



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 12:29 PM UTC

PDB ID : 5VFU / pdb_00005vfu
EMDB ID : EMD-8668
Title : Nucleotide-driven Triple-state Remodeling of the AAA-ATPase Channel in the Activated Human 26S Proteasome
Authors : Zhu, Y.; Wang, W.L.; Yu, D.; Ouyang, Q.; Lu, Y.; Mao, Y.
Deposited on : 2017-04-09
Resolution : 5.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

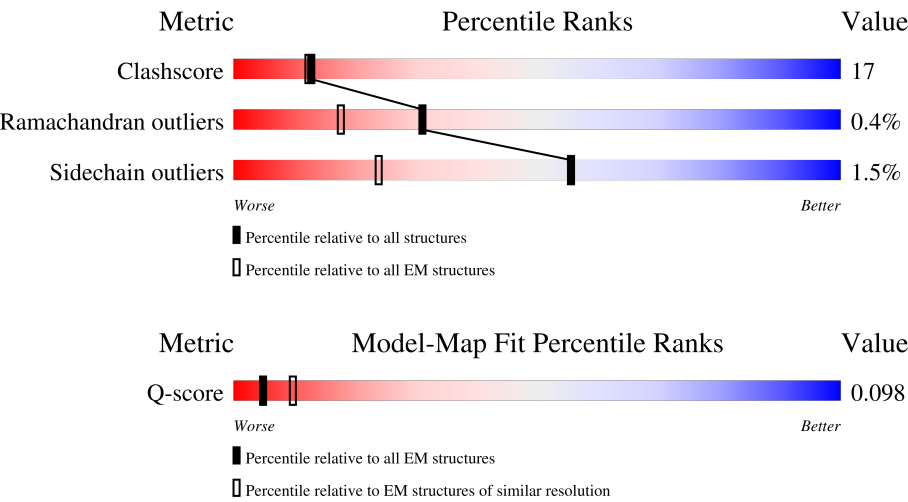
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.80 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.



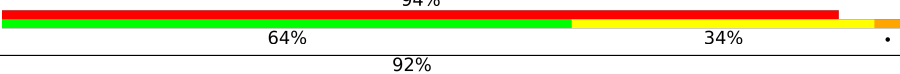
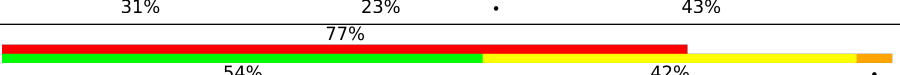
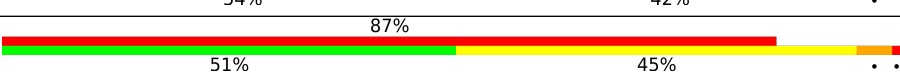
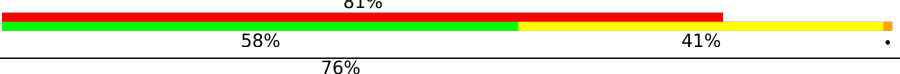
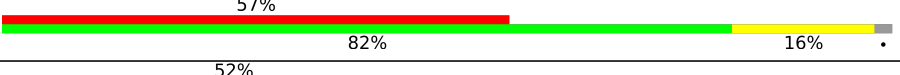
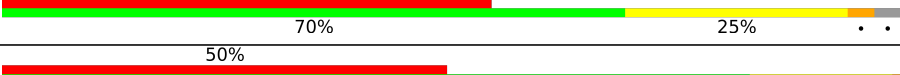
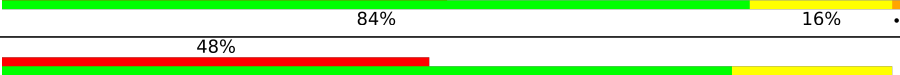
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	511 (5.30 - 6.30)

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	911	68% 60% 28% 12%
2	V	480	91% 53% 44% ..
3	W	456	94% 60% 38% .
4	X	380	60% 42% 21% 37%

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Mol	Chain	Length	Quality of chain
5	Y	378	
6	Z	286	
7	a	373	
8	b	191	
9	c	287	
10	d	257	
11	e	70	
12	A	361	
13	B	348	
14	C	384	
15	D	380	
16	E	353	
17	F	377	
18	G	240	
18	g	240	
19	H	232	
19	h	232	
20	I	250	
20	i	250	
21	J	243	
21	j	243	
22	K	234	
22	k	234	
23	L	238	
23	l	238	

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Mol	Chain	Length	Quality of chain
24	M	245	
24	m	245	
25	N	191	
25	n	191	
26	O	220	
26	o	220	
27	P	204	
27	p	204	
28	Q	199	
28	q	199	
29	R	201	
29	r	201	
30	S	213	
30	s	213	
31	T	215	
31	t	215	
32	f	908	

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 100133 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 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	806	Total	C	N	O	S	0	0
			6287	3990	1075	1178	44		

- Molecule 2 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V	480	Total	C	N	O	S	0	0
			3852	2444	684	710	14		

- Molecule 3 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	456	Total	C	N	O	S	0	0
			3703	2339	635	704	25		

- Molecule 4 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	241	Total	C	N	O	S	0	0
			1905	1212	320	365	8		

- Molecule 5 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Y	378	Total	C	N	O	S	0	0
			3115	1987	533	578	17		

- Molecule 6 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Z	286	Total	C	N	O	S	0	0
			2281	1457	392	427	5		

- Molecule 7 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	a	373	Total	C	N	O	S	0	0
			2993	1910	509	559	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	13	SER	ASN	conflict	UNP Q9UNM6

- Molecule 8 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	b	191	Total	C	N	O	S	0	0
			1458	910	261	279	8		

- Molecule 9 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	c	278	Total	C	N	O	S	0	0
			2187	1389	374	406	18		

- Molecule 10 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	d	257	Total	C	N	O	S	0	0
			2116	1371	346	390	9		

- Molecule 11 is a protein called Sem1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e	40	Total	C	N	O	S	0	0
			334	200	55	77	2		

- Molecule 12 is a protein called 26S protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	361	Total	C	N	O	S	0	0
			2834	1788	500	528	18		

- Molecule 13 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	B	348	Total	C	N	O	S	0	0
			2717	1708	460	537	12		

- Molecule 14 is a protein called 26S protease regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C	384	Total	C	N	O	S	0	0
			3015	1894	540	564	17		

- Molecule 15 is a protein called 26S protease regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D	380	Total	C	N	O	S	0	0
			3040	1923	524	580	13		

- Molecule 16 is a protein called 26S protease regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E	353	Total	C	N	O	S	0	0
			2790	1755	494	525	16		

- Molecule 17 is a protein called 26S protease regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F	366	Total	C	N	O	S	0	0
			2863	1802	496	549	16		

- Molecule 18 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	240	Total	C	N	O	S	0	0
			1825	1160	304	348	13		
18	g	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		

- Molecule 19 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		
19	h	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	I	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		
20	i	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		

- Molecule 21 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	J	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		
21	j	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		

- Molecule 22 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	K	228	Total	C	N	O	S	0	0
			1722	1080	284	348	10		
22	k	228	Total	C	N	O	S	0	0
			1722	1080	284	348	10		

- Molecule 23 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		
23	l	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		

- Molecule 24 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	M	240	Total	C	N	O	S	0	0
			1856	1178	314	353	11		
24	m	240	Total	C	N	O	S	0	0
			1856	1178	314	353	11		

- Molecule 25 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	N	191	Total	C	N	O	S	0	0
			1430	893	245	280	12		
25	n	191	Total	C	N	O	S	0	0
			1430	893	245	280	12		

- Molecule 26 is a protein called Proteasome subunit beta type-7.

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

- Molecule 27 is a protein called Proteasome subunit beta type-3.

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

- Molecule 28 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		
28	q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		

- Molecule 29 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	R	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		
29	r	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		

- Molecule 30 is a protein called Proteasome subunit beta type-1.

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

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

- Molecule 31 is a protein called Proteasome subunit beta type-4.

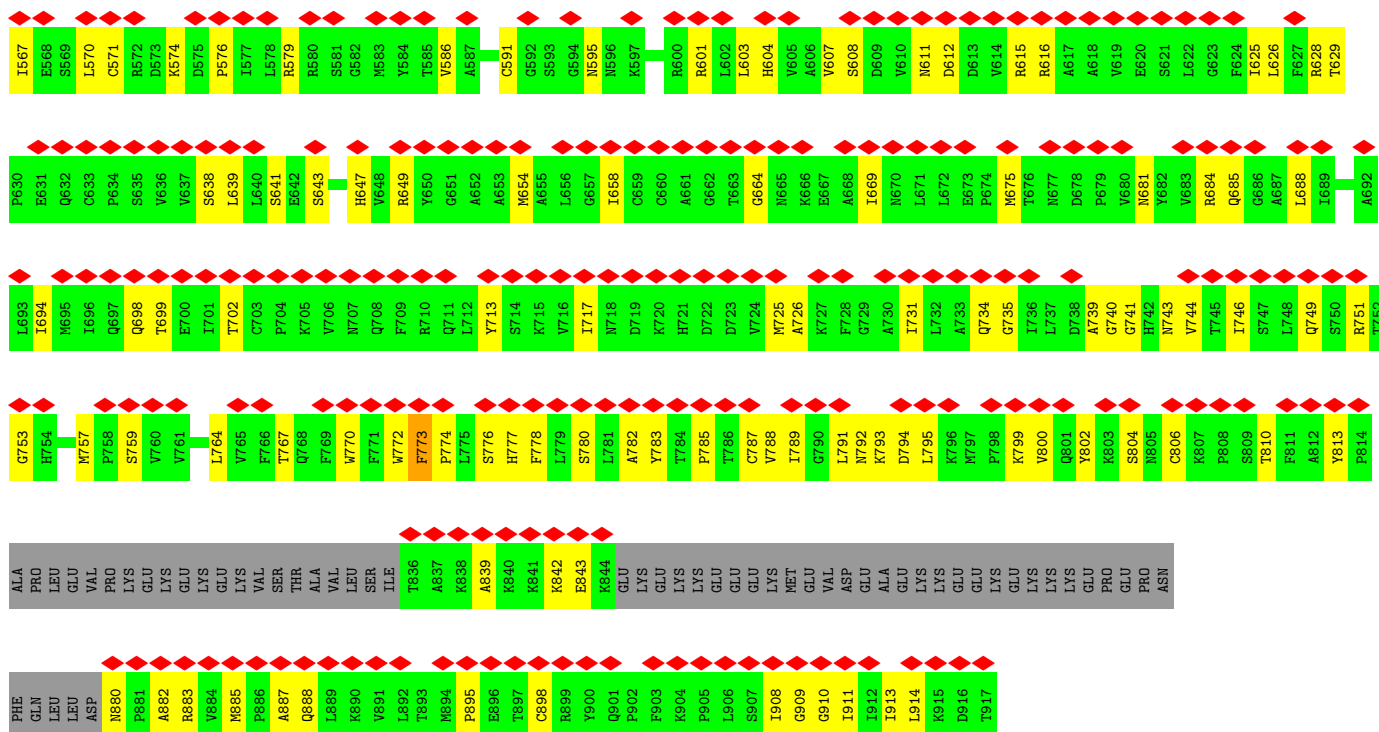
Mol	Chain	Residues	Atoms					AltConf	Trace
31	T	215	Total	C	N	O	S	0	0
			1667	1052	285	318	12		
31	t	215	Total	C	N	O	S	0	0
			1667	1052	285	318	12		

- Molecule 32 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

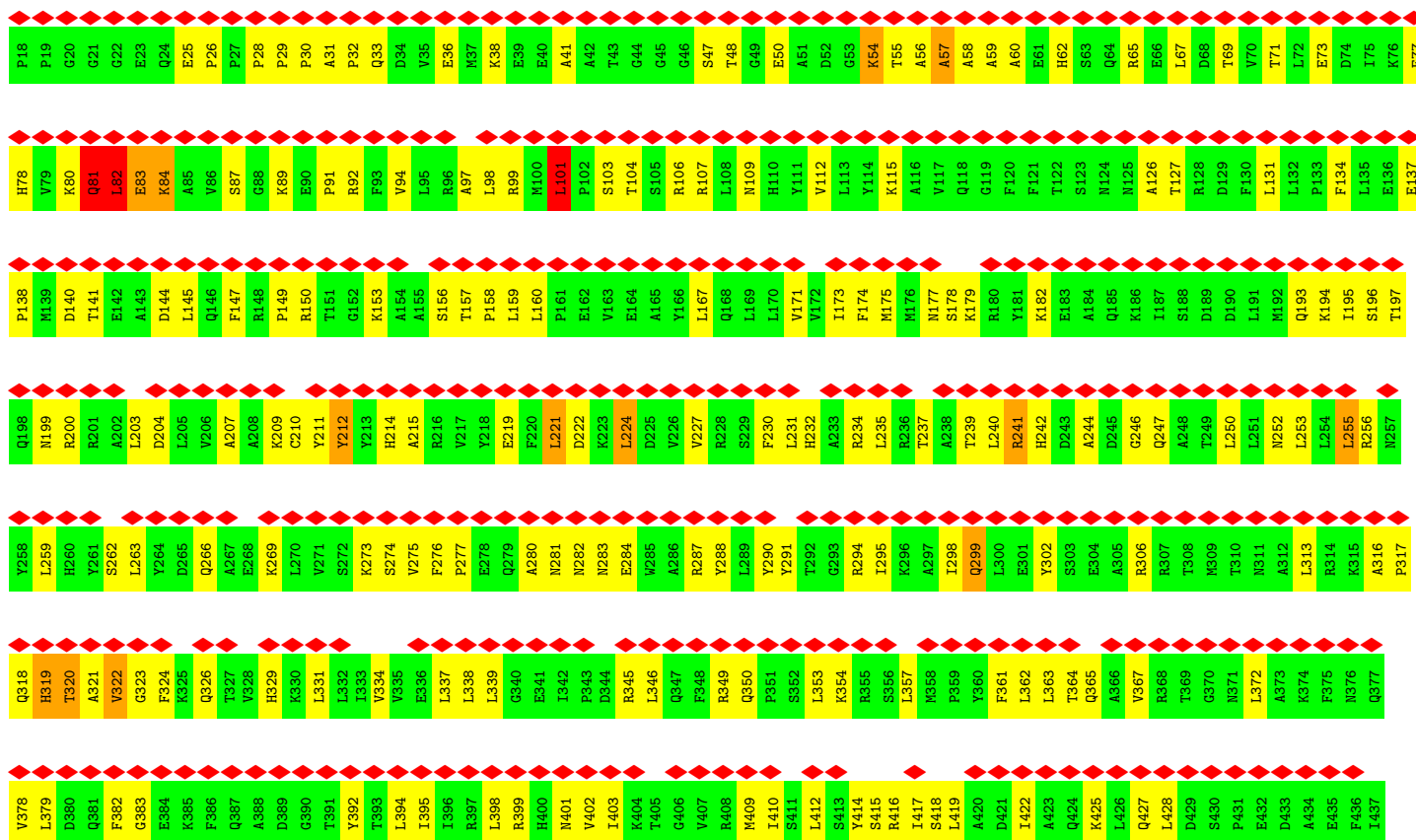
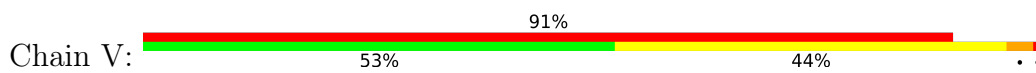
Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	689	Total	C	N	O	S	0	0
			5319	3343	904	1037	35		

- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
33	c	1	Total	Zn	0
			1	1	

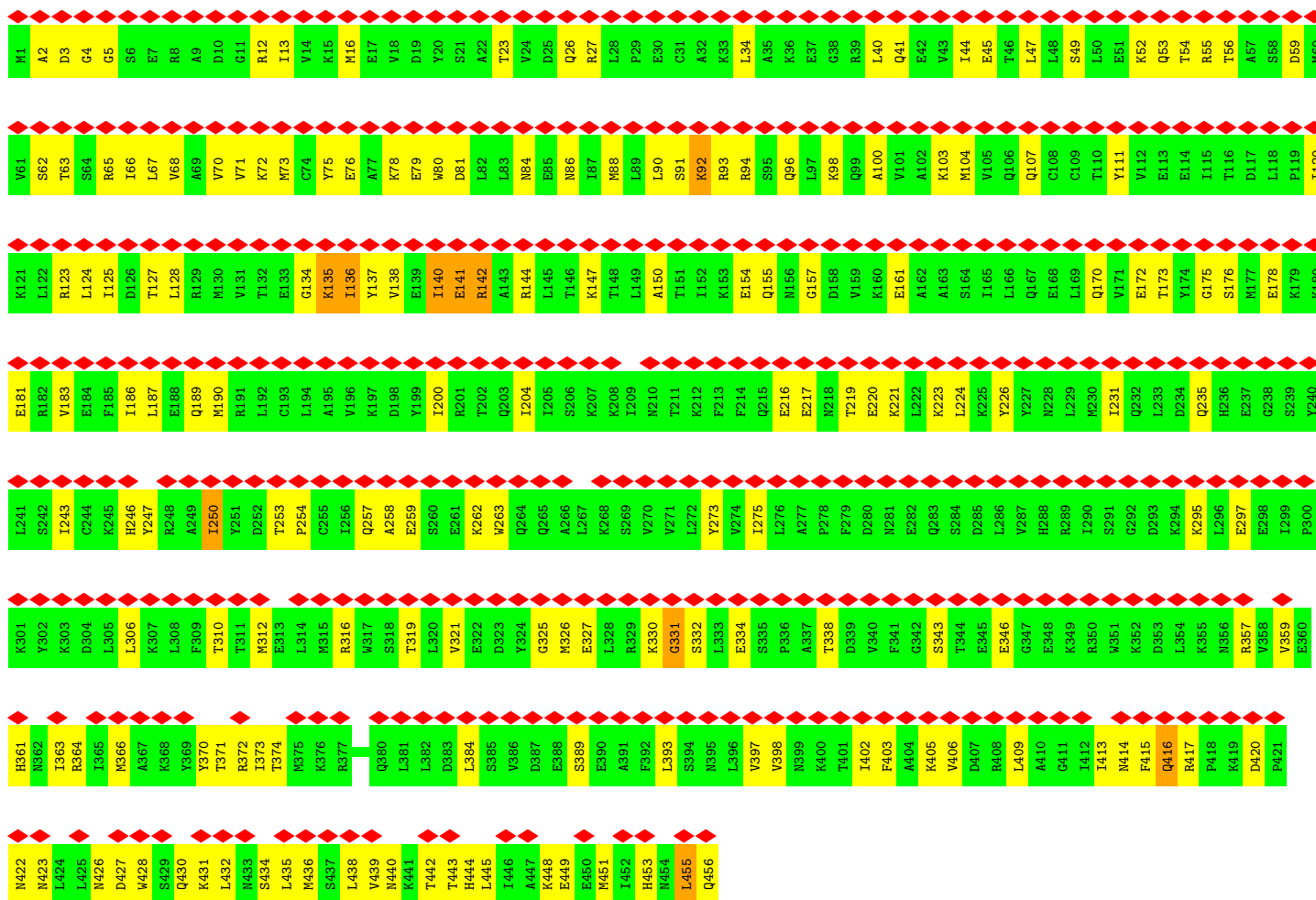


• Molecule 2: 26S proteasome non-ATPase regulatory subunit 3

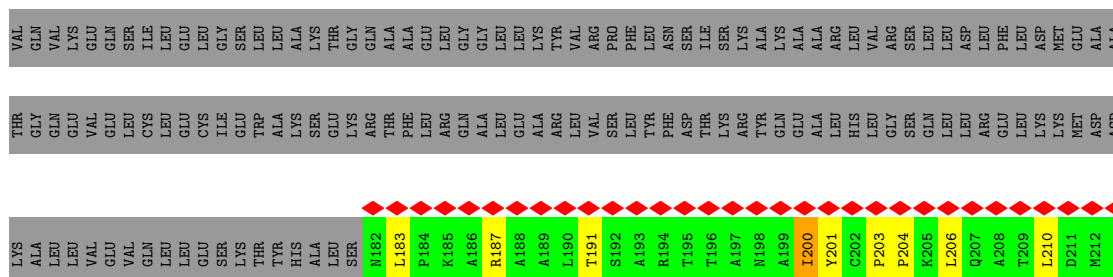
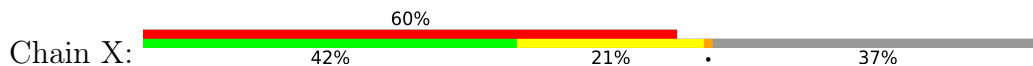


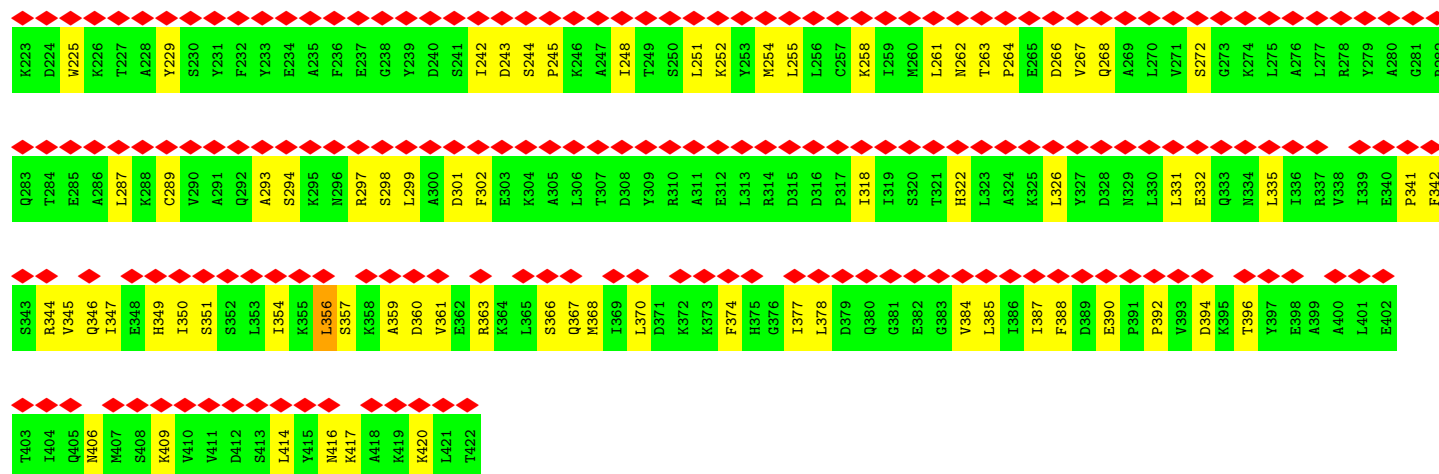


• Molecule 3: 26S proteasome non-ATPase regulatory subunit 12

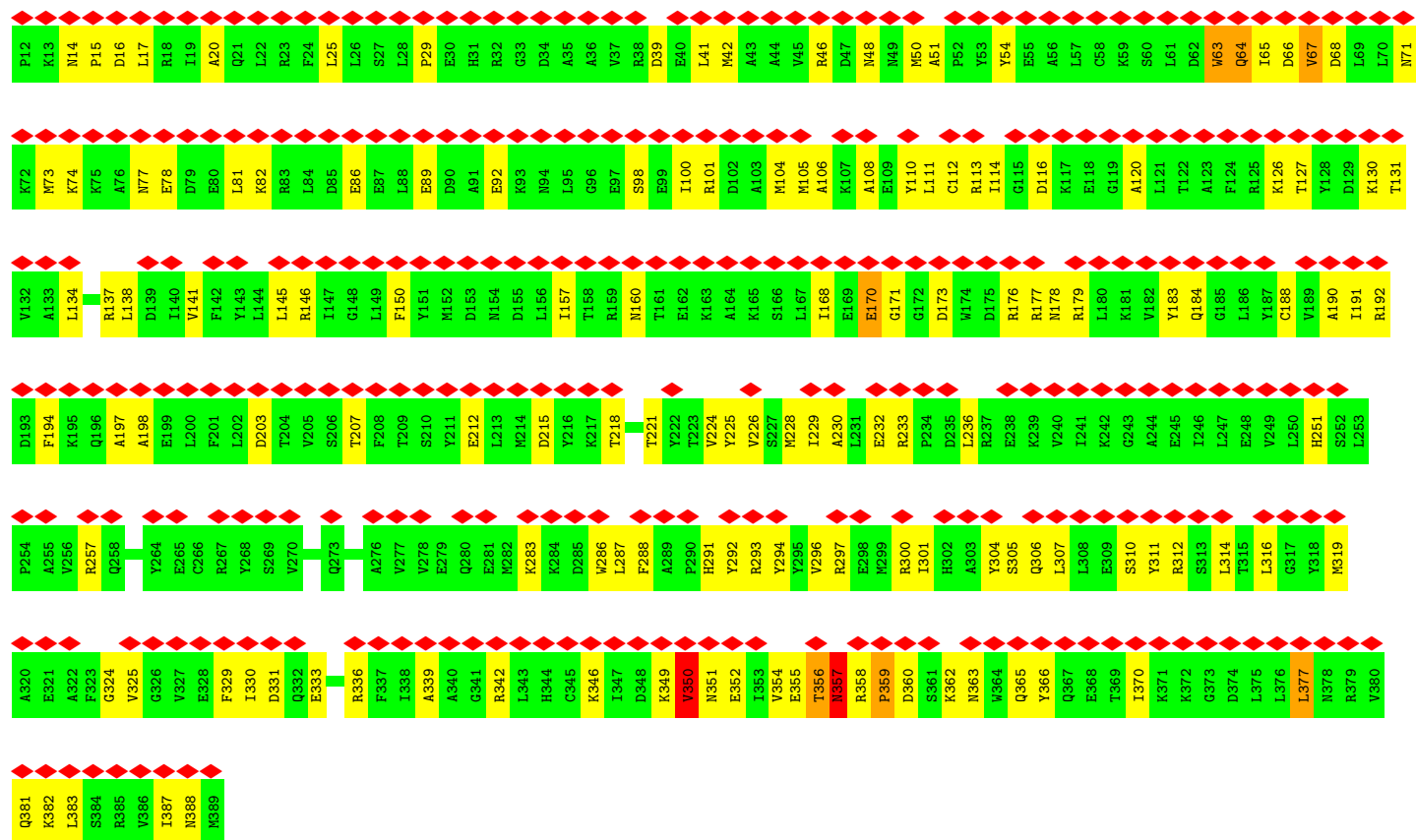
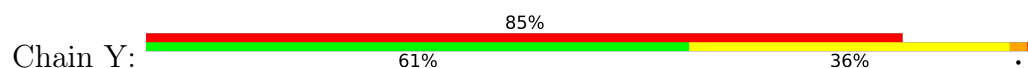


• Molecule 4: 26S proteasome non-ATPase regulatory subunit 11

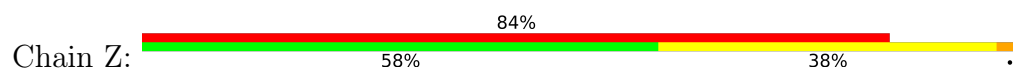


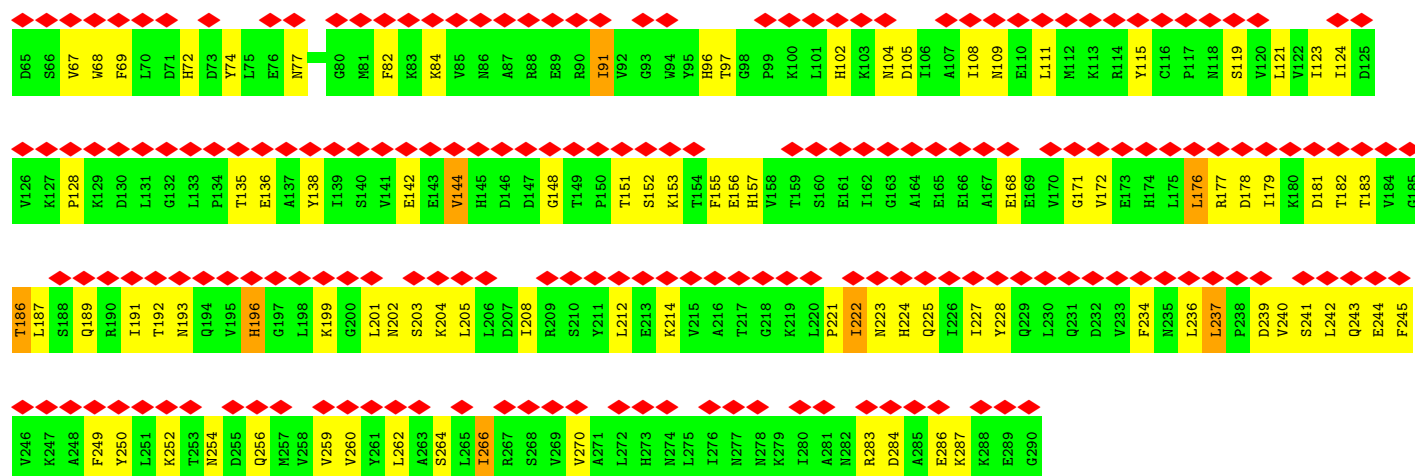


• Molecule 5: 26S proteasome non-ATPase regulatory subunit 6

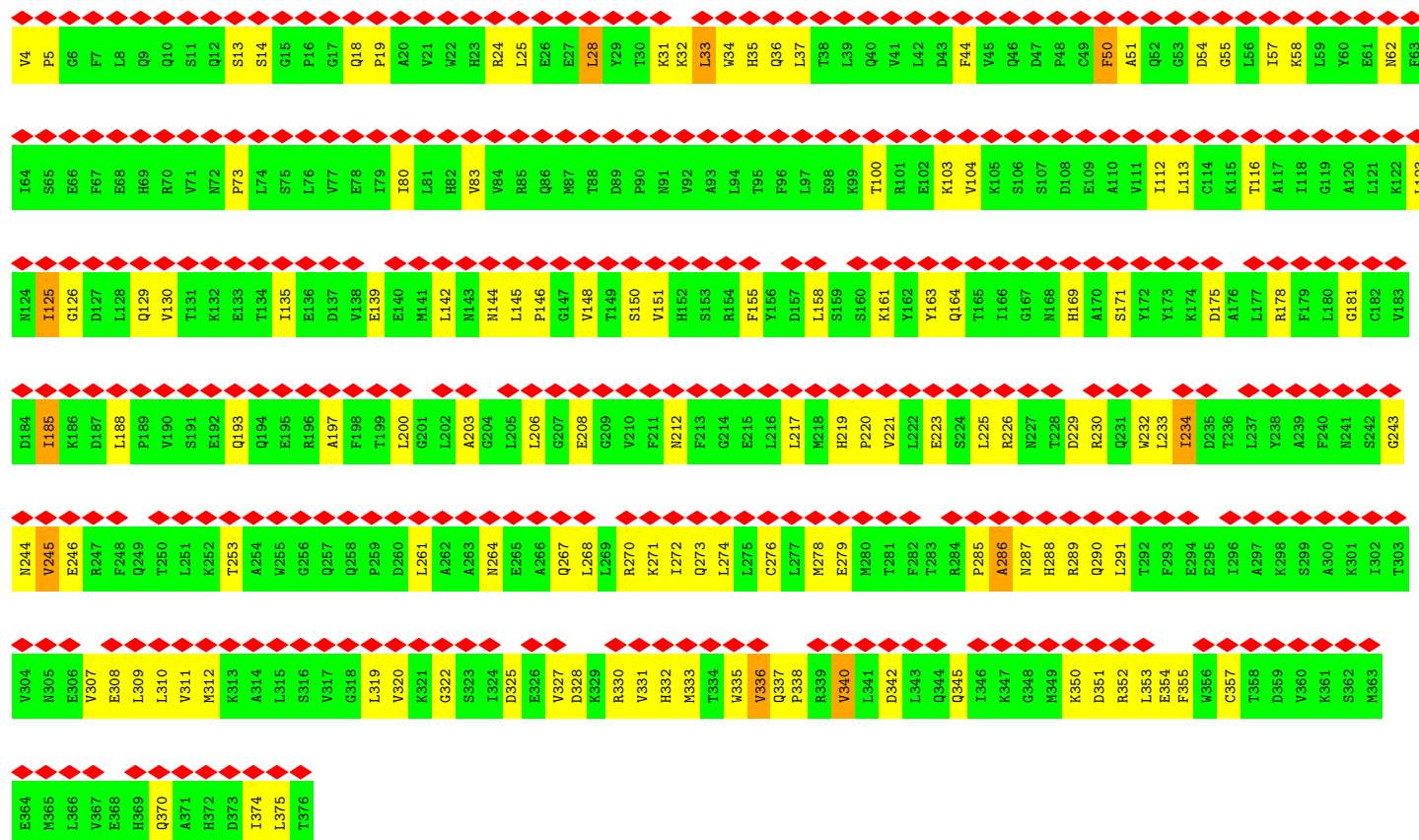


• Molecule 6: 26S proteasome non-ATPase regulatory subunit 7

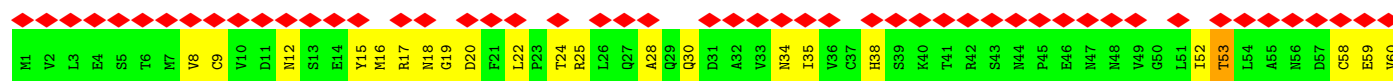


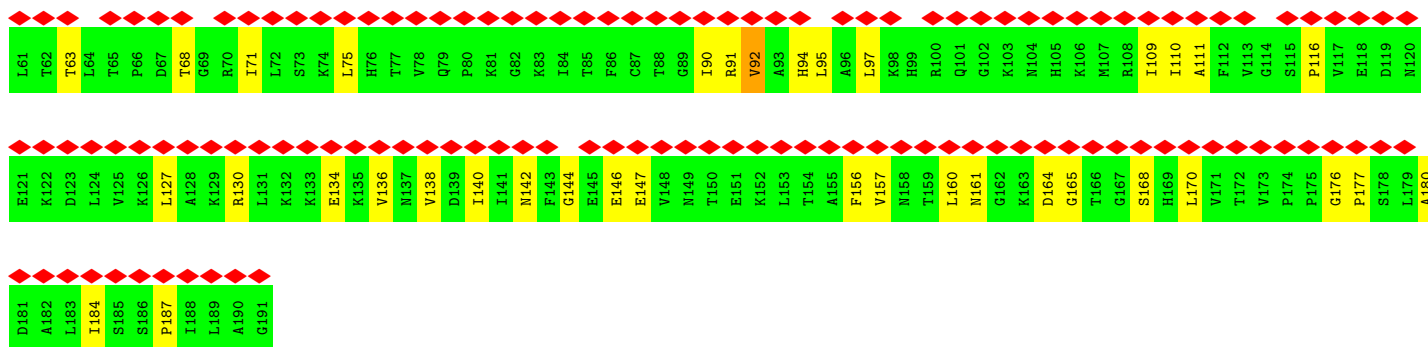


• Molecule 7: 26S proteasome non-ATPase regulatory subunit 13

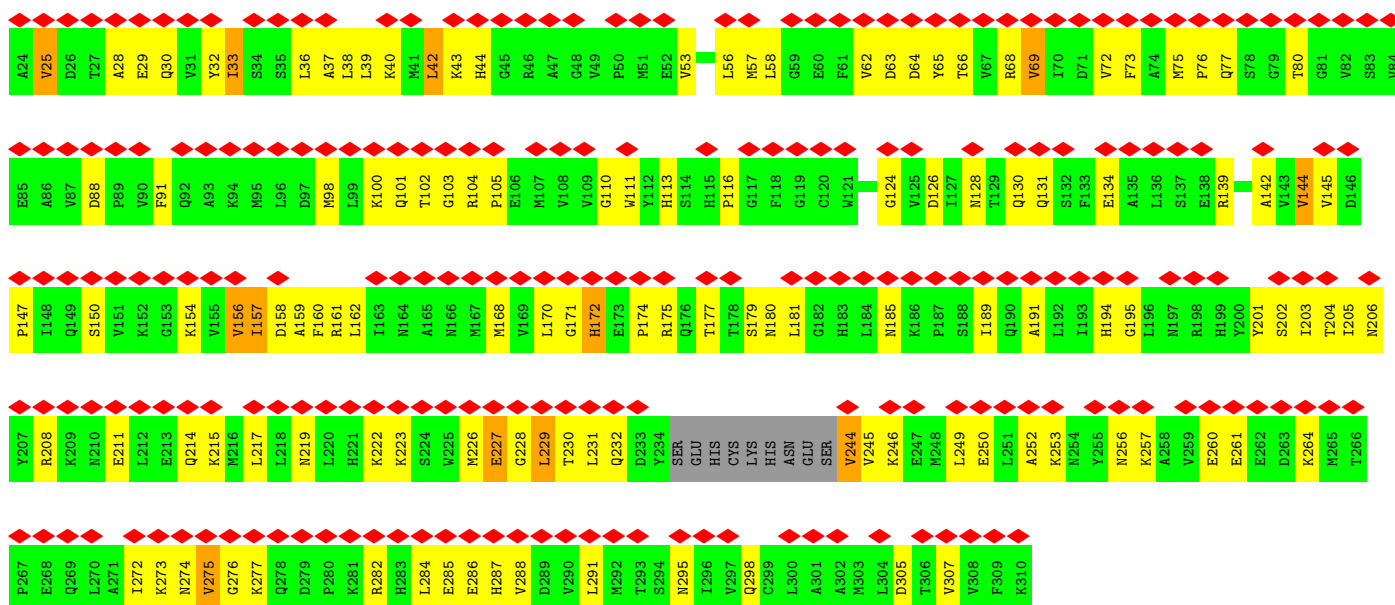
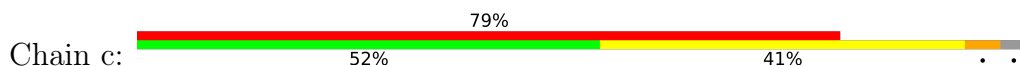


• Molecule 8: 26S proteasome non-ATPase regulatory subunit 4

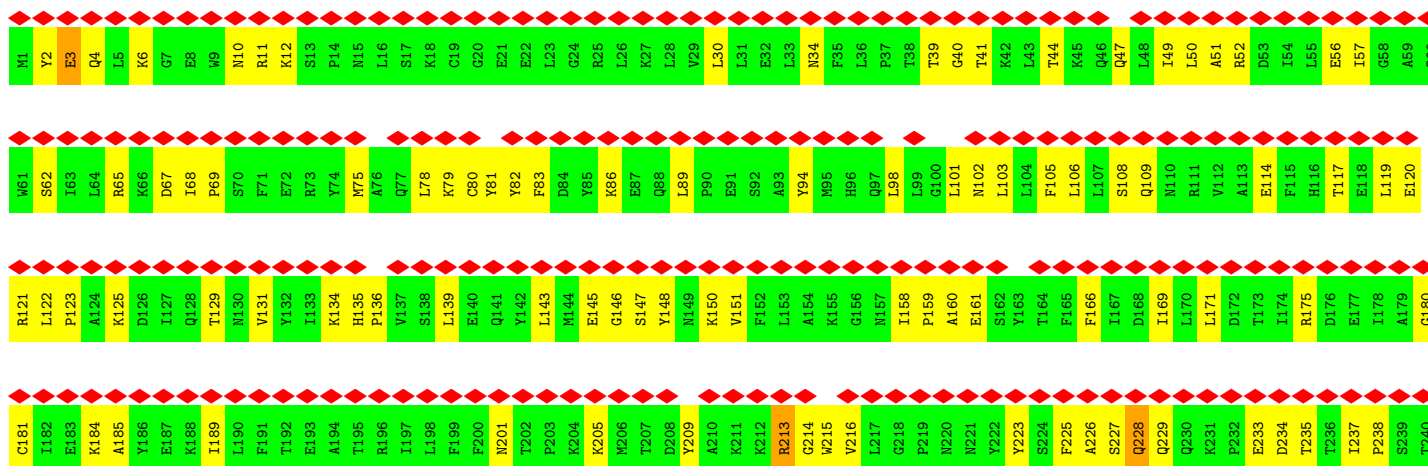


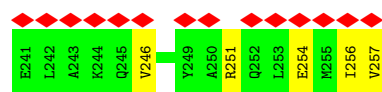


• Molecule 9: 26S proteasome non-ATPase regulatory subunit 14

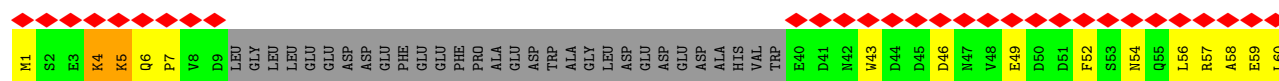
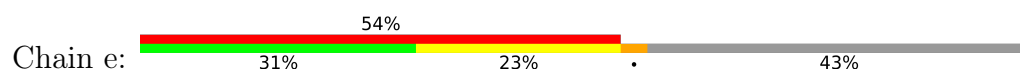


• Molecule 10: 26S proteasome non-ATPase regulatory subunit 8

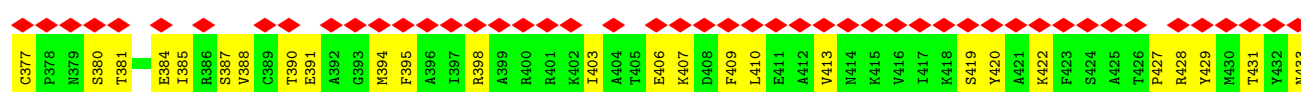
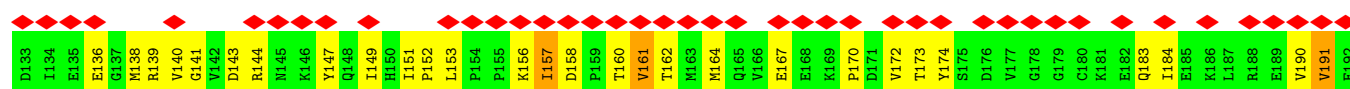
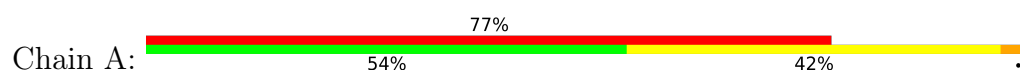




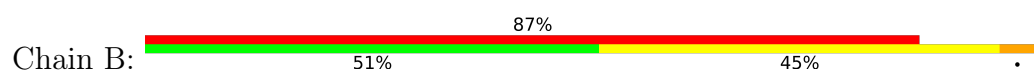
• Molecule 11: Sem1



• Molecule 12: 26S protease regulatory subunit 7



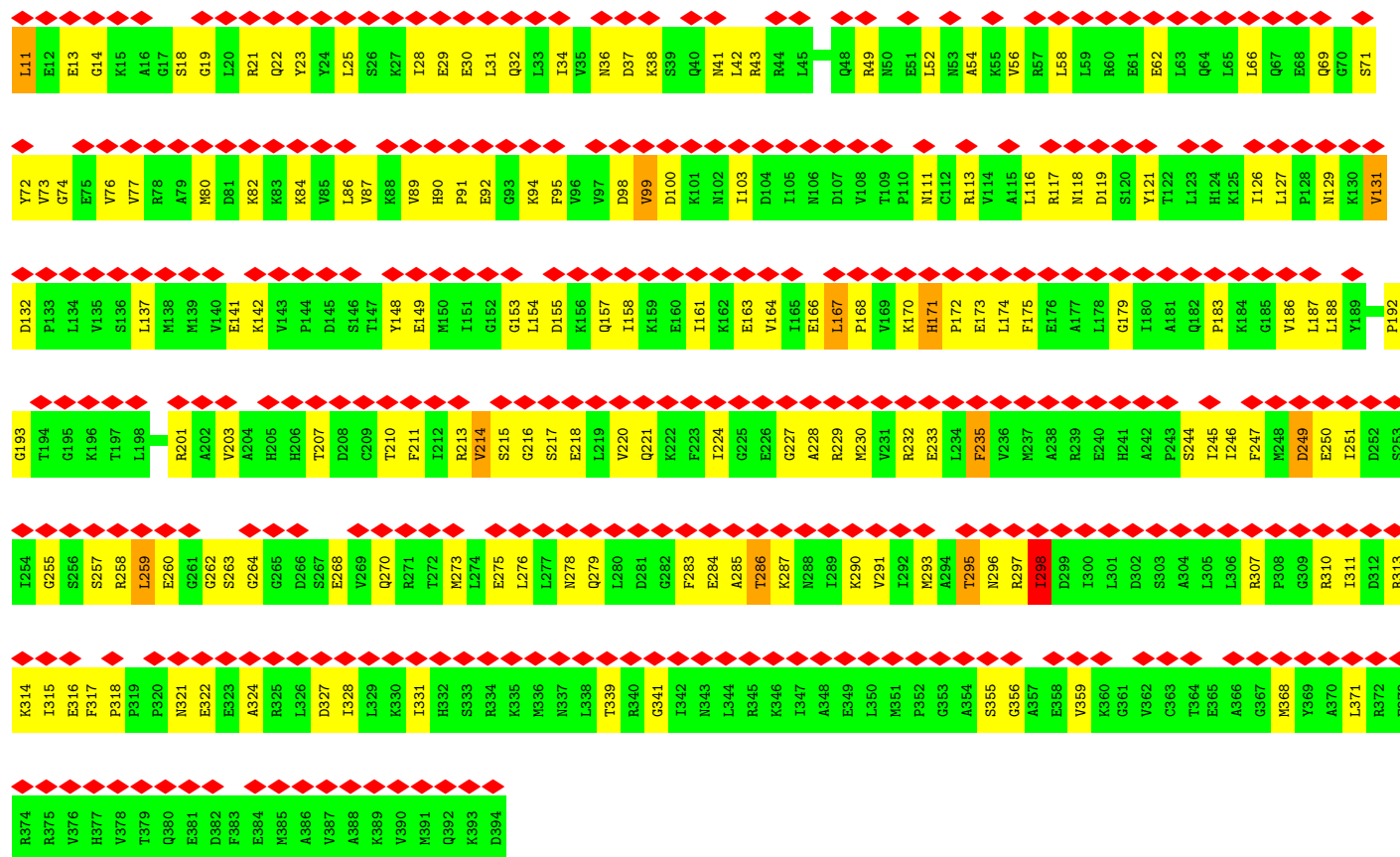
• Molecule 13: 26S protease regulatory subunit 4





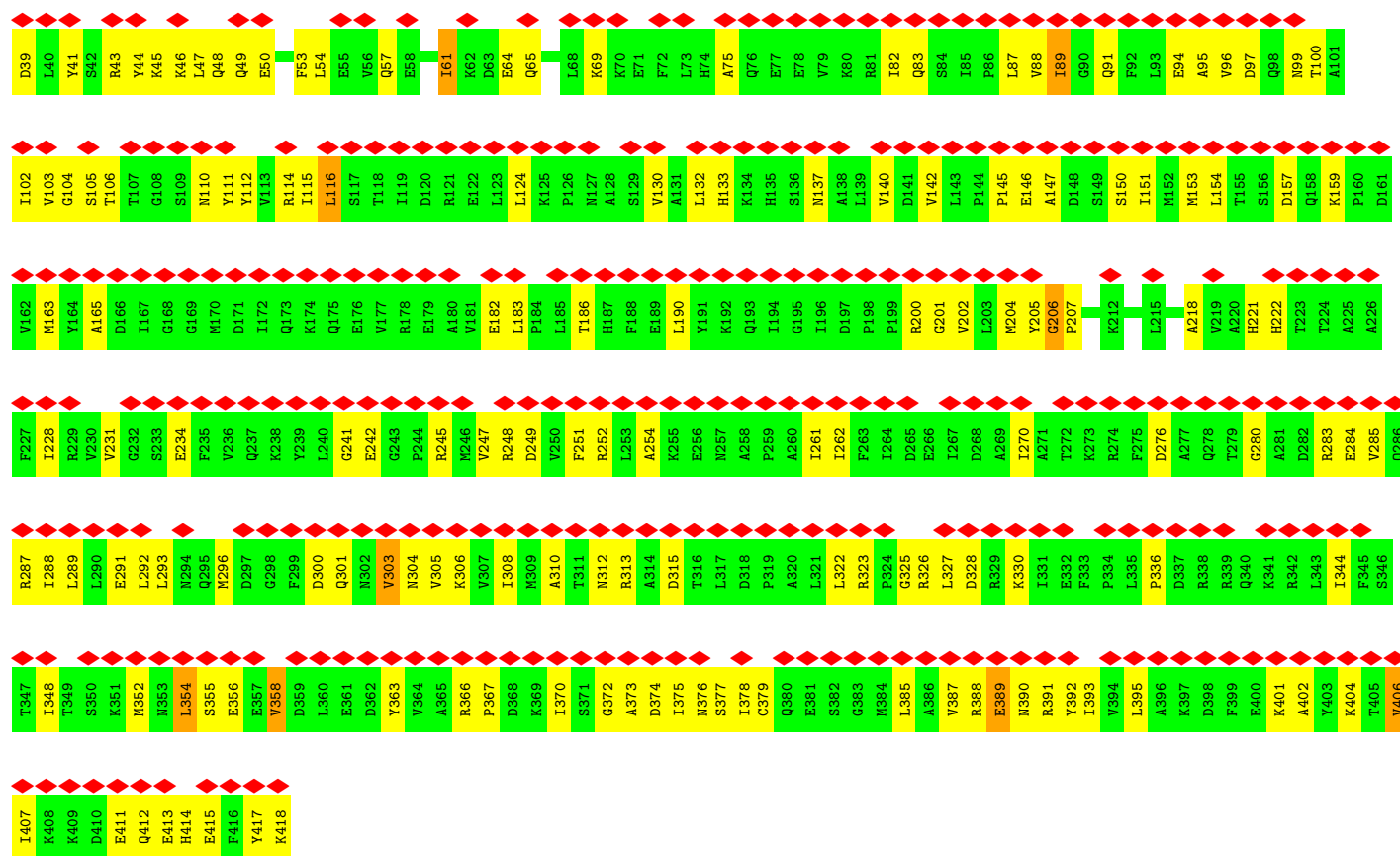
• Molecule 14: 26S protease regulatory subunit 8

Chain C:

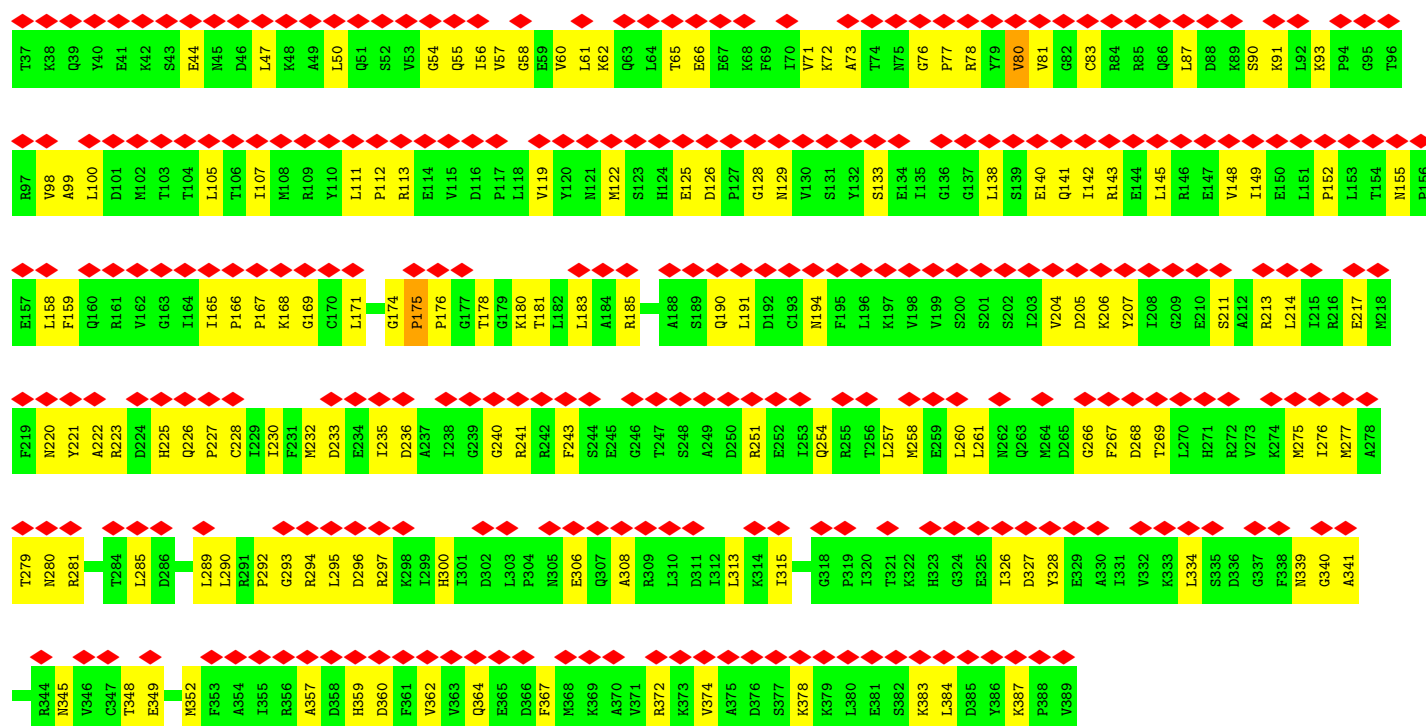
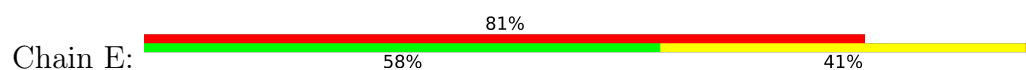


• Molecule 15: 26S protease regulatory subunit 6B

Chain D:

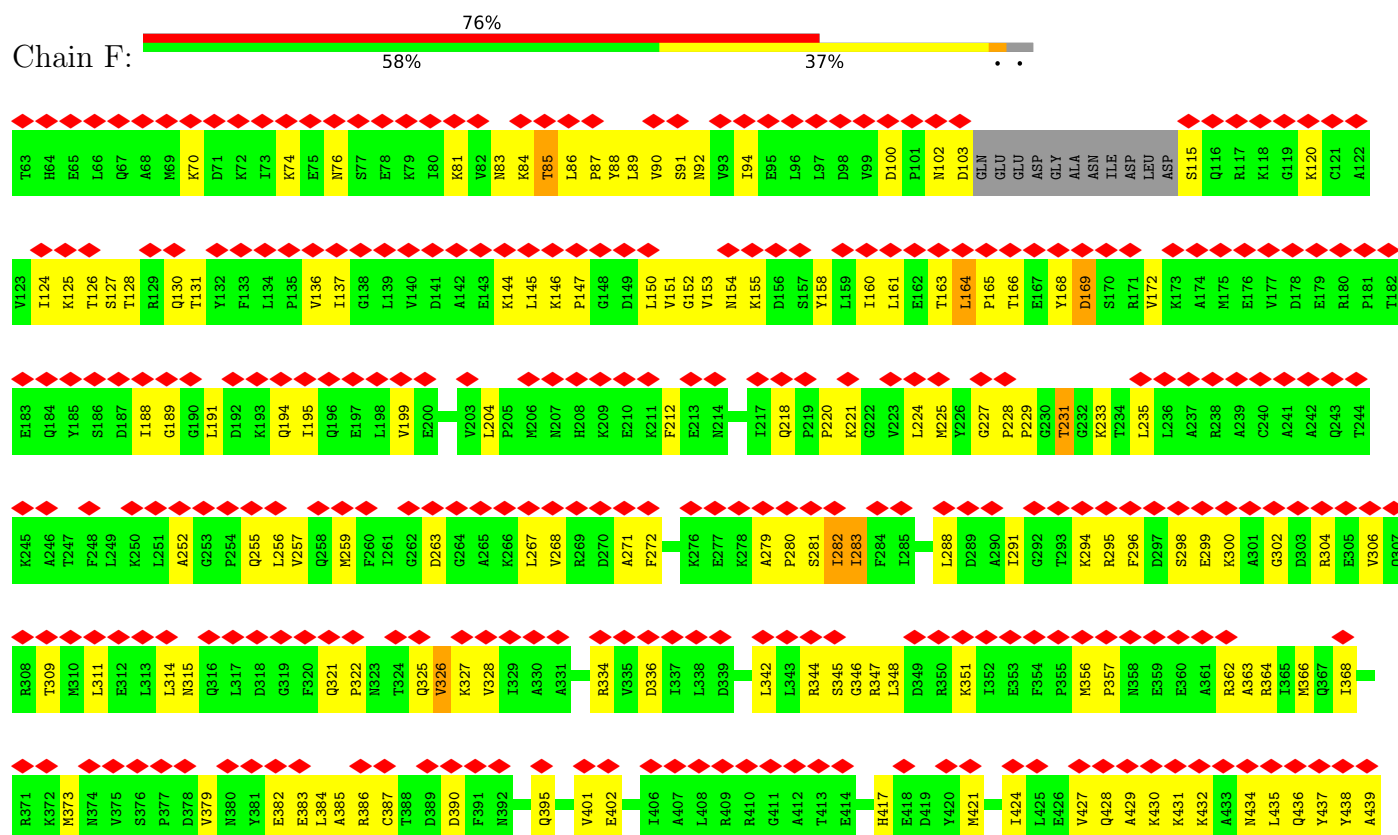


• Molecule 16: 26S protease regulatory subunit 10B



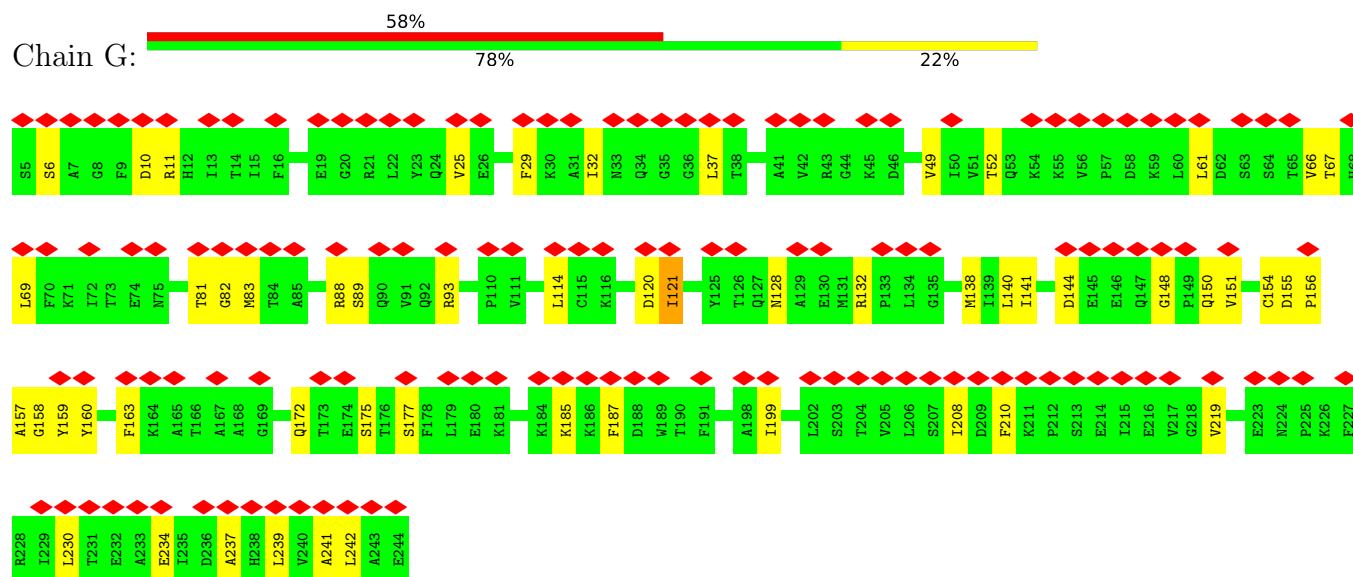
- Molecule 17: 26S protease regulatory subunit 6A

Chain F:



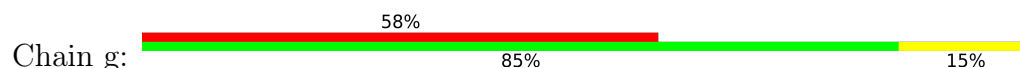
- Molecule 18: Proteasome subunit alpha type-6

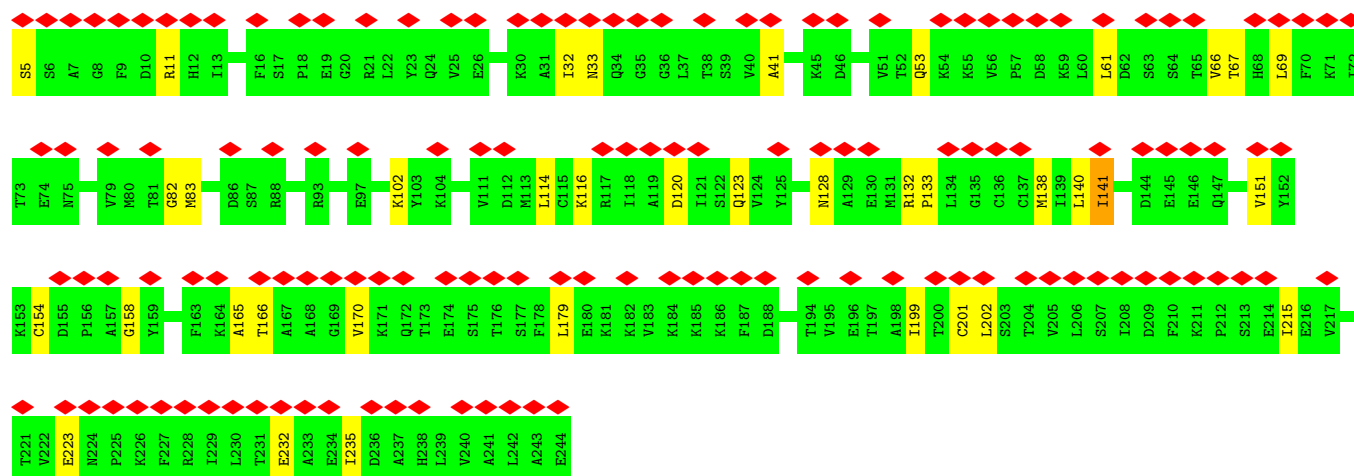
Chain G:



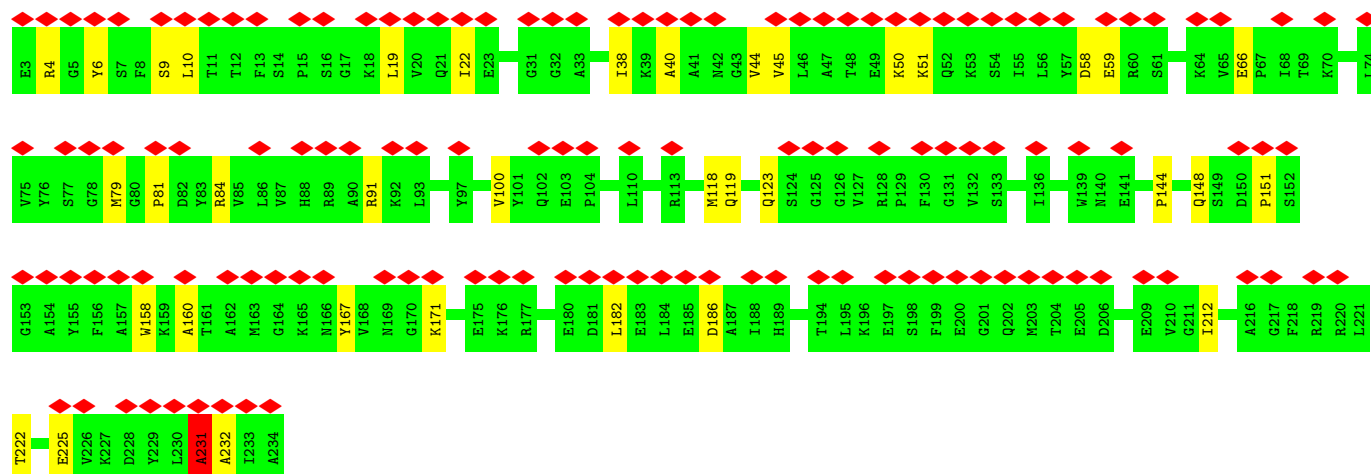
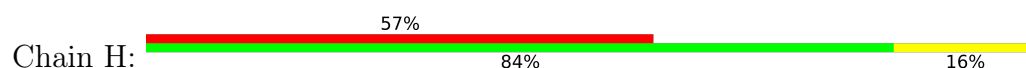
- Molecule 18: Proteasome subunit alpha type-6

Chain g:

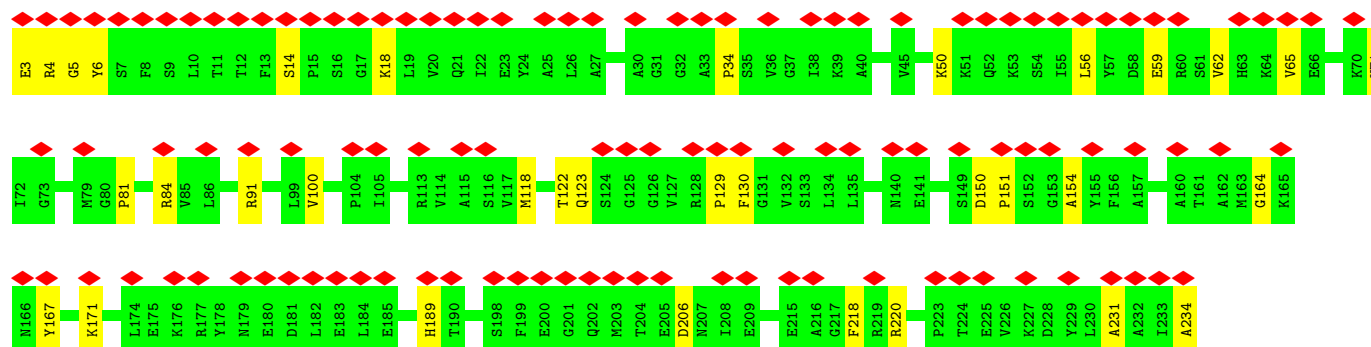
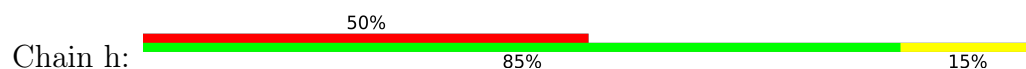




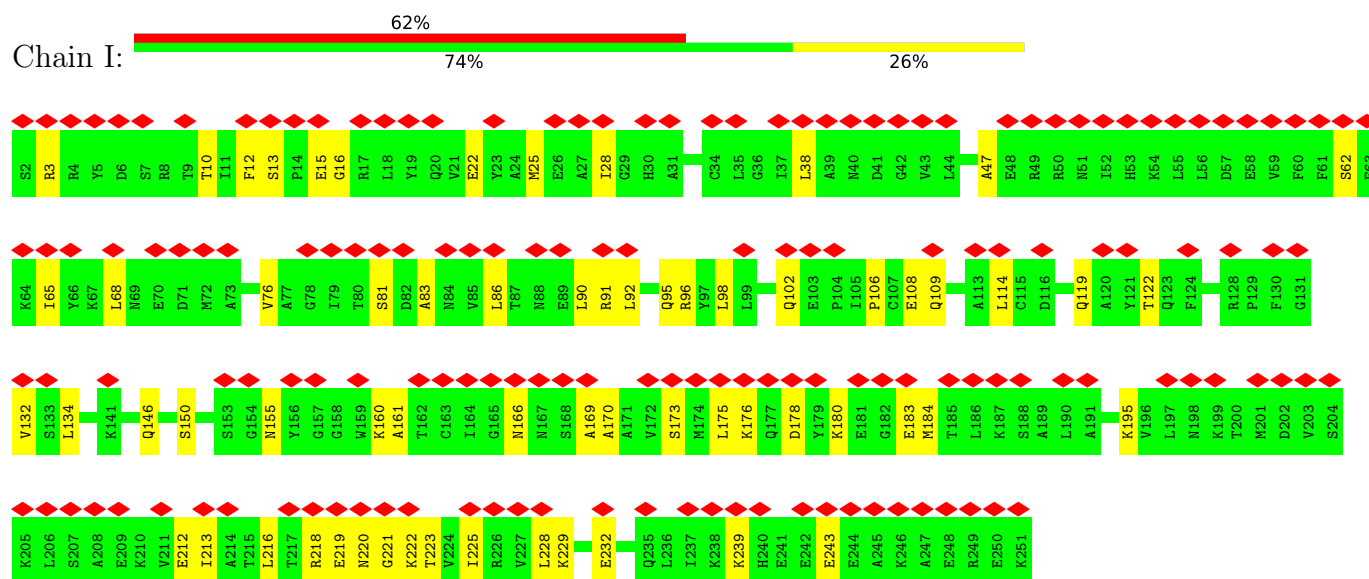
• Molecule 19: Proteasome subunit alpha type-2



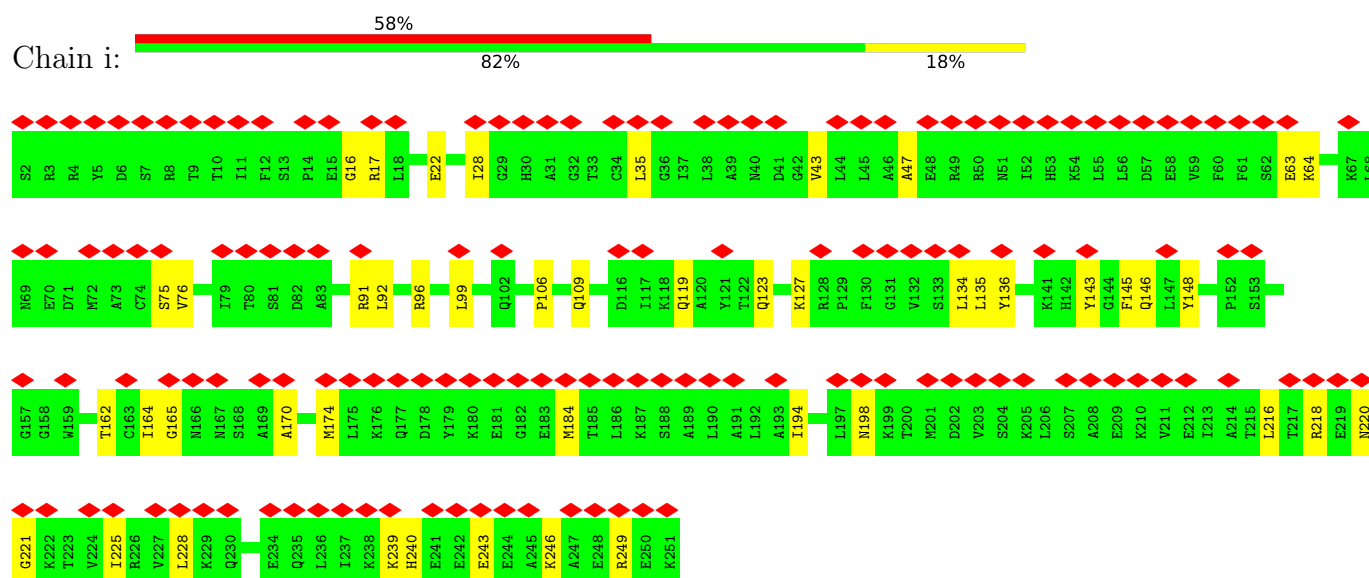
• Molecule 19: Proteasome subunit alpha type-2



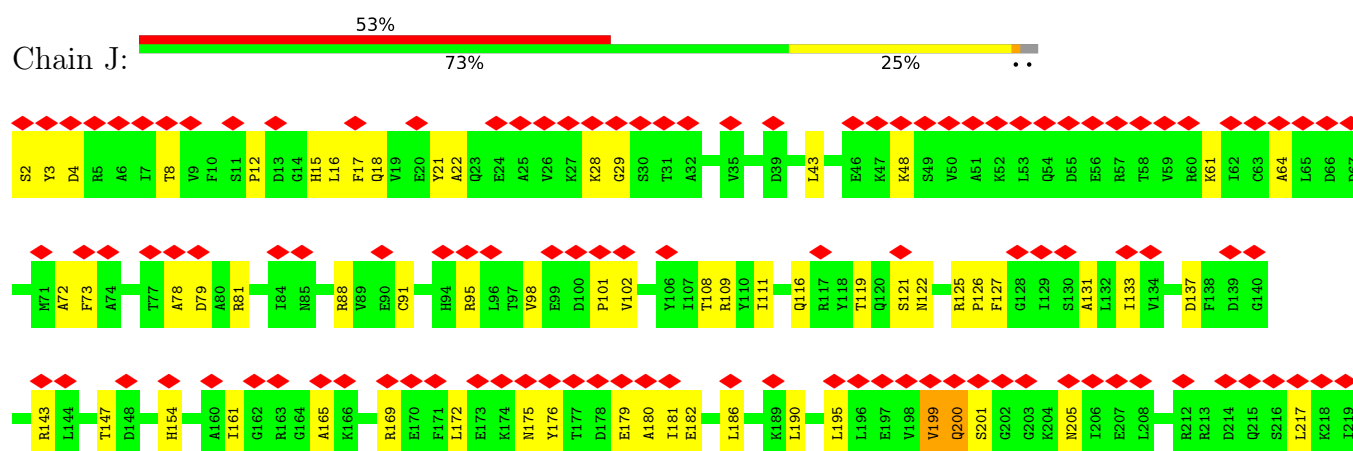
• Molecule 20: Proteasome subunit alpha type-4

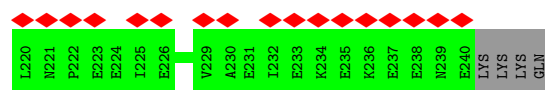


• Molecule 20: Proteasome subunit alpha type-4



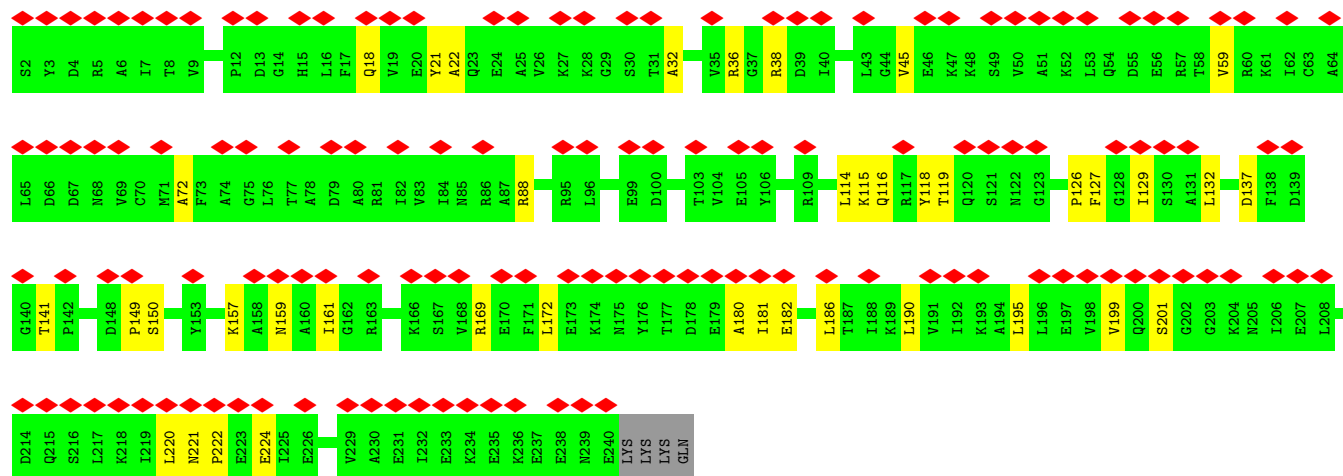
• Molecule 21: Proteasome subunit alpha type-7





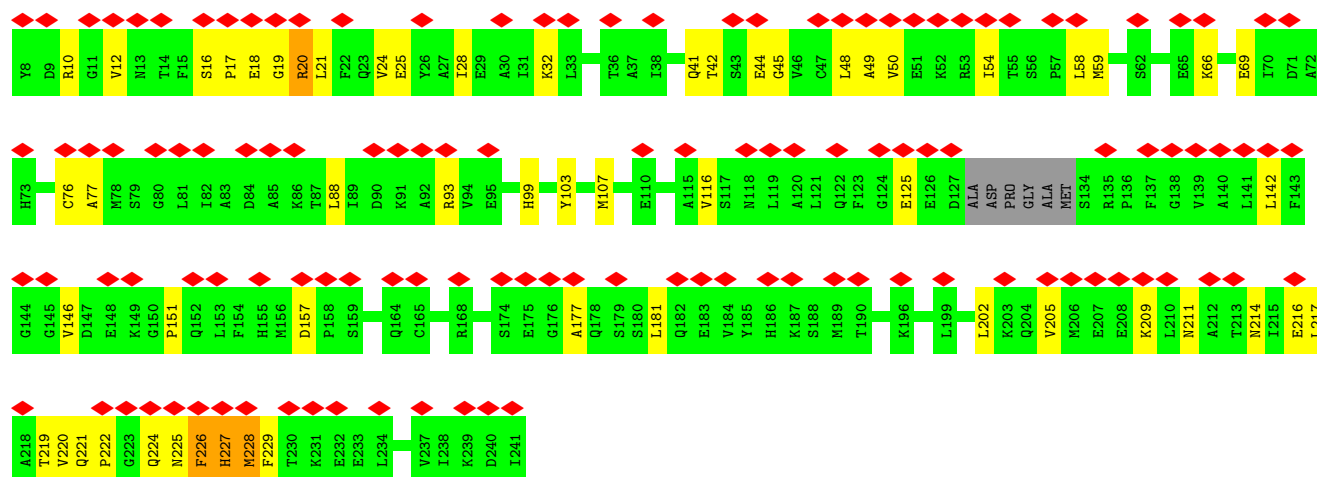
• Molecule 21: Proteasome subunit alpha type-7

Chain j: 57% 82% 16%



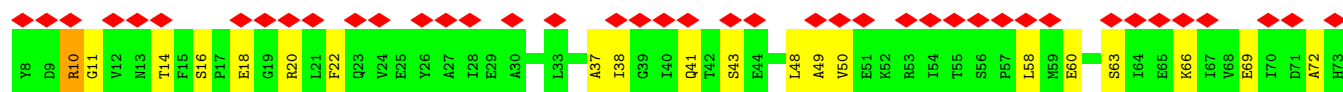
• Molecule 22: Proteasome subunit alpha type-5

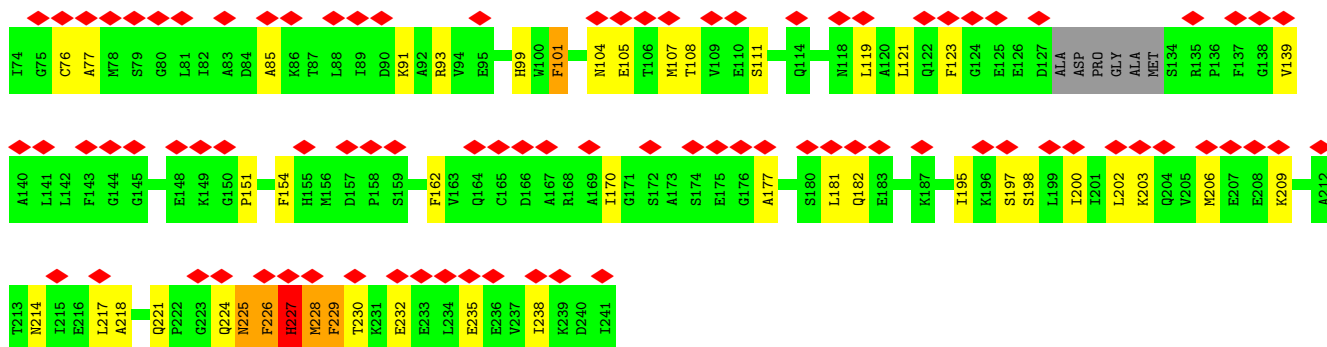
Chain K: 52% 74% 22%



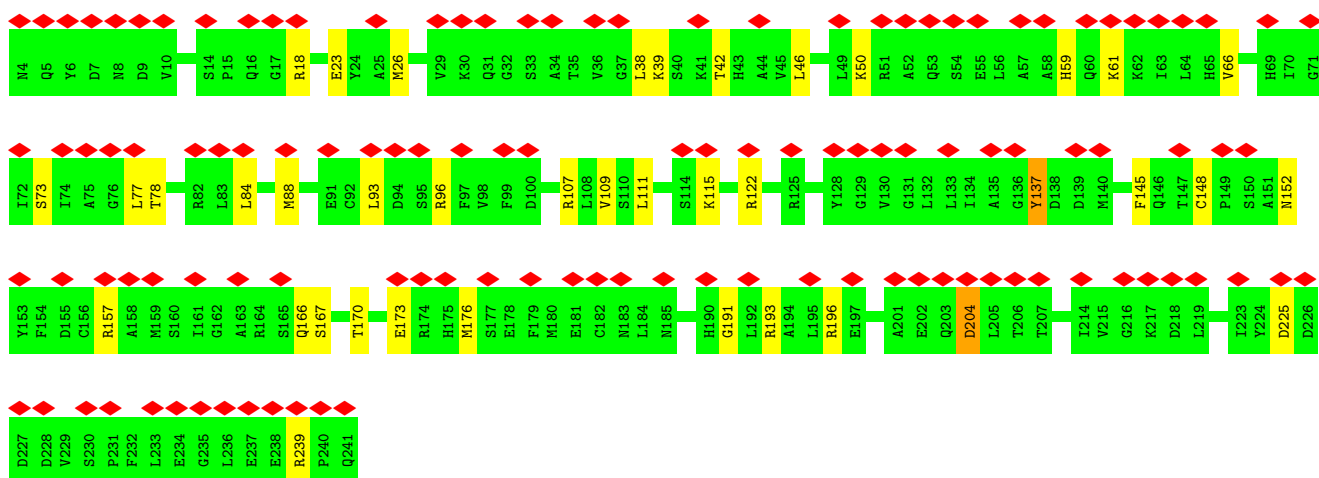
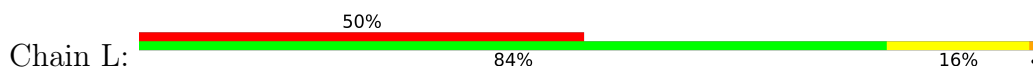
• Molecule 22: Proteasome subunit alpha type-5

Chain k: 55% 70% 25%

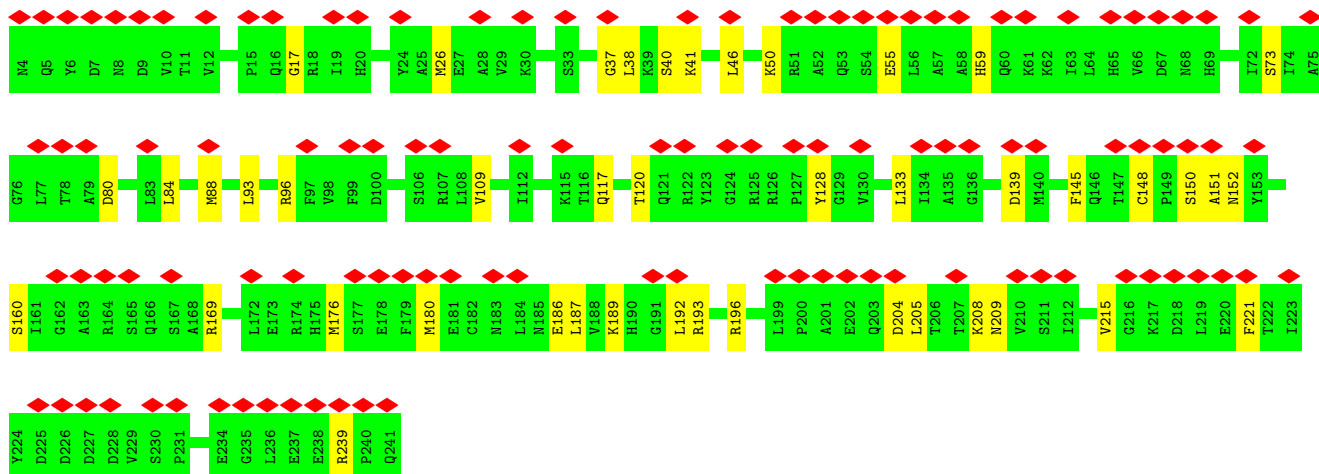
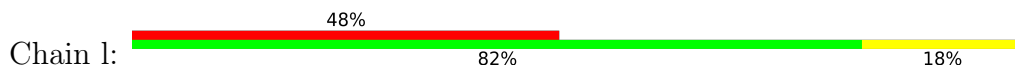




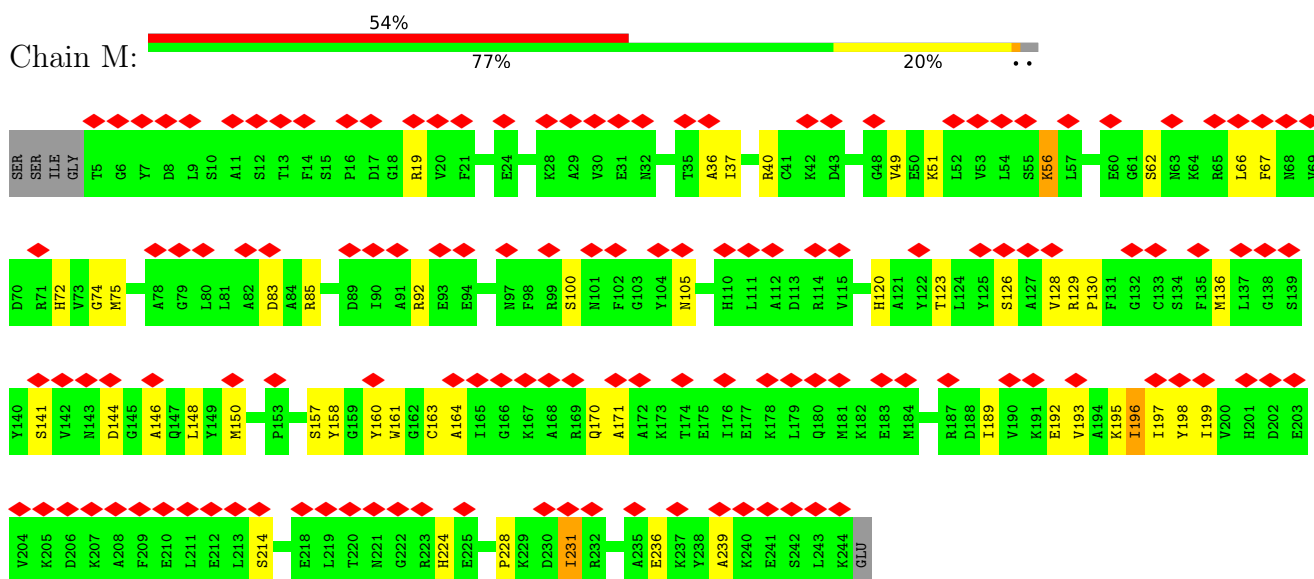
• Molecule 23: Proteasome subunit alpha type-1



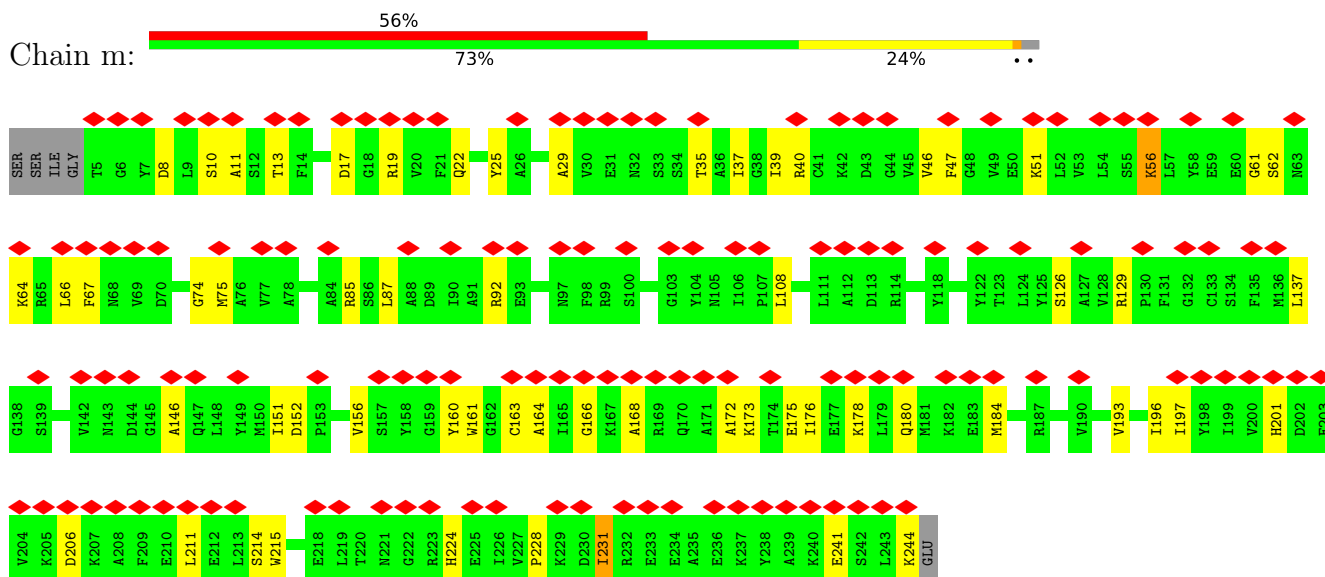
• Molecule 23: Proteasome subunit alpha type-1



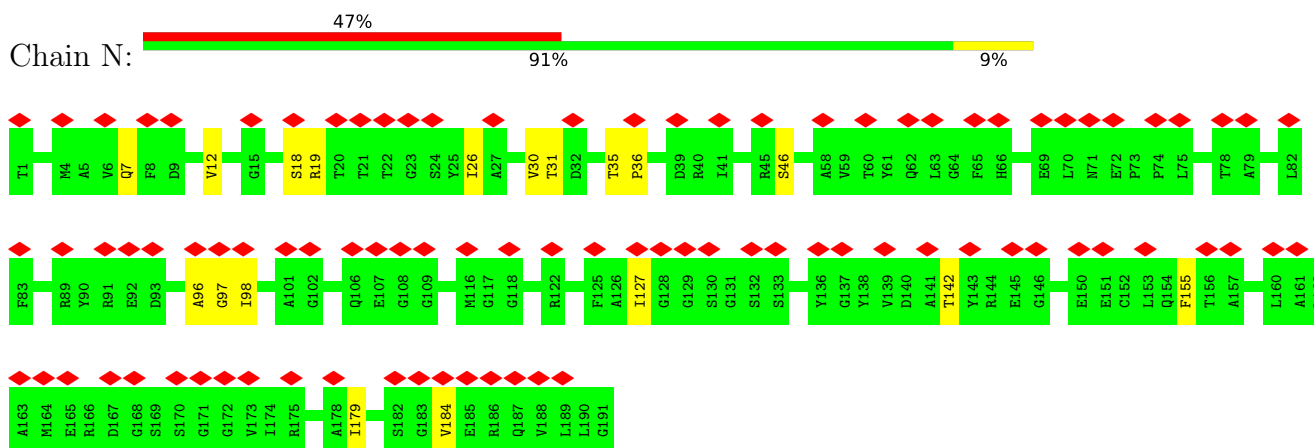
• Molecule 24: Proteasome subunit alpha type-3



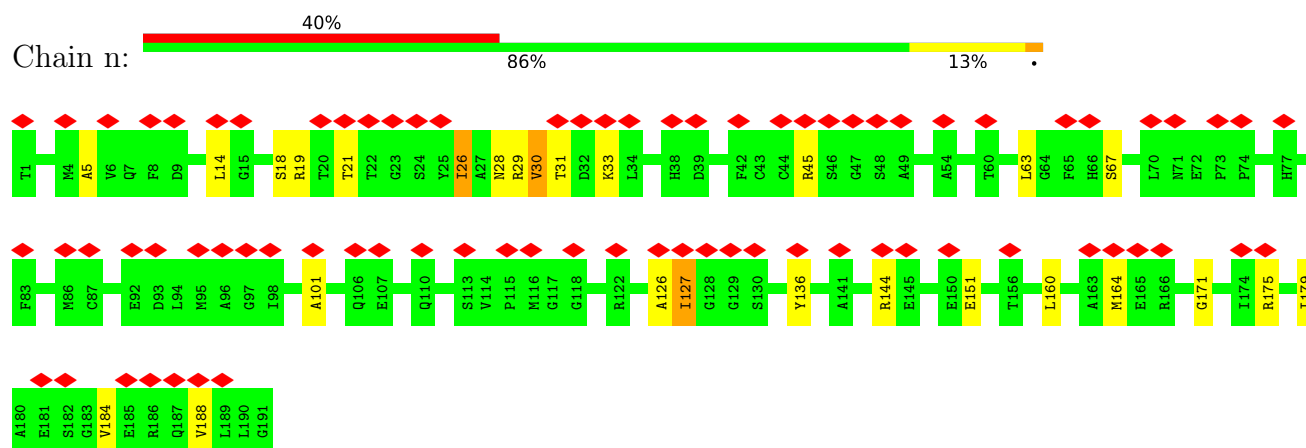
• Molecule 24: Proteasome subunit alpha type-3



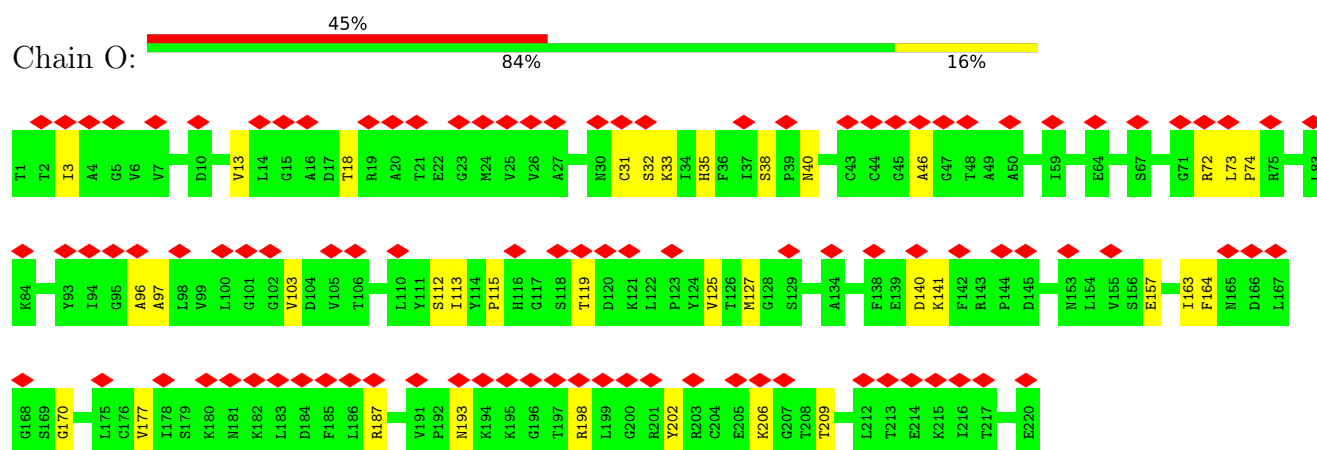
• Molecule 25: Proteasome subunit beta type-6



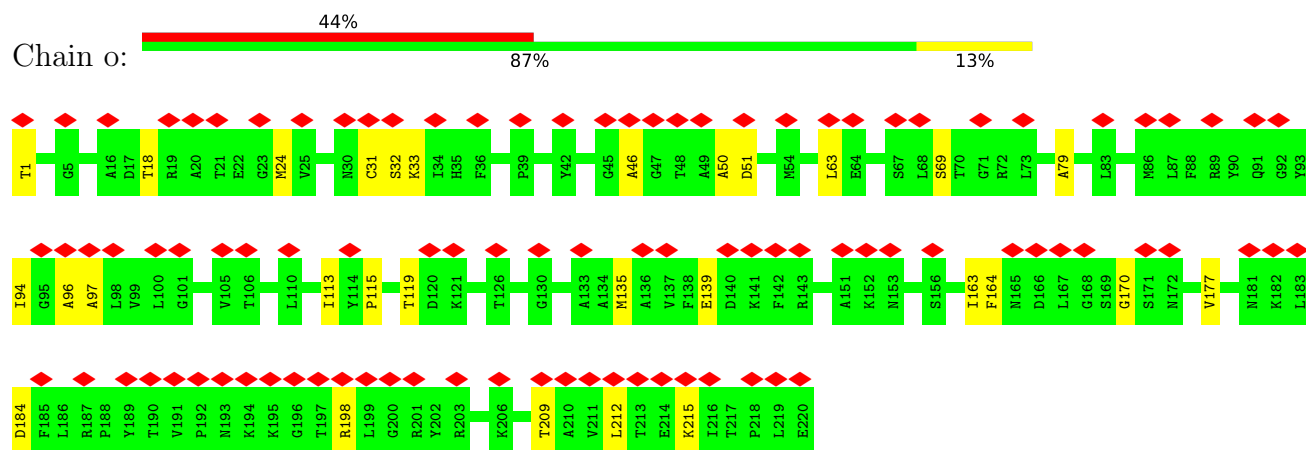
- Molecule 25: Proteasome subunit beta type-6



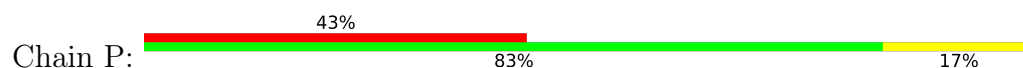
- Molecule 26: Proteasome subunit beta type-7

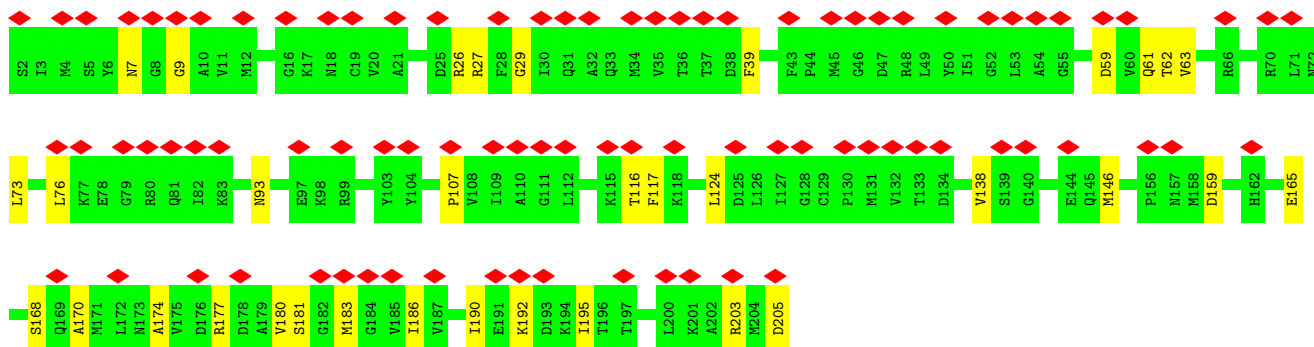


- Molecule 26: Proteasome subunit beta type-7

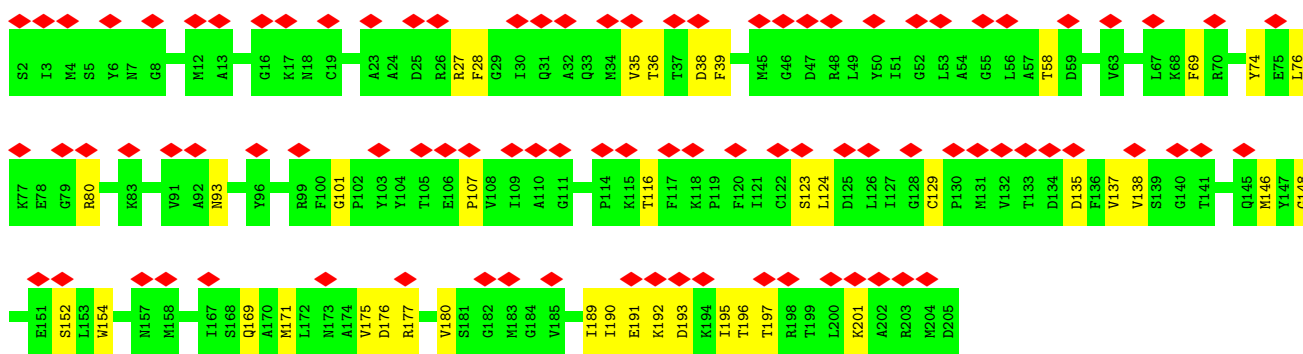
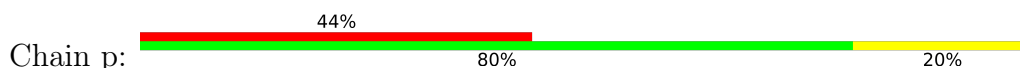


- Molecule 27: Proteasome subunit beta type-3

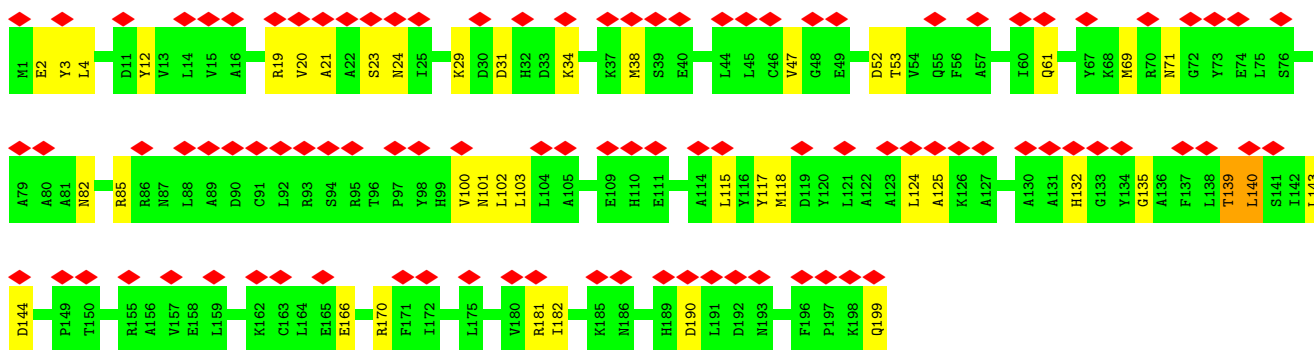
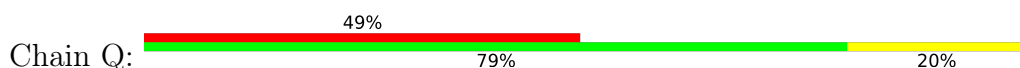




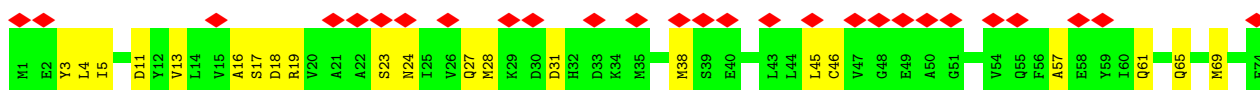
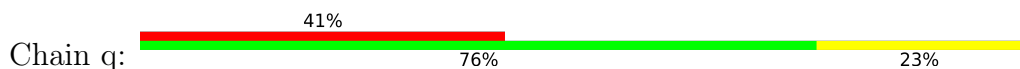
• Molecule 27: Proteasome subunit beta type-3

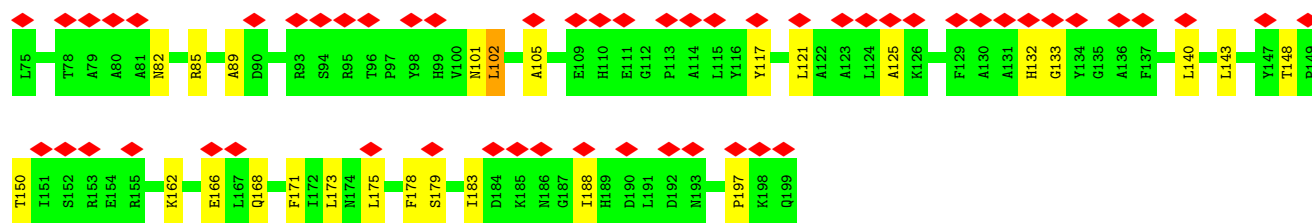


• Molecule 28: Proteasome subunit beta type-2

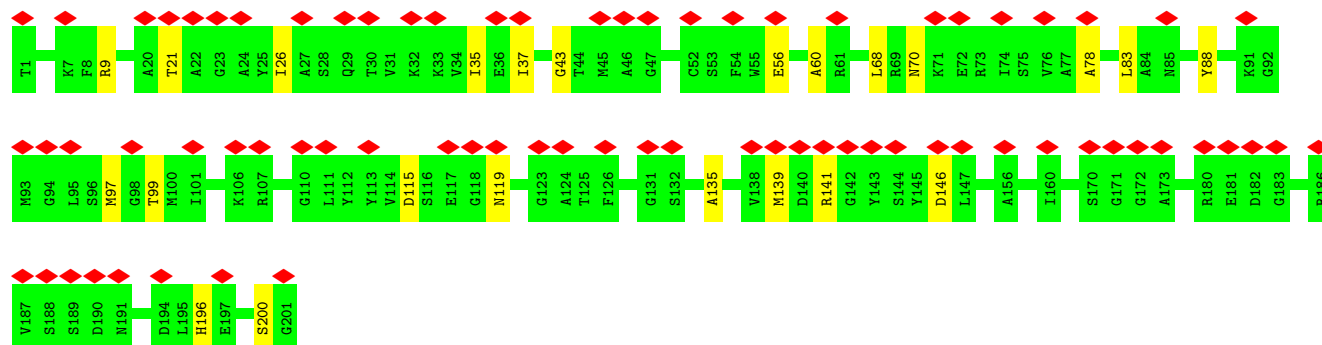
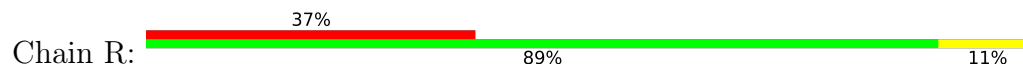


• Molecule 28: Proteasome subunit beta type-2

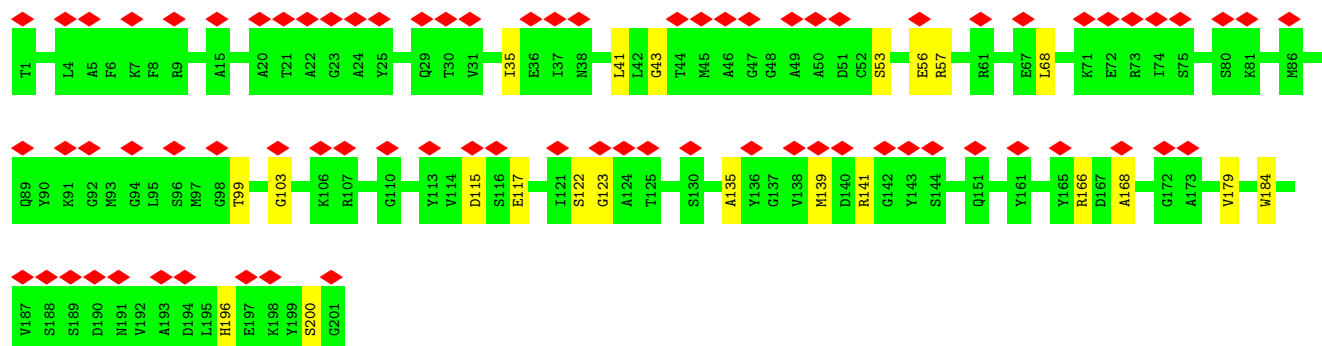
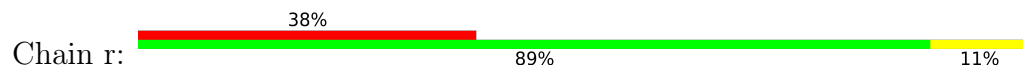




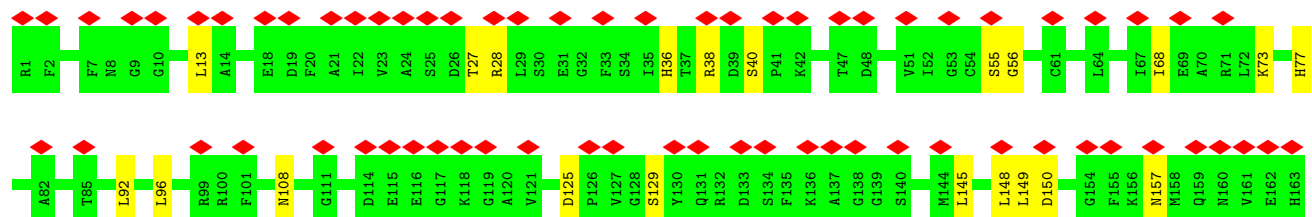
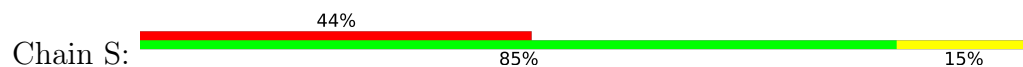
• Molecule 29: Proteasome subunit beta type-5

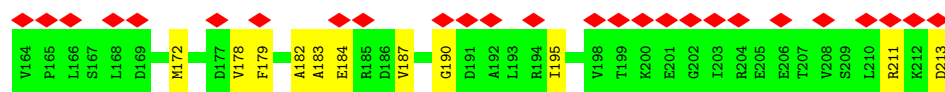


• Molecule 29: Proteasome subunit beta type-5

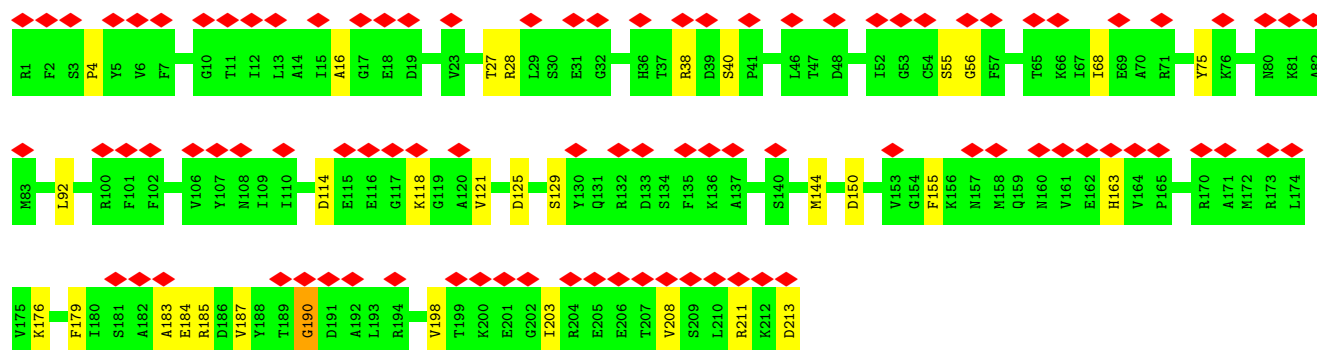
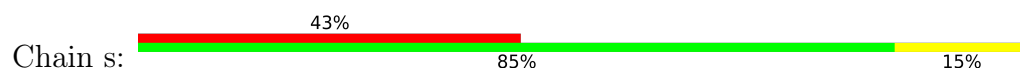


• Molecule 30: Proteasome subunit beta type-1

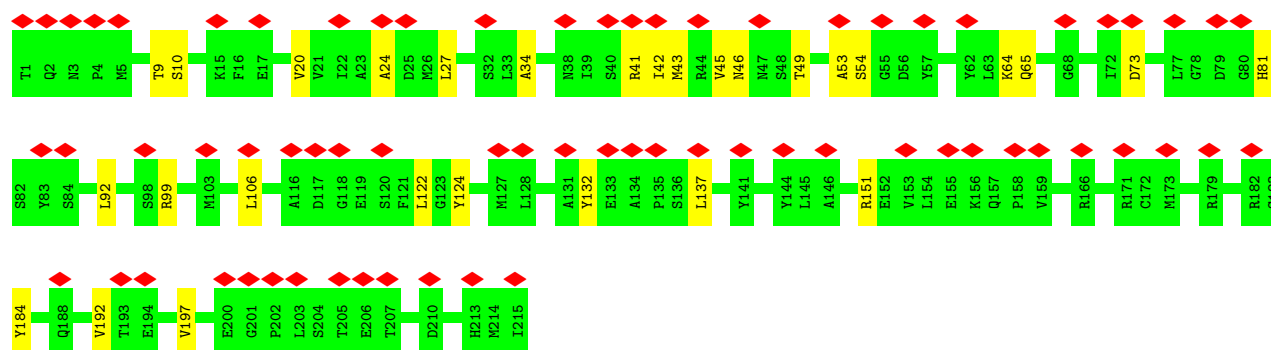
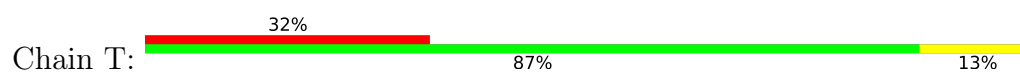




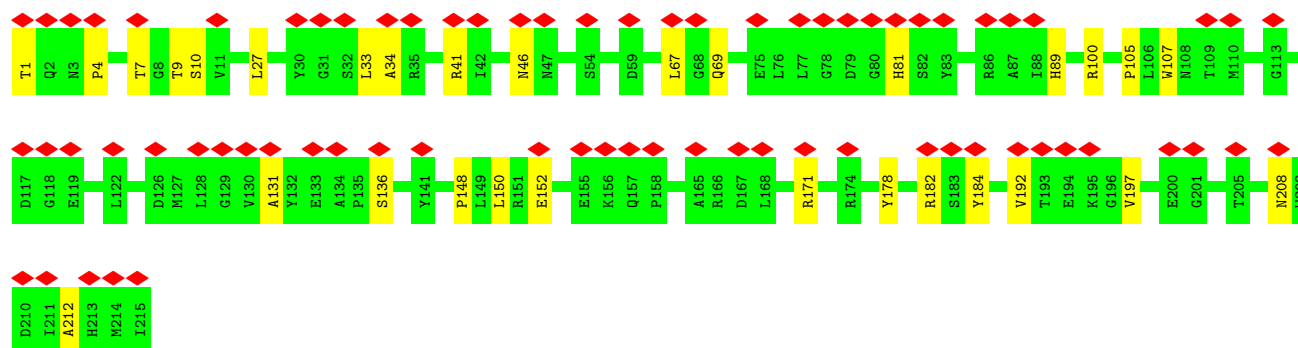
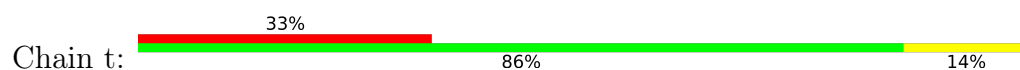
• Molecule 30: Proteasome subunit beta type-1



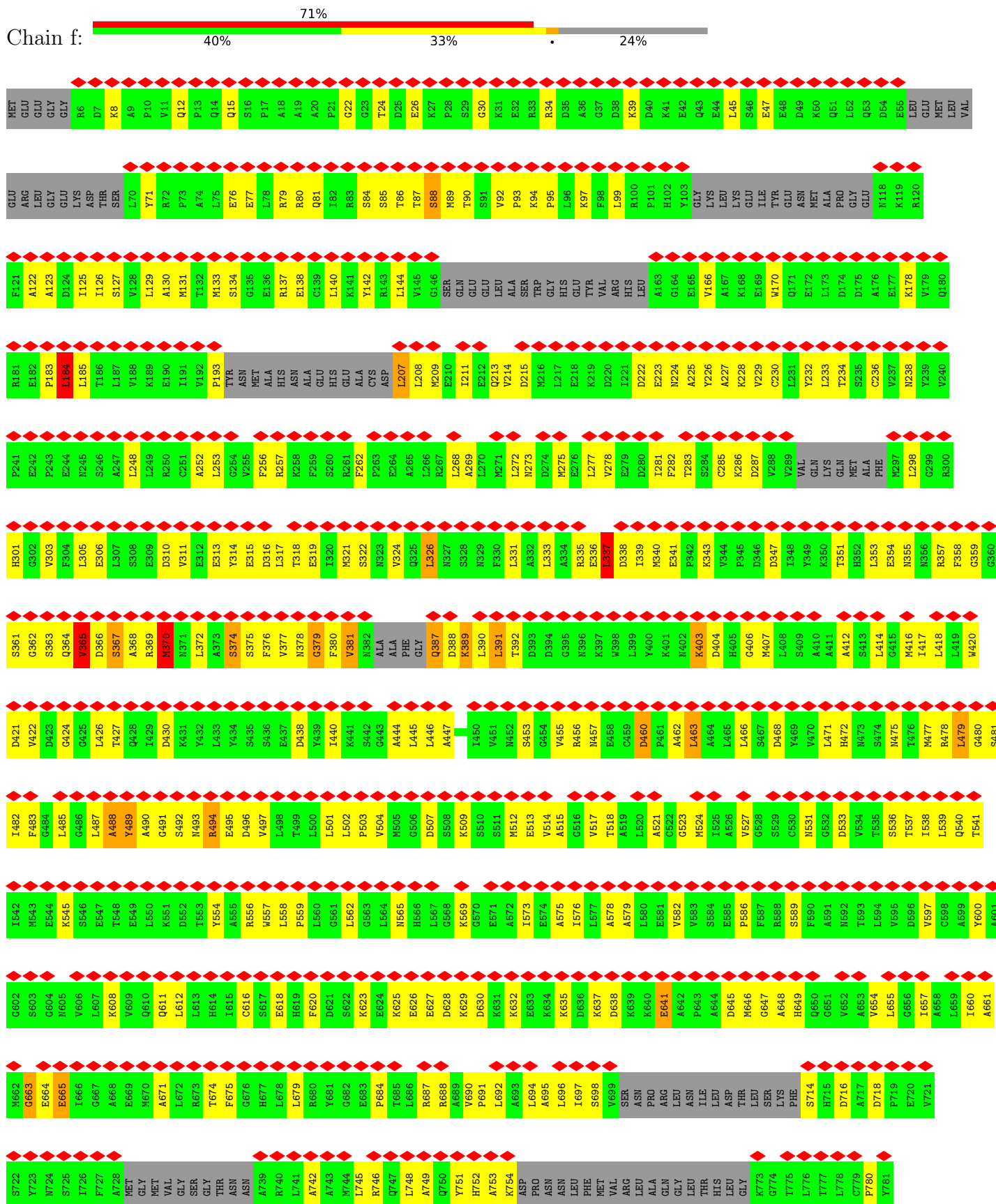
• Molecule 31: Proteasome subunit beta type-4



• Molecule 31: Proteasome subunit beta type-4



• Molecule 32: 26S proteasome non-ATPase regulatory subunit 2



LYS	VAL	H782
ASN	SER	S783
PRO	VAL	D784
ASN	ARG	R785
TYR	VAL	Q786
ASP	GLY	L787
LEU	ALA	M788
	VAL	S789
	VAL	Q790
	GLY	V791
	GLN	A792
	ALA	V793
	GLY	A794
	PRO	G795
	LYS	L796
	THR	L797
	ILE	T798
	THR	V799
	PHE	L800
	GLN	V801
	THR	S802
	HIS	F803
	THR	L804
	PRO	ASP
	VAL	VAL
	LEU	ARG
	LEU	ASN
	ALA	ILE
	HIS	ILE
	GLY	LEU
	GLU	GLY
	ARG	LYS
	ALA	SER
	ALA	HIS
	LEU	TYR
	ALA	VAL
	THR	LEU
	GLU	THR
	GLU	GLY
	PHE	LEU
	LEU	VAL
	PRO	ALA
	VAL	ALA
	THR	ALA
	PRO	GLN
	ILE	PRO
	LEU	ARG
	GLU	LEU
	GLY	MET
	PHE	LEU
	VAL	VAL
	ILE	THR
	LEU	PHE
	ARG	ASP
		GLU
		LEU
		ARG
		PRO
		LEU
		PRO

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23567	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	420.0, 420.0, 420.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.75, 0.75, 0.75	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.13	0/6396	0.42	1/8646 (0.0%)
2	V	0.20	0/3929	0.59	8/5309 (0.2%)
3	W	0.17	0/3751	0.52	3/5042 (0.1%)
4	X	0.15	0/1936	0.46	0/2614
5	Y	0.14	0/3173	0.49	1/4273 (0.0%)
6	Z	0.18	0/2324	0.56	4/3150 (0.1%)
7	a	0.16	0/3051	0.47	1/4130 (0.0%)
8	b	0.17	0/1478	0.39	0/2001
9	c	0.21	1/2226 (0.0%)	0.53	0/3007
10	d	0.21	0/2162	0.56	2/2919 (0.1%)
11	e	0.23	0/338	0.61	0/450
12	A	0.20	0/2885	0.54	6/3897 (0.2%)
13	B	0.22	0/2757	0.67	5/3724 (0.1%)
14	C	0.19	0/3054	0.54	0/4107
15	D	0.18	0/3090	0.55	6/4168 (0.1%)
16	E	0.16	0/2835	0.47	0/3821
17	F	0.17	0/2903	0.54	2/3912 (0.1%)
18	G	0.30	0/1858	0.66	0/2521
18	g	0.26	0/1859	0.63	1/2523 (0.0%)
19	H	0.31	0/1743	0.71	3/2372 (0.1%)
19	h	0.29	0/1743	0.69	2/2372 (0.1%)
20	I	0.31	0/1942	0.70	2/2628 (0.1%)
20	i	0.28	0/1942	0.71	2/2628 (0.1%)
21	J	0.33	0/1728	0.68	0/2358
21	j	0.27	0/1728	0.64	1/2358 (0.0%)
22	K	0.31	0/1747	0.68	0/2364
22	k	0.29	0/1747	0.64	2/2364 (0.1%)
23	L	0.33	0/1885	0.69	2/2552 (0.1%)
23	l	0.27	0/1885	0.66	0/2552
24	M	0.32	0/1891	0.68	2/2552 (0.1%)
24	m	0.28	0/1891	0.67	4/2552 (0.2%)
25	N	0.29	0/1454	0.55	0/1967

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
25	n	0.28	0/1454	0.56	0/1967
26	O	0.29	0/1670	0.57	0/2265
26	o	0.28	0/1670	0.51	0/2265
27	P	0.31	0/1614	0.61	0/2177
27	p	0.30	0/1614	0.58	1/2177 (0.0%)
28	Q	0.33	0/1603	0.73	0/2174
28	q	0.33	0/1603	0.75	0/2174
29	R	0.30	0/1579	0.54	0/2134
29	r	0.29	0/1579	0.52	0/2134
30	S	0.30	0/1671	0.58	0/2253
30	s	0.29	0/1671	0.61	2/2253 (0.1%)
31	T	0.32	0/1700	0.61	0/2305
31	t	0.30	0/1700	0.59	0/2305
32	f	0.33	1/5393 (0.0%)	0.87	20/7271 (0.3%)
All	All	0.25	2/101852 (0.0%)	0.60	83/137687 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	V	0	3
3	W	0	1
5	Y	0	2
7	a	0	1
10	d	0	1
11	e	0	1
12	A	0	1
13	B	0	1
14	C	0	2
18	G	0	1
19	H	0	2
21	J	0	2
21	j	0	1
22	K	0	1
22	k	0	3
23	L	0	2
23	l	0	1
24	M	0	1
26	O	0	1
27	p	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	Q	0	2
28	q	0	1
30	s	0	1
All	All	0	33

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	c	104	ARG	C-N	5.56	1.46	1.33
32	f	494	ARG	CA-C	5.21	1.59	1.52

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	f	488	ALA	N-CA-C	10.60	122.92	111.36
15	D	206	GLY	CA-C-N	-9.76	112.63	119.66
15	D	206	GLY	C-N-CA	-9.76	112.63	119.66
13	B	226	GLY	CA-C-N	9.65	130.32	120.38
13	B	226	GLY	C-N-CA	9.65	130.32	120.38
6	Z	63	LYS	N-CA-C	7.96	121.12	111.40
19	h	231	ALA	CA-C-N	7.92	135.96	121.70
19	h	231	ALA	C-N-CA	7.92	135.96	121.70
23	L	204	ASP	CA-C-N	7.64	135.46	121.70
23	L	204	ASP	C-N-CA	7.64	135.46	121.70
20	I	184	MET	CA-C-N	7.44	135.10	121.70
20	I	184	MET	C-N-CA	7.44	135.10	121.70
3	W	92	LYS	CA-C-N	7.33	134.89	121.70
3	W	92	LYS	C-N-CA	7.33	134.89	121.70
32	f	493	ASN	N-CA-C	-6.99	95.92	110.80
20	i	184	MET	CA-C-N	6.95	134.21	121.70
20	i	184	MET	C-N-CA	6.95	134.21	121.70
32	f	472	HIS	CA-C-N	6.93	130.42	120.79
32	f	472	HIS	C-N-CA	6.93	130.42	120.79
32	f	493	ASN	CA-C-N	-6.92	111.06	120.82
32	f	493	ASN	C-N-CA	-6.92	111.06	120.82
18	g	223	GLU	N-CA-C	-6.87	104.05	113.18
10	d	228	GLN	N-CA-C	6.81	124.07	113.72
2	V	57	ALA	CA-C-N	6.78	133.91	121.70
2	V	57	ALA	C-N-CA	6.78	133.91	121.70
27	p	35	VAL	N-CA-C	-6.57	106.58	111.90
19	H	231	ALA	CA-C-N	6.51	133.42	121.70
19	H	231	ALA	C-N-CA	6.51	133.42	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	f	492	SER	N-CA-C	-6.34	104.37	111.28
5	Y	170	GLU	N-CA-C	6.22	118.57	111.11
32	f	663	GLY	N-CA-C	6.14	121.39	110.95
6	Z	63	LYS	CA-C-N	6.14	132.75	121.70
6	Z	63	LYS	C-N-CA	6.14	132.75	121.70
32	f	370	MET	N-CA-C	-6.12	104.69	111.36
32	f	324	VAL	CA-C-N	6.08	133.15	121.54
32	f	324	VAL	C-N-CA	6.08	133.15	121.54
13	B	260	LEU	N-CA-C	6.03	119.83	112.23
17	F	164	LEU	CA-C-N	5.99	127.33	119.84
17	F	164	LEU	C-N-CA	5.99	127.33	119.84
3	W	331	GLY	CA-C-O	-5.97	118.34	122.22
32	f	489	TYR	N-CA-C	5.97	118.48	109.23
32	f	365	VAL	N-CA-C	5.80	121.40	109.34
19	H	231	ALA	N-CA-C	5.66	119.97	112.72
24	M	231	ILE	CA-C-N	5.66	132.35	121.54
24	M	231	ILE	C-N-CA	5.66	132.35	121.54
32	f	379	GLY	CA-C-N	-5.65	113.45	122.66
32	f	379	GLY	C-N-CA	-5.65	113.45	122.66
13	B	324	ASP	CA-C-N	5.64	131.85	121.70
13	B	324	ASP	C-N-CA	5.64	131.85	121.70
32	f	374	SER	CA-C-N	-5.64	112.72	120.28
32	f	374	SER	C-N-CA	-5.64	112.72	120.28
2	V	316	ALA	CA-C-N	5.61	126.86	119.84
2	V	316	ALA	C-N-CA	5.61	126.86	119.84
32	f	337	LEU	N-CA-C	5.54	122.60	110.80
1	U	468	ALA	CB-CA-C	-5.53	109.71	117.23
6	Z	222	ILE	N-CA-C	5.47	118.77	111.44
12	A	344	SER	CA-C-N	5.32	131.28	121.70
12	A	344	SER	C-N-CA	5.32	131.28	121.70
30	s	190	GLY	CA-C-N	5.26	129.56	121.19
30	s	190	GLY	C-N-CA	5.26	129.56	121.19
12	A	247	GLN	CA-C-N	5.25	131.14	121.70
12	A	247	GLN	C-N-CA	5.25	131.14	121.70
24	m	56	LYS	CA-C-N	5.23	131.11	121.70
24	m	56	LYS	C-N-CA	5.23	131.11	121.70
24	m	231	ILE	CA-C-N	5.22	131.50	121.54
24	m	231	ILE	C-N-CA	5.22	131.50	121.54
22	k	18	GLU	CA-C-N	5.21	131.07	121.70
22	k	18	GLU	C-N-CA	5.21	131.07	121.70
10	d	2	TYR	CB-CA-C	-5.19	110.18	117.23
2	V	54	LYS	CA-C-N	5.16	130.99	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	54	LYS	C-N-CA	5.16	130.99	121.70
15	D	389	GLU	CA-C-N	5.14	130.96	121.70
15	D	389	GLU	C-N-CA	5.14	130.96	121.70
21	j	59	VAL	N-CA-C	-5.14	107.33	111.91
2	V	212	TYR	N-CA-C	-5.14	105.13	111.40
12	A	205	GLY	CA-C-N	5.12	130.92	121.70
12	A	205	GLY	C-N-CA	5.12	130.92	121.70
15	D	354	LEU	CA-C-N	5.08	130.84	121.70
15	D	354	LEU	C-N-CA	5.08	130.84	121.70
2	V	193	GLN	CB-CA-C	-5.06	110.34	117.23
7	a	50	PHE	N-CA-C	5.06	117.18	111.11
32	f	493	ASN	CA-C-O	-5.04	113.30	120.51
32	f	404	ASP	N-CA-C	5.03	117.15	111.02

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	A	311	PRO	Peptide
13	B	278	ALA	Peptide
14	C	171	HIS	Peptide
14	C	255	GLY	Peptide
18	G	160	TYR	Peptide
19	H	231	ALA	Peptide
19	H	40	ALA	Peptide
21	J	15	HIS	Peptide
21	J	199	VAL	Peptide
22	K	226	PHE	Peptide
23	L	137	TYR	Peptide
23	L	204	ASP	Peptide
24	M	56	LYS	Peptide
26	O	187	ARG	Peptide
28	Q	101	ASN	Peptide
28	Q	139	THR	Peptide
2	V	101	LEU	Peptide
2	V	319	HIS	Peptide
2	V	81	GLN	Peptide
3	W	416	GLN	Peptide
5	Y	356	THR	Peptide
5	Y	63	TRP	Peptide
7	a	286	ALA	Peptide
10	d	3	GLU	Peptide

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Mol	Chain	Res	Type	Group
11	e	1	MET	Peptide
21	j	199	VAL	Peptide
22	k	10	ARG	Peptide
22	k	226	PHE	Peptide
22	k	232	GLU	Peptide
23	l	204	ASP	Peptide
27	p	101	GLY	Peptide
28	q	102	LEU	Peptide
30	s	190	GLY	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	U	6287	0	6338	184	0
2	V	3852	0	3889	292	0
3	W	3703	0	3822	162	0
4	X	1905	0	1951	62	0
5	Y	3115	0	3119	143	0
6	Z	2281	0	2312	133	0
7	a	2993	0	3011	108	0
8	b	1458	0	1505	46	0
9	c	2187	0	2215	111	0
10	d	2116	0	2146	71	0
11	e	334	0	292	51	0
12	A	2834	0	2875	166	0
13	B	2717	0	2755	241	0
14	C	3015	0	3124	249	0
15	D	3040	0	3076	172	0
16	E	2790	0	2844	120	0
17	F	2863	0	2931	220	0
18	G	1825	0	1795	55	0
18	g	1826	0	1796	22	0
19	H	1708	0	1594	43	0
19	h	1708	0	1594	24	0
20	I	1912	0	1851	98	0
20	i	1912	0	1851	28	0
21	J	1704	0	1517	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	j	1704	0	1517	25	0
22	K	1722	0	1673	151	0
22	k	1722	0	1673	52	0
23	L	1850	0	1822	57	0
23	l	1850	0	1822	26	0
24	M	1856	0	1814	43	0
24	m	1856	0	1814	41	0
25	N	1430	0	1398	10	0
25	n	1430	0	1398	16	0
26	O	1643	0	1644	21	0
26	o	1643	0	1644	21	0
27	P	1585	0	1598	27	0
27	p	1585	0	1598	27	0
28	Q	1570	0	1547	32	0
28	q	1570	0	1547	33	0
29	R	1548	0	1499	16	0
29	r	1548	0	1499	20	0
30	S	1641	0	1618	25	0
30	s	1641	0	1618	18	0
31	T	1667	0	1628	22	0
31	t	1667	0	1628	21	0
32	f	5319	0	5329	454	0
33	c	1	0	0	0	0
All	All	100133	0	99531	3315	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 17.

All (3315) 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)
17:F:437:TYR:CE1	22:K:28:ILE:CG2	1.76	1.59
13:B:428:TYR:CD1	20:I:170:ALA:HB2	1.25	1.59
17:F:437:TYR:CZ	22:K:28:ILE:HG21	1.08	1.57
17:F:437:TYR:CZ	22:K:28:ILE:CG2	1.82	1.54
17:F:437:TYR:CD1	22:K:28:ILE:HG13	1.01	1.54
17:F:437:TYR:CG	22:K:28:ILE:HG13	1.39	1.54
12:A:429:TYR:CG	21:J:12:PRO:HG2	1.37	1.54
17:F:437:TYR:CD1	22:K:28:ILE:CG1	1.91	1.51
22:K:18:GLU:HB2	22:K:20:ARG:NH2	1.24	1.49
2:V:495:ARG:HB3	14:C:38:LYS:CG	1.43	1.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:K:217:LEU:N	22:K:229:PHE:CZ	1.77	1.48
2:V:242:HIS:CE1	14:C:23:TYR:CG	1.98	1.48
15:D:413:GLU:CG	18:G:157:ALA:HB2	1.38	1.48
15:D:417:TYR:CZ	19:H:79:MET:HB3	1.49	1.47
13:B:428:TYR:CD1	20:I:170:ALA:CB	1.94	1.47
2:V:80:LYS:CA	2:V:81:GLN:HB2	1.43	1.44
13:B:176:VAL:HG12	14:C:283:PHE:CD2	1.50	1.44
13:B:333:ARG:NH1	20:I:15:GLU:CD	1.72	1.44
1:U:102:ALA:CA	14:C:21:ARG:HH22	1.31	1.43
2:V:495:ARG:CB	14:C:38:LYS:HG2	1.48	1.42
17:F:437:TYR:CE1	22:K:28:ILE:HG21	0.91	1.42
2:V:242:HIS:CE1	14:C:23:TYR:CD1	1.85	1.42
2:V:495:ARG:HB3	14:C:38:LYS:CB	1.47	1.42
15:D:417:TYR:CZ	19:H:79:MET:CB	1.99	1.42
17:F:435:LEU:HG	22:K:20:ARG:CG	1.50	1.41
2:V:212:TYR:OH	11:e:4:LYS:CG	1.65	1.39
2:V:492:LYS:HZ2	14:C:38:LYS:NZ	1.20	1.37
2:V:242:HIS:HE1	14:C:23:TYR:CG	1.38	1.36
3:W:98:LYS:NZ	3:W:137:TYR:HE2	1.21	1.36
1:U:102:ALA:CB	14:C:21:ARG:HH22	1.38	1.35
1:U:102:ALA:CB	14:C:21:ARG:NH2	1.89	1.35
13:B:428:TYR:CG	20:I:170:ALA:HB2	1.60	1.35
13:B:432:GLU:OE2	20:I:166:ASN:CG	1.70	1.34
2:V:212:TYR:CZ	11:e:4:LYS:CG	1.98	1.32
6:Z:45:LYS:NZ	17:F:115:SER:HA	1.40	1.32
13:B:176:VAL:HG12	14:C:283:PHE:CG	1.65	1.32
32:f:753:ALA:O	32:f:754:LYS:HE2	1.26	1.31
2:V:492:LYS:NZ	14:C:38:LYS:NZ	1.79	1.30
2:V:80:LYS:HA	2:V:81:GLN:CB	1.55	1.29
13:B:432:GLU:OE2	20:I:166:ASN:CB	1.78	1.29
13:B:432:GLU:CG	20:I:166:ASN:OD1	1.79	1.28
13:B:432:GLU:HG3	20:I:166:ASN:OD1	1.20	1.27
15:D:413:GLU:HG2	18:G:157:ALA:CB	1.62	1.27
2:V:212:TYR:CZ	11:e:4:LYS:HG3	1.03	1.26
12:A:348:LEU:HD22	22:K:32:LYS:NZ	1.48	1.26
13:B:176:VAL:CG1	14:C:283:PHE:CG	2.17	1.26
17:F:439:ALA:C	23:L:77:LEU:HD23	1.57	1.25
22:K:18:GLU:CB	22:K:20:ARG:NH2	1.99	1.25
22:K:217:LEU:N	22:K:229:PHE:HZ	1.18	1.25
17:F:387:CYS:SG	23:L:166:GLN:HG2	1.77	1.25
15:D:366:ARG:HH21	18:G:177:SER:CB	1.49	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:494:ARG:HD3	32:f:496:ASP:OD1	1.26	1.24
13:B:431:GLN:OE1	20:I:173:SER:HB3	1.13	1.24
32:f:796:LEU:O	32:f:799:VAL:HG22	1.30	1.23
3:W:98:LYS:NZ	3:W:137:TYR:CE2	2.06	1.23
17:F:439:ALA:O	23:L:77:LEU:HA	1.38	1.23
32:f:742:ALA:HA	32:f:745:LEU:CD2	1.66	1.23
2:V:212:TYR:OH	11:e:4:LYS:HG3	1.08	1.23
17:F:437:TYR:CG	22:K:28:ILE:CG1	2.10	1.22
5:Y:312:ARG:HA	5:Y:356:THR:CG2	1.69	1.21
32:f:376:PHE:CE2	32:f:798:THR:CG2	2.23	1.21
2:V:242:HIS:HE1	14:C:23:TYR:CD1	0.96	1.20
2:V:212:TYR:OH	11:e:4:LYS:CD	1.90	1.20
22:K:216:GLU:HB2	22:K:229:PHE:CE2	1.76	1.20
13:B:428:TYR:HD1	20:I:170:ALA:CA	1.54	1.20
1:U:102:ALA:CA	14:C:21:ARG:NH2	2.05	1.19
1:U:149:GLN:NE2	15:D:41:TYR:CD2	2.10	1.19
13:B:428:TYR:CD1	20:I:170:ALA:CA	2.24	1.19
5:Y:63:TRP:NE1	5:Y:66:ASP:OD1	1.73	1.19
2:V:242:HIS:CE1	14:C:23:TYR:CD2	2.11	1.19
17:F:430:LYS:NZ	22:K:17:PRO:HB2	1.53	1.19
32:f:471:LEU:CG	32:f:509:LYS:HE3	1.73	1.19
13:B:432:GLU:HA	20:I:169:ALA:HB3	1.18	1.18
13:B:431:GLN:NE2	20:I:176:LYS:HZ1	1.42	1.18
13:B:428:TYR:HD1	20:I:170:ALA:N	1.41	1.18
17:F:382:GLU:OE1	23:L:170:THR:HG22	1.43	1.18
32:f:692:LEU:HD12	32:f:748:LEU:HD21	1.19	1.17
2:V:77:GLU:HB2	2:V:81:GLN:NE2	1.59	1.17
12:A:429:TYR:CB	21:J:12:PRO:HG2	1.75	1.17
17:F:387:CYS:SG	23:L:166:GLN:CG	2.33	1.17
32:f:696:LEU:HD13	32:f:752:HIS:CD2	1.80	1.17
12:A:429:TYR:CG	21:J:12:PRO:CG	2.27	1.16
5:Y:358:ARG:HD2	5:Y:359:PRO:HD2	1.25	1.16
2:V:497:PRO:O	14:C:41:ASN:ND2	1.79	1.14
17:F:439:ALA:OXT	23:L:77:LEU:HD23	1.00	1.14
3:W:141:GLU:OE1	3:W:172:GLU:OE2	1.61	1.14
13:B:428:TYR:CD1	20:I:170:ALA:N	2.15	1.14
17:F:439:ALA:OXT	23:L:77:LEU:CD2	1.96	1.14
32:f:494:ARG:HE	32:f:495:GLU:N	1.44	1.14
17:F:435:LEU:CD1	22:K:20:ARG:HG3	1.76	1.13
13:B:176:VAL:HG12	14:C:283:PHE:CE2	1.82	1.13
32:f:311:VAL:HB	32:f:490:ALA:HB1	1.17	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:k:217:LEU:CD1	22:k:229:PHE:HZ	1.47	1.13
1:U:102:ALA:HA	14:C:21:ARG:NH2	1.59	1.12
2:V:195:ILE:HG23	14:C:23:TYR:N	1.64	1.12
32:f:479:LEU:CD2	32:f:513:GLU:HB2	1.79	1.13
2:V:77:GLU:CB	2:V:81:GLN:HE21	1.62	1.12
2:V:495:ARG:HB3	14:C:38:LYS:HB3	1.24	1.12
17:F:439:ALA:C	23:L:77:LEU:CD2	2.22	1.12
2:V:195:ILE:HA	14:C:23:TYR:HB2	1.13	1.12
32:f:389:LYS:CG	32:f:418:LEU:HD21	1.79	1.12
13:B:176:VAL:CG1	14:C:283:PHE:CD2	2.29	1.11
17:F:387:CYS:SG	23:L:166:GLN:CB	2.39	1.11
32:f:494:ARG:NH2	32:f:495:GLU:HG2	1.64	1.11
1:U:102:ALA:HB2	14:C:21:ARG:NH2	1.57	1.11
17:F:430:LYS:HZ2	22:K:17:PRO:HB2	0.95	1.11
32:f:376:PHE:CE2	32:f:798:THR:HG21	1.85	1.10
32:f:479:LEU:HD21	32:f:513:GLU:CB	1.80	1.10
1:U:102:ALA:HA	14:C:21:ARG:HH22	1.02	1.10
17:F:387:CYS:SG	23:L:166:GLN:HB3	1.90	1.10
2:V:495:ARG:CB	14:C:38:LYS:CG	2.15	1.10
17:F:435:LEU:CG	22:K:20:ARG:CG	2.29	1.10
2:V:195:ILE:HG21	14:C:22:GLN:HB3	1.22	1.09
13:B:431:GLN:OE1	20:I:173:SER:CB	1.99	1.09
32:f:389:LYS:HG2	32:f:418:LEU:HD21	1.29	1.09
32:f:483:PHE:CE2	32:f:799:VAL:HB	1.88	1.09
13:B:432:GLU:HA	20:I:169:ALA:CB	1.80	1.09
17:F:439:ALA:O	23:L:77:LEU:CA	2.00	1.09
32:f:692:LEU:HD12	32:f:748:LEU:CD2	1.82	1.09
13:B:432:GLU:CD	20:I:166:ASN:OD1	1.94	1.09
17:F:435:LEU:HA	22:K:20:ARG:HE	1.00	1.08
22:K:18:GLU:CB	22:K:20:ARG:HH22	1.62	1.08
32:f:742:ALA:O	32:f:745:LEU:HG	1.54	1.08
32:f:471:LEU:HG	32:f:509:LYS:CE	1.83	1.07
15:D:417:TYR:OH	19:H:79:MET:CB	2.01	1.07
17:F:430:LYS:HZ2	22:K:17:PRO:CB	1.68	1.07
17:F:435:LEU:HG	17:F:438:TYR:CD2	1.88	1.07
32:f:494:ARG:HH21	32:f:495:GLU:HG2	1.02	1.07
15:D:417:TYR:CZ	19:H:79:MET:HB2	1.83	1.06
22:k:217:LEU:CD1	22:k:229:PHE:CZ	2.33	1.06
16:E:372:ARG:CZ	24:M:171:ALA:N	2.09	1.06
2:V:492:LYS:NZ	14:C:38:LYS:HZ2	1.44	1.06
15:D:417:TYR:CE2	19:H:79:MET:HB3	1.91	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:413:GLU:CG	18:G:157:ALA:CB	2.25	1.05
2:V:287:ARG:HD2	11:e:4:LYS:HE3	1.39	1.04
17:F:435:LEU:CG	22:K:20:ARG:HG3	1.86	1.04
17:F:438:TYR:HD1	22:K:21:LEU:N	1.54	1.04
5:Y:312:ARG:HA	5:Y:356:THR:HG22	1.04	1.04
12:A:348:LEU:CD2	22:K:32:LYS:HZ1	1.71	1.04
13:B:438:LEU:HD12	20:I:155:ASN:ND2	1.72	1.04
22:k:72:ALA:O	22:k:226:PHE:CZ	2.10	1.04
32:f:494:ARG:CD	32:f:496:ASP:OD1	2.06	1.04
32:f:471:LEU:HD12	32:f:509:LYS:CG	1.87	1.03
22:K:18:GLU:CG	22:K:20:ARG:HH22	1.71	1.03
22:K:18:GLU:HG2	22:K:20:ARG:HH12	1.20	1.03
2:V:195:ILE:HG23	14:C:19:GLY:O	1.51	1.03
13:B:178:LYS:HZ3	14:C:278:ASN:HB3	1.15	1.02
3:W:136:ILE:HD13	3:W:175:GLY:HA3	1.40	1.02
5:Y:355:GLU:O	5:Y:357:ASN:ND2	1.92	1.02
15:D:418:LYS:HZ2	19:H:51:LYS:HD3	1.24	1.02
22:K:18:GLU:CB	22:K:20:ARG:CZ	2.36	1.02
15:D:413:GLU:OE1	18:G:29:PHE:CD1	2.13	1.01
13:B:333:ARG:NH1	20:I:15:GLU:OE2	1.91	1.01
15:D:417:TYR:CE1	19:H:79:MET:CB	2.43	1.01
17:F:430:LYS:NZ	22:K:17:PRO:CB	2.23	1.01
32:f:753:ALA:O	32:f:754:LYS:CE	2.08	1.01
17:F:439:ALA:C	23:L:77:LEU:HA	1.85	1.00
32:f:780:PRO:HB3	32:f:800:LEU:HA	1.37	1.00
6:Z:45:LYS:HZ2	17:F:115:SER:HA	1.19	0.99
32:f:494:ARG:HG3	32:f:497:VAL:HG12	1.44	0.99
17:F:435:LEU:CG	22:K:20:ARG:HG2	1.90	0.99
17:F:435:LEU:HD12	22:K:20:ARG:HG3	1.42	0.99
32:f:692:LEU:CD1	32:f:748:LEU:HD21	1.93	0.99
2:V:287:ARG:CD	11:e:4:LYS:HE3	1.85	0.99
17:F:382:GLU:OE1	23:L:170:THR:CG2	2.11	0.99
13:B:333:ARG:CZ	20:I:15:GLU:CD	2.35	0.98
32:f:479:LEU:HD21	32:f:513:GLU:HB2	0.99	0.98
6:Z:45:LYS:NZ	17:F:115:SER:CA	2.26	0.98
15:D:413:GLU:OE1	18:G:29:PHE:CE1	2.10	0.98
5:Y:63:TRP:CD1	5:Y:66:ASP:OD1	2.15	0.98
32:f:359:GLY:O	32:f:363:SER:HB3	1.63	0.98
32:f:337:LEU:HD13	32:f:420:TRP:HZ3	1.26	0.97
13:B:438:LEU:CD1	20:I:155:ASN:ND2	2.28	0.97
32:f:742:ALA:HA	32:f:745:LEU:HD23	1.46	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:k:72:ALA:O	22:k:226:PHE:CE2	2.18	0.97
32:f:456:ARG:HB3	32:f:489:TYR:CE2	2.00	0.97
5:Y:312:ARG:CA	5:Y:356:THR:HG22	1.95	0.96
13:B:432:GLU:OE2	20:I:166:ASN:CA	1.94	0.96
32:f:696:LEU:HD13	32:f:752:HIS:HD2	1.14	0.96
13:B:428:TYR:CE1	20:I:170:ALA:HB2	1.99	0.96
17:F:435:LEU:CA	22:K:20:ARG:HE	1.79	0.96
2:V:495:ARG:HB2	14:C:38:LYS:HG2	1.45	0.96
17:F:435:LEU:HA	22:K:20:ARG:NE	1.79	0.96
32:f:376:PHE:CD2	32:f:416:MET:HE1	2.01	0.95
32:f:471:LEU:HG	32:f:509:LYS:HE3	0.96	0.95
13:B:431:GLN:HE22	20:I:176:LYS:NZ	1.65	0.95
15:D:417:TYR:OH	19:H:79:MET:HB2	1.63	0.95
15:D:417:TYR:CE1	19:H:79:MET:HA	2.01	0.95
2:V:495:ARG:O	14:C:38:LYS:HA	1.66	0.95
13:B:440:LEU:C	21:J:28:LYS:O	2.10	0.95
32:f:372:LEU:HD11	32:f:406:GLY:HA3	1.47	0.95
32:f:780:PRO:CB	32:f:800:LEU:HA	1.96	0.94
5:Y:358:ARG:HD2	5:Y:359:PRO:CD	1.97	0.94
13:B:176:VAL:HG12	14:C:283:PHE:CD1	2.02	0.94
32:f:95:PRO:O	32:f:99:LEU:HB2	1.67	0.94
32:f:388:ASP:OD1	32:f:390:LEU:HB2	1.67	0.94
2:V:195:ILE:CG2	14:C:22:GLN:HB3	1.95	0.94
13:B:432:GLU:CA	20:I:169:ALA:CB	2.43	0.94
32:f:358:PHE:CZ	32:f:381:VAL:HG21	2.03	0.94
32:f:311:VAL:HB	32:f:490:ALA:CB	1.96	0.94
13:B:431:GLN:NE2	20:I:176:LYS:NZ	2.16	0.93
15:D:417:TYR:CE1	19:H:79:MET:HB2	2.02	0.93
17:F:437:TYR:CE1	22:K:28:ILE:CB	2.51	0.93
32:f:691:PRO:CB	32:f:749:ALA:HB2	1.99	0.93
2:V:495:ARG:CB	14:C:38:LYS:CB	2.44	0.93
2:V:80:LYS:HD3	2:V:81:GLN:CB	1.98	0.93
2:V:287:ARG:CD	11:e:4:LYS:CE	2.43	0.93
32:f:376:PHE:CE2	32:f:416:MET:HE1	2.03	0.93
13:B:176:VAL:CG1	14:C:283:PHE:CD1	2.51	0.92
32:f:224:ASN:O	32:f:228:LYS:HB3	1.66	0.92
22:K:224:GLN:HG2	22:K:227:HIS:CD2	2.04	0.92
22:K:18:GLU:HB2	22:K:20:ARG:CZ	1.98	0.92
15:D:366:ARG:NH2	18:G:177:SER:CB	2.33	0.92
22:k:217:LEU:HD13	22:k:229:PHE:HZ	1.35	0.92
13:B:432:GLU:CA	20:I:169:ALA:HB3	1.87	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:437:TYR:CZ	22:K:28:ILE:HG22	2.02	0.91
3:W:98:LYS:HZ1	3:W:137:TYR:HE2	0.96	0.91
12:A:429:TYR:CD2	21:J:12:PRO:HG2	2.05	0.91
12:A:348:LEU:CD2	22:K:32:LYS:NZ	2.30	0.91
13:B:432:GLU:OE2	20:I:166:ASN:OD1	1.83	0.91
32:f:315:GLU:HG2	32:f:491:GLY:HA2	1.51	0.91
15:D:418:LYS:NZ	19:H:51:LYS:HD3	1.84	0.91
22:K:18:GLU:HB3	22:K:20:ARG:NH1	1.85	0.91
32:f:366:ASP:OD1	32:f:367:SER:N	2.04	0.91
32:f:376:PHE:CE2	32:f:798:THR:HB	2.06	0.91
13:B:333:ARG:CZ	20:I:15:GLU:OE2	2.18	0.91
15:D:417:TYR:CD1	19:H:79:MET:HA	2.04	0.91
13:B:428:TYR:CE1	20:I:170:ALA:CB	2.54	0.90
2:V:324:PHE:HB3	11:e:6:GLN:HG3	1.52	0.90
13:B:178:LYS:HG3	14:C:283:PHE:HE1	1.36	0.90
17:F:438:TYR:CD1	22:K:21:LEU:N	2.34	0.90
22:K:18:GLU:CD	22:K:20:ARG:HH22	1.79	0.90
3:W:98:LYS:CD	3:W:140:ILE:HG13	2.01	0.90
17:F:439:ALA:O	23:L:78:THR:N	2.04	0.90
32:f:742:ALA:HA	32:f:745:LEU:HD21	1.53	0.90
32:f:494:ARG:HE	32:f:495:GLU:H	1.16	0.89
3:W:134:GLY:O	3:W:140:ILE:HG21	1.71	0.89
22:K:217:LEU:N	22:K:229:PHE:CE1	2.39	0.89
17:F:437:TYR:CE2	22:K:28:ILE:HB	2.08	0.89
2:V:195:ILE:CA	14:C:23:TYR:HB2	2.02	0.89
32:f:483:PHE:CZ	32:f:799:VAL:HB	2.06	0.89
1:U:149:GLN:NE2	15:D:41:TYR:HD2	1.61	0.89
32:f:363:SER:O	32:f:365:VAL:N	2.04	0.89
17:F:437:TYR:HD1	22:K:28:ILE:HG13	1.29	0.89
32:f:376:PHE:CE2	32:f:798:THR:CB	2.55	0.89
15:D:417:TYR:CE1	19:H:79:MET:CA	2.55	0.89
15:D:413:GLU:CD	18:G:25:VAL:HG13	1.98	0.89
32:f:369:ARG:HB3	32:f:370:MET:SD	2.13	0.89
32:f:389:LYS:HG2	32:f:418:LEU:CD2	2.02	0.88
5:Y:358:ARG:CD	5:Y:359:PRO:HD2	2.03	0.88
22:K:216:GLU:HB2	22:K:229:PHE:HE2	1.23	0.88
32:f:122:ALA:O	32:f:126:ILE:HB	1.72	0.88
32:f:318:THR:O	32:f:322:SER:HB3	1.74	0.88
3:W:142:ARG:HH21	3:W:178:GLU:HB2	1.38	0.88
32:f:378:ASN:HB3	32:f:391:LEU:HG	1.56	0.88
16:E:372:ARG:NH1	24:M:171:ALA:N	2.22	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:e:6:GLN:HB3	11:e:7:PRO:HD3	1.54	0.87
2:V:495:ARG:CB	14:C:38:LYS:HB3	2.02	0.87
3:W:136:ILE:HD13	3:W:175:GLY:CA	2.03	0.87
32:f:223:GLU:O	32:f:227:ALA:HB3	1.73	0.87
32:f:311:VAL:CB	32:f:490:ALA:HB1	2.03	0.87
13:B:177:GLU:N	13:B:178:LYS:HA	1.89	0.87
2:V:77:GLU:HB2	2:V:81:GLN:HE21	0.73	0.87
32:f:337:LEU:HD13	32:f:420:TRP:CZ3	2.10	0.87
22:K:18:GLU:CG	22:K:20:ARG:HH12	1.87	0.87
2:V:324:PHE:HB3	11:e:6:GLN:CG	2.04	0.86
5:Y:63:TRP:CD1	5:Y:66:ASP:CG	2.53	0.86
17:F:437:TYR:CD1	22:K:28:ILE:CB	2.57	0.86
2:V:291:TYR:CE1	11:e:5:LYS:HE2	2.10	0.86
3:W:40:LEU:HB2	3:W:41:GLN:HA	1.56	0.86
22:k:225:ASN:HA	22:k:227:HIS:HB3	1.54	0.86
32:f:378:ASN:HB3	32:f:391:LEU:CG	2.05	0.86
32:f:796:LEU:O	32:f:799:VAL:CG2	2.22	0.86
2:V:195:ILE:HA	14:C:23:TYR:CB	2.01	0.86
17:F:437:TYR:CZ	22:K:28:ILE:CB	2.58	0.86
32:f:123:ALA:O	32:f:127:SER:HB2	1.76	0.86
6:Z:45:LYS:HZ3	17:F:115:SER:HA	1.33	0.86
12:A:348:LEU:HD22	22:K:32:LYS:HZ1	0.77	0.86
15:D:389:GLU:HA	15:D:390:ASN:HB2	1.57	0.86
19:H:167:TYR:O	19:H:171:LYS:HB2	1.76	0.86
13:B:176:VAL:HG11	14:C:283:PHE:CG	2.09	0.86
22:k:217:LEU:HD12	22:k:229:PHE:HZ	1.35	0.86
22:k:217:LEU:HD12	22:k:229:PHE:CZ	2.05	0.85
32:f:88:SER:CB	32:f:92:VAL:HG23	2.06	0.85
32:f:129:LEU:O	32:f:133:MET:HB3	1.75	0.85
2:V:287:ARG:HD2	11:e:4:LYS:CE	2.03	0.85
32:f:696:LEU:CD1	32:f:752:HIS:HD2	1.90	0.85
3:W:98:LYS:HD3	3:W:140:ILE:HG13	1.59	0.85
21:J:186:LEU:O	21:J:190:LEU:HB2	1.77	0.85
17:F:439:ALA:HB3	23:L:77:LEU:HD22	1.58	0.85
32:f:471:LEU:HD12	32:f:509:LYS:HG2	1.58	0.84
32:f:691:PRO:HB2	32:f:749:ALA:HB2	1.58	0.84
2:V:495:ARG:C	14:C:38:LYS:HG2	2.01	0.84
2:V:195:ILE:CG2	14:C:19:GLY:O	2.06	0.84
11:e:6:GLN:CB	11:e:7:PRO:HD3	2.07	0.84
16:E:383:LYS:HE2	24:M:19:ARG:HH12	1.39	0.84
17:F:436:GLN:O	17:F:438:TYR:CD2	2.31	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:126:ILE:O	32:f:130:ALA:HB3	1.77	0.84
32:f:376:PHE:HE2	32:f:798:THR:CB	1.91	0.84
15:D:366:ARG:HE	18:G:177:SER:HB2	1.41	0.84
32:f:635:LYS:HZ3	32:f:641:GLU:CD	1.86	0.84
2:V:56:ALA:HB1	14:C:30:GLU:OE2	1.78	0.84
12:A:429:TYR:CD1	21:J:12:PRO:HG2	2.12	0.84
17:F:437:TYR:CD2	22:K:28:ILE:HB	2.13	0.84
32:f:336:GLU:HG3	32:f:337:LEU:HD22	1.60	0.84
32:f:376:PHE:HE2	32:f:798:THR:CG2	1.89	0.84
13:B:175:LYS:NZ	13:B:175:LYS:HB3	1.91	0.84
22:K:177:ALA:O	22:K:181:LEU:HB2	1.76	0.84
14:C:214:VAL:HG21	14:C:249:ASP:H	1.41	0.83
22:K:18:GLU:CB	22:K:20:ARG:NH1	2.41	0.83
5:Y:358:ARG:HH12	5:Y:363:ASN:HB2	1.40	0.83
13:B:178:LYS:NZ	14:C:278:ASN:HB3	1.94	0.83
32:f:695:ALA:HB3	32:f:752:HIS:HB2	1.59	0.83
12:A:429:TYR:CD1	21:J:12:PRO:HD2	2.12	0.83
3:W:98:LYS:HG2	3:W:140:ILE:CG1	2.09	0.83
2:V:80:LYS:HD3	2:V:81:GLN:HB3	1.60	0.83
2:V:256:ARG:HG3	11:e:5:LYS:HD2	1.61	0.83
2:V:495:ARG:CA	14:C:38:LYS:HG2	2.09	0.83
13:B:333:ARG:NH1	20:I:15:GLU:CG	2.41	0.83
15:D:413:GLU:HG2	18:G:157:ALA:HB2	0.84	0.83
17:F:437:TYR:HE1	22:K:28:ILE:HG21	1.31	0.83
32:f:301:HIS:O	32:f:305:LEU:HB2	1.77	0.83
32:f:714:SER:O	32:f:718:ASP:HB2	1.78	0.83
13:B:230:THR:HG23	13:B:353:PHE:HB3	1.60	0.82
15:D:366:ARG:HH21	18:G:177:SER:HB2	1.43	0.82
32:f:225:ALA:O	32:f:229:VAL:HB	1.79	0.82
2:V:492:LYS:NZ	14:C:38:LYS:HZ1	1.74	0.82
3:W:98:LYS:HG2	3:W:140:ILE:HD11	1.58	0.82
9:c:273:LYS:HD2	9:c:274:ASN:HB2	1.61	0.82
32:f:479:LEU:CD2	32:f:513:GLU:CB	2.50	0.82
32:f:494:ARG:NE	32:f:495:GLU:N	2.26	0.82
15:D:413:GLU:OE2	18:G:156:PRO:C	2.22	0.82
12:A:333:ARG:HH12	12:A:340:LYS:HD3	1.43	0.81
22:K:18:GLU:HB3	22:K:20:ARG:CZ	2.09	0.81
2:V:212:TYR:OH	11:e:4:LYS:HD3	1.76	0.81
32:f:376:PHE:CZ	32:f:416:MET:SD	2.73	0.81
32:f:378:ASN:O	32:f:381:VAL:HG12	1.80	0.81
32:f:742:ALA:C	32:f:745:LEU:HG	2.06	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:82:LEU:O	2:V:84:LYS:N	2.13	0.81
2:V:492:LYS:HZ3	14:C:38:LYS:NZ	1.78	0.81
3:W:416:GLN:HB3	3:W:417:ARG:HA	1.61	0.81
6:Z:45:LYS:HZ2	17:F:115:SER:CA	1.88	0.81
12:A:429:TYR:CE1	21:J:12:PRO:HD2	2.16	0.81
13:B:265:LYS:HD3	14:C:227:GLY:HA3	1.63	0.81
17:F:165:PRO:HB2	17:F:166:THR:HG22	1.63	0.81
22:K:18:GLU:HG2	22:K:20:ARG:NH1	1.96	0.81
22:K:216:GLU:CB	22:K:229:PHE:CE2	2.61	0.81
13:B:431:GLN:HE22	20:I:176:LYS:HZ1	0.81	0.80
32:f:376:PHE:CE2	32:f:416:MET:CE	2.64	0.80
12:A:429:TYR:CD2	21:J:12:PRO:CG	2.63	0.80
17:F:383:GLU:HA	23:L:170:THR:HG21	1.64	0.80
9:c:211:GLU:HA	9:c:214:GLN:HB3	1.64	0.80
22:K:216:GLU:CB	22:K:229:PHE:HE2	1.94	0.80
2:V:83:GLU:O	2:V:84:LYS:HB2	1.81	0.80
13:B:176:VAL:HG22	13:B:177:GLU:HB2	1.62	0.80
15:D:100:THR:HB	15:D:114:ARG:HD2	1.63	0.80
15:D:354:LEU:HA	15:D:355:SER:HB3	1.62	0.80
17:F:437:TYR:CE1	22:K:28:ILE:HG23	2.14	0.80
32:f:456:ARG:HB3	32:f:489:TYR:HE2	1.47	0.80
32:f:471:LEU:HD12	32:f:509:LYS:HG3	1.62	0.80
3:W:98:LYS:HD3	3:W:137:TYR:HD2	1.47	0.80
32:f:232:TYR:O	32:f:236:CYS:HB2	1.82	0.79
2:V:57:ALA:HB3	2:V:58:ALA:HB3	1.64	0.79
2:V:242:HIS:NE2	14:C:23:TYR:CD2	2.49	0.79
1:U:361:ARG:HG3	1:U:365:CYS:HB2	1.64	0.79
13:B:176:VAL:HG12	14:C:283:PHE:CZ	2.18	0.79
17:F:437:TYR:OH	22:K:28:ILE:CG2	2.30	0.79
9:c:272:ILE:HG21	9:c:276:GLY:H	1.47	0.79
16:E:174:GLY:HA2	16:E:176:PRO:HD2	1.65	0.79
2:V:495:ARG:HB2	14:C:38:LYS:HE3	1.64	0.79
32:f:494:ARG:HH21	32:f:495:GLU:CG	1.88	0.79
32:f:494:ARG:NE	32:f:495:GLU:H	1.80	0.79
32:f:184:LEU:HG	32:f:185:LEU:N	1.98	0.79
32:f:503:PRO:O	32:f:507:ASP:HB2	1.82	0.79
3:W:98:LYS:HG2	3:W:140:ILE:CD1	2.13	0.79
13:B:432:GLU:CD	20:I:166:ASN:CG	2.48	0.78
21:j:186:LEU:O	21:j:190:LEU:HB2	1.83	0.78
22:K:216:GLU:C	22:K:229:PHE:CZ	2.60	0.78
32:f:88:SER:HB2	32:f:92:VAL:HG23	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:82:LEU:C	2:V:84:LYS:H	1.90	0.78
32:f:691:PRO:HB3	32:f:749:ALA:HB2	1.66	0.78
17:F:256:LEU:HB2	17:F:306:VAL:HG22	1.66	0.78
32:f:494:ARG:HE	32:f:494:ARG:C	1.92	0.78
17:F:92:ASN:HB3	17:F:125:LYS:HB2	1.66	0.78
13:B:177:GLU:H	13:B:178:LYS:HA	1.48	0.78
32:f:612:LEU:O	32:f:616:CYS:HB2	1.83	0.78
32:f:745:LEU:HD12	32:f:746:ARG:N	1.99	0.78
32:f:695:ALA:C	32:f:752:HIS:HB3	2.09	0.78
15:D:104:GLY:HA2	15:D:110:ASN:HA	1.65	0.77
17:F:435:LEU:HG	17:F:438:TYR:HD2	1.41	0.77
17:F:437:TYR:CD2	22:K:25:GLU:OE1	2.37	0.77
32:f:784:ASP:HB2	32:f:800:LEU:HD21	1.67	0.77
12:A:103:ASN:ND2	17:F:169:ASP:OD1	2.17	0.77
15:D:413:GLU:CD	18:G:157:ALA:HB2	2.08	0.77
3:W:92:LYS:H	3:W:93:ARG:HB3	1.50	0.77
22:K:224:GLN:CD	22:K:227:HIS:NE2	2.42	0.77
16:E:191:LEU:HD21	16:E:227:PRO:HG2	1.64	0.77
32:f:392:THR:HG22	32:f:417:ILE:CD1	2.14	0.77
2:V:287:ARG:NH1	11:e:4:LYS:CD	2.31	0.77
15:D:413:GLU:OE2	18:G:156:PRO:O	2.02	0.77
2:V:195:ILE:HG23	14:C:23:TYR:H	1.50	0.76
32:f:796:LEU:HG	32:f:799:VAL:HG21	1.66	0.76
14:C:187:LEU:HA	14:C:293:MET:HB3	1.67	0.76
32:f:675:PHE:O	32:f:679:LEU:HB2	1.85	0.76
2:V:287:ARG:NH1	11:e:4:LYS:HD3	2.00	0.76
15:D:348:ILE:HG21	15:D:379:CYS:HB3	1.68	0.76
22:K:217:LEU:HB2	22:K:229:PHE:HE1	1.50	0.76
32:f:478:ARG:HD3	32:f:504:VAL:HG13	1.68	0.76
15:D:293:LEU:O	15:D:326:ARG:NH1	2.20	0.75
3:W:136:ILE:HD13	3:W:175:GLY:C	2.11	0.75
2:V:496:PHE:O	14:C:37:ASP:OD2	2.04	0.75
15:D:417:TYR:OH	19:H:79:MET:HB3	1.70	0.75
17:F:299:GLU:HB3	17:F:300:LYS:HB2	1.68	0.75
32:f:376:PHE:CZ	32:f:798:THR:HB	2.22	0.75
32:f:635:LYS:NZ	32:f:641:GLU:CG	2.50	0.75
19:h:167:TYR:O	19:h:171:LYS:HB2	1.85	0.75
22:K:224:GLN:NE2	22:K:227:HIS:NE2	2.35	0.75
32:f:684:PRO:O	32:f:688:ARG:HB2	1.87	0.75
2:V:99:ARG:HH22	2:V:147:PHE:H	1.34	0.75
13:B:333:ARG:HD3	20:I:15:GLU:OE2	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:439:ALA:OXT	23:L:77:LEU:HA	1.85	0.75
1:U:424:ALA:HA	1:U:427:LEU:HD13	1.69	0.74
32:f:376:PHE:CE2	32:f:798:THR:HG22	2.20	0.74
32:f:494:ARG:CG	32:f:497:VAL:HG12	2.16	0.74
1:U:799:LYS:HA	1:U:843:GLU:HG3	1.69	0.74
17:F:438:TYR:CD1	22:K:20:ARG:C	2.55	0.74
20:I:3:ARG:HH12	22:K:12:VAL:HG13	1.52	0.74
15:D:413:GLU:HG3	18:G:157:ALA:HB2	1.60	0.74
13:B:333:ARG:HH11	20:I:15:GLU:CD	1.92	0.74
22:K:20:ARG:H	22:K:20:ARG:HD2	1.52	0.74
5:Y:170:GLU:HG3	5:Y:171:GLY:HA3	1.70	0.74
2:V:81:GLN:OE1	2:V:81:GLN:HA	1.88	0.74
2:V:495:ARG:CB	14:C:38:LYS:HE3	2.18	0.74
32:f:392:THR:CG2	32:f:417:ILE:HG21	2.18	0.74
17:F:383:GLU:OE2	23:L:167:SER:N	2.20	0.74
32:f:358:PHE:O	32:f:362:GLY:HA3	1.87	0.74
5:Y:63:TRP:CE2	5:Y:66:ASP:OD1	2.40	0.73
17:F:137:ILE:HG21	17:F:160:ILE:HB	1.69	0.73
32:f:357:ARG:O	32:f:361:SER:HB2	1.87	0.73
2:V:492:LYS:HZ2	14:C:38:LYS:HZ2	0.74	0.73
12:A:170:PRO:HA	12:A:229:VAL:HG12	1.70	0.73
16:E:113:ARG:HH11	16:E:220:ASN:HD21	1.34	0.73
22:K:217:LEU:CB	22:K:229:PHE:HE1	2.00	0.73
32:f:211:ILE:O	32:f:215:ASP:HB2	1.88	0.73
32:f:471:LEU:CD1	32:f:509:LYS:CE	2.65	0.73
32:f:742:ALA:HA	32:f:745:LEU:CG	2.18	0.73
3:W:142:ARG:NH2	3:W:178:GLU:HB2	2.03	0.73
12:A:312:ARG:HG3	12:A:336:ARG:HH11	1.53	0.73
14:C:258:ARG:HD2	14:C:260:GLU:HB2	1.71	0.73
4:X:370:LEU:HD13	5:Y:306:GLN:HB2	1.68	0.73
12:A:315:ILE:HD12	12:A:317:VAL:H	1.53	0.73
1:U:173:VAL:HG13	1:U:176:MET:HB2	1.70	0.73
6:Z:102:HIS:HD2	6:Z:104:ASN:HB3	1.52	0.72
32:f:664:GLU:HB3	32:f:696:LEU:HG	1.69	0.72
2:V:255:LEU:HD22	2:V:291:TYR:HB3	1.70	0.72
14:C:229:ARG:HH11	14:C:232:ARG:HH11	1.35	0.72
17:F:357:PRO:O	17:F:362:ARG:NH1	2.22	0.72
2:V:212:TYR:OH	11:e:4:LYS:NZ	2.23	0.72
17:F:437:TYR:CG	22:K:28:ILE:CB	2.72	0.72
1:U:102:ALA:CB	14:C:21:ARG:CZ	2.65	0.72
3:W:436:MET:O	3:W:440:ASN:ND2	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:437:TYR:CE2	22:K:28:ILE:CB	2.71	0.72
32:f:691:PRO:HG2	32:f:745:LEU:HD13	1.70	0.72
22:K:18:GLU:HB2	22:K:19:GLY:HA2	1.72	0.72
2:V:291:TYR:HE1	11:e:5:LYS:HE2	1.54	0.72
15:D:417:TYR:CZ	19:H:79:MET:CA	2.73	0.72
22:K:20:ARG:HD2	22:K:20:ARG:N	2.05	0.72
4:X:366:SER:HB2	5:Y:310:SER:HB3	1.71	0.72
7:a:244:ASN:ND2	7:a:272:ILE:O	2.23	0.72
22:K:224:GLN:NE2	22:K:227:HIS:CE1	2.58	0.72
6:Z:176:LEU:HD12	6:Z:177:ARG:H	1.54	0.72
10:d:215:TRP:CD1	10:d:216:VAL:H	2.08	0.72
13:B:440:LEU:HD12	21:J:29:GLY:HA2	1.71	0.72
32:f:389:LYS:CG	32:f:418:LEU:CD2	2.63	0.72
3:W:134:GLY:O	3:W:135:LYS:O	2.08	0.71
5:Y:101:ARG:HB3	5:Y:130:LYS:HD3	1.72	0.71
32:f:389:LYS:CD	32:f:418:LEU:HD21	2.20	0.71
4:X:229:TYR:OH	4:X:258:LYS:NZ	2.23	0.71
9:c:272:ILE:HG13	9:c:275:VAL:HG23	1.70	0.71
12:A:429:TYR:CD1	21:J:12:PRO:CD	2.72	0.71
5:Y:190:ALA:O	5:Y:291:HIS:NE2	2.23	0.71
17:F:439:ALA:O	23:L:77:LEU:C	2.32	0.71
9:c:272:ILE:HD12	9:c:277:LYS:HB3	1.72	0.71
15:D:303:VAL:HG23	15:D:304:ASN:HB2	1.71	0.71
17:F:437:TYR:HD2	22:K:25:GLU:CD	1.98	0.71
1:U:337:LEU:HD13	1:U:789:ILE:HG12	1.70	0.71
3:W:417:ARG:NH1	3:W:420:ASP:OD1	2.23	0.71
5:Y:63:TRP:NE1	5:Y:66:ASP:CG	2.48	0.71
17:F:439:ALA:CB	23:L:77:LEU:HD22	2.21	0.71
2:V:447:ILE:HG13	2:V:449:ALA:H	1.56	0.71
32:f:370:MET:SD	32:f:370:MET:N	2.57	0.71
1:U:102:ALA:HB1	14:C:21:ARG:NH2	2.03	0.71
13:B:436:GLU:H	13:B:437:GLY:C	1.98	0.71
22:K:18:GLU:HB2	22:K:20:ARG:HH22	1.13	0.71
32:f:88:SER:HB3	32:f:92:VAL:HG23	1.72	0.71
2:V:195:ILE:HG21	14:C:22:GLN:CB	2.13	0.71
3:W:257:GLN:HA	3:W:258:ALA:HB3	1.72	0.71
4:X:225:TRP:HB3	4:X:261:LEU:HG	1.72	0.71
13:B:439:TYR:OH	21:J:28:LYS:HE3	1.91	0.71
2:V:241:ARG:O	14:C:23:TYR:HE2	1.74	0.71
20:i:194:ILE:O	20:i:198:ASN:HB2	1.91	0.71
2:V:492:LYS:HZ2	14:C:38:LYS:HZ3	1.37	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:416:ASN:OD1	9:c:273:LYS:NZ	2.23	0.70
2:V:495:ARG:CB	14:C:38:LYS:CE	2.69	0.70
15:D:366:ARG:NE	18:G:177:SER:HB2	2.06	0.70
1:U:413:LYS:HA	1:U:449:ILE:HG12	1.71	0.70
3:W:44:ILE:HB	3:W:93:ARG:HD2	1.73	0.70
8:b:15:TYR:O	8:b:25:ARG:NH1	2.24	0.70
10:d:12:LYS:HG2	10:d:57:ILE:HD11	1.73	0.70
17:F:435:LEU:HG	22:K:20:ARG:HG2	0.93	0.70
17:F:435:LEU:CD1	22:K:20:ARG:CG	2.61	0.70
2:V:495:ARG:O	14:C:38:LYS:CA	2.39	0.70
32:f:625:LYS:O	32:f:629:LYS:HB2	1.91	0.70
32:f:797:LEU:O	32:f:800:LEU:HD13	1.91	0.70
2:V:195:ILE:HG23	14:C:22:GLN:C	2.16	0.70
9:c:261:GLU:HA	9:c:264:LYS:HG2	1.72	0.70
14:C:168:PRO:HA	14:C:172:PRO:HG3	1.73	0.70
15:D:387:VAL:HG11	16:E:167:PRO:HD3	1.72	0.70
32:f:315:GLU:CG	32:f:491:GLY:HA2	2.20	0.70
32:f:337:LEU:CD1	32:f:420:TRP:CZ3	2.74	0.70
3:W:91:SER:HB2	3:W:92:LYS:HD2	1.73	0.70
10:d:147:SER:HA	10:d:148:TYR:HB2	1.74	0.70
17:F:437:TYR:CG	22:K:28:ILE:HG12	2.22	0.70
17:F:437:TYR:CE2	22:K:28:ILE:CG2	2.69	0.70
10:d:3:GLU:HB3	10:d:4:GLN:HA	1.73	0.70
13:B:333:ARG:NH1	20:I:15:GLU:OE1	2.24	0.70
32:f:311:VAL:O	32:f:490:ALA:O	2.09	0.70
32:f:337:LEU:CD1	32:f:420:TRP:HZ3	2.04	0.70
32:f:389:LYS:HG2	32:f:418:LEU:HD11	1.72	0.70
32:f:494:ARG:NH2	32:f:495:GLU:CG	2.48	0.70
32:f:664:GLU:O	32:f:665:GLU:O	2.10	0.70
15:D:105:SER:O	15:D:245:ARG:NH1	2.25	0.70
17:F:383:GLU:OE1	23:L:170:THR:OG1	2.04	0.70
32:f:222:ASP:O	32:f:226:TYR:HB3	1.91	0.70
32:f:311:VAL:CG2	32:f:527:VAL:O	2.39	0.70
1:U:842:LYS:HA	1:U:843:GLU:HB3	1.74	0.69
7:a:188:LEU:HD11	7:a:193:GLN:HG3	1.72	0.69
5:Y:101:ARG:HE	5:Y:127:THR:HA	1.56	0.69
32:f:376:PHE:CD2	32:f:798:THR:HG21	2.26	0.69
32:f:494:ARG:HD3	32:f:496:ASP:CG	2.16	0.69
4:X:417:LYS:HD3	5:Y:383:LEU:HD23	1.74	0.69
7:a:34:TRP:HD1	8:b:19:GLY:H	1.38	0.69
26:O:18:THR:HB	26:O:31:CYS:H	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:r:196:HIS:O	29:r:200:SER:HB3	1.91	0.69
32:f:695:ALA:HB3	32:f:752:HIS:CB	2.23	0.69
6:Z:244:GLU:HG2	7:a:287:ASN:H	1.58	0.69
7:a:286:ALA:HB1	7:a:287:ASN:HA	1.72	0.69
15:D:270:ILE:HG22	16:E:251:ARG:HH21	1.55	0.69
2:V:416:ARG:HG3	2:V:459:GLN:HA	1.73	0.69
16:E:175:PRO:HD2	16:E:387:LYS:HE3	1.74	0.69
17:F:382:GLU:CD	23:L:170:THR:HG22	2.18	0.69
32:f:742:ALA:O	32:f:745:LEU:CG	2.38	0.69
1:U:510:GLU:OE2	1:U:546:ARG:NH2	2.25	0.69
4:X:252:LYS:HD3	4:X:287:LEU:HD21	1.75	0.69
2:V:80:LYS:CD	2:V:81:GLN:HB3	2.23	0.69
13:B:176:VAL:HG12	14:C:283:PHE:CE1	2.26	0.69
13:B:438:LEU:HD12	20:I:155:ASN:HD22	1.58	0.69
17:F:84:LYS:HA	17:F:161:LEU:HD22	1.74	0.69
32:f:353:LEU:HG	32:f:387:GLN:HG3	1.75	0.69
10:d:214:GLY:N	10:d:215:TRP:HB3	2.08	0.69
15:D:413:GLU:HG3	18:G:157:ALA:CB	2.17	0.69
17:F:153:VAL:HB	17:F:160:ILE:HG13	1.74	0.69
1:U:102:ALA:HB1	14:C:21:ARG:HH22	1.54	0.69
2:V:492:LYS:HZ3	14:C:38:LYS:HZ1	1.33	0.69
12:A:258:ARG:HD2	17:F:255:GLN:HE22	1.59	0.68
2:V:283:ASN:HB2	2:V:317:PRO:HD2	1.75	0.68
12:A:80:LEU:HD23	13:B:137:SER:HB3	1.73	0.68
32:f:372:LEU:O	32:f:372:LEU:HD23	1.93	0.68
12:A:100:LYS:HZ3	12:A:140:VAL:HG23	1.57	0.68
17:F:188:ILE:HD11	17:F:195:ILE:HD12	1.76	0.68
17:F:314:LEU:HD21	17:F:342:LEU:HD23	1.76	0.68
32:f:130:ALA:O	32:f:134:SER:HB3	1.92	0.68
12:A:102:ILE:HA	12:A:113:ILE:HA	1.74	0.68
12:A:429:TYR:CB	21:J:12:PRO:CG	2.64	0.68
17:F:439:ALA:C	23:L:77:LEU:HD22	2.16	0.68
20:i:17:ARG:HD2	20:i:22:GLU:HG3	1.75	0.68
32:f:688:ARG:HA	32:f:745:LEU:HD22	1.75	0.68
2:V:440:LYS:NZ	10:d:143:LEU:O	2.27	0.68
7:a:270:ARG:NH1	7:a:310:LEU:O	2.27	0.68
13:B:217:LYS:HG3	13:B:219:PRO:HD3	1.76	0.68
7:a:135:ILE:HG12	7:a:158:LEU:HD13	1.74	0.68
8:b:12:ASN:ND2	8:b:53:THR:OG1	2.27	0.68
12:A:375:ARG:NH2	22:K:205:VAL:O	2.26	0.68
13:B:105:THR:HG23	13:B:106:PRO:HD3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:g:138:MET:HB3	18:g:154:CYS:HB3	1.75	0.68
3:W:134:GLY:O	3:W:140:ILE:CG2	2.42	0.68
32:f:392:THR:HG22	32:f:417:ILE:HD12	1.74	0.68
32:f:625:LYS:HA	32:f:657:ILE:HD11	1.75	0.68
5:Y:77:ASN:O	5:Y:81:LEU:N	2.27	0.67
13:B:372:MET:HB3	14:C:179:GLY:HA2	1.76	0.67
17:F:437:TYR:CB	22:K:25:GLU:HA	2.24	0.67
27:P:26:ARG:HB3	27:P:39:PHE:O	1.94	0.67
3:W:90:LEU:HA	3:W:94:ARG:HD2	1.75	0.67
13:B:166:ASP:HB3	13:B:167:THR:HA	1.75	0.67
22:K:224:GLN:CG	22:K:227:HIS:CD2	2.76	0.67
2:V:455:LYS:N	2:V:456:GLY:HA2	2.07	0.67
32:f:628:ASP:HB2	32:f:657:ILE:HD13	1.77	0.67
7:a:320:VAL:HG22	7:a:322:GLY:H	1.60	0.67
12:A:157:ILE:HG23	12:A:158:ASP:HB2	1.75	0.67
13:B:178:LYS:HG3	14:C:283:PHE:CE1	2.26	0.67
13:B:436:GLU:HG3	20:I:22:GLU:OE2	1.95	0.67
32:f:311:VAL:HG21	32:f:527:VAL:O	1.94	0.67
32:f:800:LEU:HD12	32:f:800:LEU:N	2.10	0.67
6:Z:138:TYR:HB3	6:Z:155:PHE:HB3	1.77	0.67
22:K:18:GLU:CG	22:K:20:ARG:NH2	2.45	0.67
32:f:372:LEU:HD23	32:f:372:LEU:C	2.20	0.67
17:F:427:VAL:HA	17:F:431:LYS:HZ2	1.58	0.67
17:F:437:TYR:OH	22:K:28:ILE:HG21	1.85	0.67
21:j:114:LEU:O	21:j:118:TYR:HB2	1.94	0.67
32:f:367:SER:HB3	32:f:370:MET:SD	2.34	0.67
1:U:155:LEU:O	1:U:158:ARG:NH1	2.28	0.67
1:U:212:ASP:O	1:U:215:ASN:ND2	2.28	0.67
4:X:406:ASN:HA	4:X:409:LYS:HD3	1.75	0.67
13:B:333:ARG:CZ	20:I:15:GLU:OE1	2.43	0.67
17:F:438:TYR:HD1	22:K:21:LEU:H	1.41	0.67
22:K:77:ALA:HB3	22:K:142:LEU:HB2	1.77	0.67
32:f:635:LYS:HZ2	32:f:641:GLU:HG3	1.58	0.67
1:U:112:CYS:SG	1:U:159:ARG:NH1	2.68	0.67
16:E:266:GLY:HA2	16:E:267:PHE:HB2	1.77	0.67
17:F:437:TYR:CD2	22:K:28:ILE:CB	2.77	0.67
5:Y:111:LEU:HA	5:Y:114:ILE:HD13	1.75	0.67
12:A:429:TYR:HB3	21:J:12:PRO:HG2	1.76	0.67
22:K:18:GLU:CG	22:K:20:ARG:NH1	2.56	0.67
32:f:478:ARG:O	32:f:482:ILE:HB	1.94	0.67
2:V:294:ARG:HH21	2:V:331:LEU:HD23	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:495:ARG:HD2	14:C:38:LYS:HB3	1.77	0.66
6:Z:111:LEU:HD12	8:b:59:GLU:HB3	1.75	0.66
32:f:578:ALA:O	32:f:582:VAL:HB	1.95	0.66
16:E:223:ARG:O	16:E:226:GLN:NE2	2.28	0.66
17:F:221:LYS:HD2	17:F:327:LYS:HG3	1.76	0.66
17:F:437:TYR:CB	22:K:28:ILE:HG13	2.22	0.66
7:a:286:ALA:HA	7:a:288:HIS:HB2	1.76	0.66
23:L:38:LEU:HD21	23:L:191:GLY:HA2	1.76	0.66
30:S:38:ARG:NH2	26:o:164:PHE:O	2.29	0.66
3:W:136:ILE:CD1	3:W:175:GLY:C	2.69	0.66
5:Y:358:ARG:NH1	5:Y:363:ASN:HB2	2.10	0.66
13:B:197:ILE:HG21	13:B:234:LEU:HD13	1.77	0.66
32:f:376:PHE:CE2	32:f:416:MET:SD	2.88	0.66
5:Y:145:LEU:HG	5:Y:160:ASN:HD21	1.59	0.66
2:V:56:ALA:CB	14:C:30:GLU:OE2	2.42	0.66
3:W:331:GLY:HA2	3:W:332:SER:HB3	1.78	0.66
12:A:304:ASN:HD21	17:F:252:ALA:HB1	1.61	0.66
15:D:89:ILE:HD11	16:E:80:VAL:HG13	1.77	0.66
16:E:138:LEU:HD22	16:E:140:GLU:HG2	1.76	0.66
27:P:27:ARG:NH1	27:P:180:VAL:O	2.29	0.66
32:f:804:LEU:H	32:f:804:LEU:HD12	1.60	0.66
16:E:277:MET:HB2	16:E:295:LEU:HD21	1.78	0.66
28:q:57:ALA:O	28:q:61:GLN:HB3	1.96	0.66
2:V:256:ARG:CG	11:e:5:LYS:HD2	2.25	0.65
2:V:492:LYS:CE	14:C:38:LYS:HZ2	2.09	0.65
3:W:98:LYS:CD	3:W:140:ILE:CG1	2.74	0.65
17:F:437:TYR:CB	22:K:28:ILE:CG1	2.74	0.65
16:E:171:LEU:HB2	16:E:295:LEU:HD22	1.77	0.65
1:U:540:GLN:OE1	9:c:68:ARG:NH1	2.30	0.65
3:W:98:LYS:HD3	3:W:137:TYR:CD2	2.31	0.65
11:e:58:ALA:HB3	11:e:59:GLU:HA	1.77	0.65
16:E:83:CYS:HB3	16:E:87:LEU:HD21	1.78	0.65
1:U:338:HIS:CD2	1:U:785:PRO:HB2	2.32	0.65
7:a:197:ALA:HA	7:a:200:LEU:HB3	1.78	0.65
13:B:248:LEU:HD22	13:B:273:VAL:HG11	1.79	0.65
2:V:197:THR:HG21	2:V:200:ARG:HG3	1.78	0.65
3:W:98:LYS:HG2	3:W:140:ILE:HG12	1.79	0.65
3:W:397:VAL:HG13	4:X:341:PRO:HB2	1.78	0.65
32:f:80:ARG:HB3	32:f:95:PRO:HB2	1.78	0.65
32:f:804:LEU:HD12	32:f:804:LEU:N	2.12	0.65
2:V:80:LYS:CB	2:V:81:GLN:HB2	2.24	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W:427:ASP:HB3	9:c:245:VAL:HG21	1.78	0.65
24:m:47:PHE:HB2	24:m:214:SER:HB3	1.79	0.65
16:E:81:VAL:HG11	16:E:105:LEU:HB2	1.78	0.65
17:F:437:TYR:CD2	22:K:25:GLU:CD	2.74	0.65
3:W:98:LYS:CG	3:W:140:ILE:HD11	2.26	0.65
17:F:430:LYS:HZ1	22:K:17:PRO:CB	2.10	0.65
12:A:293:ASN:HB2	17:F:295:ARG:HH11	1.61	0.65
15:D:411:GLU:OE1	15:D:412:GLN:NE2	2.30	0.65
22:K:224:GLN:HG2	22:K:227:HIS:CG	2.32	0.65
30:S:27:THR:HB	30:S:40:SER:H	1.61	0.65
31:t:148:PRO:O	31:t:152:GLU:HB2	1.97	0.65
32:f:337:LEU:HD11	32:f:422:VAL:HG21	1.77	0.65
12:A:345:LEU:HG	12:A:346:PRO:HD2	1.79	0.65
17:F:437:TYR:CD1	22:K:28:ILE:CD1	2.78	0.65
3:W:123:ARG:HH12	3:W:127:THR:HB	1.62	0.64
3:W:219:THR:HA	3:W:220:GLU:HB2	1.79	0.64
12:A:246:VAL:HG23	13:B:260:LEU:HD23	1.79	0.64
14:C:259:LEU:HD23	14:C:263:SER:HB3	1.79	0.64
17:F:383:GLU:OE1	23:L:170:THR:CG2	2.45	0.64
1:U:327:LYS:HE3	1:U:333:MET:HE2	1.78	0.64
3:W:430:GLN:O	3:W:434:SER:OG	2.14	0.64
13:B:103:ARG:HD3	13:B:160:ILE:HG12	1.79	0.64
13:B:178:LYS:O	13:B:178:LYS:HG2	1.95	0.64
32:f:692:LEU:HG	32:f:752:HIS:CE1	2.32	0.64
2:V:99:ARG:NH1	2:V:144:ASP:O	2.31	0.64
11:e:5:LYS:HG2	11:e:5:LYS:O	1.97	0.64
12:A:306:LEU:O	12:A:336:ARG:NE	2.29	0.64
32:f:635:LYS:HZ3	32:f:641:GLU:CG	2.10	0.64
32:f:804:LEU:H	32:f:804:LEU:CD1	2.10	0.64
2:V:266:GLN:HB3	2:V:299:GLN:HE22	1.61	0.64
6:Z:14:LEU:HG	9:c:39:LEU:HD22	1.80	0.64
6:Z:212:LEU:HB2	7:a:350:LYS:HD2	1.80	0.64
14:C:270:GLN:HA	14:C:273:MET:HE3	1.80	0.64
32:f:315:GLU:HG2	32:f:491:GLY:CA	2.24	0.64
3:W:134:GLY:O	3:W:135:LYS:C	2.40	0.64
3:W:136:ILE:HD11	3:W:176:SER:CB	2.28	0.64
13:B:177:GLU:HB3	13:B:178:LYS:HA	1.79	0.64
15:D:91:GLN:O	15:D:104:GLY:N	2.31	0.64
32:f:483:PHE:CE2	32:f:799:VAL:CB	2.75	0.64
2:V:415:SER:O	2:V:460:SER:OG	2.16	0.64
4:X:242:ILE:HG22	4:X:243:ASP:H	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:355:GLU:C	5:Y:357:ASN:HD22	2.05	0.64
6:Z:16:LEU:HD11	6:Z:135:THR:HG21	1.79	0.64
9:c:124:GLY:O	9:c:128:ASN:ND2	2.31	0.64
10:d:147:SER:OG	10:d:151:VAL:N	2.22	0.64
12:A:346:PRO:HD3	12:A:381:THR:HA	1.79	0.64
13:B:221:GLY:O	13:B:346:ARG:NE	2.28	0.64
25:n:28:ASN:ND2	25:n:31:THR:OG1	2.30	0.64
32:f:93:PRO:HB2	32:f:137:ARG:HE	1.63	0.64
32:f:379:GLY:O	32:f:417:ILE:HG12	1.97	0.64
32:f:460:ASP:N	32:f:460:ASP:OD1	2.29	0.64
1:U:137:MET:HG2	14:C:13:GLU:OE1	1.97	0.64
3:W:442:THR:HB	9:c:229:LEU:HD11	1.80	0.64
18:G:138:MET:HB3	18:G:154:CYS:HB3	1.80	0.64
19:H:119:GLN:HE21	20:I:81:SER:HB2	1.63	0.64
17:F:224:LEU:HB3	17:F:351:LYS:HG2	1.80	0.64
17:F:436:GLN:O	17:F:438:TYR:CE2	2.51	0.64
18:g:123:GLN:HE21	19:h:81:PRO:HB2	1.63	0.64
2:V:101:LEU:O	2:V:103:SER:N	2.31	0.64
2:V:242:HIS:NE2	14:C:23:TYR:CG	2.59	0.64
12:A:100:LYS:NZ	12:A:141:GLY:O	2.30	0.64
22:K:217:LEU:HB2	22:K:229:PHE:CE1	2.32	0.64
22:K:219:THR:HB	22:K:221:GLN:HE22	1.61	0.64
32:f:313:GLU:O	32:f:317:LEU:HB2	1.98	0.64
5:Y:51:ALA:HA	5:Y:54:TYR:HB2	1.79	0.64
9:c:229:LEU:HD22	9:c:231:LEU:HD13	1.79	0.64
10:d:175:ARG:HD2	10:d:205:LYS:HZ2	1.63	0.64
15:D:50:GLU:HA	15:D:53:PHE:HB2	1.81	0.64
21:J:119:THR:HG22	21:J:126:PRO:HB3	1.80	0.64
31:T:9:THR:O	31:T:41:ARG:NH2	2.31	0.64
19:h:4:ARG:NH2	24:m:126:SER:OG	2.31	0.64
32:f:494:ARG:HH21	32:f:495:GLU:H	1.46	0.64
5:Y:138:LEU:HD23	5:Y:176:ARG:HB2	1.80	0.63
15:D:373:ALA:HA	15:D:374:ASP:HB2	1.80	0.63
32:f:389:LYS:HG2	32:f:418:LEU:CG	2.27	0.63
2:V:495:ARG:C	14:C:38:LYS:CG	2.72	0.63
10:d:235:THR:HG22	10:d:237:ILE:H	1.63	0.63
14:C:153:GLY:HA3	14:C:324:ALA:HA	1.79	0.63
15:D:366:ARG:HH21	18:G:177:SER:HB3	1.55	0.63
3:W:312:MET:SD	3:W:361:HIS:ND1	2.72	0.63
24:m:11:ALA:HA	24:m:22:GLN:HG3	1.79	0.63
28:q:57:ALA:O	28:q:61:GLN:CB	2.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:275:VAL:H	2:V:276:PHE:HA	1.64	0.63
22:K:146:VAL:HG11	22:K:222:PRO:HG3	1.81	0.63
25:n:18:SER:HB2	25:n:30:VAL:HA	1.81	0.63
2:V:252:ASN:ND2	2:V:284:GLU:OE2	2.31	0.63
5:Y:98:SER:HA	5:Y:130:LYS:HD2	1.79	0.63
14:C:213:ARG:HG3	14:C:214:VAL:HG12	1.80	0.63
24:m:8:ASP:O	24:m:22:GLN:NE2	2.31	0.63
32:f:376:PHE:HE2	32:f:798:THR:HG21	1.49	0.63
6:Z:168:GLU:HA	9:c:42:LEU:HD13	1.79	0.63
6:Z:245:PHE:O	6:Z:249:PHE:N	2.32	0.63
16:E:91:LYS:HD2	16:E:107:ILE:HB	1.80	0.63
21:J:154:HIS:NE2	22:K:59:MET:SD	2.71	0.63
32:f:138:GLU:O	32:f:142:TYR:HB2	1.97	0.63
4:X:406:ASN:HD21	9:c:264:LYS:HD2	1.64	0.63
32:f:366:ASP:O	32:f:367:SER:HB2	1.97	0.63
2:V:83:GLU:O	2:V:84:LYS:CB	2.47	0.62
6:Z:142:GLU:OE2	6:Z:153:LYS:NZ	2.32	0.62
12:A:122:VAL:HG23	17:F:90:VAL:HG22	1.81	0.62
13:B:428:TYR:CG	20:I:170:ALA:CB	2.50	0.62
15:D:366:ARG:NH2	18:G:177:SER:HB2	2.06	0.62
17:F:383:GLU:OE2	23:L:166:GLN:C	2.42	0.62
32:f:376:PHE:HE2	32:f:798:THR:HB	1.53	0.62
2:V:62:HIS:HA	2:V:65:ARG:HB3	1.81	0.62
7:a:139:GLU:HA	7:a:142:LEU:HB3	1.80	0.62
8:b:19:GLY:HA2	8:b:24:THR:HA	1.80	0.62
13:B:177:GLU:H	13:B:178:LYS:CA	2.11	0.62
15:D:374:ASP:HB3	15:D:378:ILE:HD12	1.79	0.62
22:K:217:LEU:CB	22:K:229:PHE:CE1	2.81	0.62
32:f:654:VAL:HA	32:f:657:ILE:HD12	1.81	0.62
11:e:63:HIS:HA	11:e:66:LYS:HE2	1.81	0.62
13:B:432:GLU:OE2	20:I:166:ASN:HB3	1.94	0.62
17:F:439:ALA:CA	23:L:77:LEU:HD22	2.29	0.62
22:k:209:LYS:O	22:k:214:ASN:ND2	2.32	0.62
23:l:186:GLU:HA	23:l:189:LYS:HG2	1.82	0.62
32:f:687:ARG:HH21	32:f:742:ALA:HB2	1.64	0.62
1:U:156:GLU:OE2	15:D:45:LYS:HE3	1.99	0.62
2:V:321:ALA:HB1	2:V:322:VAL:HB	1.81	0.62
28:Q:140:LEU:HD13	29:r:166:ARG:HE	1.64	0.62
28:q:19:ARG:HB3	28:q:31:ASP:HA	1.82	0.62
2:V:99:ARG:HB2	2:V:104:THR:HG22	1.82	0.62
6:Z:193:ASN:HB3	9:c:307:VAL:HG11	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:69:GLN:HB2	14:C:118:ASN:HB2	1.80	0.62
24:M:51:LYS:NZ	24:M:62:SER:O	2.29	0.62
1:U:149:GLN:HE22	15:D:41:TYR:CB	2.12	0.62
2:V:416:ARG:HH12	2:V:418:SER:HB2	1.65	0.62
5:Y:71:ASN:HA	5:Y:74:LYS:HG2	1.81	0.62
6:Z:202:ASN:OD1	6:Z:203:SER:N	2.31	0.62
32:f:664:GLU:HA	32:f:697:ILE:HA	1.80	0.62
5:Y:190:ALA:HA	5:Y:287:LEU:HD13	1.82	0.62
7:a:290:GLN:HA	7:a:332:HIS:HA	1.82	0.62
9:c:160:PHE:HA	9:c:202:SER:HA	1.81	0.62
17:F:280:PRO:HB3	17:F:326:VAL:HA	1.82	0.62
2:V:266:GLN:O	2:V:269:LYS:NZ	2.32	0.62
3:W:98:LYS:CG	3:W:140:ILE:CG1	2.77	0.62
6:Z:199:LYS:HD3	6:Z:202:ASN:HD21	1.65	0.62
13:B:218:PRO:HB2	13:B:346:ARG:HH12	1.64	0.62
15:D:247:VAL:HG21	15:D:288:ILE:HG23	1.82	0.62
17:F:437:TYR:CD2	22:K:25:GLU:HA	2.35	0.62
32:f:376:PHE:CG	32:f:416:MET:HE1	2.35	0.62
1:U:149:GLN:OE1	15:D:39:ASP:N	2.32	0.62
2:V:353:LEU:HG	2:V:357:LEU:HD23	1.81	0.62
3:W:76:GLU:HA	3:W:79:GLU:HB2	1.81	0.62
5:Y:293:ARG:NH1	11:e:49:GLU:OE2	2.33	0.62
7:a:230:ARG:HE	7:a:233:LEU:HD22	1.64	0.62
26:o:18:THR:HB	26:o:31:CYS:H	1.64	0.62
6:Z:208:ILE:HD11	7:a:350:LYS:HA	1.82	0.62
8:b:164:ASP:N	8:b:165:GLY:HA2	2.15	0.62
12:A:112:ILE:HD12	17:F:150:LEU:HG	1.81	0.62
14:C:111:ASN:O	14:C:129:ASN:ND2	2.32	0.62
14:C:214:VAL:HG22	14:C:215:SER:H	1.65	0.62
2:V:212:TYR:OH	11:e:4:LYS:CE	2.47	0.61
7:a:290:GLN:HE21	7:a:330:ARG:HB2	1.65	0.61
5:Y:138:LEU:HD12	5:Y:141:VAL:HB	1.82	0.61
2:V:80:LYS:HE2	2:V:87:SER:HA	1.81	0.61
10:d:49:ILE:HD11	10:d:89:LEU:HD22	1.81	0.61
13:B:252:GLY:O	13:B:257:GLN:NE2	2.33	0.61
30:s:27:THR:HB	30:s:40:SER:H	1.66	0.61
32:f:339:ILE:HG23	32:f:340:MET:HG2	1.81	0.61
32:f:389:LYS:HD3	32:f:389:LYS:N	2.15	0.61
32:f:801:VAL:HG13	32:f:801:VAL:O	2.01	0.61
7:a:34:TRP:H	8:b:18:ASN:HB2	1.66	0.61
10:d:78:LEU:HA	10:d:81:TYR:HD2	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:B:174:MET:O	13:B:175:LYS:C	2.43	0.61
2:V:497:PRO:O	14:C:41:ASN:CG	2.43	0.61
13:B:176:VAL:HG13	14:C:283:PHE:CD1	2.35	0.61
17:F:83:ASN:O	17:F:154:ASN:ND2	2.32	0.61
17:F:231:THR:OG1	17:F:233:LYS:NZ	2.27	0.61
18:G:237:ALA:O	18:G:241:ALA:HB2	2.00	0.61
31:t:9:THR:O	31:t:41:ARG:NH2	2.31	0.61
2:V:337:LEU:O	2:V:401:ASN:ND2	2.33	0.61
13:B:139:VAL:HA	13:B:140:ASP:HB3	1.82	0.61
32:f:378:ASN:HB2	32:f:391:LEU:HD11	1.82	0.61
2:V:54:LYS:N	2:V:55:THR:OG1	2.33	0.61
4:X:332:GLU:HA	4:X:335:LEU:HB2	1.83	0.61
5:Y:64:GLN:HG2	5:Y:65:ILE:HG22	1.82	0.61
13:B:408:ARG:O	13:B:410:ARG:NH1	2.33	0.61
13:B:432:GLU:CG	20:I:166:ASN:CG	2.70	0.61
24:M:192:GLU:HA	24:M:195:LYS:HE3	1.82	0.61
1:U:189:GLN:NE2	1:U:595:ASN:OD1	2.31	0.61
10:d:147:SER:HG	10:d:151:VAL:H	1.49	0.61
12:A:141:GLY:N	12:A:151:ILE:O	2.29	0.61
12:A:429:TYR:CD1	21:J:12:PRO:CG	2.78	0.61
15:D:204:MET:HE3	15:D:310:ALA:HB2	1.80	0.61
23:l:205:LEU:HG	23:l:205:LEU:O	1.99	0.61
3:W:78:LYS:HA	3:W:81:ASP:HB3	1.81	0.61
10:d:227:SER:C	10:d:229:GLN:HA	2.26	0.61
13:B:401:GLU:HA	13:B:404:LEU:HB3	1.83	0.61
20:i:119:GLN:HE21	20:i:123:GLN:HE22	1.47	0.61
22:k:177:ALA:O	22:k:181:LEU:HB2	2.01	0.61
32:f:234:THR:O	32:f:238:ASN:HB2	2.00	0.61
2:V:241:ARG:HG3	2:V:242:HIS:H	1.65	0.61
7:a:226:ARG:HB3	7:a:234:ILE:HG12	1.83	0.61
7:a:287:ASN:HB3	7:a:289:ARG:HB2	1.82	0.61
10:d:215:TRP:CG	10:d:216:VAL:H	2.19	0.61
12:A:281:GLY:HA2	12:A:299:MET:HB3	1.82	0.61
15:D:130:VAL:HB	15:D:142:VAL:HG12	1.82	0.61
15:D:417:TYR:OH	19:H:79:MET:SD	2.59	0.61
32:f:392:THR:HG23	32:f:417:ILE:HG21	1.81	0.61
3:W:55:ARG:NH1	3:W:75:TYR:O	2.33	0.60
13:B:313:LEU:O	13:B:317:ASP:N	2.34	0.60
14:C:157:GLN:NE2	14:C:316:GLU:O	2.34	0.60
14:C:164:VAL:O	14:C:290:LYS:NZ	2.28	0.60
14:C:246:ILE:HB	14:C:291:VAL:HG12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:437:TYR:HB2	22:K:25:GLU:HA	1.83	0.60
3:W:92:LYS:N	3:W:93:ARG:HB3	2.15	0.60
3:W:220:GLU:N	3:W:221:LYS:HA	2.15	0.60
12:A:264:ALA:O	12:A:268:LYS:N	2.34	0.60
12:A:429:TYR:CE1	21:J:12:PRO:CD	2.85	0.60
24:M:40:ARG:NH1	24:M:146:ALA:O	2.35	0.60
22:k:221:GLN:O	22:k:225:ASN:ND2	2.34	0.60
2:V:211:TYR:HB3	2:V:253:LEU:HD11	1.81	0.60
3:W:187:LEU:HA	3:W:190:MET:HE3	1.82	0.60
4:X:262:ASN:HD21	4:X:326:LEU:HG	1.66	0.60
1:U:156:GLU:OE2	15:D:45:LYS:CE	2.49	0.60
3:W:431:LYS:O	3:W:435:LEU:HB2	2.02	0.60
13:B:333:ARG:CD	20:I:15:GLU:OE2	2.49	0.60
24:M:196:ILE:HA	24:M:199:ILE:HB	1.83	0.60
32:f:232:TYR:O	32:f:236:CYS:CB	2.49	0.60
32:f:380:PHE:CB	32:f:751:TYR:HE1	2.14	0.60
32:f:471:LEU:O	32:f:471:LEU:HD23	2.01	0.60
1:U:149:GLN:NE2	15:D:41:TYR:CG	2.68	0.60
1:U:524:LYS:HE3	1:U:556:MET:HA	1.83	0.60
13:B:411:ARG:HG2	13:B:412:MET:HG2	1.82	0.60
32:f:315:GLU:CB	32:f:491:GLY:HA2	2.31	0.60
32:f:471:LEU:CD1	32:f:509:LYS:HE2	2.30	0.60
1:U:789:ILE:HG22	1:U:791:LEU:H	1.65	0.60
5:Y:63:TRP:CD1	5:Y:66:ASP:OD2	2.54	0.60
5:Y:101:ARG:NH2	5:Y:126:LYS:O	2.35	0.60
10:d:145:GLU:N	10:d:146:GLY:HA2	2.17	0.60
10:d:233:GLU:N	10:d:234:ASP:HA	2.16	0.60
17:F:435:LEU:HA	17:F:438:TYR:HE2	1.67	0.60
20:I:47:ALA:HB3	20:I:212:GLU:HB3	1.84	0.60
2:V:195:ILE:CG2	14:C:23:TYR:N	2.54	0.60
2:V:262:SER:HB2	2:V:263:LEU:HB2	1.82	0.60
13:B:170:LEU:HD22	13:B:265:LYS:HE3	1.83	0.60
13:B:177:GLU:HG2	13:B:179:ALA:N	2.16	0.60
17:F:383:GLU:CA	23:L:170:THR:HG21	2.30	0.60
29:R:196:HIS:O	29:R:200:SER:HB3	2.01	0.60
28:q:168:GLN:NE2	28:q:175:LEU:O	2.35	0.60
32:f:494:ARG:NE	32:f:496:ASP:H	1.99	0.60
3:W:98:LYS:HZ2	3:W:137:TYR:HE2	1.06	0.60
7:a:125:ILE:N	7:a:126:GLY:HA2	2.17	0.60
10:d:131:VAL:HG23	10:d:134:LYS:HE2	1.83	0.60
12:A:103:ASN:HB2	12:A:112:ILE:HG23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:383:GLU:CD	23:L:167:SER:HA	2.26	0.60
17:F:439:ALA:CA	23:L:77:LEU:CD2	2.78	0.60
20:I:13:SER:O	21:J:21:TYR:OH	2.13	0.60
3:W:125:ILE:HD12	3:W:128:LEU:HD12	1.84	0.60
5:Y:349:LYS:HG3	5:Y:350:VAL:HG13	1.83	0.60
12:A:222:LYS:HD2	13:B:319:PHE:HB2	1.84	0.60
16:E:206:LYS:NZ	17:F:263:ASP:OD1	2.26	0.60
27:P:177:ARG:NH2	30:s:150:ASP:OD2	2.35	0.60
27:p:58:THR:OG1	28:q:121:LEU:O	2.19	0.60
1:U:376:MET:HA	1:U:741:GLY:H	1.67	0.60
2:V:346:LEU:O	11:e:43:TRP:NE1	2.29	0.60
12:A:429:TYR:CG	21:J:12:PRO:CD	2.85	0.60
17:F:437:TYR:HE1	22:K:28:ILE:CG2	1.98	0.60
21:J:8:THR:HG22	21:J:16:LEU:HD22	1.82	0.60
30:S:148:LEU:HD23	30:S:178:VAL:HG12	1.82	0.60
20:i:35:LEU:HB2	20:i:162:THR:HG21	1.84	0.60
28:q:19:ARG:HH21	28:q:31:ASP:HB2	1.66	0.60
32:f:501:LEU:HD22	32:f:518:THR:HG23	1.84	0.60
4:X:251:LEU:HA	4:X:254:MET:HG2	1.83	0.59
14:C:214:VAL:HG11	14:C:249:ASP:HB3	1.83	0.59
16:E:334:LEU:HD23	16:E:372:ARG:HB2	1.83	0.59
17:F:434:ASN:C	22:K:20:ARG:HH11	2.10	0.59
32:f:337:LEU:HD22	32:f:337:LEU:N	2.17	0.59
3:W:224:LEU:O	3:W:253:THR:OG1	2.19	0.59
6:Z:54:PHE:HB3	6:Z:82:PHE:HE2	1.67	0.59
13:B:190:LEU:HD12	13:B:194:ILE:HB	1.84	0.59
17:F:437:TYR:HB3	22:K:28:ILE:HG12	1.84	0.59
20:I:122:THR:O	21:J:125:ARG:NH1	2.34	0.59
1:U:102:ALA:HB2	14:C:21:ARG:CZ	2.29	0.59
4:X:346:GLN:HE21	4:X:349:HIS:HB2	1.67	0.59
6:Z:63:LYS:HB2	6:Z:64:ASP:HB2	1.84	0.59
13:B:428:TYR:HE1	20:I:170:ALA:H	1.45	0.59
17:F:256:LEU:HD12	17:F:306:VAL:HG13	1.83	0.59
32:f:618:GLU:HG2	32:f:623:LYS:HD2	1.85	0.59
1:U:12:LEU:HB2	1:U:44:LYS:HE3	1.83	0.59
2:V:349:ARG:HG3	2:V:357:LEU:HD21	1.85	0.59
15:D:370:ILE:HD13	15:D:404:LYS:HA	1.83	0.59
15:D:391:ARG:HG2	15:D:395:LEU:HG	1.85	0.59
20:I:180:LYS:HD2	20:I:183:GLU:HB2	1.83	0.59
26:O:193:ASN:ND2	30:s:213:ASP:OD2	2.35	0.59
32:f:378:ASN:CB	32:f:391:LEU:HD11	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:203:LYS:O	1:U:207:ASN:ND2	2.36	0.59
3:W:16:MET:HG2	3:W:27:ARG:HH22	1.67	0.59
3:W:422:ASN:O	3:W:426:ASN:ND2	2.35	0.59
4:X:255:LEU:HD12	4:X:287:LEU:HB3	1.85	0.59
5:Y:330:ILE:HA	5:Y:333:GLU:HB3	1.85	0.59
14:C:158:ILE:HA	14:C:161:ILE:HG22	1.84	0.59
22:k:228:MET:O	22:k:230:THR:N	2.35	0.59
3:W:397:VAL:HG21	4:X:342:PHE:HB3	1.83	0.59
7:a:33:LEU:HB3	8:b:20:ASP:HB3	1.84	0.59
13:B:438:LEU:HD13	20:I:155:ASN:ND2	2.17	0.59
32:f:494:ARG:NH2	32:f:495:GLU:H	2.00	0.59
1:U:94:SER:OG	1:U:95:GLU:OE1	2.19	0.59
24:m:92:ARG:NH2	31:t:69:GLN:OE1	2.36	0.59
32:f:89:MET:HG2	32:f:90:THR:HG23	1.84	0.59
32:f:376:PHE:CZ	32:f:416:MET:HE1	2.36	0.59
32:f:494:ARG:CZ	32:f:496:ASP:H	2.16	0.59
1:U:39:SER:HA	1:U:67:VAL:HG23	1.85	0.59
2:V:195:ILE:CG2	14:C:22:GLN:CB	2.76	0.59
5:Y:81:LEU:HD12	5:Y:111:LEU:HD13	1.85	0.59
12:A:348:LEU:CD2	22:K:32:LYS:HZ2	2.16	0.59
16:E:357:ALA:O	16:E:359:HIS:ND1	2.30	0.59
32:f:541:THR:O	32:f:545:LYS:HB2	2.02	0.59
24:m:241:GLU:O	24:m:244:LYS:NZ	2.36	0.59
32:f:477:MET:O	32:f:481:SER:HB2	2.02	0.59
4:X:262:ASN:O	4:X:297:ARG:NH2	2.33	0.58
6:Z:97:THR:HA	6:Z:124:ILE:HG13	1.83	0.58
6:Z:102:HIS:CD2	6:Z:104:ASN:HB3	2.36	0.58
10:d:184:LYS:HB2	10:d:185:ALA:HB2	1.85	0.58
13:B:431:GLN:OE1	20:I:173:SER:CA	2.51	0.58
17:F:87:PRO:HB2	17:F:152:GLY:HA3	1.84	0.58
22:K:216:GLU:C	22:K:229:PHE:HZ	2.02	0.58
21:j:116:GLN:NE2	21:j:150:SER:O	2.36	0.58
32:f:378:ASN:O	32:f:381:VAL:CG1	2.49	0.58
2:V:486:ILE:HD13	5:Y:377:LEU:HD22	1.84	0.58
5:Y:178:ASN:HB3	5:Y:207:THR:HG22	1.85	0.58
8:b:157:VAL:HG21	8:b:170:LEU:HB2	1.86	0.58
14:C:297:ARG:HG3	14:C:298:ILE:H	1.68	0.58
1:U:14:GLU:HG2	1:U:16:GLU:H	1.67	0.58
2:V:259:LEU:HD21	2:V:294:ARG:HD2	1.85	0.58
2:V:331:LEU:HD12	2:V:334:VAL:HG21	1.85	0.58
3:W:141:GLU:OE1	3:W:172:GLU:CD	2.42	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:389:GLU:HB3	15:D:391:ARG:N	2.18	0.58
17:F:435:LEU:HA	17:F:438:TYR:CE2	2.38	0.58
28:q:4:LEU:HD12	28:q:45:LEU:HB3	1.83	0.58
32:f:22:GLY:O	32:f:26:GLU:HB2	2.04	0.58
32:f:487:LEU:HD23	32:f:524:MET:HE1	1.85	0.58
32:f:780:PRO:HB2	32:f:800:LEU:HB3	1.86	0.58
1:U:68:PHE:HB3	1:U:73:ALA:HB3	1.85	0.58
2:V:383:GLY:O	2:V:392:TYR:OH	2.21	0.58
5:Y:16:ASP:HB2	5:Y:113:ARG:HE	1.68	0.58
7:a:278:MET:HE2	7:a:279:GLU:HG3	1.86	0.58
17:F:94:ILE:HA	17:F:147:PRO:HB3	1.84	0.58
18:G:158:GLY:O	19:H:84:ARG:NH2	2.36	0.58
32:f:129:LEU:O	32:f:133:MET:CB	2.50	0.58
32:f:389:LYS:HG2	32:f:418:LEU:CD1	2.32	0.58
1:U:625:ILE:HG13	1:U:626:LEU:HG	1.85	0.58
2:V:91:PRO:HG3	2:V:126:ALA:HB3	1.84	0.58
3:W:141:GLU:HG3	3:W:172:GLU:HG3	1.86	0.58
12:A:381:THR:OG1	13:B:343:ARG:NH1	2.36	0.58
32:f:635:LYS:NZ	32:f:641:GLU:HG3	2.16	0.58
13:B:317:ASP:HB3	13:B:318:GLY:HA2	1.86	0.58
26:O:140:ASP:OD2	31:t:171:ARG:NH2	2.36	0.58
1:U:759:SER:HA	1:U:782:ALA:HA	1.85	0.58
7:a:285:PRO:HB3	7:a:352:ARG:HD3	1.86	0.58
9:c:175:ARG:NH2	9:c:201:TYR:OH	2.37	0.58
12:A:140:VAL:HA	12:A:152:PRO:HA	1.86	0.58
12:A:339:ARG:NH2	17:F:402:GLU:OE1	2.35	0.58
13:B:223:ILE:HD12	13:B:346:ARG:H	1.68	0.58
13:B:440:LEU:CA	21:J:28:LYS:O	2.52	0.58
14:C:270:GLN:O	14:C:307:ARG:NH1	2.36	0.58
16:E:285:LEU:HB3	16:E:289:LEU:HB2	1.85	0.58
21:J:43:LEU:HD13	21:J:72:ALA:HB2	1.86	0.58
22:k:16:SER:HB3	22:k:20:ARG:H	1.69	0.58
24:m:108:LEU:HD11	24:m:137:LEU:HB3	1.84	0.58
32:f:127:SER:O	32:f:131:MET:CB	2.52	0.58
3:W:235:GLN:NE2	3:W:247:TYR:OH	2.36	0.58
32:f:782:HIS:HA	32:f:785:ARG:HG2	1.83	0.58
3:W:144:ARG:HA	3:W:147:LYS:HE2	1.86	0.58
8:b:25:ARG:HA	8:b:28:ALA:HB3	1.85	0.58
12:A:391:GLU:HA	12:A:394:MET:HB3	1.86	0.58
14:C:127:LEU:HD22	15:D:96:VAL:HG11	1.85	0.58
14:C:229:ARG:HE	14:C:232:ARG:HG3	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:h:3:GLU:HG3	19:h:5:GLY:H	1.68	0.58
31:t:192:VAL:HG12	31:t:197:VAL:HG22	1.85	0.58
6:Z:204:LYS:HE3	7:a:353:LEU:HG	1.85	0.58
12:A:357:ILE:HG13	12:A:360:ARG:HH21	1.68	0.58
13:B:280:SER:HB2	13:B:325:VAL:N	2.19	0.58
24:M:83:ASP:OD2	24:M:129:ARG:NH2	2.36	0.58
23:l:93:LEU:HA	23:l:96:ARG:HB3	1.85	0.58
32:f:378:ASN:HB3	32:f:391:LEU:CD2	2.34	0.58
32:f:438:ASP:N	32:f:438:ASP:OD1	2.35	0.58
32:f:456:ARG:HD3	32:f:489:TYR:OH	2.03	0.58
4:X:417:LYS:HZ2	6:Z:283:ARG:HH12	1.51	0.57
12:A:364:VAL:HG13	12:A:368:ILE:HD12	1.86	0.57
13:B:198:LYS:HD3	13:B:237:LYS:HE2	1.86	0.57
20:I:119:GLN:NE2	21:J:78:ALA:O	2.37	0.57
30:S:13:LEU:HD11	30:S:149:LEU:HD11	1.85	0.57
6:Z:21:ASP:HB2	9:c:36:LEU:HD22	1.86	0.57
9:c:131:GLN:HA	9:c:134:GLU:HG2	1.84	0.57
12:A:94:GLN:OE1	13:B:131:HIS:NE2	2.38	0.57
13:B:148:CYS:HB3	13:B:150:VAL:HG13	1.86	0.57
23:L:42:THR:O	23:L:137:TYR:OH	2.23	0.57
32:f:780:PRO:O	32:f:800:LEU:HG	2.03	0.57
1:U:541:HIS:HB2	1:U:544:ILE:HG22	1.86	0.57
6:Z:182:THR:H	6:Z:183:THR:HA	1.68	0.57
12:A:380:SER:O	13:B:343:ARG:NH1	2.38	0.57
13:B:436:GLU:HB3	13:B:437:GLY:HA3	1.84	0.57
14:C:230:MET:O	14:C:233:GLU:N	2.36	0.57
15:D:366:ARG:NH2	18:G:177:SER:OG	2.35	0.57
32:f:88:SER:HB2	32:f:92:VAL:CG2	2.33	0.57
32:f:140:LEU:O	32:f:144:LEU:HB2	2.04	0.57
6:Z:34:ARG:HH12	6:Z:102:HIS:HE1	1.51	0.57
16:E:261:LEU:HD13	16:E:294:ARG:HE	1.69	0.57
30:S:184:GLU:OE1	30:S:211:ARG:NH1	2.37	0.57
32:f:695:ALA:CB	32:f:752:HIS:CB	2.82	0.57
2:V:365:GLN:OE1	11:e:54:ASN:ND2	2.37	0.57
15:D:94:GLU:HG2	15:D:102:ILE:HD11	1.85	0.57
15:D:248:ARG:NH2	15:D:291:GLU:OE2	2.37	0.57
6:Z:222:ILE:HG23	6:Z:224:HIS:HB2	1.85	0.57
10:d:6:LYS:HD3	10:d:50:LEU:HG	1.86	0.57
13:B:176:VAL:HG11	14:C:283:PHE:CB	2.35	0.57
14:C:113:ARG:HG2	14:C:127:LEU:HD12	1.85	0.57
26:O:164:PHE:O	30:s:38:ARG:NH2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:695:ALA:CB	32:f:752:HIS:HB2	2.31	0.57
32:f:780:PRO:CB	32:f:800:LEU:CA	2.79	0.57
2:V:495:ARG:HB2	14:C:38:LYS:CE	2.30	0.57
7:a:129:GLN:HG3	7:a:130:VAL:H	1.70	0.57
32:f:353:LEU:H	32:f:387:GLN:HG2	1.68	0.57
2:V:200:ARG:O	2:V:204:ASP:N	2.36	0.57
5:Y:388:ASN:ND2	6:Z:286:GLU:OE2	2.38	0.57
24:M:163:CYS:SG	24:M:164:ALA:N	2.77	0.57
18:g:158:GLY:O	19:h:84:ARG:NH2	2.38	0.57
24:m:61:GLY:O	24:m:64:LYS:NZ	2.38	0.57
32:f:494:ARG:CZ	32:f:495:GLU:H	2.17	0.57
4:X:318:ILE:O	4:X:322:HIS:ND1	2.38	0.57
14:C:245:ILE:HD12	14:C:290:LYS:HB2	1.87	0.57
21:j:115:LYS:HE2	21:j:149:PRO:HA	1.86	0.57
28:q:117:TYR:HB3	28:q:125:ALA:HB3	1.85	0.57
32:f:358:PHE:HZ	32:f:381:VAL:HG21	1.66	0.57
32:f:471:LEU:CD1	32:f:509:LYS:HE3	2.26	0.57
2:V:73:GLU:HB3	2:V:78:HIS:HA	1.87	0.57
4:X:203:PRO:HB3	4:X:206:LEU:HB2	1.85	0.57
4:X:203:PRO:HB2	4:X:204:PRO:C	2.30	0.57
12:A:310:ASP:N	12:A:312:ARG:HB2	2.19	0.57
13:B:177:GLU:CB	13:B:178:LYS:HA	2.32	0.57
22:K:76:CYS:SG	22:K:77:ALA:N	2.78	0.57
30:S:150:ASP:OD2	27:p:177:ARG:NH2	2.36	0.57
3:W:223:LYS:HA	3:W:226:TYR:HB3	1.86	0.56
5:Y:82:LYS:O	5:Y:86:GLU:N	2.36	0.56
10:d:254:GLU:HA	10:d:257:VAL:HG23	1.87	0.56
13:B:133:VAL:HG11	13:B:159:VAL:HG12	1.85	0.56
13:B:229:GLY:O	13:B:233:THR:N	2.37	0.56
15:D:411:GLU:HB3	15:D:412:GLN:HB2	1.85	0.56
20:I:108:GLU:OE2	20:I:146:GLN:NE2	2.37	0.56
23:L:173:GLU:HG3	24:M:56:LYS:HD3	1.87	0.56
20:i:198:ASN:HD22	20:i:240:HIS:HD2	1.52	0.56
24:m:160:TYR:HD2	24:m:163:CYS:HB2	1.70	0.56
32:f:226:TYR:O	32:f:230:CYS:CB	2.53	0.56
1:U:213:PHE:HE2	1:U:244:MET:HB2	1.69	0.56
2:V:175:MET:O	2:V:178:SER:OG	2.21	0.56
5:Y:314:LEU:HD21	5:Y:319:MET:HG2	1.87	0.56
8:b:161:ASN:ND2	8:b:168:SER:H	2.03	0.56
9:c:64:ASP:HA	9:c:139:ARG:HH21	1.70	0.56
18:g:165:ALA:HB3	19:h:56:LEU:HD22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:536:SER:O	32:f:540:GLN:HB2	2.05	0.56
2:V:410:ILE:HD13	2:V:425:LYS:HE3	1.88	0.56
2:V:479:ARG:HD2	5:Y:370:ILE:HG12	1.86	0.56
3:W:52:LYS:HD3	3:W:55:ARG:HD3	1.86	0.56
3:W:334:GLU:OE1	3:W:338:THR:OG1	2.23	0.56
6:Z:224:HIS:CG	6:Z:225:GLN:HA	2.39	0.56
10:d:101:LEU:HD22	10:d:166:PHE:HE2	1.70	0.56
12:A:343:PHE:HA	12:A:344:SER:OG	2.05	0.56
13:B:177:GLU:HG2	13:B:179:ALA:H	1.71	0.56
15:D:372:GLY:HA3	15:D:374:ASP:HB2	1.87	0.56
17:F:430:LYS:NZ	22:K:17:PRO:HB3	2.19	0.56
20:I:218:ARG:NH1	20:I:223:THR:OG1	2.39	0.56
22:K:209:LYS:O	22:K:214:ASN:ND2	2.37	0.56
32:f:269:ALA:HB2	32:f:277:LEU:HD22	1.87	0.56
1:U:102:ALA:HB1	14:C:21:ARG:NH1	2.20	0.56
6:Z:212:LEU:HD22	7:a:350:LYS:HE2	1.86	0.56
6:Z:244:GLU:HG2	7:a:287:ASN:N	2.21	0.56
9:c:157:ILE:HG12	9:c:158:ASP:H	1.69	0.56
13:B:316:LEU:HD11	13:B:327:VAL:HG11	1.86	0.56
14:C:42:LEU:HD21	15:D:65:GLN:HE22	1.69	0.56
15:D:87:LEU:HB2	16:E:80:VAL:HG23	1.86	0.56
16:E:383:LYS:HE2	24:M:19:ARG:NH1	2.16	0.56
18:g:120:ASP:OD1	19:h:84:ARG:NH1	2.38	0.56
23:l:151:ALA:O	24:m:85:ARG:NH2	2.38	0.56
30:s:4:PRO:O	31:t:100:ARG:NH2	2.37	0.56
32:f:471:LEU:HD12	32:f:509:LYS:CE	2.36	0.56
32:f:742:ALA:CA	32:f:745:LEU:HG	2.35	0.56
32:f:780:PRO:HB2	32:f:800:LEU:CB	2.36	0.56
1:U:740:GLY:HA3	1:U:744:VAL:HG22	1.86	0.56
2:V:291:TYR:OH	11:e:5:LYS:CE	2.53	0.56
2:V:466:ILE:HD11	2:V:471:GLU:HB2	1.88	0.56
2:V:495:ARG:HG3	14:C:38:LYS:CE	2.36	0.56
3:W:440:ASN:O	3:W:443:THR:OG1	2.19	0.56
12:A:296:GLN:HB3	12:A:300:LEU:HD12	1.87	0.56
13:B:205:LEU:HD21	13:B:245:ALA:HB2	1.87	0.56
14:C:157:GLN:HE22	14:C:318:PRO:HD3	1.71	0.56
22:K:18:GLU:OE1	22:K:20:ARG:NH2	2.38	0.56
30:S:157:ASN:ND2	27:p:176:ASP:OD2	2.38	0.56
25:n:144:ARG:NH2	25:n:151:GLU:OE1	2.39	0.56
32:f:358:PHE:CE1	32:f:381:VAL:HG21	2.40	0.56
4:X:414:LEU:HD23	4:X:417:LYS:HD2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:d:80:CYS:HA	10:d:83:PHE:HB3	1.88	0.56
12:A:167:GLU:HB2	12:A:239:ARG:HG2	1.87	0.56
23:L:66:VAL:O	30:S:77:HIS:NE2	2.39	0.56
24:M:214:SER:OG	24:M:224:HIS:NE2	2.36	0.56
29:r:135:ALA:O	29:r:139:MET:CB	2.54	0.56
1:U:428:PRO:HB3	1:U:439:GLU:HB2	1.88	0.56
2:V:302:TYR:HB3	2:V:339:LEU:HD23	1.87	0.56
8:b:109:ILE:HB	8:b:138:VAL:HG13	1.86	0.56
27:P:27:ARG:HD2	27:P:183:MET:HG2	1.88	0.56
32:f:623:LYS:O	32:f:627:GLU:CB	2.54	0.56
1:U:102:ALA:HB1	14:C:21:ARG:CZ	2.35	0.56
2:V:38:LYS:HA	2:V:41:ALA:HB3	1.88	0.56
5:Y:14:ASN:HA	5:Y:17:LEU:HB3	1.88	0.56
12:A:373:LEU:HD21	12:A:413:VAL:HG21	1.88	0.56
13:B:256:ILE:HG12	14:C:268:GLU:HG3	1.88	0.56
14:C:28:ILE:O	14:C:32:GLN:N	2.26	0.56
17:F:437:TYR:OH	22:K:28:ILE:HG22	1.97	0.56
21:J:172:LEU:HD22	21:J:175:ASN:HD22	1.71	0.56
22:k:48:LEU:HD21	22:k:77:ALA:HB2	1.88	0.56
28:q:183:ILE:HG12	28:q:188:ILE:HG13	1.87	0.56
32:f:456:ARG:HB3	32:f:489:TYR:CZ	2.39	0.56
5:Y:358:ARG:NH2	5:Y:359:PRO:HG2	2.21	0.56
6:Z:62:ASP:OD2	6:Z:63:LYS:NZ	2.39	0.56
7:a:14:SER:HB2	7:a:18:GLN:HG2	1.87	0.56
13:B:432:GLU:HA	20:I:169:ALA:HB2	1.79	0.56
16:E:60:VAL:HG22	16:E:71:VAL:HG12	1.88	0.56
17:F:89:LEU:HG	17:F:153:VAL:HG13	1.86	0.56
22:K:18:GLU:CB	22:K:20:ARG:HH12	2.11	0.56
32:f:742:ALA:CA	32:f:745:LEU:HD21	2.32	0.56
1:U:685:GLN:HB2	1:U:726:ALA:HA	1.88	0.56
2:V:443:ARG:NH2	10:d:180:GLY:O	2.39	0.56
4:X:345:VAL:HG21	4:X:350:ILE:HD13	1.87	0.56
4:X:420:LYS:O	6:Z:287:LYS:NZ	2.28	0.56
6:Z:236:LEU:HD11	7:a:335:TRP:HD1	1.72	0.56
9:c:170:LEU:HG	9:c:171:GLY:H	1.71	0.56
12:A:139:ARG:H	12:A:156:LYS:HE3	1.71	0.56
12:A:143:ASP:O	12:A:147:TYR:N	2.33	0.56
28:Q:117:TYR:HB3	28:Q:125:ALA:HB3	1.88	0.56
19:h:118:MET:HE2	19:h:151:PRO:HA	1.88	0.56
22:k:37:ALA:HB2	22:k:50:VAL:HG23	1.88	0.56
3:W:65:ARG:HB2	3:W:66:ILE:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:B:188:GLY:HA3	13:B:367:ILE:HD12	1.87	0.55
14:C:32:GLN:O	14:C:36:ASN:N	2.36	0.55
17:F:168:TYR:HB2	17:F:169:ASP:HB2	1.88	0.55
17:F:227:GLY:HA3	17:F:231:THR:HG21	1.87	0.55
32:f:377:VAL:HG22	32:f:751:TYR:HB2	1.88	0.55
2:V:495:ARG:CG	14:C:38:LYS:HB3	2.36	0.55
4:X:299:LEU:HA	4:X:302:PHE:HB3	1.88	0.55
5:Y:105:MET:HG3	5:Y:106:ALA:H	1.71	0.55
6:Z:225:GLN:HB2	6:Z:228:TYR:CE1	2.41	0.55
2:V:324:PHE:CE2	11:e:7:PRO:HB3	2.41	0.55
2:V:484:LEU:HA	2:V:487:HIS:HD2	1.71	0.55
6:Z:266:ILE:HB	9:c:295:ASN:HD21	1.72	0.55
24:m:51:LYS:NZ	24:m:62:SER:O	2.36	0.55
32:f:380:PHE:CG	32:f:751:TYR:HE1	2.24	0.55
1:U:474:ARG:HH21	1:U:500:ASN:HB2	1.71	0.55
1:U:506:ALA:HB3	9:c:65:TYR:HE1	1.71	0.55
6:Z:214:LYS:HE3	6:Z:221:PRO:HG2	1.89	0.55
13:B:178:LYS:CE	14:C:278:ASN:O	2.54	0.55
14:C:19:GLY:O	14:C:23:TYR:N	2.37	0.55
29:r:196:HIS:O	29:r:200:SER:CB	2.54	0.55
32:f:229:VAL:O	32:f:233:LEU:HB2	2.07	0.55
1:U:356:THR:HG22	1:U:717:ILE:HG21	1.89	0.55
3:W:66:ILE:HA	3:W:67:LEU:HB2	1.89	0.55
8:b:91:ARG:HH22	8:b:130:ARG:HE	1.51	0.55
17:F:306:VAL:HA	17:F:309:THR:HB	1.88	0.55
21:J:108:THR:HG22	21:J:133:ILE:HD13	1.88	0.55
22:K:217:LEU:CA	22:K:229:PHE:CZ	2.63	0.55
18:g:53:GLN:HA	18:g:215:ILE:HA	1.88	0.55
24:m:17:ASP:OD2	24:m:19:ARG:NH2	2.40	0.55
32:f:426:LEU:O	32:f:430:ASP:HB3	2.07	0.55
1:U:773:PHE:O	1:U:776:SER:OG	2.18	0.55
2:V:372:LEU:H	2:V:427:GLN:NE2	2.05	0.55
6:Z:34:ARG:HB2	6:Z:97:THR:HG22	1.87	0.55
7:a:31:LYS:HA	8:b:177:PRO:HD3	1.88	0.55
7:a:264:ASN:ND2	7:a:267:GLN:OE1	2.39	0.55
8:b:8:VAL:HA	8:b:110:ILE:HG13	1.89	0.55
14:C:90:HIS:HB2	14:C:91:PRO:HD3	1.89	0.55
31:T:99:ARG:HD2	31:T:106:LEU:HG	1.88	0.55
30:s:184:GLU:OE2	30:s:211:ARG:NH1	2.40	0.55
2:V:30:PRO:HA	2:V:33:GLN:HB2	1.88	0.55
3:W:216:GLU:CD	3:W:217:GLU:H	2.15	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:301:ILE:HD12	5:Y:342:ARG:HB3	1.88	0.55
6:Z:91:ILE:HD13	6:Z:115:TYR:HB3	1.89	0.55
20:I:38:LEU:HG	20:I:160:LYS:HB3	1.88	0.55
21:J:17:PHE:O	21:J:21:TYR:N	2.36	0.55
2:V:159:LEU:HD13	2:V:178:SER:HB3	1.88	0.55
2:V:319:HIS:HB2	2:V:320:THR:HA	1.88	0.55
5:Y:283:LYS:HZ1	11:e:60:LEU:HB3	1.71	0.55
6:Z:17:LEU:HD13	9:c:39:LEU:HD21	1.89	0.55
6:Z:240:VAL:O	6:Z:243:GLN:N	2.39	0.55
12:A:205:GLY:HA2	12:A:206:ILE:HG22	1.89	0.55
13:B:170:LEU:HD13	14:C:228:ALA:HA	1.88	0.55
29:R:141:ARG:HH21	28:q:166:GLU:HG2	1.71	0.55
19:h:71:HIS:HA	19:h:218:PHE:H	1.72	0.55
32:f:278:VAL:HA	32:f:281:ILE:HG22	1.89	0.55
32:f:317:LEU:O	32:f:321:MET:HB2	2.05	0.55
32:f:586:PRO:HA	32:f:589:SER:HB2	1.89	0.55
32:f:688:ARG:HH12	32:f:788:MET:HA	1.71	0.55
1:U:208:LEU:HD23	1:U:210:LYS:H	1.72	0.55
2:V:28:PRO:HG2	2:V:84:LYS:HE2	1.87	0.55
3:W:40:LEU:HB2	3:W:41:GLN:CA	2.31	0.55
3:W:259:GLU:HG2	3:W:262:LYS:HB3	1.88	0.55
13:B:257:GLN:OE1	13:B:257:GLN:N	2.37	0.55
14:C:155:ASP:HA	14:C:158:ILE:HG12	1.88	0.55
23:L:18:ARG:NH1	23:L:23:GLU:OE2	2.39	0.55
28:q:38:MET:O	28:q:65:GLN:NE2	2.39	0.55
1:U:842:LYS:HG2	1:U:882:ALA:HB2	1.89	0.55
2:V:173:ILE:O	2:V:177:ASN:ND2	2.40	0.55
2:V:196:SER:H	14:C:23:TYR:HD1	1.54	0.55
2:V:317:PRO:HD3	5:Y:382:LYS:HD2	1.89	0.55
8:b:94:HIS:HD2	8:b:136:VAL:HG21	1.71	0.55
12:A:323:ARG:HE	12:A:431:THR:HB	1.72	0.55
17:F:256:LEU:HD13	17:F:309:THR:HG21	1.88	0.55
22:K:18:GLU:CB	22:K:19:GLY:HA2	2.35	0.55
22:K:93:ARG:NH1	29:R:68:LEU:O	2.40	0.55
21:j:115:LYS:NZ	21:j:129:ILE:O	2.35	0.55
21:j:172:LEU:HD13	22:k:58:LEU:HD11	1.89	0.55
23:l:73:SER:HB3	23:l:133:LEU:HB2	1.87	0.55
2:V:468:SER:O	2:V:472:PRO:HD2	2.08	0.54
2:V:495:ARG:CD	14:C:38:LYS:HB3	2.37	0.54
5:Y:197:ALA:HB3	5:Y:226:VAL:HG21	1.89	0.54
5:Y:225:TYR:HA	5:Y:228:MET:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:c:253:LYS:O	9:c:257:LYS:N	2.39	0.54
12:A:344:SER:N	12:A:345:LEU:HB3	2.22	0.54
13:B:221:GLY:HA2	13:B:326:LYS:HE3	1.88	0.54
14:C:28:ILE:HA	14:C:31:LEU:HB3	1.89	0.54
14:C:171:HIS:O	14:C:173:GLU:N	2.39	0.54
17:F:267:LEU:O	17:F:271:ALA:N	2.35	0.54
20:i:91:ARG:NH1	27:p:76:LEU:O	2.40	0.54
30:s:28:ARG:NH1	30:s:187:VAL:O	2.40	0.54
32:f:15:GLN:NE2	32:f:47:GLU:OE1	2.41	0.54
32:f:229:VAL:O	32:f:233:LEU:CB	2.56	0.54
32:f:663:GLY:O	32:f:697:ILE:HB	2.07	0.54
1:U:375:PHE:O	1:U:740:GLY:N	2.30	0.54
1:U:505:ASP:HB3	1:U:508:THR:HG22	1.89	0.54
4:X:359:ALA:O	4:X:363:ARG:NE	2.37	0.54
5:Y:232:GLU:O	5:Y:236:LEU:N	2.39	0.54
6:Z:33:LYS:HD3	6:Z:60:GLU:N	2.21	0.54
14:C:11:LEU:HD12	14:C:14:GLY:HA2	1.90	0.54
16:E:293:GLY:N	16:E:296:ASP:OD1	2.40	0.54
18:g:5:SER:O	18:g:11:ARG:NH2	2.40	0.54
24:m:214:SER:HG	24:m:224:HIS:HE2	1.52	0.54
32:f:253:LEU:O	32:f:257:ARG:HB2	2.07	0.54
12:A:427:PRO:HB2	12:A:429:TYR:HD1	1.71	0.54
15:D:88:VAL:N	15:D:132:LEU:O	2.30	0.54
16:E:241:ARG:HG2	16:E:243:PHE:H	1.72	0.54
32:f:684:PRO:O	32:f:688:ARG:CB	2.54	0.54
1:U:82:LEU:O	1:U:129:ARG:NE	2.40	0.54
2:V:320:THR:HG23	2:V:321:ALA:HB2	1.90	0.54
3:W:178:GLU:OE1	3:W:181:GLU:N	2.40	0.54
9:c:272:ILE:HG21	9:c:276:GLY:N	2.20	0.54
14:C:72:TYR:HB2	14:C:116:LEU:HD23	1.90	0.54
15:D:287:ARG:O	15:D:291:GLU:N	2.40	0.54
28:Q:2:GLU:HB2	28:Q:47:VAL:HG11	1.90	0.54
32:f:80:ARG:O	32:f:84:SER:HB3	2.07	0.54
1:U:505:ASP:OD1	9:c:65:TYR:OH	2.26	0.54
2:V:80:LYS:CD	2:V:81:GLN:CB	2.80	0.54
4:X:183:LEU:HD22	5:Y:251:HIS:HD2	1.72	0.54
5:Y:179:ARG:NH2	5:Y:212:GLU:OE2	2.38	0.54
9:c:253:LYS:HA	9:c:256:ASN:HB2	1.89	0.54
12:A:380:SER:HB3	12:A:384:GLU:HB3	1.89	0.54
32:f:138:GLU:O	32:f:142:TYR:CB	2.56	0.54
1:U:628:ARG:NH1	1:U:749:GLN:OE1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:33:LYS:HG2	6:Z:34:ARG:HG2	1.90	0.54
6:Z:179:ILE:HG12	9:c:222:LYS:HE3	1.90	0.54
6:Z:241:SER:HB2	6:Z:242:LEU:HD12	1.88	0.54
8:b:52:ILE:HD11	8:b:58:CYS:HB3	1.90	0.54
13:B:175:LYS:HB3	13:B:175:LYS:HZ2	1.73	0.54
14:C:371:LEU:HG	15:D:190:LEU:HD21	1.90	0.54
15:D:354:LEU:HD23	15:D:356:GLU:HB3	1.89	0.54
16:E:57:VAL:HA	16:E:99:ALA:HA	1.87	0.54
19:h:65:VAL:O	19:h:220:ARG:NH1	2.41	0.54
32:f:76:GLU:OE1	32:f:79:ARG:NH2	2.41	0.54
32:f:353:LEU:HG	32:f:387:GLN:CG	2.36	0.54
2:V:67:LEU:O	2:V:71:THR:OG1	2.21	0.54
2:V:131:LEU:HD23	2:V:134:PHE:HD2	1.72	0.54
3:W:247:TYR:HD2	3:W:273:TYR:HD2	1.56	0.54
13:B:304:GLU:HA	13:B:307:ARG:HG2	1.90	0.54
13:B:333:ARG:NH1	20:I:15:GLU:HG2	2.23	0.54
15:D:413:GLU:CD	18:G:25:VAL:CG1	2.78	0.54
16:E:285:LEU:HB2	16:E:290:LEU:HG	1.90	0.54
31:T:41:ARG:HH21	31:T:54:SER:HA	1.72	0.54
32:f:273:ASN:ND2	32:f:310:ASP:OD2	2.41	0.54
32:f:313:GLU:O	32:f:317:LEU:CB	2.55	0.54
32:f:403:LYS:O	32:f:407:MET:N	2.40	0.54
1:U:792:ASN:OD1	1:U:793:LYS:N	2.38	0.54
2:V:495:ARG:CG	14:C:38:LYS:HE3	2.38	0.54
9:c:191:ALA:O	9:c:195:GLY:N	2.39	0.54
15:D:182:GLU:HG3	15:D:183:LEU:HD12	1.90	0.54
16:E:56:ILE:HG23	16:E:100:LEU:HB2	1.90	0.54
27:P:7:ASN:ND2	27:P:29:GLY:O	2.40	0.54
32:f:8:LYS:O	32:f:12:GLN:CB	2.56	0.54
32:f:8:LYS:O	32:f:12:GLN:HB2	2.08	0.54
32:f:688:ARG:HA	32:f:745:LEU:CD2	2.38	0.54
2:V:322:VAL:HG13	2:V:323:GLY:H	1.73	0.54
3:W:136:ILE:HD11	3:W:176:SER:N	2.23	0.54
3:W:389:SER:O	3:W:393:LEU:N	2.41	0.54
3:W:435:LEU:HA	3:W:438:LEU:HG	1.89	0.54
7:a:327:VAL:HG13	7:a:328:ASP:H	1.72	0.54
12:A:428:ARG:HH22	13:B:340:ALA:HB2	1.72	0.54
13:B:106:PRO:HB2	13:B:154:HIS:HD2	1.73	0.54
15:D:366:ARG:CZ	18:G:177:SER:HB2	2.37	0.54
17:F:280:PRO:HA	17:F:281:SER:HB2	1.89	0.54
19:H:66:GLU:OE2	19:H:91:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:I:161:ALA:HB1	20:I:175:LEU:HD13	1.88	0.54
32:f:211:ILE:O	32:f:215:ASP:CB	2.56	0.54
32:f:281:ILE:O	32:f:285:CYS:CB	2.56	0.54
32:f:314:TYR:CE1	32:f:490:ALA:HB3	2.43	0.54
32:f:575:ALA:O	32:f:579:ALA:HB2	2.07	0.54
5:Y:74:LYS:HA	5:Y:77:ASN:HB3	1.90	0.54
14:C:164:VAL:HG21	14:C:313:ARG:HB2	1.89	0.54
15:D:153:MET:HG3	15:D:154:LEU:HD13	1.90	0.54
17:F:257:VAL:HG23	17:F:306:VAL:HG23	1.89	0.54
23:L:84:LEU:O	23:L:88:MET:HB2	2.08	0.54
23:L:93:LEU:HA	23:L:96:ARG:HB3	1.90	0.54
31:T:45:VAL:HB	31:T:49:THR:HG23	1.89	0.54
32:f:477:MET:O	32:f:481:SER:CB	2.56	0.54
1:U:802:TYR:HB3	1:U:895:PRO:HD3	1.89	0.53
2:V:234:ARG:HG3	2:V:250:LEU:HD11	1.91	0.53
2:V:495:ARG:HG3	14:C:38:LYS:HE3	1.89	0.53
15:D:354:LEU:HB3	15:D:356:GLU:H	1.73	0.53
28:Q:139:THR:OG1	28:Q:140:LEU:N	2.38	0.53
22:k:93:ARG:NH1	29:r:68:LEU:O	2.41	0.53
26:o:31:CYS:SG	26:o:32:SER:N	2.80	0.53
32:f:515:ALA:HB1	32:f:558:LEU:HD21	1.91	0.53
1:U:474:ARG:NH2	1:U:496:LEU:O	2.41	0.53
5:Y:68:ASP:HA	5:Y:71:ASN:HB2	1.91	0.53
5:Y:358:ARG:O	5:Y:360:ASP:N	2.40	0.53
15:D:280:GLY:O	15:D:284:GLU:N	2.41	0.53
16:E:285:LEU:HD12	16:E:290:LEU:HD23	1.90	0.53
30:S:211:ARG:NE	30:S:213:ASP:OD1	2.41	0.53
27:p:191:GLU:HG3	27:p:193:ASP:H	1.73	0.53
2:V:33:GLN:HB3	2:V:115:LYS:HD3	1.91	0.53
3:W:55:ARG:NH1	3:W:79:GLU:HG3	2.24	0.53
5:Y:194:PHE:HB3	5:Y:230:ALA:HB2	1.89	0.53
6:Z:25:ARG:HB3	9:c:103:GLY:HA3	1.89	0.53
7:a:145:LEU:HD12	7:a:146:PRO:HD2	1.91	0.53
12:A:218:PRO:HD3	12:A:428:ARG:HH21	1.73	0.53
22:K:42:THR:HG22	22:K:44:GLU:H	1.73	0.53
22:K:99:HIS:HB2	22:K:107:MET:HE3	1.89	0.53
22:K:216:GLU:CA	22:K:229:PHE:CZ	2.91	0.53
26:o:198:ARG:NH1	27:p:154:TRP:O	2.42	0.53
32:f:301:HIS:O	32:f:305:LEU:CB	2.53	0.53
32:f:742:ALA:HA	32:f:745:LEU:HG	1.88	0.53
1:U:616:ARG:HH21	1:U:647:HIS:HA	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:192:THR:O	6:Z:196:HIS:N	2.37	0.53
14:C:82:LYS:HE2	14:C:84:LYS:HD3	1.90	0.53
14:C:321:ASN:OD1	14:C:322:GLU:N	2.40	0.53
17:F:279:ALA:HA	17:F:325:GLN:HE21	1.73	0.53
20:I:106:PRO:HD2	20:I:109:GLN:HE21	1.74	0.53
28:Q:21:ALA:HB3	28:Q:29:LYS:HB3	1.89	0.53
26:o:209:THR:OG1	27:p:169:GLN:NE2	2.41	0.53
1:U:774:PRO:HA	1:U:777:HIS:CD2	2.44	0.53
2:V:345:ARG:HH12	2:V:357:LEU:HB2	1.72	0.53
2:V:379:LEU:HD13	2:V:395:ILE:HG12	1.89	0.53
3:W:5:GLY:HA3	3:W:47:LEU:HD13	1.91	0.53
3:W:423:ASN:HD22	9:c:246:LYS:HD2	1.72	0.53
6:Z:68:TRP:CD2	6:Z:108:ILE:HG13	2.43	0.53
8:b:34:ASN:O	8:b:38:HIS:ND1	2.32	0.53
17:F:386:ARG:HB3	23:L:166:GLN:NE2	2.23	0.53
20:i:99:LEU:HD13	27:p:69:PHE:HB2	1.90	0.53
32:f:80:ARG:O	32:f:84:SER:CB	2.57	0.53
8:b:28:ALA:HB1	8:b:180:ALA:HB2	1.91	0.53
10:d:44:THR:O	10:d:47:GLN:NE2	2.41	0.53
14:C:153:GLY:N	14:C:327:ASP:OD2	2.41	0.53
14:C:214:VAL:HG13	14:C:215:SER:O	2.09	0.53
23:l:84:LEU:O	23:l:88:MET:HB2	2.08	0.53
32:f:600:TYR:HB3	32:f:608:LYS:HE2	1.91	0.53
32:f:714:SER:C	32:f:718:ASP:HB2	2.33	0.53
2:V:451:ILE:HG13	2:V:458:VAL:HG13	1.89	0.53
3:W:445:LEU:HA	3:W:448:LYS:HZ3	1.74	0.53
4:X:351:SER:OG	4:X:357:SER:OG	2.19	0.53
7:a:73:PRO:HG2	7:a:113:LEU:HD21	1.89	0.53
9:c:37:ALA:HB1	9:c:72:VAL:HG23	1.90	0.53
23:L:196:ARG:HH21	23:L:239:ARG:HG3	1.74	0.53
2:V:412:LEU:O	5:Y:346:LYS:NZ	2.31	0.53
5:Y:173:ASP:H	5:Y:177:ARG:HD3	1.74	0.53
13:B:175:LYS:O	14:C:283:PHE:CE2	2.61	0.53
14:C:142:LYS:HB2	14:C:213:ARG:HG2	1.90	0.53
15:D:336:PRO:HG2	15:D:375:ILE:HG21	1.91	0.53
17:F:437:TYR:HD2	22:K:25:GLU:OE1	1.84	0.53
32:f:24:THR:HG22	32:f:71:TYR:HB2	1.91	0.53
32:f:537:THR:OG1	32:f:538:ILE:N	2.42	0.53
13:B:333:ARG:NE	20:I:15:GLU:OE2	2.40	0.53
17:F:195:ILE:HG12	17:F:199:VAL:HG23	1.91	0.53
18:G:141:ILE:HG22	18:G:151:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:h:14:SER:HG	19:h:18:LYS:H	1.56	0.53
24:m:197:ILE:HG21	24:m:211:LEU:HD13	1.91	0.53
1:U:137:MET:CG	14:C:13:GLU:OE1	2.56	0.53
5:Y:329:PHE:HB3	11:e:66:LYS:HZ2	1.74	0.53
8:b:30:GLN:HG3	8:b:75:LEU:HD13	1.91	0.53
13:B:440:LEU:HA	21:J:28:LYS:O	2.09	0.53
15:D:91:GLN:HB2	15:D:245:ARG:HE	1.74	0.53
15:D:242:GLU:OE2	16:E:78:ARG:NH2	2.42	0.53
16:E:141:GLN:NE2	16:E:300:HIS:O	2.41	0.53
16:E:152:PRO:HG3	16:E:159:PHE:HE2	1.74	0.53
17:F:383:GLU:HB3	17:F:417:HIS:NE2	2.24	0.53
22:k:226:PHE:HA	22:k:227:HIS:HB3	1.91	0.53
5:Y:191:ILE:HG13	5:Y:192:ARG:H	1.74	0.52
13:B:261:GLY:C	13:B:263:GLY:H	2.17	0.52
13:B:338:ASP:H	13:B:341:LEU:HG	1.74	0.52
15:D:293:LEU:O	15:D:296:MET:HG2	2.09	0.52
16:E:145:LEU:HA	16:E:148:VAL:HB	1.91	0.52
18:g:201:CYS:SG	18:g:202:LEU:N	2.82	0.52
22:k:177:ALA:O	22:k:181:LEU:CB	2.56	0.52
29:r:135:ALA:O	29:r:139:MET:HB3	2.09	0.52
32:f:262:PHE:HB3	32:f:281:ILE:HD11	1.91	0.52
32:f:714:SER:O	32:f:718:ASP:CB	2.55	0.52
2:V:372:LEU:HD21	2:V:399:ARG:HH22	1.73	0.52
6:Z:270:VAL:HG13	9:c:288:VAL:HG13	1.91	0.52
7:a:28:LEU:HD23	7:a:37:LEU:HA	1.90	0.52
13:B:390:LEU:HD13	13:B:430:LYS:HE2	1.89	0.52
18:G:6:SER:HB2	18:G:11:ARG:HE	1.74	0.52
19:H:45:VAL:HG22	19:H:212:ILE:HG22	1.90	0.52
22:K:41:GLN:NE2	22:K:151:PRO:O	2.43	0.52
26:O:198:ARG:HH21	26:O:202:TYR:H	1.56	0.52
19:h:34:PRO:HA	19:h:164:GLY:HA3	1.90	0.52
32:f:311:VAL:CB	32:f:490:ALA:CB	2.77	0.52
32:f:378:ASN:HB3	32:f:391:LEU:CD1	2.39	0.52
8:b:90:ILE:HD13	8:b:127:LEU:HD13	1.90	0.52
11:e:6:GLN:CB	11:e:7:PRO:CD	2.83	0.52
13:B:364:ILE:O	13:B:368:HIS:ND1	2.32	0.52
15:D:201:GLY:HA3	15:D:327:LEU:HA	1.91	0.52
17:F:88:TYR:CD2	17:F:155:LYS:HG3	2.43	0.52
20:I:216:LEU:HD12	20:I:225:ILE:HG12	1.90	0.52
24:M:236:GLU:HA	24:M:239:ALA:HB3	1.90	0.52
29:R:196:HIS:O	29:R:200:SER:CB	2.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:k:50:VAL:HG11	22:k:66:LYS:HB2	1.91	0.52
3:W:361:HIS:CD2	3:W:364:ARG:HH11	2.27	0.52
5:Y:46:ARG:C	5:Y:48:ASN:H	2.16	0.52
6:Z:37:GLY:HA2	6:Z:56:VAL:HG12	1.91	0.52
7:a:370:GLN:O	10:d:251:ARG:NH1	2.43	0.52
8:b:116:PRO:HA	8:b:146:GLU:HG3	1.91	0.52
10:d:225:PHE:HB3	10:d:226:ALA:HB2	1.92	0.52
14:C:49:ARG:HA	14:C:52:LEU:HB2	1.91	0.52
14:C:89:VAL:HG12	14:C:91:PRO:HD2	1.91	0.52
27:p:27:ARG:NH1	27:p:180:VAL:O	2.43	0.52
1:U:649:ARG:HB3	1:U:675:MET:HE1	1.90	0.52
2:V:495:ARG:CB	14:C:38:LYS:CD	2.86	0.52
5:Y:20:ALA:HB2	5:Y:150:PHE:HD1	1.75	0.52
9:c:57:MET:N	9:c:110:GLY:O	2.38	0.52
12:A:120:LYS:H	17:F:127:SER:HB2	1.73	0.52
14:C:119:ASP:OD1	14:C:119:ASP:N	2.41	0.52
14:C:193:GLY:H	14:C:355:SER:HB2	1.75	0.52
24:M:67:PHE:HB2	24:M:75:MET:HB2	1.92	0.52
24:M:189:ILE:HA	24:M:192:GLU:HB2	1.91	0.52
22:k:105:GLU:OE2	30:s:75:TYR:OH	2.28	0.52
32:f:692:LEU:HD12	32:f:748:LEU:HD23	1.84	0.52
2:V:324:PHE:CD1	11:e:7:PRO:HA	2.45	0.52
2:V:496:PHE:CE1	14:C:34:ILE:CG2	2.93	0.52
5:Y:192:ARG:NH2	5:Y:294:TYR:HB3	2.24	0.52
32:f:376:PHE:CD2	32:f:416:MET:CE	2.83	0.52
32:f:632:LYS:HD2	32:f:661:ALA:HA	1.92	0.52
12:A:334:PRO:HB3	17:F:395:GLN:HE21	1.74	0.52
14:C:193:GLY:H	14:C:356:GLY:H	1.58	0.52
21:J:88:ARG:HH22	28:Q:69:MET:HB3	1.75	0.52
22:k:69:GLU:OE1	22:k:228:MET:HE2	2.10	0.52
25:n:160:LEU:O	25:n:164:MET:HB2	2.10	0.52
27:p:58:THR:O	28:q:85:ARG:NH2	2.42	0.52
30:s:176:LYS:HE2	30:s:208:VAL:HG21	1.90	0.52
1:U:806:CYS:SG	1:U:888:GLN:HG2	2.50	0.52
4:X:394:ASP:N	4:X:394:ASP:OD1	2.41	0.52
15:D:41:TYR:HA	15:D:44:TYR:HB3	1.92	0.52
20:I:91:ARG:NH1	27:P:76:LEU:O	2.43	0.52
21:J:91:CYS:HB2	21:J:102:VAL:HG21	1.90	0.52
30:S:13:LEU:HD13	30:S:145:LEU:HD13	1.92	0.52
26:o:163:ILE:HG23	26:o:170:GLY:HA2	1.91	0.52
32:f:306:GLU:HB3	32:f:339:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:885:MET:HG2	1:U:887:ALA:H	1.75	0.52
2:V:80:LYS:HD3	2:V:81:GLN:HB2	1.75	0.52
9:c:145:VAL:HA	9:c:157:ILE:HA	1.92	0.52
13:B:280:SER:HB2	13:B:325:VAL:H	1.73	0.52
27:P:39:PHE:HE1	27:P:61:GLN:HE21	1.58	0.52
18:g:33:ASN:HA	18:g:170:VAL:HG22	1.91	0.52
24:m:40:ARG:NH1	24:m:146:ALA:O	2.43	0.52
27:p:189:ILE:HG23	27:p:196:THR:HB	1.91	0.52
32:f:336:GLU:HG3	32:f:337:LEU:CD2	2.38	0.52
32:f:366:ASP:O	32:f:367:SER:CB	2.57	0.52
32:f:485:LEU:HD12	32:f:488:ALA:HB3	1.92	0.52
32:f:691:PRO:HB3	32:f:749:ALA:CB	2.39	0.52
2:V:59:ALA:N	2:V:60:ALA:HB3	2.25	0.52
2:V:227:VAL:HA	2:V:230:PHE:HB3	1.92	0.52
2:V:338:LEU:HD21	2:V:394:LEU:HB2	1.91	0.52
5:Y:16:ASP:HB3	5:Y:146:ARG:HH21	1.75	0.52
9:c:56:LEU:HA	9:c:111:TRP:HA	1.92	0.52
9:c:252:ALA:O	9:c:256:ASN:N	2.42	0.52
19:H:100:VAL:HG13	27:P:93:ASN:HD22	1.74	0.52
30:S:55:SER:OG	30:S:56:GLY:N	2.42	0.52
18:g:41:ALA:HB3	18:g:166:THR:HB	1.91	0.52
24:m:168:ALA:HB1	24:m:172:ALA:HB2	1.92	0.52
1:U:774:PRO:O	1:U:778:PHE:N	2.43	0.51
2:V:362:LEU:HD12	2:V:365:GLN:HB3	1.92	0.51
3:W:5:GLY:HA2	3:W:34:LEU:HD13	1.92	0.51
8:b:91:ARG:NH1	8:b:134:GLU:OE2	2.42	0.51
14:C:221:GLN:HB2	15:D:283:ARG:NH1	2.25	0.51
16:E:122:MET:SD	16:E:225:HIS:NE2	2.79	0.51
16:E:348:THR:HG21	17:F:218:GLN:HB2	1.92	0.51
19:h:14:SER:OG	19:h:18:LYS:N	2.38	0.51
32:f:337:LEU:N	32:f:337:LEU:CD2	2.73	0.51
32:f:800:LEU:N	32:f:800:LEU:CD1	2.73	0.51
1:U:102:ALA:HB1	14:C:21:ARG:HH12	1.75	0.51
1:U:220:LEU:HD11	1:U:252:LEU:HD13	1.90	0.51
5:Y:73:MET:O	5:Y:77:ASN:N	2.28	0.51
12:A:277:ILE:HG13	12:A:280:ILE:HD11	1.93	0.51
14:C:99:VAL:HA	14:C:100:ASP:HB3	1.91	0.51
15:D:163:MET:HG3	15:D:165:ALA:H	1.75	0.51
15:D:218:ALA:O	15:D:222:HIS:ND1	2.39	0.51
18:G:88:ARG:NH1	24:M:157:SER:O	2.41	0.51
20:I:213:ILE:HB	20:I:228:LEU:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:g:128:ASN:OD1	19:h:6:TYR:OH	2.26	0.51
26:o:51:ASP:HB3	26:o:94:ILE:HG23	1.93	0.51
7:a:112:ILE:HD13	7:a:151:VAL:HG11	1.92	0.51
12:A:260:LEU:HD13	12:A:272:ILE:HG13	1.92	0.51
25:N:179:ILE:HG12	25:N:184:VAL:HG22	1.91	0.51
32:f:647:GLY:HA2	32:f:655:LEU:HG	1.93	0.51
1:U:57:ARG:HA	1:U:60:ALA:HB3	1.92	0.51
2:V:195:ILE:CG2	14:C:22:GLN:C	2.81	0.51
3:W:321:VAL:O	3:W:325:GLY:N	2.44	0.51
5:Y:67:VAL:O	5:Y:71:ASN:N	2.41	0.51
17:F:70:LYS:HE2	17:F:74:LYS:HE3	1.93	0.51
19:H:44:VAL:HG23	19:H:144:PRO:HB2	1.92	0.51
23:l:189:LYS:HA	23:l:192:LEU:HG	1.93	0.51
32:f:468:ASP:OD2	32:f:475:ASN:N	2.42	0.51
1:U:237:VAL:HG13	1:U:321:GLN:HG3	1.91	0.51
15:D:251:PHE:CE2	15:D:292:LEU:HB2	2.45	0.51
30:S:211:ARG:NH2	30:S:213:ASP:OD2	2.42	0.51
22:k:182:GLN:NE2	23:l:55:GLU:OE1	2.44	0.51
28:q:140:LEU:HA	28:q:143:LEU:HB3	1.92	0.51
32:f:336:GLU:CG	32:f:337:LEU:HD22	2.36	0.51
32:f:790:GLN:HG3	32:f:792:ALA:H	1.75	0.51
1:U:842:LYS:H	1:U:882:ALA:HB2	1.76	0.51
2:V:480:ILE:HD11	6:Z:264:SER:HA	1.92	0.51
5:Y:346:LYS:HB2	5:Y:355:GLU:HB3	1.92	0.51
13:B:427:LEU:CD2	20:I:173:SER:HB2	2.41	0.51
14:C:201:ARG:HH11	14:C:211:PHE:HB3	1.76	0.51
22:K:99:HIS:O	22:K:103:TYR:HB2	2.11	0.51
24:M:228:PRO:HB2	24:M:231:ILE:HB	1.93	0.51
27:P:107:PRO:HG2	27:P:124:LEU:HB2	1.93	0.51
28:Q:23:SER:OG	28:Q:24:ASN:N	2.43	0.51
21:j:88:ARG:NH1	28:q:69:MET:O	2.44	0.51
23:l:160:SER:O	23:l:169:ARG:NH2	2.44	0.51
32:f:127:SER:O	32:f:131:MET:HB3	2.10	0.51
32:f:380:PHE:CG	32:f:751:TYR:CE1	2.99	0.51
32:f:440:ILE:O	32:f:444:ALA:HB2	2.10	0.51
32:f:463:LEU:HD22	32:f:466:LEU:CD1	2.40	0.51
1:U:576:PRO:HB3	1:U:611:ASN:HD22	1.76	0.51
1:U:908:ILE:HG12	1:U:909:GLY:H	1.76	0.51
3:W:374:THR:HG23	7:a:327:VAL:HA	1.93	0.51
6:Z:189:GLN:O	6:Z:192:THR:OG1	2.27	0.51
10:d:106:LEU:HG	10:d:109:GLN:HE21	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:d:228:GLN:N	10:d:229:GLN:HA	2.25	0.51
12:A:270:CYS:O	12:A:315:ILE:HG12	2.10	0.51
13:B:110:GLY:HA3	13:B:152:LEU:HD13	1.93	0.51
16:E:292:PRO:HA	16:E:295:LEU:O	2.10	0.51
17:F:126:THR:OG1	17:F:130:GLN:O	2.25	0.51
22:K:177:ALA:O	22:K:181:LEU:CB	2.53	0.51
18:g:165:ALA:HB1	18:g:179:LEU:HD13	1.92	0.51
21:j:186:LEU:O	21:j:190:LEU:CB	2.56	0.51
22:k:154:PHE:HB3	22:k:162:PHE:HE1	1.74	0.51
32:f:268:LEU:O	32:f:272:LEU:HB2	2.10	0.51
1:U:643:SER:O	1:U:649:ARG:NH1	2.43	0.51
2:V:80:LYS:CA	2:V:81:GLN:CB	2.33	0.51
7:a:58:LYS:HD2	7:a:83:VAL:HG11	1.91	0.51
9:c:29:GLU:HB2	9:c:203:ILE:HD11	1.93	0.51
9:c:174:PRO:HB3	9:c:175:ARG:HD3	1.93	0.51
12:A:102:ILE:HD11	12:A:136:GLU:HA	1.92	0.51
15:D:202:VAL:HB	15:D:308:ILE:HA	1.92	0.51
16:E:327:ASP:O	16:E:364:GLN:NE2	2.38	0.51
17:F:334:ARG:HG2	17:F:336:ASP:H	1.75	0.51
32:f:376:PHE:CZ	32:f:798:THR:CG2	2.91	0.51
32:f:463:LEU:HD22	32:f:466:LEU:HD11	1.92	0.51
32:f:523:GLY:O	32:f:527:VAL:N	2.43	0.51
1:U:529:ILE:HD11	1:U:555:VAL:HG11	1.93	0.51
1:U:764:LEU:HA	1:U:767:THR:HG23	1.92	0.51
6:Z:17:LEU:HB3	9:c:39:LEU:HD11	1.92	0.51
13:B:175:LYS:O	14:C:283:PHE:HE2	1.94	0.51
14:C:49:ARG:HH22	15:D:69:LYS:HG3	1.75	0.51
14:C:246:ILE:HG22	14:C:247:PHE:H	1.76	0.51
16:E:372:ARG:NE	24:M:170:GLN:C	2.46	0.51
17:F:325:GLN:HG2	17:F:326:VAL:HG23	1.93	0.51
18:G:114:LEU:HD22	18:G:140:LEU:HD21	1.91	0.51
27:P:116:THR:O	27:P:192:LYS:NZ	2.41	0.51
20:i:145:PHE:HZ	20:i:218:ARG:HB2	1.76	0.51
21:j:119:THR:HG22	21:j:126:PRO:HB3	1.92	0.51
30:s:125:ASP:OD1	30:s:129:SER:N	2.43	0.51
1:U:149:GLN:HE22	15:D:41:TYR:H	1.58	0.51
2:V:378:VAL:HG13	2:V:382:PHE:HD2	1.76	0.51
2:V:496:PHE:HE1	14:C:34:ILE:HG21	1.75	0.51
3:W:98:LYS:NZ	3:W:137:TYR:CD2	2.75	0.51
3:W:372:ARG:HG2	3:W:414:ASN:HB3	1.93	0.51
6:Z:199:LYS:HA	6:Z:202:ASN:ND2	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:d:98:LEU:HA	10:d:101:LEU:HG	1.93	0.51
12:A:138:MET:SD	12:A:156:LYS:NZ	2.69	0.51
12:A:160:THR:C	12:A:162:THR:H	2.19	0.51
12:A:191:VAL:HG21	12:A:271:LEU:HD21	1.93	0.51
12:A:205:GLY:HA2	12:A:206:ILE:CG2	2.41	0.51
20:I:92:LEU:HD22	20:I:96:ARG:HH21	1.76	0.51
22:K:45:GLY:HA3	22:K:221:GLN:HG3	1.93	0.51
25:N:7:GLN:HA	25:N:12:VAL:HA	1.92	0.51
28:Q:38:MET:HA	28:Q:61:GLN:HE22	1.76	0.51
32:f:226:TYR:O	32:f:230:CYS:HB2	2.11	0.51
32:f:531:ASN:HA	32:f:569:LYS:HA	1.93	0.51
32:f:745:LEU:HD12	32:f:745:LEU:C	2.36	0.51
2:V:326:GLN:HB3	2:V:353:LEU:HD22	1.93	0.50
6:Z:223:ASN:HB2	6:Z:227:ILE:HG12	1.93	0.50
9:c:88:ASP:HB3	9:c:91:PHE:HB2	1.93	0.50
12:A:95:VAL:HB	12:A:144:ARG:H	1.76	0.50
12:A:333:ARG:HG3	12:A:334:PRO:HD3	1.92	0.50
12:A:384:GLU:H	13:B:343:ARG:HH11	1.57	0.50
13:B:224:LEU:O	13:B:330:ALA:HA	2.11	0.50
26:O:46:ALA:HB3	26:O:97:ALA:HB3	1.93	0.50
30:S:96:LEU:HD11	30:S:108:ASN:HD22	1.76	0.50
23:l:41:LYS:NZ	23:l:180:MET:O	2.37	0.50
23:l:120:THR:O	24:m:129:ARG:NH1	2.35	0.50
32:f:347:ASP:O	32:f:351:THR:OG1	2.25	0.50
32:f:502:LEU:HG	32:f:540:GLN:HE22	1.75	0.50
32:f:556:ARG:NH1	32:f:786:GLN:OE1	2.44	0.50
13:B:337:LEU:HA	13:B:341:LEU:HD12	1.93	0.50
19:H:38:ILE:HG12	19:H:160:ALA:HB1	1.94	0.50
22:K:16:SER:OG	22:K:18:GLU:OE1	2.24	0.50
28:q:23:SER:OG	28:q:24:ASN:N	2.44	0.50
32:f:479:LEU:HA	32:f:517:VAL:HG21	1.93	0.50
7:a:123:LEU:HD21	7:a:161:LYS:HG3	1.94	0.50
10:d:209:TYR:HB3	10:d:213:ARG:HE	1.76	0.50
14:C:137:LEU:O	14:C:141:GLU:HG3	2.11	0.50
23:l:139:ASP:H	31:t:81:HIS:HE1	1.58	0.50
32:f:343:LYS:NZ	32:f:804:LEU:HD23	2.26	0.50
2:V:69:THR:O	2:V:73:GLU:N	2.35	0.50
2:V:492:LYS:NZ	14:C:38:LYS:HZ3	1.98	0.50
5:Y:312:ARG:HA	5:Y:356:THR:HG21	1.79	0.50
8:b:25:ARG:CZ	8:b:144:GLY:HA2	2.42	0.50
9:c:130:GLN:HE21	9:c:162:LEU:HB2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:d:40:GLY:HA3	10:d:41:THR:C	2.36	0.50
10:d:52:ARG:NH2	10:d:82:TYR:OH	2.44	0.50
10:d:237:ILE:N	10:d:238:PRO:HD2	2.27	0.50
14:C:13:GLU:N	14:C:14:GLY:HA3	2.27	0.50
17:F:383:GLU:OE1	23:L:166:GLN:O	2.30	0.50
17:F:436:GLN:C	17:F:438:TYR:H	2.20	0.50
23:L:152:ASN:HA	24:M:85:ARG:HH22	1.76	0.50
22:k:43:SER:HA	22:k:151:PRO:HG3	1.92	0.50
23:l:17:GLY:HA3	24:m:29:ALA:HB2	1.93	0.50
32:f:392:THR:HG22	32:f:417:ILE:HD13	1.92	0.50
32:f:478:ARG:NE	32:f:504:VAL:HG22	2.27	0.50
32:f:623:LYS:O	32:f:627:GLU:HB2	2.11	0.50
1:U:792:ASN:HA	1:U:914:LEU:HB3	1.93	0.50
2:V:367:VAL:HG13	2:V:402:VAL:HG22	1.93	0.50
3:W:366:MET:HB3	3:W:370:TYR:CE2	2.47	0.50
9:c:63:ASP:OD1	9:c:66:THR:OG1	2.23	0.50
12:A:333:ARG:O	12:A:337:LEU:N	2.45	0.50
12:A:373:LEU:HD13	12:A:410:LEU:HB2	1.93	0.50
19:H:118:MET:HE2	19:H:151:PRO:HA	1.92	0.50
24:M:195:LYS:HG3	24:M:196:ILE:HG13	1.92	0.50
21:j:32:ALA:HB2	21:j:45:VAL:HG23	1.93	0.50
22:k:228:MET:O	22:k:230:THR:HG23	2.10	0.50
32:f:455:VAL:HG12	32:f:457:ASN:H	1.76	0.50
32:f:517:VAL:O	32:f:521:ALA:CB	2.60	0.50
32:f:517:VAL:O	32:f:521:ALA:HB3	2.12	0.50
32:f:536:SER:HA	32:f:539:LEU:HB3	1.93	0.50
32:f:691:PRO:HA	32:f:694:LEU:HB3	1.93	0.50
32:f:804:LEU:N	32:f:804:LEU:CD1	2.74	0.50
4:X:298:SER:O	4:X:301:ASP:N	2.43	0.50
7:a:219:HIS:ND1	7:a:221:VAL:HG22	2.26	0.50
12:A:101:ILE:N	12:A:114:ASN:O	2.45	0.50
12:A:151:ILE:HD12	12:A:152:PRO:HD2	1.94	0.50
18:G:239:LEU:HD12	18:G:242:LEU:HD21	1.93	0.50
18:g:32:ILE:HA	18:g:82:GLY:HA2	1.92	0.50
22:k:85:ALA:HB2	22:k:139:VAL:HG21	1.94	0.50
32:f:612:LEU:O	32:f:616:CYS:CB	2.56	0.50
1:U:27:LEU:O	1:U:31:VAL:N	2.45	0.50
1:U:574:LYS:HD2	9:c:211:GLU:HG3	1.93	0.50
2:V:474:LEU:HA	2:V:477:HIS:HD2	1.76	0.50
14:C:71:SER:HB2	15:D:112:TYR:O	2.12	0.50
14:C:229:ARG:HB3	14:C:232:ARG:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:I:10:THR:HG22	21:J:125:ARG:HB2	1.94	0.50
22:K:54:ILE:HA	22:K:59:MET:HE1	1.94	0.50
30:S:125:ASP:OD1	30:S:129:SER:N	2.45	0.50
32:f:343:LYS:O	32:f:347:ASP:N	2.40	0.50
32:f:692:LEU:HG	32:f:752:HIS:HE1	1.77	0.50
1:U:403:THR:HA	1:U:406:ALA:HB3	1.93	0.50
2:V:219:GLU:OE2	2:V:256:ARG:NH1	2.45	0.50
7:a:335:TRP:CG	7:a:336:VAL:H	2.28	0.50
13:B:178:LYS:HE3	14:C:278:ASN:O	2.11	0.50
13:B:216:ILE:O	13:B:217:LYS:HG2	2.12	0.50
14:C:188:LEU:HB3	14:C:317:PHE:HB2	1.93	0.50
26:O:31:CYS:SG	26:O:32:SER:N	2.85	0.50
28:Q:103:LEU:HD13	28:Q:115:LEU:HD11	1.93	0.50
30:S:178:VAL:O	30:S:182:ALA:HB3	2.11	0.50
32:f:691:PRO:HG2	32:f:745:LEU:CD1	2.41	0.50
2:V:227:VAL:O	2:V:231:LEU:N	2.43	0.50
4:X:258:LYS:HD3	4:X:267:VAL:HG22	1.93	0.50
5:Y:131:THR:O	5:Y:137:ARG:NH1	2.45	0.50
7:a:32:LYS:HD3	8:b:22:LEU:HD11	1.94	0.50
20:I:134:LEU:N	20:I:150:SER:OG	2.42	0.50
28:Q:53:THR:HG22	28:Q:100:VAL:HG12	1.94	0.50
32:f:657:ILE:HA	32:f:660:ILE:HD12	1.94	0.50
1:U:345:ASN:ND2	1:U:743:ASN:OD1	2.45	0.49
5:Y:362:LYS:HZ3	5:Y:366:TYR:HE2	1.60	0.49
9:c:211:GLU:O	9:c:215:LYS:N	2.36	0.49
12:A:86:THR:O	12:A:90:GLU:N	2.45	0.49
20:I:16:GLY:N	21:J:21:TYR:OH	2.44	0.49
20:i:198:ASN:HD22	20:i:240:HIS:CD2	2.30	0.49
32:f:337:LEU:HD22	32:f:337:LEU:H	1.75	0.49
1:U:885:MET:HB3	1:U:888:GLN:HG3	1.93	0.49
6:Z:105:ASP:HA	6:Z:108:ILE:HD13	1.94	0.49
7:a:193:GLN:HB3	7:a:225:LEU:HD13	1.93	0.49
11:e:57:ARG:HB2	11:e:59:GLU:HB2	1.95	0.49
12:A:217:PRO:HD2	12:A:343:PHE:HB2	1.94	0.49
12:A:218:PRO:O	12:A:221:GLY:N	2.45	0.49
15:D:414:HIS:HE1	19:H:79:MET:CE	2.26	0.49
21:J:18:GLN:O	21:J:22:ALA:CB	2.61	0.49
21:J:186:LEU:O	21:J:190:LEU:CB	2.55	0.49
23:L:46:LEU:HD13	23:L:73:SER:HB2	1.94	0.49
32:f:392:THR:CG2	32:f:417:ILE:HD13	2.42	0.49
2:V:496:PHE:CD1	14:C:34:ILE:HG23	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W:136:ILE:CD1	3:W:176:SER:N	2.76	0.49
5:Y:233:ARG:NH1	5:Y:306:GLN:OE1	2.45	0.49
9:c:223:LYS:HZ2	9:c:230:THR:HG23	1.77	0.49
12:A:297:ARG:NE	17:F:302:GLY:O	2.45	0.49
13:B:436:GLU:OE2	20:I:22:GLU:OE1	2.30	0.49
15:D:231:VAL:HG11	16:E:258:MET:HB3	1.94	0.49
22:K:224:GLN:CD	22:K:227:HIS:CD2	2.90	0.49
26:O:96:ALA:H	26:O:115:PRO:HB3	1.77	0.49
27:P:27:ARG:NH2	29:r:168:ALA:HB2	2.27	0.49
1:U:639:LEU:HD23	15:D:64:GLU:OE1	2.12	0.49
2:V:287:ARG:HH12	11:e:4:LYS:HD3	1.74	0.49
2:V:417:ILE:HG12	2:V:422:ILE:HD12	1.94	0.49
6:Z:256:GLN:HG3	6:Z:260:VAL:HG23	1.93	0.49
12:A:125:LEU:HB3	12:A:149:ILE:HD12	1.94	0.49
13:B:199:GLU:O	13:B:203:LEU:N	2.45	0.49
13:B:254:GLU:HG3	13:B:292:THR:HG22	1.94	0.49
16:E:281:ARG:NH1	17:F:294:LYS:O	2.45	0.49
28:q:4:LEU:HD22	28:q:18:ASP:H	1.77	0.49
4:X:368:MET:HB3	4:X:374:PHE:HB3	1.95	0.49
12:A:164:MET:HG2	12:A:244:GLU:HG3	1.95	0.49
16:E:345:ASN:HD21	17:F:345:SER:HA	1.78	0.49
20:i:75:SER:HB2	20:i:135:LEU:HB2	1.95	0.49
24:m:163:CYS:SG	24:m:164:ALA:N	2.85	0.49
32:f:336:GLU:HG3	32:f:337:LEU:H	1.76	0.49
32:f:641:GLU:HG3	32:f:641:GLU:O	2.10	0.49
1:U:20:LYS:HE2	1:U:48:LEU:HD21	1.93	0.49
6:Z:39:LEU:HD11	6:Z:50:VAL:HG11	1.94	0.49
7:a:351:ASP:O	7:a:355:PHE:HB2	2.13	0.49
8:b:68:THR:HA	8:b:71:ILE:HD13	1.95	0.49
10:d:30:LEU:HA	10:d:34:ASN:HA	1.94	0.49
10:d:39:THR:HG23	10:d:86:LYS:HE3	1.94	0.49
16:E:165:ILE:HD12	16:E:166:PRO:HD2	1.93	0.49
18:G:155:ASP:OD2	18:G:159:TYR:OH	2.25	0.49
21:J:109:ARG:NH2	29:R:70:ASN:OD1	2.45	0.49
23:L:111:LEU:O	23:L:115:LYS:HB2	2.11	0.49
25:N:46:SER:HB2	25:N:97:GLY:HA3	1.94	0.49
30:S:178:VAL:O	30:S:182:ALA:CB	2.61	0.49
28:q:3:TYR:HB2	28:q:133:GLY:HA3	1.94	0.49
32:f:234:THR:HG23	32:f:637:LYS:HE2	1.94	0.49
2:V:26:PRO:O	2:V:29:PRO:HD2	2.12	0.49
2:V:306:ARG:HB3	2:V:339:LEU:HD21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W:91:SER:HB2	3:W:92:LYS:HA	1.94	0.49
13:B:106:PRO:HB3	14:C:121:TYR:HB2	1.95	0.49
13:B:109:VAL:HG22	13:B:151:LEU:HD22	1.95	0.49
19:H:9:SER:OG	19:H:123:GLN:O	2.30	0.49
22:K:225:ASN:HB2	22:K:226:PHE:CD1	2.48	0.49
18:g:83:MET:SD	18:g:132:ARG:NH1	2.75	0.49
21:j:18:GLN:O	21:j:22:ALA:HB2	2.13	0.49
22:k:217:LEU:HD13	22:k:229:PHE:CZ	2.24	0.49
32:f:387:GLN:N	32:f:387:GLN:NE2	2.60	0.49
1:U:472:ILE:HG22	1:U:475:HIS:CE1	2.47	0.49
2:V:495:ARG:NE	14:C:42:LEU:HD22	2.28	0.49
5:Y:63:TRP:HB3	5:Y:65:ILE:N	2.28	0.49
6:Z:77:ASN:HB2	9:c:98:MET:HE1	1.94	0.49
6:Z:256:GLN:HG2	10:d:246:VAL:HG21	1.95	0.49
7:a:103:LYS:HG3	7:a:104:VAL:HG23	1.94	0.49
12:A:247:GLN:HB2	12:A:248:LYS:O	2.13	0.49
14:C:89:VAL:HB	14:C:92:GLU:HB2	1.95	0.49
15:D:254:ALA:HB1	15:D:305:VAL:HG23	1.95	0.49
25:n:5:ALA:HB3	25:n:126:ALA:HB3	1.94	0.49
31:t:27:LEU:HD11	31:t:34:ALA:HB1	1.94	0.49
32:f:140:LEU:O	32:f:144:LEU:CB	2.61	0.49
32:f:372:LEU:C	32:f:372:LEU:CD2	2.86	0.49
32:f:389:LYS:HB3	32:f:392:THR:HG21	1.95	0.49
2:V:273:LYS:HA	2:V:274:SER:HB2	1.94	0.49
6:Z:222:ILE:N	6:Z:223:ASN:HA	2.28	0.49
10:d:125:LYS:HB3	10:d:129:THR:HG22	1.95	0.49
14:C:43:ARG:HG2	15:D:61:ILE:HD12	1.94	0.49
19:H:4:ARG:NH2	24:M:126:SER:OG	2.45	0.49
21:J:2:SER:OG	21:J:3:TYR:N	2.45	0.49
30:S:68:ILE:HD11	30:S:92:LEU:HD13	1.94	0.49
32:f:597:VAL:HG22	32:f:630:ASP:HB2	1.95	0.49
1:U:612:ASP:HA	1:U:615:ARG:HD3	1.95	0.49
3:W:52:LYS:HA	3:W:55:ARG:HB3	1.95	0.49
15:D:241:GLY:O	15:D:245:ARG:NH2	2.46	0.49
16:E:206:LYS:HG3	16:E:207:TYR:H	1.77	0.49
16:E:339:ASN:OD1	16:E:340:GLY:N	2.46	0.49
18:G:93:ARG:HH21	18:G:121:ILE:HG12	1.78	0.49
19:h:100:VAL:HG13	27:p:93:ASN:HD22	1.77	0.49
21:j:38:ARG:HH12	21:j:182:GLU:HA	1.77	0.49
25:n:136:TYR:HE2	31:t:33:LEU:HD21	1.77	0.49
25:n:175:ARG:HG2	25:n:188:VAL:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:376:PHE:CZ	32:f:798:THR:CB	2.91	0.49
2:V:291:TYR:CZ	11:e:5:LYS:HE2	2.48	0.48
2:V:495:ARG:CZ	14:C:42:LEU:HD22	2.43	0.48
3:W:2:ALA:HA	3:W:47:LEU:HD11	1.95	0.48
3:W:186:ILE:O	3:W:189:GLN:NE2	2.44	0.48
5:Y:101:ARG:HD3	5:Y:130:LYS:HD3	1.95	0.48
9:c:63:ASP:O	9:c:139:ARG:NH2	2.45	0.48
13:B:182:GLU:HB2	13:B:239:VAL:HG21	1.96	0.48
15:D:417:TYR:CZ	19:H:79:MET:HA	2.44	0.48
16:E:178:THR:HG21	16:E:340:GLY:H	1.77	0.48
16:E:235:ILE:HG22	16:E:279:THR:HB	1.95	0.48
26:o:96:ALA:H	26:o:115:PRO:HB3	1.78	0.48
32:f:645:ASP:HB3	32:f:648:ALA:HB3	1.95	0.48
1:U:384:GLN:HG2	1:U:385:PHE:H	1.78	0.48
3:W:170:GLN:HA	3:W:173:THR:HG23	1.94	0.48
8:b:146:GLU:HG2	8:b:147:GLU:H	1.78	0.48
10:d:159:PRO:N	10:d:160:ALA:HA	2.27	0.48
12:A:219:GLY:HA2	12:A:220:THR:HA	1.49	0.48
14:C:87:VAL:O	14:C:95:PHE:N	2.26	0.48
17:F:437:TYR:HD2	22:K:25:GLU:HA	1.76	0.48
21:J:176:TYR:HE2	22:K:58:LEU:HA	1.78	0.48
22:K:211:ASN:OD1	22:K:214:ASN:ND2	2.46	0.48
31:T:20:VAL:HG11	31:T:122:LEU:HD13	1.96	0.48
19:h:50:LYS:NZ	19:h:62:VAL:O	2.47	0.48
32:f:94:LYS:HA	32:f:97:LYS:HG2	1.94	0.48
32:f:453:SER:O	32:f:488:ALA:O	2.31	0.48
1:U:401:LYS:HB3	1:U:438:GLN:NE2	2.29	0.48
1:U:520:MET:HE2	1:U:525:ASN:HD22	1.78	0.48
2:V:137:GLU:O	2:V:141:THR:N	2.40	0.48
3:W:88:MET:O	3:W:91:SER:OG	2.26	0.48
9:c:282:ARG:HG3	9:c:284:LEU:HD13	1.94	0.48
12:A:428:ARG:NH2	13:B:340:ALA:HB2	2.28	0.48
13:B:428:TYR:CE1	20:I:170:ALA:HB3	2.47	0.48
14:C:84:LYS:NZ	14:C:98:ASP:OD1	2.32	0.48
18:G:128:ASN:OD1	19:H:6:TYR:OH	2.30	0.48
24:M:150:MET:HG2	24:M:160:TYR:HE2	1.78	0.48
18:g:114:LEU:HD22	18:g:140:LEU:HD21	1.94	0.48
25:n:19:ARG:HH11	25:n:171:GLY:HA3	1.79	0.48
32:f:315:GLU:HA	32:f:318:THR:HG22	1.95	0.48
32:f:389:LYS:HD2	32:f:418:LEU:HD21	1.92	0.48
32:f:471:LEU:CG	32:f:509:LYS:CE	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:324:PHE:HB3	11:e:6:GLN:HG2	1.92	0.48
3:W:16:MET:HG3	3:W:54:THR:HB	1.96	0.48
3:W:438:LEU:HD22	6:Z:234:PHE:CD1	2.47	0.48
12:A:206:ILE:HG23	12:A:207:GLU:H	1.79	0.48
16:E:341:ALA:HB1	17:F:345:SER:H	1.78	0.48
22:K:224:GLN:HE21	22:K:227:HIS:CE1	2.31	0.48
26:O:33:LYS:O	26:O:35:HIS:ND1	2.47	0.48
28:Q:19:ARG:HH21	28:Q:31:ASP:HB2	1.78	0.48
31:T:27:LEU:HD22	31:T:184:TYR:HB2	1.96	0.48
24:m:46:VAL:HG22	24:m:215:TRP:HD1	1.79	0.48
24:m:67:PHE:HB2	24:m:75:MET:HB2	1.93	0.48
32:f:333:LEU:HA	32:f:338:ASP:HB2	1.95	0.48
1:U:800:VAL:HG21	1:U:914:LEU:HD21	1.94	0.48
5:Y:134:LEU:HD13	5:Y:168:ILE:HG23	1.94	0.48
6:Z:74:TYR:HD1	9:c:101:GLN:HE21	1.61	0.48
14:C:131:VAL:HG13	14:C:132:ASP:H	1.78	0.48
15:D:285:VAL:HA	15:D:288:ILE:HB	1.94	0.48
16:E:257:LEU:HA	16:E:260:LEU:HD12	1.96	0.48
23:L:107:ARG:HH22	31:T:81:HIS:HB2	1.79	0.48
24:M:141:SER:HB3	24:M:144:ASP:HB2	1.96	0.48
32:f:487:LEU:HD22	32:f:801:VAL:HG11	1.95	0.48
1:U:591:CYS:HA	1:U:625:ILE:HA	1.96	0.48
5:Y:346:LYS:H	5:Y:357:ASN:HD21	1.60	0.48
7:a:319:LEU:HA	7:a:337:GLN:HE21	1.78	0.48
10:d:256:ILE:N	10:d:257:VAL:HA	2.28	0.48
11:e:6:GLN:CG	11:e:7:PRO:HD3	2.43	0.48
13:B:409:GLU:CD	13:B:413:LYS:HB3	2.39	0.48
16:E:65:THR:HG22	16:E:66:GLU:H	1.79	0.48
17:F:363:ALA:HB2	17:F:385:ALA:HB2	1.96	0.48
29:R:115:ASP:HB2	29:R:119:ASN:HB2	1.96	0.48
32:f:30:GLY:O	32:f:34:ARG:HB2	2.14	0.48
32:f:253:LEU:O	32:f:257:ARG:CB	2.61	0.48
32:f:559:PRO:HA	32:f:562:LEU:HB2	1.96	0.48
1:U:571:CYS:HB2	1:U:601:ARG:HH21	1.78	0.48
3:W:451:MET:HE1	6:Z:156:GLU:HA	1.96	0.48
3:W:455:LEU:HD12	3:W:456:GLN:H	1.78	0.48
4:X:414:LEU:HA	4:X:417:LYS:HD2	1.94	0.48
4:X:420:LYS:NZ	6:Z:284:ASP:OD1	2.40	0.48
5:Y:51:ALA:CB	5:Y:116:ASP:H	2.27	0.48
7:a:62:ASN:OD1	7:a:103:LYS:NZ	2.47	0.48
13:B:174:MET:O	13:B:175:LYS:O	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:E:133:SER:HA	16:E:142:ILE:HD13	1.95	0.48
17:F:85:THR:HA	17:F:86:LEU:HA	1.59	0.48
22:k:197:SER:HA	22:k:200:ILE:HD12	1.95	0.48
22:k:203:LYS:HA	22:k:206:MET:HG2	1.94	0.48
27:p:74:TYR:OH	27:p:80:ARG:NH2	2.46	0.48
32:f:248:LEU:O	32:f:252:ALA:CB	2.62	0.48
1:U:148:LYS:HD2	15:D:39:ASP:HB2	1.94	0.48
1:U:446:LEU:O	1:U:450:HIS:ND1	2.34	0.48
2:V:80:LYS:HA	2:V:81:GLN:HB2	0.58	0.48
3:W:442:THR:HA	3:W:445:LEU:HB2	1.94	0.48
6:Z:45:LYS:HZ2	17:F:115:SER:N	2.10	0.48
6:Z:228:TYR:CE2	7:a:338:PRO:HB2	2.49	0.48
7:a:244:ASN:ND2	7:a:276:CYS:HB3	2.29	0.48
9:c:30:GLN:HB3	9:c:66:THR:HG22	1.95	0.48
12:A:354:ILE:O	12:A:358:HIS:ND1	2.40	0.48
12:A:384:GLU:O	12:A:387:SER:OG	2.30	0.48
13:B:260:LEU:N	13:B:261:GLY:HA2	2.29	0.48
15:D:116:LEU:HD12	15:D:140:VAL:HG22	1.94	0.48
16:E:211:SER:HA	16:E:214:LEU:HB3	1.96	0.48
19:H:50:LYS:HE2	19:H:59:GLU:HG3	1.95	0.48
24:M:158:TYR:HH	24:M:160:TYR:HH	1.57	0.48
32:f:336:GLU:CG	32:f:337:LEU:CD2	2.92	0.48
1:U:654:MET:HE1	1:U:767:THR:HG22	1.95	0.48
2:V:47:SER:HA	2:V:50:GLU:HB2	1.94	0.48
5:Y:145:LEU:HA	5:Y:157:ILE:HG22	1.95	0.48
6:Z:58:PHE:CZ	6:Z:68:TRP:HB2	2.49	0.48
12:A:322:ASN:OD1	12:A:428:ARG:NH1	2.46	0.48
13:B:99:VAL:O	13:B:103:ARG:HG2	2.14	0.48
13:B:103:ARG:HG3	13:B:104:GLY:H	1.78	0.48
14:C:142:LYS:HA	15:D:323:ARG:HD2	1.95	0.48
14:C:295:THR:HG22	14:C:296:ASN:H	1.79	0.48
15:D:348:ILE:HG13	15:D:352:MET:HE3	1.94	0.48
23:l:215:VAL:HB	23:l:221:PHE:HD1	1.78	0.48
32:f:127:SER:O	32:f:131:MET:HB2	2.13	0.48
32:f:479:LEU:CD2	32:f:513:GLU:HB3	2.39	0.48
32:f:695:ALA:CB	32:f:752:HIS:HB3	2.44	0.48
1:U:202:VAL:HG11	1:U:219:CYS:HB3	1.95	0.48
1:U:388:ASP:OD1	1:U:389:ASN:N	2.46	0.48
2:V:77:GLU:CB	2:V:81:GLN:NE2	2.42	0.48
4:X:360:ASP:OD1	4:X:361:VAL:N	2.45	0.48
5:Y:297:ARG:HD3	11:e:52:PHE:CE1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:109:ASN:ND2	6:Z:119:SER:O	2.43	0.48
13:B:440:LEU:CD1	21:J:29:GLY:HA2	2.41	0.48
14:C:103:ILE:HG13	14:C:126:ILE:HG22	1.95	0.48
16:E:372:ARG:CZ	24:M:171:ALA:H	2.18	0.48
20:I:86:LEU:HD22	20:I:114:LEU:HD11	1.96	0.48
23:L:50:LYS:HB3	23:L:59:HIS:HB3	1.95	0.48
28:Q:47:VAL:H	28:Q:102:LEU:HG	1.79	0.48
31:T:192:VAL:HG12	31:T:197:VAL:HG22	1.95	0.48
32:f:209:MET:SD	32:f:213:GLN:NE2	2.87	0.48
2:V:495:ARG:HB2	14:C:38:LYS:CG	2.16	0.47
9:c:180:ASN:HB2	9:c:204:THR:HG21	1.94	0.47
12:A:120:LYS:HE2	17:F:90:VAL:HG11	1.95	0.47
13:B:178:LYS:HZ1	14:C:278:ASN:C	2.22	0.47
14:C:163:GLU:OE1	14:C:163:GLU:N	2.44	0.47
27:P:203:ARG:NH2	27:P:205:ASP:OD2	2.47	0.47
23:l:117:GLN:O	23:l:120:THR:OG1	2.30	0.47
32:f:166:VAL:O	32:f:170:TRP:HB2	2.14	0.47
32:f:456:ARG:HD3	32:f:489:TYR:CZ	2.49	0.47
1:U:149:GLN:HE22	15:D:41:TYR:HB2	1.79	0.47
2:V:99:ARG:NH2	2:V:147:PHE:H	2.08	0.47
3:W:231:ILE:HG21	3:W:250:ILE:HG22	1.96	0.47
5:Y:138:LEU:HD22	5:Y:168:ILE:HD13	1.96	0.47
7:a:155:PHE:HE2	7:a:178:ARG:HD3	1.79	0.47
10:d:10:ASN:OD1	10:d:11:ARG:N	2.47	0.47
12:A:174:TYR:HD1	12:A:227:ARG:HD2	1.78	0.47
13:B:428:TYR:CD1	20:I:170:ALA:HA	2.39	0.47
16:E:58:GLY:HA2	16:E:73:ALA:HA	1.96	0.47
16:E:360:ASP:N	16:E:360:ASP:OD1	2.44	0.47
20:I:219:GLU:O	20:I:222:LYS:N	2.47	0.47
31:T:122:LEU:HG	31:T:137:LEU:HD12	1.96	0.47
18:g:67:THR:HG22	18:g:69:LEU:H	1.78	0.47
30:s:68:ILE:HD11	30:s:92:LEU:HD13	1.95	0.47
32:f:336:GLU:HB3	32:f:337:LEU:HD23	1.95	0.47
32:f:671:ALA:O	32:f:674:THR:OG1	2.26	0.47
1:U:118:LEU:HD21	1:U:123:LYS:HA	1.95	0.47
12:A:97:ARG:HA	12:A:98:CYS:HA	1.52	0.47
15:D:377:SER:CB	16:E:292:PRO:HB2	2.44	0.47
15:D:417:TYR:CG	19:H:79:MET:HA	2.49	0.47
17:F:224:LEU:HB2	17:F:348:LEU:HD13	1.96	0.47
18:G:208:ILE:HB	18:G:210:PHE:HD2	1.78	0.47
26:O:38:SER:OG	26:O:40:ASN:OD1	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:k:76:CYS:SG	22:k:77:ALA:N	2.87	0.47
24:m:8:ASP:HB2	24:m:25:TYR:HE2	1.80	0.47
24:m:180:GLN:HB2	24:m:184:MET:HG2	1.96	0.47
27:p:107:PRO:HG2	27:p:124:LEU:HB2	1.95	0.47
27:p:148:GLY:O	27:p:152:SER:OG	2.26	0.47
32:f:359:GLY:O	32:f:363:SER:CB	2.50	0.47
32:f:392:THR:HA	32:f:414:LEU:CD2	2.44	0.47
32:f:626:GLU:OE1	32:f:782:HIS:NE2	2.47	0.47
1:U:681:ASN:ND2	1:U:725:MET:SD	2.87	0.47
2:V:468:SER:HA	5:Y:363:ASN:HD21	1.79	0.47
3:W:120:ILE:O	3:W:124:LEU:N	2.45	0.47
7:a:24:ARG:O	7:a:28:LEU:HD13	2.14	0.47
12:A:362:MET:HE3	13:B:210:TYR:HB3	1.96	0.47
12:A:375:ARG:HG3	12:A:376:LEU:HD12	1.96	0.47
13:B:93:GLU:HG3	13:B:94:GLU:H	1.79	0.47
14:C:328:ILE:HG23	14:C:359:VAL:HG11	1.95	0.47
15:D:89:ILE:HD13	16:E:78:ARG:HB3	1.96	0.47
16:E:47:LEU:HA	16:E:50:LEU:HD12	1.96	0.47
20:I:12:PHE:HB3	21:J:21:TYR:HE2	1.80	0.47
23:L:148:CYS:SG	23:L:152:ASN:N	2.83	0.47
21:j:115:LYS:HG3	21:j:127:PHE:HD2	1.79	0.47
32:f:252:ALA:O	32:f:256:PHE:HB2	2.14	0.47
32:f:742:ALA:CA	32:f:745:LEU:CD2	2.62	0.47
1:U:437:TYR:HE2	9:c:25:VAL:HG21	1.80	0.47
1:U:443:LEU:HD21	1:U:464:GLN:HB2	1.97	0.47
3:W:405:LYS:HG3	4:X:344:ARG:HG2	1.95	0.47
5:Y:77:ASN:ND2	5:Y:114:ILE:HG21	2.29	0.47
6:Z:32:GLN:HG3	6:Z:33:LYS:H	1.78	0.47
13:B:103:ARG:HD2	13:B:107:MET:HE1	1.95	0.47
13:B:176:VAL:HA	13:B:177:GLU:HA	1.73	0.47
16:E:306:GLU:C	16:E:308:ALA:H	2.22	0.47
18:G:159:TYR:HB3	19:H:81:PRO:HG3	1.96	0.47
23:L:122:ARG:HG2	24:M:128:VAL:HG12	1.96	0.47
26:O:141:LYS:NZ	26:O:157:GLU:OE2	2.44	0.47
28:Q:140:LEU:HA	28:Q:143:LEU:HB3	1.97	0.47
26:o:50:ALA:HB2	27:p:129:CYS:HB2	1.96	0.47
30:s:16:ALA:HB2	30:s:121:VAL:HG23	1.96	0.47
1:U:336:GLU:HA	1:U:339:LEU:HB3	1.96	0.47
12:A:80:LEU:HD21	13:B:138:PHE:HB2	1.96	0.47
15:D:145:PRO:HB2	15:D:146:GLU:HB2	1.97	0.47
26:O:112:SER:HB3	26:O:125:VAL:HG11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:n:21:THR:HG22	25:n:26:ILE:HG13	1.97	0.47
29:r:35:ILE:N	29:r:43:GLY:O	2.47	0.47
32:f:635:LYS:NZ	32:f:641:GLU:CD	2.66	0.47
1:U:751:ARG:HG3	1:U:908:ILE:HG21	1.97	0.47
2:V:259:LEU:HD11	2:V:294:ARG:HD2	1.97	0.47
2:V:363:LEU:HA	2:V:378:VAL:HG11	1.97	0.47
2:V:479:ARG:NH1	5:Y:370:ILE:HG21	2.30	0.47
3:W:316:ARG:O	3:W:319:THR:OG1	2.27	0.47
3:W:436:MET:HA	3:W:439:VAL:HG22	1.97	0.47
5:Y:316:LEU:HG	5:Y:352:GLU:HG3	1.97	0.47
6:Z:151:THR:OG1	7:a:146:PRO:O	2.23	0.47
7:a:31:LYS:HG3	8:b:176:GLY:HA2	1.96	0.47
9:c:223:LYS:NZ	9:c:230:THR:HG23	2.30	0.47
12:A:387:SER:HA	12:A:390:THR:HB	1.97	0.47
13:B:175:LYS:HB3	13:B:175:LYS:HZ1	1.73	0.47
13:B:177:GLU:HB3	13:B:178:LYS:CA	2.44	0.47
13:B:255:LEU:HD11	14:C:264:GLY:HA2	1.96	0.47
14:C:56:VAL:HG21	15:D:75:ALA:HB1	1.96	0.47
14:C:166:GLU:OE2	14:C:207:THR:OG1	2.33	0.47
14:C:251:ILE:HG23	14:C:262:GLY:HA2	1.97	0.47
15:D:200:ARG:NH1	15:D:300:ASP:OD1	2.39	0.47
18:G:32:ILE:HA	18:G:82:GLY:HA2	1.97	0.47
24:M:100:SER:O	31:T:65:GLN:NE2	2.47	0.47
29:R:35:ILE:N	29:R:43:GLY:O	2.47	0.47
32:f:79:ARG:HE	32:f:95:PRO:HG3	1.80	0.47
32:f:331:LEU:O	32:f:335:ARG:NH1	2.47	0.47
32:f:424:GLY:HA2	32:f:427:THR:HG22	1.96	0.47
5:Y:358:ARG:HH21	5:Y:359:PRO:HG2	1.79	0.47
7:a:232:TRP:HZ3	7:a:253:THR:HA	1.80	0.47
14:C:245:ILE:HG23	14:C:290:LYS:HB2	1.97	0.47
15:D:377:SER:HB3	16:E:292:PRO:HB2	1.96	0.47
17:F:151:VAL:HG12	17:F:163:THR:HA	1.97	0.47
17:F:379:VAL:HG13	17:F:417:HIS:HD1	1.80	0.47
27:P:170:ALA:O	27:P:174:ALA:CB	2.63	0.47
30:S:172:MET:HE1	30:S:195:ILE:HG21	1.97	0.47
32:f:538:ILE:HA	32:f:541:THR:HG22	1.97	0.47
2:V:196:SER:H	14:C:23:TYR:CB	2.28	0.47
3:W:428:TRP:HE1	9:c:244:VAL:C	2.23	0.47
5:Y:89:GLU:HA	5:Y:92:GLU:HG2	1.97	0.47
6:Z:186:THR:HG23	6:Z:187:LEU:H	1.80	0.47
12:A:311:PRO:N	12:A:312:ARG:HA	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:358:VAL:HG12	15:D:363:TYR:HE2	1.80	0.47
27:P:59:ASP:O	27:P:63:VAL:HB	2.15	0.47
24:m:37:ILE:HD11	24:m:193:VAL:HG13	1.96	0.47
26:o:46:ALA:HB3	26:o:97:ALA:HB3	1.97	0.47
26:o:177:VAL:HB	26:o:184:ASP:HB2	1.97	0.47
29:r:53:SER:O	29:r:57:ARG:HB2	2.15	0.47
32:f:664:GLU:HB3	32:f:696:LEU:CG	2.43	0.47
1:U:176:MET:HA	1:U:179:TYR:CE2	2.50	0.47
1:U:337:LEU:HD12	1:U:338:HIS:N	2.30	0.47
1:U:735:GLY:O	1:U:739:ALA:N	2.48	0.47
4:X:347:ILE:HG22	4:X:385:LEU:HB2	1.96	0.47
5:Y:48:ASN:O	5:Y:114:ILE:HG13	2.15	0.47
6:Z:69:PHE:HZ	8:b:92:VAL:HG22	1.79	0.47
7:a:273:GLN:HB3	7:a:310:LEU:HD11	1.97	0.47
9:c:100:LYS:HA	9:c:105:PRO:HB3	1.97	0.47
12:A:184:ILE:HD13	12:A:224:LEU:HD22	1.97	0.47
12:A:217:PRO:HA	12:A:428:ARG:NE	2.29	0.47
13:B:178:LYS:O	13:B:179:ALA:O	2.32	0.47
13:B:333:ARG:NH2	20:I:15:GLU:OE1	2.48	0.47
15:D:300:ASP:HA	15:D:301:GLN:HA	1.64	0.47
19:H:148:GLN:OE1	19:H:158:TRP:NE1	2.48	0.47
23:L:26:MET:HE1	23:L:148:CYS:HB2	1.96	0.47
25:n:19:ARG:HE	25:n:26:ILE:HG12	1.80	0.47
26:o:215:LYS:HB3	27:p:197:THR:HB	1.97	0.47
31:t:178:TYR:OH	31:t:208:ASN:N	2.42	0.47
32:f:378:ASN:HB3	32:f:391:LEU:HD21	1.97	0.47
32:f:445:LEU:HG	32:f:462:ALA:HB2	1.95	0.47
1:U:813:TYR:OH	1:U:883:ARG:NH1	2.49	0.46
2:V:56:ALA:O	2:V:59:ALA:HB3	2.15	0.46
2:V:144:ASP:N	2:V:145:LEU:HA	2.29	0.46
5:Y:251:HIS:HA	5:Y:257:ARG:HD3	1.97	0.46
5:Y:314:LEU:O	5:Y:354:VAL:N	2.48	0.46
6:Z:33:LYS:HZ1	6:Z:34:ARG:C	2.18	0.46
7:a:25:LEU:HA	7:a:28:LEU:HD22	1.96	0.46
12:A:157:ILE:HG21	12:A:259:GLU:OE1	2.16	0.46
15:D:313:ARG:NH2	15:D:315:ASP:OD2	2.47	0.46
15:D:417:TYR:OH	19:H:79:MET:HE2	2.15	0.46
31:T:43:MET:HE3	31:T:45:VAL:HG22	1.96	0.46
1:U:378:CYS:SG	1:U:783:TYR:HD2	2.39	0.46
1:U:842:LYS:HB3	1:U:843:GLU:O	2.15	0.46
2:V:496:PHE:CE1	14:C:34:ILE:HG23	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:B:239:VAL:HA	13:B:242:GLN:HG3	1.97	0.46
13:B:261:GLY:O	13:B:264:PRO:HD3	2.15	0.46
18:G:49:VAL:HG22	18:G:219:VAL:HG23	1.97	0.46
20:I:95:GLN:HE22	20:I:98:LEU:HD23	1.80	0.46
27:P:117:PHE:HB3	27:P:192:LYS:HD3	1.96	0.46
28:q:23:SER:HB2	28:q:28:MET:HE2	1.97	0.46
4:X:377:ILE:HB	4:X:388:PHE:HE1	1.79	0.46
4:X:396:THR:HG23	5:Y:366:TYR:CD1	2.50	0.46
6:Z:96:HIS:HE1	6:Z:121:LEU:HD13	1.80	0.46
7:a:54:ASP:HA	7:a:57:ILE:HG22	1.96	0.46
15:D:322:LEU:HB3	15:D:330:LYS:HE2	1.97	0.46
18:G:61:LEU:HD21	18:G:66:VAL:HG21	1.96	0.46
28:Q:4:LEU:HD21	28:Q:132:HIS:HB2	1.96	0.46
22:k:101:PHE:HE1	29:r:57:ARG:HG2	1.81	0.46
31:t:46:ASN:OD1	31:t:46:ASN:N	2.47	0.46
1:U:16:GLU:OE1	1:U:18:GLN:HG2	2.15	0.46
2:V:153:LYS:O	2:V:157:THR:OG1	2.29	0.46
2:V:471:GLU:HB3	2:V:472:PRO:HD3	1.96	0.46
5:Y:92:GLU:HA	5:Y:100:ILE:HD13	1.98	0.46
7:a:13:SER:HA	7:a:19:PRO:HG3	1.96	0.46
13:B:415:THR:HB	13:B:418:ASP:HB3	1.98	0.46
14:C:170:LYS:C	14:C:172:PRO:HD3	2.40	0.46
15:D:261:ILE:HG12	15:D:306:LYS:HB2	1.95	0.46
18:G:37:LEU:HD23	18:G:81:THR:HG22	1.97	0.46
21:J:61:LYS:HD2	21:J:73:PHE:HZ	1.81	0.46
26:O:113:ILE:HG12	26:O:119:THR:HG22	1.96	0.46
30:S:38:ARG:HH12	31:T:151:ARG:HD3	1.80	0.46
32:f:796:LEU:HD12	32:f:799:VAL:HG11	1.98	0.46
1:U:338:HIS:HD2	1:U:785:PRO:HB2	1.76	0.46
1:U:378:CYS:HB2	1:U:740:GLY:HA2	1.97	0.46
1:U:485:ALA:HB3	1:U:519:VAL:HG12	1.97	0.46
3:W:136:ILE:HD11	3:W:176:SER:HB3	1.98	0.46
5:Y:203:ASP:OD1	5:Y:203:ASP:N	2.46	0.46
6:Z:59:ASP:HB2	8:b:95:LEU:HD11	1.98	0.46
6:Z:72:HIS:HB2	8:b:63:THR:OG1	2.16	0.46
7:a:163:TYR:HE1	7:a:169:HIS:HA	1.79	0.46
9:c:28:ALA:HB1	9:c:180:ASN:HD21	1.80	0.46
9:c:226:MET:C	9:c:228:GLY:H	2.24	0.46
12:A:398:ARG:NH2	13:B:195:GLN:HB2	2.31	0.46
14:C:77:VAL:HG22	14:C:86:LEU:HD22	1.97	0.46
14:C:86:LEU:HD21	14:C:94:LYS:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:54:LEU:HA	15:D:57:GLN:HB2	1.97	0.46
15:D:159:LYS:HD2	15:D:221:HIS:CE1	2.50	0.46
15:D:413:GLU:OE2	18:G:157:ALA:N	2.48	0.46
17:F:283:ILE:HG22	17:F:328:VAL:HG13	1.98	0.46
24:M:37:ILE:HD11	24:M:193:VAL:HG13	1.97	0.46
22:k:227:HIS:ND1	22:k:227:HIS:C	2.74	0.46
23:l:196:ARG:HE	23:l:239:ARG:HH21	1.61	0.46
32:f:193:PRO:C	32:f:208:LEU:HD12	2.40	0.46
1:U:664:GLY:HA2	1:U:698:GLN:HE22	1.81	0.46
2:V:282:ASN:OD1	5:Y:382:LYS:HG3	2.16	0.46
3:W:275:ILE:O	3:W:357:ARG:NE	2.49	0.46
6:Z:34:ARG:HH12	6:Z:102:HIS:CE1	2.34	0.46
13:B:155:LYS:HA	13:B:156:VAL:HA	1.62	0.46
15:D:95:ALA:HB2	15:D:124:LEU:HD21	1.97	0.46
15:D:401:LYS:HA	15:D:404:LYS:HE2	1.97	0.46
22:K:59:MET:HE2	22:K:59:MET:HB3	1.86	0.46
28:Q:12:TYR:HB2	28:Q:182:ILE:HD11	1.96	0.46
28:Q:52:ASP:OD1	29:R:88:TYR:OH	2.31	0.46
32:f:226:TYR:O	32:f:230:CYS:HB3	2.16	0.46
32:f:695:ALA:O	32:f:752:HIS:HB3	2.15	0.46
2:V:137:GLU:HA	2:V:140:ASP:HB2	1.97	0.46
2:V:239:THR:HA	2:V:240:LEU:HA	1.68	0.46
3:W:45:GLU:HA	3:W:96:GLN:HB3	1.98	0.46
3:W:155:GLN:NE2	3:W:161:GLU:HG3	2.31	0.46
3:W:403:PHE:HB3	3:W:416:GLN:HG3	1.97	0.46
9:c:295:ASN:HA	9:c:298:GLN:HG2	1.96	0.46
12:A:318:LEU:HD23	12:A:319:MET:N	2.31	0.46
14:C:69:GLN:H	14:C:118:ASN:HD22	1.63	0.46
14:C:74:GLY:HA3	14:C:87:VAL:HG13	1.97	0.46
15:D:153:MET:HB3	15:D:228:ILE:HD13	1.96	0.46
17:F:128:THR:HG23	17:F:130:GLN:H	1.81	0.46
18:g:116:LYS:NZ	26:o:69:SER:O	2.49	0.46
21:j:220:LEU:HD13	21:j:224:GLU:HB2	1.97	0.46
26:o:1:THR:HG23	26:o:33:LYS:HE3	1.97	0.46
32:f:389:LYS:HD3	32:f:389:LYS:H	1.81	0.46
2:V:196:SER:N	14:C:23:TYR:HD1	2.13	0.46
5:Y:110:TYR:O	5:Y:113:ARG:HB3	2.16	0.46
6:Z:68:TRP:HH2	6:Z:111:LEU:HD22	1.81	0.46
6:Z:181:ASP:OD1	6:Z:181:ASP:N	2.48	0.46
10:d:62:SER:HA	10:d:65:ARG:HG2	1.98	0.46
12:A:368:ILE:HG23	12:A:406:GLU:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:B:392:GLY:O	13:B:395:ILE:HG22	2.16	0.46
13:B:409:GLU:OE1	13:B:413:LYS:HB3	2.16	0.46
13:B:428:TYR:HA	13:B:431:GLN:HB2	1.98	0.46
15:D:366:ARG:HB3	15:D:367:PRO:HD3	1.96	0.46
16:E:119:VAL:HG21	17:F:147:PRO:HD2	1.97	0.46
17:F:366:MET:HE1	17:F:384:LEU:HD22	1.97	0.46
21:J:4:ASP:HB3	22:K:125:GLU:HB3	1.97	0.46
25:N:19:ARG:HE	25:N:26:ILE:HG13	1.80	0.46
25:n:179:ILE:HG12	25:n:184:VAL:HG22	1.98	0.46
30:s:179:PHE:O	30:s:183:ALA:HB2	2.15	0.46
32:f:483:PHE:HE2	32:f:799:VAL:HB	1.69	0.46
2:V:197:THR:C	2:V:199:ASN:H	2.24	0.46
4:X:200:ILE:HG22	4:X:201:TYR:H	1.81	0.46
6:Z:187:LEU:O	6:Z:191:ILE:HD12	2.16	0.46
9:c:75:MET:HE3	9:c:76:PRO:HD2	1.98	0.46
9:c:181:LEU:O	9:c:185:ASN:N	2.43	0.46
12:A:290:GLY:HA2	12:A:291:GLY:HA3	1.56	0.46
16:E:100:LEU:HD23	16:E:107:ILE:HG13	1.97	0.46
19:H:19:LEU:HD13	19:H:22:ILE:HD12	1.97	0.46
19:H:222:THR:OG1	19:H:225:GLU:OE1	2.33	0.46
22:K:221:GLN:OE1	22:K:227:HIS:HD2	1.99	0.46
20:i:170:ALA:O	20:i:174:MET:HB2	2.16	0.46
1:U:469:SER:OG	1:U:472:ILE:HG13	2.16	0.46
2:V:82:LEU:HD22	2:V:82:LEU:HA	1.82	0.46
2:V:291:TYR:OH	11:e:5:LYS:HE3	2.16	0.46
4:X:289:CYS:O	4:X:293:ALA:N	2.49	0.46
5:Y:25:LEU:O	5:Y:29:PRO:HG2	2.16	0.46
7:a:80:ILE:HD12	7:a:83:VAL:HB	1.98	0.46
9:c:154:LYS:HG2	9:c:156:VAL:H	1.81	0.46
12:A:115:VAL:HG13	12:A:117:GLN:H	1.81	0.46
14:C:310:ARG:HA	14:C:311:ILE:HA	1.67	0.46
17:F:298:SER:HB2	17:F:299:GLU:HA	1.97	0.46
19:H:182:LEU:HB3	19:H:186:ASP:HB2	1.98	0.46
21:J:95:ARG:HH22	21:J:101:PRO:HB3	1.81	0.46
20:i:43:VAL:HG12	20:i:216:LEU:HB3	1.98	0.46
24:m:66:LEU:HD13	24:m:214:SER:HB2	1.97	0.46
28:q:11:ASP:N	28:q:11:ASP:OD1	2.48	0.46
28:q:101:ASN:HB3	28:q:132:HIS:CD2	2.50	0.46
31:t:1:THR:N	31:t:105:PRO:O	2.47	0.46
3:W:398:VAL:HA	4:X:341:PRO:HB3	1.98	0.45
5:Y:336:ARG:NH1	11:e:56:LEU:HB3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:a:116:THR:HA	7:a:158:LEU:HD21	1.98	0.45
7:a:309:LEU:H	7:a:309:LEU:HD12	1.80	0.45
13:B:177:GLU:CB	13:B:178:LYS:CA	2.93	0.45
13:B:254:GLU:HB2	13:B:288:ASP:HB2	1.98	0.45
15:D:49:GLN:O	15:D:53:PHE:N	2.40	0.45
17:F:145:LEU:HG	17:F:146:LYS:H	1.81	0.45
17:F:221:LYS:HA	17:F:327:LYS:HG3	1.97	0.45
17:F:344:ARG:HB3	17:F:347:ARG:HB2	1.99	0.45
23:L:157:ARG:HD2	23:L:176:MET:HE3	1.97	0.45
24:M:136:MET:HE3	24:M:148:LEU:HD11	1.98	0.45
24:M:198:TYR:CG	24:M:239:ALA:HB1	2.52	0.45
28:Q:170:ARG:NH1	28:q:27:GLN:O	2.49	0.45
29:R:9:ARG:NH2	29:R:146:ASP:OD1	2.40	0.45
29:r:122:SER:OG	29:r:123:GLY:N	2.49	0.45
32:f:353:LEU:H	32:f:387:GLN:CG	2.29	0.45
32:f:420:TRP:CG	32:f:421:ASP:H	2.34	0.45
32:f:675:PHE:O	32:f:679:LEU:CB	2.59	0.45
4:X:244:SER:O	4:X:248:ILE:N	2.45	0.45
5:Y:286:TRP:O	5:Y:287:LEU:HG	2.16	0.45
6:Z:45:LYS:HG3	6:Z:46:LYS:H	1.80	0.45
7:a:31:LYS:HG3	8:b:177:PRO:HD3	1.99	0.45
7:a:261:LEU:HD11	7:a:268:LEU:HD12	1.98	0.45
12:A:279:ALA:HB2	13:B:310:LEU:HD23	1.97	0.45
12:A:420:TYR:CE2	13:B:350:LYS:HG2	2.51	0.45
14:C:203:VAL:O	14:C:207:THR:OG1	2.22	0.45
15:D:276:ASP:O	15:D:280:GLY:N	2.49	0.45
16:E:232:MET:HB2	16:E:277:MET:HG2	1.97	0.45
28:Q:4:LEU:HD13	28:Q:102:LEU:HD13	1.97	0.45
24:m:74:GLY:HA3	24:m:224:HIS:CE1	2.50	0.45
27:p:138:VAL:HB	27:p:146:MET:HE3	1.98	0.45
32:f:378:ASN:CB	32:f:391:LEU:CD1	2.94	0.45
32:f:475:ASN:O	32:f:478:ARG:HB3	2.15	0.45
32:f:664:GLU:O	32:f:665:GLU:C	2.57	0.45
1:U:377:HIS:O	1:U:380:THR:HG22	2.17	0.45
2:V:290:TYR:OH	2:V:294:ARG:NH2	2.49	0.45
3:W:23:THR:HA	3:W:26:GLN:HB2	1.98	0.45
4:X:396:THR:HG21	5:Y:365:GLN:HB3	1.98	0.45
8:b:164:ASP:H	8:b:165:GLY:HA2	1.79	0.45
9:c:33:ILE:HA	9:c:69:VAL:HG13	1.97	0.45
13:B:428:TYR:HD1	20:I:170:ALA:HA	1.64	0.45
13:B:438:LEU:HD13	20:I:155:ASN:HD21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:E:230:ILE:HB	16:E:275:MET:HA	1.98	0.45
22:K:88:LEU:HD22	22:K:116:VAL:HG13	1.99	0.45
22:K:216:GLU:CA	22:K:229:PHE:CE2	2.99	0.45
27:P:190:ILE:HG22	27:P:195:ILE:HG23	1.97	0.45
28:Q:3:TYR:HD1	28:Q:135:GLY:HA3	1.80	0.45
22:k:41:GLN:NE2	22:k:151:PRO:O	2.50	0.45
32:f:178:LYS:NZ	32:f:215:ASP:O	2.42	0.45
32:f:541:THR:O	32:f:545:LYS:CB	2.63	0.45
1:U:794:ASP:OD1	1:U:795:LEU:N	2.50	0.45
2:V:89:LYS:HD3	2:V:92:ARG:HH11	1.82	0.45
3:W:128:LEU:HD23	3:W:147:LYS:HZ2	1.81	0.45
5:Y:349:LYS:O	5:Y:350:VAL:HG22	2.16	0.45
13:B:151:LEU:HD11	13:B:163:LEU:HD13	1.96	0.45
14:C:285:ALA:HA	14:C:286:THR:HA	1.78	0.45
15:D:385:LEU:HD22	15:D:402:ALA:HB2	1.97	0.45
17:F:437:TYR:CB	22:K:28:ILE:HG12	2.38	0.45
20:I:155:ASN:HA	21:J:81:ARG:HH22	1.81	0.45
22:K:225:ASN:HA	22:K:226:PHE:HA	1.50	0.45
25:N:96:ALA:HB1	25:N:98:ILE:HG12	1.99	0.45
29:r:56:GLU:OE2	29:r:99:THR:OG1	2.33	0.45
32:f:376:PHE:CZ	32:f:798:THR:HG22	2.50	0.45
2:V:318:GLN:O	2:V:319:HIS:ND1	2.50	0.45
3:W:55:ARG:NH1	3:W:78:LYS:HG3	2.32	0.45
3:W:253:THR:HB	3:W:254:PRO:HD3	1.97	0.45
4:X:417:LYS:HG2	6:Z:283:ARG:NH1	2.31	0.45
6:Z:14:LEU:HD23	9:c:43:LYS:HD3	1.96	0.45
6:Z:128:PRO:HB2	9:c:219:ASN:HD22	1.82	0.45
7:a:125:ILE:HG22	7:a:126:GLY:C	2.42	0.45
10:d:184:LYS:HA	10:d:185:ALA:HA	1.75	0.45
12:A:250:VAL:O	17:F:259:MET:N	2.50	0.45
13:B:126:SER:HA	13:B:127:VAL:HA	1.51	0.45
13:B:176:VAL:CG1	14:C:283:PHE:CE1	2.93	0.45
13:B:201:VAL:HB	13:B:241:ASN:HD21	1.82	0.45
17:F:288:LEU:HD12	17:F:291:ILE:HD11	1.98	0.45
26:O:163:ILE:HG23	26:O:170:GLY:HA2	1.99	0.45
20:i:143:TYR:HB2	20:i:146:GLN:HE21	1.81	0.45
27:p:36:THR:OG1	27:p:38:ASP:OD1	2.31	0.45
32:f:281:ILE:O	32:f:285:CYS:HB3	2.15	0.45
32:f:533:ASP:OD1	32:f:565:ASN:ND2	2.50	0.45
32:f:688:ARG:CA	32:f:745:LEU:HD22	2.44	0.45
1:U:106:ASP:HA	1:U:109:THR:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:242:LEU:HD13	1:U:324:LYS:HD2	1.99	0.45
2:V:455:LYS:HD2	2:V:457:TYR:CE2	2.52	0.45
5:Y:301:ILE:O	5:Y:305:SER:N	2.45	0.45
6:Z:242:LEU:C	6:Z:244:GLU:H	2.25	0.45
7:a:287:ASN:HA	7:a:288:HIS:C	2.41	0.45
12:A:292:ASP:OD1	13:B:303:ARG:NH1	2.49	0.45
12:A:395:PHE:HA	12:A:398:ARG:HB2	1.99	0.45
12:A:409:PHE:O	12:A:413:VAL:HG23	2.16	0.45
16:E:372:ARG:NH1	24:M:171:ALA:H	2.09	0.45
16:E:372:ARG:NH1	24:M:171:ALA:CA	2.79	0.45
17:F:383:GLU:OE1	23:L:170:THR:HG23	2.17	0.45
18:G:144:ASP:OD2	26:O:72:ARG:NH2	2.44	0.45
21:J:98:VAL:HG13	29:R:78:ALA:HB2	1.99	0.45
23:l:80:ASP:HB3	23:l:128:TYR:HD1	1.82	0.45
31:t:4:PRO:HG3	31:t:107:TRP:CE2	2.52	0.45
31:t:136:SER:HB2	31:t:150:LEU:HD13	1.97	0.45
32:f:316:ASP:HA	32:f:319:GLU:HG2	1.99	0.45
2:V:275:VAL:HB	2:V:277:PRO:HD3	1.98	0.45
3:W:136:ILE:O	3:W:136:ILE:HG23	2.17	0.45
3:W:259:GLU:HB3	3:W:263:TRP:HB2	1.99	0.45
3:W:327:GLU:HA	3:W:330:LYS:HB3	1.98	0.45
6:Z:136:GLU:OE2	6:Z:157:HIS:ND1	2.34	0.45
13:B:96:ARG:HH22	14:C:84:LYS:HG3	1.82	0.45
14:C:368:MET:HA	14:C:371:LEU:HB3	1.99	0.45
15:D:89:ILE:O	15:D:106:THR:OG1	2.29	0.45
15:D:130:VAL:HA	15:D:142:VAL:HA	1.99	0.45
15:D:207:PRO:HG2	15:D:312:ASN:HA	1.99	0.45
21:J:18:GLN:O	21:J:22:ALA:HB3	2.17	0.45
28:Q:19:ARG:HB3	28:Q:31:ASP:HA	1.97	0.45
28:Q:20:VAL:O	28:Q:34:LYS:NZ	2.46	0.45
32:f:392:THR:HB	32:f:414:LEU:HD22	1.97	0.45
32:f:664:GLU:C	32:f:665:GLU:O	2.59	0.45
1:U:54:PHE:CZ	1:U:56:SER:HB2	2.52	0.45
1:U:156:GLU:OE2	15:D:45:LYS:HE2	2.16	0.45
1:U:510:GLU:HA	1:U:547:GLY:HA3	1.98	0.45
2:V:179:LYS:HD3	2:V:214:HIS:HA	1.97	0.45
3:W:431:LYS:HA	3:W:435:LEU:HD13	1.97	0.45
12:A:160:THR:O	12:A:162:THR:N	2.49	0.45
13:B:364:ILE:HG23	13:B:368:HIS:CE1	2.52	0.45
16:E:168:LYS:O	16:E:275:MET:HG2	2.17	0.45
16:E:205:ASP:OD2	16:E:211:SER:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:91:SER:OG	17:F:125:LYS:O	2.21	0.45
17:F:300:LYS:HE3	17:F:304:ARG:HB3	1.98	0.45
29:R:56:GLU:OE2	29:R:99:THR:OG1	2.29	0.45
20:i:106:PRO:HD2	20:i:109:GLN:HE21	1.81	0.45
28:q:13:VAL:HG11	28:q:105:ALA:HB1	1.99	0.45
32:f:125:ILE:HA	32:f:129:LEU:HD12	1.98	0.45
32:f:608:LYS:HA	32:f:611:GLN:HB3	1.99	0.45
32:f:675:PHE:CG	32:f:694:LEU:HD23	2.51	0.45
32:f:688:ARG:HG3	32:f:745:LEU:HB3	1.99	0.45
1:U:328:ILE:HG13	1:U:329:LEU:N	2.31	0.45
1:U:500:ASN:HA	1:U:503:GLN:HG2	1.99	0.45
2:V:209:LYS:O	2:V:212:TYR:HB2	2.17	0.45
3:W:263:TRP:HH2	3:W:295:LYS:HG3	1.80	0.45
5:Y:349:LYS:C	5:Y:351:ASN:H	2.23	0.45
9:c:226:MET:O	9:c:228:GLY:N	2.50	0.45
12:A:206:ILE:HG12	17:F:401:VAL:HA	1.99	0.45
14:C:167:LEU:HD22	14:C:175:PHE:CZ	2.52	0.45
14:C:232:ARG:NE	14:C:275:GLU:OE1	2.42	0.45
20:I:95:GLN:HG2	27:P:73:LEU:HG	1.98	0.45
31:T:24:ALA:H	31:T:42:ILE:HD11	1.80	0.45
23:l:189:LYS:HZ3	23:l:193:ARG:HH22	1.63	0.45
32:f:354:GLU:HG3	32:f:355:ASN:H	1.82	0.45
1:U:586:VAL:HG11	1:U:601:ARG:HH12	1.81	0.45
2:V:32:PRO:O	2:V:36:GLU:HB3	2.17	0.45
2:V:280:ALA:HB1	2:V:281:ASN:ND2	2.32	0.45
5:Y:301:ILE:HA	5:Y:304:TYR:HB2	1.99	0.45
7:a:33:LEU:HD13	7:a:36:GLN:HB2	1.99	0.45
7:a:161:LYS:HA	7:a:164:GLN:HG2	1.98	0.45
7:a:243:GLY:HA3	7:a:244:ASN:HA	1.61	0.45
9:c:40:LYS:O	9:c:44:HIS:HB3	2.17	0.45
10:d:225:PHE:HA	10:d:226:ALA:HA	1.73	0.45
12:A:363:SER:HB2	12:A:403:ILE:HG22	1.99	0.45
12:A:419:SER:HA	12:A:422:LYS:HE3	1.99	0.45
13:B:139:VAL:HA	13:B:140:ASP:CB	2.46	0.45
14:C:117:ARG:O	14:C:121:TYR:HA	2.17	0.45
16:E:236:ASP:OD1	16:E:236:ASP:N	2.50	0.45
18:G:230:LEU:HD23	18:G:234:GLU:HG3	1.99	0.45
21:J:116:GLN:O	21:J:119:THR:OG1	2.35	0.45
21:J:179:GLU:O	21:J:182:GLU:N	2.48	0.45
21:J:180:ALA:HA	21:J:181:ILE:HA	1.60	0.45
23:L:225:ASP:OD1	23:L:225:ASP:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:g:141:ILE:HG22	18:g:151:VAL:HG22	1.99	0.45
19:h:91:ARG:HH12	26:o:69:SER:HA	1.82	0.45
28:q:17:SER:OG	28:q:179:SER:OG	2.30	0.45
32:f:45:LEU:HD22	32:f:86:THR:HG21	1.99	0.45
32:f:509:LYS:HB3	32:f:514:VAL:HG21	1.99	0.45
1:U:561:GLU:HG2	1:U:562:GLU:H	1.82	0.44
4:X:406:ASN:ND2	9:c:264:LYS:HD2	2.31	0.44
12:A:206:ILE:HA	17:F:373:MET:SD	2.57	0.44
15:D:406:VAL:HA	15:D:407:ILE:HA	1.51	0.44
17:F:144:LYS:HA	17:F:145:LEU:HA	1.71	0.44
23:l:40:SER:HB3	23:l:187:LEU:HD22	1.98	0.44
23:l:109:VAL:HG21	23:l:145:PHE:HD2	1.81	0.44
32:f:357:ARG:NH2	32:f:754:LYS:HG3	2.33	0.44
1:U:20:LYS:HD2	1:U:48:LEU:HD11	1.99	0.44
1:U:173:VAL:N	1:U:174:PRO:HD3	2.32	0.44
2:V:203:LEU:O	2:V:207:ALA:N	2.25	0.44
2:V:486:ILE:HG12	5:Y:381:GLN:HE21	1.83	0.44
3:W:403:PHE:HD2	3:W:416:GLN:HA	1.83	0.44
5:Y:112:CYS:SG	5:Y:120:ALA:HB2	2.58	0.44
6:Z:26:ILE:HA	6:Z:29:VAL:HG12	1.99	0.44
6:Z:182:THR:N	6:Z:183:THR:HA	2.30	0.44
6:Z:252:LYS:HE2	9:c:305:ASP:HB3	2.00	0.44
9:c:144:VAL:HB	9:c:158:ASP:HB3	1.99	0.44
10:d:147:SER:OG	10:d:150:LYS:N	2.51	0.44
10:d:226:ALA:HA	10:d:227:SER:HA	1.69	0.44
13:B:324:ASP:HB2	13:B:326:LYS:HG2	1.98	0.44
20:I:109:GLN:OE1	28:Q:71:ASN:ND2	2.38	0.44
24:M:74:GLY:HA3	24:M:224:HIS:CE1	2.52	0.44
31:T:124:TYR:HB2	31:T:137:LEU:HD13	1.99	0.44
30:s:198:VAL:HG22	30:s:203:ILE:HG12	1.99	0.44
1:U:713:TYR:HB2	1:U:734:GLN:HE21	1.83	0.44
2:V:419:LEU:HD23	2:V:458:VAL:HG23	1.99	0.44
2:V:495:ARG:HB2	14:C:38:LYS:CD	2.47	0.44
9:c:249:LEU:HA	9:c:252:ALA:HB3	1.98	0.44
11:e:46:ASP:HA	11:e:49:GLU:HB3	1.99	0.44
12:A:105:ASP:N	12:A:105:ASP:OD1	2.50	0.44
14:C:76:VAL:O	14:C:111:ASN:N	2.44	0.44
16:E:128:GLY:HA2	16:E:129:ASN:HB2	2.00	0.44
16:E:349:GLU:HG2	16:E:374:VAL:HG21	1.99	0.44
22:k:91:LYS:HD2	22:k:119:LEU:HD21	1.99	0.44
23:l:50:LYS:N	23:l:209:ASN:O	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:p:116:THR:O	27:p:192:LYS:NZ	2.48	0.44
28:q:18:ASP:HA	28:q:178:PHE:HD1	1.83	0.44
3:W:306:LEU:O	3:W:310:THR:HG22	2.17	0.44
5:Y:41:LEU:HD22	5:Y:63:TRP:HZ2	1.82	0.44
7:a:100:THR:HA	7:a:103:LYS:HE2	1.98	0.44
9:c:161:ARG:NH1	9:c:162:LEU:O	2.50	0.44
9:c:191:ALA:HA	9:c:194:HIS:CE1	2.52	0.44
14:C:154:LEU:O	14:C:157:GLN:N	2.51	0.44
14:C:257:SER:O	14:C:258:ARG:HB2	2.17	0.44
16:E:149:ILE:O	16:E:152:PRO:HD2	2.17	0.44
22:k:235:GLU:HA	22:k:238:ILE:HD12	1.98	0.44
32:f:286:LYS:HD3	32:f:326:LEU:HD23	2.00	0.44
1:U:374:SER:HB2	1:U:410:VAL:HG11	1.99	0.44
2:V:173:ILE:O	2:V:177:ASN:N	2.42	0.44
2:V:182:LYS:NZ	2:V:210:CYS:HB2	2.33	0.44
2:V:439:ALA:HB1	10:d:181:CYS:O	2.17	0.44
3:W:416:GLN:HB3	3:W:417:ARG:CA	2.42	0.44
5:Y:300:ARG:HH12	11:e:63:HIS:CG	2.36	0.44
8:b:156:PHE:O	8:b:160:LEU:HB2	2.17	0.44
10:d:65:ARG:HG3	10:d:67:ASP:H	1.82	0.44
10:d:160:ALA:N	10:d:161:GLU:HA	2.32	0.44
10:d:216:VAL:HG11	10:d:223:TYR:HB2	2.00	0.44
12:A:221:GLY:C	12:A:223:THR:H	2.26	0.44
12:A:261:PHE:O	12:A:265:ARG:HG3	2.17	0.44
12:A:312:ARG:HA	12:A:313:GLY:HA2	1.58	0.44
12:A:328:ASP:HB3	12:A:329:PRO:HD3	1.98	0.44
13:B:388:ASP:HA	13:B:389:ASP:HA	1.72	0.44
17:F:356:MET:HG2	17:F:390:ASP:HA	1.99	0.44
22:K:48:LEU:HD21	22:K:77:ALA:HB2	2.00	0.44
24:M:92:ARG:HH21	31:T:73:ASP:HA	1.81	0.44
29:R:141:ARG:NH2	28:q:162:LYS:O	2.50	0.44
2:V:99:ARG:NH1	2:V:150:ARG:HH21	2.16	0.44
2:V:156:SER:HB2	2:V:160:LEU:HD12	1.99	0.44
2:V:244:ALA:C	2:V:246:GLY:H	2.25	0.44
2:V:323:GLY:HA2	2:V:326:GLN:HB2	1.99	0.44
2:V:492:LYS:CE	14:C:38:LYS:NZ	2.71	0.44
3:W:88:MET:SD	3:W:96:GLN:NE2	2.90	0.44
7:a:342:ASP:HB2	7:a:345:GLN:HG2	1.99	0.44
10:d:201:ASN:N	10:d:201:ASN:OD1	2.50	0.44
13:B:438:LEU:CD1	20:I:155:ASN:HD21	2.20	0.44
14:C:285:ALA:HB1	14:C:286:THR:HB	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:E:129:ASN:H	16:E:190:GLN:HG2	1.81	0.44
17:F:228:PRO:O	17:F:231:THR:HG23	2.16	0.44
17:F:437:TYR:HB3	22:K:24:VAL:HG12	2.00	0.44
20:I:178:ASP:OD2	20:I:195:LYS:NZ	2.39	0.44
19:h:167:TYR:O	19:h:171:LYS:CB	2.62	0.44
32:f:471:LEU:HD11	32:f:509:LYS:HE2	2.00	0.44
1:U:470:ASN:OD1	1:U:471:ASP:HA	2.18	0.44
2:V:291:TYR:OH	11:e:4:LYS:HD2	2.18	0.44
4:X:245:PRO:HA	4:X:248:ILE:HG22	2.00	0.44
6:Z:241:SER:HA	6:Z:242:LEU:HA	1.40	0.44
7:a:171:SER:O	7:a:175:ASP:N	2.45	0.44
7:a:212:ASN:OD1	7:a:212:ASN:N	2.45	0.44
9:c:256:ASN:OD1	9:c:291:LEU:HD22	2.17	0.44
12:A:427:PRO:HB2	12:A:429:TYR:CD1	2.50	0.44
13:B:176:VAL:CG1	14:C:283:PHE:CE2	2.74	0.44
14:C:72:TYR:N	14:C:116:LEU:O	2.50	0.44
15:D:82:ILE:HA	15:D:83:GLN:HA	1.64	0.44
16:E:155:ASN:HB3	16:E:158:LEU:HG	1.99	0.44
17:F:100:ASP:OD1	17:F:100:ASP:N	2.47	0.44
17:F:120:LYS:HG2	17:F:136:VAL:HG21	2.00	0.44
22:k:99:HIS:HB2	22:k:107:MET:HE3	1.99	0.44
27:p:123:SER:HB3	27:p:137:VAL:HB	2.00	0.44
31:t:148:PRO:O	31:t:152:GLU:CB	2.65	0.44
32:f:130:ALA:O	32:f:134:SER:CB	2.64	0.44
1:U:26:LYS:O	1:U:30:VAL:HG22	2.18	0.44
2:V:221:LEU:HD12	2:V:222:ASP:H	1.82	0.44
2:V:324:PHE:CE1	11:e:7:PRO:HA	2.53	0.44
3:W:247:TYR:HA	3:W:250:ILE:HG23	1.98	0.44
3:W:326:MET:O	3:W:330:LYS:N	2.48	0.44
6:Z:199:LYS:HA	6:Z:202:ASN:HD21	1.83	0.44
7:a:245:VAL:HA	7:a:246:GLU:C	2.43	0.44
8:b:52:ILE:HD13	8:b:60:VAL:HG23	2.00	0.44
12:A:433:ASN:OD1	22:K:10:ARG:NH2	2.51	0.44
15:D:96:VAL:HG23	15:D:97:ASP:OD1	2.18	0.44
16:E:281:ARG:NH2	17:F:296:PHE:HA	2.32	0.44
17:F:81:LYS:O	17:F:85:THR:HG22	2.18	0.44
27:p:171:MET:O	27:p:175:VAL:HB	2.17	0.44
30:s:55:SER:OG	30:s:56:GLY:N	2.48	0.44
32:f:412:ALA:HA	32:f:447:ALA:HB2	2.00	0.44
32:f:698:SER:OG	32:f:716:ASP:OD1	2.36	0.44
1:U:340:GLN:HG3	1:U:880:ASN:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W:13:ILE:HG22	3:W:54:THR:HG21	1.99	0.44
6:Z:171:GLY:HA3	9:c:38:LEU:HD11	2.00	0.44
7:a:274:LEU:HB2	7:a:319:LEU:HD21	2.00	0.44
12:A:271:LEU:HA	12:A:315:ILE:HD13	2.00	0.44
13:B:111:THR:OG1	13:B:124:SER:O	2.21	0.44
21:J:165:ALA:O	21:J:169:ARG:CB	2.66	0.44
22:K:220:VAL:HG23	22:K:226:PHE:HE2	1.83	0.44
27:P:159:ASP:N	27:P:159:ASP:OD1	2.48	0.44
19:h:122:THR:HG22	19:h:129:PRO:HB3	2.00	0.44
20:i:76:VAL:HG23	20:i:134:LEU:HB3	2.00	0.44
20:i:136:TYR:HB2	20:i:148:TYR:HB2	2.00	0.44
20:i:220:ASN:HA	20:i:221:GLY:HA2	1.66	0.44
32:f:479:LEU:HD23	32:f:513:GLU:CB	2.42	0.44
32:f:623:LYS:O	32:f:627:GLU:HB3	2.18	0.44
1:U:563:ALA:O	1:U:567:ILE:HG12	2.18	0.43
1:U:804:SER:HB3	1:U:839:ALA:HB3	1.99	0.43
2:V:167:LEU:HD11	2:V:171:VAL:HB	2.00	0.43
4:X:264:PRO:C	4:X:266:ASP:H	2.26	0.43
4:X:417:LYS:HZ3	6:Z:283:ARG:HH22	1.64	0.43
5:Y:191:ILE:HD12	5:Y:191:ILE:HA	1.91	0.43
5:Y:286:TRP:CD1	5:Y:287:LEU:HD23	2.53	0.43
5:Y:311:TYR:HD2	5:Y:314:LEU:HD12	1.83	0.43
7:a:185:ILE:H	7:a:185:ILE:HG13	1.57	0.43
9:c:287:HIS:O	9:c:291:LEU:HG	2.18	0.43
12:A:310:ASP:HA	12:A:311:PRO:HA	1.58	0.43
13:B:277:HIS:HB3	13:B:279:PRO:HD2	2.00	0.43
14:C:25:LEU:HD23	15:D:47:LEU:HB2	2.00	0.43
15:D:147:ALA:O	16:E:62:LYS:HD2	2.18	0.43
16:E:374:VAL:O	16:E:378:LYS:HG2	2.18	0.43
17:F:421:MET:HA	17:F:424:ILE:HB	1.99	0.43
31:T:9:THR:OG1	31:T:10:SER:N	2.47	0.43
28:q:57:ALA:O	28:q:61:GLN:HB2	2.17	0.43
1:U:181:LEU:HB3	1:U:218:GLN:NE2	2.33	0.43
2:V:80:LYS:CB	2:V:81:GLN:CB	2.92	0.43
3:W:98:LYS:HD2	3:W:140:ILE:HG13	1.94	0.43
4:X:187:ARG:O	4:X:191:THR:N	2.45	0.43
6:Z:205:LEU:HA	6:Z:208:ILE:HG22	1.99	0.43
6:Z:287:LYS:HB2	6:Z:287:LYS:HE3	1.79	0.43
7:a:144:ASN:HA	7:a:145:LEU:HA	1.58	0.43
13:B:173:VAL:HG23	13:B:174:MET:H	1.83	0.43
13:B:300:GLY:HA3	13:B:301:GLY:HA2	1.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:235:PHE:HD1	14:C:276:LEU:HG	1.83	0.43
15:D:91:GLN:N	15:D:104:GLY:O	2.33	0.43
15:D:105:SER:HB3	15:D:111:TYR:CE2	2.53	0.43
17:F:364:ARG:O	17:F:368:ILE:HG12	2.18	0.43
19:H:167:TYR:O	19:H:171:LYS:CB	2.57	0.43
20:I:62:SER:OG	20:I:65:ILE:O	2.22	0.43
22:K:49:ALA:HB1	22:K:202:LEU:HD11	2.00	0.43
21:j:32:ALA:HB3	21:j:161:ILE:HD11	2.00	0.43
24:m:152:ASP:OD1	24:m:156:VAL:N	2.51	0.43
26:o:212:LEU:HD21	27:p:201:LYS:HD2	1.99	0.43
6:Z:91:ILE:H	6:Z:91:ILE:HG13	1.45	0.43
6:Z:176:LEU:C	6:Z:178:ASP:H	2.27	0.43
9:c:32:TYR:HB3	9:c:208:ARG:HD3	2.00	0.43
9:c:40:LYS:HE3	9:c:43:LYS:HZ1	1.82	0.43
12:A:250:VAL:HG11	12:A:297:ARG:NH2	2.34	0.43
16:E:76:GLY:N	16:E:77:PRO:HD2	2.32	0.43
16:E:112:PRO:O	16:E:113:ARG:HG3	2.18	0.43
16:E:222:ALA:HB1	16:E:228:CYS:SG	2.58	0.43
16:E:327:ASP:C	16:E:364:GLN:HE22	2.23	0.43
16:E:383:LYS:HG3	16:E:384:LEU:HD12	2.00	0.43
17:F:268:VAL:HA	17:F:271:ALA:HB3	1.99	0.43
18:G:185:LYS:HG3	18:G:187:PHE:H	1.84	0.43
28:Q:199:GLN:HA	28:q:197:PRO:HD2	1.99	0.43
29:R:37:ILE:HG23	29:R:60:ALA:HB2	2.00	0.43
20:i:216:LEU:HD12	20:i:225:ILE:HG12	2.00	0.43
22:k:195:ILE:O	22:k:198:SER:OG	2.30	0.43
25:n:14:LEU:HD11	25:n:101:ALA:HB3	2.00	0.43
26:o:113:ILE:HG12	26:o:119:THR:HG22	2.00	0.43
32:f:22:GLY:O	32:f:26:GLU:CB	2.66	0.43
32:f:303:VAL:HG22	32:f:339:ILE:HA	2.00	0.43
32:f:380:PHE:CD2	32:f:380:PHE:O	2.70	0.43
32:f:664:GLU:CB	32:f:696:LEU:HG	2.45	0.43
1:U:428:PRO:HD2	1:U:464:GLN:NE2	2.32	0.43
3:W:86:ASN:HD22	3:W:88:MET:HG3	1.83	0.43
6:Z:33:LYS:HE3	6:Z:33:LYS:HB3	1.79	0.43
7:a:208:GLU:HG2	7:a:271:LYS:HD2	2.01	0.43
7:a:308:GLU:OE1	7:a:308:GLU:N	2.40	0.43
9:c:53:VAL:HG12	9:c:77:GLN:HG2	2.00	0.43
9:c:150:SER:OG	9:c:154:LYS:HB3	2.18	0.43
10:d:120:GLU:O	10:d:123:PRO:HD3	2.18	0.43
12:A:83:ASP:HB2	13:B:102:LEU:HD23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:237:PHE:HB2	12:A:271:LEU:HB2	2.01	0.43
13:B:107:MET:HB2	13:B:153:ASN:HA	1.99	0.43
13:B:285:ASP:OD2	13:B:286:GLU:HG2	2.18	0.43
16:E:313:LEU:HD21	16:E:328:TYR:CD2	2.54	0.43
17:F:125:LYS:HD2	17:F:131:THR:HG23	2.00	0.43
19:h:123:GLN:O	20:i:127:LYS:NZ	2.45	0.43
24:m:201:HIS:HE1	24:m:206:ASP:HB2	1.83	0.43
27:p:148:GLY:O	27:p:152:SER:CB	2.66	0.43
31:t:9:THR:OG1	31:t:10:SER:N	2.51	0.43
32:f:376:PHE:CZ	32:f:416:MET:CE	2.95	0.43
32:f:446:LEU:HD13	32:f:480:GLY:HA2	2.00	0.43
2:V:496:PHE:HE1	14:C:34:ILE:CG2	2.28	0.43
3:W:49:SER:O	3:W:53:GLN:N	2.51	0.43
3:W:370:TYR:OH	3:W:373:ILE:HD12	2.18	0.43
10:d:52:ARG:O	10:d:56:GLU:N	2.47	0.43
13:B:139:VAL:HB	13:B:141:LYS:N	2.34	0.43
14:C:73:VAL:HB	15:D:110:ASN:HB2	1.99	0.43
18:G:148:GLY:O	18:G:150:GLN:NE2	2.52	0.43
22:K:225:ASN:HB2	22:K:226:PHE:CE1	2.53	0.43
24:m:35:THR:H	24:m:166:GLY:HA3	1.84	0.43
28:q:171:PHE:HB3	28:q:173:LEU:H	1.83	0.43
32:f:343:LYS:HZ2	32:f:804:LEU:HD23	1.83	0.43
32:f:646:MET:HA	32:f:649:HIS:HD1	1.82	0.43
1:U:181:LEU:HB3	1:U:218:GLN:HE22	1.84	0.43
1:U:465:LEU:HA	1:U:473:VAL:HG11	1.99	0.43
3:W:444:HIS:HD2	3:W:448:LYS:NZ	2.16	0.43
5:Y:108:ALA:HA	5:Y:111:LEU:HG	2.00	0.43
6:Z:250:TYR:O	6:Z:254:ASN:HB2	2.18	0.43
7:a:308:GLU:HB3	7:a:312:MET:HE2	2.00	0.43
11:e:6:GLN:HG2	11:e:7:PRO:HD3	2.00	0.43
13:B:320:ASP:OD1	13:B:320:ASP:N	2.52	0.43
13:B:437:GLY:N	20:I:25:MET:HE1	2.04	0.43
14:C:217:SER:N	14:C:218:GLU:HB3	2.34	0.43
15:D:392:TYR:CD2	15:D:393:ILE:HG13	2.53	0.43
17:F:189:GLY:HA3	17:F:364:ARG:HB3	2.00	0.43
17:F:430:LYS:O	17:F:431:LYS:HG3	2.18	0.43
18:G:237:ALA:O	18:G:241:ALA:CB	2.65	0.43
20:I:102:GLN:HG2	28:Q:82:ASN:ND2	2.34	0.43
27:P:26:ARG:CB	27:P:39:PHE:O	2.64	0.43
29:r:41:LEU:HD23	29:r:103:GLY:HA3	2.00	0.43
32:f:645:ASP:O	32:f:649:HIS:ND1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:338:HIS:CE1	1:U:787:CYS:HB3	2.54	0.43
1:U:457:ILE:HG23	1:U:460:TYR:HB3	1.99	0.43
2:V:475:ALA:O	2:V:479:ARG:HG2	2.19	0.43
3:W:66:ILE:HG23	3:W:67:LEU:HB2	2.01	0.43
3:W:183:VAL:HA	3:W:186:ILE:HG22	2.00	0.43
4:X:258:LYS:HD2	4:X:294:SER:OG	2.18	0.43
4:X:356:LEU:HD11	4:X:360:ASP:OD1	2.19	0.43
4:X:378:LEU:HG	4:X:385:LEU:HD13	2.01	0.43
6:Z:67:VAL:HG13	8:b:92:VAL:HG23	2.00	0.43
6:Z:191:ILE:HD11	7:a:375:LEU:HD11	2.01	0.43
7:a:203:ALA:HA	7:a:206:LEU:HD12	2.00	0.43
13:B:437:GLY:N	20:I:25:MET:CE	2.67	0.43
14:C:25:LEU:O	14:C:29:GLU:N	2.43	0.43
14:C:161:ILE:HD13	14:C:186:VAL:HG21	2.00	0.43
17:F:191:LEU:HG	17:F:194:GLN:HE21	1.84	0.43
17:F:204:LEU:HB2	17:F:212:PHE:HZ	1.84	0.43
31:T:27:LEU:HD11	31:T:34:ALA:HB1	2.01	0.43
22:k:101:PHE:CE1	29:r:57:ARG:HG2	2.53	0.43
32:f:282:PHE:HE2	32:f:317:LEU:HD21	1.83	0.43
32:f:283:THR:O	32:f:287:ASP:HB2	2.18	0.43
32:f:664:GLU:HA	32:f:697:ILE:CA	2.46	0.43
32:f:690:VAL:O	32:f:694:LEU:HB2	2.18	0.43
1:U:347:ASN:HB3	1:U:813:TYR:HB2	2.01	0.43
1:U:669:ILE:HG12	1:U:694:ILE:HG21	2.00	0.43
2:V:174:PHE:HA	2:V:177:ASN:HB2	2.00	0.43
3:W:70:VAL:HA	3:W:73:MET:HE3	1.99	0.43
3:W:200:ILE:O	3:W:204:ILE:HG12	2.19	0.43
3:W:343:SER:HB2	3:W:346:GLU:HB3	2.00	0.43
4:X:377:ILE:HG12	5:Y:312:ARG:HB3	2.01	0.43
6:Z:237:LEU:HB2	6:Z:239:ASP:OD1	2.19	0.43
9:c:229:LEU:O	9:c:230:THR:OG1	2.23	0.43
9:c:272:ILE:HB	9:c:274:ASN:HA	2.01	0.43
10:d:135:HIS:HB3	10:d:136:PRO:HD3	2.00	0.43
12:A:385:ILE:HA	12:A:388:VAL:HG23	2.00	0.43
13:B:324:ASP:OD1	13:B:324:ASP:N	2.51	0.43
13:B:358:GLU:OE2	21:J:200:GLN:HA	2.19	0.43
15:D:414:HIS:HE1	19:H:79:MET:HE1	1.84	0.43
16:E:57:VAL:HG12	16:E:111:LEU:HD21	2.00	0.43
17:F:439:ALA:O	23:L:77:LEU:CB	2.62	0.43
21:J:48:LYS:H	21:J:205:ASN:HB3	1.84	0.43
23:L:109:VAL:HG21	23:L:145:PHE:HD2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:S:28:ARG:HB2	30:S:190:GLY:HA3	2.00	0.43
20:i:63:GLU:CD	20:i:64:LYS:H	2.26	0.43
22:k:218:ALA:HA	22:k:229:PHE:CB	2.49	0.43
32:f:122:ALA:HB1	32:f:126:ILE:HD12	2.01	0.43
1:U:413:LYS:NZ	1:U:448:LEU:O	2.51	0.43
2:V:357:LEU:O	2:V:361:PHE:N	2.52	0.43
2:V:455:LYS:H	2:V:456:GLY:HA2	1.83	0.43
2:V:495:ARG:HG3	14:C:38:LYS:HE2	2.00	0.43
3:W:124:LEU:O	3:W:128:LEU:HG	2.18	0.43
3:W:221:LYS:HG3	3:W:224:LEU:HB2	2.01	0.43
5:Y:286:TRP:C	5:Y:288:PHE:H	2.27	0.43
8:b:142:ASN:HD21	8:b:170:LEU:HD21	1.84	0.43
13:B:182:GLU:HB2	13:B:239:VAL:HG11	2.00	0.43
14:C:215:SER:HB3	14:C:216:GLY:HA2	2.01	0.43
14:C:279:GLN:O	14:C:283:PHE:N	2.43	0.43
15:D:83:GLN:HG3	15:D:133:HIS:CD2	2.54	0.43
27:P:9:GLY:H	27:P:181:SER:HG	1.62	0.43
22:k:227:HIS:O	22:k:227:HIS:CG	2.70	0.43
25:n:33:LYS:O	25:n:45:ARG:NH2	2.51	0.43
29:r:179:VAL:HA	29:r:184:TRP:HA	2.01	0.43
32:f:248:LEU:O	32:f:252:ALA:HB3	2.19	0.43
32:f:494:ARG:HE	32:f:494:ARG:CA	2.32	0.43
32:f:536:SER:O	32:f:540:GLN:CB	2.66	0.43
2:V:414:TYR:OH	5:Y:331:ASP:O	2.37	0.43
2:V:495:ARG:CG	14:C:38:LYS:CE	2.95	0.43
4:X:206:LEU:O	4:X:210:LEU:N	2.41	0.43
5:Y:50:MET:SD	5:Y:74:LYS:HB3	2.58	0.43
5:Y:78:GLU:HA	5:Y:81:LEU:HB3	1.99	0.43
5:Y:105:MET:HB3	5:Y:127:THR:HG21	2.01	0.43
5:Y:307:LEU:HD11	5:Y:319:MET:SD	2.59	0.43
6:Z:121:LEU:HG	6:Z:138:TYR:HB2	2.01	0.43
12:A:100:LYS:HB3	12:A:115:VAL:HG23	2.01	0.43
13:B:226:GLY:C	13:B:230:THR:HB	2.43	0.43
14:C:220:VAL:O	14:C:224:ILE:HB	2.19	0.43
15:D:157:ASP:O	15:D:159:LYS:HG2	2.19	0.43
15:D:218:ALA:HA	15:D:221:HIS:HD2	1.84	0.43
15:D:315:ASP:OD1	15:D:315:ASP:N	2.50	0.43
16:E:180:LYS:HG3	16:E:181:THR:N	2.34	0.43
28:Q:181:ARG:NH1	28:Q:190:ASP:OD1	2.52	0.43
29:R:21:THR:HG22	29:R:26:ILE:HG12	2.01	0.43
31:T:41:ARG:NH2	31:T:53:ALA:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:i:16:GLY:N	21:j:21:TYR:OH	2.52	0.43
22:k:10:ARG:HD2	22:k:22:PHE:HE2	1.83	0.43
24:m:228:PRO:HB2	24:m:231:ILE:HG12	2.00	0.43
28:q:85:ARG:O	28:q:89:ALA:HB2	2.18	0.43
32:f:281:ILE:O	32:f:285:CYS:HB2	2.18	0.43
32:f:368:ALA:O	32:f:372:LEU:HB2	2.18	0.43
1:U:107:HIS:HA	1:U:110:LYS:HE3	2.00	0.42
2:V:25:GLU:O	2:V:28:PRO:HD2	2.19	0.42
2:V:394:LEU:O	2:V:398:LEU:N	2.49	0.42
3:W:3:ASP:OD1	3:W:4:GLY:N	2.52	0.42
4:X:354:ILE:HG21	4:X:361:VAL:HG11	2.00	0.42
5:Y:170:GLU:CG	5:Y:171:GLY:HA3	2.44	0.42
6:Z:30:GLY:HA3	6:Z:31:ASN:HA	1.83	0.42
6:Z:208:ILE:HD13	7:a:354:GLU:HB2	2.01	0.42
9:c:116:PRO:HA	9:c:147:PRO:HD2	2.01	0.42
12:A:139:ARG:HG3	12:A:156:LYS:HG3	2.01	0.42
13:B:108:SER:HA	14:C:95:PHE:HA	2.01	0.42
13:B:178:LYS:HZ3	14:C:278:ASN:CB	2.06	0.42
13:B:431:GLN:HB3	20:I:169:ALA:O	2.19	0.42
14:C:141:GLU:OE2	15:D:326:ARG:NH2	2.51	0.42
16:E:54:GLY:H	17:F:158:TYR:HD2	1.67	0.42
16:E:214:LEU:HA	16:E:217:GLU:HB3	2.00	0.42
18:G:120:ASP:OD1	19:H:84:ARG:NH1	2.51	0.42
23:L:50:LYS:HE2	23:L:61:LYS:HA	2.01	0.42
28:Q:166:GLU:HG2	29:r:141:ARG:HH21	1.83	0.42
22:k:224:GLN:O	22:k:225:ASN:HB3	2.19	0.42
23:l:37:GLY:HA2	23:l:46:LEU:HA	2.01	0.42
24:m:173:LYS:HA	24:m:176:ILE:HD12	2.01	0.42
28:q:38:MET:HA	28:q:61:GLN:HE22	1.83	0.42
32:f:380:PHE:CB	32:f:751:TYR:CE1	2.99	0.42
1:U:566:LEU:O	1:U:570:LEU:HG	2.19	0.42
1:U:638:SER:O	1:U:641:SER:OG	2.31	0.42
2:V:48:THR:HG23	2:V:147:PHE:HE2	1.84	0.42
2:V:224:LEU:HB2	2:V:227:VAL:HB	2.01	0.42
3:W:409:LEU:HD23	4:X:384:VAL:HG21	2.00	0.42
3:W:445:LEU:HD12	3:W:448:LYS:HZ1	1.84	0.42
6:Z:208:ILE:HD12	7:a:353:LEU:HD23	2.00	0.42
7:a:25:LEU:HD22	7:a:44:PHE:HE2	1.84	0.42
7:a:35:HIS:CE1	8:b:17:ARG:HB2	2.54	0.42
8:b:35:ILE:HD13	8:b:184:ILE:HD13	2.02	0.42
9:c:260:GLU:O	9:c:264:LYS:N	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:d:79:LYS:HA	10:d:121:ARG:HH21	1.83	0.42
12:A:206:ILE:HG13	12:A:207:GLU:H	1.84	0.42
15:D:325:GLY:N	15:D:328:ASP:OD1	2.52	0.42
15:D:388:ARG:HH12	16:E:143:ARG:HG2	1.83	0.42
15:D:412:GLN:NE2	15:D:415:GLU:H	2.16	0.42
16:E:55:GLN:HB3	16:E:100:LEU:O	2.19	0.42
17:F:321:GLN:HG3	17:F:322:PRO:HD3	2.01	0.42
17:F:428:GLN:CG	17:F:429:ALA:HA	2.49	0.42
24:M:92:ARG:NH2	31:T:73:ASP:OD1	2.52	0.42
25:N:35:THR:HA	25:N:36:PRO:HD3	1.90	0.42
24:m:40:ARG:HH21	24:m:161:TRP:NE1	2.17	0.42
31:t:7:THR:OG1	31:t:182:ARG:NH2	2.52	0.42
32:f:228:LYS:O	32:f:232:TYR:HB3	2.19	0.42
32:f:513:GLU:HG3	32:f:557:TRP:HZ3	1.84	0.42
32:f:796:LEU:HG	32:f:799:VAL:CG2	2.42	0.42
1:U:517:GLY:HA3	1:U:554:LEU:HB3	2.01	0.42
1:U:772:TRP:CD1	1:U:774:PRO:HD2	2.54	0.42
2:V:409:MET:HG3	5:Y:339:ALA:HB2	2.01	0.42
3:W:80:TRP:CD1	3:W:84:ASN:HD21	2.37	0.42
5:Y:387:ILE:HD13	6:Z:283:ARG:HD3	2.00	0.42
7:a:55:GLY:O	7:a:58:LYS:HG2	2.19	0.42
7:a:155:PHE:CE2	7:a:178:ARG:HD3	2.54	0.42
8:b:16:MET:HA	8:b:25:ARG:HD2	2.01	0.42
9:c:58:LEU:HB2	9:c:73:PHE:HE1	1.84	0.42
12:A:291:GLY:O	12:A:294:GLU:HG2	2.19	0.42
13:B:227:PRO:HD3	13:B:332:ASN:O	2.19	0.42
14:C:14:GLY:O	14:C:18:SER:N	2.25	0.42
20:I:229:LYS:N	20:I:232:GLU:OE2	2.46	0.42
21:J:195:LEU:O	21:J:201:SER:OG	2.36	0.42
25:N:18:SER:HB2	25:N:31:THR:H	1.83	0.42
20:i:164:ILE:HA	20:i:165:GLY:HA2	1.74	0.42
26:o:135:MET:O	26:o:139:GLU:HB2	2.19	0.42
1:U:356:THR:HG21	1:U:731:ILE:HD13	2.02	0.42
2:V:82:LEU:C	2:V:84:LYS:N	2.59	0.42
2:V:157:THR:OG1	2:V:158:PRO:HD3	2.19	0.42
2:V:197:THR:HG22	2:V:199:ASN:H	1.83	0.42
2:V:372:LEU:H	2:V:427:GLN:HE22	1.67	0.42
3:W:56:THR:HG21	3:W:103:LYS:HE3	2.02	0.42
6:Z:33:LYS:HD3	6:Z:60:GLU:H	1.84	0.42
7:a:253:THR:HG23	7:a:261:LEU:HD21	2.01	0.42
10:d:52:ARG:O	10:d:56:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:d:171:LEU:O	10:d:175:ARG:HG2	2.19	0.42
13:B:164:MET:HE2	13:B:164:MET:HA	2.02	0.42
13:B:313:LEU:HD13	13:B:341:LEU:HD22	2.00	0.42
14:C:154:LEU:O	14:C:158:ILE:HG23	2.19	0.42
17:F:172:VAL:HG22	17:F:267:LEU:HD11	2.01	0.42
18:G:67:THR:HG22	18:G:69:LEU:H	1.85	0.42
28:Q:31:ASP:OD1	28:Q:31:ASP:N	2.50	0.42
19:h:189:HIS:NE2	19:h:234:ALA:O	2.51	0.42
21:j:195:LEU:O	21:j:201:SER:OG	2.32	0.42
31:t:27:LEU:HD22	31:t:184:TYR:HB2	2.00	0.42
32:f:86:THR:HG23	32:f:87:THR:H	1.85	0.42
32:f:207:LEU:HD13	32:f:207:LEU:HA	1.86	0.42
32:f:629:LYS:HE2	32:f:660:ILE:HG21	2.02	0.42
32:f:688:ARG:HA	32:f:745:LEU:CB	2.49	0.42
1:U:780:SER:HA	1:U:783:TYR:CD1	2.54	0.42
1:U:913:ILE:H	1:U:913:ILE:HG13	1.67	0.42
2:V:31:ALA:HB3	2:V:32:PRO:HD3	2.01	0.42
2:V:59:ALA:HA	2:V:60:ALA:C	2.45	0.42
2:V:345:ARG:HG2	2:V:364:THR:HG21	2.01	0.42
3:W:150:ALA:O	3:W:154:GLU:HG3	2.20	0.42
5:Y:111:LEU:HD23	5:Y:114:ILE:HD13	2.01	0.42
5:Y:215:ASP:O	5:Y:218:THR:OG1	2.27	0.42
7:a:325:ASP:OD1	7:a:327:VAL:HG12	2.19	0.42
13:B:360:THR:O	13:B:364:ILE:N	2.52	0.42
13:B:432:GLU:CA	20:I:169:ALA:HB2	2.40	0.42
14:C:283:PHE:HD2	14:C:284:GLU:HG2	1.85	0.42
15:D:375:ILE:HG23	15:D:376:ASN:H	1.84	0.42
17:F:225:MET:HG2	17:F:233:LYS:HD2	2.02	0.42
17:F:439:ALA:C	23:L:77:LEU:CA	2.68	0.42
23:L:111:LEU:O	23:L:115:LYS:CB	2.67	0.42
24:M:36:ALA:HB1	24:M:49:VAL:HG22	2.02	0.42
24:m:175:GLU:HA	24:m:178:LYS:HD3	2.01	0.42
32:f:311:VAL:CA	32:f:490:ALA:HB1	2.48	0.42
32:f:635:LYS:HD3	32:f:641:GLU:HG2	2.01	0.42
1:U:607:VAL:O	1:U:615:ARG:NH1	2.52	0.42
2:V:496:PHE:O	14:C:37:ASP:CG	2.62	0.42
3:W:45:GLU:HB2	3:W:93:ARG:HA	2.02	0.42
3:W:439:VAL:HG21	9:c:232:GLN:HA	2.02	0.42
6:Z:181:ASP:HA	6:Z:182:THR:HA	1.46	0.42
8:b:16:MET:O	8:b:25:ARG:HB2	2.19	0.42
9:c:32:TYR:HE1	9:c:206:ASN:HD21	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:c:80:THR:O	17:F:155:LYS:NZ	2.52	0.42
10:d:49:ILE:HD12	10:d:52:ARG:HH11	1.85	0.42
13:B:191:ASP:OD1	13:B:191:ASP:N	2.52	0.42
13:B:376:ASP:O	13:B:378:VAL:N	2.53	0.42
14:C:210:THR:HG23	14:C:244:SER:HB3	2.01	0.42
14:C:327:ASP:O	14:C:331:ILE:HG12	2.20	0.42
15:D:200:ARG:HH12	15:D:300:ASP:CG	2.27	0.42
16:E:113:ARG:HB3	16:E:221:TYR:OH	2.19	0.42
16:E:126:ASP:OD2	16:E:185:ARG:HG2	2.20	0.42
16:E:169:GLY:O	16:E:296:ASP:HB2	2.18	0.42
16:E:194:ASN:ND2	16:E:227:PRO:O	2.53	0.42
17:F:436:GLN:N	17:F:438:TYR:CE2	2.87	0.42
24:M:37:ILE:HG12	24:M:197:ILE:HD11	2.02	0.42
27:P:26:ARG:CG	27:P:39:PHE:O	2.68	0.42
21:j:115:LYS:HE3	21:j:127:PHE:HB2	2.00	0.42
24:m:231:ILE:HD13	24:m:231:ILE:HA	1.94	0.42
26:o:63:LEU:HD11	26:o:79:ALA:HB2	2.01	0.42
27:p:28:PHE:HB2	27:p:39:PHE:HB2	2.01	0.42
29:r:135:ALA:O	29:r:139:MET:HB2	2.19	0.42
1:U:470:ASN:HA	1:U:471:ASP:HA	1.84	0.42
2:V:287:ARG:HD2	11:e:4:LYS:HE2	1.96	0.42
2:V:480:ILE:HG22	2:V:484:LEU:HD23	2.00	0.42
3:W:107:GLN:HB3	3:W:111:TYR:CZ	2.55	0.42
7:a:320:VAL:HG21	7:a:333:MET:SD	2.59	0.42
10:d:40:GLY:HA3	10:d:41:THR:O	2.20	0.42
12:A:102:ILE:HG22	12:A:113:ILE:HG12	2.02	0.42
15:D:228:ILE:HB	15:D:262:ILE:HG12	2.01	0.42
15:D:413:GLU:OE2	18:G:25:VAL:HG13	2.19	0.42
16:E:141:GLN:HB3	16:E:183:LEU:HD11	2.01	0.42
16:E:232:MET:N	16:E:276:ILE:O	2.53	0.42
16:E:254:GLN:O	16:E:258:MET:HG2	2.19	0.42
20:I:86:LEU:O	20:I:90:LEU:HB2	2.19	0.42
20:I:220:ASN:HA	20:I:221:GLY:HA2	1.58	0.42
21:J:79:ASP:HB3	21:J:127:PHE:HD1	1.85	0.42
26:O:209:THR:HG21	27:P:168:SER:HB3	2.01	0.42
21:j:72:ALA:HB3	21:j:132:LEU:HB2	2.01	0.42
23:l:150:SER:OG	23:l:152:ASN:ND2	2.53	0.42
1:U:788:VAL:HG12	1:U:910:GLY:H	1.84	0.42
2:V:313:LEU:HD22	2:V:329:HIS:CE1	2.54	0.42
4:X:261:LEU:C	4:X:263:THR:H	2.28	0.42
4:X:390:GLU:O	4:X:392:PRO:HD3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:121:LEU:HD11	6:Z:138:TYR:HD2	1.85	0.42
6:Z:172:VAL:HG13	9:c:217:LEU:HD11	2.01	0.42
7:a:148:VAL:C	7:a:150:SER:H	2.28	0.42
9:c:229:LEU:C	9:c:231:LEU:H	2.27	0.42
12:A:106:SER:HB2	17:F:165:PRO:O	2.20	0.42
13:B:153:ASN:HD21	13:B:160:ILE:HB	1.85	0.42
13:B:294:ARG:HG2	13:B:295:TYR:H	1.85	0.42
14:C:214:VAL:HG22	14:C:215:SER:N	2.33	0.42
14:C:259:LEU:H	14:C:259:LEU:HD13	1.85	0.42
16:E:352:MET:HE1	17:F:220:PRO:HG3	2.02	0.42
17:F:102:ASN:HA	17:F:103:ASP:HA	1.51	0.42
18:G:83:MET:SD	18:G:132:ARG:NH1	2.92	0.42
20:I:239:LYS:NZ	20:I:243:GLU:OE2	2.52	0.42
22:K:50:VAL:HG11	22:K:66:LYS:HB2	2.02	0.42
30:S:187:VAL:HG21	26:o:24:MET:HE3	2.02	0.42
18:g:61:LEU:HD21	18:g:66:VAL:HG21	2.00	0.42
19:h:59:GLU:HG2	19:h:206:ASP:HB3	2.01	0.42
30:s:114:ASP:OD1	30:s:118:LYS:N	2.49	0.42
32:f:77:GLU:O	32:f:81:GLN:HB2	2.19	0.42
32:f:374:SER:O	32:f:375:SER:C	2.59	0.42
32:f:379:GLY:O	32:f:417:ILE:CG1	2.65	0.42
32:f:494:ARG:NE	32:f:494:ARG:CA	2.82	0.42
32:f:573:ILE:HG22	32:f:576:ILE:HB	2.01	0.42
32:f:780:PRO:HB2	32:f:800:LEU:HA	1.94	0.42
32:f:794:ALA:HA	32:f:797:LEU:HB2	2.01	0.42
1:U:800:VAL:HG22	1:U:898:CYS:SG	2.60	0.42
2:V:91:PRO:HA	2:V:94:VAL:HG12	2.02	0.42
2:V:112:VAL:HG22	2:V:115:LYS:HZ1	1.85	0.42
2:V:127:THR:HA	2:V:131:LEU:HG	2.01	0.42
2:V:232:HIS:HA	2:V:235:LEU:HB3	2.02	0.42
2:V:234:ARG:HA	2:V:237:THR:HG22	2.02	0.42
2:V:256:ARG:CD	11:e:5:LYS:HD2	2.50	0.42
3:W:449:GLU:HG2	3:W:453:HIS:CE1	2.55	0.42
10:d:68:ILE:HB	10:d:69:PRO:HD3	2.01	0.42
10:d:139:LEU:HD11	10:d:151:VAL:HG13	2.01	0.42
12:A:183:GLN:HG2	12:A:344:SER:OG	2.19	0.42
12:A:212:VAL:O	12:A:319:MET:HB2	2.20	0.42
14:C:183:PRO:HA	14:C:311:ILE:HG13	2.02	0.42
14:C:215:SER:HB3	14:C:216:GLY:CA	2.49	0.42
15:D:205:TYR:CG	15:D:206:GLY:N	2.88	0.42
16:E:171:LEU:N	16:E:297:ARG:O	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:I:68:LEU:HD22	20:I:90:LEU:HD22	2.02	0.42
28:Q:140:LEU:HD22	29:r:166:ARG:HH21	1.85	0.42
19:h:150:ASP:OD1	19:h:154:ALA:N	2.53	0.42
28:q:46:CYS:HA	28:q:102:LEU:HB2	2.02	0.42
32:f:358:PHE:O	32:f:362:GLY:CA	2.63	0.42
32:f:512:MET:HE1	32:f:554:TYR:HA	2.02	0.42
32:f:620:PHE:HD2	32:f:623:LYS:HG2	1.85	0.42
1:U:684:ARG:O	1:U:688:LEU:HG	2.19	0.42
2:V:215:ALA:HB1	2:V:256:ARG:NH2	2.34	0.42
3:W:243:ILE:HA	3:W:246:HIS:HB3	2.02	0.42
4:X:268:GLN:O	4:X:272:SER:HB2	2.20	0.42
6:Z:148:GLY:HA2	7:a:181:GLY:C	2.44	0.42
7:a:4:VAL:HB	7:a:5:PRO:HD3	2.02	0.42
10:d:103:LEU:HD22	10:d:119:LEU:HD21	2.02	0.42
12:A:173:THR:HA	12:A:230:ALA:HB3	2.01	0.42
15:D:150:SER:HB3	16:E:61:LEU:HD22	2.02	0.42
16:E:240:GLY:HA2	17:F:299:GLU:HB2	2.01	0.42
16:E:341:ALA:O	16:E:345:ASN:N	2.52	0.42
22:K:69:GLU:OE1	22:K:228:MET:HG3	2.20	0.42
26:O:40:ASN:ND2	26:O:103:VAL:O	2.51	0.42
26:O:206:LYS:HA	27:P:165:GLU:HG3	2.01	0.42
27:P:138:VAL:HB	27:P:146:MET:HE3	2.01	0.42
21:j:137:ASP:HB2	21:j:141:THR:H	1.85	0.42
22:k:60:GLU:OE1	22:k:63:SER:N	2.48	0.42
28:q:5:ILE:HG22	28:q:16:ALA:HB3	2.01	0.42
30:s:155:PHE:HB2	30:s:163:HIS:CE1	2.55	0.42
32:f:355:ASN:HA	32:f:358:PHE:HD2	1.83	0.42
1:U:654:MET:O	1:U:658:ILE:HG12	2.19	0.41
5:Y:48:ASN:ND2	5:Y:77:ASN:HB2	2.35	0.41
5:Y:198:ALA:HB2	5:Y:226:VAL:HG13	2.03	0.41
12:A:206:ILE:HG23	12:A:207:GLU:N	2.35	0.41
14:C:84:LYS:HG2	14:C:98:ASP:HA	2.02	0.41
31:T:46:ASN:OD1	31:T:46:ASN:N	2.49	0.41
20:i:194:ILE:O	20:i:198:ASN:CB	2.66	0.41
21:j:32:ALA:O	21:j:159:ASN:ND2	2.53	0.41
24:m:10:SER:HB3	24:m:13:THR:HG23	2.02	0.41
32:f:298:LEU:HA	32:f:301:HIS:CD2	2.55	0.41
32:f:797:LEU:HA	32:f:797:LEU:HD22	1.76	0.41
1:U:770:TRP:CG	9:c:179:SER:HB2	2.55	0.41
2:V:94:VAL:HG11	2:V:134:PHE:HB3	2.01	0.41
5:Y:145:LEU:HD23	5:Y:157:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:109:ASN:OD1	6:Z:119:SER:HB2	2.20	0.41
7:a:175:ASP:HA	7:a:178:ARG:HH11	1.85	0.41
8:b:9:CYS:HB3	8:b:111:ALA:HA	2.01	0.41
9:c:272:ILE:HB	9:c:273:LYS:HA	2.01	0.41
10:d:47:GLN:O	10:d:51:ALA:N	2.53	0.41
12:A:252:GLU:O	12:A:256:MET:N	2.40	0.41
13:B:222:VAL:HG22	13:B:328:ILE:HG12	2.02	0.41
13:B:338:ASP:N	13:B:341:LEU:HG	2.34	0.41
15:D:289:LEU:HD12	15:D:292:LEU:HD11	2.02	0.41
16:E:58:GLY:N	16:E:98:VAL:O	2.41	0.41
16:E:266:GLY:C	16:E:268:ASP:H	2.28	0.41
17:F:311:LEU:HD23	17:F:314:LEU:HD22	2.01	0.41
18:G:172:GLN:HA	18:G:175:SER:HB3	2.03	0.41
21:J:199:VAL:O	21:J:201:SER:N	2.53	0.41
26:O:3:ILE:HD11	26:O:127:MET:HB2	2.02	0.41
26:O:73:LEU:HA	26:O:74:PRO:HD3	1.93	0.41
30:S:36:HIS:HB3	31:T:132:TYR:CZ	2.55	0.41
31:T:43:MET:SD	31:T:64:LYS:HG3	2.60	0.41
18:g:232:GLU:HA	18:g:235:ILE:HD12	2.02	0.41
21:j:36:ARG:HE	21:j:157:LYS:HA	1.85	0.41
22:k:108:THR:O	22:k:111:SER:OG	2.37	0.41
23:l:26:MET:HE1	23:l:148:CYS:HB2	2.01	0.41
32:f:8:LYS:HD3	32:f:39:LYS:HD2	2.02	0.41
32:f:80:ARG:HE	32:f:99:LEU:HD13	1.85	0.41
32:f:303:VAL:HG13	32:f:339:ILE:HG13	2.03	0.41
1:U:789:ILE:HB	1:U:911:ILE:HB	2.02	0.41
2:V:474:LEU:HA	2:V:477:HIS:CD2	2.55	0.41
3:W:428:TRP:CD1	9:c:245:VAL:HG23	2.54	0.41
5:Y:104:MET:O	5:Y:108:ALA:HB3	2.19	0.41
6:Z:245:PHE:HD1	6:Z:245:PHE:HA	1.75	0.41
7:a:220:PRO:HA	7:a:223:GLU:HG2	2.00	0.41
10:d:215:TRP:CG	10:d:216:VAL:N	2.85	0.41
12:A:90:GLU:O	12:A:94:GLN:HB2	2.19	0.41
14:C:54:ALA:O	14:C:58:LEU:N	2.53	0.41
15:D:53:PHE:O	15:D:57:GLN:HG2	2.19	0.41
16:E:119:VAL:HG11	17:F:146:LYS:HD2	2.02	0.41
19:H:231:ALA:H	19:H:232:ALA:HB3	1.84	0.41
30:s:144:MET:HE1	30:s:185:ARG:HB2	2.02	0.41
32:f:311:VAL:HG22	32:f:527:VAL:O	2.19	0.41
32:f:392:THR:CG2	32:f:417:ILE:CG2	2.94	0.41
2:V:104:THR:HA	2:V:107:ARG:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W:455:LEU:HD12	3:W:456:GLN:N	2.34	0.41
5:Y:324:GLY:N	5:Y:325:VAL:HA	2.35	0.41
7:a:374:ILE:HD12	10:d:254:GLU:HG2	2.02	0.41
9:c:157:ILE:HG23	9:c:158:ASP:N	2.35	0.41
12:A:113:ILE:O	12:A:121:PHE:N	2.32	0.41
12:A:212:VAL:HG12	12:A:339:ARG:HB3	2.02	0.41
12:A:384:GLU:N	13:B:343:ARG:HH11	2.18	0.41
14:C:192:PRO:HA	14:C:193:GLY:HA3	1.68	0.41
16:E:364:GLN:HA	16:E:367:PHE:HB2	2.03	0.41
17:F:188:ILE:O	17:F:188:ILE:HG13	2.20	0.41
18:G:163:PHE:HD1	19:H:58:ASP:H	1.68	0.41
27:P:62:THR:HG1	28:Q:85:ARG:HH22	1.64	0.41
18:g:102:LYS:HD2	18:g:102:LYS:HA	1.91	0.41
24:m:39:ILE:HG22	24:m:46:VAL:HB	2.02	0.41
1:U:427:LEU:HG	1:U:464:GLN:HE21	1.85	0.41
2:V:288:TYR:HA	2:V:291:TYR:HD2	1.86	0.41
3:W:406:VAL:HA	3:W:413:ILE:HG22	2.03	0.41
4:X:367:GLN:HA	4:X:370:LEU:HD12	2.02	0.41
5:Y:145:LEU:HD13	5:Y:183:TYR:CD1	2.56	0.41
5:Y:184:GLN:O	5:Y:188:CYS:N	2.45	0.41
6:Z:96:HIS:NE2	6:Z:123:ILE:HG12	2.36	0.41
8:b:140:ILE:HD13	8:b:157:VAL:HG22	2.01	0.41
10:d:56:GLU:HB3	10:d:94:TYR:HB2	2.02	0.41
12:A:190:VAL:HG11	12:A:212:VAL:HG11	2.03	0.41
12:A:210:LYS:O	12:A:336:ARG:NH2	2.53	0.41
12:A:309:PHE:CZ	17:F:235:LEU:HD12	2.56	0.41
13:B:283:PHE:CE2	13:B:285:ASP:HB2	2.55	0.41
13:B:431:GLN:HA	13:B:434:THR:OG1	2.21	0.41
14:C:186:VAL:HG23	14:C:313:ARG:HB3	2.03	0.41
16:E:240:GLY:HA2	17:F:299:GLU:CD	2.45	0.41
24:M:66:LEU:HD13	24:M:214:SER:HB2	2.02	0.41
18:g:132:ARG:HA	18:g:133:PRO:HD3	1.81	0.41
21:j:169:ARG:HA	21:j:172:LEU:HD12	2.02	0.41
22:k:121:LEU:HD22	22:k:123:PHE:HE1	1.86	0.41
32:f:81:GLN:O	32:f:85:SER:HB2	2.21	0.41
32:f:479:LEU:HD23	32:f:513:GLU:HB3	2.02	0.41
32:f:638:ASP:OD1	32:f:638:ASP:N	2.50	0.41
1:U:358:ASP:O	1:U:360:VAL:HG23	2.20	0.41
2:V:137:GLU:N	2:V:138:PRO:HD2	2.35	0.41
3:W:373:ILE:HG23	3:W:413:ILE:HG13	2.03	0.41
5:Y:292:TYR:O	5:Y:296:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:36:VAL:HG22	6:Z:96:HIS:HB3	2.02	0.41
10:d:108:SER:HB3	10:d:169:ILE:HG22	2.02	0.41
15:D:43:ARG:HA	15:D:46:LYS:HD2	2.02	0.41
16:E:362:VAL:HB	16:E:367:PHE:CE1	2.56	0.41
17:F:150:LEU:HB3	17:F:164:LEU:O	2.20	0.41
21:J:131:ALA:N	21:J:147:THR:OG1	2.54	0.41
22:K:18:GLU:CG	22:K:20:ARG:CZ	2.89	0.41
24:M:123:THR:HG22	24:M:130:PRO:HB3	2.02	0.41
25:N:30:VAL:HG11	31:t:212:ALA:HA	2.01	0.41
28:Q:118:MET:HE1	28:Q:124:LEU:HD23	2.03	0.41
20:i:92:LEU:HD22	20:i:96:ARG:HH21	1.86	0.41
32:f:275:MET:SD	32:f:275:MET:N	2.90	0.41
32:f:780:PRO:HB2	32:f:800:LEU:CA	2.50	0.41
1:U:576:PRO:HA	1:U:579:ARG:HE	1.85	0.41
2:V:106:ARG:HA	2:V:109:ASN:HB2	2.02	0.41
2:V:259:LEU:HD12	2:V:295:ILE:HG12	2.02	0.41
2:V:403:ILE:HD11	2:V:428:LEU:HD11	2.02	0.41
3:W:359:VAL:O	3:W:363:ILE:HG12	2.21	0.41
5:Y:41:LEU:HD22	5:Y:63:TRP:CZ2	2.56	0.41
7:a:34:TRP:CE3	7:a:37:LEU:HD23	2.55	0.41
7:a:307:VAL:O	7:a:311:VAL:HG22	2.21	0.41
9:c:285:GLU:HB3	9:c:286:GLU:HA	2.01	0.41
10:d:175:ARG:O	10:d:209:TYR:OH	2.37	0.41
12:A:164:MET:HE3	12:A:239:ARG:HH12	1.84	0.41
13:B:226:GLY:HA2	13:B:227:PRO:HD3	1.90	0.41
13:B:436:GLU:HG2	13:B:439:TYR:CD1	2.56	0.41
14:C:287:LYS:HE3	14:C:287:LYS:HB2	1.95	0.41
15:D:385:LEU:O	15:D:388:ARG:HB3	2.20	0.41
15:D:412:GLN:O	18:G:159:TYR:OH	2.38	0.41
16:E:90:SER:O	16:E:93:LYS:NZ	2.40	0.41
17:F:221:LYS:HG3	17:F:346:GLY:HA2	2.01	0.41
21:J:73:PHE:HA	21:J:131:ALA:HA	2.03	0.41
21:J:121:SER:OG	21:J:122:ASN:N	2.53	0.41
25:N:142:THR:HB	25:N:155:PHE:HE1	1.85	0.41
30:S:179:PHE:O	30:S:183:ALA:CB	2.68	0.41
21:j:180:ALA:HA	21:j:181:ILE:HA	1.66	0.41
21:j:221:ASN:HA	21:j:222:PRO:HD3	1.90	0.41
22:k:225:ASN:HA	22:k:226:PHE:HA	1.51	0.41
24:m:56:LYS:HB3	24:m:56:LYS:HE3	1.84	0.41
32:f:479:LEU:HG	32:f:513:GLU:O	2.21	0.41
32:f:533:ASP:OD1	32:f:533:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:810:THR:O	1:U:883:ARG:NH1	2.52	0.41
2:V:235:LEU:HD12	2:V:247:GLN:HG3	2.02	0.41
3:W:155:GLN:HG2	3:W:157:GLY:H	1.86	0.41
6:Z:123:ILE:HB	6:Z:136:GLU:HB3	2.02	0.41
6:Z:262:LEU:O	6:Z:266:ILE:HD12	2.20	0.41
7:a:100:THR:HG22	7:a:103:LYS:HE2	2.03	0.41
9:c:42:LEU:HD12	9:c:43:LYS:N	2.36	0.41
9:c:98:MET:O	9:c:102:THR:OG1	2.25	0.41
12:A:325:ASP:HA	12:A:326:THR:HA	1.77	0.41
14:C:149:GLU:O	14:C:331:ILE:HD12	2.20	0.41
14:C:171:HIS:HD2	14:C:174:LEU:HD21	1.85	0.41
14:C:235:PHE:CD1	14:C:275:GLU:HG3	2.55	0.41
15:D:358:VAL:HG12	15:D:363:TYR:CE2	2.55	0.41
16:E:44:GLU:OE1	17:F:76:ASN:ND2	2.54	0.41
16:E:72:LYS:HB2	16:E:78:ARG:HG2	2.02	0.41
22:K:157:ASP:OD1	22:K:157:ASP:N	2.50	0.41
1:U:363:SER:C	1:U:365:CYS:H	2.28	0.41
1:U:495:ASP:HA	1:U:498:LYS:NZ	2.36	0.41
1:U:604:HIS:O	1:U:608:SER:OG	2.35	0.41
1:U:628:ARG:NH2	1:U:753:GLY:O	2.36	0.41
2:V:97:ALA:N	2:V:98:LEU:HA	2.35	0.41
2:V:149:PRO:HG3	2:V:203:LEU:HG	2.03	0.41
2:V:455:LYS:HD2	2:V:457:TYR:HE2	1.86	0.41
2:V:497:PRO:HG3	6:Z:286:GLU:HG3	2.02	0.41
5:Y:16:ASP:OD2	5:Y:113:ARG:HG3	2.21	0.41
5:Y:300:ARG:HH12	11:e:63:HIS:CD2	2.39	0.41
6:Z:201:LEU:HD22	7:a:357:CYS:HA	2.02	0.41
7:a:229:ASP:HB3	7:a:234:ILE:HD11	2.02	0.41
7:a:291:LEU:O	7:a:331:VAL:N	2.54	0.41
8:b:24:THR:O	8:b:28:ALA:N	2.47	0.41
10:d:114:GLU:HA	10:d:117:THR:HG22	2.02	0.41
12:A:120:LYS:H	17:F:127:SER:CB	2.34	0.41
12:A:315:ILE:H	12:A:315:ILE:HG13	1.54	0.41
12:A:377:CYS:HB2	12:A:380:SER:OG	2.21	0.41
13:B:194:ILE:O	13:B:237:LYS:NZ	2.35	0.41
13:B:343:ARG:HB2	13:B:344:PRO:HD3	2.02	0.41
13:B:437:GLY:HA3	13:B:438:LEU:C	2.46	0.41
15:D:45:LYS:O	15:D:48:GLN:NE2	2.54	0.41
16:E:181:THR:O	16:E:185:ARG:HB2	2.20	0.41
16:E:213:ARG:O	16:E:217:GLU:N	2.53	0.41
16:E:236:ASP:OD2	16:E:280:ASN:ND2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:431:LYS:HG2	17:F:432:LYS:HD2	2.02	0.41
18:G:37:LEU:HD11	18:G:52:THR:HG22	2.03	0.41
20:I:83:ALA:HB2	20:I:132:VAL:HG11	2.02	0.41
21:J:137:ASP:OD2	21:J:143:ARG:NH1	2.54	0.41
22:K:18:GLU:CD	22:K:20:ARG:NH2	2.63	0.41
28:Q:85:ARG:HD2	28:Q:124:LEU:HG	2.02	0.41
29:R:135:ALA:O	29:R:139:MET:HB2	2.20	0.41
30:S:73:LYS:O	30:S:77:HIS:ND1	2.36	0.41
19:h:118:MET:HE3	19:h:130:PHE:HB2	2.03	0.41
20:i:47:ALA:HB1	20:i:64:LYS:HD2	2.01	0.41
20:i:64:LYS:HG3	20:i:76:VAL:HG12	2.03	0.41
20:i:246:LYS:HD2	20:i:249:ARG:HG3	2.02	0.41
22:k:11:GLY:O	22:k:14:THR:OG1	2.28	0.41
22:k:49:ALA:HB2	22:k:217:LEU:HD23	2.03	0.41
24:m:46:VAL:HG22	24:m:215:TRP:CD1	2.56	0.41
27:p:135:ASP:OD1	27:p:135:ASP:N	2.48	0.41
28:q:148:THR:HG22	28:q:150:THR:H	1.86	0.41
31:t:89:HIS:CE1	31:t:131:ALA:HB1	2.55	0.41
32:f:86:THR:O	32:f:87:THR:HB	2.21	0.41
32:f:89:MET:SD	32:f:89:MET:N	2.94	0.41
32:f:478:ARG:HD3	32:f:504:VAL:HG22	2.03	0.41
1:U:699:THR:O	1:U:702:THR:OG1	2.30	0.41
2:V:417:ILE:HD11	2:V:422:ILE:HB	2.03	0.41
5:Y:39:ASP:HA	5:Y:42:MET:HB3	2.03	0.41
6:Z:67:VAL:HG12	8:b:95:LEU:HD23	2.02	0.41
6:Z:148:GLY:HA2	7:a:181:GLY:O	2.21	0.41
9:c:177:THR:O	9:c:177:THR:OG1	2.39	0.41
12:A:250:VAL:HG23	17:F:259:MET:HA	2.03	0.41
13:B:163:LEU:HD23	14:C:80:MET:HG3	2.03	0.41
13:B:198:LYS:N	13:B:237:LYS:HZ3	2.19	0.41
13:B:319:PHE:HA	13:B:320:ASP:HA	1.49	0.41
13:B:427:LEU:HD23	20:I:173:SER:HB2	2.02	0.41
15:D:249:ASP:HA	15:D:252:ARG:HG2	2.03	0.41
16:E:125:GLU:N	16:E:125:GLU:OE1	2.54	0.41
17:F:88:TYR:HB2	17:F:154:ASN:HA	2.02	0.41
17:F:228:PRO:HA	17:F:229:PRO:HD3	1.84	0.41
18:G:10:ASP:OD1	18:G:10:ASP:N	2.54	0.41
23:L:39:LYS:HE2	23:L:157:ARG:HA	2.03	0.41
20:i:239:LYS:NZ	20:i:243:GLU:OE2	2.54	0.41
23:l:59:HIS:ND1	23:l:208:LYS:O	2.37	0.41
27:p:190:ILE:HG22	27:p:195:ILE:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:687:ARG:O	32:f:745:LEU:HD22	2.21	0.41
32:f:742:ALA:CA	32:f:745:LEU:CG	2.93	0.41
2:V:283:ASN:ND2	2:V:317:PRO:O	2.54	0.40
2:V:295:ILE:O	2:V:298:ILE:HG22	2.21	0.40
2:V:349:ARG:HD2	2:V:354:LYS:HG3	2.03	0.40
3:W:62:SER:HB2	3:W:71:VAL:HG11	2.03	0.40
5:Y:221:THR:HA	5:Y:224:VAL:HG12	2.04	0.40
5:Y:358:ARG:HH21	5:Y:359:PRO:CG	2.34	0.40
8:b:184:ILE:C	8:b:187:PRO:HD2	2.45	0.40
9:c:113:HIS:CE1	9:c:144:VAL:HG22	2.56	0.40
9:c:168:MET:HA	9:c:172:HIS:ND1	2.36	0.40
12:A:115:VAL:HG12	12:A:119:ALA:O	2.21	0.40
13:B:439:TYR:CE2	21:J:28:LYS:HD2	2.55	0.40
14:C:217:SER:HB3	14:C:220:VAL:CG2	2.51	0.40
14:C:339:THR:HG23	14:C:341:GLY:H	1.85	0.40
15:D:412:GLN:OE1	15:D:415:GLU:HB2	2.21	0.40
22:K:18:GLU:N	22:K:19:GLY:CA	2.84	0.40
24:m:87:LEU:HD23	24:m:87:LEU:HA	1.94	0.40
25:n:63:LEU:O	25:n:67:SER:CB	2.69	0.40
32:f:380:PHE:CD2	32:f:751:TYR:CE1	3.09	0.40
1:U:9:ILE:HD12	1:U:9:ILE:H	1.86	0.40
1:U:757:MET:H	1:U:757:MET:HG2	1.71	0.40
2:V:350:GLN:O	2:V:354:LYS:N	2.52	0.40
3:W:12:ARG:O	3:W:27:ARG:NH2	2.54	0.40
5:Y:101:ARG:HG3	5:Y:104:MET:SD	2.62	0.40
6:Z:34:ARG:NH1	6:Z:102:HIS:HE1	2.18	0.40
7:a:50:PHE:N	7:a:51:ALA:HA	2.35	0.40
9:c:113:HIS:NE2	9:c:126:ASP:OD2	2.53	0.40
9:c:142:ALA:O	9:c:160:PHE:N	2.48	0.40
9:c:159:ALA:HB3	9:c:205:ILE:HD11	2.03	0.40
11:e:60:LEU:O	11:e:64:GLY:N	2.49	0.40
12:A:406:GLU:HG3	12:A:407:LYS:H	1.86	0.40
14:C:62:GLU:HG2	15:D:114:ARG:NH2	2.36	0.40
14:C:157:GLN:NE2	14:C:318:PRO:HD3	2.34	0.40
14:C:229:ARG:NE	14:C:232:ARG:HG3	2.36	0.40
14:C:313:ARG:HH11	14:C:314:LYS:H	1.69	0.40
15:D:99:ASN:C	15:D:115:ILE:HG12	2.45	0.40
15:D:132:LEU:HB3	15:D:137:ASN:HA	2.02	0.40
16:E:268:ASP:OD1	16:E:269:THR:N	2.49	0.40
18:G:89:SER:OG	24:M:120:HIS:ND1	2.43	0.40
23:L:193:ARG:O	23:L:196:ARG:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:M:72:HIS:CE1	24:M:105:ASN:HB3	2.57	0.40
27:P:76:LEU:HD23	27:P:76:LEU:HA	1.95	0.40
28:Q:140:LEU:O	28:Q:144:ASP:HB2	2.21	0.40
22:k:38:ILE:HD12	22:k:202:LEU:HG	2.03	0.40
22:k:104:ASN:OD1	29:r:57:ARG:NH2	2.43	0.40
1:U:501:LEU:HD13	1:U:548:LEU:HD11	2.02	0.40
2:V:194:LYS:HG2	2:V:200:ARG:HH22	1.86	0.40
3:W:72:LYS:HD2	3:W:123:ARG:HD3	2.02	0.40
3:W:172:GLU:OE1	3:W:172:GLU:N	2.54	0.40
6:Z:84:LYS:HE3	9:c:76:PRO:HB3	2.03	0.40
6:Z:204:LYS:HG2	7:a:357:CYS:HB2	2.04	0.40
7:a:100:THR:HA	7:a:103:LYS:HG2	2.04	0.40
10:d:67:ASP:OD1	10:d:69:PRO:HD2	2.22	0.40
10:d:105:PHE:HB2	10:d:166:PHE:CE1	2.56	0.40
12:A:95:VAL:HG21	12:A:143:ASP:OD1	2.22	0.40
12:A:95:VAL:HG12	12:A:144:ARG:HG2	2.04	0.40
13:B:109:VAL:HB	14:C:94:LYS:HB2	2.03	0.40
13:B:150:VAL:HG12	13:B:162:VAL:HG12	2.03	0.40
13:B:174:MET:HE3	13:B:272:ARG:NH2	2.36	0.40
13:B:313:LEU:HD22	13:B:341:LEU:HD22	2.03	0.40
13:B:387:LYS:HD2	13:B:430:LYS:HZ2	1.86	0.40
16:E:372:ARG:NH1	24:M:171:ALA:HB2	2.35	0.40
21:J:64:ALA:HB2	21:J:217:LEU:HD21	2.02	0.40
22:K:217:LEU:H	22:K:229:PHE:HZ	0.48	0.40
25:N:18:SER:HB2	25:N:30:VAL:HA	2.03	0.40
26:O:13:VAL:HG22	26:O:177:VAL:HG22	2.03	0.40
27:P:26:ARG:NH1	27:P:186:ILE:HD12	2.35	0.40
29:R:83:LEU:HD11	29:R:97:MET:HE1	2.03	0.40
22:k:225:ASN:HB2	22:k:226:PHE:CG	2.56	0.40
24:m:201:HIS:CE1	24:m:206:ASP:HB2	2.55	0.40
29:r:115:ASP:HB3	29:r:117:GLU:H	1.86	0.40
1:U:68:PHE:HE2	1:U:80:TYR:HE2	1.70	0.40
1:U:93:ASN:OD1	1:U:94:SER:N	2.54	0.40
1:U:253:TYR:HE1	1:U:453:HIS:HE1	1.69	0.40
2:V:392:TYR:O	2:V:395:ILE:HG22	2.21	0.40
3:W:100:ALA:O	3:W:104:MET:N	2.50	0.40
3:W:363:ILE:HG23	3:W:415:PHE:CE2	2.57	0.40
3:W:445:LEU:HD12	3:W:448:LYS:NZ	2.36	0.40
5:Y:228:MET:HG3	5:Y:229:ILE:HD12	2.04	0.40
6:Z:62:ASP:OD1	6:Z:62:ASP:N	2.55	0.40
6:Z:144:VAL:HA	6:Z:152:SER:H	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:259:VAL:HG13	9:c:298:GLN:HG3	2.04	0.40
12:A:354:ILE:HB	12:A:385:ILE:HD11	2.04	0.40
12:A:357:ILE:HG13	12:A:360:ARG:NH2	2.36	0.40
14:C:249:ASP:HA	14:C:250:GLU:HA	1.72	0.40
16:E:87:LEU:HD22	16:E:91:LYS:HD3	2.04	0.40
17:F:166:THR:O	17:F:166:THR:OG1	2.39	0.40
24:M:40:ARG:HE	24:M:161:TRP:CD1	2.39	0.40
23:l:176:MET:SD	24:m:56:LYS:HE2	2.61	0.40
25:n:29:ARG:NH2	26:o:139:GLU:OE2	2.55	0.40
31:t:67:LEU:HD23	31:t:67:LEU:HA	1.97	0.40
32:f:170:TRP:CZ3	32:f:208:LEU:HB3	2.55	0.40
32:f:482:ILE:HD13	32:f:482:ILE:HA	1.96	0.40
2:V:200:ARG:HA	2:V:203:LEU:HB2	2.04	0.40
3:W:59:ASP:HA	3:W:63:THR:HG23	2.02	0.40
5:Y:15:PRO:HB2	5:Y:113:ARG:NH1	2.36	0.40
5:Y:300:ARG:O	5:Y:304:TYR:N	2.51	0.40
6:Z:262:LEU:HD12	9:c:249:LEU:HD22	2.02	0.40
9:c:227:GLU:HB2	9:c:230:THR:CA	2.52	0.40
9:c:250:GLU:O	9:c:253:LYS:HG2	2.20	0.40
10:d:75:MET:HG2	10:d:102:ASN:HD22	1.86	0.40
16:E:233:ASP:OD2	17:F:315:ASN:ND2	2.54	0.40
30:S:179:PHE:O	30:S:183:ALA:HB2	2.21	0.40
25:n:127:ILE:HD12	25:n:136:TYR:CD1	2.56	0.40
32:f:211:ILE:HA	32:f:214:VAL:HG22	2.04	0.40
32:f:338:ASP:HA	32:f:341:GLU:HG3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	U	798/911 (88%)	735 (92%)	62 (8%)	1 (0%)	48	83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	V	478/480 (100%)	413 (86%)	59 (12%)	6 (1%)	9	41
3	W	454/456 (100%)	406 (89%)	45 (10%)	3 (1%)	18	56
4	X	239/380 (63%)	213 (89%)	26 (11%)	0	100	100
5	Y	376/378 (100%)	333 (89%)	38 (10%)	5 (1%)	9	41
6	Z	284/286 (99%)	253 (89%)	30 (11%)	1 (0%)	30	67
7	a	371/373 (100%)	331 (89%)	38 (10%)	2 (0%)	24	63
8	b	189/191 (99%)	174 (92%)	15 (8%)	0	100	100
9	c	274/287 (96%)	242 (88%)	28 (10%)	4 (2%)	8	39
10	d	255/257 (99%)	227 (89%)	27 (11%)	1 (0%)	30	67
11	e	36/70 (51%)	30 (83%)	6 (17%)	0	100	100
12	A	359/361 (99%)	312 (87%)	43 (12%)	4 (1%)	11	45
13	B	346/348 (99%)	295 (85%)	46 (13%)	5 (1%)	9	40
14	C	382/384 (100%)	339 (89%)	41 (11%)	2 (0%)	24	63
15	D	378/380 (100%)	333 (88%)	44 (12%)	1 (0%)	36	72
16	E	351/353 (99%)	321 (92%)	29 (8%)	1 (0%)	36	72
17	F	362/377 (96%)	322 (89%)	38 (10%)	2 (1%)	21	59
18	G	238/240 (99%)	224 (94%)	14 (6%)	0	100	100
18	g	238/240 (99%)	226 (95%)	12 (5%)	0	100	100
19	H	230/232 (99%)	213 (93%)	17 (7%)	0	100	100
19	h	230/232 (99%)	215 (94%)	15 (6%)	0	100	100
20	I	248/250 (99%)	236 (95%)	12 (5%)	0	100	100
20	i	248/250 (99%)	228 (92%)	20 (8%)	0	100	100
21	J	237/243 (98%)	216 (91%)	20 (8%)	1 (0%)	30	67
21	j	237/243 (98%)	222 (94%)	15 (6%)	0	100	100
22	K	224/234 (96%)	205 (92%)	19 (8%)	0	100	100
22	k	224/234 (96%)	203 (91%)	18 (8%)	3 (1%)	9	41
23	L	236/238 (99%)	224 (95%)	12 (5%)	0	100	100
23	l	236/238 (99%)	222 (94%)	14 (6%)	0	100	100
24	M	238/245 (97%)	221 (93%)	17 (7%)	0	100	100
24	m	238/245 (97%)	220 (92%)	18 (8%)	0	100	100
25	N	189/191 (99%)	179 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	n	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
26	O	218/220 (99%)	210 (96%)	8 (4%)	0	100	100
26	o	218/220 (99%)	211 (97%)	7 (3%)	0	100	100
27	P	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
27	p	202/204 (99%)	186 (92%)	16 (8%)	0	100	100
28	Q	197/199 (99%)	179 (91%)	18 (9%)	0	100	100
28	q	197/199 (99%)	177 (90%)	20 (10%)	0	100	100
29	R	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
29	r	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
30	S	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
30	s	211/213 (99%)	201 (95%)	10 (5%)	0	100	100
31	T	213/215 (99%)	204 (96%)	9 (4%)	0	100	100
31	t	213/215 (99%)	201 (94%)	12 (6%)	0	100	100
32	f	669/908 (74%)	579 (86%)	82 (12%)	8 (1%)	10	43
All	All	12761/13430 (95%)	11639 (91%)	1072 (8%)	50 (0%)	31	67

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	U	364	VAL
2	V	82	LEU
2	V	83	GLU
2	V	84	LYS
3	W	68	VAL
3	W	135	LYS
5	Y	64	GLN
5	Y	350	VAL
12	A	161	VAL
22	k	229	PHE
32	f	337	LEU
32	f	364	GLN
32	f	367	SER
32	f	665	GLU
2	V	81	GLN
3	W	138	VAL
5	Y	357	ASN
5	Y	359	PRO

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Mol	Chain	Res	Type
9	c	157	ILE
9	c	227	GLU
13	B	175	LYS
13	B	176	VAL
14	C	214	VAL
22	k	227	HIS
32	f	183	PRO
32	f	365	VAL
7	a	340	VAL
12	A	206	ILE
12	A	317	VAL
13	B	218	PRO
15	D	151	ILE
32	f	184	LEU
32	f	326	LEU
5	Y	67	VAL
9	c	156	VAL
14	C	298	ILE
17	F	282	ILE
2	V	241	ARG
6	Z	144	VAL
21	J	200	GLN
22	k	225	ASN
10	d	213	ARG
2	V	101	LEU
7	a	336	VAL
9	c	189	ILE
13	B	179	ALA
13	B	325	VAL
12	A	172	VAL
17	F	326	VAL
16	E	175	PRO

5.3.2 Protein sidechains [i](#)

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	685/779 (88%)	679 (99%)	6 (1%)	70	78
2	V	414/414 (100%)	405 (98%)	9 (2%)	45	64
3	W	416/416 (100%)	405 (97%)	11 (3%)	40	61
4	X	208/327 (64%)	204 (98%)	4 (2%)	50	66
5	Y	334/334 (100%)	331 (99%)	3 (1%)	70	78
6	Z	257/257 (100%)	251 (98%)	6 (2%)	44	63
7	a	333/333 (100%)	325 (98%)	8 (2%)	43	63
8	b	167/167 (100%)	164 (98%)	3 (2%)	51	67
9	c	243/252 (96%)	233 (96%)	10 (4%)	27	48
10	d	231/231 (100%)	228 (99%)	3 (1%)	61	73
11	e	38/63 (60%)	36 (95%)	2 (5%)	20	41
12	A	308/308 (100%)	300 (97%)	8 (3%)	40	61
13	B	304/304 (100%)	291 (96%)	13 (4%)	26	47
14	C	332/332 (100%)	319 (96%)	13 (4%)	28	49
15	D	333/333 (100%)	323 (97%)	10 (3%)	36	57
16	E	308/308 (100%)	304 (99%)	4 (1%)	61	73
17	F	312/321 (97%)	305 (98%)	7 (2%)	45	64
18	G	192/205 (94%)	190 (99%)	2 (1%)	68	77
18	g	193/205 (94%)	191 (99%)	2 (1%)	68	77
19	H	164/190 (86%)	163 (99%)	1 (1%)	78	82
19	h	164/190 (86%)	164 (100%)	0	100	100
20	I	193/210 (92%)	191 (99%)	2 (1%)	68	77
20	i	193/210 (92%)	191 (99%)	2 (1%)	68	77
21	J	152/207 (73%)	150 (99%)	2 (1%)	61	73
21	j	152/207 (73%)	152 (100%)	0	100	100
22	K	186/196 (95%)	183 (98%)	3 (2%)	55	69
22	k	186/196 (95%)	182 (98%)	4 (2%)	45	64
23	L	198/204 (97%)	198 (100%)	0	100	100
23	l	198/204 (97%)	197 (100%)	1 (0%)	81	83
24	M	192/202 (95%)	191 (100%)	1 (0%)	81	83
24	m	192/202 (95%)	190 (99%)	2 (1%)	68	77
25	N	148/148 (100%)	147 (99%)	1 (1%)	76	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	n	148/148 (100%)	145 (98%)	3 (2%)	48	66
26	O	177/181 (98%)	177 (100%)	0	100	100
26	o	177/181 (98%)	177 (100%)	0	100	100
27	P	172/173 (99%)	172 (100%)	0	100	100
27	p	172/173 (99%)	172 (100%)	0	100	100
28	Q	164/170 (96%)	163 (99%)	1 (1%)	78	82
28	q	164/170 (96%)	163 (99%)	1 (1%)	78	82
29	R	153/156 (98%)	153 (100%)	0	100	100
29	r	153/156 (98%)	153 (100%)	0	100	100
30	S	174/178 (98%)	174 (100%)	0	100	100
30	s	174/178 (98%)	174 (100%)	0	100	100
31	T	175/178 (98%)	174 (99%)	1 (1%)	78	82
31	t	175/178 (98%)	175 (100%)	0	100	100
32	f	580/763 (76%)	564 (97%)	16 (3%)	38	59
All	All	10684/11438 (93%)	10519 (98%)	165 (2%)	55	71

All (165) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	U	473	VAL
1	U	554	LEU
1	U	603	LEU
1	U	629	THR
1	U	746	ILE
1	U	773	PHE
2	V	81	GLN
2	V	82	LEU
2	V	221	LEU
2	V	224	LEU
2	V	255	LEU
2	V	299	GLN
2	V	320	THR
2	V	322	VAL
2	V	453	HIS
3	W	136	ILE
3	W	140	ILE
3	W	141	GLU

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Mol	Chain	Res	Type
3	W	142	ARG
3	W	250	ILE
3	W	297	GLU
3	W	371	THR
3	W	384	LEU
3	W	402	ILE
3	W	432	LEU
3	W	455	LEU
4	X	200	ILE
4	X	331	LEU
4	X	356	LEU
4	X	387	ILE
5	Y	350	VAL
5	Y	357	ASN
5	Y	377	LEU
6	Z	91	ILE
6	Z	176	LEU
6	Z	186	THR
6	Z	196	HIS
6	Z	237	LEU
6	Z	266	ILE
7	a	28	LEU
7	a	33	LEU
7	a	125	ILE
7	a	185	ILE
7	a	217	LEU
7	a	234	ILE
7	a	245	VAL
7	a	340	VAL
8	b	53	THR
8	b	92	VAL
8	b	97	LEU
9	c	25	VAL
9	c	33	ILE
9	c	42	LEU
9	c	62	VAL
9	c	69	VAL
9	c	144	VAL
9	c	172	HIS
9	c	229	LEU
9	c	244	VAL
9	c	275	VAL

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Mol	Chain	Res	Type
10	d	122	LEU
10	d	158	ILE
10	d	189	ILE
11	e	4	LYS
11	e	5	LYS
12	A	125	LEU
12	A	153	LEU
12	A	157	ILE
12	A	161	VAL
12	A	191	VAL
12	A	220	THR
12	A	250	VAL
12	A	315	ILE
13	B	105	THR
13	B	135	ILE
13	B	136	LEU
13	B	159	VAL
13	B	164	MET
13	B	173	VAL
13	B	175	LYS
13	B	176	VAL
13	B	177	GLU
13	B	190	LEU
13	B	256	ILE
13	B	281	ILE
13	B	334	ILE
14	C	11	LEU
14	C	66	LEU
14	C	99	VAL
14	C	131	VAL
14	C	148	TYR
14	C	167	LEU
14	C	235	PHE
14	C	249	ASP
14	C	259	LEU
14	C	286	THR
14	C	295	THR
14	C	298	ILE
14	C	315	ILE
15	D	61	ILE
15	D	89	ILE
15	D	103	VAL

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Mol	Chain	Res	Type
15	D	116	LEU
15	D	186	THR
15	D	234	GLU
15	D	303	VAL
15	D	344	ILE
15	D	358	VAL
15	D	406	VAL
16	E	80	VAL
16	E	204	VAL
16	E	315	ILE
16	E	326	ILE
17	F	85	THR
17	F	124	ILE
17	F	169	ASP
17	F	231	THR
17	F	272	PHE
17	F	282	ILE
17	F	283	ILE
18	G	121	ILE
18	G	199	ILE
19	H	10	LEU
20	I	28	ILE
20	I	76	VAL
21	J	111	ILE
21	J	161	ILE
22	K	20	ARG
22	K	227	HIS
22	K	228	MET
24	M	196	ILE
25	N	127	ILE
28	Q	140	LEU
31	T	92	LEU
18	g	141	ILE
18	g	199	ILE
20	i	28	ILE
20	i	228	LEU
22	k	101	PHE
22	k	170	ILE
22	k	227	HIS
22	k	228	MET
23	l	38	LEU
24	m	151	ILE

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Mol	Chain	Res	Type
24	m	196	ILE
25	n	26	ILE
25	n	30	VAL
25	n	127	ILE
28	q	82	ASN
32	f	88	SER
32	f	184	LEU
32	f	207	LEU
32	f	337	LEU
32	f	370	MET
32	f	381	VAL
32	f	387	GLN
32	f	389	LYS
32	f	391	LEU
32	f	403	LYS
32	f	460	ASP
32	f	463	LEU
32	f	479	LEU
32	f	641	GLU
32	f	797	LEU
32	f	800	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (162) such sidechains are listed below:

Mol	Chain	Res	Type
1	U	70	HIS
1	U	107	HIS
1	U	111	GLN
1	U	149	GLN
1	U	267	ASN
1	U	345	ASN
1	U	389	ASN
1	U	438	GLN
1	U	453	HIS
1	U	464	GLN
1	U	467	ASN
1	U	475	HIS
1	U	491	GLN
1	U	500	ASN
1	U	604	HIS
1	U	685	GLN
1	U	698	GLN

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Mol	Chain	Res	Type
1	U	777	HIS
1	U	805	ASN
2	V	81	GLN
2	V	281	ASN
2	V	299	GLN
2	V	400	HIS
2	V	427	GLN
2	V	459	GLN
2	V	487	HIS
3	W	106	GLN
3	W	235	GLN
3	W	426	ASN
3	W	444	HIS
4	X	207	GLN
4	X	262	ASN
4	X	406	ASN
5	Y	48	ASN
5	Y	251	HIS
5	Y	363	ASN
5	Y	367	GLN
5	Y	378	ASN
6	Z	77	ASN
6	Z	102	HIS
6	Z	194	GLN
6	Z	224	HIS
6	Z	231	GLN
6	Z	256	GLN
7	a	23	HIS
7	a	46	GLN
7	a	164	GLN
7	a	227	ASN
7	a	257	GLN
7	a	290	GLN
7	a	337	GLN
8	b	47	ASN
8	b	76	HIS
8	b	105	HIS
8	b	137	ASN
8	b	149	ASN
9	c	30	GLN
9	c	92	GLN
9	c	115	HIS

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Mol	Chain	Res	Type
9	c	190	GLN
9	c	199	HIS
9	c	219	ASN
9	c	283	HIS
9	c	287	HIS
10	d	102	ASN
10	d	109	GLN
12	A	304	ASN
12	A	314	ASN
13	B	153	ASN
13	B	154	HIS
13	B	241	ASN
13	B	431	GLN
15	D	187	HIS
15	D	221	HIS
15	D	302	ASN
15	D	376	ASN
15	D	412	GLN
15	D	414	HIS
16	E	86	GLN
16	E	190	GLN
16	E	220	ASN
16	E	307	GLN
16	E	364	GLN
17	F	116	GLN
17	F	255	GLN
17	F	325	GLN
18	G	68	HIS
18	G	75	ASN
18	G	127	GLN
19	H	71	HIS
19	H	119	GLN
20	I	40	ASN
20	I	53	HIS
20	I	95	GLN
20	I	119	GLN
20	I	149	GLN
20	I	155	ASN
21	J	116	GLN
21	J	122	ASN
22	K	41	GLN
22	K	155	HIS

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Mol	Chain	Res	Type
22	K	214	ASN
22	K	224	GLN
22	K	227	HIS
23	L	59	HIS
23	L	60	GLN
23	L	90	GLN
23	L	146	GLN
23	L	152	ASN
23	L	166	GLN
24	M	97	ASN
26	O	116	HIS
26	O	193	ASN
27	P	93	ASN
28	Q	61	GLN
28	Q	82	ASN
29	R	85	ASN
31	T	81	HIS
31	T	185	ASN
31	T	213	HIS
18	g	12	HIS
18	g	75	ASN
18	g	193	GLN
19	h	21	GLN
19	h	71	HIS
20	i	53	HIS
20	i	95	GLN
20	i	102	GLN
20	i	119	GLN
20	i	149	GLN
20	i	198	ASN
21	j	85	ASN
21	j	120	GLN
22	k	114	GLN
23	l	65	HIS
23	l	90	GLN
23	l	152	ASN
25	n	7	GLN
25	n	77	HIS
25	n	158	ASN
26	o	193	ASN
27	p	93	ASN
27	p	169	GLN

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Mol	Chain	Res	Type
28	q	61	GLN
28	q	101	ASN
29	r	70	ASN
30	s	58	HIS
30	s	146	GLN
30	s	159	GLN
30	s	163	HIS
31	t	81	HIS
31	t	89	HIS
31	t	213	HIS
32	f	102	HIS
32	f	213	GLN
32	f	352	HIS
32	f	387	GLN
32	f	473	ASN
32	f	493	ASN
32	f	540	GLN
32	f	565	ASN
32	f	650	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

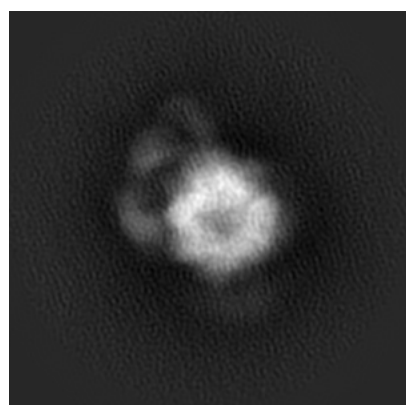
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8668. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

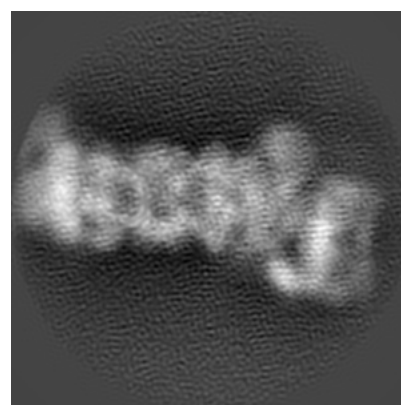
6.1.1 Primary map



X



Y

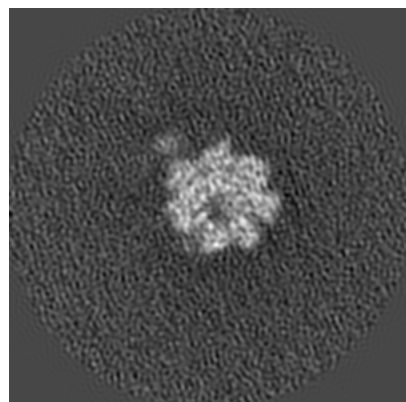


Z

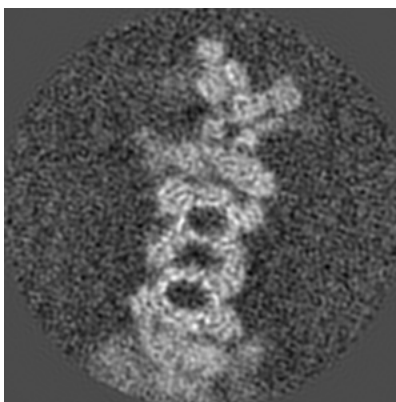
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

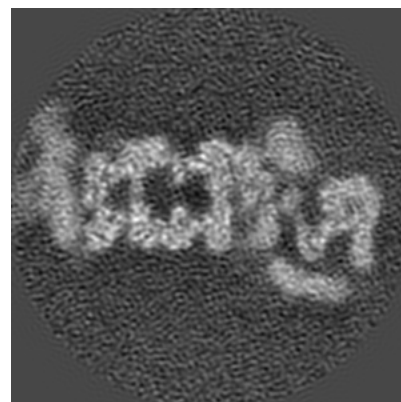
6.2.1 Primary map



X Index: 280



Y Index: 280

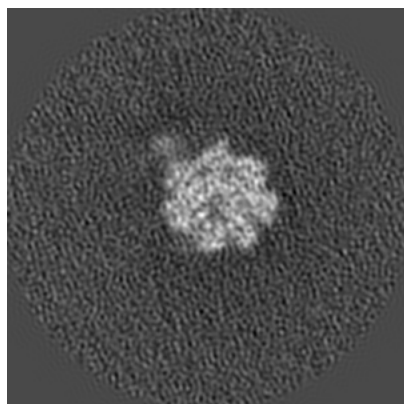


Z Index: 280

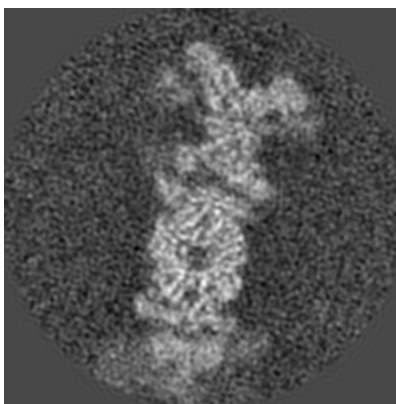
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

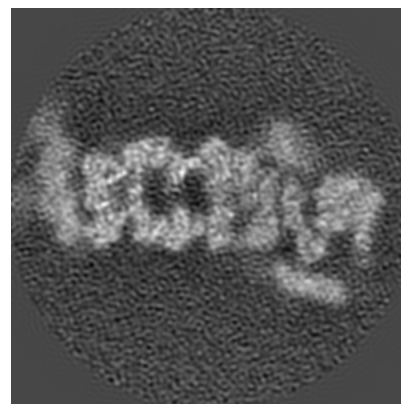
6.3.1 Primary map



X Index: 282



Y Index: 264

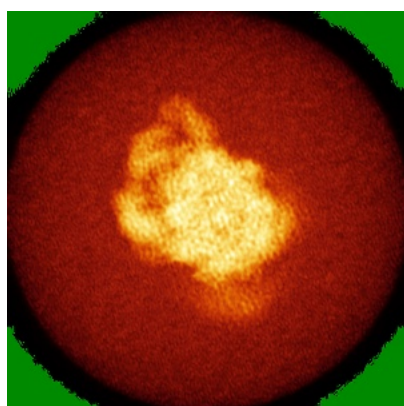


Z Index: 286

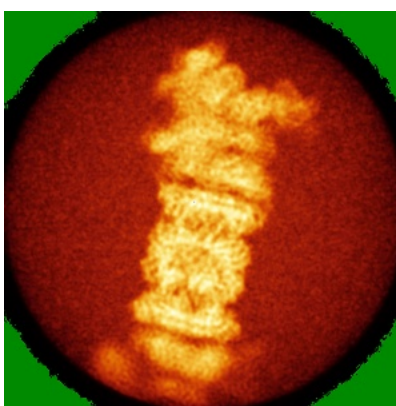
The images above show the largest variance slices of the map in three orthogonal directions.

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

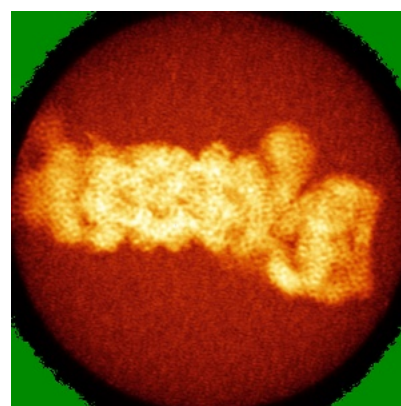
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

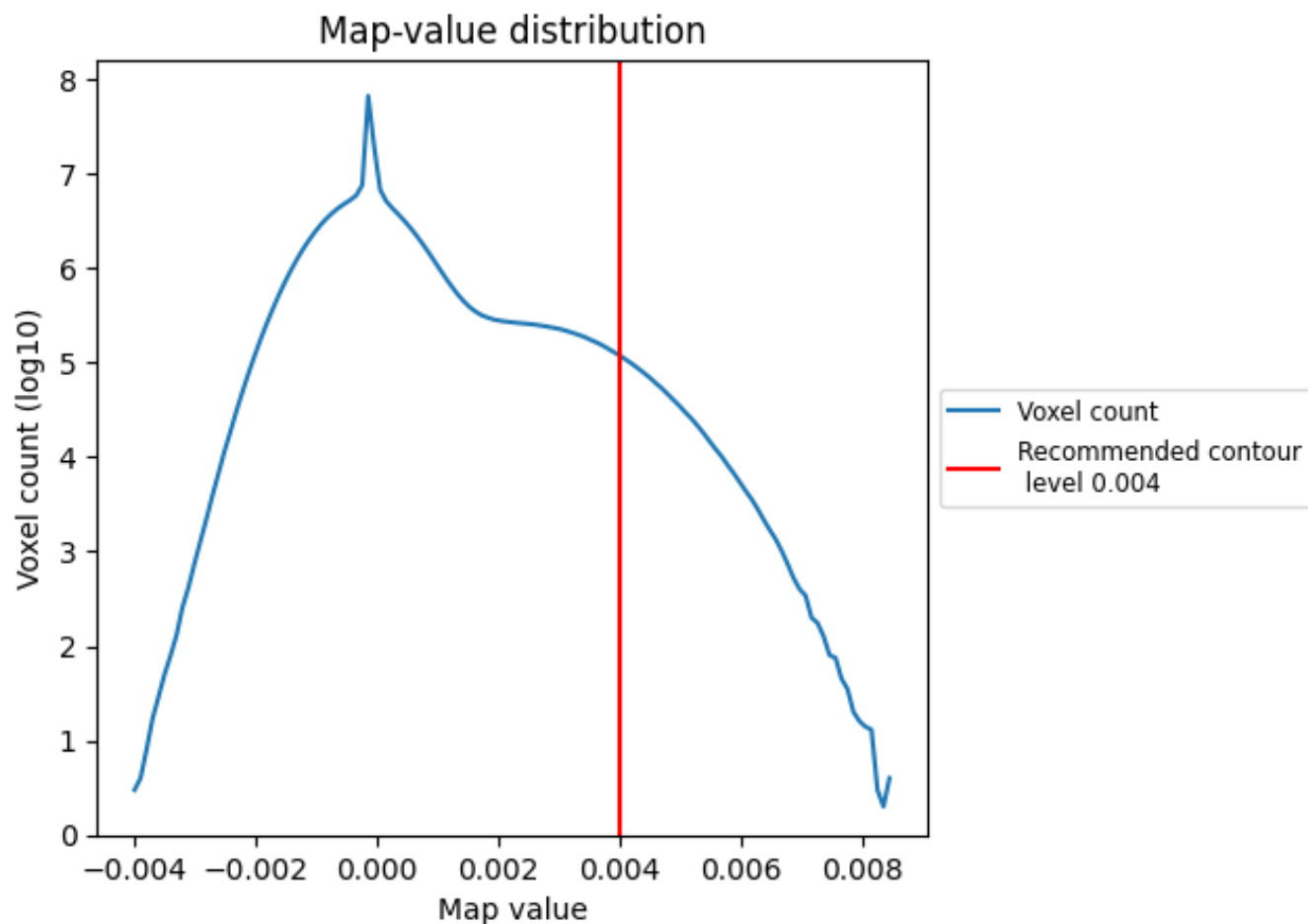
6.6 Mask visualisation

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

7 Map analysis [i](#)

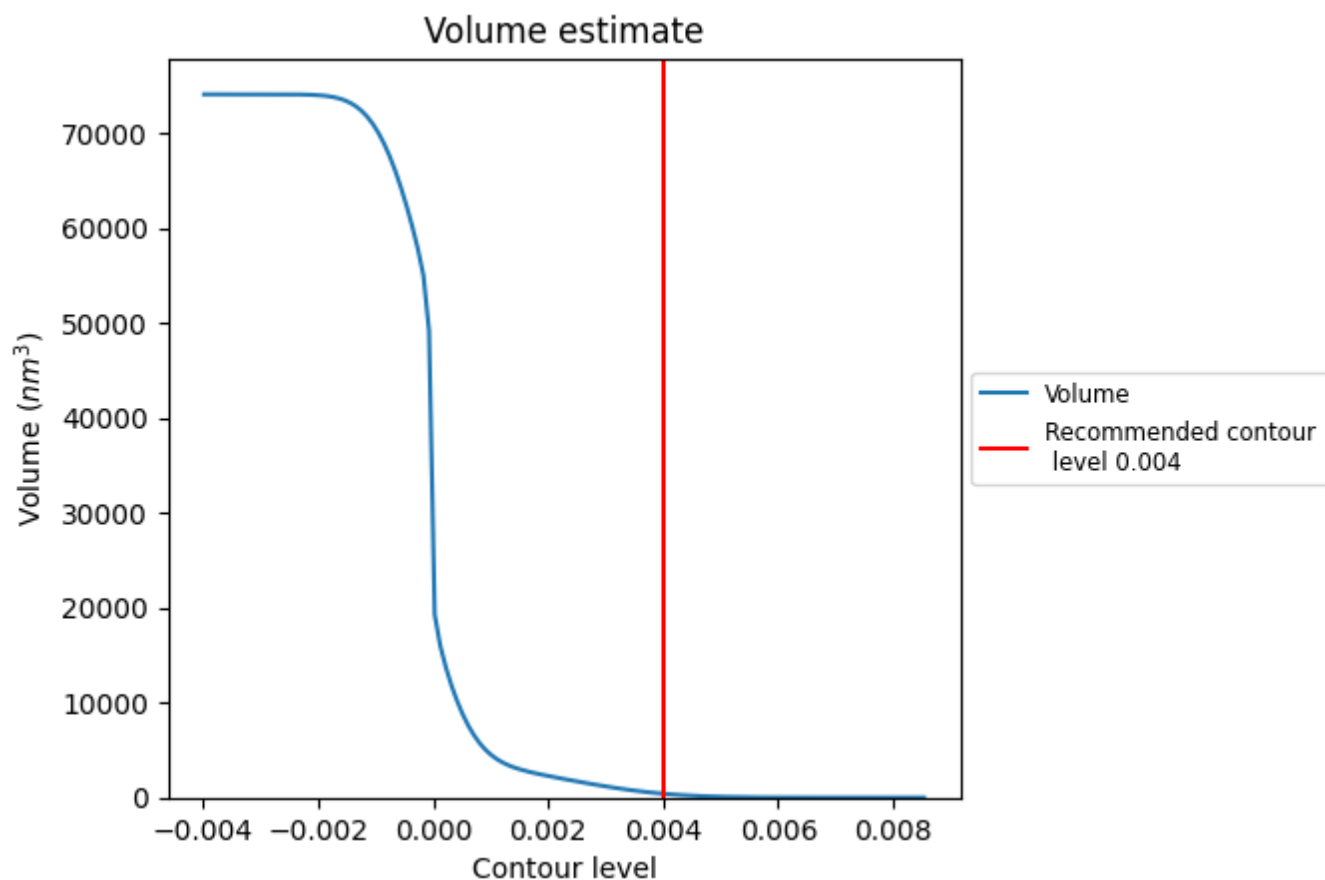
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

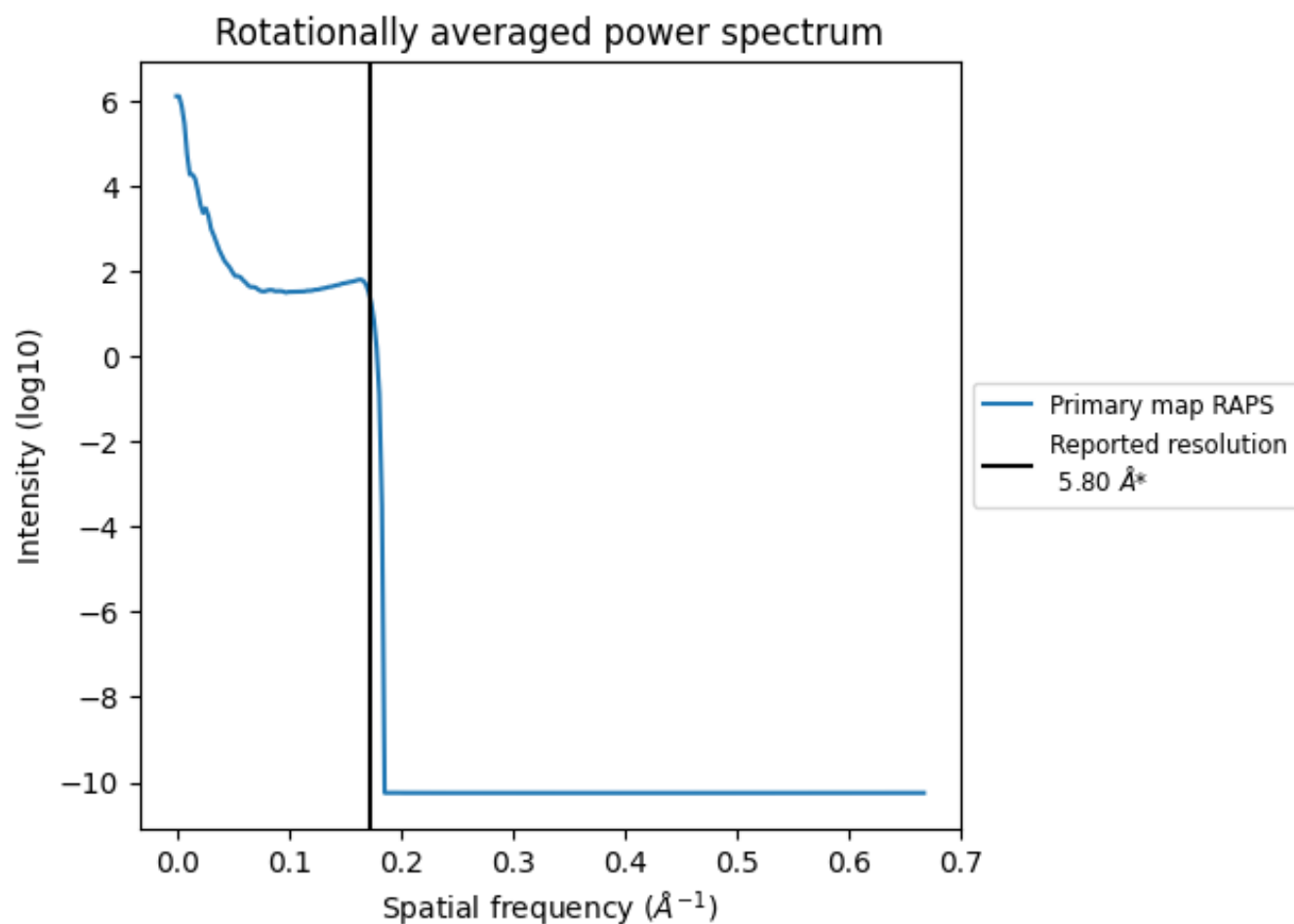
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 405 nm³; this corresponds to an approximate mass of 366 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 0.172 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

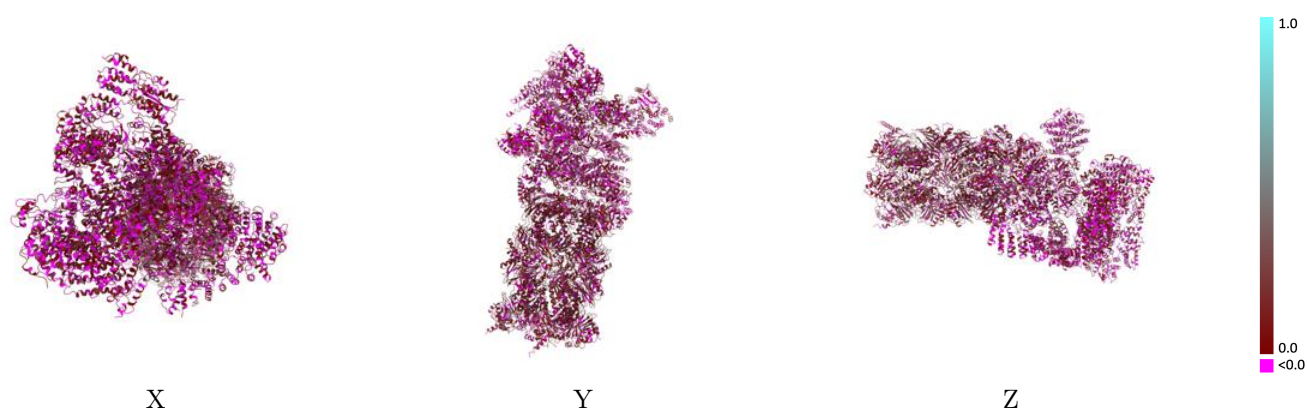
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8668 and PDB model 5VFU. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

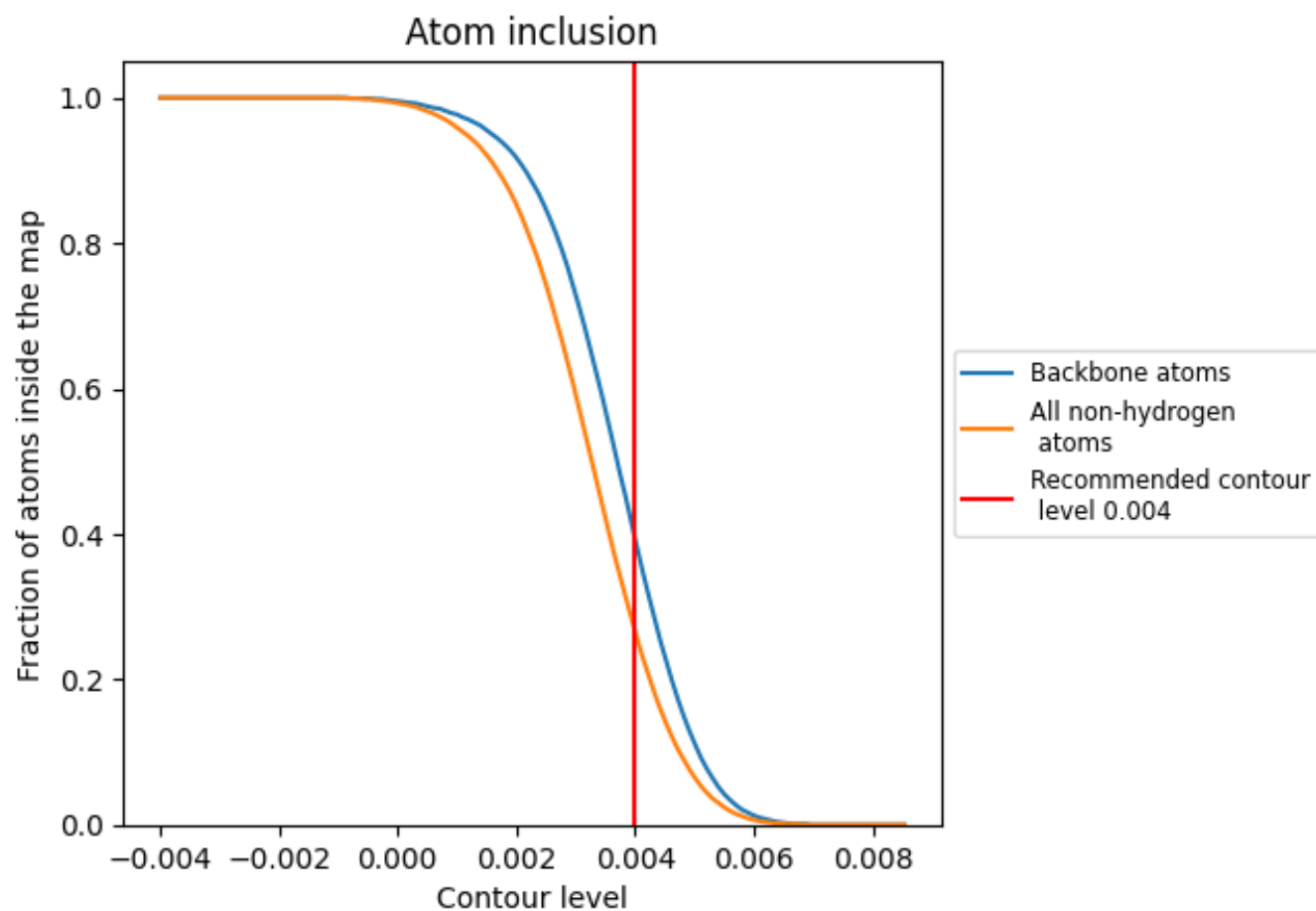


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 27% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2660	 0.0980
A	 0.2200	 0.0990
B	 0.1390	 0.0780
C	 0.1390	 0.0700
D	 0.1580	 0.0620
E	 0.1750	 0.0740
F	 0.1900	 0.0820
G	 0.3340	 0.1230
H	 0.3590	 0.1240
I	 0.3240	 0.1260
J	 0.3840	 0.1400
K	 0.3600	 0.1350
L	 0.4080	 0.1320
M	 0.3730	 0.1270
N	 0.4330	 0.1320
O	 0.4280	 0.1470
P	 0.4560	 0.1280
Q	 0.4330	 0.1480
R	 0.4850	 0.1440
S	 0.4390	 0.1460
T	 0.4970	 0.1530
U	 0.2190	 0.0670
V	 0.1150	 0.0620
W	 0.0590	 0.0590
X	 0.0580	 0.0180
Y	 0.1650	 0.0630
Z	 0.1760	 0.0760
a	 0.0840	 0.0600
b	 0.0790	 0.0550
c	 0.2020	 0.0920
d	 0.0790	 0.0290
e	 0.0610	 0.0310
f	 0.0640	 0.0400
g	 0.3650	 0.1320
h	 0.3980	 0.1420



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Chain	Atom inclusion	Q-score
i	 0.3310	 0.1280
j	 0.3490	 0.1290
k	 0.3650	 0.1410
l	 0.4020	 0.1280
m	 0.3610	 0.1150
n	 0.4620	 0.1440
o	 0.4440	 0.1520
p	 0.4520	 0.1350
q	 0.4460	 0.1370
r	 0.4670	 0.1380
s	 0.4490	 0.1400
t	 0.4980	 0.1630