH12	24:f:326:LEU:CD2	2.19	0.55
19:V:36:GLU:CD	19:V:77:GLU:HG2	2.32	0.55
19:V:163:VAL:HG22	19:V:175:MET:HG2	1.87	0.55
19:V:183:GLU:HA	19:V:186:LYS:HD2	1.87	0.55
27:Y:202:LEU:HD11	27:Y:239:LYS:HB3	1.86	0.55
17:q:49:GLU:OE2	17:q:50:ALA:N	2.39	0.55
24:f:815:HIS:HB2	24:f:881:GLU:H	1.72	0.55
23:h:71:HIS:HA	23:h:218:PHE:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:116:ASP:O	27:Y:120:ALA:N	2.34	0.55
3:M:31:VAL:HG21	3:M:154:PRO:HG3	1.87	0.55
29:Z:69:PHE:C	29:Z:69:PHE:CD1	2.84	0.55
32:L:185:ASN:OD1	32:L:189:LYS:NZ	2.38	0.55
34:c:259:VAL:O	34:c:262:GLU:CG	2.54	0.55
1:u:77:ASP:CG	34:c:94:LYS:HE3	2.31	0.55
9:o:69:VAL:O	10:S:213:ARG:NH1	2.37	0.55
14:U:682:TYR:CA	14:U:685:GLN:HG2	2.37	0.55
15:C:36:ASN:ND2	19:V:55:THR:OG1	2.40	0.55
15:C:351:MET:CE	15:C:354:ALA:HB2	2.36	0.55
17:q:69:MET:O	28:j:88:ARG:NH1	2.39	0.55
24:f:553:THR:OG1	24:f:556:ARG:NH2	2.39	0.55
16:g:49:VAL:HG22	16:g:219:VAL:HG23	1.89	0.55
29:Z:123:ILE:O	29:Z:135:THR:HA	2.07	0.55
30:k:47:CYS:SG	30:k:219:THR:HG22	2.46	0.55
2:d:175:TYR:CE2	2:d:188:MET:SD	2.99	0.55
6:E:344:ARG:NH1	6:E:348:THR:OG1	2.40	0.55
24:f:680:ARG:HA	24:f:716:ASP:OD1	2.05	0.55
27:Y:24:PHE:HZ	27:Y:152:MET:HG2	1.70	0.55
32:L:225:ASP:OD1	32:L:225:ASP:N	2.39	0.55
34:c:42:LEU:HD21	34:c:155:VAL:CG2	2.36	0.55
1:u:74:LEU:CD2	34:c:90:VAL:HG22	2.36	0.55
6:E:322:LYS:HD3	6:E:326:ILE:HG13	1.88	0.55
10:S:96:ILE:HD11	10:S:120:LEU:HD13	1.89	0.55
17:q:35:MET:CG	17:q:181:ARG:NH2	2.68	0.55
19:V:163:VAL:HG11	19:V:213:TYR:HB2	1.87	0.55
19:V:204:ASP:O	19:V:208:ALA:N	2.38	0.55
22:W:315:MET:HE3	22:W:320:LEU:HB2	1.88	0.55
24:f:236:CYS:HB3	24:f:260:SER:HB3	1.88	0.55
24:f:541:THR:C	24:f:543:MET:H	2.15	0.55
27:Y:376:LEU:HD21	29:Z:265:LEU:HD21	1.86	0.55
5:N:196:LEU:HD21	5:N:228:ILE:HD13	1.87	0.55
28:j:4:ASP:HB2	30:k:127:ASP:OD1	2.07	0.55
2:d:113:GLY:HA2	2:d:116:LEU:HD12	1.89	0.55
15:C:251:ILE:O	15:C:255:GLY:N	2.38	0.55
22:W:93:ARG:HH12	22:W:97:LEU:HD23	1.71	0.55
22:W:302:TYR:O	22:W:306:LEU:N	2.36	0.55
24:f:616:CYS:CB	24:f:629:LYS:HE3	2.34	0.55
27:Y:169:GLU:OE1	27:Y:176:ARG:NH2	2.38	0.55
5:N:45:GLY:HA3	5:N:213:ILE:O	2.07	0.55
6:E:84:ARG:HG2	34:c:50:PRO:HG3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:V:276:PHE:N	19:V:276:PHE:CD1	2.73	0.55
22:W:155:GLN:HG3	22:W:158:ASP:OD2	2.07	0.55
29:Z:62:ASP:N	29:Z:62:ASP:OD1	2.39	0.55
32:L:72:ILE:HD12	32:L:132:LEU:HD22	1.88	0.55
4:R:61:THR:CG2	4:R:219:ILE:HD13	2.34	0.55
5:n:223:LEU:CD1	5:n:227:GLN:CB	2.81	0.55
14:U:265:ILE:HG23	14:U:269:ARG:HD2	1.80	0.55
4:r:96:ILE:HG22	4:r:97:ASN:HB2	1.88	0.55
19:V:228:ARG:O	19:V:232:HIS:ND1	2.40	0.55
3:M:130:ARG:NH1	32:L:120:THR:O	2.40	0.55
34:c:265:MET:HE2	34:c:265:MET:O	2.07	0.55
13:p:135:ASP:OD1	13:p:135:ASP:N	2.40	0.55
14:U:708:GLN:OE1	14:U:709:PHE:CD1	2.60	0.55
18:A:400:ARG:NH1	24:f:50:LYS:O	2.40	0.55
22:W:268:LYS:CG	22:W:299:ILE:CD1	2.66	0.55
24:f:257:ARG:HB3	24:f:272:LEU:HD21	1.87	0.55
31:a:73:PRO:HB3	31:a:104:VAL:HG11	1.89	0.55
13:P:51:ILE:CD1	13:P:87:LEU:HD21	2.27	0.55
13:P:153:LEU:HB3	13:P:166:THR:HG23	1.89	0.55
2:d:164:PHE:CE1	2:d:168:MET:CG	2.89	0.55
4:R:59:GLY:HA3	4:R:92:LYS:CE	2.36	0.55
13:p:65:GLN:OE1	17:q:86:ARG:NH2	2.40	0.55
14:U:117:ASP:OD1	14:U:158:ARG:NH2	2.40	0.55
14:U:539:THR:HG21	14:U:544:ILE:HD13	1.89	0.55
17:q:35:MET:HG3	17:q:181:ARG:NH2	2.22	0.55
22:W:191:ARG:HD2	22:W:192:LEU:HD22	1.89	0.55
24:f:463:LEU:HD13	24:f:497:VAL:HG12	1.88	0.55
24:f:558:LEU:CD1	24:f:559:PRO:CG	2.85	0.55
26:i:123:GLN:OE1	28:j:125:ARG:NH1	2.40	0.55
5:N:207:VAL:HG11	5:N:224:LEU:HD21	1.89	0.55
2:d:251:ILE:CD1	2:d:255:SER:HA	2.36	0.54
9:o:54:GLY:HA3	9:o:221:ILE:O	2.06	0.54
14:U:423:MET:HE1	14:U:449:ILE:HG13	1.87	0.54
14:U:556:MET:SD	14:U:563:ALA:HB2	2.46	0.54
18:A:99:THR:HG22	18:A:115:VAL:HA	1.88	0.54
27:Y:23:ARG:O	27:Y:27:SER:HB3	2.07	0.54
3:M:109:LEU:HD23	3:M:148:GLN:HB2	1.89	0.54
26:i:132:VAL:HG12	26:i:134:LEU:HD23	1.89	0.54
31:a:66:GLU:HG3	31:a:67:PHE:CE2	2.42	0.54
9:o:44:THR:N	9:o:211:GLY:O	2.41	0.54
15:C:99:VAL:HB	15:C:103:ILE:HD11	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:351:MET:CE	15:C:354:ALA:CB	2.84	0.54
16:G:190:THR:OG1	16:G:191:PHE:N	2.40	0.54
24:f:19:ALA:HB2	24:f:34:ARG:CD	2.36	0.54
27:Y:387:ILE:HG22	27:Y:388:ASN:N	2.21	0.54
10:S:153:ASP:OD1	10:S:157:SER:N	2.40	0.54
14:U:58:GLN:O	14:U:61:ALA:HB3	2.07	0.54
22:W:98:LYS:HG2	22:W:138:VAL:HA	1.88	0.54
33:b:97:LEU:O	33:b:100:ARG:NE	2.39	0.54
34:c:173:GLU:OE2	34:c:201:TYR:CE2	2.60	0.54
2:d:147:ILE:CA	2:d:150:ILE:HG22	2.34	0.54
2:d:200:LEU:HD11	2:d:236:LEU:HD11	1.90	0.54
4:R:197:VAL:CG2	17:q:141:SER:HB2	2.36	0.54
7:B:407:LEU:HG	15:C:178:LEU:HD23	1.90	0.54
22:W:206:SER:HA	22:W:209:ILE:HG12	1.89	0.54
23:H:186:ASP:OD1	23:H:186:ASP:N	2.41	0.54
24:f:381:VAL:HG23	24:f:755:ASP:O	2.07	0.54
25:X:80:ILE:HD11	25:X:85:ALA:HA	1.90	0.54
31:a:270:ARG:HD2	31:a:273:GLN:HE21	1.72	0.54
1:u:402:LYS:O	1:u:406:ARG:CG	2.46	0.54
10:S:175:PRO:O	10:S:178:ASP:HB2	2.08	0.54
20:T:155:MET:CA	20:T:155:MET:CE	2.85	0.54
22:W:41:GLN:O	22:W:92:LYS:NZ	2.40	0.54
22:W:408:ARG:NH2	25:X:349:HIS:HB2	2.23	0.54
24:f:555:ALA:HB3	24:f:590:PHE:CD2	2.42	0.54
25:X:80:ILE:HB	25:X:84:LYS:HE3	1.89	0.54
25:X:306:LEU:HD23	25:X:310:ARG:NH1	2.16	0.54
26:I:218:ARG:NH1	26:I:223:THR:OG1	2.41	0.54
29:Z:235:ASN:OD1	29:Z:235:ASN:O	2.25	0.54
9:O:206:ILE:HG23	9:O:213:GLY:HA2	1.88	0.54
6:E:226:GLN:NE2	6:E:271:HIS:O	2.39	0.54
14:U:486:MET:HG2	14:U:518:LEU:HB3	1.89	0.54
18:A:254:ALA:O	18:A:258:ARG:HG3	2.07	0.54
19:V:74:ASP:O	19:V:78:HIS:NE2	2.40	0.54
32:L:192:LEU:HD12	32:L:205:LEU:HD13	1.88	0.54
34:c:90:VAL:CG1	34:c:94:LYS:HE3	2.38	0.54
3:m:50:GLU:OE2	3:m:52:LEU:HD13	2.08	0.54
6:E:46:ASP:CG	12:F:139:LEU:CD2	2.72	0.54
13:p:164:PHE:HB2	13:p:189:ILE:HD12	1.88	0.54
22:W:307:LYS:HG3	22:W:307:LYS:O	2.07	0.54
24:f:326:LEU:H	24:f:326:LEU:CD2	2.10	0.54
25:X:153:LEU:CD2	25:X:169:VAL:CG1	2.80	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:g:51:VAL:HG12	16:g:217:VAL:HG22	1.88	0.54
23:h:150:ASP:OD1	23:h:150:ASP:N	2.41	0.54
30:K:76:CYS:SG	30:K:77:ALA:N	2.79	0.54
32:l:34:ALA:HA	32:l:162:GLY:HA3	1.90	0.54
32:l:67:ASP:OD2	32:l:96:ARG:NH2	2.40	0.54
5:n:192:ASN:CG	5:n:228:ILE:HG21	2.33	0.54
7:B:135:ILE:HD12	7:B:141:LYS:HZ1	1.72	0.54
7:B:152:LEU:HD23	7:B:159:VAL:HG12	1.89	0.54
11:D:416:PHE:CZ	16:G:25:VAL:CG2	2.87	0.54
22:W:82:LEU:HG	22:W:86:ASN:OD1	2.07	0.54
24:f:616:CYS:CA	24:f:629:LYS:HE3	2.37	0.54
5:n:161:ILE:HD11	5:n:170:TYR:CE1	2.42	0.54
7:B:307:ARG:HD2	18:A:246:VAL:HG21	1.90	0.54
15:C:209:CYS:HB3	15:C:244:SER:HA	1.89	0.54
15:C:223:PHE:O	15:C:225:GLY:N	2.40	0.54
22:W:381:LEU:C	22:W:382:LEU:HD12	2.32	0.54
16:g:191:PHE:O	16:g:191:PHE:HD1	1.91	0.54
2:d:147:ILE:C	2:d:150:ILE:HG22	2.33	0.54
5:n:187:LEU:CD1	5:n:210:LEU:CD1	2.86	0.54
14:U:52:GLU:OE1	14:U:57:ARG:NH1	2.40	0.54
14:U:81:ALA:O	14:U:89:ASN:ND2	2.41	0.54
22:W:244:CYS:SG	22:W:274:VAL:HG22	2.48	0.54
24:f:466:LEU:HD13	24:f:484:GLY:HA3	1.90	0.54
16:g:86:ASP:O	16:g:90:GLN:HG2	2.08	0.54
16:g:111:VAL:HG21	16:g:142:GLY:HA3	1.90	0.54
3:M:124:THR:O	3:M:124:THR:CG2	2.53	0.54
29:Z:94:TRP:HB3	29:Z:112:MET:HE1	1.89	0.54
34:c:219:ASN:N	34:c:219:ASN:OD1	2.40	0.54
14:U:524:LYS:O	14:U:524:LYS:HG2	2.08	0.53
14:U:803:LYS:HG2	14:U:892:LEU:HD22	1.90	0.53
15:C:258:ARG:HG2	15:C:302:ASP:HB3	1.89	0.53
17:q:39:SER:OG	17:q:40:GLU:N	2.40	0.53
24:f:371:ASN:HD22	24:f:398:TRP:HE1	1.55	0.53
16:g:191:PHE:HD1	16:g:191:PHE:C	2.16	0.53
27:Y:144:LEU:O	27:Y:147:ILE:CG2	2.55	0.53
32:L:215:VAL:CG2	32:L:221:PHE:HB2	2.32	0.53
30:k:71:ASP:OD1	30:k:72:ALA:N	2.33	0.53
2:d:197:LEU:HG	2:d:229:PRO:HB3	1.89	0.53
5:n:63:ARG:HG2	20:T:254:TRP:HZ3	1.73	0.53
6:E:281:ARG:HD2	12:F:295:ARG:HE	1.74	0.53
6:E:310:LEU:HG	6:E:314:LYS:HE3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:388:PRO:HB2	11:D:409:LYS:HE3	1.90	0.53
17:q:33:ASP:N	17:q:33:ASP:OD1	2.40	0.53
23:H:74:LEU:HD21	23:H:134:LEU:HD22	1.90	0.53
24:f:39:LYS:HZ2	24:f:86:THR:H	1.55	0.53
24:f:83:ARG:O	24:f:120:ARG:NH2	2.40	0.53
24:f:131:MET:CG	24:f:181:ARG:HH12	2.21	0.53
24:f:829:MET:HG3	24:f:830:LEU:H	1.72	0.53
24:f:845:ARG:CZ	24:f:860:LYS:HE2	2.38	0.53
26:i:45:LEU:O	26:i:213:ILE:HA	2.08	0.53
34:c:54:MET:HE3	34:c:55:GLY:H	1.73	0.53
4:R:58:HIS:HB2	4:R:106:GLY:O	2.08	0.53
6:E:135:ILE:CG1	6:E:182:LEU:HD21	2.38	0.53
6:E:265:ASP:OD2	6:E:291:ARG:NH2	2.42	0.53
7:B:176:VAL:HG22	7:B:249:ARG:HB2	1.90	0.53
7:B:293:LYS:HG2	7:B:295:TYR:HE2	1.71	0.53
11:D:415:GLU:HG2	16:G:159:TYR:CZ	2.42	0.53
14:U:43:ASP:OD1	14:U:43:ASP:N	2.39	0.53
14:U:708:GLN:OE1	14:U:709:PHE:CE1	2.61	0.53
26:I:68:LEU:CD1	26:I:69:ASN:HB2	2.35	0.53
23:h:44:VAL:HG11	23:h:137:CYS:HB2	1.88	0.53
27:Y:157:ILE:HD12	27:Y:186:LEU:HD12	1.90	0.53
28:J:31:THR:HA	28:J:161:ILE:O	2.09	0.53
26:i:42:GLY:HA2	26:i:216:LEU:O	2.08	0.53
28:j:158:ALA:HB1	28:j:172:LEU:HD13	1.89	0.53
2:d:308:TRP:H	2:d:318:PHE:HB3	1.72	0.53
5:n:187:LEU:HD11	5:n:210:LEU:CD1	2.38	0.53
6:E:182:LEU:HD12	35:E:401:ADP:H3'	1.89	0.53
7:B:65:LEU:HD13	18:A:49:GLU:HB3	1.89	0.53
18:A:97:ARG:HH21	18:A:144:ARG:HA	1.74	0.53
20:t:88:MET:HE2	20:t:96:LEU:HD23	1.90	0.53
23:h:72:ILE:CG1	23:h:107:THR:HG22	2.28	0.53
27:Y:259:TYR:HH	27:Y:299:MET:HE2	1.71	0.53
28:j:70:CYS:SG	28:j:217:LEU:HD22	2.47	0.53
31:a:289:ARG:O	31:a:291:LEU:CD1	2.56	0.53
2:d:281:LYS:NZ	2:d:282:ILE:O	2.40	0.53
3:m:46:VAL:HG22	3:m:215:TRP:HB3	1.90	0.53
10:S:41:LEU:HD11	10:S:177:LEU:HD11	1.91	0.53
14:U:695:MET:HE2	14:U:709:PHE:CD2	2.36	0.53
24:f:415:GLY:HA3	24:f:447:ALA:CB	2.39	0.53
24:f:888:LEU:HD12	24:f:889:PRO:HD2	1.89	0.53
25:X:80:ILE:HD11	25:X:85:ALA:CA	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:k:84:ASP:OD2	30:k:135:ARG:NH2	2.42	0.53
5:n:225:GLY:C	5:n:227:GLN:H	2.16	0.53
7:B:288:ASP:OD1	7:B:288:ASP:N	2.40	0.53
16:G:13:ILE:HG22	16:G:14:THR:N	2.23	0.53
22:W:231:ILE:HD12	22:W:243:ILE:HG23	1.90	0.53
23:H:64:LYS:HG2	23:H:76:TYR:HE1	1.73	0.53
24:f:38:ASP:OD1	24:f:38:ASP:O	2.27	0.53
24:f:652:VAL:HB	24:f:686:LEU:HD21	1.89	0.53
5:n:72:HIS:ND1	5:n:73:ASP:OD1	2.40	0.53
7:B:190:LEU:HB3	7:B:193:GLN:HB2	1.90	0.53
14:U:766:PHE:HD1	14:U:776:SER:HB3	1.72	0.53
14:U:879:ASP:OD1	14:U:879:ASP:N	2.42	0.53
15:C:311:ILE:CG2	15:C:312:ASP:H	2.21	0.53
24:f:326:LEU:HD13	24:f:326:LEU:N	2.24	0.53
17:Q:12:TYR:HB2	17:Q:182:ILE:HD11	1.90	0.53
3:m:161:TRP:O	3:m:181:MET:SD	2.67	0.53
6:E:283:ASP:OD1	6:E:283:ASP:N	2.42	0.53
13:p:71:LEU:HD11	13:p:82:ILE:HG21	1.91	0.53
14:U:661:ALA:CB	14:U:693:LEU:CD2	2.86	0.53
16:G:93:ARG:HE	16:G:121:ILE:HD11	1.69	0.53
19:V:350:GLN:HB2	19:V:353:LEU:HB2	1.91	0.53
22:W:373:ILE:HA	31:a:326:GLU:HB2	1.91	0.53
24:f:370:MET:HG2	24:f:747:GLN:NE2	2.24	0.53
24:f:399:LEU:CB	24:f:440:ILE:CD1	2.57	0.53
24:f:560:LEU:HD23	24:f:594:LEU:HD21	1.90	0.53
26:I:90:LEU:HB3	26:I:114:LEU:HD13	1.91	0.53
13:P:65:GLN:OE1	17:Q:86:ARG:NH2	2.38	0.53
34:c:279:ASP:OD1	34:c:280:PRO:HD3	2.08	0.53
16:G:128:ASN:OD1	23:H:127:VAL:CG1	2.49	0.53
18:A:101:ILE:HD11	18:A:140:VAL:HG21	1.90	0.53
19:V:215:ALA:O	19:V:219:GLU:N	2.42	0.53
23:H:79:MET:H	23:H:132:VAL:HG22	1.74	0.53
24:f:396:ASN:OD1	24:f:399:LEU:CD2	2.55	0.53
29:Z:43:TRP:CE2	29:Z:45:LYS:O	2.62	0.53
32:L:46:LEU:HD13	32:L:73:SER:HB2	1.90	0.53
1:u:385:ASN:CB	24:f:434:TYR:HD1	2.19	0.53
6:E:194:ASN:HB2	6:E:228:CYS:HA	1.91	0.53
24:f:91:SER:OG	24:f:125:ILE:CG2	2.57	0.53
24:f:301:HIS:NE2	24:f:321:MET:SD	2.83	0.53
24:f:387:GLN:OE1	24:f:418:LEU:CD1	2.49	0.53
5:N:74:ARG:NH1	5:N:214:ALA:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:50:PHE:O	31:a:86:GLN:NE2	2.41	0.53
13:P:22:ILE:HD11	13:P:50:TYR:CD2	2.44	0.53
1:u:385:ASN:CB	24:f:434:TYR:CD1	2.92	0.52
6:E:40:TYR:HA	12:F:73:ILE:HD12	1.90	0.52
7:B:135:ILE:CD1	7:B:141:LYS:NZ	2.71	0.52
18:A:101:ILE:HD13	18:A:113:ILE:CG1	2.36	0.52
22:W:268:LYS:HG3	22:W:299:ILE:HD13	1.90	0.52
22:W:366:MET:HE3	22:W:378:MET:HE2	1.89	0.52
6:E:349:GLU:HA	6:E:352:MET:HG3	1.90	0.52
7:B:71:TYR:O	7:B:74:MET:HG3	2.09	0.52
7:B:183:THR:OG1	7:B:184:TYR:N	2.43	0.52
20:T:144:ARG:HG2	20:T:151:LEU:HG	1.91	0.52
24:f:403:LYS:O	24:f:407:MET:N	2.42	0.52
29:Z:225:GLN:HA	29:Z:228:TYR:CE2	2.43	0.52
2:d:104:ARG:HG2	2:d:105:LYS:H	1.74	0.52
17:q:31:ASP:N	17:q:31:ASP:OD1	2.42	0.52
19:V:203:LEU:O	19:V:207:ALA:N	2.38	0.52
26:I:121:TYR:HE2	26:I:130:PHE:CZ	2.27	0.52
26:I:248:GLU:HG3	26:I:252:LYS:HE3	1.90	0.52
30:K:21:LEU:HD23	30:K:24:VAL:N	2.21	0.52
31:a:87:MET:HG2	31:a:93:ALA:HB2	1.91	0.52
13:P:111:GLY:HA2	13:P:190:ILE:CD1	2.40	0.52
6:E:265:ASP:OD1	6:E:265:ASP:N	2.42	0.52
12:F:306:VAL:HG21	18:A:297:ARG:HH12	1.75	0.52
14:U:70:HIS:C	14:U:72:GLY:H	2.17	0.52
15:C:261:GLY:O	15:C:265:GLY:N	2.40	0.52
19:V:212:TYR:O	19:V:215:ALA:HB3	2.10	0.52
19:V:342:ILE:HG12	19:V:368:ARG:HG3	1.90	0.52
22:W:169:LEU:C	22:W:169:LEU:HD12	2.34	0.52
20:t:141:MET:HE3	20:t:151:LEU:HB2	1.90	0.52
23:H:189:HIS:HD2	25:X:124:PHE:CB	2.22	0.52
24:f:187:LEU:O	24:f:191:ILE:CD1	2.50	0.52
24:f:347:ASP:HA	24:f:350:LYS:HB2	1.91	0.52
3:M:24:VAL:CG1	3:M:124:THR:HG21	2.37	0.52
29:Z:19:VAL:HG21	29:Z:124:ILE:HD12	1.91	0.52
31:a:320:VAL:HG13	31:a:333:MET:HE1	1.91	0.52
13:P:22:ILE:HD13	13:P:50:TYR:HB2	1.91	0.52
2:d:95:TYR:CD2	2:d:95:TYR:O	2.63	0.52
5:n:161:ILE:HD11	5:n:170:TYR:CD1	2.45	0.52
11:D:131:ALA:HB3	11:D:141:ASP:HB3	1.91	0.52
11:D:376:ASN:ND2	36:D:501:ATP:O2'	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:s:107:ASN:ND2	30:k:111:SER:HB3	2.24	0.52
24:f:365:VAL:HG11	24:f:370:MET:SD	2.50	0.52
16:g:175:SER:HB2	16:g:205:VAL:HG21	1.91	0.52
27:Y:71:ASN:HA	27:Y:74:LYS:HG2	1.91	0.52
27:Y:124:PHE:CE2	27:Y:147:ILE:HG21	2.44	0.52
28:j:70:CYS:SG	28:j:217:LEU:HD21	2.49	0.52
31:a:223:GLU:HG2	31:a:234:ILE:HD11	1.91	0.52
34:c:265:MET:SD	34:c:269:GLN:HB3	2.49	0.52
2:d:147:ILE:O	2:d:150:ILE:CG2	2.57	0.52
2:d:208:PHE:CD2	2:d:209:HIS:CD2	2.90	0.52
7:B:144:LEU:CD1	7:B:162:VAL:HG21	2.38	0.52
18:A:368:ILE:CD1	18:A:409:PHE:HE2	2.06	0.52
24:f:605:ASN:HD21	24:f:639:LYS:HE3	1.75	0.52
25:X:149:LEU:HD12	25:X:153:LEU:HD13	1.91	0.52
30:k:74:ILE:HG23	30:k:109:VAL:HG22	1.90	0.52
6:E:267:PHE:CE1	11:D:160:PRO:HG2	2.45	0.52
22:W:48:LEU:HD13	22:W:96:GLN:HG3	1.91	0.52
22:W:408:ARG:HH21	25:X:349:HIS:HB3	1.73	0.52
24:f:376:PHE:CE2	24:f:380:PHE:CE2	2.90	0.52
16:g:191:PHE:CE1	16:g:195:VAL:HG23	2.45	0.52
27:Y:79:ASP:O	27:Y:82:LYS:HD2	2.09	0.52
27:Y:376:LEU:HD23	29:Z:265:LEU:HD11	1.91	0.52
33:b:12:ASN:HB2	33:b:80:PRO:HA	1.90	0.52
2:d:200:LEU:HD23	2:d:232:LEU:HD23	1.92	0.52
16:G:79:VAL:HG12	16:G:139:ILE:HB	1.92	0.52
10:s:197:ASP:OD2	10:s:201:ARG:NH1	2.43	0.52
24:f:399:LEU:CD2	24:f:440:ILE:HD13	2.06	0.52
27:Y:61:LEU:HD12	27:Y:63:TRP:H	1.74	0.52
27:Y:269:SER:OG	27:Y:270:VAL:N	2.43	0.52
32:L:18:ARG:NH1	32:L:23:GLU:OE2	2.43	0.52
7:B:234:LEU:CD2	35:B:501:ADP:C4	2.92	0.52
4:r:92:LYS:HG2	4:r:104:MET:HB2	1.92	0.52
19:V:322:VAL:O	19:V:322:VAL:CG1	2.56	0.52
22:W:393:LEU:HD23	22:W:393:LEU:O	2.10	0.52
22:W:446:ILE:HB	29:Z:226:ILE:HD11	1.92	0.52
24:f:374:SER:O	24:f:378:ASN:ND2	2.42	0.52
10:S:178:ASP:OD2	13:p:177:ARG:NH2	2.43	0.52
14:U:247:GLN:NE2	14:U:911:ILE:O	2.39	0.52
24:f:652:VAL:HG11	24:f:686:LEU:HD11	1.92	0.52
27:Y:387:ILE:CG2	27:Y:388:ASN:N	2.73	0.52
31:a:70:ARG:O	33:b:17:ARG:NH2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:293:PHE:CG	31:a:329:LYS:HG3	2.41	0.52
34:c:121:TRP:HE3	34:c:122:LEU:O	1.93	0.52
34:c:163:ILE:HD13	34:c:201:TYR:HE1	1.75	0.52
6:E:135:ILE:HG13	6:E:182:LEU:HD21	1.92	0.51
11:D:123:LEU:HB3	11:D:142:VAL:HG11	1.92	0.51
17:q:24:ASN:N	17:q:24:ASN:OD1	2.42	0.51
19:V:210:CYS:SG	19:V:211:TYR:N	2.83	0.51
3:M:215:SER:OG	3:M:225:HIS:NE2	2.40	0.51
29:Z:235:ASN:OD1	31:a:289:ARG:NH1	2.44	0.51
33:b:65:THR:HG22	33:b:67:ASP:OD1	2.10	0.51
34:c:65:TYR:OH	34:c:176:GLN:NE2	2.43	0.51
1:u:403:ARG:C	1:u:406:ARG:HG3	2.35	0.51
14:U:524:LYS:NZ	14:U:562:GLU:O	2.28	0.51
19:V:159:LEU:HD22	19:V:163:VAL:HG23	1.91	0.51
22:W:33:LYS:O	22:W:33:LYS:NZ	2.34	0.51
30:k:78:MET:HE3	30:k:85:ALA:HB1	1.86	0.51
3:m:71:ARG:HD3	20:t:117:ILE:HG12	1.91	0.51
10:S:179:ASN:OD1	13:p:173:ASN:ND2	2.44	0.51
18:A:403:ILE:HD12	18:A:405:THR:N	2.24	0.51
22:W:264:GLN:HE21	22:W:299:ILE:HG13	1.75	0.51
24:f:88:SER:O	24:f:92:VAL:CB	2.52	0.51
24:f:250:ARG:NH2	24:f:281:ILE:O	2.36	0.51
24:f:434:TYR:O	24:f:434:TYR:CD2	2.63	0.51
16:g:191:PHE:C	16:g:191:PHE:CD1	2.89	0.51
26:I:38:LEU:HD23	26:I:43:VAL:HG21	1.92	0.51
30:k:31:ILE:HD13	30:k:140:ALA:HB2	1.93	0.51
7:B:74:MET:SD	7:B:74:MET:C	2.94	0.51
12:F:410:ARG:NH1	12:F:419:ASP:OD1	2.40	0.51
15:C:149:GLU:HB2	15:C:206:HIS:HE1	1.75	0.51
16:G:221:THR:OG1	16:G:222:VAL:N	2.43	0.51
17:q:45:LEU:O	17:q:46:CYS:SG	2.67	0.51
29:Z:165:GLU:OE1	29:Z:167:ALA:N	2.41	0.51
33:b:184:ILE:O	33:b:184:ILE:CG2	2.56	0.51
2:d:240:SER:O	2:d:240:SER:OG	2.25	0.51
14:U:542:GLU:N	14:U:542:GLU:OE1	2.44	0.51
14:U:557:TYR:O	14:U:559:ARG:NH2	2.37	0.51
14:U:632:GLN:O	14:U:635:SER:OG	2.28	0.51
16:G:60:LEU:HD22	3:M:182:MET:CE	2.40	0.51
20:T:171:ASP:OD1	20:T:172:MET:N	2.40	0.51
24:f:190:GLU:HB3	24:f:194:TYR:HA	1.93	0.51
24:f:326:LEU:HD22	24:f:326:LEU:N	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:96:THR:O	17:Q:96:THR:OG1	2.28	0.51
1:u:60:LEU:HD21	1:u:73:LEU:HD11	1.92	0.51
7:B:152:LEU:HD22	7:B:159:VAL:HG12	1.84	0.51
7:B:401:GLU:OE1	7:B:429:LYS:NZ	2.44	0.51
19:V:52:ASP:OD2	19:V:147:PHE:CZ	2.64	0.51
22:W:93:ARG:HH12	22:W:97:LEU:CD2	2.23	0.51
24:f:396:ASN:O	24:f:399:LEU:CD2	2.59	0.51
31:a:321:LYS:HB2	31:a:335:TRP:HB3	1.93	0.51
2:d:135:LYS:HA	2:d:138:LYS:HG3	1.91	0.51
19:V:52:ASP:CG	19:V:147:PHE:CE1	2.88	0.51
19:V:91:PRO:HA	19:V:94:VAL:HG12	1.93	0.51
19:V:407:VAL:CG2	19:V:426:LEU:HD22	2.40	0.51
10:s:82:CYS:CB	10:s:89:CYS:SG	2.97	0.51
24:f:414:LEU:HD21	24:f:428:GLN:CB	2.40	0.51
27:Y:20:ALA:HB2	27:Y:150:PHE:HA	1.93	0.51
33:b:52:ILE:HD11	33:b:58:CYS:HB3	1.93	0.51
11:D:370:ILE:HG23	11:D:374:ASP:HB2	1.93	0.51
20:T:72:LEU:HD11	20:T:79:ALA:HB1	1.91	0.51
24:f:82:ILE:O	24:f:86:THR:OG1	2.28	0.51
26:i:71:ASP:HA	26:i:223:THR:HG21	1.92	0.51
29:Z:12:HIS:ND1	29:Z:50:VAL:O	2.41	0.51
29:Z:48:LEU:HD21	29:Z:92:VAL:HG11	1.92	0.51
31:a:111:VAL:O	31:a:115:LYS:HG3	2.11	0.51
32:l:47:VAL:HG12	32:l:195:LEU:HD12	1.93	0.51
6:E:71:VAL:HG21	6:E:100:LEU:HD21	1.92	0.51
7:B:60:LEU:HD11	24:f:223:GLU:HB3	1.93	0.51
14:U:82:LEU:HD23	14:U:129:ARG:HA	1.93	0.51
14:U:751:ARG:HG3	14:U:752:THR:HG22	1.92	0.51
22:W:231:ILE:HG13	22:W:243:ILE:CG2	2.41	0.51
24:f:385:PHE:HZ	24:f:421:ASP:CG	2.16	0.51
16:g:137:CYS:SG	16:g:138:MET:N	2.79	0.51
5:N:196:LEU:HG	5:N:228:ILE:CD1	2.41	0.51
2:d:215:LEU:HD22	2:d:218:LYS:HD3	1.93	0.51
2:d:251:ILE:O	2:d:251:ILE:HG13	2.11	0.51
16:G:86:ASP:OD1	3:M:121:HIS:NE2	2.42	0.51
20:t:224:ARG:NH2	9:O:178:MET:SD	2.84	0.51
24:f:404:ASP:OD2	24:f:439:TYR:OH	2.28	0.51
24:f:545:LYS:CE	24:f:588:ARG:HD2	2.41	0.51
16:g:90:GLN:OE1	16:g:134:LEU:CD2	2.59	0.51
27:Y:124:PHE:CE2	27:Y:147:ILE:CD1	2.89	0.51
31:a:289:ARG:HG2	31:a:333:MET:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:d:271:ILE:O	2:d:274:CYS:SG	2.68	0.50
11:D:415:GLU:CG	16:G:159:TYR:CZ	2.94	0.50
14:U:609:ASP:O	14:U:615:ARG:NH1	2.44	0.50
14:U:642:GLU:O	15:C:53:ASN:ND2	2.44	0.50
23:H:123:GLN:NE2	26:I:130:PHE:CE1	2.71	0.50
24:f:20:ALA:CB	24:f:75:LEU:HD23	2.33	0.50
24:f:145:VAL:HG13	24:f:149:GLU:HB2	1.92	0.50
24:f:399:LEU:CD1	24:f:440:ILE:HD11	2.39	0.50
24:f:872:VAL:HG11	24:f:881:GLU:HB3	1.93	0.50
3:M:189:ASP:OD1	3:M:189:ASP:N	2.40	0.50
26:i:3:ARG:HG2	26:i:3:ARG:O	2.11	0.50
34:c:49:VAL:HG13	34:c:50:PRO:HD3	1.92	0.50
2:d:112:CYS:O	2:d:115:GLU:HB2	2.10	0.50
12:F:137:ILE:HG23	12:F:160:ILE:HD12	1.93	0.50
19:V:280:ALA:HB1	19:V:284:GLU:HB3	1.94	0.50
22:W:82:LEU:HB3	22:W:90:LEU:CD2	2.42	0.50
22:W:228:ASN:HA	22:W:231:ILE:HG22	1.93	0.50
24:f:63:LEU:O	24:f:67:ASP:HB2	2.11	0.50
25:X:304:LYS:NZ	25:X:308:ASP:OD2	2.38	0.50
23:h:212:ILE:HG22	23:h:213:CYS:N	2.26	0.50
27:Y:124:PHE:HE2	27:Y:147:ILE:HD12	1.73	0.50
13:P:205:ASP:OD1	13:P:205:ASP:N	2.40	0.50
33:b:51:LEU:HD11	33:b:61:LEU:HD23	1.93	0.50
33:b:61:LEU:HD21	33:b:74:LYS:HB3	1.93	0.50
11:D:234:GLU:O	11:D:237:GLN:NE2	2.44	0.50
13:p:7:ASN:ND2	13:p:29:GLY:O	2.42	0.50
17:q:62:LYS:HD2	28:j:96:LEU:HD22	1.92	0.50
17:q:102:LEU:HD22	17:q:103:LEU:HG	1.94	0.50
18:A:277:ILE:HG21	18:A:319:MET:HG2	1.92	0.50
22:W:155:GLN:HG3	22:W:155:GLN:O	2.12	0.50
24:f:744:MET:C	24:f:744:MET:SD	2.94	0.50
27:Y:82:LYS:NZ	27:Y:82:LYS:CB	2.73	0.50
33:b:121:GLU:HG2	33:b:152:LYS:HG2	1.85	0.50
10:S:56:ARG:NH2	10:S:219:ASP:OD1	2.44	0.50
14:U:265:ILE:O	14:U:269:ARG:HG3	2.12	0.50
24:f:90:THR:O	24:f:133:MET:SD	2.70	0.50
16:g:50:ILE:CD1	16:g:79:VAL:HG23	2.35	0.50
29:Z:8:LYS:HE2	29:Z:159:THR:HG21	1.93	0.50
7:B:63:LEU:O	7:B:67:ARG:N	2.41	0.50
12:F:225:MET:HB3	12:F:354:PHE:HE2	1.75	0.50
17:q:192:ASP:OD1	17:q:192:ASP:N	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:169:TYR:O	20:T:176:ALA:HA	2.11	0.50
27:Y:12:PRO:CD	27:Y:113:ARG:HE	2.14	0.50
5:N:196:LEU:CD2	5:N:228:ILE:CD1	2.89	0.50
4:R:156:MET:HE3	4:R:158:THR:HG22	1.94	0.50
14:U:608:SER:O	14:U:608:SER:OG	2.29	0.50
4:r:172:TYR:O	4:r:179:ARG:HA	2.11	0.50
20:t:54:THR:O	20:t:86:ARG:NH2	2.42	0.50
24:f:570:GLY:H	24:f:600:TYR:HB3	1.76	0.50
24:f:850:VAL:HG11	24:f:852:VAL:CG2	2.40	0.50
25:X:45:VAL:HA	25:X:48:GLN:HG2	1.93	0.50
25:X:319:ILE:O	25:X:323:LEU:HB2	2.11	0.50
6:E:135:ILE:HG13	6:E:182:LEU:CD2	2.42	0.50
20:T:54:THR:HG22	20:T:55:SER:H	1.75	0.50
25:X:119:SER:O	25:X:121:LYS:NZ	2.44	0.50
13:P:22:ILE:CG2	13:P:110:ALA:CB	2.90	0.50
9:o:108:LEU:C	9:o:108:LEU:CD2	2.85	0.50
11:D:82:ILE:HD11	15:C:66:LEU:HG	1.92	0.50
22:W:395:ASN:HA	22:W:398:VAL:HG22	1.93	0.50
20:t:224:ARG:NH1	5:N:60:ILE:O	2.43	0.50
24:f:571:GLU:O	24:f:571:GLU:HG2	2.12	0.50
26:I:79:ILE:HG22	26:I:82:ASP:H	1.75	0.50
23:h:121:TYR:O	23:h:127:VAL:HG23	2.11	0.50
27:Y:191:ILE:HD13	27:Y:290:PRO:HB2	1.94	0.50
5:N:196:LEU:CD2	5:N:228:ILE:HD12	2.41	0.50
8:e:60:LEU:HD12	27:Y:329:PHE:CG	2.46	0.50
11:D:79:VAL:HG23	15:C:63:LEU:HG	1.94	0.50
13:p:20:VAL:CG2	13:p:119:PRO:HB3	2.40	0.50
15:C:336:MET:CG	15:C:338:LEU:HD11	2.42	0.50
10:s:153:ASP:OD1	10:s:157:SER:N	2.45	0.50
23:H:189:HIS:CD2	25:X:124:PHE:CG	3.00	0.50
26:I:28:ILE:HG21	26:I:133:SER:HB3	1.93	0.50
27:Y:165:LYS:NZ	27:Y:188:CYS:SG	2.84	0.50
13:P:51:ILE:HG12	13:P:109:ILE:HG12	1.94	0.50
2:d:275:ILE:HD11	2:d:279:TYR:H	1.75	0.49
10:S:52:ALA:HB1	10:S:221:LEU:HD11	1.92	0.49
14:U:497:LEU:HD13	14:U:515:ALA:HB1	1.92	0.49
15:C:235:PHE:HD2	15:C:239:ARG:NH1	2.08	0.49
15:C:311:ILE:CG2	15:C:312:ASP:N	2.74	0.49
22:W:15:LYS:HG3	22:W:27:ARG:HH12	1.77	0.49
23:H:4:ARG:HD3	3:M:128:ALA:HB2	1.93	0.49
24:f:399:LEU:CD1	24:f:440:ILE:CD1	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:f:399:LEU:HD11	24:f:400:TYR:CD1	2.17	0.49
24:f:404:ASP:OD1	24:f:439:TYR:CE2	2.64	0.49
24:f:850:VAL:HG12	24:f:852:VAL:CG2	2.41	0.49
16:g:210:PHE:CE2	16:g:215:ILE:HG21	2.47	0.49
26:I:21:VAL:HG11	26:I:153:SER:HB3	1.92	0.49
26:I:33:THR:HA	26:I:165:GLY:HA3	1.93	0.49
23:h:44:VAL:HG11	23:h:137:CYS:CB	2.42	0.49
33:b:3:LEU:HD11	33:b:104:ASN:O	2.11	0.49
30:k:178:GLN:NE2	30:k:178:GLN:CA	2.72	0.49
34:c:61:PHE:HD1	34:c:67:VAL:HG23	1.77	0.49
6:E:84:ARG:HB2	6:E:87:LEU:HD23	1.94	0.49
11:D:173:GLN:NE2	11:D:332:GLU:O	2.45	0.49
16:G:11:ARG:O	16:G:24:GLN:NE2	2.45	0.49
18:A:299:MET:SD	18:A:303:ILE:HG12	2.50	0.49
22:W:8:ARG:HH21	22:W:12:ARG:HE	1.60	0.49
24:f:261:ARG:HG3	24:f:269:ALA:CB	2.41	0.49
25:X:90:ARG:HD2	25:X:125:LEU:CD1	2.22	0.49
27:Y:88:LEU:HA	27:Y:91:ALA:HB3	1.93	0.49
27:Y:144:LEU:HD12	27:Y:147:ILE:CG2	2.43	0.49
17:Q:192:ASP:OD1	17:Q:192:ASP:N	2.45	0.49
34:c:178:THR:HA	34:c:181:LEU:CD1	2.42	0.49
1:u:403:ARG:CA	1:u:406:ARG:HG3	2.41	0.49
9:o:189:MET:HE2	9:o:193:GLU:HB3	1.93	0.49
16:G:25:VAL:O	16:G:29:PHE:HD1	1.95	0.49
24:f:761:MET:C	24:f:858:LYS:HZ1	2.20	0.49
27:Y:217:LYS:HB3	27:Y:253:LEU:HD11	1.94	0.49
29:Z:133:LEU:HD12	29:Z:134:PRO:HD2	1.94	0.49
33:b:65:THR:HG23	33:b:66:PRO:HD2	1.94	0.49
9:o:44:THR:N	9:o:212:SER:OG	2.41	0.49
14:U:568:GLU:O	14:U:572:ARG:NH1	2.45	0.49
18:A:325:ASP:OD1	18:A:325:ASP:N	2.44	0.49
19:V:483:CYS:O	29:Z:268:SER:OG	2.31	0.49
24:f:111:GLU:HG3	24:f:141:LYS:HZ3	1.76	0.49
9:O:81:SER:OG	9:O:83:ASN:OD1	2.30	0.49
33:b:121:GLU:CG	33:b:152:LYS:CG	2.66	0.49
30:k:37:ALA:HB2	30:k:50:VAL:HG13	1.94	0.49
2:d:236:LEU:O	19:V:440:LYS:NZ	2.45	0.49
4:R:103:THR:O	4:R:158:THR:OG1	2.31	0.49
14:U:527:GLN:NE2	14:U:531:ASP:OD2	2.46	0.49
16:G:130:GLU:HG2	16:G:131:MET:HE2	1.94	0.49
22:W:421:PRO:CB	29:Z:251:LEU:HD23	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:f:603:SER:H	24:f:639:LYS:HD3	1.77	0.49
26:i:132:VAL:CG1	26:i:134:LEU:HD23	2.43	0.49
33:b:161:ASN:HB2	33:b:167:GLY:H	1.76	0.49
9:o:61:THR:HB	9:o:74:CYS:H	1.77	0.49
15:C:219:LEU:HD12	15:C:220:VAL:HG23	1.94	0.49
19:V:94:VAL:HG21	19:V:134:PHE:HB3	1.95	0.49
24:f:408:LEU:CD1	24:f:439:TYR:CA	2.85	0.49
27:Y:50:MET:SD	27:Y:116:ASP:HB2	2.53	0.49
32:l:130:VAL:HG21	32:l:132:LEU:CD1	2.42	0.49
2:d:164:PHE:CZ	2:d:168:MET:HG3	2.47	0.49
3:m:40:ARG:HD3	3:m:161:TRP:NE1	2.28	0.49
7:B:148:CYS:HB3	7:B:165:ASP:OD2	2.12	0.49
7:B:405:MET:HA	7:B:408:ARG:HG2	1.94	0.49
15:C:351:MET:HB3	15:C:387:VAL:HG13	1.94	0.49
18:A:217:PRO:O	18:A:222:LYS:NZ	2.43	0.49
27:Y:103:ALA:HB3	27:Y:105:MET:HE1	1.95	0.49
26:i:139:TRP:HA	26:i:144:GLY:O	2.13	0.49
30:K:210:LEU:HD11	30:K:215:ILE:HG12	1.95	0.49
10:S:99:ARG:HD3	10:S:123:ILE:HD11	1.93	0.49
11:D:213:THR:OG1	36:D:501:ATP:O1B	2.25	0.49
18:A:368:ILE:HG12	18:A:409:PHE:CE2	2.47	0.49
22:W:144:ARG:NH2	22:W:168:GLU:OE2	2.46	0.49
24:f:83:ARG:NH2	24:f:112:ASN:O	2.45	0.49
24:f:385:PHE:CZ	24:f:421:ASP:HB2	2.48	0.49
25:X:134:VAL:HG11	25:X:149:LEU:HD13	1.95	0.49
16:g:191:PHE:CZ	16:g:219:VAL:HG21	2.48	0.49
3:M:55:LEU:HD23	3:M:58:LEU:HD23	1.95	0.49
5:N:138:ASP:OD1	5:N:139:PRO:CD	2.60	0.49
30:K:211:ASN:CG	30:K:212:ALA:H	2.21	0.49
13:P:126:LEU:HD12	13:P:126:LEU:C	2.37	0.49
33:b:25:ARG:NH1	33:b:114:GLY:O	2.45	0.49
2:d:330:ILE:HG13	2:d:331:PRO:HD3	1.94	0.49
10:S:40:ILE:HD11	10:S:82:CYS:N	2.28	0.49
12:F:289:ASP:OD1	12:F:289:ASP:N	2.45	0.49
14:U:130:LEU:O	14:U:132:GLY:N	2.45	0.49
16:G:212:PRO:HG3	16:G:239:LEU:HD12	1.94	0.49
18:A:45:ILE:HA	18:A:48:VAL:HG12	1.95	0.49
19:V:407:VAL:HG22	19:V:426:LEU:HD22	1.93	0.49
22:W:449:GLU:HA	22:W:452:ILE:HD12	1.95	0.49
23:H:122:THR:HG22	23:H:129:PRO:HB3	1.95	0.49
23:h:86:LEU:HD13	23:h:134:LEU:HD21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:34:TRP:HD1	33:b:18:ASN:HA	1.77	0.49
31:a:189:PRO:O	31:a:193:GLN:N	2.45	0.49
33:b:121:GLU:HG2	33:b:152:LYS:CD	2.39	0.49
17:Q:31:ASP:N	17:Q:31:ASP:OD1	2.46	0.49
5:n:72:HIS:HD1	5:n:73:ASP:H	1.61	0.49
11:D:135:HIS:O	15:C:69:GLN:NE2	2.46	0.49
11:D:229:ARG:C	11:D:229:ARG:CD	2.85	0.49
14:U:261:LEU:HD22	14:U:328:ILE:HD11	1.93	0.49
14:U:418:GLU:HB3	14:U:422:LEU:HB2	1.95	0.49
14:U:542:GLU:OE2	34:c:66:THR:HG23	2.13	0.49
14:U:555:VAL:O	14:U:556:MET:HE2	2.12	0.49
14:U:661:ALA:HB2	14:U:693:LEU:CD2	2.43	0.49
18:A:35:THR:OG1	18:A:36:TYR:N	2.46	0.49
18:A:103:ASN:HB3	18:A:112:ILE:HD12	1.94	0.49
19:V:274:SER:HA	19:V:276:PHE:CD1	2.47	0.49
24:f:372:LEU:HD13	24:f:406:GLY:HA2	1.95	0.49
26:I:119:GLN:HG3	28:J:78:ALA:HB1	1.94	0.49
26:I:123:GLN:NE2	28:J:125:ARG:O	2.45	0.49
26:i:33:THR:HB	26:i:48:GLU:HB2	1.94	0.49
9:O:94:ASP:HB3	9:O:137:ILE:HG23	1.94	0.49
13:P:36:THR:OG1	13:P:38:ASP:OD1	2.30	0.49
10:S:173:LEU:HD22	10:S:206:VAL:HB	1.95	0.48
14:U:129:ARG:C	14:U:130:LEU:HG	2.37	0.48
18:A:333:ARG:HH21	18:A:336:ARG:CZ	2.26	0.48
24:f:385:PHE:CZ	24:f:421:ASP:OD2	2.66	0.48
24:f:602:GLY:HA2	24:f:639:LYS:HA	1.95	0.48
24:f:682:GLY:HA3	24:f:687:ARG:HE	1.78	0.48
16:g:120:ASP:OD1	23:h:84:ARG:NH1	2.46	0.48
13:P:171:MET:O	13:P:175:VAL:CG2	2.60	0.48
33:b:52:ILE:HD13	33:b:60:VAL:HG22	1.95	0.48
6:E:199:VAL:HG13	6:E:201:SER:H	1.77	0.48
14:U:173:VAL:HA	14:U:177:LEU:HD12	1.94	0.48
22:W:2:ALA:HB2	22:W:43:VAL:HG13	1.94	0.48
22:W:56:THR:HA	22:W:59:ASP:HB2	1.95	0.48
22:W:97:LEU:HD21	22:W:135:LYS:CE	2.40	0.48
23:H:89:ARG:O	23:H:93:LEU:HG	2.13	0.48
24:f:685:THR:OG1	24:f:686:LEU:N	2.46	0.48
32:L:29:VAL:HG21	32:L:149:PRO:HG2	1.95	0.48
32:L:140:MET:O	32:L:140:MET:CG	2.59	0.48
33:b:112:PHE:HE1	33:b:141:ILE:HD12	1.78	0.48
33:b:161:ASN:HB3	33:b:168:SER:OG	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:146:TYR:HB2	17:Q:159:LEU:HD13	1.95	0.48
34:c:279:ASP:H	34:c:280:PRO:HD2	1.77	0.48
1:u:410:ARG:CZ	24:f:326:LEU:CD2	2.90	0.48
7:B:233:THR:CG2	7:B:285:ASP:OD2	2.61	0.48
14:U:54:PHE:CZ	14:U:56:SER:OG	2.67	0.48
15:C:252:ASP:N	15:C:252:ASP:OD1	2.46	0.48
22:W:421:PRO:HG3	29:Z:251:LEU:HD21	1.94	0.48
31:a:80:ILE:O	31:a:84:VAL:HG23	2.14	0.48
2:d:202:GLN:OE1	2:d:204:ARG:NH1	2.47	0.48
7:B:105:THR:OG1	7:B:106:PRO:HD3	2.12	0.48
7:B:176:VAL:HG21	7:B:247:PHE:HD2	1.77	0.48
14:U:226:PRO:HB3	14:U:264:VAL:HG12	1.94	0.48
19:V:214:HIS:NE2	19:V:218:TYR:CE2	2.81	0.48
24:f:234:THR:O	24:f:238:ASN:ND2	2.47	0.48
24:f:545:LYS:CE	24:f:588:ARG:CD	2.76	0.48
16:g:164:LYS:NZ	23:h:56:LEU:O	2.46	0.48
27:Y:186:LEU:CG	27:Y:187:TYR:H	2.26	0.48
27:Y:295:TYR:O	27:Y:299:MET:HG2	2.13	0.48
26:i:119:GLN:NE2	28:j:82:ILE:HG13	2.26	0.48
29:Z:170:VAL:HG22	34:c:152:LYS:HA	1.96	0.48
30:k:41:GLN:HA	30:k:46:VAL:HG22	1.94	0.48
2:d:193:GLY:HA2	2:d:196:LEU:HD12	1.96	0.48
7:B:234:LEU:HD21	35:B:501:ADP:C4	2.49	0.48
14:U:129:ARG:O	14:U:130:LEU:CG	2.60	0.48
19:V:416:ARG:HG3	19:V:459:GLN:HB3	1.95	0.48
22:W:59:ASP:O	22:W:63:THR:N	2.47	0.48
22:W:435:LEU:HD13	29:Z:236:LEU:HD21	1.94	0.48
23:H:74:LEU:HD11	23:H:134:LEU:HD13	1.94	0.48
24:f:33:ARG:HA	24:f:36:ALA:HB3	1.96	0.48
24:f:582:VAL:CG2	24:f:588:ARG:NH2	2.59	0.48
25:X:380:GLN:OE1	27:Y:318:TYR:CE2	2.66	0.48
23:h:198:SER:O	23:h:198:SER:OG	2.29	0.48
29:Z:181:ASP:OD1	29:Z:181:ASP:N	2.46	0.48
28:j:41:VAL:HB	28:j:211:MET:HB3	1.95	0.48
31:a:106:SER:OG	31:a:107:SER:N	2.45	0.48
2:d:131:THR:HG22	2:d:138:LYS:HD3	1.96	0.48
7:B:361:LYS:HE3	7:B:361:LYS:HB2	1.71	0.48
14:U:378:CYS:SG	14:U:780:SER:HB2	2.54	0.48
24:f:352:HIS:HB2	24:f:355:ASN:HD22	1.77	0.48
25:X:299:LEU:HD11	25:X:331:LEU:HG	1.94	0.48
29:Z:225:GLN:CG	29:Z:226:ILE:H	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:156:TYR:HE1	31:a:175:ASP:HB3	1.78	0.48
13:P:22:ILE:CD1	13:P:50:TYR:CB	2.92	0.48
30:k:69:GLU:O	30:k:93:ARG:NH2	2.38	0.48
34:c:287:HIS:HA	34:c:290:VAL:HG12	1.95	0.48
34:c:306:THR:HG23	34:c:307:VAL:HG13	1.95	0.48
2:d:345:GLN:HB2	19:V:484:LEU:CD2	2.44	0.48
5:n:138:ASP:OD2	5:n:140:GLN:CB	2.62	0.48
6:E:61:LEU:HD13	11:D:148:ASP:HA	1.96	0.48
7:B:176:VAL:O	7:B:176:VAL:CG1	2.61	0.48
7:B:303:ARG:HA	7:B:306:GLN:HG3	1.95	0.48
11:D:338:ARG:HH12	11:D:365:ALA:HA	1.78	0.48
15:C:73:VAL:HG12	15:C:74:GLY:N	2.27	0.48
15:C:246:ILE:HB	15:C:291:VAL:HG12	1.94	0.48
15:C:336:MET:HG2	15:C:338:LEU:CD1	2.43	0.48
22:W:362:ASN:HB3	22:W:382:LEU:CD1	2.44	0.48
27:Y:123:ALA:HA	27:Y:126:LYS:HE3	1.96	0.48
1:u:33:LEU:CD1	1:u:90:VAL:HG11	2.42	0.48
5:n:68:LEU:HD13	5:n:76:PHE:HD2	1.76	0.48
7:B:189:GLY:HA3	7:B:360:THR:CG2	2.44	0.48
10:S:102:MET:HG3	32:L:93:LEU:HD21	1.95	0.48
14:U:115:ASN:ND2	14:U:123:LYS:O	2.47	0.48
14:U:201:LEU:O	14:U:205:TYR:CD2	2.67	0.48
22:W:76:GLU:O	22:W:130:MET:HE3	2.13	0.48
24:f:695:ALA:HA	24:f:729:MET:HE1	1.96	0.48
25:X:207:GLN:NE2	25:X:211:ASP:OD2	2.47	0.48
25:X:251:LEU:HA	25:X:254:MET:HE2	1.96	0.48
23:h:74:LEU:HD22	23:h:83:TYR:HE1	1.78	0.48
23:h:82:ASP:OD2	23:h:128:ARG:NH2	2.47	0.48
33:b:143:PHE:HE1	33:b:183:LEU:HD13	1.78	0.48
2:d:270:GLU:O	2:d:274:CYS:CB	2.62	0.48
10:S:173:LEU:HD21	10:S:210:ALA:HB2	1.95	0.48
11:D:113:VAL:HB	11:D:138:ALA:HA	1.96	0.48
11:D:370:ILE:HD11	11:D:407:ILE:HG13	1.94	0.48
14:U:460:TYR:O	14:U:464:GLN:HB2	2.14	0.48
14:U:500:ASN:OD1	14:U:508:THR:OG1	2.30	0.48
14:U:640:LEU:HD13	14:U:648:VAL:HG12	1.96	0.48
19:V:159:LEU:HD22	19:V:163:VAL:HG21	1.95	0.48
25:X:50:ILE:HG23	25:X:88:LEU:HD11	1.96	0.48
27:Y:149:LEU:HG	27:Y:186:LEU:HD13	1.96	0.48
3:m:50:GLU:OE2	3:m:52:LEU:CD1	2.62	0.48
4:R:57:LEU:C	4:R:57:LEU:CD1	2.85	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:94:SER:HB2	14:U:97:VAL:HG12	1.95	0.48
18:A:351:ARG:NH1	18:A:378:PRO:O	2.47	0.48
24:f:399:LEU:HB3	24:f:440:ILE:HD11	1.80	0.48
16:g:90:GLN:OE1	16:g:134:LEU:HD23	2.13	0.48
30:K:78:MET:HE2	30:K:89:ILE:HD12	1.96	0.48
31:a:6:GLY:O	31:a:10:GLN:HG3	2.14	0.48
2:d:331:PRO:O	2:d:334:GLU:HB3	2.14	0.47
7:B:133:VAL:HB	7:B:158:ALA:HA	1.96	0.47
14:U:595:ASN:OD1	14:U:595:ASN:N	2.45	0.47
14:U:661:ALA:HB1	14:U:693:LEU:CD2	2.44	0.47
15:C:187:LEU:CB	15:C:314:LYS:HG2	2.12	0.47
18:A:255:ARG:NH2	18:A:259:GLU:OE2	2.46	0.47
19:V:87:SER:OG	19:V:124:ASN:O	2.27	0.47
19:V:418:SER:OG	19:V:419:LEU:N	2.46	0.47
22:W:169:LEU:CD1	22:W:170:GLN:NE2	2.76	0.47
25:X:374:PHE:HZ	25:X:387:ILE:HG12	1.77	0.47
33:b:40:LYS:O	33:b:43:SER:OG	2.32	0.47
4:R:59:GLY:CA	4:R:92:LYS:HZ1	2.06	0.47
6:E:334:LEU:HG	16:G:57:PRO:O	2.13	0.47
9:o:94:ASP:HB3	9:o:137:ILE:HG23	1.95	0.47
9:o:234:VAL:HG13	9:o:234:VAL:O	2.14	0.47
12:F:386:ARG:HH22	32:L:170:THR:HG22	1.75	0.47
14:U:490:ARG:HD2	14:U:493:VAL:HG23	1.96	0.47
14:U:661:ALA:CB	14:U:693:LEU:HD21	2.43	0.47
14:U:697:GLN:NE2	14:U:744:VAL:O	2.47	0.47
16:G:83:MET:SD	16:G:132:ARG:NH2	2.87	0.47
18:A:362:MET:HA	18:A:362:MET:HE2	1.92	0.47
4:r:101:LEU:HB2	4:r:161:CYS:SG	2.54	0.47
4:r:238:VAL:HG22	4:r:243:TRP:HB3	1.96	0.47
19:V:415:SER:HB2	27:Y:346:LYS:HB3	1.95	0.47
10:s:212:GLU:OE1	10:s:239:ARG:NH1	2.47	0.47
23:H:205:GLU:HG3	23:H:223:PRO:HB3	1.96	0.47
24:f:39:LYS:HE3	24:f:84:SER:HB2	1.96	0.47
24:f:376:PHE:CZ	24:f:380:PHE:HD2	2.24	0.47
25:X:150:GLY:O	25:X:154:LEU:HB2	2.14	0.47
28:j:146:GLN:HG3	28:j:159:ASN:HD21	1.77	0.47
2:d:159:LYS:HE3	2:d:159:LYS:HB3	1.66	0.47
4:R:233:VAL:O	4:R:248:SER:HA	2.15	0.47
5:n:227:GLN:O	5:n:228:ILE:CG1	2.53	0.47
12:F:347:ARG:H	12:F:347:ARG:HG2	1.36	0.47
14:U:68:PHE:CE1	14:U:71:LEU:HD11	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:235:PHE:HD2	15:C:279:GLN:NE2	2.06	0.47
18:A:286:ASP:O	18:A:288:GLY:N	2.48	0.47
19:V:333:ILE:HA	19:V:336:GLU:HB2	1.96	0.47
24:f:616:CYS:HB2	24:f:629:LYS:CE	2.41	0.47
16:g:47:CYS:SG	16:g:194:THR:HG21	2.55	0.47
31:a:345:GLN:O	31:a:349:MET:HG2	2.13	0.47
32:L:61:LYS:NZ	32:L:63:ILE:O	2.48	0.47
2:d:95:TYR:O	2:d:95:TYR:CG	2.65	0.47
6:E:304:PRO:O	6:E:309:ARG:NH1	2.48	0.47
14:U:130:LEU:C	14:U:132:GLY:H	2.22	0.47
14:U:390:LEU:O	14:U:390:LEU:HD23	2.15	0.47
14:U:678:ASP:O	14:U:684:ARG:NH1	2.47	0.47
22:W:169:LEU:HD12	22:W:170:GLN:N	2.29	0.47
22:W:403:PHE:HE2	22:W:417:ARG:HA	1.80	0.47
26:I:86:LEU:HD12	26:I:132:VAL:HG11	1.97	0.47
27:Y:12:PRO:HD2	27:Y:113:ARG:HD3	1.92	0.47
27:Y:49:ASN:OD1	27:Y:49:ASN:N	2.47	0.47
26:i:161:ALA:HB1	26:i:175:LEU:HD13	1.95	0.47
31:a:289:ARG:CG	31:a:333:MET:HB2	2.44	0.47
32:L:54:SER:OG	32:L:55:GLU:N	2.48	0.47
2:d:200:LEU:CD2	2:d:232:LEU:HD23	2.44	0.47
5:n:223:LEU:CB	5:n:227:GLN:CB	2.87	0.47
6:E:294:ARG:NH2	36:D:501:ATP:O3G	2.41	0.47
7:B:56:THR:OG1	24:f:178:LYS:NZ	2.43	0.47
7:B:230:THR:HG23	7:B:355:LEU:HD23	1.95	0.47
7:B:343:ARG:HH21	7:B:346:ARG:HH21	1.62	0.47
12:F:84:LYS:HZ1	12:F:139:LEU:CD1	2.28	0.47
13:p:164:PHE:CB	13:p:189:ILE:CD1	2.81	0.47
19:V:84:LYS:HG3	19:V:123:SER:H	1.79	0.47
24:f:387:GLN:NE2	24:f:414:LEU:HG	2.27	0.47
25:X:248:ILE:HD12	25:X:251:LEU:HD12	1.96	0.47
27:Y:75:LYS:O	27:Y:79:ASP:N	2.44	0.47
31:a:136:GLU:HA	31:a:139:GLU:HG2	1.96	0.47
31:a:206:LEU:HD11	31:a:264:ASN:HD21	1.79	0.47
17:Q:116:TYR:HB3	17:Q:124:LEU:HD11	1.95	0.47
34:c:42:LEU:HD21	34:c:155:VAL:HG23	1.95	0.47
34:c:121:TRP:CE3	34:c:194:HIS:CB	2.97	0.47
32:l:225:ASP:OD1	32:l:225:ASP:N	2.45	0.47
2:d:117:GLY:HA2	2:d:120:LYS:HG2	1.97	0.47
7:B:144:LEU:HD12	7:B:162:VAL:HG21	1.96	0.47
10:S:42:ALA:HA	10:S:50:ILE:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:290:LEU:HD13	15:C:222:LYS:CB	2.37	0.47
12:F:168:TYR:HB2	12:F:173:LYS:HE2	1.96	0.47
13:p:58:THR:OG1	17:q:121:LEU:O	2.30	0.47
13:p:126:LEU:CD1	13:p:127:ILE:HG23	2.37	0.47
14:U:685:GLN:NE2	14:U:770:TRP:HE1	2.12	0.47
16:G:169:GLY:O	16:G:172:GLN:NE2	2.48	0.47
18:A:101:ILE:HG12	18:A:140:VAL:HG21	1.96	0.47
20:T:81:PHE:HB3	20:T:84:ILE:CD1	2.37	0.47
24:f:27:LYS:HE2	24:f:34:ARG:HH11	1.80	0.47
27:Y:116:ASP:OD1	27:Y:151:TYR:OH	2.33	0.47
26:i:45:LEU:HD13	26:i:65:ILE:HD12	1.96	0.47
30:K:85:ALA:HB2	30:K:139:VAL:HG11	1.96	0.47
2:d:227:LYS:HA	2:d:227:LYS:HD2	1.68	0.47
4:R:94:ILE:HD11	4:R:104:MET:HE2	1.94	0.47
7:B:51:LEU:HD21	24:f:646:MET:HE1	1.95	0.47
12:F:125:LYS:HA	12:F:131:THR:HA	1.96	0.47
12:F:175:MET:HB3	12:F:250:LYS:O	2.14	0.47
19:V:33:GLN:HA	19:V:89:LYS:HZ1	1.79	0.47
22:W:83:LEU:HD12	22:W:84:ASN:N	2.30	0.47
20:t:144:ARG:HG2	20:t:151:LEU:HG	1.97	0.47
20:t:167:LEU:HG	20:t:182:LEU:HD12	1.96	0.47
24:f:87:THR:OG1	24:f:113:MET:O	2.29	0.47
24:f:131:MET:HG2	24:f:181:ARG:NH1	2.30	0.47
24:f:388:ASP:HB3	24:f:391:LEU:HB3	1.96	0.47
24:f:494:ARG:HG3	24:f:496:ASP:OD1	2.14	0.47
24:f:697:ILE:O	24:f:706:ILE:HG12	2.15	0.47
24:f:733:GLY:HA2	24:f:737:ASN:HD21	1.80	0.47
25:X:386:ILE:HG13	27:Y:312:ARG:HH21	1.80	0.47
26:I:42:GLY:HA3	26:I:186:LEU:HD22	1.96	0.47
26:i:34:CYS:SG	26:i:164:ILE:HD11	2.55	0.47
31:a:42:LEU:HD23	31:a:79:ILE:HG23	1.97	0.47
32:L:214:ILE:O	32:L:221:PHE:HA	2.15	0.47
13:P:78:GLU:N	13:P:78:GLU:OE2	2.48	0.47
34:c:226:MET:O	34:c:230:THR:OG1	2.29	0.47
2:d:113:GLY:O	2:d:116:LEU:HB2	2.14	0.47
6:E:207:TYR:CD2	11:D:238:LYS:HD2	2.49	0.47
6:E:267:PHE:CE1	11:D:160:PRO:CG	2.96	0.47
7:B:189:GLY:HA3	7:B:360:THR:HG21	1.97	0.47
11:D:45:LYS:HA	11:D:45:LYS:HD2	1.71	0.47
14:U:181:LEU:CD1	14:U:201:LEU:HD13	2.40	0.47
14:U:596:ASN:O	14:U:600:ARG:HB3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:619:VAL:O	14:U:622:LEU:HB2	2.14	0.47
22:W:243:ILE:HA	22:W:246:HIS:HB3	1.97	0.47
22:W:340:VAL:HG22	22:W:350:ARG:HH21	1.78	0.47
24:f:741:LEU:HD11	24:f:788:MET:SD	2.55	0.47
31:a:15:GLY:HA3	31:a:22:TRP:HZ2	1.79	0.47
31:a:329:LYS:HA	31:a:329:LYS:HD2	1.67	0.47
13:P:22:ILE:CD1	13:P:50:TYR:HB2	2.45	0.47
13:P:83:LYS:O	13:P:86:THR:OG1	2.26	0.47
33:b:24:THR:HG23	33:b:27:GLN:H	1.80	0.47
2:d:148:LEU:HB3	2:d:171:LEU:HD21	1.95	0.47
4:R:172:TYR:O	4:R:179:ARG:HA	2.15	0.47
14:U:693:LEU:HD23	14:U:693:LEU:O	2.14	0.47
15:C:227:GLY:HA2	15:C:230:MET:HB3	1.96	0.47
19:V:36:GLU:OE2	19:V:77:GLU:CG	2.61	0.47
24:f:180:GLN:HG2	24:f:835:GLU:HG2	1.97	0.47
26:I:44:LEU:HD21	26:I:190:LEU:HD23	1.85	0.47
27:Y:157:ILE:HD12	27:Y:186:LEU:CD1	2.45	0.47
34:c:121:TRP:CE2	34:c:194:HIS:CD2	3.03	0.47
1:u:33:LEU:CD2	1:u:90:VAL:HG13	2.45	0.47
1:u:410:ARG:HH12	24:f:326:LEU:HD21	1.80	0.47
18:A:125:LEU:C	18:A:125:LEU:HD12	2.40	0.47
22:W:414:ASN:N	22:W:414:ASN:OD1	2.47	0.47
23:H:222:THR:HG1	23:H:225:GLU:HG3	1.80	0.47
24:f:601:ALA:O	24:f:639:LYS:NZ	2.39	0.47
3:M:13:SER:O	3:M:13:SER:OG	2.32	0.47
3:M:54:VAL:HG23	3:M:209:ALA:HB1	1.97	0.47
26:i:218:ARG:HD2	26:i:223:THR:OG1	2.15	0.47
13:P:126:LEU:HD11	13:P:127:ILE:HG13	1.92	0.47
2:d:94:MET:HE3	2:d:121:LEU:CD1	2.44	0.46
5:n:196:LEU:CG	5:n:230:LYS:CB	2.93	0.46
6:E:279:THR:OG1	6:E:280:ASN:N	2.47	0.46
9:o:98:THR:HG23	9:o:129:MET:HE1	1.98	0.46
11:D:127:ASN:O	11:D:252:ARG:NH1	2.47	0.46
11:D:228:ILE:HG23	11:D:262:ILE:HA	1.97	0.46
14:U:103:LYS:HE3	14:U:103:LYS:HB3	1.72	0.46
14:U:772:TRP:CD1	14:U:774:PRO:HD2	2.50	0.46
19:V:285:TRP:HD1	19:V:315:LYS:HE2	1.80	0.46
22:W:227:TYR:HD1	22:W:230:MET:HE3	1.79	0.46
24:f:354:GLU:OE1	24:f:354:GLU:N	2.48	0.46
24:f:408:LEU:CD1	24:f:439:TYR:CB	2.93	0.46
26:I:234:GLU:O	26:I:238:LYS:HG3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:87:GLU:O	27:Y:91:ALA:CB	2.62	0.46
27:Y:202:LEU:O	27:Y:202:LEU:HD23	2.15	0.46
5:N:48:LEU:HD21	5:N:135:ALA:HB3	1.97	0.46
31:a:135:ILE:HG12	31:a:158:LEU:HD13	1.97	0.46
13:P:58:THR:OG1	17:Q:121:LEU:O	2.28	0.46
33:b:140:ILE:HD11	33:b:156:PHE:HE2	1.79	0.46
7:B:180:PRO:HG2	7:B:237:LYS:HB3	1.97	0.46
7:B:260:LEU:HB2	21:v:2:UNK:HA	1.97	0.46
8:e:60:LEU:CD1	27:Y:329:PHE:HB2	2.40	0.46
14:U:382:SER:O	14:U:382:SER:OG	2.32	0.46
14:U:543:LYS:HD3	14:U:543:LYS:HA	1.80	0.46
18:A:177:VAL:HG12	18:A:224:LEU:HD13	1.96	0.46
24:f:58:MET:HE1	24:f:96:LEU:HD13	1.96	0.46
27:Y:38:ARG:H	27:Y:38:ARG:HG2	1.54	0.46
5:N:48:LEU:CB	5:N:68:LEU:HD21	2.44	0.46
30:K:190:THR:OG1	30:K:191:LEU:N	2.49	0.46
6:E:267:PHE:CZ	11:D:160:PRO:CG	2.99	0.46
10:S:144:GLU:N	10:S:144:GLU:OE2	2.47	0.46
15:C:336:MET:SD	15:C:338:LEU:HD11	2.55	0.46
16:G:60:LEU:HD11	3:M:177:ILE:HG22	1.98	0.46
18:A:360:ARG:HG2	24:f:839:PRO:HG2	1.96	0.46
19:V:399:ARG:O	19:V:402:VAL:HB	2.14	0.46
20:T:72:LEU:HD22	20:T:229:TYR:HB2	1.96	0.46
22:W:128:LEU:O	22:W:132:THR:OG1	2.23	0.46
22:W:231:ILE:HG13	22:W:243:ILE:HG23	1.97	0.46
24:f:32:GLU:O	24:f:36:ALA:N	2.48	0.46
27:Y:130:LYS:CG	27:Y:131:THR:N	2.73	0.46
34:c:56:LEU:CD1	34:c:92:GLN:CD	2.88	0.46
32:l:229:VAL:O	32:l:233:LEU:CD1	2.59	0.46
13:p:164:PHE:HA	13:p:189:ILE:HD11	1.97	0.46
14:U:106:ASP:HA	14:U:109:THR:HG22	1.98	0.46
14:U:701:ILE:HG13	14:U:810:THR:HA	1.97	0.46
19:V:200:ARG:HH22	19:V:237:THR:HG22	1.81	0.46
10:s:226:VAL:HG22	10:s:231:ILE:HG12	1.97	0.46
24:f:128:VAL:CG2	24:f:129:LEU:N	2.68	0.46
25:X:225:TRP:O	25:X:261:LEU:HD23	2.16	0.46
27:Y:213:LEU:HD21	27:Y:219:PHE:HB2	1.97	0.46
27:Y:242:LYS:HE3	27:Y:242:LYS:HB3	1.71	0.46
12:F:296:PHE:HE1	12:F:298:SER:HB3	1.71	0.46
14:U:373:ASN:OD1	14:U:377:HIS:ND1	2.48	0.46
15:C:193:GLY:H	15:C:196:LYS:HD3	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:336:MET:CG	15:C:338:LEU:CD1	2.93	0.46
18:A:307:ASP:HB3	18:A:336:ARG:HE	1.79	0.46
22:W:272:LEU:HD22	22:W:305:LEU:HD11	1.98	0.46
24:f:288:VAL:HG21	24:f:872:VAL:HB	1.97	0.46
24:f:393:ASP:O	24:f:393:ASP:OD1	2.33	0.46
27:Y:134:LEU:C	27:Y:134:LEU:HD12	2.40	0.46
31:a:264:ASN:N	31:a:264:ASN:OD1	2.49	0.46
33:b:11:ASP:OD1	33:b:84:ILE:HD12	2.16	0.46
34:c:64:ASP:N	34:c:64:ASP:OD1	2.47	0.46
1:u:33:LEU:CD2	1:u:90:VAL:HG11	2.45	0.46
1:u:406:ARG:HG2	1:u:406:ARG:H	1.42	0.46
15:C:231:VAL:HG11	15:C:276:LEU:HB2	1.98	0.46
15:C:351:MET:HB3	15:C:387:VAL:CG1	2.46	0.46
27:Y:17:LEU:HA	27:Y:150:PHE:HE1	1.81	0.46
26:i:223:THR:O	26:i:223:THR:HG22	2.15	0.46
31:a:211:PHE:HD1	31:a:271:LYS:HE2	1.80	0.46
2:d:145:ARG:HG2	2:d:171:LEU:HD22	1.97	0.46
6:E:85:ARG:NH2	29:Z:165:GLU:OE2	2.47	0.46
10:S:211:ALA:HA	10:S:217:THR:HB	1.96	0.46
10:S:213:ARG:HG3	13:p:151:GLU:HG3	1.97	0.46
11:D:92:PHE:HA	11:D:103:VAL:HG23	1.97	0.46
14:U:144:ASP:HB3	14:U:146:LYS:HE2	1.97	0.46
17:q:118:MET:HE2	17:q:118:MET:HB3	1.83	0.46
18:A:133:ASP:OD1	18:A:133:ASP:N	2.39	0.46
10:s:178:ASP:OD2	13:P:177:ARG:NH2	2.48	0.46
22:W:328:LEU:HG	22:W:329:ARG:HG2	1.98	0.46
24:f:462:ALA:HB3	24:f:489:TYR:CZ	2.50	0.46
24:f:697:ILE:C	24:f:706:ILE:HG13	2.39	0.46
24:f:797:LEU:HA	24:f:800:LEU:HG	1.98	0.46
32:L:133:LEU:HD12	32:L:144:ILE:HD11	1.97	0.46
34:c:150:SER:HB2	34:c:155:VAL:HA	1.97	0.46
7:B:380:LEU:C	7:B:380:LEU:HD12	2.41	0.46
14:U:725:MET:HE2	34:c:178:THR:HB	1.96	0.46
10:s:209:SER:HG	13:P:152:SER:HG	1.64	0.46
22:W:184:GLU:HG3	22:W:222:LEU:HD11	1.97	0.46
22:W:274:VAL:CG1	22:W:283:GLN:CD	2.88	0.46
24:f:845:ARG:NH1	24:f:848:GLN:NE2	2.63	0.46
27:Y:176:ARG:HE	27:Y:177:ARG:HH12	1.64	0.46
27:Y:181:LYS:HA	27:Y:200:LEU:HD21	1.98	0.46
5:N:56:THR:O	5:N:56:THR:OG1	2.33	0.46
31:a:198:PHE:CE2	31:a:202:LEU:CD1	2.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:3:LEU:HD11	33:b:104:ASN:C	2.41	0.46
6:E:144:GLU:HB3	6:E:297:ARG:HH22	1.80	0.46
11:D:338:ARG:HH22	11:D:365:ALA:HA	1.81	0.46
14:U:269:ARG:HH11	14:U:329:LEU:HD11	1.77	0.46
15:C:301:LEU:CD1	15:C:302:ASP:OD1	2.63	0.46
18:A:72:LEU:HD12	18:A:72:LEU:HA	1.84	0.46
22:W:216:GLU:HB2	22:W:224:LEU:HG	1.98	0.46
24:f:329:ASN:HD22	24:f:421:ASP:HA	1.81	0.46
24:f:681:TYR:O	24:f:687:ARG:NH2	2.49	0.46
24:f:719:PRO:HG3	24:f:754:LYS:HA	1.97	0.46
25:X:303:GLU:O	25:X:307:THR:OG1	2.27	0.46
30:K:147:ASP:OD1	30:K:147:ASP:N	2.48	0.46
33:b:20:ASP:OD1	33:b:20:ASP:N	2.49	0.46
3:m:70:ASP:OD2	3:m:99:ARG:NH2	2.49	0.46
6:E:77:PRO:HB3	11:D:107:THR:HG22	1.97	0.46
7:B:59:ARG:O	7:B:63:LEU:N	2.40	0.46
7:B:214:MET:SD	7:B:214:MET:N	2.83	0.46
7:B:293:LYS:HD2	7:B:293:LYS:HA	1.82	0.46
13:p:111:GLY:HA2	13:p:190:ILE:HD11	1.98	0.46
15:C:144:PRO:HB2	15:C:205:HIS:HB2	1.97	0.46
18:A:347:ASP:OD1	18:A:347:ASP:N	2.49	0.46
19:V:216:ARG:HA	19:V:219:GLU:HB2	1.98	0.46
19:V:224:LEU:HD13	19:V:227:VAL:CB	2.35	0.46
19:V:253:LEU:HD23	19:V:256:ARG:HE	1.81	0.46
19:V:482:PHE:HE2	27:Y:377:LEU:HB2	1.81	0.46
19:V:484:LEU:HD11	29:Z:267:ARG:NH1	2.26	0.46
22:W:83:LEU:HB2	22:W:89:LEU:H	1.81	0.46
24:f:399:LEU:HB2	24:f:440:ILE:CG1	2.46	0.46
27:Y:88:LEU:O	27:Y:92:GLU:N	2.45	0.46
27:Y:329:PHE:CE1	27:Y:333:GLU:OE2	2.69	0.46
33:b:61:LEU:HG	33:b:62:THR:HG23	1.97	0.46
17:Q:5:ILE:HD12	17:Q:16:ALA:HB3	1.98	0.46
1:u:70:ARG:NH1	34:c:128:ASN:OD1	2.49	0.45
2:d:195:ASN:O	2:d:199:LEU:CD1	2.59	0.45
4:R:92:LYS:HA	4:R:104:MET:HE3	1.97	0.45
7:B:246:THR:HG21	7:B:277:HIS:ND1	2.31	0.45
9:o:246:ARG:HE	9:o:247:CYS:H	1.64	0.45
13:p:91:VAL:HG12	13:p:124:LEU:HD22	1.96	0.45
18:A:73:ALA:HB3	18:A:78:TRP:HB3	1.98	0.45
22:W:87:ILE:HG22	22:W:88:MET:N	2.31	0.45
16:g:22:LEU:HD12	16:g:22:LEU:C	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:76:ALA:O	27:Y:80:GLU:N	2.48	0.45
27:Y:195:LYS:H	27:Y:195:LYS:HG3	1.46	0.45
31:a:184:ASP:OD1	31:a:184:ASP:N	2.45	0.45
33:b:65:THR:CG2	33:b:67:ASP:OD1	2.64	0.45
34:c:145:VAL:HG23	34:c:157:ILE:HD13	1.98	0.45
34:c:267:PRO:HA	34:c:270:LEU:CB	2.47	0.45
2:d:165:GLU:CD	2:d:198:PHE:CZ	2.94	0.45
6:E:331:ILE:HG23	6:E:371:VAL:HG21	1.99	0.45
7:B:440:LEU:O	28:J:28:LYS:C	2.58	0.45
15:C:351:MET:HE1	15:C:354:ALA:HB3	1.97	0.45
19:V:39:GLU:OE1	19:V:65:ARG:NH2	2.49	0.45
22:W:76:GLU:O	22:W:130:MET:CE	2.64	0.45
22:W:254:PRO:HB3	22:W:262:LYS:HB2	1.98	0.45
20:t:124:ASP:OD1	20:t:124:ASP:N	2.46	0.45
23:H:185:GLU:HB2	25:X:122:ARG:HH22	1.81	0.45
26:I:250:GLU:O	26:I:254:LYS:HD2	2.17	0.45
31:a:78:GLU:HA	31:a:81:LEU:CD1	2.44	0.45
9:O:89:ALA:HB3	9:O:140:ALA:HB3	1.98	0.45
1:u:37:SER:OG	1:u:39:THR:HG22	2.16	0.45
7:B:114:GLU:HB3	7:B:122:ILE:HD11	1.99	0.45
14:U:130:LEU:C	14:U:132:GLY:N	2.75	0.45
3:M:48:PHE:HB2	3:M:215:SER:HB3	1.99	0.45
3:M:50:VAL:HG11	3:M:66:ARG:HB2	1.97	0.45
26:i:115:CYS:HB3	28:j:81:ARG:HH22	1.80	0.45
5:N:63:ARG:NH1	9:O:182:GLU:OE1	2.43	0.45
31:a:42:LEU:HD23	31:a:79:ILE:CG2	2.47	0.45
32:L:120:THR:O	32:L:120:THR:OG1	2.29	0.45
10:S:32:PRO:O	20:T:145:ARG:NH2	2.48	0.45
14:U:214:ILE:HD13	14:U:904:LYS:HB2	1.97	0.45
20:T:88:MET:HB2	20:T:88:MET:HE3	1.70	0.45
22:W:231:ILE:HB	22:W:246:HIS:CE1	2.51	0.45
20:t:171:ASP:OD1	20:t:172:MET:N	2.46	0.45
24:f:205:CYS:HA	24:f:208:LEU:HB2	1.97	0.45
24:f:385:PHE:CE2	24:f:421:ASP:OD2	2.70	0.45
24:f:555:ALA:HB1	24:f:590:PHE:CE2	2.51	0.45
25:X:222:GLU:HB2	25:X:225:TRP:HE1	1.82	0.45
23:h:73:GLY:O	23:h:136:ILE:HG13	2.16	0.45
27:Y:117:LYS:HA	27:Y:120:ALA:HB3	1.98	0.45
28:J:137:ASP:OD2	28:J:143:ARG:NH1	2.50	0.45
29:Z:282:ASN:OD1	29:Z:286:GLU:OE2	2.35	0.45
31:a:42:LEU:HD21	31:a:75:SER:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:46:GLN:O	31:a:46:GLN:HG2	2.17	0.45
31:a:84:VAL:CG1	31:a:121:LEU:HD21	2.46	0.45
13:P:164:PHE:HB2	13:P:189:ILE:HD11	1.99	0.45
9:o:44:THR:HA	9:o:76:LYS:HE3	1.98	0.45
11:D:83:GLN:CD	11:D:140:VAL:CG1	2.89	0.45
14:U:99:THR:HG21	19:V:240:LEU:HD22	1.99	0.45
19:V:268:GLU:HA	19:V:271:VAL:HG12	1.99	0.45
22:W:67:LEU:HD12	22:W:67:LEU:HA	1.84	0.45
22:W:316:ARG:O	22:W:319:THR:OG1	2.30	0.45
24:f:450:ILE:CD1	24:f:801:VAL:HG11	2.46	0.45
24:f:539:LEU:O	24:f:543:MET:CG	2.31	0.45
25:X:365:LEU:HB2	25:X:378:LEU:HD21	1.98	0.45
23:h:182:LEU:HD12	23:h:182:LEU:HA	1.88	0.45
26:i:26:GLU:OE2	26:i:26:GLU:HA	2.17	0.45
28:j:188:ILE:HA	28:j:191:VAL:HG12	1.99	0.45
2:d:92:THR:HG21	2:d:125:GLU:HG3	1.98	0.45
2:d:222:THR:OG1	2:d:223:ASN:N	2.41	0.45
3:m:161:TRP:CZ2	3:m:182:LYS:CE	2.99	0.45
4:R:78:ARG:NE	4:R:230:GLY:HA3	2.32	0.45
14:U:695:MET:HE2	14:U:709:PHE:CE2	2.48	0.45
15:C:346:LYS:O	15:C:350:LEU:HB2	2.16	0.45
17:q:3:TYR:HE2	17:q:5:ILE:HD11	1.81	0.45
19:V:145:LEU:HD13	19:V:151:THR:HG21	1.99	0.45
24:f:216:MET:O	24:f:219:LYS:HB3	2.16	0.45
24:f:286:LYS:HA	24:f:289:VAL:HG23	1.98	0.45
16:g:22:LEU:CD1	16:g:22:LEU:O	2.50	0.45
27:Y:110:TYR:CE1	27:Y:114:ILE:HD13	2.51	0.45
30:k:210:LEU:HD23	30:k:210:LEU:HA	1.86	0.45
34:c:121:TRP:CE3	34:c:122:LEU:O	2.68	0.45
5:n:207:VAL:HG23	5:n:224:LEU:HA	1.98	0.45
14:U:388:ASP:OD1	14:U:388:ASP:N	2.50	0.45
14:U:564:ASP:OD1	14:U:590:TYR:OH	2.34	0.45
14:U:769:PHE:HB3	14:U:776:SER:HB2	1.98	0.45
16:G:21:ARG:HD3	16:G:23:TYR:CE1	2.50	0.45
16:G:158:GLY:O	23:H:84:ARG:NH2	2.50	0.45
19:V:89:LYS:HD3	19:V:92:ARG:HH12	1.82	0.45
19:V:201:ARG:HD2	19:V:244:ALA:HB3	1.99	0.45
20:t:86:ARG:HH21	20:t:99:SER:HA	1.81	0.45
24:f:98:PHE:HA	24:f:102:HIS:CE1	2.51	0.45
24:f:600:TYR:HE1	24:f:603:SER:HG	1.64	0.45
24:f:805:ASP:O	24:f:807:ARG:NH2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:108:THR:HG22	28:J:133:ILE:HG13	1.99	0.45
31:a:221:VAL:O	31:a:221:VAL:HG23	2.17	0.45
6:E:142:ILE:HD13	6:E:142:ILE:HA	1.89	0.45
6:E:223:ARG:HE	6:E:270:LEU:HD23	1.82	0.45
14:U:539:THR:HG22	14:U:541:HIS:HD2	1.82	0.45
16:G:50:ILE:O	16:G:217:VAL:HA	2.16	0.45
17:q:166:GLU:CD	17:q:166:GLU:C	2.85	0.45
10:s:52:ALA:HB1	10:s:221:LEU:HD11	1.98	0.45
22:W:3:ASP:OD1	22:W:3:ASP:N	2.48	0.45
24:f:287:ASP:OD1	24:f:320:ILE:HD13	2.16	0.45
23:h:203:MET:HE3	23:h:208:ILE:HD13	1.98	0.45
29:Z:43:TRP:CE3	29:Z:43:TRP:O	2.70	0.45
31:a:289:ARG:CG	31:a:333:MET:CB	2.92	0.45
31:a:328:ASP:HB2	31:a:330:ARG:HD3	1.99	0.45
4:R:58:HIS:CD2	4:R:108:ALA:HB2	2.52	0.45
4:R:181:SER:OG	4:R:182:GLY:N	2.49	0.45
5:n:195:ALA:HA	5:n:198:MET:HE2	1.99	0.45
6:E:102:MET:HE2	6:E:102:MET:HB3	1.74	0.45
7:B:152:LEU:HD22	7:B:159:VAL:CG1	2.47	0.45
14:U:229:VAL:HA	14:U:232:ILE:HG12	1.99	0.45
15:C:119:ASP:OD1	15:C:120:SER:N	2.46	0.45
17:q:3:TYR:CE2	17:q:5:ILE:HD11	2.52	0.45
10:s:99:ARG:HD3	10:s:123:ILE:HD11	1.99	0.45
22:W:76:GLU:HG3	22:W:130:MET:SD	2.56	0.45
22:W:371:THR:OG1	31:a:325:ASP:OD1	2.34	0.45
23:H:105:ILE:HG12	23:H:110:LEU:HD13	1.97	0.45
24:f:682:GLY:HA3	24:f:687:ARG:HH21	1.80	0.45
25:X:306:LEU:O	25:X:310:ARG:NH1	2.50	0.45
27:Y:100:ILE:HD12	27:Y:100:ILE:HA	1.86	0.45
3:m:129:ARG:HB3	32:l:11:THR:HG23	1.98	0.45
5:n:221:GLN:NE2	5:n:223:LEU:HD21	2.22	0.45
9:o:186:ARG:NH2	9:o:193:GLU:OE1	2.46	0.45
12:F:195:ILE:HD12	12:F:195:ILE:HA	1.88	0.45
14:U:108:TYR:OH	14:U:159:ARG:NE	2.50	0.45
14:U:746:ILE:HG13	14:U:783:TYR:CD1	2.52	0.45
17:q:102:LEU:HD13	17:q:103:LEU:HD12	1.99	0.45
18:A:368:ILE:HD11	18:A:409:PHE:CE2	2.30	0.45
4:r:243:TRP:O	4:r:243:TRP:CE3	2.70	0.45
22:W:82:LEU:HB3	22:W:90:LEU:HD21	1.98	0.45
24:f:126:ILE:HA	24:f:131:MET:HB2	1.99	0.45
28:j:221:ASN:OD1	28:j:221:ASN:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:58:CYS:SG	33:b:88:THR:OG1	2.73	0.45
34:c:62:VAL:HG13	34:c:63:ASP:OD1	2.17	0.45
2:d:94:MET:HE3	2:d:121:LEU:HB2	1.99	0.44
2:d:168:MET:SD	2:d:171:LEU:HD12	2.57	0.44
4:R:174:ASP:HB2	4:R:178:ASN:HB2	1.98	0.44
7:B:233:THR:HG22	7:B:285:ASP:OD2	2.17	0.44
11:D:203:LEU:HD13	11:D:309:MET:HG2	1.99	0.44
22:W:263:TRP:HH2	22:W:298:GLU:HG3	1.81	0.44
25:X:292:GLN:HA	25:X:295:LYS:HE2	1.99	0.44
16:g:191:PHE:CD1	16:g:195:VAL:HG23	2.52	0.44
26:i:246:LYS:HA	26:i:246:LYS:HD2	1.80	0.44
29:Z:235:ASN:CG	31:a:289:ARG:HH12	2.25	0.44
30:k:101:PHE:CD1	30:k:101:PHE:O	2.70	0.44
7:B:122:ILE:O	7:B:122:ILE:HG13	2.17	0.44
9:o:72:LYS:NZ	13:p:151:GLU:OE2	2.48	0.44
9:o:110:SER:HB3	9:o:117:PRO:HG3	1.99	0.44
11:D:204:MET:HG2	11:D:331:ILE:CD1	2.48	0.44
12:F:84:LYS:HZ1	12:F:139:LEU:HD12	1.82	0.44
12:F:303:ASP:OD1	12:F:303:ASP:N	2.45	0.44
14:U:401:LYS:HE3	14:U:438:GLN:HE22	1.83	0.44
14:U:545:LEU:HB3	14:U:577:ILE:HG21	1.98	0.44
17:q:30:ASP:OD1	17:q:30:ASP:N	2.49	0.44
19:V:33:GLN:NE2	19:V:84:LYS:O	2.50	0.44
22:W:317:TRP:CZ2	22:W:321:VAL:CG2	3.00	0.44
20:t:169:TYR:O	20:t:176:ALA:HA	2.16	0.44
24:f:405:HIS:ND1	24:f:406:GLY:N	2.65	0.44
24:f:411:ALA:CB	24:f:443:GLY:HA3	2.39	0.44
27:Y:134:LEU:HD12	27:Y:135:GLY:N	2.32	0.44
3:M:84:ASP:OD1	32:L:117:GLN:NE2	2.49	0.44
28:J:91:CYS:SG	28:J:102:VAL:CG2	3.04	0.44
14:U:320:ASP:OD1	14:U:320:ASP:N	2.49	0.44
14:U:661:ALA:HB1	14:U:693:LEU:HD21	2.00	0.44
15:C:352:PRO:HD2	15:C:391:MET:HE2	1.99	0.44
17:q:171:PHE:O	17:Q:27:GLN:NE2	2.51	0.44
17:Q:3:TYR:CE2	17:Q:5:ILE:HD11	2.45	0.44
2:d:341:GLU:CD	2:d:341:GLU:C	2.84	0.44
5:n:38:MET:SD	5:n:161:ILE:CG2	3.02	0.44
6:E:101:ASP:OD2	6:E:106:THR:OG1	2.29	0.44
8:e:60:LEU:HD12	27:Y:329:PHE:CD1	2.49	0.44
9:o:203:ALA:HA	9:o:206:ILE:HD12	1.98	0.44
14:U:640:LEU:HD13	14:U:648:VAL:CG1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:r:181:SER:OG	4:r:182:GLY:N	2.50	0.44
19:V:92:ARG:O	19:V:96:ARG:NH1	2.50	0.44
24:f:246:SER:OG	24:f:247:ALA:N	2.51	0.44
24:f:266:LEU:HG	24:f:569:LYS:NZ	2.33	0.44
24:f:408:LEU:HD11	24:f:439:TYR:CD1	2.45	0.44
23:h:213:CYS:HB2	23:h:218:PHE:HD1	1.81	0.44
31:a:77:VAL:O	31:a:81:LEU:HG	2.18	0.44
6:E:40:TYR:HA	12:F:73:ILE:CD1	2.47	0.44
7:B:56:THR:OG1	7:B:57:GLN:N	2.49	0.44
9:o:102:ILE:HD12	9:o:125:MET:HB3	1.99	0.44
11:D:193:GLN:HE21	15:C:376:VAL:HG21	1.82	0.44
12:F:100:ASP:OD1	12:F:100:ASP:N	2.48	0.44
14:U:139:GLN:HA	14:U:142:LEU:HD12	1.99	0.44
14:U:236:LEU:HD11	14:U:244:MET:HG3	1.99	0.44
14:U:756:HIS:CE1	14:U:758:PRO:HD2	2.52	0.44
19:V:213:TYR:O	19:V:216:ARG:HB2	2.17	0.44
22:W:366:MET:HE1	22:W:378:MET:CE	2.46	0.44
24:f:204:ALA:HA	24:f:207:LEU:HD12	1.99	0.44
24:f:330:PHE:HD1	24:f:330:PHE:HA	1.68	0.44
24:f:600:TYR:HE1	24:f:603:SER:HB2	1.82	0.44
24:f:639:LYS:HD3	24:f:639:LYS:HA	1.74	0.44
25:X:382:GLU:N	25:X:382:GLU:OE2	2.50	0.44
23:h:212:ILE:CG2	23:h:213:CYS:N	2.80	0.44
27:Y:23:ARG:O	27:Y:27:SER:CB	2.65	0.44
9:O:155:SER:HB3	9:O:168:VAL:HG11	1.99	0.44
3:m:56:LYS:HD2	32:l:157:ARG:HD2	1.99	0.44
6:E:388:PRO:HG2	11:D:409:LYS:NZ	2.33	0.44
7:B:234:LEU:CD1	35:B:501:ADP:H2'	2.48	0.44
12:F:250:LYS:HD3	18:A:309:PHE:CE2	2.50	0.44
24:f:333:LEU:HD12	24:f:333:LEU:HA	1.88	0.44
24:f:387:GLN:HG3	24:f:389:LYS:HG3	2.00	0.44
16:g:71:LYS:HE3	16:g:74:GLU:HA	1.99	0.44
27:Y:117:LYS:O	27:Y:121:LEU:HB2	2.17	0.44
17:Q:118:MET:HE2	17:Q:124:LEU:HD13	2.00	0.44
30:k:67:ILE:HD13	30:k:218:ALA:HB2	1.99	0.44
34:c:119:GLY:CA	34:c:121:TRP:HD1	2.31	0.44
32:l:7:ASP:OD1	32:l:7:ASP:N	2.35	0.44
2:d:215:LEU:HD12	2:d:219:ASP:HB3	1.99	0.44
2:d:288:THR:HG21	2:d:295:THR:CG2	2.47	0.44
7:B:199:GLU:O	7:B:211:TYR:OH	2.35	0.44
9:o:49:VAL:CG2	9:o:181:PHE:CZ	3.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:83:GLN:OE1	11:D:140:VAL:HG12	2.17	0.44
15:C:376:VAL:O	15:C:376:VAL:HG12	2.17	0.44
18:A:101:ILE:CD1	18:A:140:VAL:HG21	2.47	0.44
22:W:169:LEU:HD11	22:W:170:GLN:HE21	1.82	0.44
24:f:198:HIS:CE1	24:f:238:ASN:HB3	2.52	0.44
24:f:330:PHE:O	24:f:334:ALA:N	2.39	0.44
25:X:374:PHE:HE2	25:X:385:LEU:HD21	1.83	0.44
3:M:109:LEU:HD11	3:M:138:LEU:HB3	1.98	0.44
26:i:185:THR:OG1	26:i:186:LEU:N	2.51	0.44
34:c:258:ALA:O	34:c:262:GLU:OE2	2.36	0.44
2:d:191:LEU:HA	2:d:194:LEU:HD12	1.98	0.44
2:d:207:GLU:O	2:d:211:GLU:CB	2.65	0.44
3:m:66:LEU:HD23	3:m:66:LEU:HA	1.81	0.44
3:m:77:VAL:HG11	3:m:84:ALA:HB1	1.99	0.44
15:C:166:GLU:OE1	15:C:170:LYS:NZ	2.49	0.44
15:C:351:MET:CE	15:C:354:ALA:HB3	2.48	0.44
22:W:103:LYS:HB3	22:W:103:LYS:HE3	1.77	0.44
22:W:133:GLU:OE1	22:W:135:LYS:HD3	2.18	0.44
24:f:568:GLY:H	24:f:600:TYR:HA	1.82	0.44
24:f:607:LEU:HA	24:f:610:GLN:HG2	1.99	0.44
24:f:694:LEU:HD11	24:f:710:LEU:HB2	1.99	0.44
31:a:172:TYR:O	31:a:176:ALA:CB	2.66	0.44
33:b:9:CYS:SG	33:b:111:ALA:HA	2.58	0.44
33:b:179:LEU:HG	33:b:181:ASP:H	1.82	0.44
6:E:160:GLN:CD	6:E:160:GLN:C	2.85	0.44
7:B:59:ARG:H	24:f:184:LEU:HD21	1.82	0.44
11:D:212:LYS:NZ	36:D:501:ATP:O1G	2.51	0.44
14:U:69:TYR:O	14:U:69:TYR:CG	2.70	0.44
22:W:274:VAL:HG13	22:W:283:GLN:CD	2.43	0.44
22:W:274:VAL:HG11	22:W:287:VAL:HG12	1.99	0.44
27:Y:387:ILE:CD1	29:Z:276:ILE:CG2	2.94	0.44
28:j:139:ASP:OD1	28:j:139:ASP:N	2.51	0.44
31:a:42:LEU:HD11	31:a:75:SER:HB2	2.00	0.44
17:Q:38:MET:HE3	17:Q:64:VAL:HG21	2.00	0.44
34:c:37:ALA:O	34:c:41:MET:HB2	2.18	0.44
2:d:288:THR:HG21	2:d:295:THR:HG22	2.00	0.43
5:n:196:LEU:HD21	5:n:230:LYS:CB	2.48	0.43
5:n:233:VAL:CG2	20:T:82:ARG:HH21	2.08	0.43
7:B:78:PHE:O	7:B:82:GLN:N	2.50	0.43
7:B:234:LEU:HD22	35:B:501:ADP:N9	2.33	0.43
7:B:234:LEU:HD13	35:B:501:ADP:C2'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:256:ILE:O	7:B:257:GLN:NE2	2.51	0.43
11:D:229:ARG:NE	11:D:229:ARG:O	2.50	0.43
12:F:195:ILE:HD13	12:F:236:LEU:HD22	1.99	0.43
13:p:20:VAL:HG21	13:p:119:PRO:CB	2.44	0.43
14:U:542:GLU:HG2	14:U:543:LYS:N	2.32	0.43
15:C:383:PHE:O	15:C:387:VAL:HG23	2.18	0.43
22:W:274:VAL:HG11	22:W:287:VAL:CG1	2.48	0.43
24:f:227:ALA:HB1	24:f:231:LEU:HD23	2.00	0.43
24:f:522:CYS:HA	24:f:525:ILE:HG12	2.00	0.43
24:f:652:VAL:HG11	24:f:686:LEU:CD2	2.41	0.43
24:f:845:ARG:NH1	24:f:860:LYS:HE2	2.33	0.43
25:X:297:ARG:O	25:X:334:ASN:ND2	2.41	0.43
16:g:50:ILE:HD11	16:g:69:LEU:HD11	2.00	0.43
26:I:102:GLN:HG3	17:Q:82:ASN:HD22	1.83	0.43
17:Q:11:ASP:N	17:Q:11:ASP:OD1	2.48	0.43
3:m:34:SER:HB2	3:m:52:LEU:HD21	2.00	0.43
5:n:48:LEU:HD21	5:n:135:ALA:HB3	2.00	0.43
5:n:191:ALA:HB1	5:n:228:ILE:HD12	1.92	0.43
7:B:440:LEU:H	7:B:440:LEU:HG	1.37	0.43
10:S:83:SER:OG	10:S:84:GLY:N	2.51	0.43
11:D:214:MET:O	11:D:218:ALA:N	2.51	0.43
18:A:125:LEU:HA	18:A:149:ILE:HB	1.99	0.43
18:A:213:LEU:HB2	18:A:337:LEU:HD22	2.00	0.43
18:A:354:ILE:O	18:A:358:HIS:HB2	2.18	0.43
22:W:155:GLN:CG	22:W:158:ASP:OD2	2.66	0.43
24:f:414:LEU:CD1	24:f:432:TYR:HE2	2.29	0.43
24:f:600:TYR:CE1	24:f:603:SER:HB2	2.54	0.43
24:f:828:ARG:HH12	24:f:863:THR:HG1	1.62	0.43
24:f:845:ARG:NH1	24:f:860:LYS:HZ1	2.16	0.43
25:X:172:LEU:HA	25:X:175:LYS:HG2	2.00	0.43
27:Y:82:LYS:H	27:Y:82:LYS:HG2	1.49	0.43
27:Y:140:ILE:HD12	27:Y:140:ILE:HA	1.86	0.43
3:M:82:LEU:HD23	3:M:82:LEU:HA	1.89	0.43
28:j:187:THR:O	28:j:191:VAL:HG12	2.18	0.43
34:c:104:ARG:HA	34:c:105:PRO:HD3	1.90	0.43
7:B:440:LEU:O	28:J:29:GLY:N	2.50	0.43
11:D:59:GLU:OE1	14:U:600:ARG:HD3	2.17	0.43
11:D:125:LYS:HG3	11:D:126:PRO:HD3	2.00	0.43
12:F:435:LEU:HD22	30:K:20:ARG:HE	1.83	0.43
14:U:41:SER:O	14:U:44:LYS:HB2	2.18	0.43
15:C:187:LEU:HD12	15:C:314:LYS:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:267:SER:O	15:C:267:SER:OG	2.31	0.43
18:A:151:ILE:HD12	18:A:152:PRO:HD2	2.00	0.43
19:V:134:PHE:HA	19:V:137:GLU:HB2	2.00	0.43
22:W:349:LYS:HE3	22:W:349:LYS:HB3	1.82	0.43
24:f:372:LEU:HD23	24:f:744:MET:HG3	1.99	0.43
24:f:774:GLY:O	24:f:778:LEU:N	2.46	0.43
16:g:208:ILE:CD1	16:g:210:PHE:CD2	2.91	0.43
3:M:24:VAL:CG1	3:M:124:THR:CG2	2.96	0.43
29:Z:8:LYS:CG	29:Z:159:THR:HB	2.30	0.43
33:b:22:LEU:HD12	33:b:28:ALA:HB2	1.99	0.43
2:d:223:ASN:O	2:d:227:LYS:N	2.52	0.43
14:U:24:LEU:HB3	14:U:56:SER:OG	2.17	0.43
15:C:274:LEU:O	15:C:277:LEU:HB2	2.19	0.43
24:f:508:SER:O	24:f:508:SER:OG	2.30	0.43
24:f:764:LEU:HG	24:f:775:THR:HG23	2.00	0.43
26:I:86:LEU:HD21	26:I:130:PHE:CD2	2.53	0.43
3:M:78:VAL:HG12	3:M:136:PHE:HB3	1.99	0.43
3:M:190:ILE:HD12	3:M:190:ILE:HA	1.92	0.43
30:K:224:GLN:OE1	30:K:225:ASN:N	2.51	0.43
31:a:289:ARG:O	31:a:291:LEU:HD12	2.18	0.43
31:a:312:MET:O	31:a:316:SER:N	2.51	0.43
32:l:109:VAL:HG22	32:l:134:ILE:HD13	1.99	0.43
2:d:175:TYR:CE2	2:d:188:MET:CE	3.00	0.43
2:d:251:ILE:HD12	2:d:255:SER:O	2.18	0.43
7:B:74:MET:HE2	7:B:74:MET:HB2	1.77	0.43
11:D:300:ASP:OD1	11:D:303:VAL:N	2.46	0.43
11:D:385:LEU:HD23	11:D:398:ASP:HA	2.01	0.43
13:p:14:MET:HE3	13:p:14:MET:HB2	1.86	0.43
14:U:15:ASP:N	14:U:15:ASP:OD1	2.50	0.43
16:G:200:THR:HA	16:G:203:SER:HB2	1.99	0.43
16:G:239:LEU:HD23	16:G:239:LEU:HA	1.88	0.43
22:W:357:ARG:HD3	22:W:357:ARG:HA	1.86	0.43
25:X:170:GLN:HB3	25:X:193:ALA:HB2	2.01	0.43
25:X:319:ILE:HD12	25:X:319:ILE:HA	1.90	0.43
23:h:110:LEU:HD21	23:h:136:ILE:HD11	1.99	0.43
27:Y:186:LEU:CG	27:Y:187:TYR:N	2.80	0.43
27:Y:231:LEU:HD22	27:Y:234:PRO:CG	2.48	0.43
28:J:13:ASP:OD2	28:J:15:HIS:NE2	2.51	0.43
31:a:127:ASP:O	31:a:131:THR:OG1	2.37	0.43
17:Q:171:PHE:CE2	17:Q:173:LEU:HB2	2.53	0.43
30:k:167:ALA:HB1	30:k:181:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:56:LEU:HD11	34:c:92:GLN:CD	2.43	0.43
1:u:75:HIS:ND1	1:u:88:PHE:CE2	2.76	0.43
2:d:198:PHE:CD2	2:d:199:LEU:HD12	2.54	0.43
7:B:249:ARG:HG3	7:B:283:PHE:HD2	1.84	0.43
7:B:259:TYR:HD2	18:A:248:LYS:HE2	1.83	0.43
9:o:124:ARG:CG	9:o:128:GLN:HE21	2.16	0.43
12:F:79:LYS:HA	12:F:79:LYS:HD3	1.77	0.43
12:F:224:LEU:HB2	12:F:348:LEU:HG	2.00	0.43
14:U:746:ILE:HG12	14:U:782:ALA:O	2.19	0.43
19:V:64:GLN:O	19:V:67:LEU:HB2	2.18	0.43
19:V:127:THR:O	19:V:127:THR:CG2	2.62	0.43
10:s:107:ASN:HD21	30:k:111:SER:CB	2.31	0.43
22:W:219:THR:HG21	22:W:222:LEU:HD23	2.00	0.43
24:f:202:HIS:CE1	24:f:241:PRO:HB2	2.54	0.43
24:f:414:LEU:HD13	24:f:432:TYR:CE2	2.49	0.43
24:f:463:LEU:N	24:f:489:TYR:OH	2.49	0.43
24:f:649:HIS:HA	24:f:652:VAL:HG22	1.99	0.43
23:h:22:ILE:HD12	23:h:152:SER:HA	2.00	0.43
28:J:198:VAL:O	28:J:200:GLN:N	2.52	0.43
30:k:42:THR:HG22	30:k:44:GLU:H	1.84	0.43
2:d:209:HIS:CE1	19:V:397:ARG:HD3	2.53	0.43
4:R:71:VAL:HB	4:R:238:VAL:HB	2.01	0.43
7:B:234:LEU:O	7:B:237:LYS:N	2.52	0.43
7:B:301:GLY:HA2	7:B:304:GLU:HB3	2.00	0.43
7:B:412:MET:SD	7:B:412:MET:N	2.82	0.43
12:F:105:GLU:HG2	12:F:116:GLN:HE22	1.83	0.43
15:C:336:MET:CB	15:C:338:LEU:CD1	2.95	0.43
22:W:166:LEU:CD2	22:W:201:ARG:CD	2.81	0.43
20:t:95:MET:HE2	20:t:237:VAL:HG13	2.01	0.43
24:f:420:TRP:HZ2	24:f:806:VAL:O	2.02	0.43
25:X:103:THR:HA	25:X:106:GLU:HG3	2.00	0.43
25:X:207:GLN:HA	25:X:210:LEU:HD12	2.01	0.43
26:i:119:GLN:HA	26:i:122:THR:HG22	2.01	0.43
34:c:223:LYS:HB2	34:c:223:LYS:HE2	1.78	0.43
3:m:126:SER:OG	16:g:130:GLU:OE1	2.31	0.43
12:F:95:GLU:HA	12:F:147:PRO:HG3	2.00	0.43
18:A:41:TYR:HB2	18:A:44:GLN:HE21	1.84	0.43
18:A:368:ILE:CG1	18:A:409:PHE:CE2	3.02	0.43
19:V:204:ASP:HA	19:V:207:ALA:HB3	2.00	0.43
22:W:231:ILE:CG1	22:W:243:ILE:CG2	2.97	0.43
23:H:48:THR:OG1	23:H:49:GLU:N	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:f:828:ARG:O	24:f:861:THR:N	2.39	0.43
27:Y:19:ILE:O	27:Y:23:ARG:CB	2.67	0.43
28:J:115:LYS:HG3	28:J:127:PHE:HD2	1.84	0.43
2:d:161:ILE:HG23	2:d:162:PRO:HD3	2.01	0.43
4:R:61:THR:O	4:R:219:ILE:HD11	2.18	0.43
6:E:40:TYR:CA	12:F:73:ILE:CD1	2.93	0.43
19:V:139:MET:HA	19:V:143:ALA:HB3	2.01	0.43
24:f:547:GLU:C	24:f:548:THR:HG23	2.44	0.43
24:f:828:ARG:HH21	24:f:842:VAL:HB	1.84	0.43
24:f:845:ARG:O	24:f:847:GLY:N	2.51	0.43
2:d:274:CYS:HB2	19:V:443:ARG:HD3	2.00	0.43
5:n:196:LEU:HD11	5:N:175:ALA:HB2	2.00	0.43
6:E:109:ARG:HH21	12:F:114:ASP:HA	1.84	0.43
7:B:99:VAL:HA	7:B:102:LEU:HB3	2.00	0.43
12:F:291:ILE:HG23	12:F:291:ILE:O	2.19	0.43
15:C:171:HIS:HB3	15:C:174:LEU:HB2	2.01	0.43
15:C:276:LEU:O	15:C:280:LEU:N	2.50	0.43
4:r:88:GLN:HE21	4:r:88:GLN:HB3	1.64	0.43
10:s:56:ARG:HB2	10:s:218:GLY:HA3	2.00	0.43
10:s:164:LYS:HD2	10:s:164:LYS:HA	1.85	0.43
22:W:421:PRO:HG3	29:Z:251:LEU:HD23	2.00	0.43
24:f:718:ASP:HB2	24:f:760:PHE:CD1	2.53	0.43
24:f:850:VAL:HG13	24:f:852:VAL:CG2	2.34	0.43
27:Y:157:ILE:HG21	27:Y:186:LEU:CD1	2.43	0.43
27:Y:184:GLN:CB	27:Y:201:PHE:CZ	2.95	0.43
32:L:73:SER:OG	32:L:74:ILE:N	2.52	0.43
34:c:54:MET:HE1	34:c:111:TRP:HE3	1.84	0.43
1:u:32:SER:HA	1:u:46:ALA:HA	2.01	0.42
3:m:56:LYS:HE2	32:l:176:MET:HE1	2.01	0.42
9:o:127:LYS:HD3	9:o:162:THR:HG22	2.00	0.42
24:f:791:VAL:HA	24:f:796:LEU:HB2	2.01	0.42
24:f:850:VAL:HG12	24:f:852:VAL:HG22	1.96	0.42
25:X:134:VAL:HG12	25:X:172:LEU:HD21	2.01	0.42
25:X:306:LEU:CD1	25:X:323:LEU:HD11	2.45	0.42
26:I:134:LEU:HD11	26:I:136:TYR:CE2	2.49	0.42
29:Z:33:LYS:HA	29:Z:33:LYS:HD2	1.58	0.42
31:a:217:LEU:HD21	31:a:237:LEU:HB3	2.01	0.42
30:k:198:SER:HA	30:k:201:ILE:HG22	2.00	0.42
34:c:216:MET:HE3	34:c:216:MET:HB3	1.90	0.42
32:l:196:ARG:NH1	32:l:238:GLU:O	2.52	0.42
6:E:216:ARG:HH21	11:D:234:GLU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:343:ARG:HH12	36:A:501:ATP:H5'1	1.83	0.42
11:D:39:ASP:N	11:D:39:ASP:OD1	2.50	0.42
13:p:73:LEU:HG	26:i:95:GLN:HG3	2.00	0.42
14:U:224:ASP:CG	14:U:224:ASP:O	2.62	0.42
18:A:124:ASP:OD1	18:A:125:LEU:N	2.50	0.42
18:A:265:ARG:NH2	18:A:305:GLN:OE1	2.51	0.42
19:V:361:PHE:HA	19:V:364:THR:HG22	2.01	0.42
19:V:426:LEU:HG	19:V:426:LEU:O	2.19	0.42
10:s:219:ASP:O	10:s:238:LEU:N	2.52	0.42
22:W:294:LYS:HA	22:W:294:LYS:HD2	1.87	0.42
26:I:10:THR:HG23	28:J:125:ARG:HB2	2.01	0.42
26:I:236:LEU:HD23	26:I:236:LEU:HA	1.90	0.42
28:J:11:SER:OG	28:J:13:ASP:OD1	2.30	0.42
26:i:108:GLU:OE2	28:j:57:ARG:NH2	2.43	0.42
26:i:213:ILE:HG22	26:i:228:LEU:HD13	2.01	0.42
30:K:76:CYS:HA	30:K:142:LEU:O	2.19	0.42
28:j:31:THR:HG21	28:j:197:GLU:CB	2.48	0.42
28:j:79:ASP:OD2	28:j:125:ARG:NH2	2.53	0.42
28:j:144:LEU:C	28:j:144:LEU:HD12	2.44	0.42
32:L:84:LEU:O	32:L:88:MET:HG2	2.20	0.42
34:c:63:ASP:OD1	34:c:63:ASP:N	2.52	0.42
2:d:178:TYR:OH	14:U:2:ILE:CG1	2.63	0.42
2:d:271:ILE:C	2:d:274:CYS:SG	3.02	0.42
6:E:125:GLU:HG2	12:F:321:GLN:NE2	2.34	0.42
11:D:183:LEU:HD21	15:C:374:ARG:HH12	1.82	0.42
12:F:172:VAL:HG21	12:F:270:ASP:HB3	2.01	0.42
12:F:276:LYS:HA	12:F:276:LYS:HD2	1.86	0.42
14:U:2:ILE:CG2	14:U:2:ILE:O	2.64	0.42
14:U:157:THR:O	14:U:157:THR:OG1	2.36	0.42
14:U:210:LYS:HA	14:U:210:LYS:HD2	1.75	0.42
14:U:324:LYS:HA	14:U:327:LYS:HD3	2.00	0.42
14:U:424:ALA:HA	14:U:427:LEU:HG	2.02	0.42
22:W:317:TRP:CE3	22:W:321:VAL:CG2	3.02	0.42
22:W:393:LEU:HD23	22:W:393:LEU:C	2.44	0.42
16:g:10:ASP:OD1	16:g:11:ARG:HG3	2.19	0.42
26:I:229:LYS:N	26:I:232:GLU:OE2	2.52	0.42
30:k:234:LEU:C	30:k:234:LEU:HD12	2.44	0.42
1:u:403:ARG:CA	1:u:406:ARG:CG	2.94	0.42
4:r:184:THR:HB	4:r:198:MET:HE3	2.01	0.42
22:W:170:GLN:O	22:W:173:THR:OG1	2.28	0.42
23:H:189:HIS:HD2	25:X:124:PHE:CG	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:f:290:VAL:HG22	24:f:321:MET:HG2	2.01	0.42
26:I:44:LEU:CD1	26:I:213:ILE:HG22	2.44	0.42
27:Y:186:LEU:O	27:Y:189:VAL:N	2.51	0.42
27:Y:207:THR:HA	27:Y:216:TYR:CZ	2.55	0.42
30:K:119:LEU:O	30:K:133:MET:HE1	2.19	0.42
31:a:298:LYS:HA	31:a:298:LYS:HD2	1.92	0.42
17:Q:53:THR:HG22	17:Q:100:VAL:HG22	2.01	0.42
30:k:101:PHE:O	30:k:101:PHE:CG	2.70	0.42
32:l:50:LYS:HB3	32:l:59:HIS:HB3	2.01	0.42
1:u:38:THR:HG23	1:u:39:THR:N	2.34	0.42
1:u:385:ASN:CG	24:f:434:TYR:CD1	2.97	0.42
7:B:346:ARG:NH2	36:A:501:ATP:O1G	2.43	0.42
11:D:415:GLU:HG3	16:G:159:TYR:CZ	2.55	0.42
12:F:331:ALA:C	12:F:332:THR:HG23	2.44	0.42
14:U:912:ILE:HD12	14:U:914:LEU:HD21	2.01	0.42
15:C:187:LEU:CD1	15:C:314:LYS:CD	2.84	0.42
20:T:137:LEU:HD23	20:T:157:ILE:HD11	2.01	0.42
22:W:15:LYS:H	22:W:15:LYS:HG2	1.70	0.42
23:H:86:LEU:HD13	23:H:134:LEU:HD11	2.00	0.42
24:f:39:LYS:HD2	24:f:85:SER:HB2	2.00	0.42
24:f:689:ALA:HA	24:f:692:LEU:HD12	2.01	0.42
24:f:769:THR:OG1	24:f:769:THR:O	2.36	0.42
24:f:845:ARG:HD3	24:f:860:LYS:HE2	2.01	0.42
16:g:50:ILE:HD11	16:g:69:LEU:CD1	2.50	0.42
16:g:78:CYS:HA	16:g:139:ILE:O	2.20	0.42
3:M:241:LYS:HA	3:M:241:LYS:HD2	1.83	0.42
28:J:89:VAL:HG22	17:Q:66:LEU:HD21	2.02	0.42
5:N:52:SER:HB2	5:N:65:THR:H	1.85	0.42
30:K:203:LYS:HA	30:K:203:LYS:HD2	1.78	0.42
5:n:104:LEU:HD23	5:n:104:LEU:HA	1.94	0.42
12:F:72:LYS:H	12:F:72:LYS:HG2	1.62	0.42
14:U:146:LYS:H	14:U:146:LYS:HG2	1.69	0.42
14:U:165:LYS:O	14:U:169:GLU:N	2.53	0.42
14:U:714:SER:HA	14:U:717:ILE:HG22	2.00	0.42
20:T:96:LEU:HD13	20:T:157:ILE:HG13	2.00	0.42
23:H:148:GLN:OE1	23:H:158:TRP:NE1	2.52	0.42
24:f:306:GLU:CA	24:f:314:TYR:CE1	3.02	0.42
24:f:482:ILE:HD13	24:f:518:THR:HA	2.01	0.42
31:a:27:GLU:O	31:a:31:LYS:NZ	2.46	0.42
13:P:12:MET:HG2	13:P:171:MET:HE2	2.00	0.42
3:m:160:TYR:HB3	3:m:162:GLY:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:233:THR:N	35:B:501:ADP:O1A	2.51	0.42
18:A:165:GLN:HE22	18:A:267:LYS:HZ2	1.64	0.42
18:A:365:GLU:HB3	18:A:406:GLU:HG2	2.01	0.42
20:T:95:MET:HE3	20:T:95:MET:HB2	1.78	0.42
24:f:370:MET:CE	24:f:747:GLN:NE2	2.56	0.42
16:g:114:LEU:HD23	16:g:114:LEU:HA	1.93	0.42
26:I:68:LEU:HD11	26:I:72:MET:HB2	2.01	0.42
29:Z:259:VAL:HG13	34:c:291:LEU:HD13	2.00	0.42
30:K:184:VAL:O	30:K:184:VAL:HG13	2.19	0.42
31:a:138:VAL:O	31:a:142:LEU:N	2.52	0.42
17:Q:2:GLU:OE1	17:Q:2:GLU:N	2.53	0.42
3:m:123:THR:O	3:m:123:THR:OG1	2.33	0.42
5:n:35:THR:N	5:n:204:SER:OG	2.45	0.42
14:U:557:TYR:HE1	14:U:588:MET:HE1	1.85	0.42
15:C:188:LEU:N	15:C:293:MET:O	2.51	0.42
17:q:68:LYS:HE2	17:q:74:GLU:HG2	2.01	0.42
10:s:151:SER:HB3	10:s:164:LYS:HG3	2.00	0.42
22:W:263:TRP:HZ2	22:W:295:LYS:HB3	1.85	0.42
25:X:354:ILE:O	25:X:354:ILE:HG22	2.19	0.42
26:I:25:MET:HE2	26:I:151:ASP:HB3	2.00	0.42
30:K:47:CYS:SG	30:K:195:ILE:HG12	2.60	0.42
9:O:140:ALA:HB1	9:O:170:MET:HE3	2.01	0.42
34:c:28:ALA:HA	34:c:175:ARG:HH12	1.84	0.42
34:c:282:ARG:NH1	34:c:282:ARG:O	2.53	0.42
32:l:41:LYS:HB2	32:l:41:LYS:HE3	1.85	0.42
1:u:407:LYS:HE2	1:u:411:ASP:OD2	2.20	0.42
3:m:37:ILE:HD11	3:m:193:VAL:HG13	2.02	0.42
6:E:151:LEU:HD23	6:E:151:LEU:HA	1.91	0.42
7:B:107:MET:HB3	7:B:151:LEU:HD13	2.01	0.42
13:p:3:ILE:HG21	13:p:104:TYR:CD1	2.55	0.42
14:U:246:TYR:HE1	14:U:913:ILE:HD13	1.85	0.42
15:C:226:GLU:O	15:C:230:MET:N	2.52	0.42
22:W:82:LEU:O	22:W:82:LEU:HD23	2.20	0.42
24:f:324:VAL:HA	24:f:455:VAL:CG1	2.49	0.42
25:X:74:ARG:O	25:X:74:ARG:NH1	2.42	0.42
31:a:327:VAL:HG13	31:a:328:ASP:N	2.35	0.42
32:L:27:GLU:HA	32:L:30:LYS:HG2	2.02	0.42
13:P:7:ASN:ND2	13:P:29:GLY:O	2.41	0.42
34:c:265:MET:HE2	34:c:265:MET:HB2	1.65	0.42
6:E:298:LYS:HG2	6:E:389:VAL:HG22	2.02	0.42
7:B:223:ILE:CG2	7:B:347:ILE:HD12	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:214:ILE:CD1	14:U:904:LYS:HB2	2.50	0.42
18:A:40:THR:OG1	24:f:181:ARG:NH2	2.47	0.42
18:A:384:GLU:O	18:A:388:VAL:HG23	2.20	0.42
19:V:38:LYS:HD2	19:V:38:LYS:HA	1.82	0.42
19:V:102:PRO:O	19:V:106:ARG:HG3	2.20	0.42
10:s:208:ILE:O	10:s:212:GLU:HG2	2.19	0.42
10:s:241:ASP:OD1	10:s:241:ASP:N	2.52	0.42
20:t:237:VAL:HA	20:t:241:GLY:O	2.20	0.42
28:J:88:ARG:NH1	17:Q:69:MET:O	2.53	0.42
31:a:251:LEU:HD12	31:a:251:LEU:HA	1.92	0.42
9:O:192:GLU:OE1	9:O:192:GLU:N	2.53	0.42
32:L:49:LEU:HB2	32:L:195:LEU:HD21	2.02	0.42
32:l:23:GLU:HA	32:l:26:MET:HG2	2.02	0.42
7:B:343:ARG:HD3	18:A:218:PRO:HB2	2.01	0.41
10:S:143:GLU:OE1	10:S:143:GLU:N	2.43	0.41
12:F:304:ARG:HE	12:F:304:ARG:HB3	1.74	0.41
14:U:246:TYR:CE1	14:U:913:ILE:HD13	2.54	0.41
14:U:789:ILE:HG22	14:U:790:GLY:H	1.78	0.41
19:V:176:MET:N	19:V:176:MET:SD	2.93	0.41
19:V:280:ALA:HB3	19:V:285:TRP:HB2	2.01	0.41
20:T:223:TYR:OH	20:T:253:ASN:N	2.52	0.41
22:W:231:ILE:CG1	22:W:243:ILE:HG23	2.50	0.41
22:W:314:LEU:HD11	31:a:312:MET:HG2	2.01	0.41
24:f:326:LEU:HD12	24:f:330:PHE:CE2	2.55	0.41
24:f:472:HIS:ND1	24:f:472:HIS:C	2.78	0.41
27:Y:157:ILE:CD1	27:Y:186:LEU:HD11	2.50	0.41
3:M:187:CYS:HA	3:M:190:ILE:HG22	2.02	0.41
30:K:181:LEU:CD2	30:K:201:ILE:HG13	2.49	0.41
33:b:11:ASP:CG	33:b:84:ILE:HD12	2.45	0.41
34:c:55:GLY:HA3	34:c:112:TYR:CE1	2.54	0.41
4:R:100:LEU:HD23	4:R:162:GLY:HA3	2.02	0.41
6:E:295:LEU:HD23	6:E:295:LEU:HA	1.91	0.41
16:G:175:SER:O	16:G:179:LEU:HB2	2.20	0.41
18:A:34:LYS:HG3	18:A:35:THR:HG22	2.03	0.41
19:V:465:ASP:HB3	19:V:469:THR:HG23	2.02	0.41
22:W:244:CYS:SG	22:W:274:VAL:CG2	3.08	0.41
25:X:193:ALA:HA	25:X:196:THR:HG22	2.02	0.41
25:X:203:PRO:HB2	25:X:206:LEU:HB2	2.03	0.41
23:h:72:ILE:HG12	23:h:107:THR:CG2	2.34	0.41
26:i:71:ASP:OD1	26:i:223:THR:HG21	2.21	0.41
31:a:253:THR:HB	31:a:261:LEU:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:347:LYS:HA	31:a:347:LYS:HD3	1.95	0.41
33:b:7:MET:HG3	33:b:97:LEU:HD21	2.02	0.41
34:c:195:GLY:HA3	34:c:200:TYR:OH	2.21	0.41
2:d:345:GLN:CB	19:V:484:LEU:CD2	2.97	0.41
5:n:60:ILE:O	20:T:224:ARG:NH1	2.49	0.41
14:U:444:TYR:OH	14:U:774:PRO:O	2.37	0.41
14:U:529:ILE:HD11	14:U:566:LEU:HD13	2.02	0.41
15:C:73:VAL:CG1	15:C:74:GLY:N	2.83	0.41
15:C:160:GLU:O	15:C:164:VAL:HB	2.20	0.41
15:C:360:LYS:O	15:C:364:THR:HG23	2.20	0.41
16:G:212:PRO:HB3	16:G:235:ILE:HG22	2.00	0.41
18:A:40:THR:CG2	18:A:41:TYR:CD2	3.03	0.41
19:V:73:GLU:HA	19:V:76:LYS:HB3	2.03	0.41
22:W:12:ARG:HD2	22:W:27:ARG:HD3	2.02	0.41
22:W:128:LEU:O	22:W:132:THR:CB	2.68	0.41
24:f:326:LEU:HD12	24:f:330:PHE:CD2	2.55	0.41
24:f:821:LEU:HD23	24:f:821:LEU:HA	1.90	0.41
27:Y:13:LYS:HA	27:Y:16:ASP:HB2	2.01	0.41
26:i:147:LEU:HD23	26:i:148:TYR:N	2.35	0.41
29:Z:121:LEU:C	29:Z:121:LEU:HD12	2.46	0.41
7:B:49:LEU:HD11	24:f:650:GLN:HG2	2.03	0.41
11:D:249:ASP:OD1	11:D:252:ARG:NH2	2.48	0.41
11:D:327:LEU:O	11:D:327:LEU:CD1	2.51	0.41
12:F:344:ARG:CB	12:F:347:ARG:HE	2.33	0.41
14:U:155:LEU:HD23	14:U:155:LEU:HA	1.89	0.41
15:C:337:ASN:ND2	15:C:376:VAL:CG1	2.84	0.41
17:q:11:ASP:OD1	17:q:11:ASP:N	2.53	0.41
22:W:12:ARG:HA	22:W:12:ARG:HD3	1.82	0.41
20:t:202:GLN:HA	20:t:203:PRO:HD3	1.87	0.41
24:f:78:LEU:HD13	24:f:82:ILE:HD13	2.01	0.41
24:f:645:ASP:HA	24:f:648:ALA:HB3	2.01	0.41
26:I:38:LEU:HB3	26:I:43:VAL:CG2	2.36	0.41
27:Y:347:ILE:HG13	27:Y:354:VAL:HG22	2.03	0.41
3:M:216:TRP:HB3	3:M:221:THR:HG21	2.01	0.41
28:J:31:THR:HG22	28:J:32:ALA:N	2.35	0.41
28:J:119:THR:HG22	28:J:126:PRO:HB3	2.03	0.41
5:N:196:LEU:HD21	5:N:228:ILE:CD1	2.49	0.41
31:a:194:GLN:HG2	31:a:225:LEU:HD13	2.03	0.41
9:O:181:PHE:HD1	9:O:181:PHE:HA	1.77	0.41
32:L:227:ASP:OD1	32:L:228:ASP:N	2.54	0.41
13:P:49:LEU:HD21	13:P:87:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:15:TYR:HD2	33:b:116:PRO:HD2	1.85	0.41
6:E:352:MET:SD	12:F:350:ARG:NH1	2.93	0.41
12:F:265:ALA:HA	12:F:312:GLU:HG2	2.01	0.41
14:U:405:THR:CG2	14:U:438:GLN:OE1	2.68	0.41
15:C:349:GLU:O	15:C:349:GLU:HG2	2.20	0.41
18:A:45:ILE:O	18:A:49:GLU:HG3	2.19	0.41
4:r:225:ARG:HD3	4:r:225:ARG:HA	1.84	0.41
22:W:192:LEU:HD13	22:W:192:LEU:HA	1.94	0.41
22:W:264:GLN:CD	22:W:299:ILE:HD11	2.45	0.41
22:W:268:LYS:CD	22:W:299:ILE:HD13	2.48	0.41
23:H:42:ASN:HD21	23:H:184:LEU:H	1.68	0.41
24:f:24:THR:HG21	24:f:76:GLU:HB2	2.01	0.41
24:f:357:ARG:HE	24:f:357:ARG:HB3	1.51	0.41
24:f:701:ASN:OD1	24:f:705:ASN:ND2	2.53	0.41
25:X:281:GLY:H	25:X:284:THR:HG22	1.84	0.41
25:X:397:TYR:CZ	29:Z:258:VAL:HG21	2.55	0.41
27:Y:20:ALA:HB2	27:Y:150:PHE:HD1	1.86	0.41
28:J:153:TYR:O	28:J:154:HIS:ND1	2.53	0.41
29:Z:43:TRP:CD2	29:Z:45:LYS:O	2.74	0.41
5:N:68:LEU:CG	5:N:78:CYS:SG	3.06	0.41
30:k:117:SER:OG	30:k:160:GLY:HA2	2.20	0.41
3:m:108:LEU:HD22	3:m:139:SER:HB3	2.03	0.41
3:m:117:MET:HE2	3:m:117:MET:HB3	1.92	0.41
7:B:107:MET:CE	7:B:151:LEU:HD13	2.43	0.41
12:F:120:LYS:O	12:F:121:CYS:SG	2.77	0.41
12:F:437:TYR:CD2	30:K:159:SER:CB	3.04	0.41
15:C:194:THR:HG22	15:C:320:PRO:HD3	2.03	0.41
15:C:287:LYS:HB3	15:C:288:ASN:H	1.70	0.41
16:G:21:ARG:HD2	16:G:23:TYR:OH	2.17	0.41
16:G:88:ARG:NH2	3:M:158:SER:H	2.19	0.41
10:s:44:ALA:HB2	10:s:149:VAL:HG23	2.03	0.41
27:Y:18:ARG:HH21	27:Y:22:LEU:HB3	1.86	0.41
27:Y:83:ARG:HD3	27:Y:107:LYS:HD3	2.01	0.41
27:Y:157:ILE:O	27:Y:161:THR:CG2	2.68	0.41
26:i:17:ARG:NH1	26:i:22:GLU:OE1	2.52	0.41
29:Z:69:PHE:HE2	33:b:96:ALA:O	2.03	0.41
5:N:52:SER:HB2	5:N:64:VAL:HA	2.02	0.41
31:a:172:TYR:O	31:a:176:ALA:HB2	2.20	0.41
2:d:101:GLU:H	2:d:111:LYS:HE3	1.84	0.41
8:e:56:LEU:HA	8:e:59:GLU:HG2	2.02	0.41
9:o:49:VAL:HG23	9:o:181:PHE:CZ	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:7:GLY:O	14:U:10:SER:OG	2.35	0.41
14:U:242:LEU:HA	14:U:245:ALA:HB3	2.03	0.41
14:U:804:SER:OG	14:U:805:ASN:N	2.53	0.41
16:G:60:LEU:CD1	3:M:177:ILE:HG22	2.51	0.41
18:A:403:ILE:HD12	18:A:404:ALA:C	2.46	0.41
4:r:91:LYS:HB2	4:r:91:LYS:HE2	1.89	0.41
22:W:120:ILE:HD12	22:W:120:ILE:HA	1.91	0.41
22:W:206:SER:O	22:W:210:ASN:HB2	2.20	0.41
23:H:76:TYR:HD2	23:H:132:VAL:HG13	1.85	0.41
24:f:593:THR:OG1	24:f:628:ASP:OD1	2.31	0.41
25:X:203:PRO:HA	25:X:204:PRO:HD3	1.91	0.41
28:J:132:LEU:HD12	28:J:132:LEU:HA	1.91	0.41
26:i:71:ASP:HA	26:i:223:THR:CG2	2.50	0.41
26:i:147:LEU:C	26:i:147:LEU:CD2	2.93	0.41
29:Z:70:LEU:HD11	29:Z:108:ILE:HG23	2.03	0.41
13:P:25:ASP:OD1	13:P:25:ASP:N	2.53	0.41
17:Q:7:ILE:HD11	17:Q:143:LEU:HG	2.02	0.41
34:c:49:VAL:CG1	34:c:50:PRO:HD3	2.50	0.41
34:c:57:MET:HE3	34:c:57:MET:HB2	1.97	0.41
3:m:110:HIS:O	3:m:114:ARG:HG2	2.21	0.41
9:o:88:GLY:HA2	9:o:141:LEU:HD23	2.03	0.41
9:o:130:LEU:HD23	9:o:130:LEU:HA	1.96	0.41
10:S:44:ALA:HB2	10:S:149:VAL:HG23	2.02	0.41
14:U:192:GLN:HG3	14:U:193:PHE:N	2.36	0.41
14:U:622:LEU:HD23	14:U:622:LEU:HA	1.91	0.41
20:T:83:ASN:C	20:T:84:ILE:HG13	2.46	0.41
22:W:227:TYR:O	22:W:246:HIS:NE2	2.48	0.41
24:f:64:GLY:HA2	24:f:67:ASP:HB3	2.03	0.41
24:f:744:MET:SD	24:f:744:MET:O	2.78	0.41
25:X:200:ILE:H	25:X:200:ILE:HG13	1.69	0.41
3:M:91:ILE:O	3:M:95:GLU:HG2	2.21	0.41
9:O:156:ILE:HG23	9:O:162:THR:HG22	2.02	0.41
32:L:184:LEU:HD11	32:L:214:ILE:HG21	2.02	0.41
34:c:193:ILE:N	34:c:193:ILE:HD13	2.36	0.41
2:d:248:LYS:HE3	2:d:264:LEU:HD13	2.02	0.41
3:m:58:TYR:HD2	3:m:62:SER:HB3	1.85	0.41
4:R:156:MET:HB3	4:R:175:SER:HB3	2.03	0.41
7:B:199:GLU:OE2	7:B:349:ARG:NH2	2.44	0.41
12:F:134:LEU:HD12	12:F:134:LEU:C	2.44	0.41
15:C:217:SER:OG	15:C:218:GLU:N	2.54	0.41
16:G:224:ASN:HA	16:G:225:PRO:HD3	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:r:100:LEU:HD23	4:r:162:GLY:HA3	2.03	0.41
4:r:150:LYS:NZ	4:r:176:GLU:O	2.53	0.41
19:V:290:TYR:OH	19:V:294:ARG:NH2	2.54	0.41
10:s:83:SER:OG	10:s:84:GLY:N	2.54	0.41
22:W:34:LEU:HA	22:W:37:GLU:HG3	2.02	0.41
22:W:187:LEU:HA	22:W:190:MET:HE1	2.02	0.41
22:W:272:LEU:HD21	22:W:341:PHE:HE2	1.86	0.41
20:t:224:ARG:HD3	20:t:224:ARG:HA	1.88	0.41
24:f:290:VAL:HG23	24:f:321:MET:SD	2.60	0.41
24:f:512:MET:HE1	24:f:554:TYR:CZ	2.55	0.41
24:f:602:GLY:HA3	24:f:642:ALA:HB3	2.02	0.41
24:f:667:GLY:HA2	24:f:671:ALA:HB3	2.03	0.41
24:f:866:GLN:HG2	24:f:866:GLN:O	2.21	0.41
25:X:157:LEU:HB3	25:X:166:LEU:HD12	2.02	0.41
16:g:194:THR:HA	16:g:197:THR:HG22	2.02	0.41
29:Z:198:LEU:HD22	34:c:229:LEU:HD21	2.03	0.41
29:Z:224:HIS:CE1	31:a:340:VAL:HG11	2.47	0.41
31:a:168:ASN:ND2	31:a:171:SER:OG	2.51	0.41
31:a:343:LEU:HD23	31:a:343:LEU:HA	1.91	0.41
30:k:13:ASN:HB3	32:l:126:ARG:HB3	2.03	0.41
5:n:184:GLU:O	5:n:188:GLN:HG2	2.21	0.41
6:E:36:LEU:HB3	6:E:37:THR:H	1.66	0.41
14:U:188:MET:SD	14:U:189:GLN:N	2.94	0.41
17:q:102:LEU:HD22	17:q:103:LEU:H	1.85	0.41
18:A:110:LYS:HE3	18:A:110:LYS:HB3	1.94	0.41
10:s:132:TYR:HB3	10:s:134:VAL:HG12	2.03	0.41
22:W:307:LYS:O	22:W:307:LYS:CG	2.70	0.41
23:H:229:TYR:CZ	25:X:83:ALA:HB2	2.56	0.41
24:f:655:LEU:CD1	24:f:675:PHE:HE1	2.34	0.41
24:f:694:LEU:HG	24:f:729:MET:HE2	2.03	0.41
24:f:845:ARG:HG2	24:f:845:ARG:O	2.21	0.41
25:X:306:LEU:CD1	25:X:323:LEU:CD2	2.99	0.41
3:M:51:GLU:OE2	3:M:211:GLU:N	2.52	0.41
17:Q:184:ASP:N	17:Q:184:ASP:OD1	2.51	0.41
2:d:164:PHE:CE1	2:d:168:MET:HG3	2.56	0.40
7:B:153:ASN:OD1	7:B:157:HIS:N	2.54	0.40
7:B:234:LEU:HD13	35:B:501:ADP:H2'	2.03	0.40
11:D:61:ILE:HD13	11:D:61:ILE:HA	1.92	0.40
11:D:232:GLY:HA3	11:D:266:GLU:OE2	2.20	0.40
11:D:391:ARG:HG2	11:D:393:ILE:H	1.85	0.40
15:C:233:GLU:O	15:C:236:VAL:HB	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:13:ILE:HG23	16:G:129:ALA:CB	2.31	0.40
18:A:299:MET:HE3	18:A:299:MET:HB3	1.52	0.40
22:W:317:TRP:CE3	22:W:321:VAL:HG21	2.47	0.40
23:h:121:TYR:CD1	23:h:127:VAL:HG21	2.56	0.40
27:Y:309:GLU:CA	27:Y:358:ARG:HH22	2.19	0.40
28:J:64:ALA:O	28:J:88:ARG:NH1	2.54	0.40
26:i:3:ARG:CZ	30:k:10:ARG:O	2.69	0.40
29:Z:14:LEU:CD1	34:c:36:LEU:HD12	2.51	0.40
28:j:66:ASP:CG	28:j:91:CYS:SG	3.02	0.40
31:a:170:ALA:HB2	31:a:208:GLU:H	1.86	0.40
9:O:224:ASN:OD1	9:O:224:ASN:N	2.54	0.40
34:c:49:VAL:HG23	34:c:148:ILE:HD11	2.03	0.40
3:m:76:ALA:HB3	3:m:136:MET:HB2	2.02	0.40
4:R:241:ASP:OD1	4:R:241:ASP:N	2.54	0.40
10:S:211:ALA:HB2	10:S:238:LEU:HD13	2.03	0.40
11:D:200:ARG:NH1	11:D:303:VAL:O	2.54	0.40
14:U:405:THR:HG21	14:U:438:GLN:HA	2.03	0.40
15:C:165:ILE:HD12	15:C:165:ILE:HA	1.94	0.40
16:G:117:ARG:HE	16:G:117:ARG:HB3	1.71	0.40
19:V:33:GLN:HE21	19:V:85:ALA:HA	1.87	0.40
19:V:449:ALA:HB2	19:V:460:SER:HB3	2.04	0.40
22:W:76:GLU:HA	22:W:79:GLU:HG2	2.03	0.40
20:t:224:ARG:HG2	5:N:63:ARG:HH21	1.87	0.40
24:f:131:MET:CG	24:f:181:ARG:NH1	2.84	0.40
24:f:288:VAL:HG11	24:f:872:VAL:HB	2.02	0.40
16:g:33:ASN:HB3	16:g:170:VAL:HG22	2.02	0.40
26:i:71:ASP:OD1	26:i:223:THR:CG2	2.70	0.40
28:j:130:SER:HB3	28:j:161:ILE:HD11	2.03	0.40
13:P:155:GLU:HB3	13:P:158:MET:HE3	2.03	0.40
33:b:65:THR:HG21	33:b:70:ARG:HH22	1.82	0.40
33:b:117:VAL:HG13	33:b:117:VAL:O	2.22	0.40
30:k:82:ILE:HD12	30:k:82:ILE:HA	1.98	0.40
2:d:207:GLU:HA	2:d:210:THR:HG22	2.04	0.40
4:R:89:THR:O	4:R:89:THR:OG1	2.34	0.40
6:E:60:VAL:HG22	6:E:71:VAL:HG12	2.03	0.40
7:B:59:ARG:HA	7:B:62:LEU:HB2	2.03	0.40
14:U:46:GLU:O	14:U:50:GLU:N	2.53	0.40
14:U:536:ALA:HB2	14:U:548:LEU:HD23	2.03	0.40
14:U:570:LEU:C	14:U:570:LEU:CD2	2.91	0.40
14:U:586:VAL:HG12	14:U:602:LEU:HD12	2.04	0.40
18:A:306:LEU:O	18:A:312:ARG:NH1	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:413:VAL:HA	18:A:416:VAL:HG22	2.03	0.40
22:W:230:MET:HA	22:W:233:LEU:HG	2.03	0.40
22:W:393:LEU:CD2	22:W:406:VAL:CG2	2.98	0.40
23:H:40:ALA:HB1	23:H:182:LEU:HB2	2.02	0.40
24:f:431:LYS:HE3	24:f:432:TYR:CZ	2.57	0.40
16:g:22:LEU:CD1	16:g:25:VAL:CG2	2.93	0.40
27:Y:81:LEU:HD23	27:Y:81:LEU:HA	1.82	0.40
3:M:64:ASN:OD1	3:M:64:ASN:O	2.39	0.40
26:i:168:SER:O	26:i:168:SER:OG	2.34	0.40
31:a:66:GLU:CG	31:a:67:PHE:CE2	3.05	0.40
31:a:363:MET:HE1	34:c:304:LEU:HA	2.04	0.40
13:P:107:PRO:HG2	13:P:124:LEU:HB2	2.03	0.40
33:b:91:ARG:HD2	33:b:91:ARG:HA	1.89	0.40
30:k:178:GLN:CA	30:k:178:GLN:HE21	2.33	0.40
3:m:50:GLU:OE2	3:m:209:PHE:CB	2.64	0.40
5:n:102:ILE:HD13	5:n:102:ILE:HA	1.95	0.40
11:D:401:LYS:HE2	11:D:401:LYS:HB2	1.93	0.40
12:F:249:LEU:HD23	12:F:283:ILE:HD13	2.03	0.40
14:U:62:LEU:HD11	14:U:87:LEU:HB3	2.02	0.40
14:U:496:LEU:O	14:U:499:THR:OG1	2.39	0.40
14:U:527:GLN:O	14:U:531:ASP:CG	2.65	0.40
14:U:772:TRP:CD1	14:U:775:LEU:HG	2.57	0.40
15:C:88:LYS:HB3	15:C:94:LYS:HG2	2.02	0.40
15:C:161:ILE:HD12	15:C:161:ILE:HA	1.88	0.40
16:G:13:ILE:CG2	16:G:14:THR:N	2.84	0.40
16:G:65:THR:HG21	3:M:160:GLY:H	1.86	0.40
22:W:141:GLU:HB3	22:W:142:ARG:HH21	1.86	0.40
23:H:62:VAL:HG12	23:H:63:HIS:N	2.37	0.40
24:f:871:PRO:HG2	24:f:872:VAL:HG13	2.03	0.40
25:X:66:LEU:HD21	25:X:95:LEU:HD23	2.04	0.40
25:X:208:ALA:HB2	25:X:238:GLY:HA3	2.04	0.40
3:M:78:VAL:HG11	3:M:85:ALA:HB1	2.02	0.40
28:J:54:GLN:HE22	28:J:59:VAL:HB	1.87	0.40
28:J:146:GLN:O	28:J:153:TYR:HA	2.22	0.40
29:Z:70:LEU:HA	29:Z:70:LEU:HD23	1.87	0.40
29:Z:236:LEU:HB3	29:Z:237:LEU:H	1.73	0.40
28:j:214:ASP:OD1	28:j:214:ASP:N	2.52	0.40
31:a:293:PHE:HE2	31:a:329:LYS:HB3	1.79	0.40
30:k:90:ASP:HA	30:k:93:ARG:HG2	2.03	0.40
2:d:94:MET:SD	2:d:118:ARG:CD	3.09	0.40
2:d:219:ASP:OD1	2:d:219:ASP:N	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:118:LEU:HD22	4:R:142:LEU:HD22	2.03	0.40
6:E:219:PHE:HZ	6:E:275:MET:SD	2.45	0.40
6:E:348:THR:HA	12:F:217:ILE:HD12	2.03	0.40
7:B:434:THR:HA	7:B:435:PRO:HD3	1.94	0.40
12:F:94:ILE:HB	12:F:123:VAL:HG13	2.03	0.40
16:G:78:CYS:HA	16:G:139:ILE:O	2.21	0.40
18:A:77:LEU:HA	24:f:692:LEU:HD13	2.03	0.40
10:s:107:ASN:HD21	30:k:111:SER:HB3	1.85	0.40
24:f:369:ARG:HA	24:f:369:ARG:HD2	1.97	0.40
24:f:790:GLN:O	24:f:796:LEU:N	2.54	0.40
34:c:61:PHE:CD1	34:c:67:VAL:HG23	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	u	110/491 (22%)	101 (92%)	8 (7%)	1 (1%)	14	47
2	d	258/350 (74%)	215 (83%)	40 (16%)	3 (1%)	10	41
3	M	238/255 (93%)	218 (92%)	19 (8%)	1 (0%)	30	62
3	m	237/255 (93%)	222 (94%)	15 (6%)	0	100	100
4	R	204/263 (78%)	188 (92%)	14 (7%)	2 (1%)	12	44
4	r	199/263 (76%)	190 (96%)	9 (4%)	0	100	100
5	N	197/239 (82%)	184 (93%)	11 (6%)	2 (1%)	12	44
5	n	199/239 (83%)	185 (93%)	12 (6%)	2 (1%)	12	44
6	E	352/389 (90%)	317 (90%)	34 (10%)	1 (0%)	36	67
7	B	393/440 (89%)	344 (88%)	48 (12%)	1 (0%)	36	67
8	e	29/70 (41%)	21 (72%)	8 (28%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	O	218/277 (79%)	209 (96%)	9 (4%)	0	100	100
9	o	218/277 (79%)	205 (94%)	13 (6%)	0	100	100
10	S	211/241 (88%)	205 (97%)	6 (3%)	0	100	100
10	s	211/241 (88%)	203 (96%)	7 (3%)	1 (0%)	24	57
11	D	378/418 (90%)	332 (88%)	44 (12%)	2 (0%)	24	57
12	F	367/439 (84%)	326 (89%)	40 (11%)	1 (0%)	36	67
13	P	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
13	p	202/205 (98%)	192 (95%)	10 (5%)	0	100	100
14	U	808/953 (85%)	719 (89%)	83 (10%)	6 (1%)	18	51
15	C	372/406 (92%)	338 (91%)	32 (9%)	2 (0%)	24	57
16	G	238/246 (97%)	231 (97%)	7 (3%)	0	100	100
16	g	237/246 (96%)	224 (94%)	13 (6%)	0	100	100
17	Q	197/201 (98%)	183 (93%)	14 (7%)	0	100	100
17	q	196/201 (98%)	175 (89%)	21 (11%)	0	100	100
18	A	391/433 (90%)	340 (87%)	48 (12%)	3 (1%)	16	49
19	V	470/534 (88%)	413 (88%)	56 (12%)	1 (0%)	43	74
20	T	213/264 (81%)	201 (94%)	12 (6%)	0	100	100
20	t	213/264 (81%)	203 (95%)	10 (5%)	0	100	100
22	W	454/456 (100%)	412 (91%)	40 (9%)	2 (0%)	30	62
23	H	229/234 (98%)	218 (95%)	11 (5%)	0	100	100
23	h	227/234 (97%)	214 (94%)	13 (6%)	0	100	100
24	f	887/908 (98%)	717 (81%)	156 (18%)	14 (2%)	7	36
25	X	378/422 (90%)	345 (91%)	31 (8%)	2 (0%)	24	57
26	I	254/261 (97%)	232 (91%)	22 (9%)	0	100	100
26	i	248/261 (95%)	225 (91%)	22 (9%)	1 (0%)	30	62
27	Y	376/389 (97%)	319 (85%)	54 (14%)	3 (1%)	16	49
28	J	237/248 (96%)	216 (91%)	20 (8%)	1 (0%)	30	62
28	j	236/248 (95%)	211 (89%)	23 (10%)	2 (1%)	16	49
29	Z	284/324 (88%)	261 (92%)	22 (8%)	1 (0%)	30	62
30	K	232/241 (96%)	211 (91%)	20 (9%)	1 (0%)	30	62
30	k	232/241 (96%)	207 (89%)	22 (10%)	3 (1%)	9	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	a	371/376 (99%)	329 (89%)	41 (11%)	1 (0%)	36	67
32	L	237/263 (90%)	220 (93%)	17 (7%)	0	100	100
32	l	235/263 (89%)	216 (92%)	19 (8%)	0	100	100
33	b	188/377 (50%)	172 (92%)	15 (8%)	1 (0%)	24	57
34	c	285/310 (92%)	259 (91%)	24 (8%)	2 (1%)	18	51
All	All	13348/15361 (87%)	12062 (90%)	1223 (9%)	63 (0%)	26	57

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	u	90	VAL
4	R	61	THR
5	n	229	PRO
7	B	232	LYS
11	D	125	LYS
12	F	86	LEU
14	U	161	ASP
15	C	224	ILE
18	A	346	PRO
19	V	277	PRO
10	s	108	ASN
22	W	258	ALA
24	f	92	VAL
24	f	100	ARG
24	f	294	MET
24	f	324	VAL
26	i	60	PHE
28	j	199	VAL
2	d	98	LEU
11	D	85	ILE
14	U	130	LEU
14	U	131	GLU
18	A	287	ASP
24	f	128	VAL
27	Y	269	SER
3	M	222	ASN
28	J	212	ARG
28	j	200	GLN
31	a	69	HIS
33	b	22	LEU

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Mol	Chain	Res	Type
5	n	233	VAL
6	E	360	ASP
14	U	903	PHE
15	C	267	SER
18	A	107	GLU
22	W	253	THR
24	f	300	ARG
24	f	305	LEU
24	f	308	SER
24	f	881	GLU
29	Z	7	GLN
5	N	226	ASP
30	k	225	ASN
34	c	279	ASP
2	d	293	PHE
24	f	544	GLU
24	f	817	VAL
25	X	393	VAL
27	Y	63	TRP
27	Y	212	GLU
5	N	232	ALA
34	c	266	THR
4	R	59	GLY
14	U	70	HIS
2	d	94	MET
24	f	101	PRO
25	X	380	GLN
30	K	129	ASP
30	k	130	PRO
24	f	755	ASP
30	k	131	GLY
24	f	542	ILE
14	U	174	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	u	99/398 (25%)	96 (97%)	3 (3%)	36	60
2	d	224/294 (76%)	224 (100%)	0	100	100
3	M	189/212 (89%)	188 (100%)	1 (0%)	81	80
3	m	191/212 (90%)	190 (100%)	1 (0%)	81	80
4	R	153/202 (76%)	151 (99%)	2 (1%)	61	72
4	r	152/202 (75%)	151 (99%)	1 (1%)	76	78
5	N	154/181 (85%)	154 (100%)	0	100	100
5	n	153/181 (84%)	153 (100%)	0	100	100
6	E	305/341 (89%)	305 (100%)	0	100	100
7	B	332/385 (86%)	331 (100%)	1 (0%)	86	83
8	e	10/63 (16%)	10 (100%)	0	100	100
9	O	177/228 (78%)	177 (100%)	0	100	100
9	o	177/228 (78%)	177 (100%)	0	100	100
10	S	174/199 (87%)	174 (100%)	0	100	100
10	s	174/199 (87%)	174 (100%)	0	100	100
11	D	324/366 (88%)	320 (99%)	4 (1%)	63	73
12	F	310/379 (82%)	308 (99%)	2 (1%)	78	79
13	P	172/174 (99%)	172 (100%)	0	100	100
13	p	172/174 (99%)	172 (100%)	0	100	100
14	U	683/816 (84%)	683 (100%)	0	100	100
15	C	308/352 (88%)	307 (100%)	1 (0%)	86	83
16	G	192/210 (91%)	192 (100%)	0	100	100
16	g	186/210 (89%)	185 (100%)	1 (0%)	81	80
17	Q	164/171 (96%)	164 (100%)	0	100	100
17	q	164/171 (96%)	164 (100%)	0	100	100
18	A	330/372 (89%)	329 (100%)	1 (0%)	86	83
19	V	400/460 (87%)	398 (100%)	2 (0%)	81	80
20	T	173/215 (80%)	172 (99%)	1 (1%)	78	79
20	t	173/215 (80%)	173 (100%)	0	100	100
22	W	407/416 (98%)	403 (99%)	4 (1%)	68	75
23	H	164/191 (86%)	164 (100%)	0	100	100
23	h	160/191 (84%)	160 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	f	695/763 (91%)	686 (99%)	9 (1%)	61	72
25	X	326/362 (90%)	324 (99%)	2 (1%)	78	79
26	I	199/221 (90%)	198 (100%)	1 (0%)	81	80
26	i	191/221 (86%)	191 (100%)	0	100	100
27	Y	308/344 (90%)	307 (100%)	1 (0%)	86	83
28	J	151/211 (72%)	150 (99%)	1 (1%)	76	78
28	j	149/211 (71%)	149 (100%)	0	100	100
29	Z	251/295 (85%)	249 (99%)	2 (1%)	73	77
30	K	186/203 (92%)	184 (99%)	2 (1%)	65	74
30	k	186/203 (92%)	185 (100%)	1 (0%)	81	80
31	a	331/336 (98%)	331 (100%)	0	100	100
32	L	196/224 (88%)	196 (100%)	0	100	100
32	l	197/224 (88%)	196 (100%)	1 (0%)	81	80
33	b	164/312 (53%)	164 (100%)	0	100	100
34	c	246/268 (92%)	242 (98%)	4 (2%)	55	70
All	All	10922/13006 (84%)	10873 (100%)	49 (0%)	81	81

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	u	378	ASP
1	u	389	ARG
1	u	406	ARG
3	m	161	TRP
4	R	58	HIS
4	R	195	TYR
7	B	440	LEU
11	D	60	TYR
11	D	164	TYR
11	D	229	ARG
11	D	235	PHE
12	F	320	PHE
12	F	347	ARG
15	C	369	TYR
18	A	362	MET
4	r	195	TYR
19	V	276	PHE

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Mol	Chain	Res	Type
19	V	436	PHE
20	T	155	MET
22	W	227	TYR
22	W	247	TYR
22	W	272	LEU
22	W	273	TYR
24	f	309	GLU
24	f	326	LEU
24	f	327	ASN
24	f	329	ASN
24	f	330	PHE
24	f	473	ASN
24	f	474	SER
24	f	475	ASN
24	f	476	THR
25	X	87	ARG
25	X	234	GLU
16	g	210	PHE
26	I	128	ARG
27	Y	82	LYS
3	M	216	TRP
28	J	17	PHE
29	Z	58	PHE
29	Z	69	PHE
30	K	22	PHE
30	K	186	HIS
30	k	178	GLN
34	c	133	PHE
34	c	193	ILE
34	c	265	MET
34	c	310	LYS
32	l	179	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (159) such sidechains are listed below:

Mol	Chain	Res	Type
2	d	139	GLN
2	d	234	GLN
2	d	321	GLN
2	d	322	GLN
3	m	63	ASN
3	m	68	ASN

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Mol	Chain	Res	Type
4	R	58	HIS
5	n	100	HIS
5	n	221	GLN
6	E	55	GLN
6	E	263	GLN
6	E	271	HIS
6	E	323	HIS
7	B	84	GLN
7	B	257	GLN
7	B	368	HIS
7	B	425	ASN
9	o	128	GLN
9	o	159	HIS
10	S	159	GLN
10	S	174	GLN
11	D	57	GLN
11	D	67	ASN
11	D	98	GLN
11	D	173	GLN
11	D	193	GLN
11	D	295	GLN
11	D	302	ASN
12	F	243	GLN
12	F	315	ASN
12	F	333	ASN
13	p	18	ASN
13	p	33	GLN
13	p	72	ASN
13	p	169	GLN
14	U	18	GLN
14	U	111	GLN
14	U	115	ASN
14	U	139	GLN
14	U	453	HIS
14	U	464	GLN
14	U	491	GLN
14	U	540	GLN
14	U	541	HIS
14	U	596	ASN
14	U	685	GLN
14	U	718	ASN
14	U	754	HIS

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Mol	Chain	Res	Type
14	U	801	GLN
15	C	36	ASN
15	C	90	HIS
15	C	296	ASN
16	G	75	ASN
16	G	90	GLN
18	A	38	GLN
18	A	91	GLN
18	A	165	GLN
18	A	203	ASN
18	A	314	ASN
18	A	353	HIS
4	r	234	ASN
19	V	33	GLN
19	V	118	GLN
19	V	214	HIS
19	V	257	ASN
19	V	283	ASN
10	s	107	ASN
10	s	174	GLN
10	s	180	GLN
10	s	187	GLN
20	T	202	GLN
22	W	99	GLN
22	W	107	GLN
22	W	155	GLN
22	W	170	GLN
22	W	264	GLN
22	W	426	ASN
22	W	454	ASN
23	H	179	ASN
23	H	189	HIS
24	f	43	GLN
24	f	198	HIS
24	f	199	ASN
24	f	224	ASN
24	f	238	ASN
24	f	352	HIS
24	f	355	ASN
24	f	378	ASN
24	f	402	ASN
24	f	473	ASN

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Mol	Chain	Res	Type
24	f	592	ASN
24	f	611	GLN
24	f	619	HIS
24	f	650	GLN
24	f	747	GLN
24	f	750	GLN
24	f	766	GLN
24	f	786	GLN
24	f	826	GLN
24	f	848	GLN
25	X	178	HIS
25	X	268	GLN
25	X	292	GLN
16	g	53	GLN
26	I	123	GLN
26	I	166	ASN
23	h	21	GLN
23	h	95	GLN
23	h	119	GLN
23	h	207	ASN
27	Y	160	ASN
27	Y	388	ASN
3	M	98	ASN
28	J	85	ASN
28	J	215	GLN
26	i	102	GLN
26	i	119	GLN
26	i	149	GLN
29	Z	32	GLN
29	Z	223	ASN
29	Z	224	HIS
29	Z	243	GLN
29	Z	256	GLN
5	N	105	ASN
30	K	152	GLN
31	a	40	GLN
31	a	52	GLN
31	a	72	ASN
31	a	86	GLN
31	a	169	HIS
31	a	231	GLN
31	a	257	GLN

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Mol	Chain	Res	Type
31	a	273	GLN
9	O	109	HIS
32	L	31	GLN
13	P	72	ASN
13	P	81	GLN
13	P	93	ASN
33	b	12	ASN
33	b	79	GLN
33	b	137	ASN
33	b	158	ASN
33	b	161	ASN
17	Q	32	HIS
17	Q	82	ASN
17	Q	193	ASN
30	k	13	ASN
30	k	178	GLN
30	k	221	GLN
34	c	92	GLN
34	c	176	GLN
34	c	190	GLN
34	c	194	HIS
34	c	269	GLN
32	l	5	GLN
32	l	8	ASN
32	l	20	HIS
32	l	60	GLN
32	l	90	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	ATP	D	501	-	29,33,33	0.35	0	44,52,52	0.52	0
36	ATP	F	501	-	29,33,33	0.36	0	44,52,52	0.52	0
35	ADP	E	401	-	27,29,29	1.35	4 (14%)	42,45,45	2.03	9 (21%)
36	ATP	A	501	-	29,33,33	0.34	0	44,52,52	0.52	0
35	ADP	B	501	-	27,29,29	1.35	4 (14%)	42,45,45	1.97	9 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	ATP	D	501	-	-	6/22/38/38	0/3/3/3
36	ATP	F	501	-	-	3/22/38/38	0/3/3/3
35	ADP	E	401	-	-	3/16/32/32	0/3/3/3
36	ATP	A	501	-	-	7/22/38/38	0/3/3/3
35	ADP	B	501	-	-	4/16/32/32	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	E	401	ADP	C5-C4	4.39	1.47	1.39
35	B	501	ADP	C5-C4	4.37	1.47	1.39
35	B	501	ADP	C5-N7	-2.55	1.34	1.39
35	E	401	ADP	C5-N7	-2.47	1.34	1.39
35	E	401	ADP	C5-C6	2.40	1.47	1.41
35	B	501	ADP	C5-C6	2.37	1.47	1.41
35	E	401	ADP	C8-N7	2.21	1.35	1.31
35	B	501	ADP	C8-N7	2.07	1.35	1.31

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B	501	ADP	C5-C4-N3	-6.43	118.36	126.75
35	E	401	ADP	C5-C4-N3	-6.29	118.55	126.75
35	B	501	ADP	N3-C4-N9	5.30	135.81	127.08
35	E	401	ADP	N3-C4-N9	4.97	135.28	127.08
35	E	401	ADP	PA-O3A-PB	-4.41	117.70	132.83
35	E	401	ADP	C2-N3-C4	3.84	120.83	111.75
35	B	501	ADP	C2-N3-C4	3.77	120.66	111.75
35	E	401	ADP	N3-C2-N1	-3.18	123.63	128.60
35	E	401	ADP	C4-C5-N7	-3.07	106.88	110.62
35	B	501	ADP	N3-C2-N1	-2.94	124.00	128.60
35	B	501	ADP	C4-C5-N7	-2.92	107.06	110.62
35	E	401	ADP	C3'-C2'-C1'	2.78	106.72	101.43
35	B	501	ADP	PA-O3A-PB	-2.73	123.46	132.83
35	B	501	ADP	C3'-C2'-C1'	2.73	106.61	101.43
35	E	401	ADP	C5-N7-C8	2.54	107.12	103.51
35	B	501	ADP	C5-N7-C8	2.52	107.09	103.51
35	B	501	ADP	C4-N9-C8	2.46	108.39	105.73
35	E	401	ADP	C4-N9-C8	2.41	108.34	105.73

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	E	401	ADP	C5'-O5'-PA-O2A
36	D	501	ATP	C5'-O5'-PA-O3A
36	D	501	ATP	C4'-C5'-O5'-PA
36	F	501	ATP	C5'-O5'-PA-O3A
36	A	501	ATP	C5'-O5'-PA-O1A
36	A	501	ATP	C5'-O5'-PA-O2A
36	D	501	ATP	C3'-C4'-C5'-O5'
35	B	501	ADP	O4'-C4'-C5'-O5'
36	F	501	ATP	C4'-C5'-O5'-PA
35	E	401	ADP	C5'-O5'-PA-O3A
36	D	501	ATP	PG-O3B-PB-O1B
35	E	401	ADP	C5'-O5'-PA-O1A
36	D	501	ATP	C5'-O5'-PA-O1A
36	F	501	ATP	C5'-O5'-PA-O1A
36	A	501	ATP	C4'-C5'-O5'-PA
35	B	501	ADP	C3'-C4'-C5'-O5'
36	D	501	ATP	O4'-C4'-C5'-O5'
36	A	501	ATP	O4'-C4'-C5'-O5'

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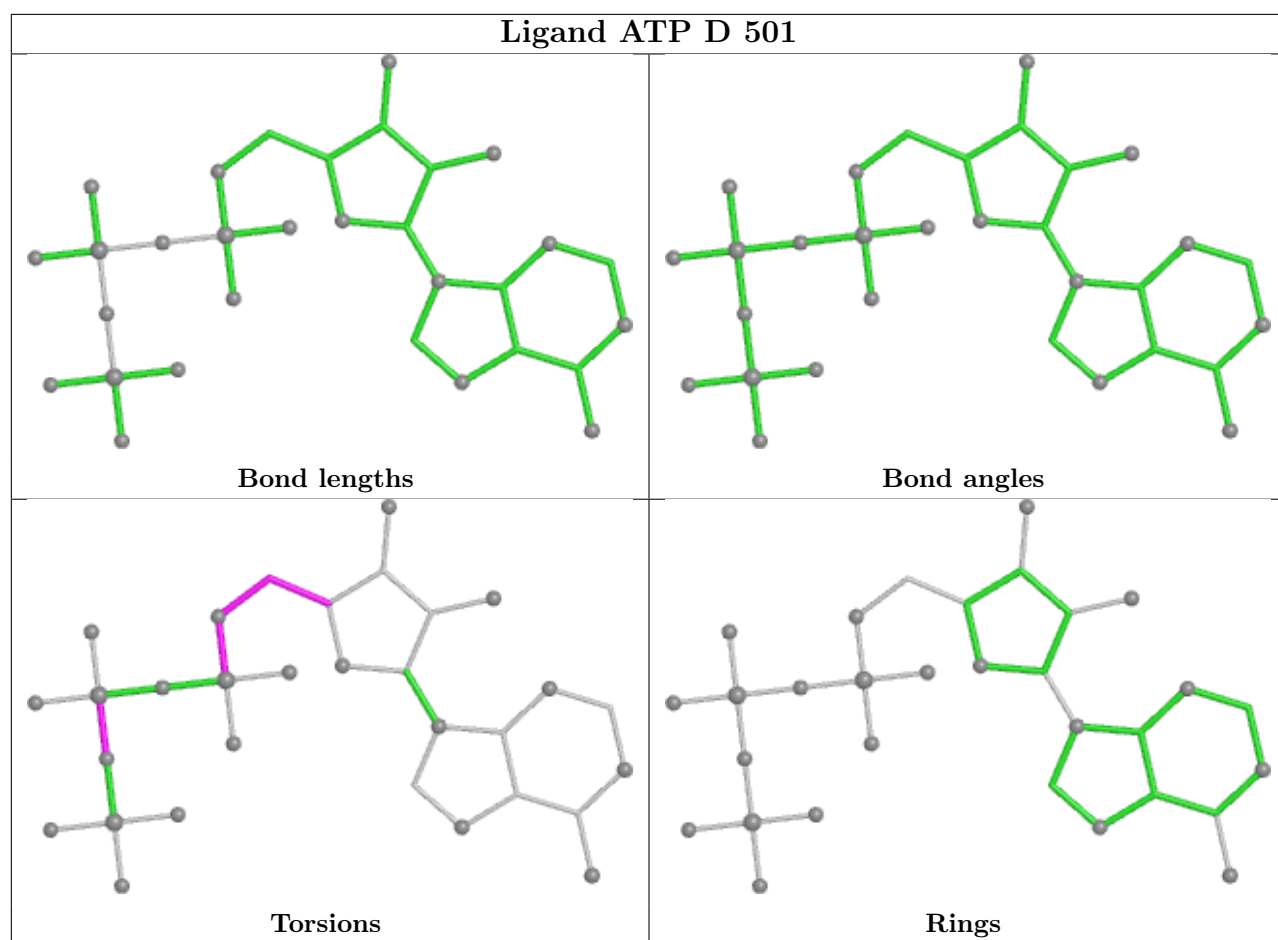
Mol	Chain	Res	Type	Atoms
36	A	501	ATP	C5'-O5'-PA-O3A
35	B	501	ADP	PB-O3A-PA-O1A
35	B	501	ADP	PB-O3A-PA-O2A
36	A	501	ATP	PB-O3A-PA-O1A
36	A	501	ATP	PB-O3A-PA-O2A

There are no ring outliers.

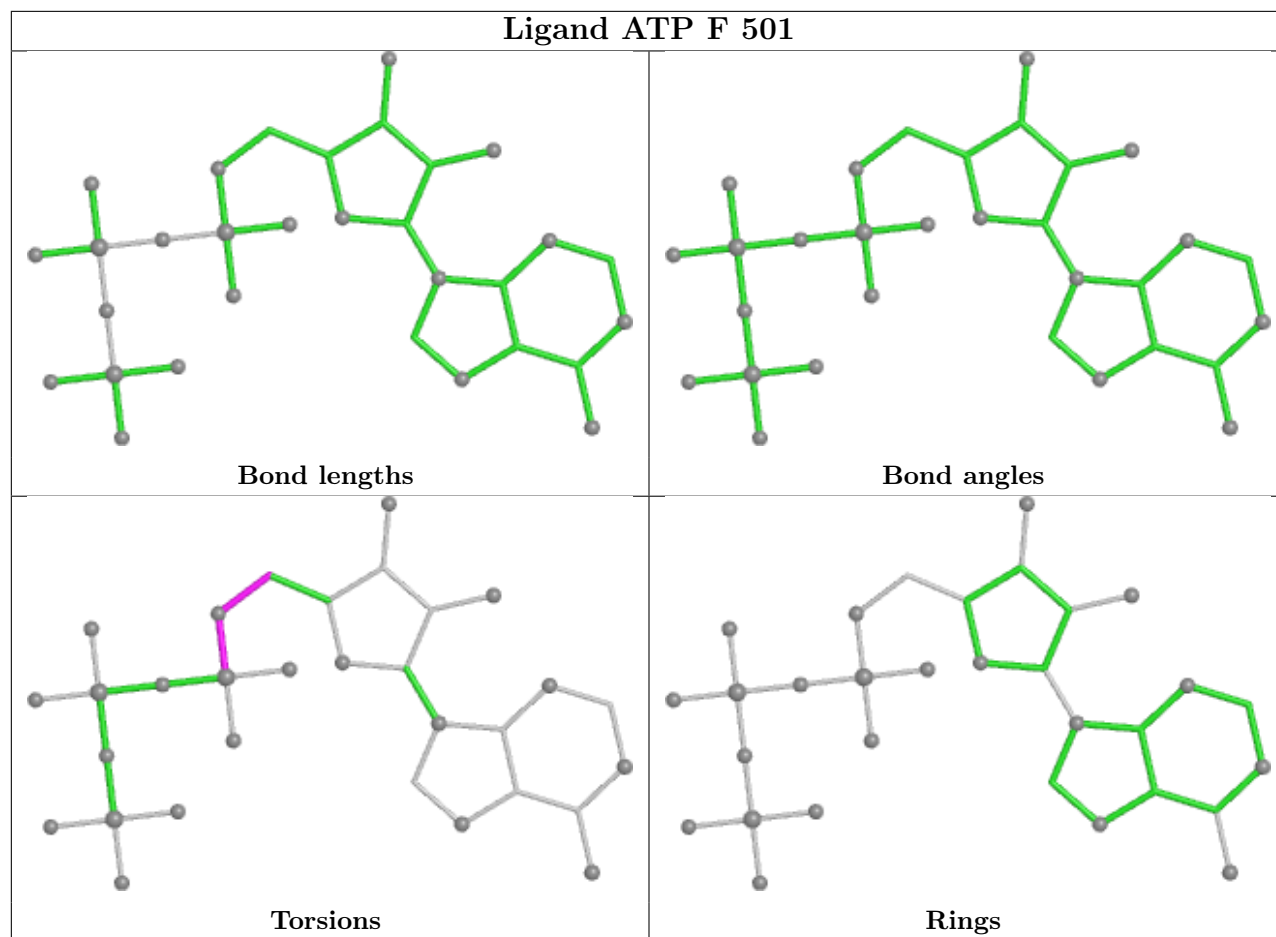
4 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	D	501	ATP	4	0
35	E	401	ADP	2	0
36	A	501	ATP	2	0
35	B	501	ADP	10	0

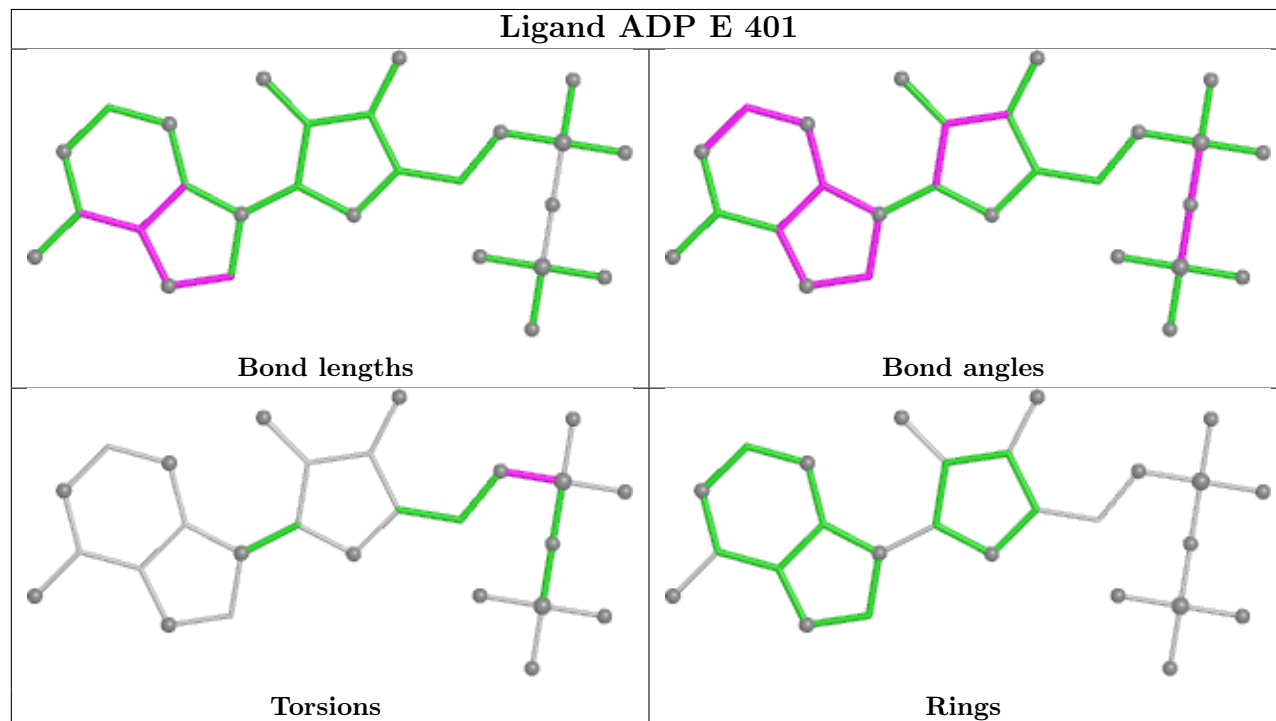
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



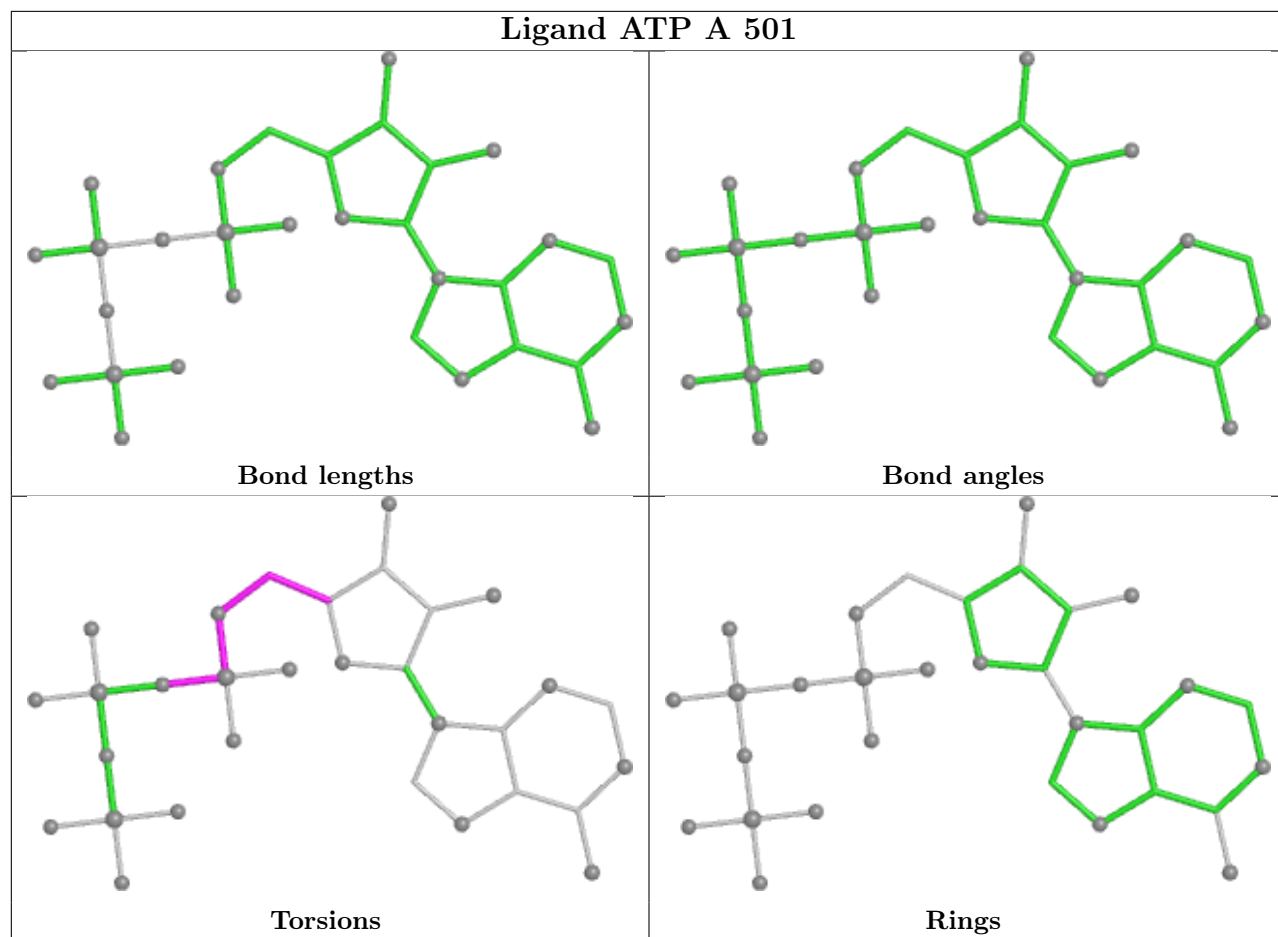
Ligand ATP F 501



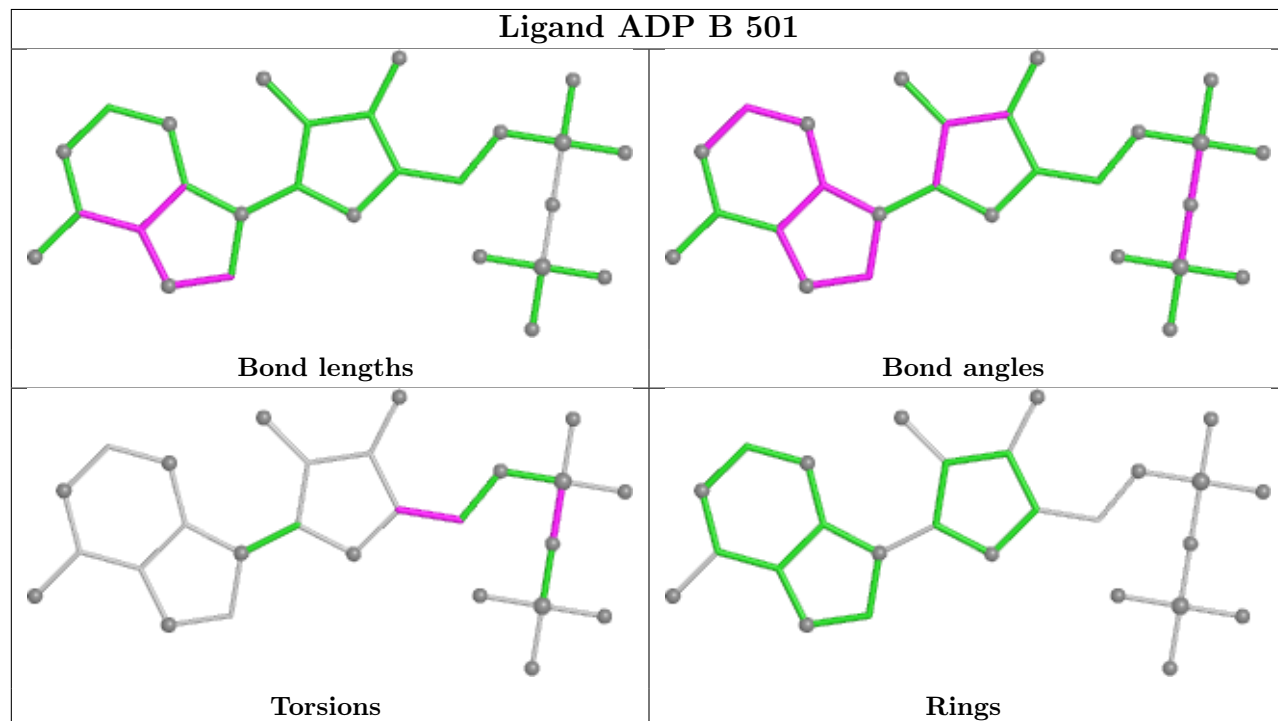
Ligand ADP E 401



Ligand ATP A 501



Ligand ADP B 501



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.

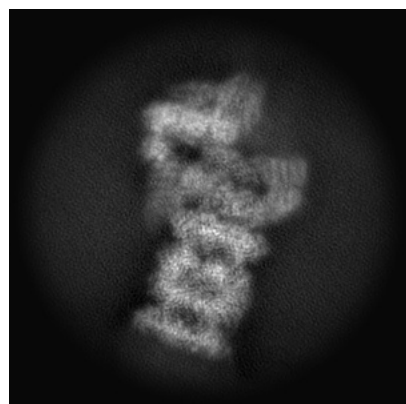
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64133. These allow visual inspection of the internal detail of the map and identification of artifacts.

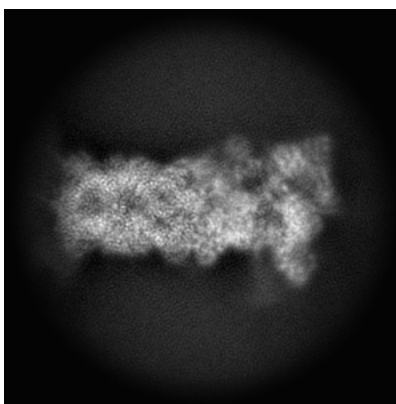
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

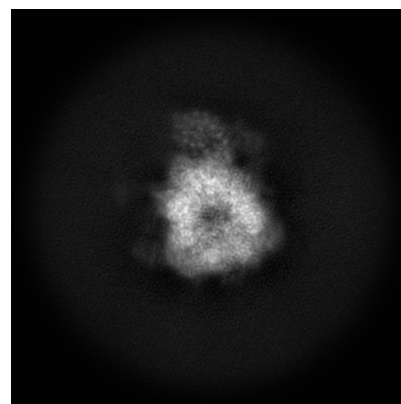
6.1.1 Primary map



X

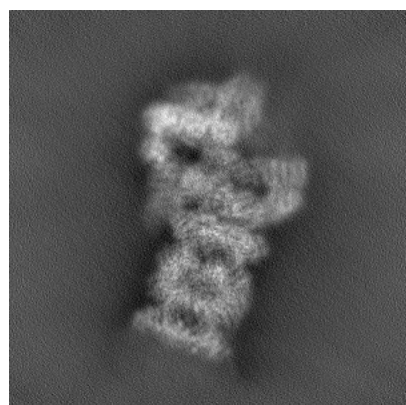


Y

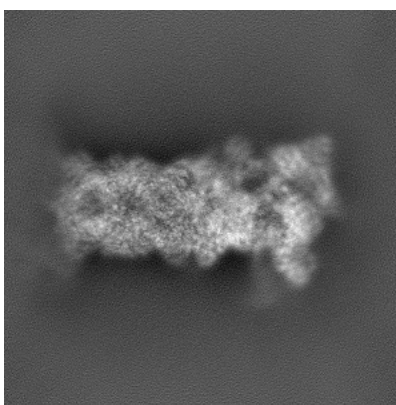


Z

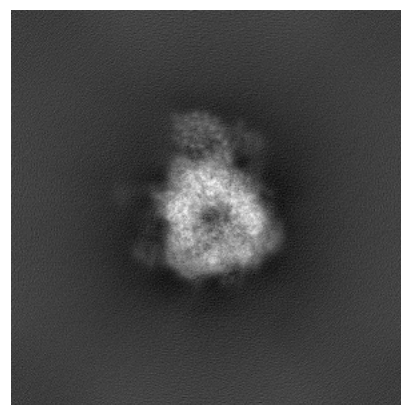
6.1.2 Raw map



X



Y

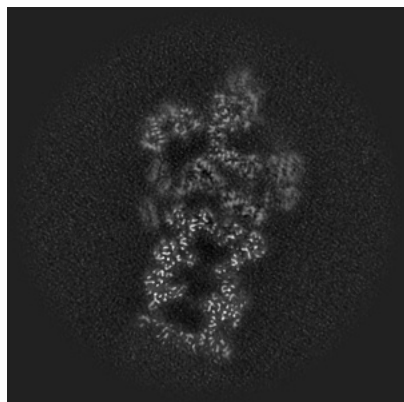


Z

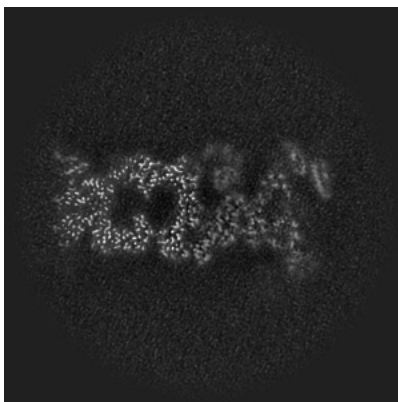
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

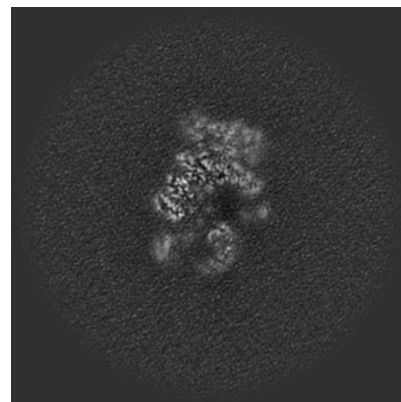
6.2.1 Primary map



X Index: 210

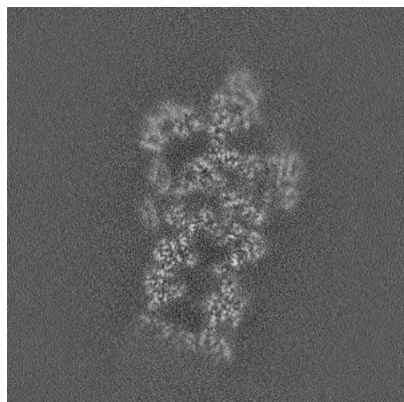


Y Index: 210

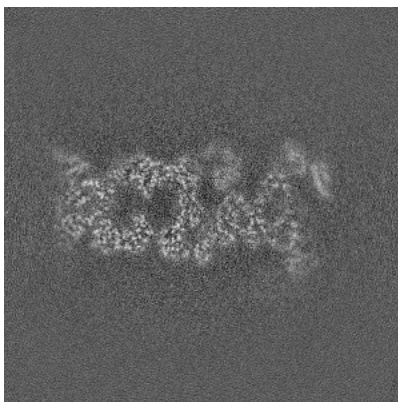


Z Index: 210

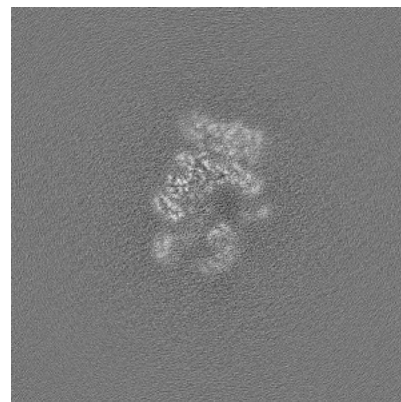
6.2.2 Raw map



X Index: 210



Y Index: 210

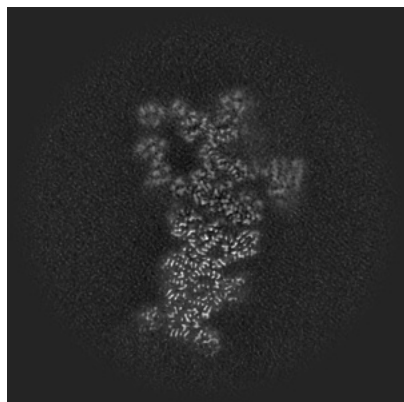


Z Index: 210

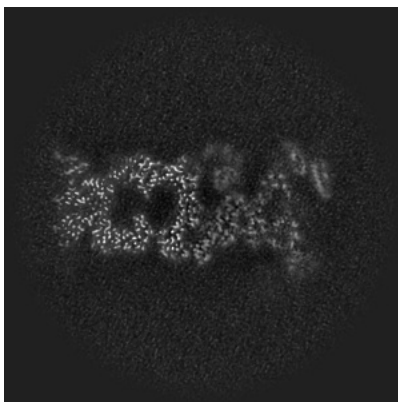
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

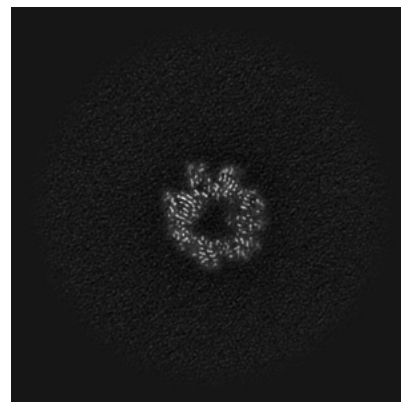
6.3.1 Primary map



X Index: 184

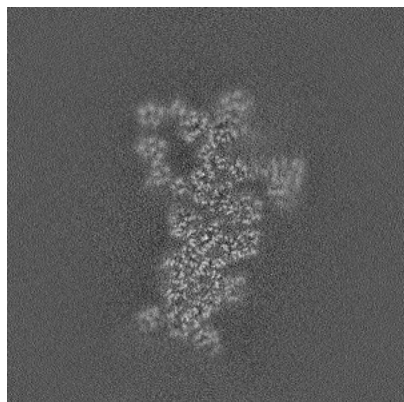


Y Index: 210

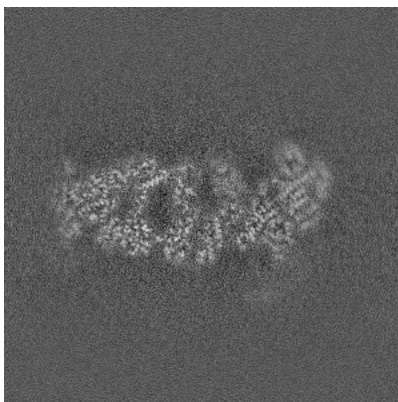


Z Index: 139

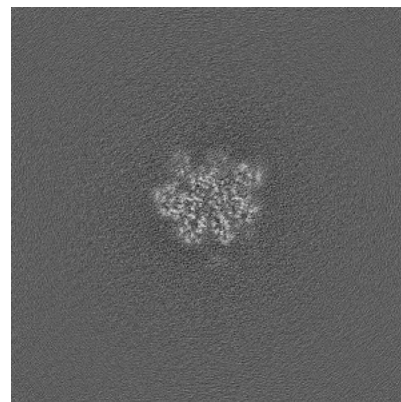
6.3.2 Raw map



X Index: 184



Y Index: 219

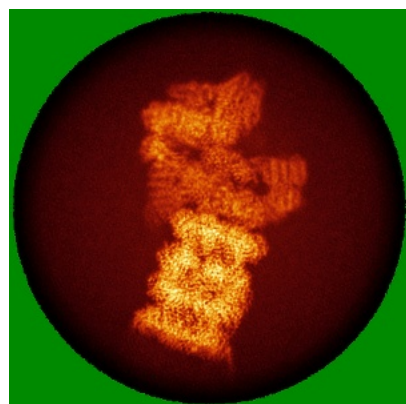


Z Index: 184

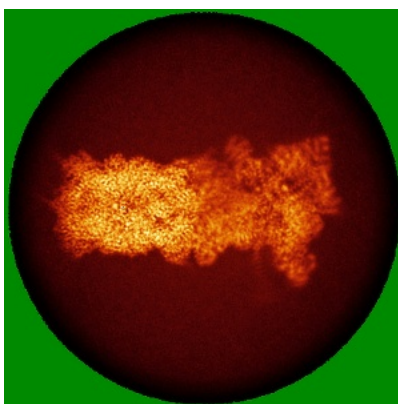
The images above show the largest variance slices of the map in three orthogonal directions.

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

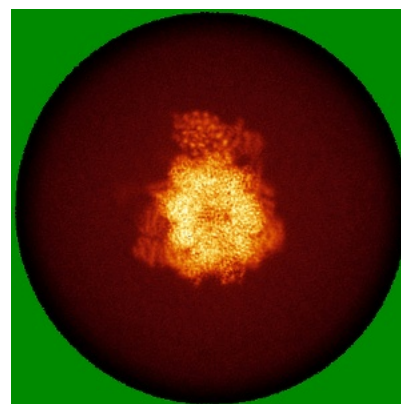
6.4.1 Primary map



X

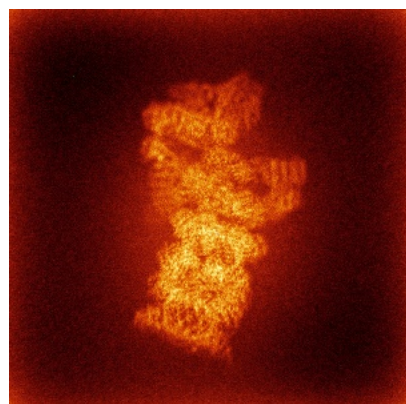


Y

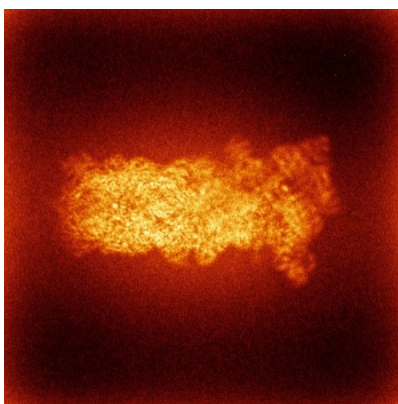


Z

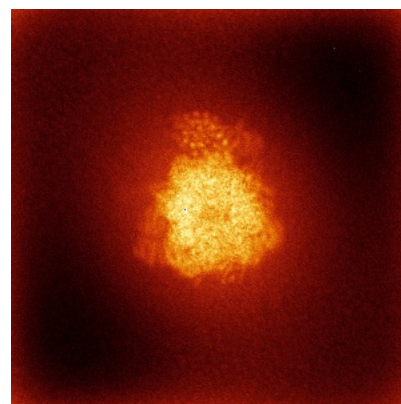
6.4.2 Raw map



X



Y

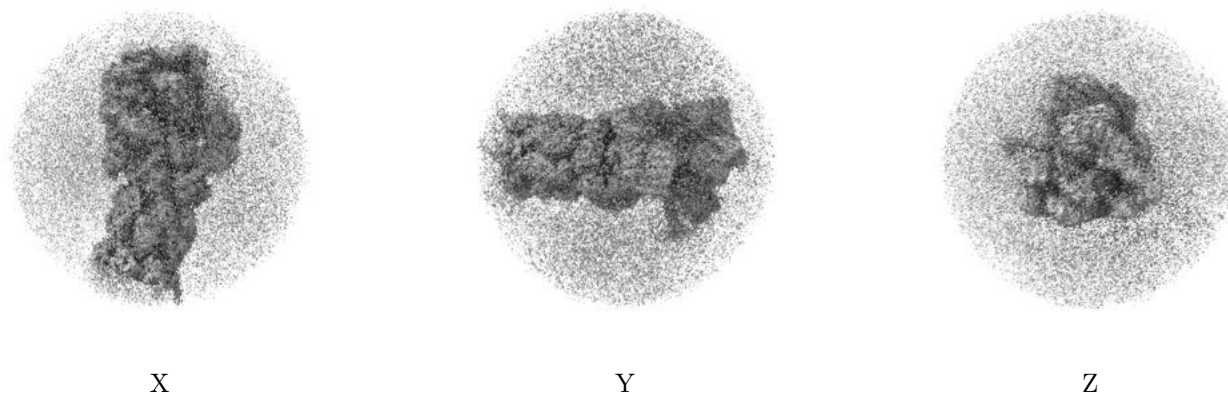


Z

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

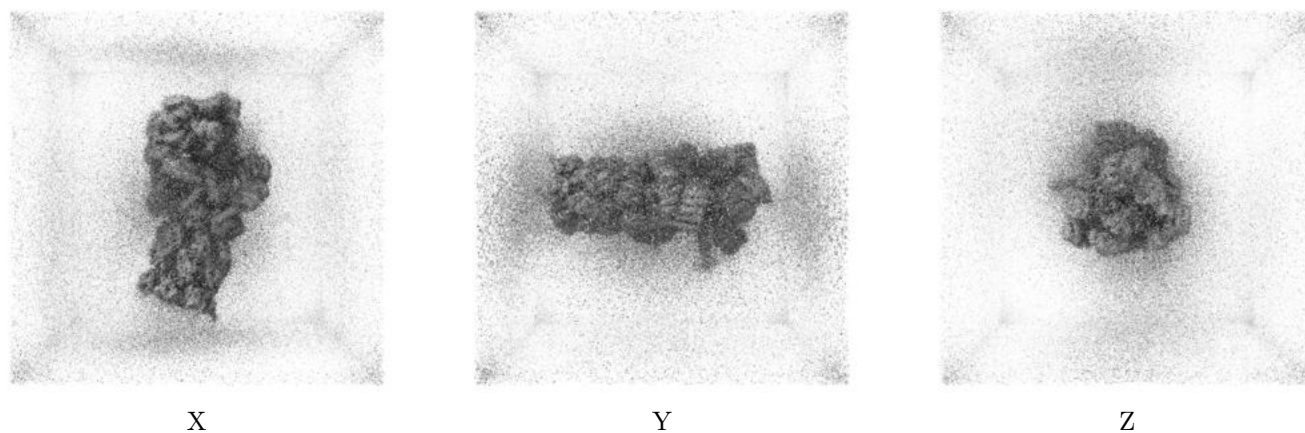
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

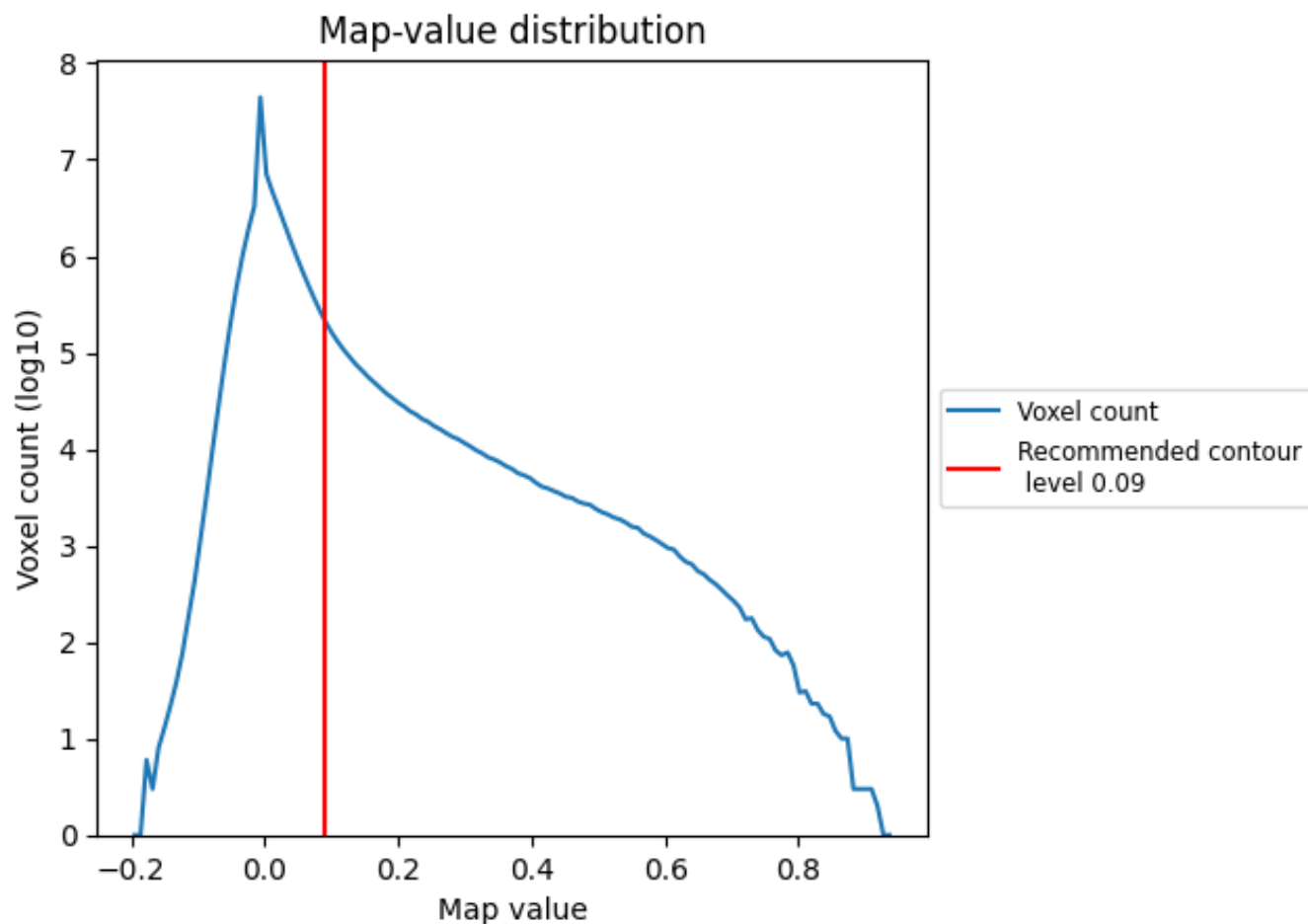
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

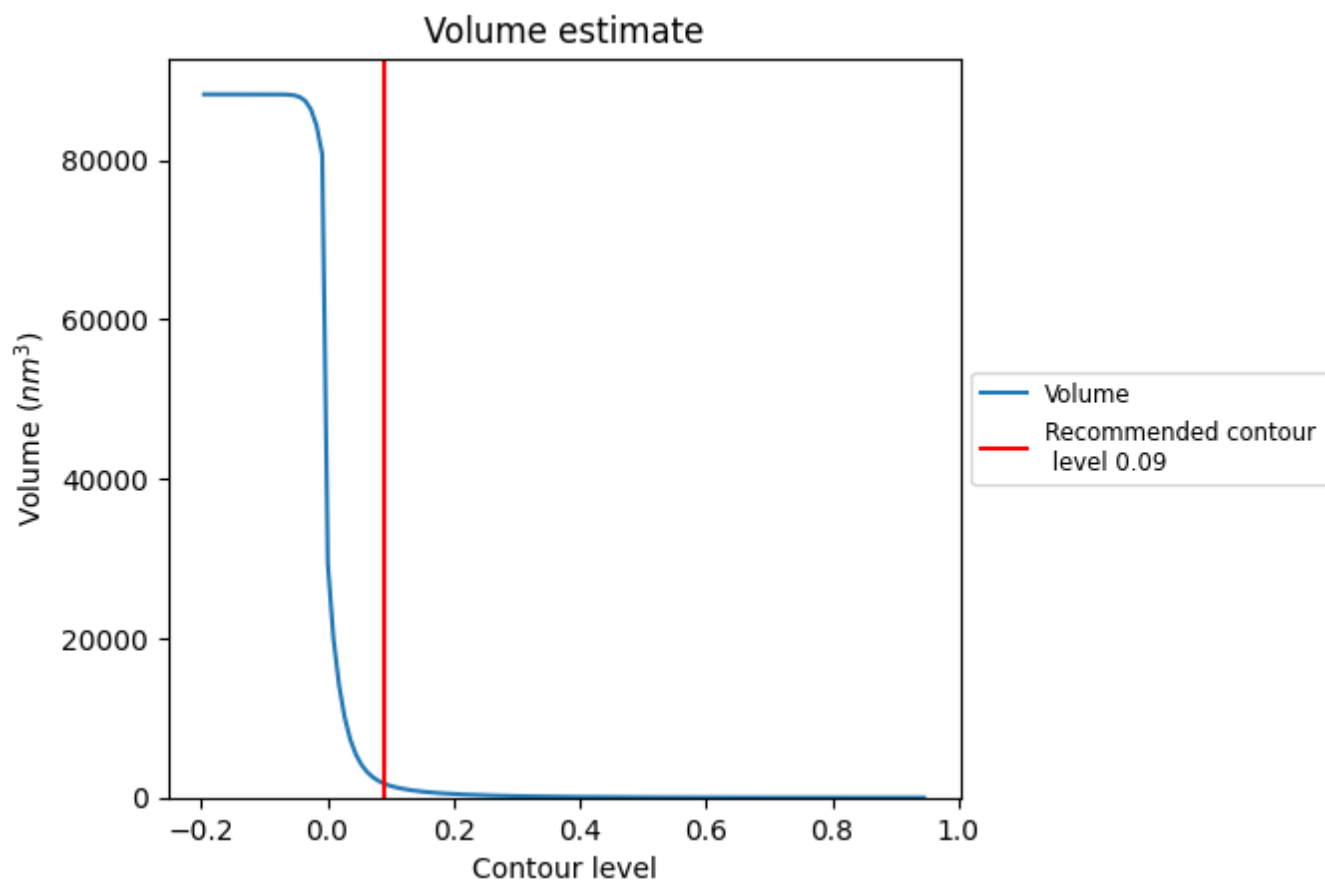
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

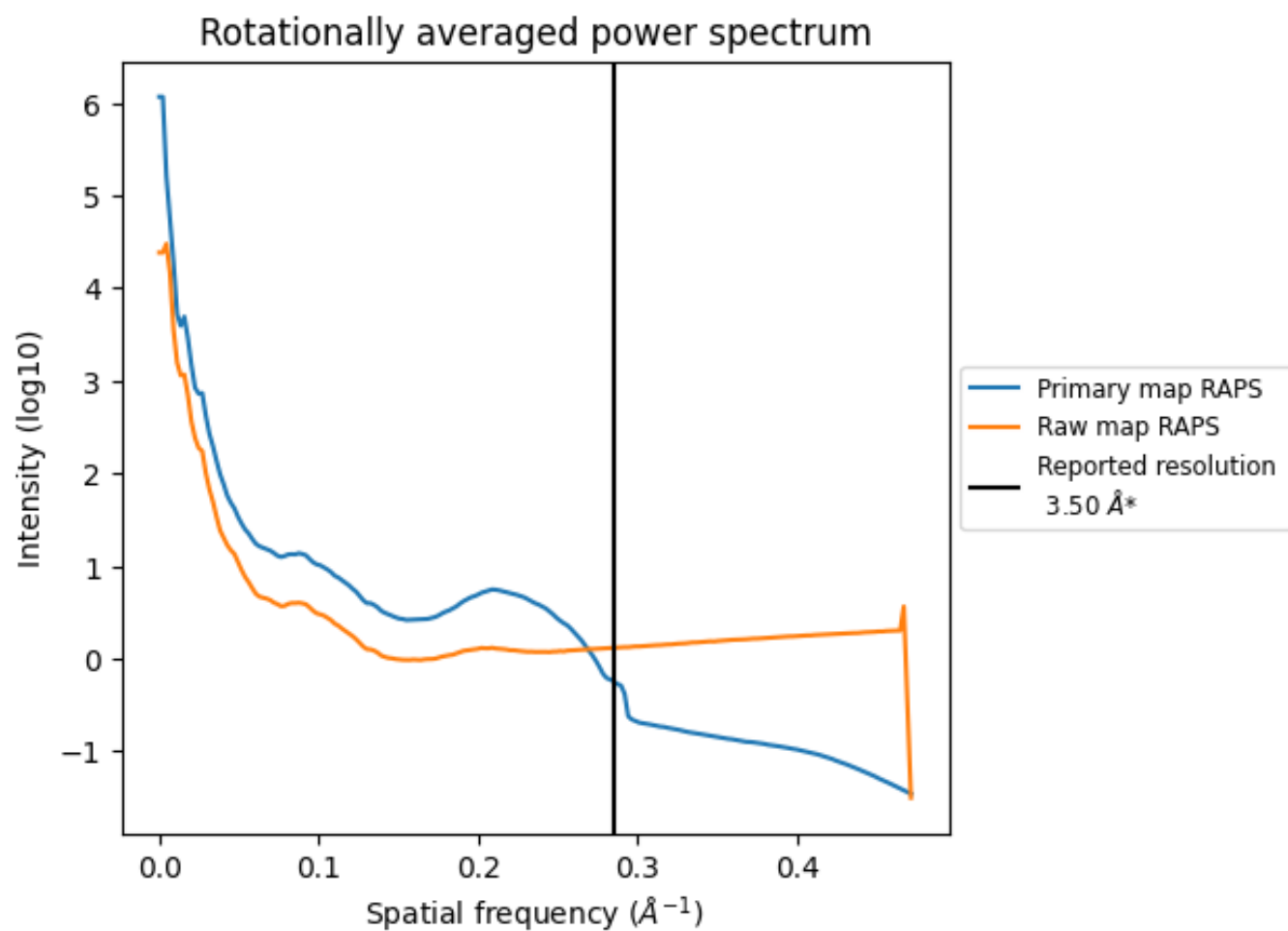
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1756 nm³; this corresponds to an approximate mass of 1586 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

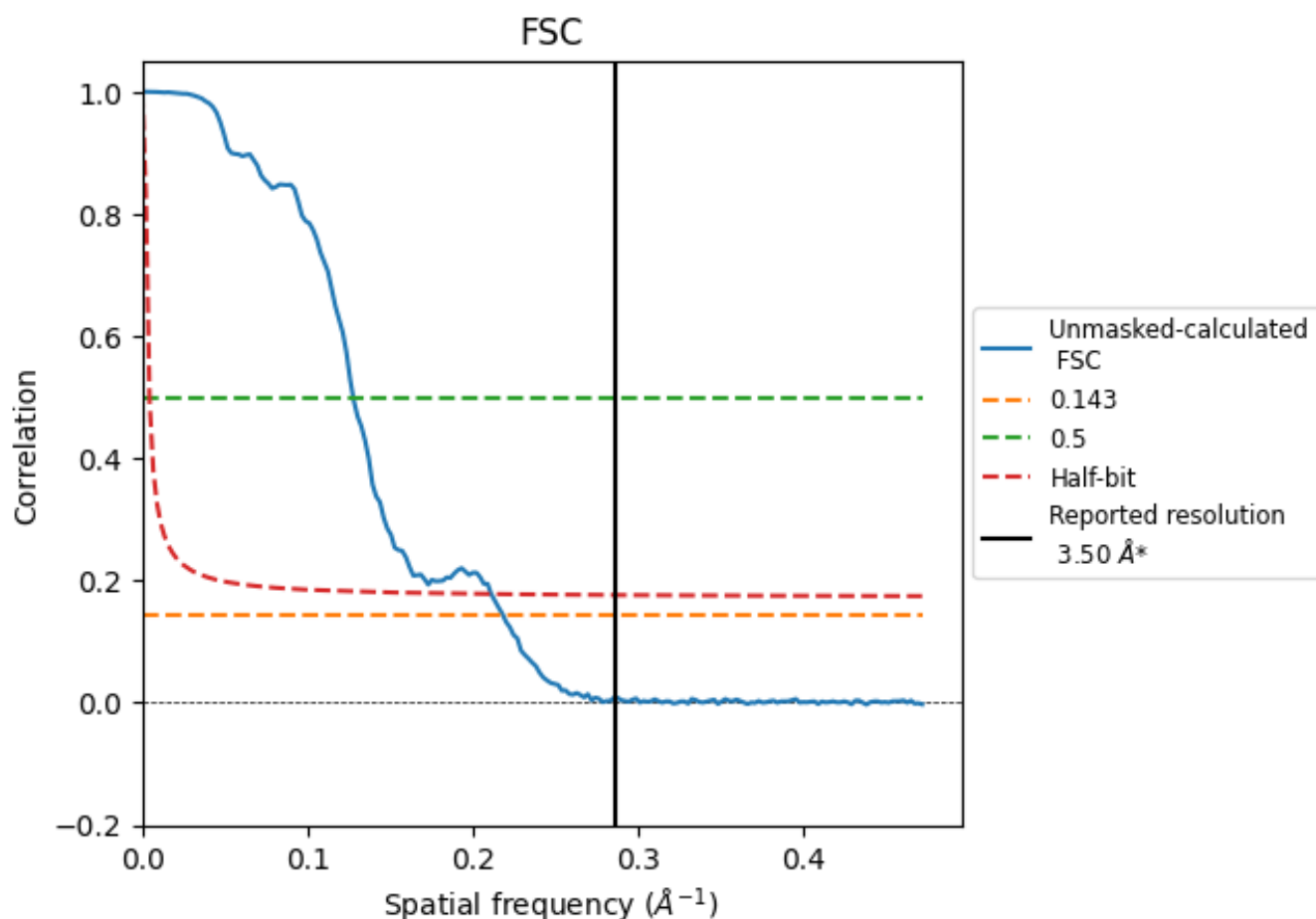


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

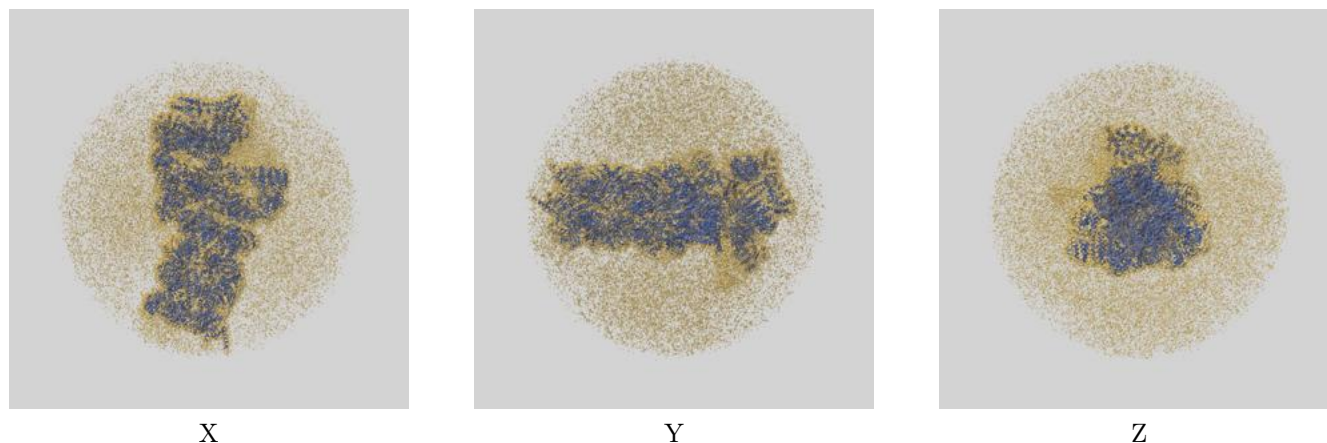
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.58	7.84	4.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.58 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

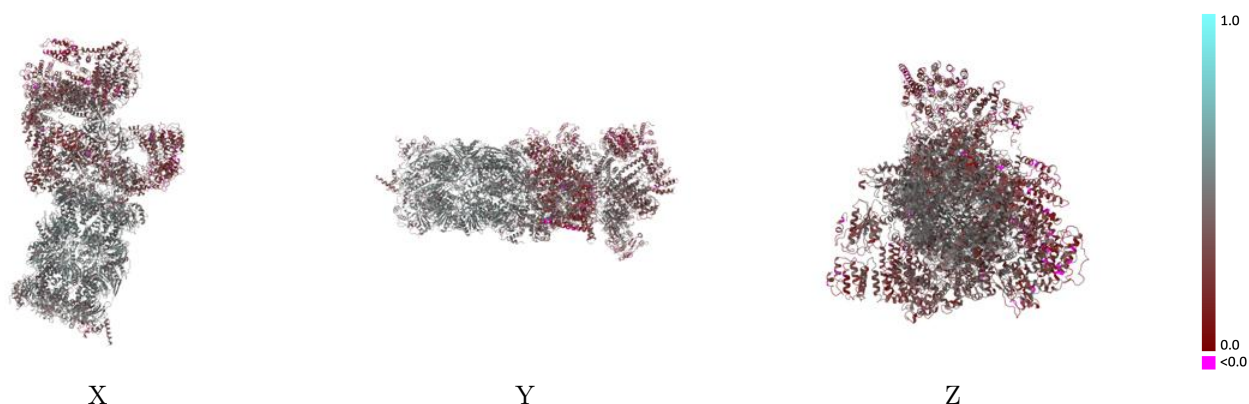
This section contains information regarding the fit between EMDB map EMD-64133 and PDB model 9UG9. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



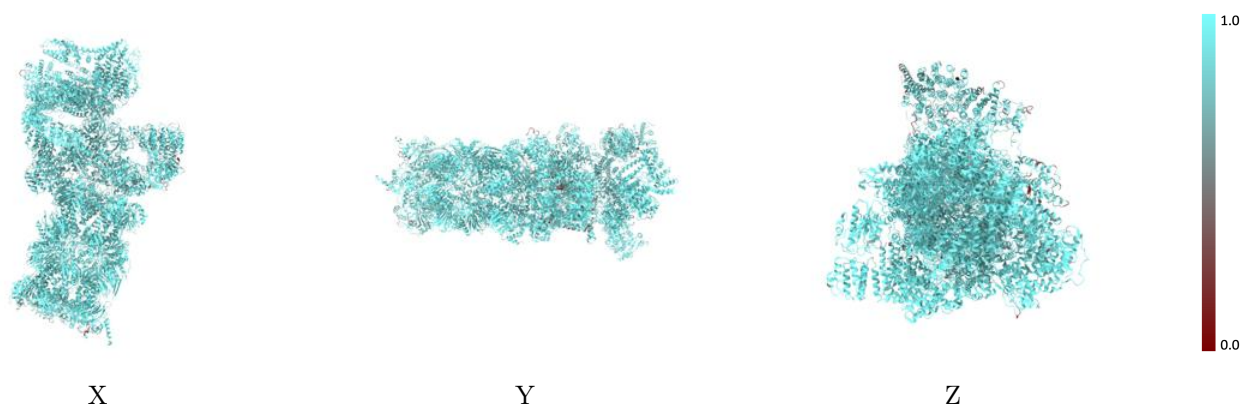
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



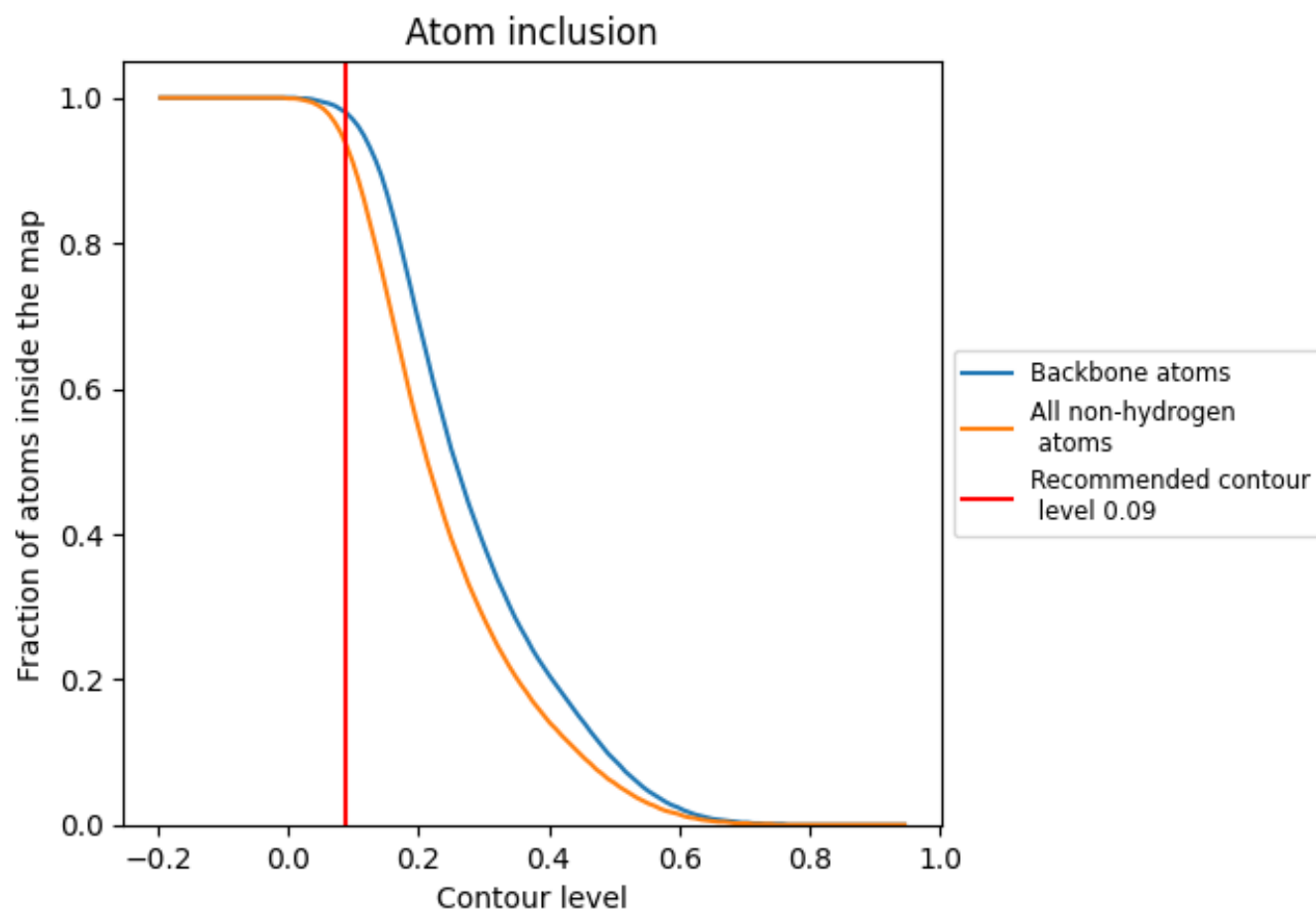
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.3990
A	 0.9250	 0.3800
B	 0.9190	 0.3780
C	 0.8750	 0.3450
D	 0.9160	 0.4090
E	 0.9400	 0.4240
F	 0.9420	 0.4290
G	 0.9650	 0.4670
H	 0.9710	 0.4780
I	 0.9610	 0.4480
J	 0.9840	 0.4710
K	 0.9760	 0.4730
L	 0.9740	 0.4760
M	 0.9710	 0.4760
N	 0.9800	 0.4960
O	 0.9900	 0.5020
P	 0.9840	 0.4940
Q	 0.9880	 0.5090
R	 0.9920	 0.4990
S	 0.9830	 0.4950
T	 0.9860	 0.5030
U	 0.9530	 0.3290
V	 0.8690	 0.2550
W	 0.9150	 0.3040
X	 0.8860	 0.3330
Y	 0.9190	 0.3070
Z	 0.9390	 0.4000
a	 0.9520	 0.3010
b	 0.9370	 0.3410
c	 0.9420	 0.3960
d	 0.8920	 0.2400
e	 0.9780	 0.3130
f	 0.8700	 0.2480
g	 0.8770	 0.4470
h	 0.9160	 0.4600



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Chain	Atom inclusion	Q-score
i	 0.9150	 0.4420
j	 0.8900	 0.4240
k	 0.8930	 0.4420
l	 0.9200	 0.4670
m	 0.8750	 0.4500
n	 0.9900	 0.4870
o	 0.9920	 0.4870
p	 0.9880	 0.4940
q	 0.9870	 0.4900
r	 0.9910	 0.5030
s	 0.9840	 0.4970
t	 0.9850	 0.5030
u	 0.8250	 0.2830
v	 0.8530	 0.4750