



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:25 AM UTC

PDB ID : 5T0G / pdb_00005t0g
EMDB ID : EMD-8334
Title : Structural basis for dynamic regulation of the human 26S proteasome
Authors : Chen, S.; Wu, J.; Lu, Y.; Ma, Y.B.; Lee, B.H.; Yu, Z.; Ouyang, Q.; Finley, D.; Kirschner, M.W.; Mao, Y.
Deposited on : 2016-08-16
Resolution : 4.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

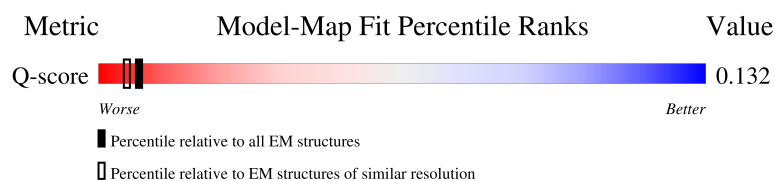
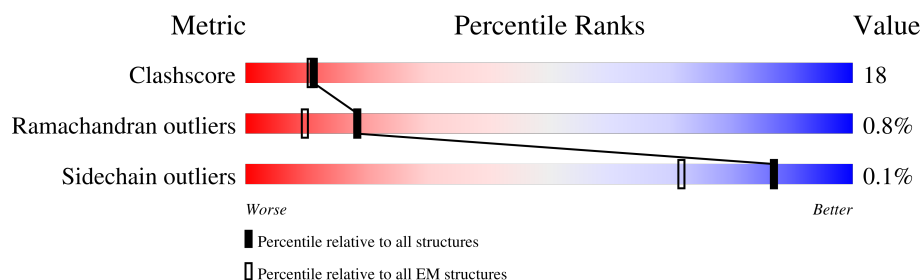
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	G	245	42% 62% 35% ..
2	H	233	39% 73% 27%
3	I	260	42% 65% 31% .
4	J	247	43% 66% 31% .

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Mol	Chain	Length	Quality of chain
5	K	240	
6	L	268	
7	M	254	
8	N	238	
9	O	276	
10	P	204	
11	Q	201	
12	R	262	
13	S	240	
14	T	263	
15	A	433	
16	B	440	
17	D	418	
18	E	403	
19	F	439	
20	C	398	
21	U	953	
22	V	533	
23	W	456	
24	X	422	
25	Y	389	
26	Z	324	
27	a	376	
28	b	377	
29	c	309	

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Mol	Chain	Length	Quality of chain
30	d	349	50% 42% 31% 26%
31	e	70	44% 27% 30% 43%
32	f	749	93% 40% 51% 7%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 77800 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 Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	233	Total	C	N	O	S	0	0
			1713	1084	290	334	5		

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

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

- Molecule 4 is a protein called Proteasome subunit alpha type-7.

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

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

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

- Molecule 6 is a protein called Proteasome subunit alpha type-1.

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

- Molecule 7 is a protein called Proteasome subunit alpha type-3.

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

- Molecule 8 is a protein called Proteasome subunit beta type-6.

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

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

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

- Molecule 10 is a protein called Proteasome subunit beta type-3.

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

- Molecule 11 is a protein called Proteasome subunit beta type-2.

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

- Molecule 12 is a protein called Proteasome subunit beta type-5.

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

- Molecule 13 is a protein called Proteasome subunit beta type-1.

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

- Molecule 14 is a protein called Proteasome subunit beta type-4.

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

- Molecule 15 is a protein called 26S protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	A	361	Total	C	N	O	S	0	0
			2835	1788	501	528	18		

- Molecule 16 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	341	Total	C	N	O	S	0	0
			2662	1671	453	526	12		

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

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

- Molecule 18 is a protein called 26S protease regulatory subunit 10B.

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

- Molecule 19 is a protein called 26S protease regulatory subunit 6A.

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

- Molecule 20 is a protein called 26S protease regulatory subunit 8.

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

- Molecule 21 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

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

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

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

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

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

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	380	Total	C	N	O	S	0	0
			3009	1918	509	570	12		

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

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

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

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

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	373	Total	C	N	O	S	0	0
			2995	1911	510	559	15		

- Molecule 28 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

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

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	287	Total	C	N	O	S	0	0
			2260	1430	389	422	19		

- Molecule 30 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

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

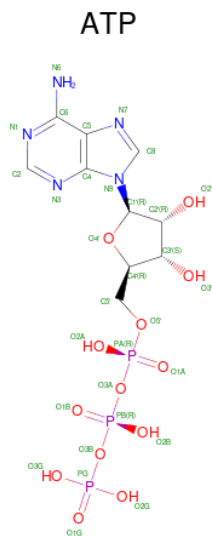
- Molecule 31 is a protein called 26S proteasome complex subunit DSS1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	694	Total	C	N	O	S	0	0
			5331	3364	899	1027	41		

- Molecule 33 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
33	A	1	Total 31	C 10	N 5	O 13	P 3	0
33	B	1	Total 31	C 10	N 5	O 13	P 3	0
33	D	1	Total 31	C 10	N 5	O 13	P 3	0
33	E	1	Total 31	C 10	N 5	O 13	P 3	0
33	F	1	Total 31	C 10	N 5	O 13	P 3	0
33	C	1	Total 31	C 10	N 5	O 13	P 3	0

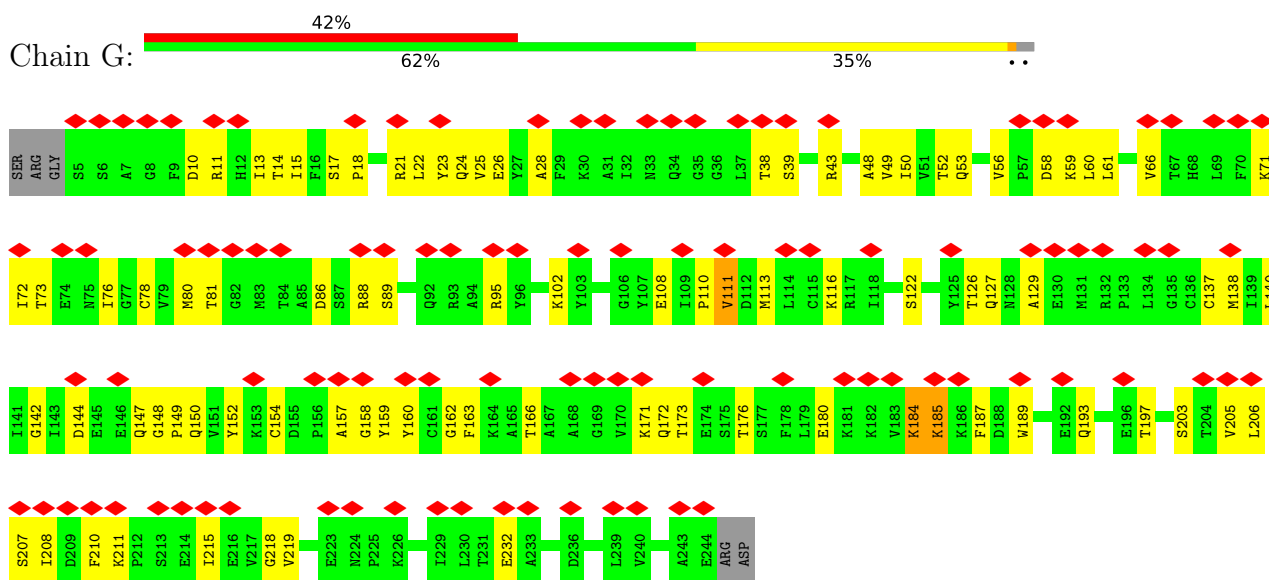
- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

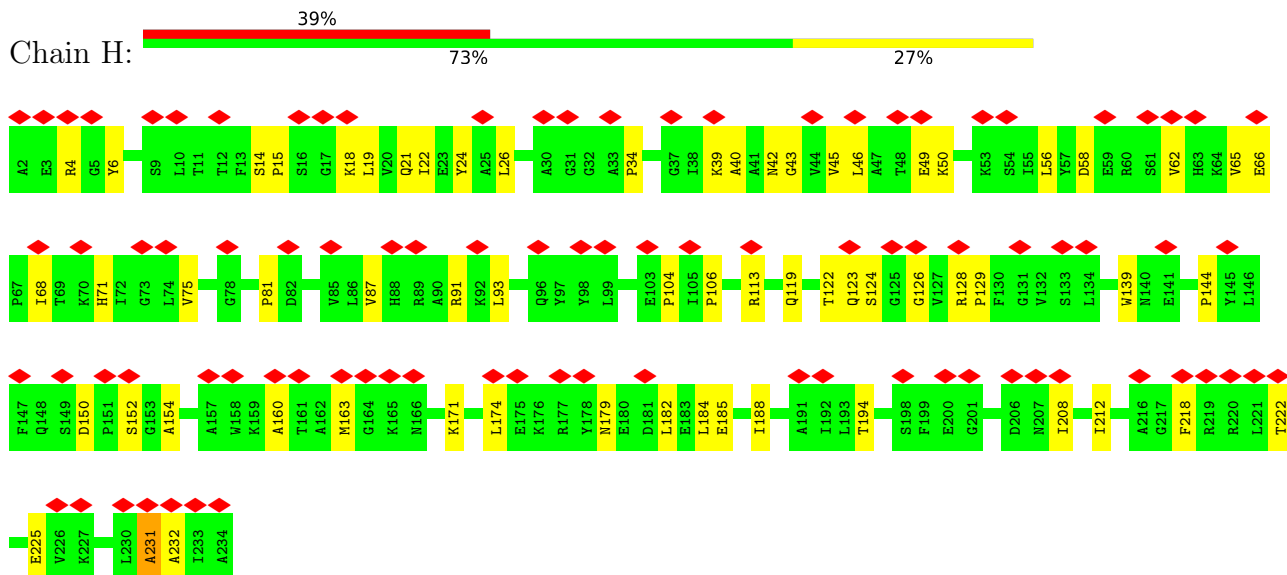
3 Residue-property plots [i](#)

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

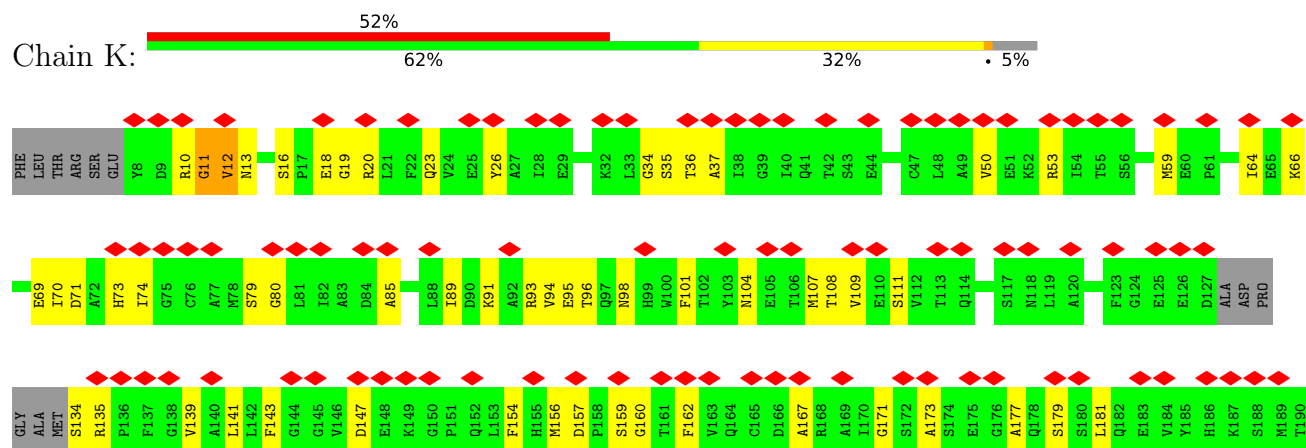
- Molecule 1: Proteasome subunit alpha type-6

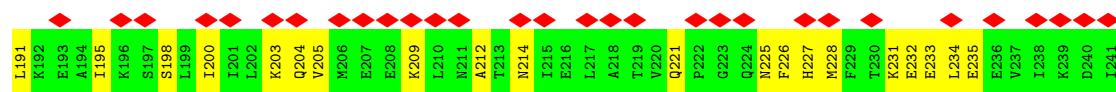


- Molecule 2: Proteasome subunit alpha type-2

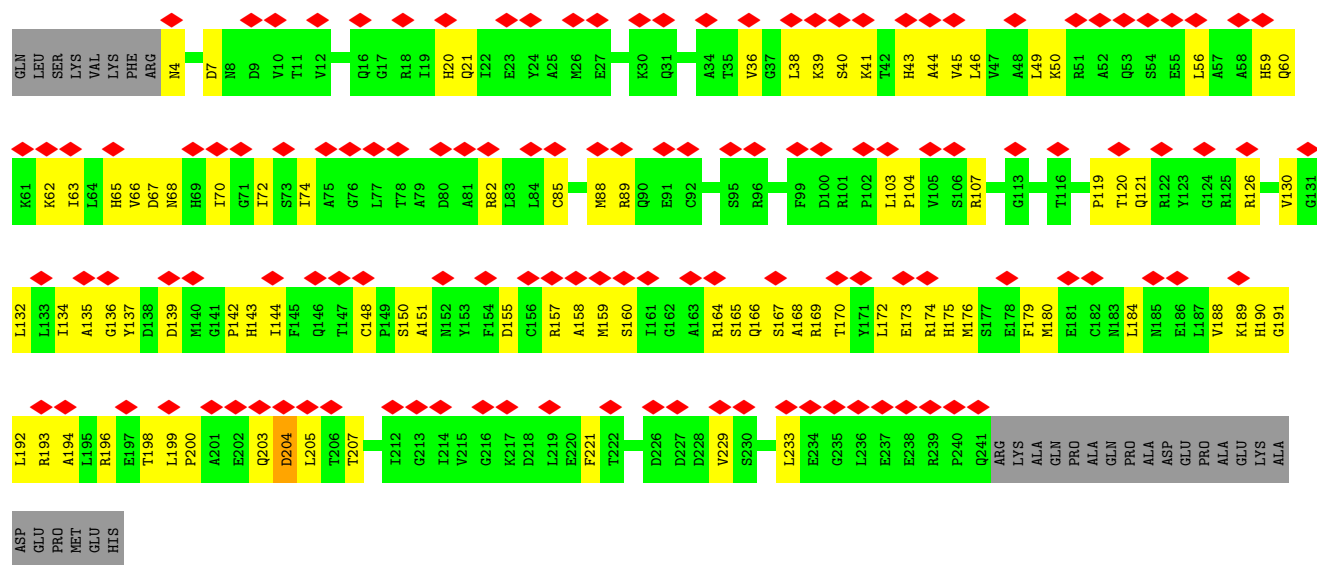


- Molecule 3: Proteasome subunit alpha type-4

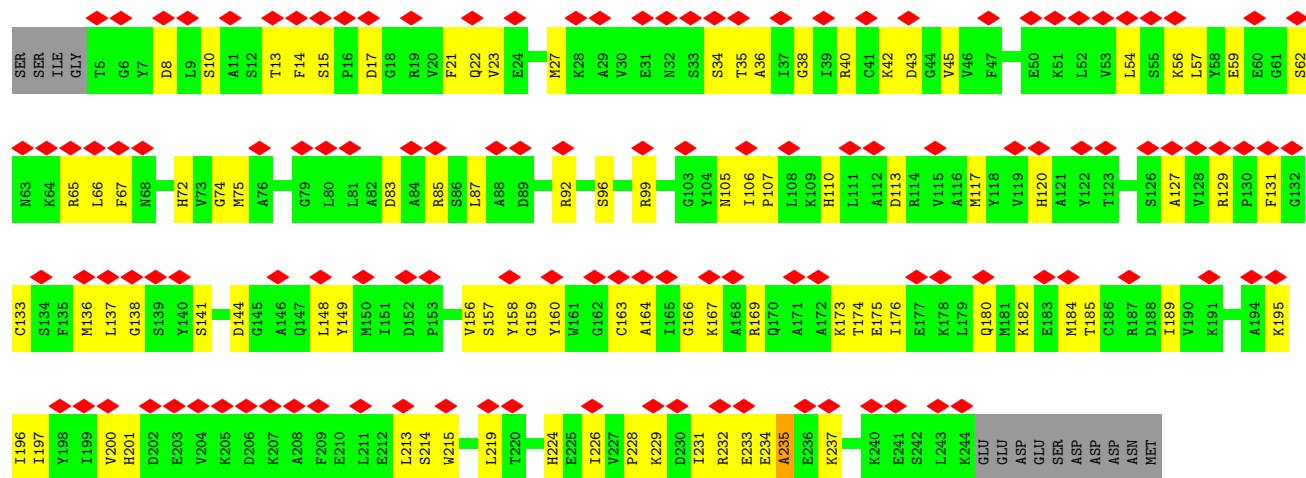




• Molecule 6: Proteasome subunit alpha type-1

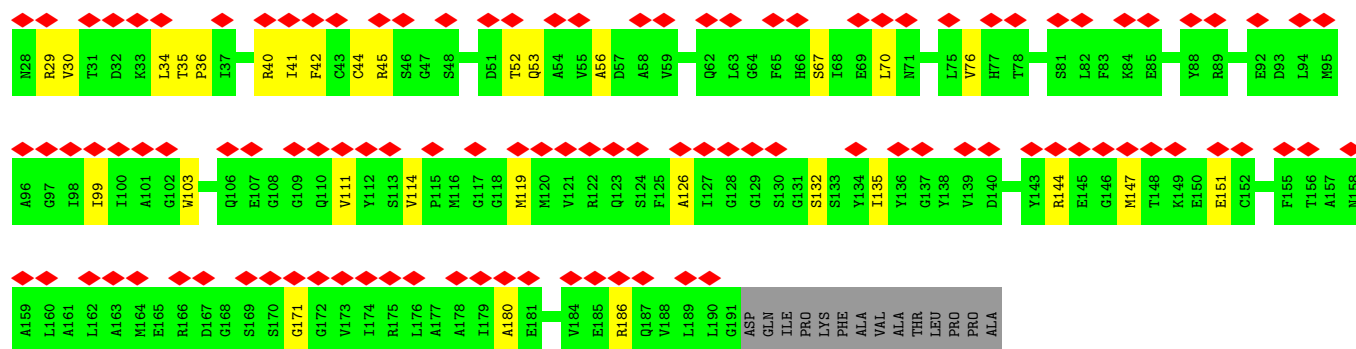


• Molecule 7: Proteasome subunit alpha type-3

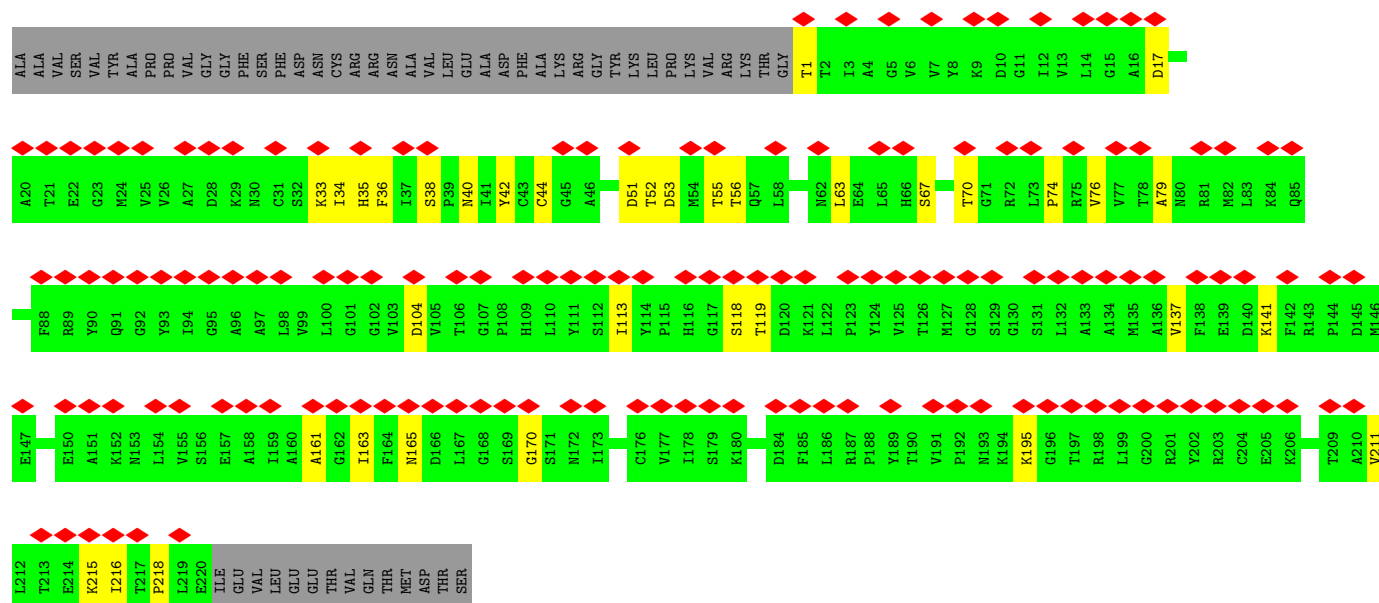


• Molecule 8: Proteasome subunit beta type-6



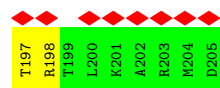


• Molecule 9: Proteasome subunit beta type-7

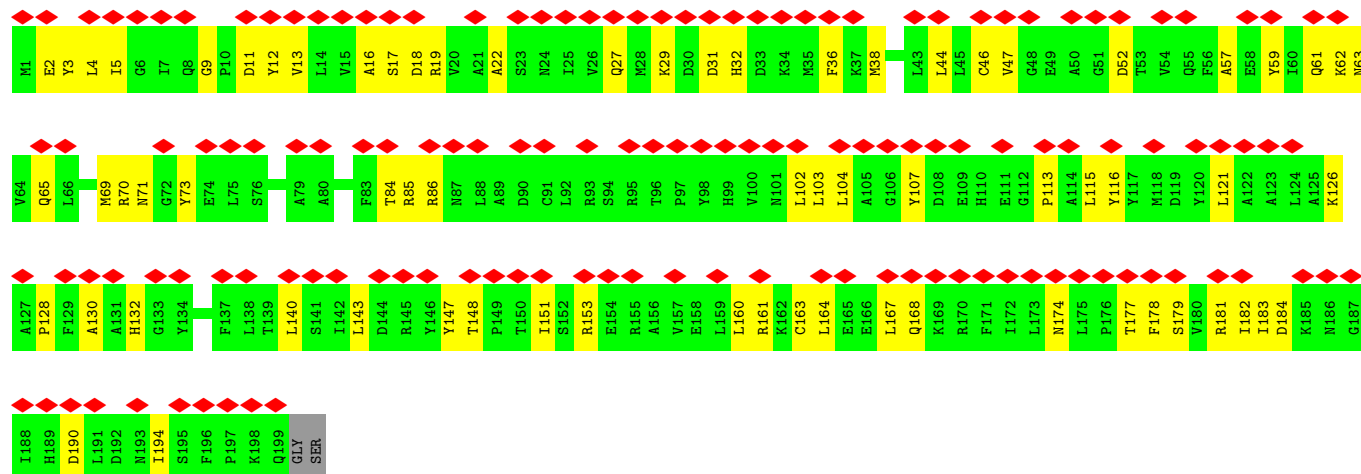


• Molecule 10: Proteasome subunit beta type-3

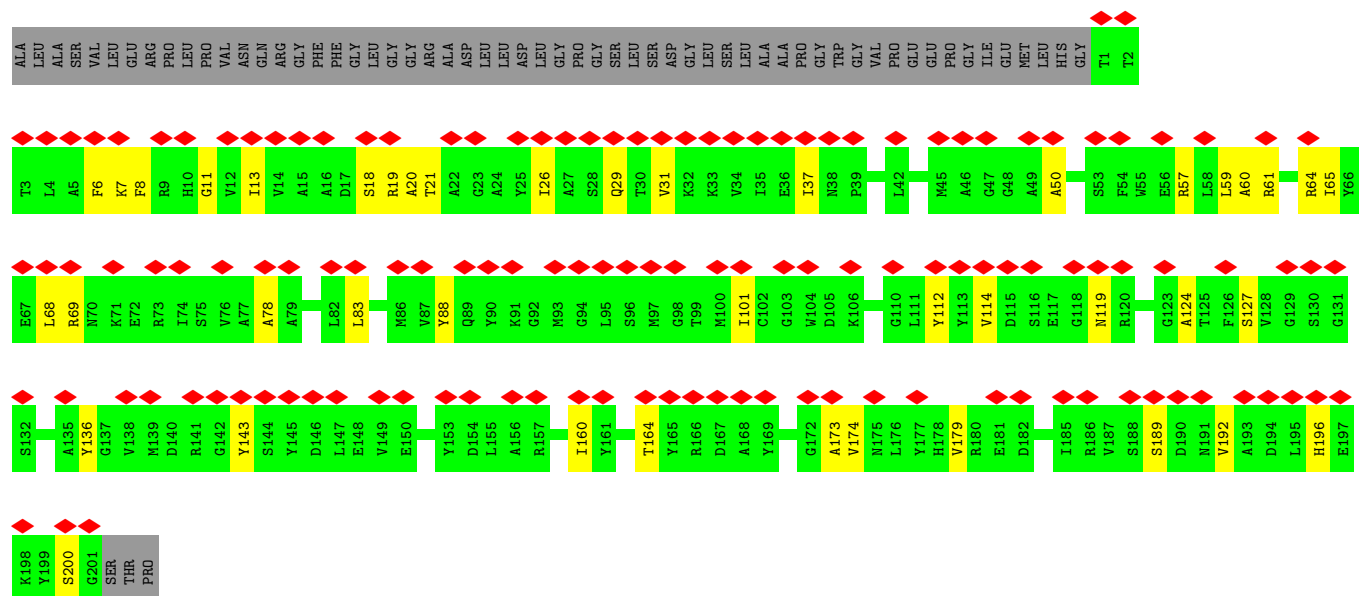




• Molecule 11: Proteasome subunit beta type-2

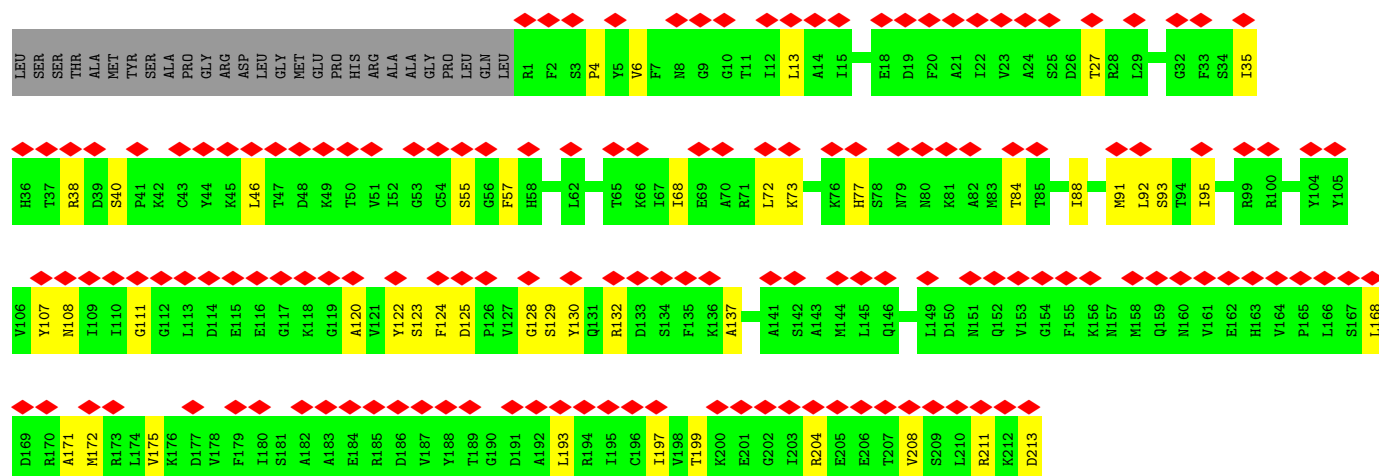


• Molecule 12: Proteasome subunit beta type-5

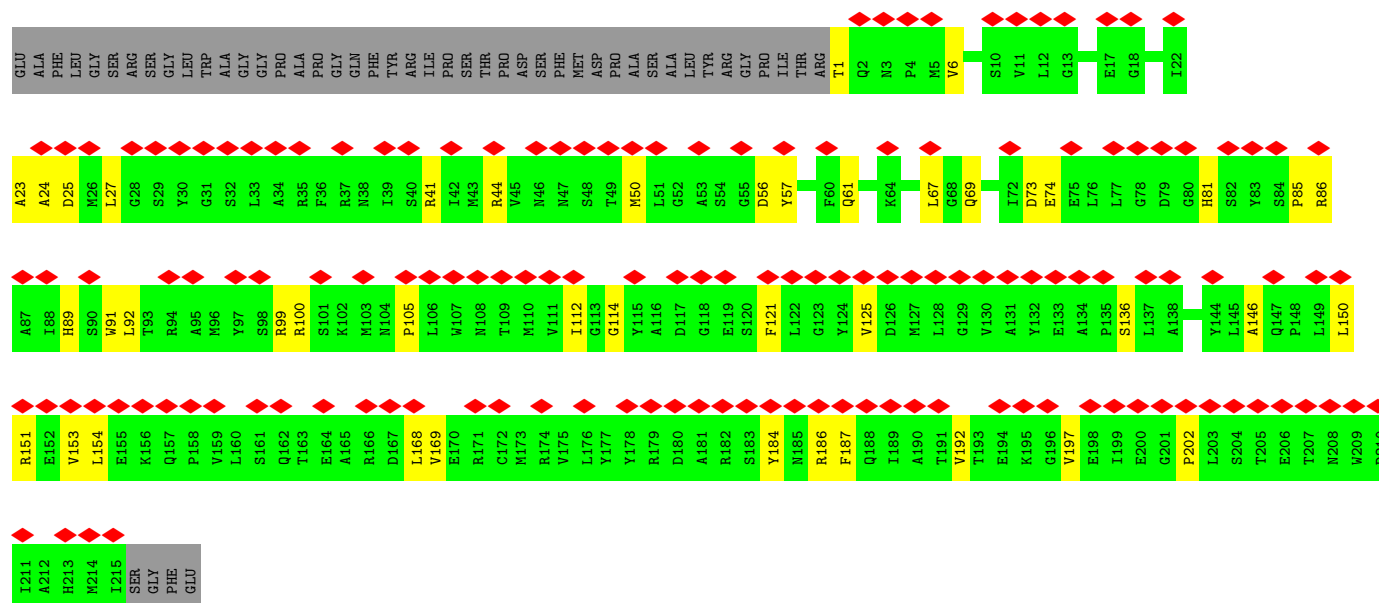


• Molecule 13: Proteasome subunit beta type-1

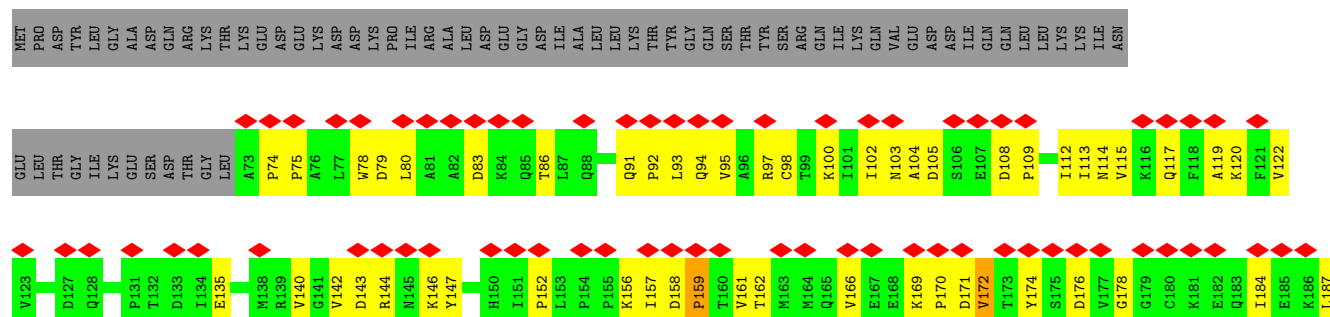


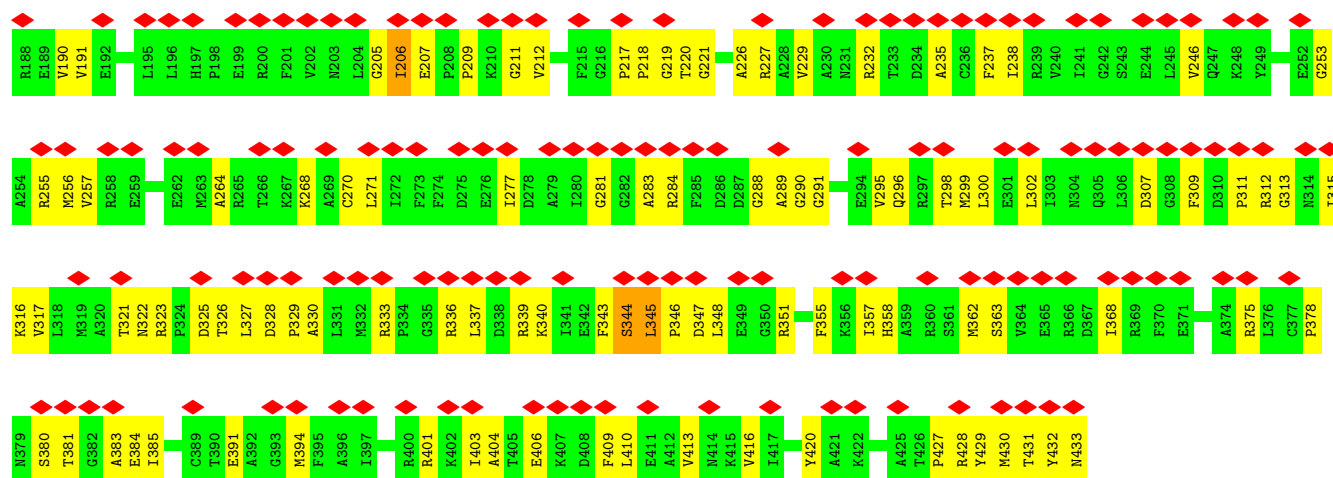


• Molecule 14: Proteasome subunit beta type-4

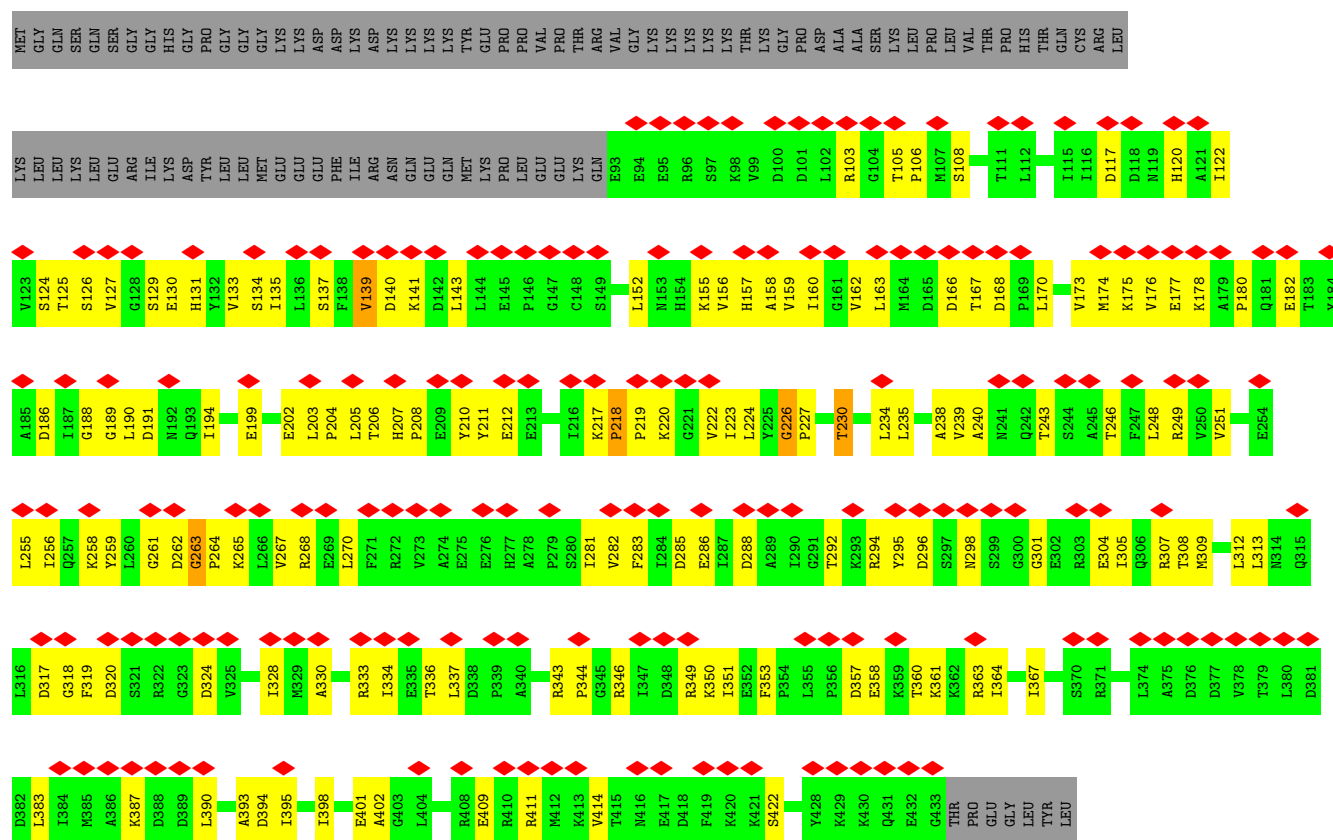
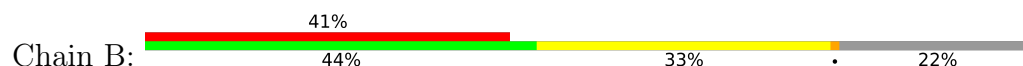


• Molecule 15: 26S protease regulatory subunit 7

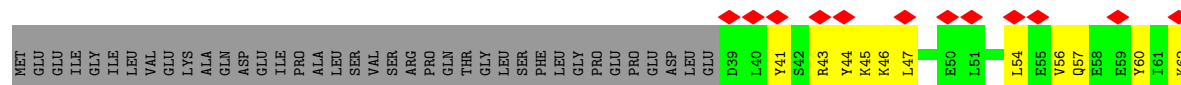
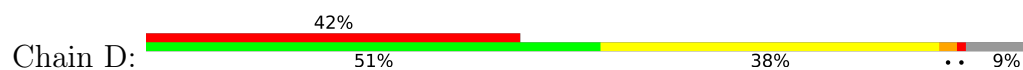


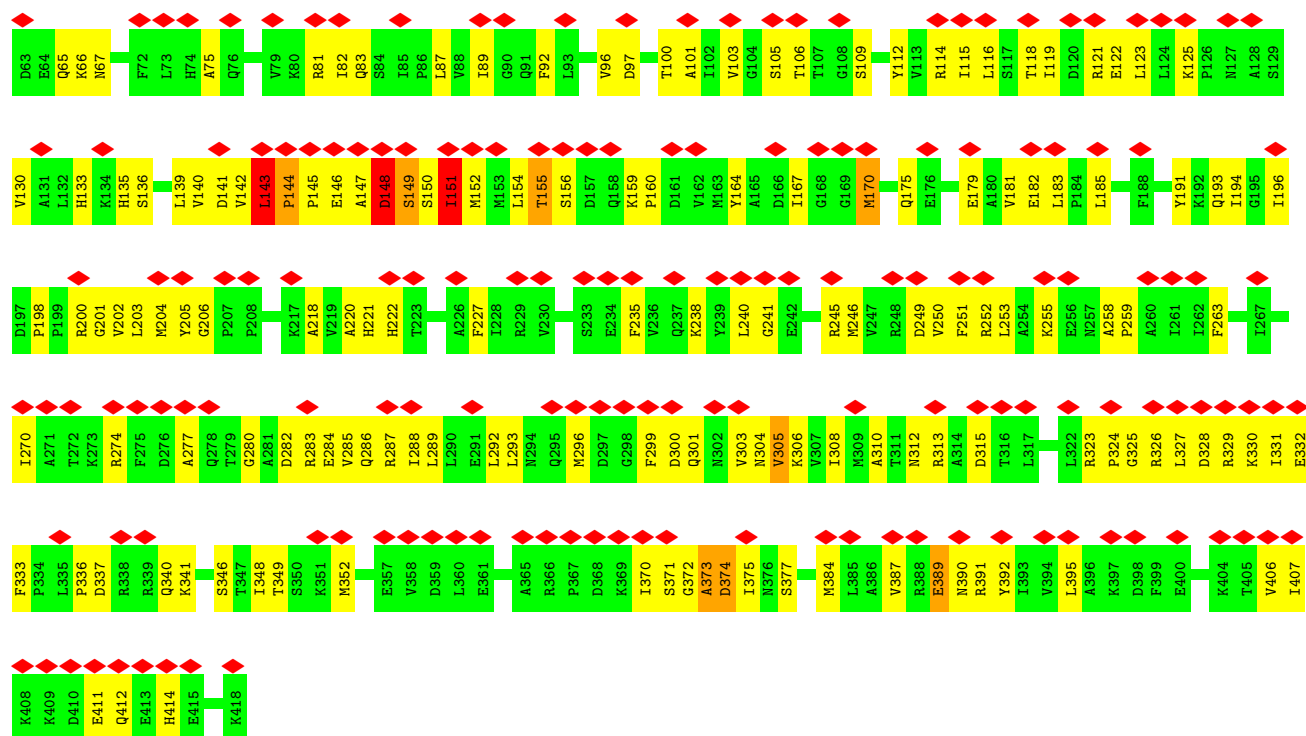


• Molecule 16: 26S protease regulatory subunit 4

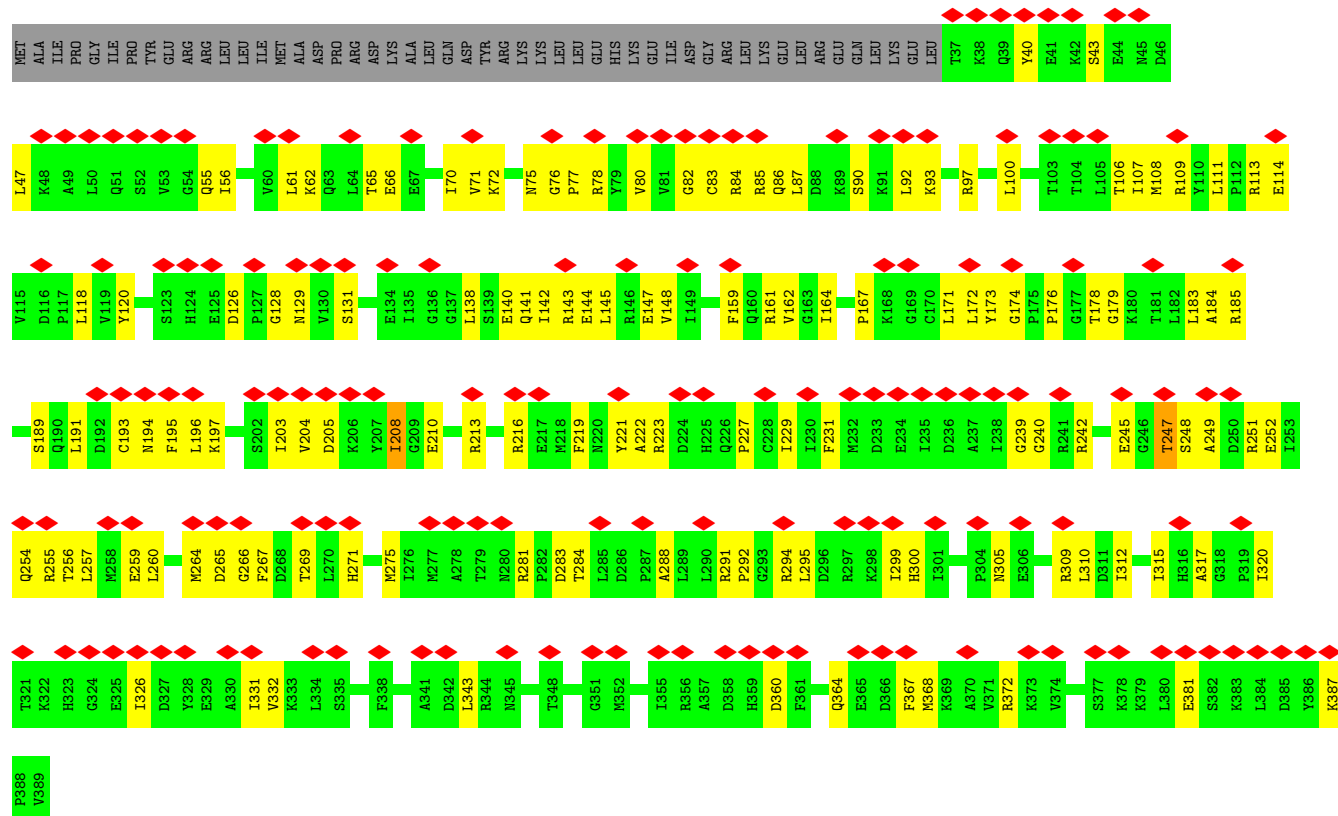
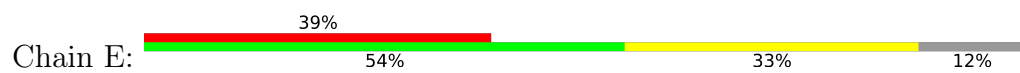


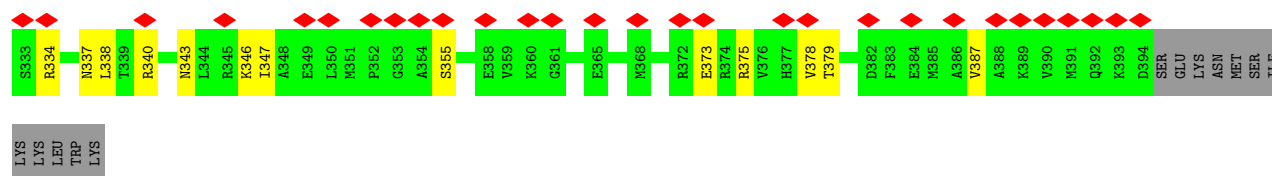
• Molecule 17: 26S protease regulatory subunit 6B



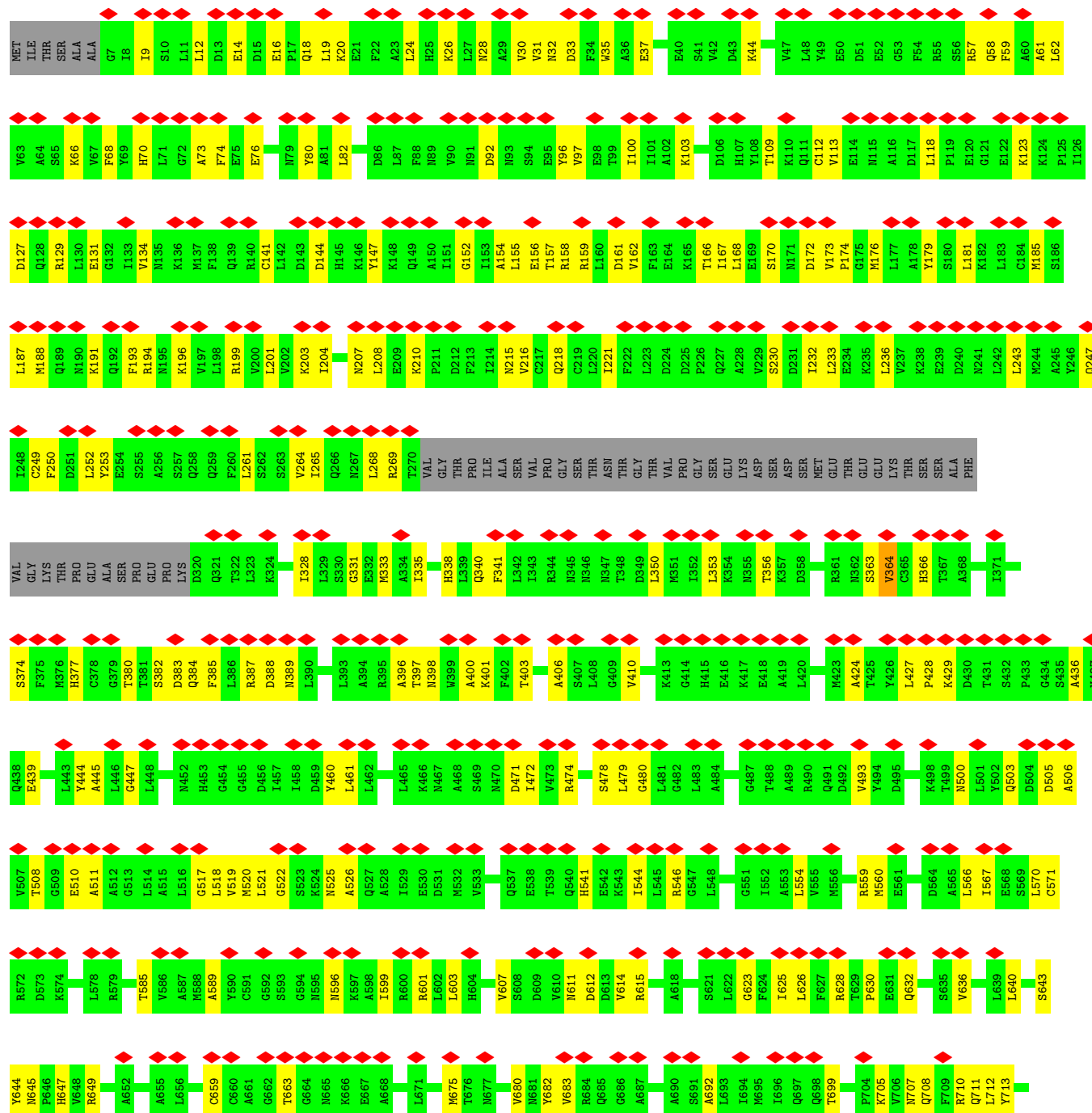


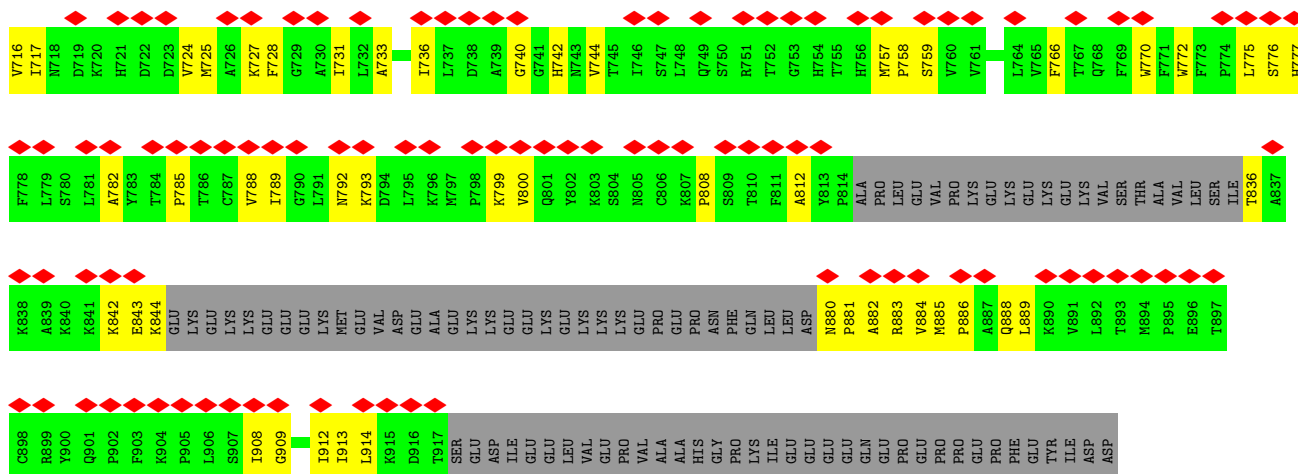
• Molecule 18: 26S protease regulatory subunit 10B



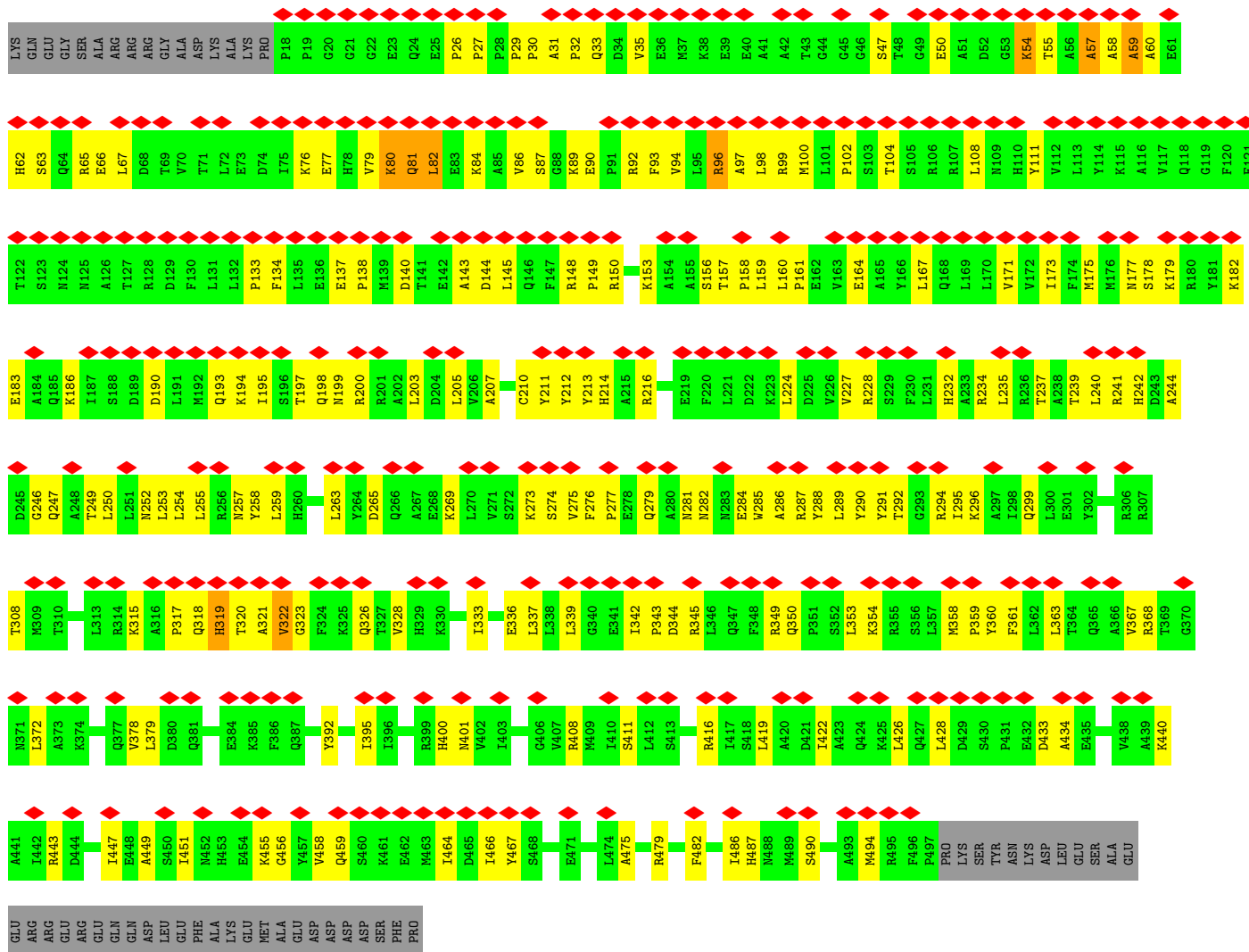


• Molecule 21: 26S proteasome non-ATPase regulatory subunit 1

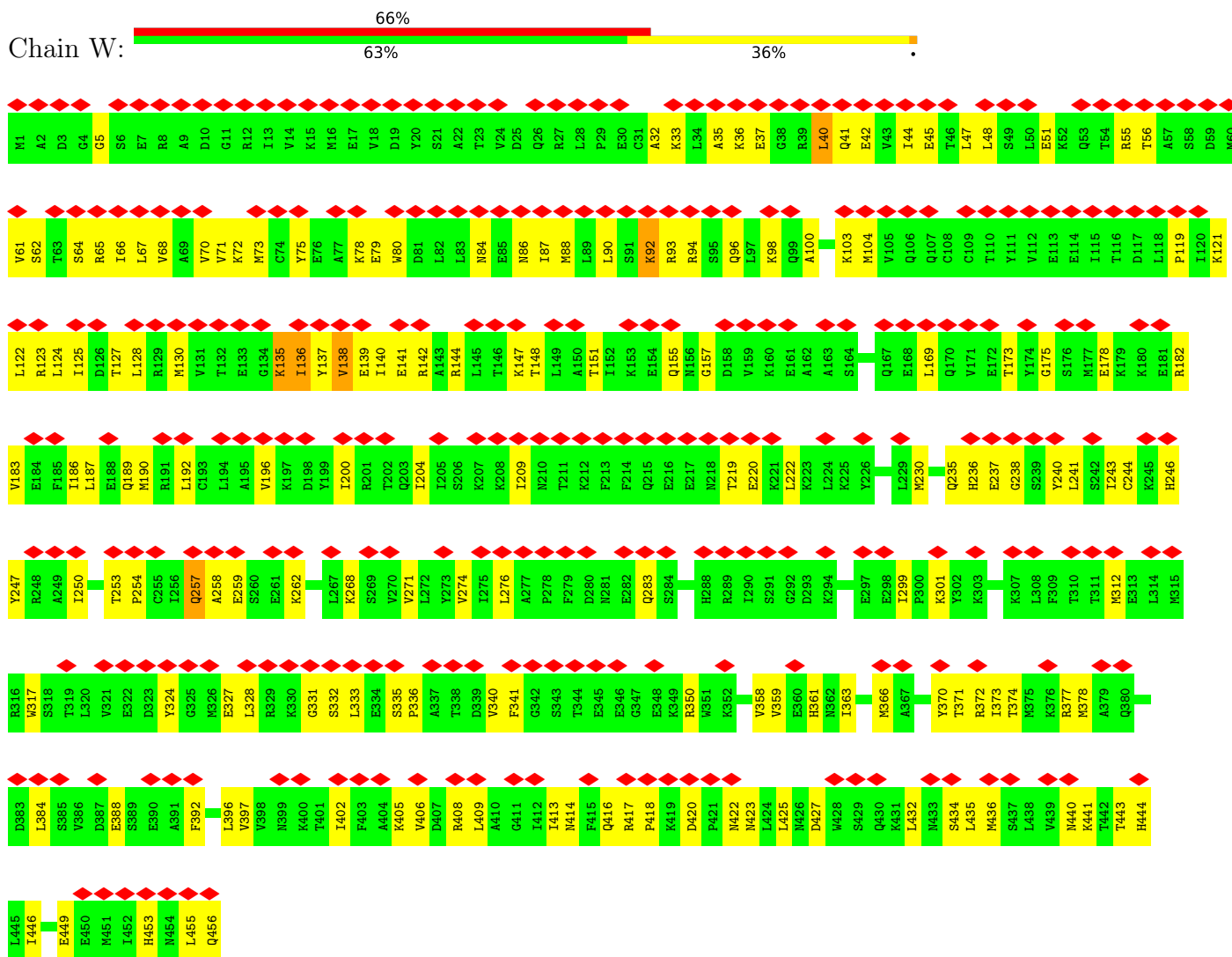




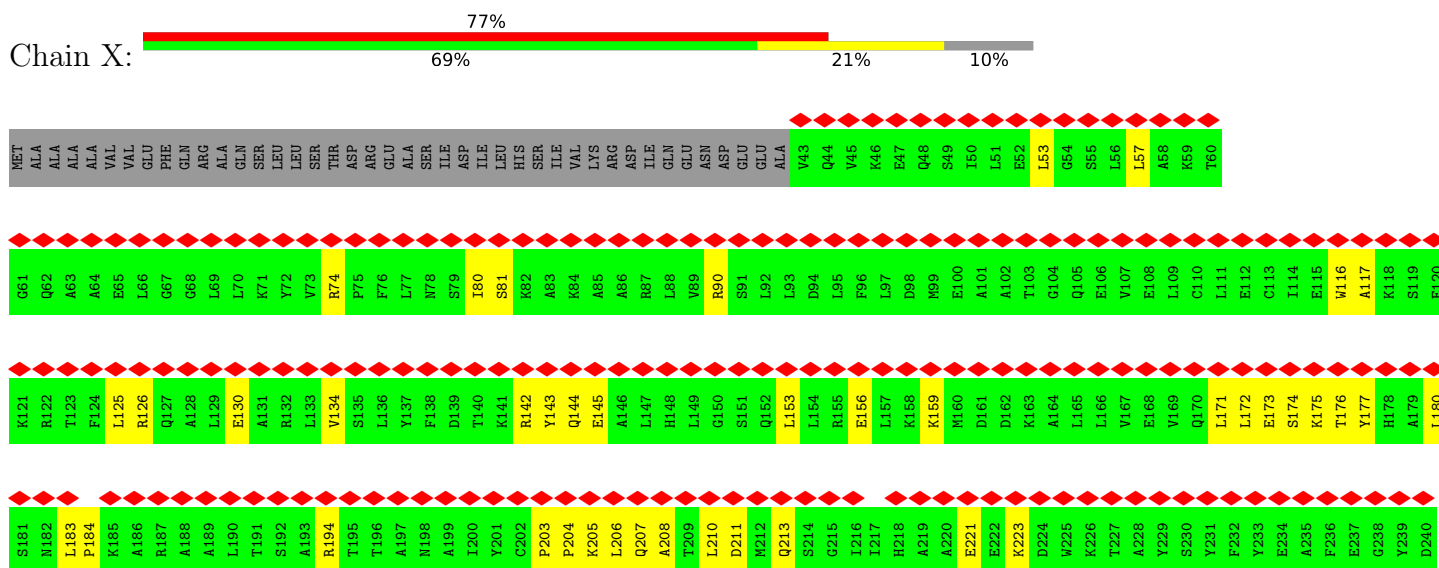
• Molecule 22: 26S proteasome non-ATPase regulatory subunit 3

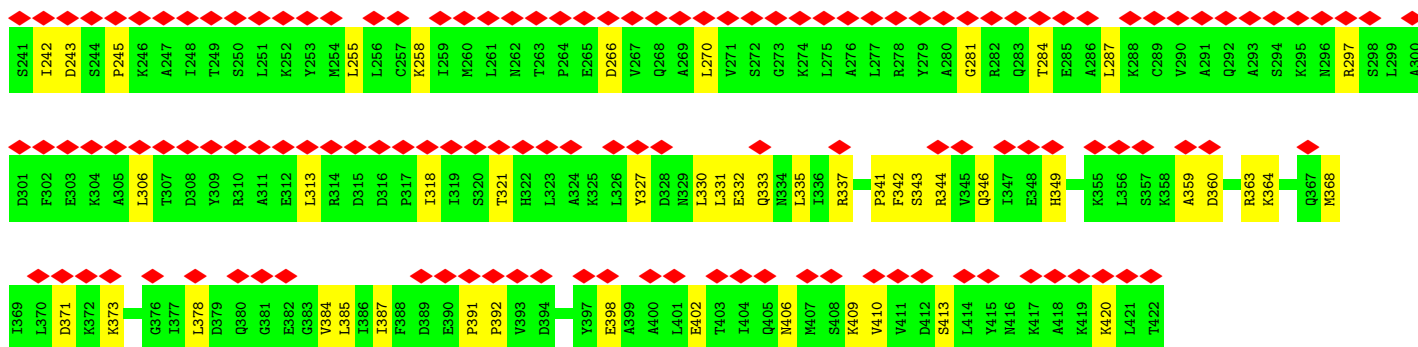


• Molecule 23: 26S proteasome non-ATPase regulatory subunit 12

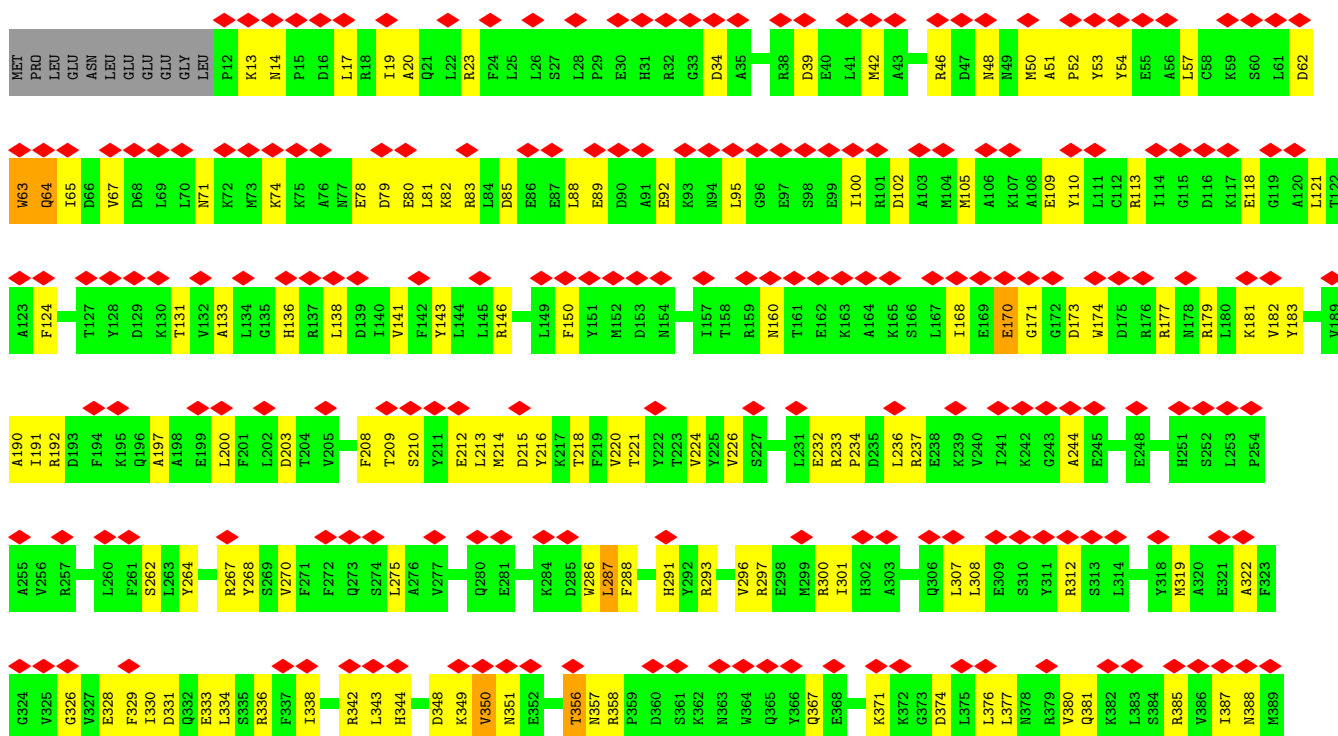


• Molecule 24: 26S proteasome non-ATPase regulatory subunit 11

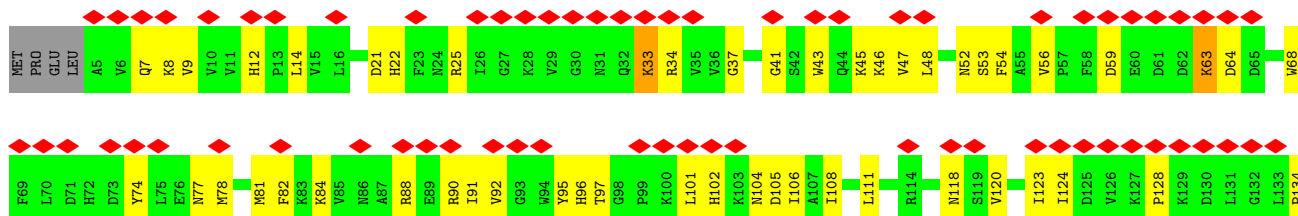


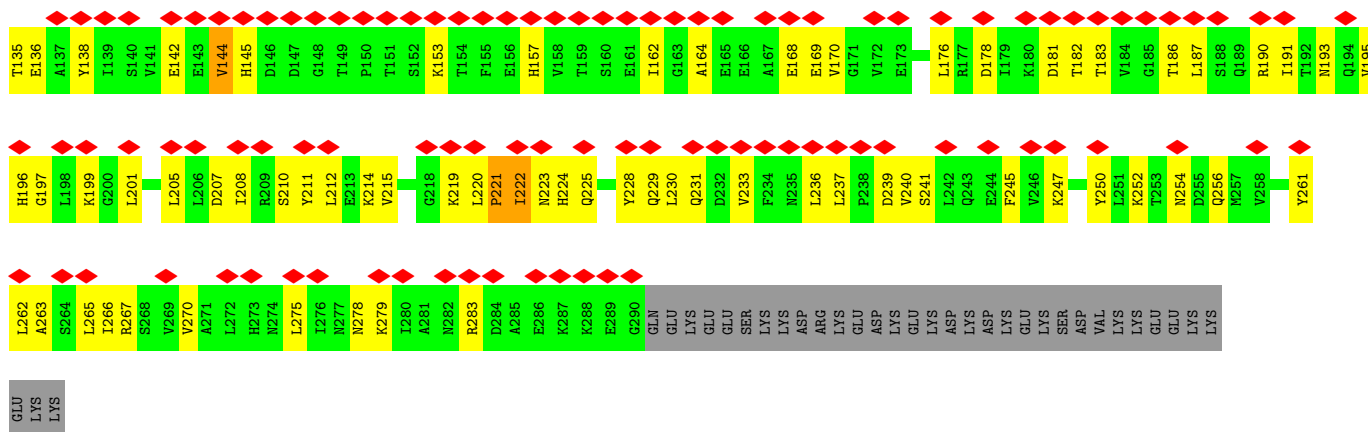


• Molecule 25: 26S proteasome non-ATPase regulatory subunit 6



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

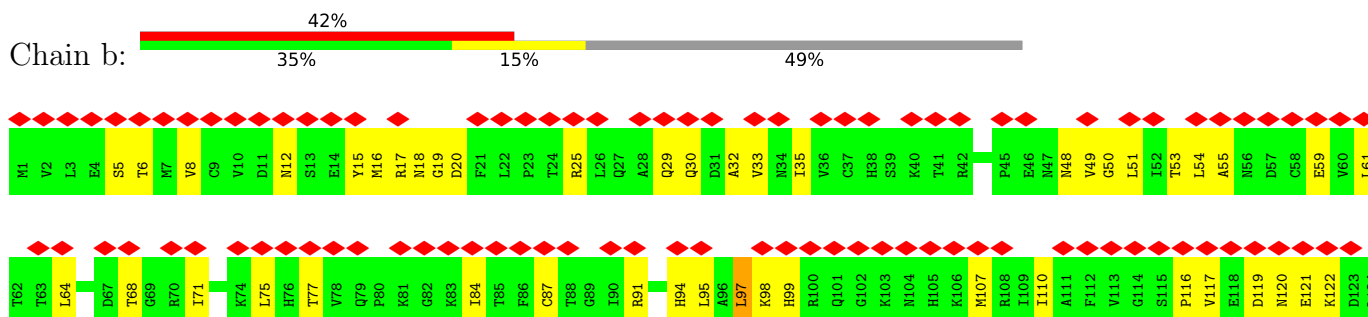


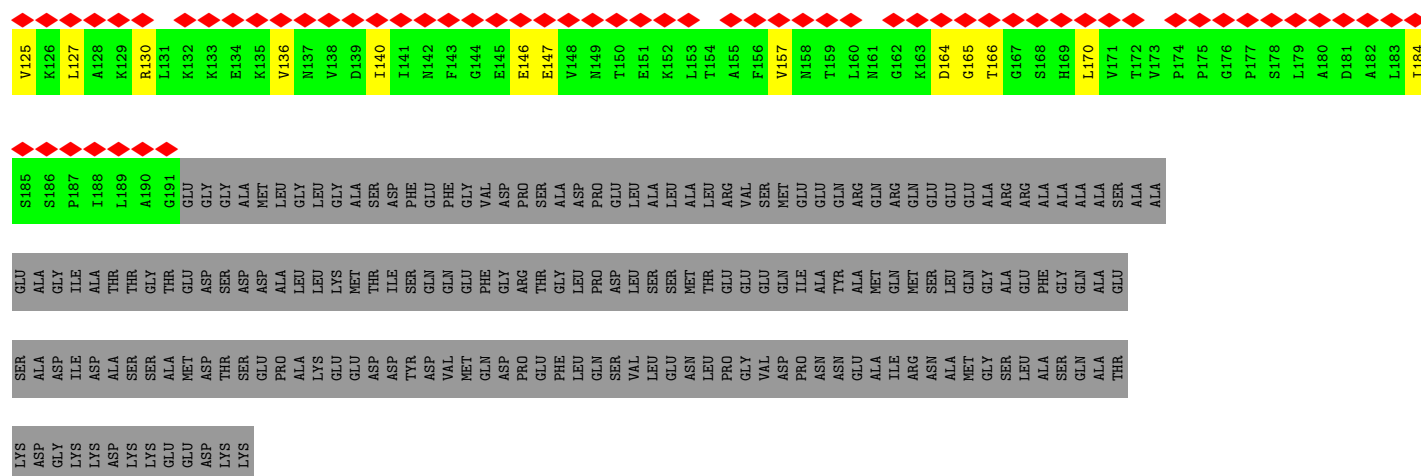


• Molecule 27: 26S proteasome non-ATPase regulatory subunit 13

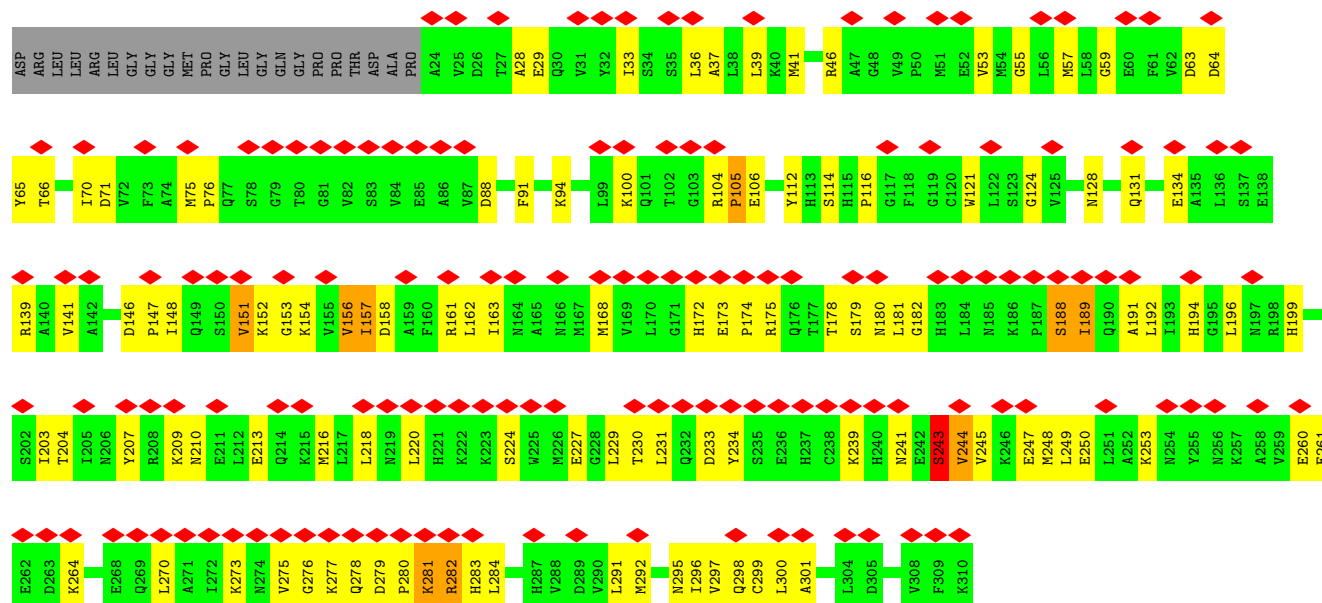


• Molecule 28: 26S proteasome non-ATPase regulatory subunit 4

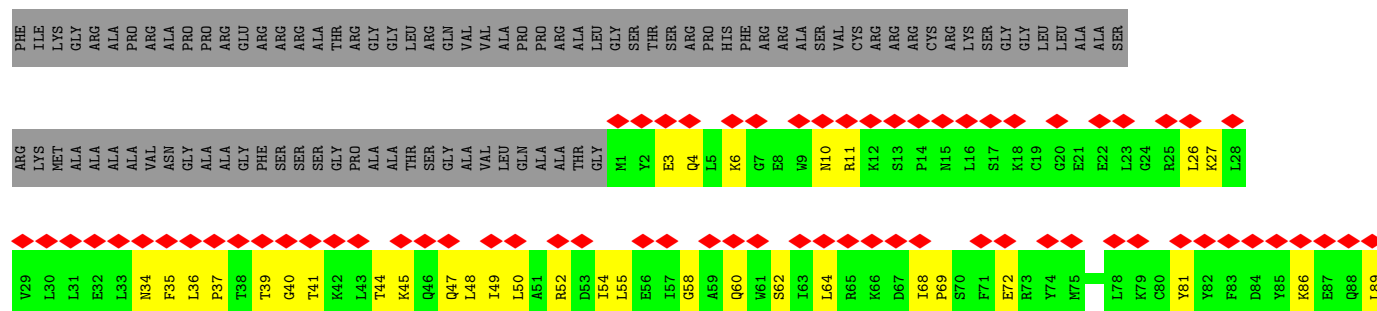


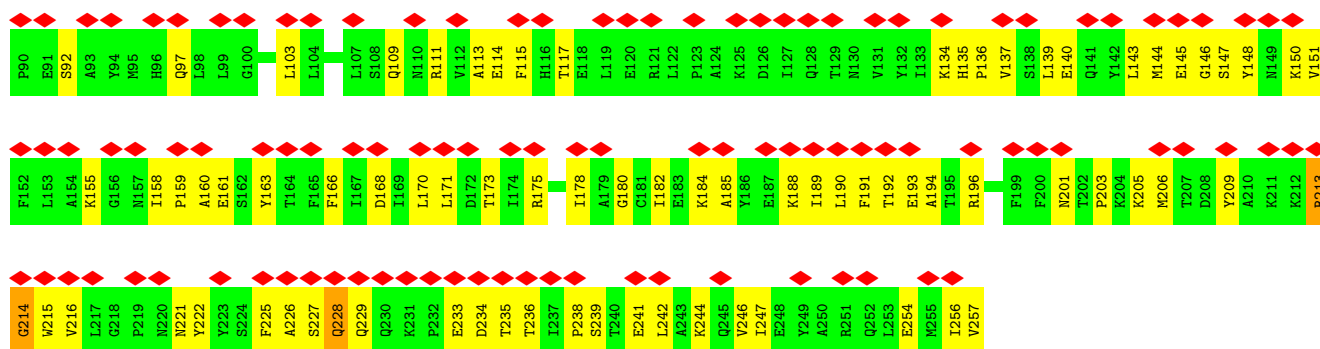


• Molecule 29: 26S proteasome non-ATPase regulatory subunit 14

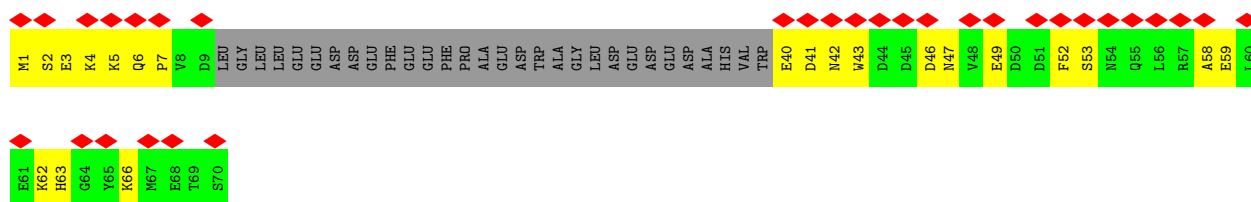
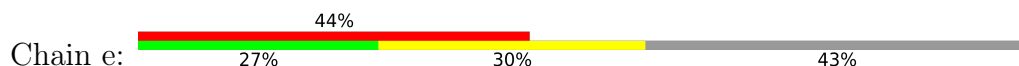


• Molecule 30: 26S proteasome non-ATPase regulatory subunit 8

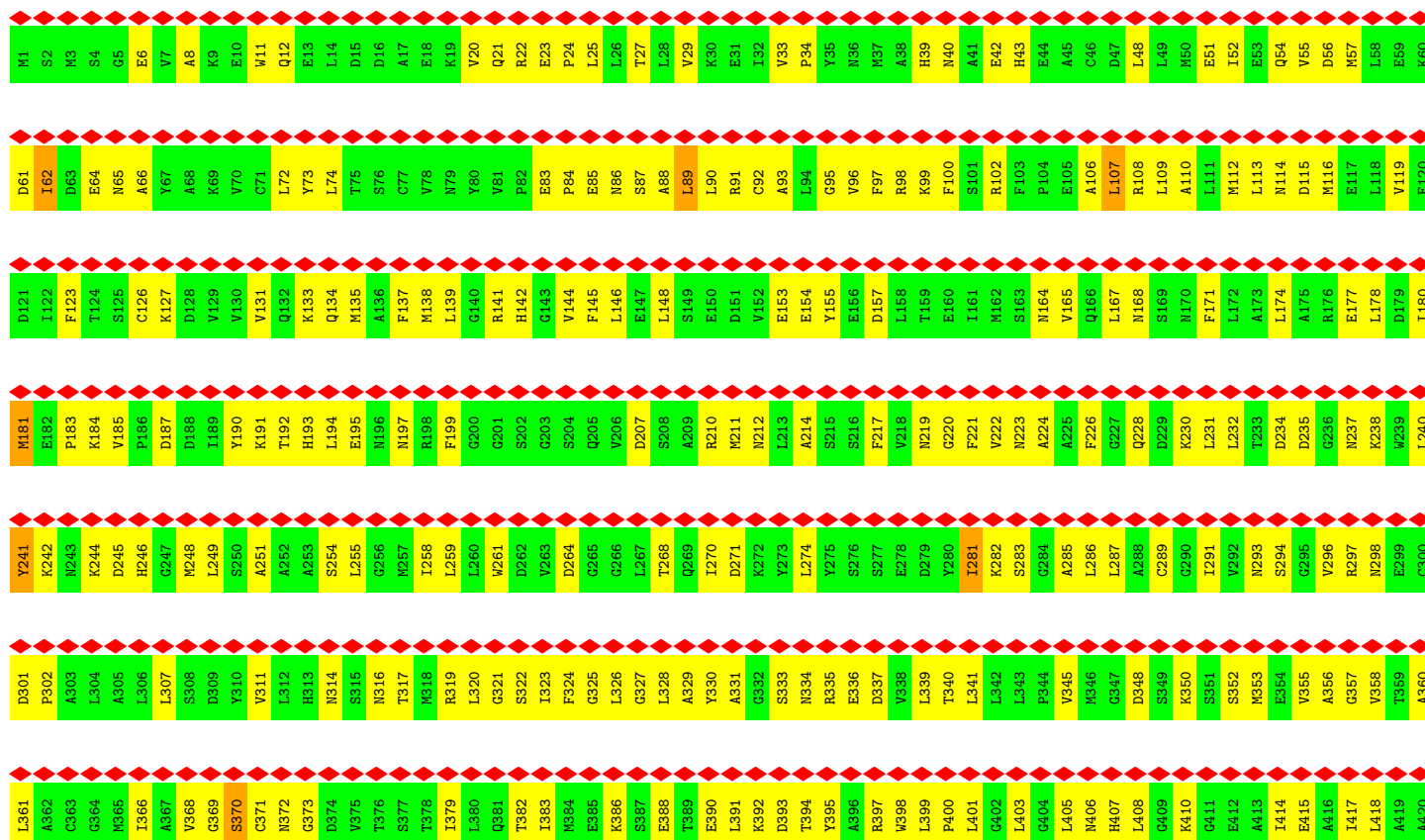




• Molecule 31: 26S proteasome complex subunit DSS1



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





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	139236	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	0.010	Depositor
Minimum map value	-0.004	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0033	Depositor
Map size (Å)	309.6, 309.6, 309.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	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, ATP

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	G	0.20	0/1859	0.46	2/2523 (0.1%)
2	H	0.20	0/1747	0.44	2/2376 (0.1%)
3	I	0.21	0/1942	0.48	0/2628
4	J	0.19	0/1728	0.40	0/2358
5	K	0.19	0/1747	0.44	0/2364
6	L	0.19	0/1885	0.44	2/2552 (0.1%)
7	M	0.17	0/1891	0.39	0/2552
8	N	0.17	0/1454	0.37	0/1967
9	O	0.15	0/1670	0.36	0/2265
10	P	0.17	0/1614	0.37	0/2177
11	Q	0.19	0/1603	0.39	0/2174
12	R	0.17	0/1579	0.37	0/2134
13	S	0.18	0/1671	0.37	0/2253
14	T	0.17	0/1700	0.40	0/2305
15	A	0.23	0/2886	0.55	2/3899 (0.1%)
16	B	0.24	0/2700	0.58	6/3645 (0.2%)
17	D	0.27	0/3090	0.72	13/4168 (0.3%)
18	E	0.23	0/2835	0.51	0/3821
19	F	0.21	0/2903	0.51	2/3912 (0.1%)
20	C	0.25	0/3054	0.60	4/4107 (0.1%)
21	U	0.22	1/6396 (0.0%)	0.46	0/8646
22	V	0.26	0/3929	0.63	6/5309 (0.1%)
23	W	0.24	0/3751	0.58	6/5042 (0.1%)
24	X	0.19	0/3053	0.41	0/4115
25	Y	0.24	0/3173	0.56	5/4273 (0.1%)
26	Z	0.22	0/2324	0.56	4/3150 (0.1%)
27	a	0.28	1/3053 (0.0%)	0.52	0/4133
28	b	0.18	0/1478	0.41	0/2001
29	c	0.28	0/2302	0.66	8/3110 (0.3%)
30	d	0.27	0/2162	0.60	1/2919 (0.0%)
31	e	0.27	0/338	0.60	0/450
32	f	0.30	2/5413 (0.0%)	0.72	13/7317 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.23	4/78930 (0.0%)	0.53	76/106645 (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
17	D	0	1
20	C	0	1
29	c	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	a	145	LEU	C-N	9.86	1.56	1.33
32	f	181	MET	C-N	-7.40	1.21	1.33
32	f	681	LEU	C-N	5.39	1.46	1.33
21	U	644	TYR	C-N	5.11	1.44	1.33

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	f	636	GLY	N-CA-C	11.02	126.68	113.79
17	D	206	GLY	CA-C-N	-10.38	112.18	119.66
17	D	206	GLY	C-N-CA	-10.38	112.18	119.66
20	C	217	SER	CA-C-N	8.27	136.58	121.70
20	C	217	SER	C-N-CA	8.27	136.58	121.70
17	D	151	ILE	CA-C-N	8.12	136.32	121.70
17	D	151	ILE	C-N-CA	8.12	136.32	121.70
32	f	459	GLU	N-CA-C	7.72	127.25	110.80
25	Y	63	TRP	CA-C-N	7.67	135.51	121.70
25	Y	63	TRP	C-N-CA	7.67	135.51	121.70
23	W	92	LYS	CA-C-N	7.56	135.31	121.70
23	W	92	LYS	C-N-CA	7.56	135.31	121.70
32	f	181	MET	CA-C-N	7.54	131.44	120.51
32	f	181	MET	C-N-CA	7.54	131.44	120.51
23	W	135	LYS	CA-C-N	7.41	135.04	121.70
23	W	135	LYS	C-N-CA	7.41	135.04	121.70
29	c	243	SER	CA-C-N	7.41	135.03	121.70
29	c	243	SER	C-N-CA	7.41	135.03	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	B	226	GLY	CA-C-N	7.17	127.77	120.38
16	B	226	GLY	C-N-CA	7.17	127.77	120.38
17	D	373	ALA	CA-C-N	7.00	134.31	121.70
17	D	373	ALA	C-N-CA	7.00	134.31	121.70
26	Z	222	ILE	CA-C-N	6.89	134.09	121.70
26	Z	222	ILE	C-N-CA	6.89	134.09	121.70
22	V	81	GLN	CA-C-N	6.29	133.03	121.70
22	V	81	GLN	C-N-CA	6.29	133.03	121.70
26	Z	63	LYS	CA-C-N	6.23	132.92	121.70
26	Z	63	LYS	C-N-CA	6.23	132.92	121.70
22	V	57	ALA	CA-C-N	6.17	132.80	121.70
22	V	57	ALA	C-N-CA	6.17	132.80	121.70
32	f	459	GLU	CA-C-N	6.16	132.80	121.70
32	f	459	GLU	C-N-CA	6.16	132.80	121.70
17	D	143	LEU	CA-C-N	6.08	126.64	120.38
17	D	143	LEU	C-N-CA	6.08	126.64	120.38
32	f	617	LEU	CA-C-N	6.07	132.62	121.70
32	f	617	LEU	C-N-CA	6.07	132.62	121.70
20	C	255	GLY	CA-C-N	5.95	132.41	121.70
20	C	255	GLY	C-N-CA	5.95	132.41	121.70
29	c	188	SER	CA-C-N	5.94	132.40	121.70
29	c	188	SER	C-N-CA	5.94	132.40	121.70
17	D	148	ASP	CA-C-N	5.82	132.17	121.70
17	D	148	ASP	C-N-CA	5.82	132.17	121.70
17	D	389	GLU	CA-C-N	5.79	132.12	121.70
17	D	389	GLU	C-N-CA	5.79	132.12	121.70
25	Y	170	GLU	N-CA-C	5.76	117.56	111.28
2	H	231	ALA	CA-C-N	5.68	131.93	121.70
2	H	231	ALA	C-N-CA	5.68	131.93	121.70
32	f	656	HIS	CB-CA-C	-5.68	109.03	115.79
32	f	617	LEU	N-CA-C	5.59	117.17	111.14
32	f	370	SER	CA-C-N	5.50	131.59	121.70
32	f	370	SER	C-N-CA	5.50	131.59	121.70
25	Y	356	THR	CA-C-N	5.48	131.56	121.70
25	Y	356	THR	C-N-CA	5.48	131.56	121.70
29	c	281	LYS	CA-C-N	5.47	131.55	121.70
29	c	281	LYS	C-N-CA	5.47	131.55	121.70
17	D	144	PRO	N-CA-C	5.47	117.37	110.70
19	F	164	LEU	CA-C-N	5.43	126.72	120.85
19	F	164	LEU	C-N-CA	5.43	126.72	120.85
30	d	228	GLN	N-CA-C	5.41	124.35	113.31
29	c	282	ARG	CA-C-N	5.37	131.36	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	c	282	ARG	C-N-CA	5.37	131.36	121.70
16	B	139	VAL	CA-C-N	5.33	131.30	121.70
16	B	139	VAL	C-N-CA	5.33	131.30	121.70
22	V	80	LYS	CA-C-N	5.33	131.30	121.70
22	V	80	LYS	C-N-CA	5.33	131.30	121.70
15	A	344	SER	CA-C-N	5.30	131.24	121.70
15	A	344	SER	C-N-CA	5.30	131.24	121.70
16	B	324	ASP	CA-C-N	5.25	131.16	121.70
16	B	324	ASP	C-N-CA	5.25	131.16	121.70
1	G	184	LYS	CA-C-N	5.15	130.97	121.70
1	G	184	LYS	C-N-CA	5.15	130.97	121.70
23	W	257	GLN	CA-C-N	5.05	130.79	121.70
23	W	257	GLN	C-N-CA	5.05	130.79	121.70
32	f	241	TYR	CB-CA-C	-5.05	109.78	115.79
6	L	204	ASP	CA-C-N	5.02	130.73	121.70
6	L	204	ASP	C-N-CA	5.02	130.73	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
20	C	171	HIS	Peptide
17	D	148	ASP	Peptide
29	c	243	SER	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	G	1826	0	1796	71	0
2	H	1713	0	1598	58	0
3	I	1912	0	1851	64	0
4	J	1704	0	1517	62	0
5	K	1722	0	1673	66	0
6	L	1850	0	1822	72	0
7	M	1856	0	1814	71	0
8	N	1430	0	1398	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	O	1643	0	1644	24	0
10	P	1585	0	1598	42	0
11	Q	1570	0	1547	51	0
12	R	1548	0	1499	29	0
13	S	1641	0	1618	30	0
14	T	1667	0	1628	31	0
15	A	2835	0	2879	151	0
16	B	2662	0	2702	147	0
17	D	3040	0	3076	170	0
18	E	2790	0	2846	119	0
19	F	2863	0	2931	115	0
20	C	3015	0	3125	161	0
21	U	6287	0	6338	180	0
22	V	3852	0	3893	169	0
23	W	3703	0	3822	139	0
24	X	3009	0	3113	64	0
25	Y	3115	0	3120	105	0
26	Z	2281	0	2312	122	0
27	a	2995	0	3012	100	0
28	b	1458	0	1505	51	0
29	c	2260	0	2276	109	0
30	d	2116	0	2146	87	0
31	e	334	0	294	24	0
32	f	5331	0	5344	419	0
33	A	31	0	12	2	0
33	B	31	0	12	3	0
33	C	31	0	12	1	0
33	D	31	0	12	3	0
33	E	31	0	12	4	0
33	F	31	0	12	3	0
34	c	1	0	0	0	0
All	All	77800	0	77809	2815	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 18.

All (2815) 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)
15:A:74:PRO:CG	32:f:521:ARG:HE	1.30	1.42
27:a:13:ASN:OD1	27:a:19:PRO:HG3	1.17	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:261:TYR:O	26:Z:265:LEU:HD13	1.20	1.35
27:a:13:ASN:OD1	27:a:19:PRO:CG	1.76	1.31
26:Z:261:TYR:O	26:Z:265:LEU:CD1	1.86	1.24
15:A:74:PRO:HG3	32:f:521:ARG:NE	1.59	1.16
16:B:117:ASP:OD2	32:f:588:GLN:NE2	1.79	1.16
32:f:231:LEU:O	32:f:235:ASP:HB2	1.45	1.15
29:c:168:MET:HA	29:c:172:HIS:HE1	1.15	1.09
32:f:85:GLU:O	32:f:89:LEU:HB2	1.52	1.07
15:A:74:PRO:CG	32:f:521:ARG:NE	2.15	1.06
26:Z:261:TYR:C	26:Z:265:LEU:HD13	1.79	1.05
16:B:117:ASP:CB	32:f:588:GLN:HE22	1.69	1.05
15:A:74:PRO:HG3	32:f:521:ARG:HE	0.89	1.04
20:C:217:SER:HB3	20:C:218:GLU:HB3	1.38	1.02
29:c:168:MET:HA	29:c:172:HIS:CE1	1.97	0.99
17:D:152:MET:CE	18:E:62:LYS:HG3	1.94	0.97
32:f:548:LEU:O	32:f:552:SER:HB2	1.65	0.97
17:D:83:GLN:HE22	17:D:140:VAL:HG21	1.29	0.96
15:A:74:PRO:HG2	32:f:521:ARG:HE	1.26	0.96
16:B:117:ASP:CG	32:f:588:GLN:HE22	1.74	0.96
32:f:230:LYS:O	32:f:234:ASP:HB2	1.64	0.95
32:f:600:LEU:O	32:f:604:ARG:HB3	1.66	0.95
6:L:148:CYS:HG	6:L:150:SER:HG	1.10	0.94
32:f:371:CYS:SG	32:f:406:ASN:ND2	2.39	0.94
31:e:1:MET:H3	31:e:2:SER:HA	1.33	0.94
21:U:517:GLY:O	21:U:554:LEU:HD22	1.69	0.93
12:R:19:ARG:HE	12:R:29:GLN:HE22	1.18	0.90
26:Z:222:ILE:HG23	26:Z:223:ASN:HB3	1.54	0.89
32:f:617:LEU:HB3	32:f:618:THR:HB	1.55	0.89
32:f:20:VAL:HG12	32:f:24:PRO:HD3	1.53	0.88
25:Y:179:ARG:NH2	25:Y:212:GLU:OE2	2.07	0.88
32:f:391:LEU:HD12	32:f:392:LYS:H	1.37	0.87
17:D:201:GLY:HA3	17:D:327:LEU:HA	1.56	0.86
32:f:651:ILE:O	32:f:655:SER:HB3	1.74	0.86
32:f:496:LEU:O	32:f:500:LEU:HB2	1.75	0.86
20:C:86:LEU:HD23	20:C:96:VAL:HB	1.58	0.86
7:M:36:ALA:HB2	7:M:65:ARG:HH21	1.41	0.85
20:C:229:ARG:HH12	20:C:232:ARG:HE	1.25	0.84
32:f:453:LEU:O	32:f:457:CYS:HB3	1.76	0.84
16:B:296:ASP:HB2	20:C:268:GLU:HG3	1.59	0.84
32:f:146:LEU:HG	32:f:178:LEU:HD13	1.58	0.84
15:A:74:PRO:HB3	32:f:521:ARG:HB3	1.57	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:180:PRO:HG2	16:B:239:VAL:HG23	1.59	0.83
23:W:40:LEU:HB2	23:W:41:GLN:HA	1.60	0.83
4:J:88:ARG:HH22	11:Q:69:MET:HB2	1.42	0.83
16:B:117:ASP:CB	32:f:588:GLN:NE2	2.41	0.83
22:V:57:ALA:HB3	22:V:58:ALA:HB3	1.60	0.83
6:L:67:ASP:HB3	6:L:70:ILE:HB	1.61	0.83
26:Z:224:HIS:HB3	26:Z:225:GLN:HA	1.60	0.83
32:f:311:VAL:HB	32:f:319:ARG:HG2	1.60	0.83
6:L:151:ALA:O	7:M:85:ARG:NH2	2.12	0.83
15:A:78:TRP:CB	32:f:528:ARG:HH12	1.92	0.83
17:D:143:LEU:HD11	17:D:147:ALA:H	1.43	0.83
20:C:22:GLN:HA	20:C:25:LEU:HD13	1.61	0.83
23:W:47:LEU:O	23:W:51:GLU:OE1	1.97	0.83
27:a:13:ASN:OD1	27:a:19:PRO:HG2	1.75	0.82
19:F:300:LYS:HD2	19:F:304:ARG:HE	1.43	0.82
22:V:153:LYS:O	22:V:157:THR:HG23	1.79	0.82
26:Z:33:LYS:NZ	26:Z:34:ARG:O	2.12	0.82
22:V:321:ALA:HB1	22:V:322:VAL:HB	1.59	0.82
32:f:503:MET:SD	32:f:669:ARG:NH1	2.54	0.81
23:W:92:LYS:H	23:W:93:ARG:HB3	1.47	0.80
19:F:183:GLU:HG2	19:F:239:ALA:HB2	1.63	0.80
32:f:85:GLU:O	32:f:89:LEU:CB	2.29	0.80
1:G:22:LEU:HD13	1:G:25:VAL:HB	1.63	0.80
29:c:124:GLY:O	29:c:128:ASN:ND2	2.14	0.80
32:f:251:ALA:HA	32:f:254:SER:HB2	1.62	0.80
2:H:231:ALA:HB3	2:H:232:ALA:HB3	1.62	0.80
32:f:663:VAL:HG13	32:f:664:ALA:HB2	1.64	0.80
15:A:368:ILE:HG12	15:A:406:GLU:HB3	1.63	0.79
20:C:99:VAL:HA	20:C:100:ASP:HB2	1.64	0.79
19:F:191:LEU:HG	19:F:194:GLN:HE21	1.48	0.79
21:U:154:ALA:HB2	21:U:166:THR:HG21	1.64	0.79
21:U:799:LYS:HA	21:U:843:GLU:HG3	1.65	0.79
32:f:339:LEU:HD12	32:f:340:THR:HG23	1.65	0.79
22:V:255:LEU:HD22	22:V:291:TYR:HB3	1.65	0.79
14:T:99:ARG:HG3	14:T:105:PRO:HA	1.63	0.79
30:d:147:SER:HA	30:d:148:TYR:HB2	1.65	0.79
2:H:123:GLN:HB2	3:I:128:ARG:HH21	1.49	0.78
30:d:244:LYS:HA	30:d:247:ILE:HD12	1.66	0.78
23:W:268:LYS:HD3	23:W:299:ILE:HG21	1.64	0.78
4:J:104:VAL:HB	4:J:143:ARG:HD3	1.64	0.78
32:f:72:LEU:HD21	32:f:113:LEU:HD13	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:406:VAL:HG12	23:W:413:ILE:HB	1.65	0.78
30:d:188:LYS:HD2	30:d:221:ASN:HD21	1.48	0.78
26:Z:14:LEU:HG	29:c:39:LEU:HB3	1.65	0.78
29:c:121:TRP:HA	29:c:196:LEU:HD11	1.66	0.78
32:f:222:VAL:HA	32:f:231:LEU:HD11	1.64	0.78
11:Q:36:PHE:HB2	11:Q:44:LEU:HB3	1.66	0.78
23:W:257:GLN:HA	23:W:258:ALA:HB3	1.64	0.78
21:U:554:LEU:O	21:U:554:LEU:HD23	1.84	0.77
17:D:286:GLN:NE2	20:C:218:GLU:OE2	2.17	0.77
23:W:136:ILE:H	23:W:141:GLU:HG2	1.48	0.77
22:V:228:ARG:HH21	22:V:257:ASN:HB3	1.48	0.77
19:F:168:TYR:HB2	19:F:169:ASP:HB2	1.66	0.77
15:A:190:VAL:HG23	15:A:209:PRO:HG2	1.67	0.77
15:A:383:ALA:HB3	16:B:343:ARG:HH11	1.50	0.77
20:C:78:ARG:HB3	20:C:86:LEU:HD12	1.67	0.77
32:f:119:VAL:O	32:f:123:PHE:CB	2.33	0.77
16:B:105:THR:HG23	16:B:106:PRO:HD3	1.67	0.77
32:f:548:LEU:O	32:f:552:SER:CB	2.32	0.77
19:F:83:ASN:O	19:F:154:ASN:ND2	2.18	0.76
22:V:67:LEU:HD21	22:V:205:LEU:HD23	1.67	0.76
17:D:152:MET:HE1	18:E:62:LYS:HG3	1.67	0.76
23:W:257:GLN:HE22	23:W:262:LYS:HD2	1.51	0.76
32:f:119:VAL:O	32:f:123:PHE:HB2	1.85	0.76
15:A:413:VAL:HA	15:A:416:VAL:HG12	1.67	0.76
21:U:474:ARG:HH21	21:U:500:ASN:HB2	1.48	0.76
16:B:333:ARG:HD2	16:B:336:THR:HG23	1.66	0.76
26:Z:164:ALA:HB1	26:Z:168:GLU:HG3	1.66	0.76
26:Z:261:TYR:O	26:Z:265:LEU:HD12	1.86	0.76
22:V:494:MET:HG3	26:Z:278:ASN:HD22	1.49	0.76
17:D:116:LEU:HD23	17:D:118:THR:H	1.51	0.76
3:I:8:ARG:HE	4:J:5:ARG:HH21	1.34	0.76
7:M:175:GLU:HG3	7:M:196:ILE:HG12	1.68	0.76
15:A:211:GLY:HA3	15:A:317:VAL:HG23	1.67	0.76
26:Z:128:PRO:HG3	29:c:216:MET:HB3	1.67	0.76
3:I:213:ILE:HB	3:I:228:LEU:HD11	1.66	0.76
27:a:70:ARG:NH1	27:a:70:ARG:O	2.19	0.76
4:J:11:SER:OG	4:J:15:HIS:O	2.02	0.75
17:D:115:ILE:HG22	17:D:139:LEU:HD12	1.66	0.75
23:W:44:ILE:HB	23:W:93:ARG:HD2	1.68	0.75
2:H:222:THR:OG1	2:H:225:GLU:OE1	2.04	0.75
32:f:296:VAL:HG12	32:f:297:ARG:HG2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:168:MET:CA	29:c:172:HIS:HE1	1.97	0.75
16:B:117:ASP:HB2	32:f:588:GLN:NE2	2.02	0.75
23:W:416:GLN:HB3	23:W:417:ARG:HA	1.67	0.75
16:B:240:ALA:O	16:B:243:THR:OG1	2.05	0.74
32:f:319:ARG:NH1	32:f:348:ASP:OD2	2.15	0.74
15:A:232:ARG:NE	15:A:235:ALA:O	2.12	0.74
24:X:420:LYS:O	26:Z:283:ARG:NH2	2.19	0.74
21:U:607:VAL:O	21:U:615:ARG:NH1	2.20	0.74
27:a:286:ALA:HB1	27:a:287:ASN:HA	1.68	0.74
8:N:5:ALA:HB3	8:N:126:ALA:HB3	1.69	0.74
5:K:107:MET:HG2	5:K:111:SER:OG	1.87	0.74
23:W:414:ASN:ND2	23:W:416:GLN:O	2.21	0.73
23:W:186:ILE:O	23:W:189:GLN:NE2	2.21	0.73
29:c:243:SER:HB3	29:c:244:VAL:HB	1.70	0.73
2:H:39:LYS:HE2	2:H:144:PRO:HG2	1.69	0.73
17:D:154:LEU:HD23	17:D:155:THR:H	1.51	0.73
23:W:340:VAL:HG13	23:W:350:ARG:HD2	1.70	0.73
30:d:103:LEU:HD11	30:d:115:PHE:HD1	1.53	0.73
15:A:218:PRO:HD3	15:A:428:ARG:HE	1.53	0.73
21:U:147:TYR:OH	21:U:170:SER:O	2.06	0.73
24:X:409:LYS:HZ2	29:c:264:LYS:HD3	1.54	0.73
25:Y:89:GLU:HA	25:Y:92:GLU:HG2	1.70	0.73
26:Z:37:GLY:HA2	26:Z:56:VAL:HG12	1.70	0.73
23:W:90:LEU:HD11	23:W:135:LYS:HD3	1.71	0.73
15:A:217:PRO:HA	15:A:428:ARG:HG2	1.69	0.73
16:B:117:ASP:CG	32:f:588:GLN:NE2	2.39	0.73
17:D:312:ASN:HD21	18:E:242:ARG:HH22	1.34	0.73
25:Y:268:TYR:HB2	25:Y:322:ALA:HB1	1.70	0.73
15:A:166:VAL:HA	15:A:238:ILE:HG13	1.71	0.73
23:W:173:THR:HG23	23:W:182:ARG:HH11	1.53	0.73
2:H:4:ARG:HD3	7:M:127:ALA:HB2	1.70	0.73
32:f:559:ASP:HB3	32:f:562:VAL:HG22	1.69	0.73
30:d:147:SER:HG	30:d:151:VAL:H	1.36	0.72
18:E:381:GLU:HG3	19:F:351:LYS:HD2	1.70	0.72
10:P:62:THR:OG1	11:Q:85:ARG:NH2	2.18	0.72
17:D:193:GLN:O	20:C:337:ASN:ND2	2.21	0.72
21:U:842:LYS:HA	21:U:843:GLU:HB3	1.71	0.72
32:f:223:ASN:HA	32:f:254:SER:HB3	1.72	0.72
27:a:123:LEU:HD21	27:a:161:LYS:HG3	1.71	0.72
29:c:151:VAL:HG13	29:c:152:LYS:H	1.53	0.72
32:f:52:ILE:O	32:f:56:ASP:HB2	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:176:VAL:HG22	16:B:177:GLU:HB2	1.70	0.72
18:E:128:GLY:O	18:E:189:SER:OG	2.07	0.72
18:E:266:GLY:HA2	18:E:267:PHE:HB2	1.71	0.72
20:C:18:SER:HA	20:C:21:ARG:HB2	1.69	0.72
32:f:294:SER:OG	32:f:321:GLY:O	2.08	0.72
25:Y:192:ARG:NH1	31:e:42:ASN:OD1	2.23	0.72
5:K:85:ALA:HB2	5:K:139:VAL:HG21	1.72	0.71
6:L:160:SER:O	6:L:169:ARG:NH2	2.23	0.71
15:A:174:TYR:HD1	15:A:227:ARG:HD2	1.56	0.71
20:C:187:LEU:HD11	20:C:314:LYS:HD2	1.72	0.71
28:b:54:LEU:HD13	28:b:84:ILE:HG13	1.72	0.71
32:f:314:ASN:HA	32:f:319:ARG:HD2	1.71	0.71
18:E:97:ARG:HD2	18:E:111:LEU:HD11	1.71	0.71
30:d:109:GLN:O	30:d:111:ARG:NH2	2.23	0.71
15:A:218:PRO:HB3	15:A:428:ARG:HH21	1.55	0.71
19:F:137:ILE:HG21	19:F:160:ILE:HB	1.71	0.71
26:Z:233:VAL:HA	26:Z:236:LEU:HD13	1.72	0.71
17:D:89:ILE:HD11	18:E:80:VAL:HG13	1.72	0.71
19:F:276:LYS:NZ	19:F:325:GLN:OE1	2.24	0.71
15:A:74:PRO:HG3	32:f:521:ARG:CD	2.20	0.71
11:Q:38:MET:HA	11:Q:61:GLN:HE22	1.55	0.71
5:K:167:ALA:HB3	5:K:181:LEU:HD21	1.73	0.71
21:U:518:LEU:HD23	21:U:554:LEU:HD11	1.73	0.71
21:U:611:ASN:HB3	21:U:614:VAL:HG12	1.72	0.71
1:G:144:ASP:HB3	1:G:147:GLN:HB2	1.73	0.70
15:A:94:GLN:O	16:B:131:HIS:NE2	2.23	0.70
23:W:373:ILE:HG23	23:W:413:ILE:HG13	1.71	0.70
26:Z:7:GLN:OE1	26:Z:46:LYS:NZ	2.24	0.70
4:J:115:LYS:HE2	4:J:149:PRO:HA	1.72	0.70
32:f:183:PRO:HG3	32:f:481:LYS:HE2	1.72	0.70
32:f:676:GLU:HB3	32:f:691:VAL:HG22	1.71	0.70
4:J:120:GLN:OE1	5:K:134:SER:N	2.24	0.70
10:P:29:GLY:HA2	10:P:35:VAL:HG23	1.73	0.70
32:f:255:LEU:HD23	32:f:258:ILE:HD11	1.73	0.70
20:C:175:PHE:CE2	20:C:182:GLN:HG3	2.26	0.70
22:V:212:TYR:OH	22:V:287:ARG:NH2	2.24	0.70
25:Y:381:GLN:HB3	25:Y:385:ARG:HH12	1.55	0.70
32:f:97:PHE:CD1	32:f:139:LEU:HA	2.26	0.70
32:f:453:LEU:O	32:f:457:CYS:CB	2.39	0.70
19:F:238:ARG:HH11	19:F:250:LYS:HG2	1.57	0.70
17:D:204:MET:HE3	17:D:310:ALA:HB2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:167:LEU:O	32:f:171:PHE:HB2	1.91	0.70
6:L:168:ALA:HB1	6:L:194:ALA:HB1	1.73	0.70
15:A:191:VAL:HG23	15:A:316:LYS:HE2	1.72	0.70
16:B:177:GLU:H	16:B:178:LYS:HA	1.57	0.70
26:Z:222:ILE:HG23	26:Z:223:ASN:CB	2.21	0.70
29:c:116:PRO:HA	29:c:146:ASP:OD1	1.92	0.70
21:U:356:THR:HG21	21:U:731:ILE:HD13	1.74	0.70
27:a:340:VAL:HG12	27:a:341:LEU:H	1.56	0.70
30:d:209:TYR:HB3	30:d:213:ARG:HE	1.57	0.70
3:I:218:ARG:NH1	3:I:223:THR:OG1	2.25	0.70
17:D:121:ARG:HB3	29:c:280:PRO:HG2	1.74	0.70
21:U:522:GLY:O	21:U:559:ARG:NH2	2.25	0.70
16:B:103:ARG:HD3	16:B:160:ILE:HG12	1.71	0.69
6:L:66:VAL:HG13	6:L:89:ARG:HD3	1.73	0.69
6:L:174:ARG:HG3	6:L:175:HIS:ND1	2.07	0.69
22:V:80:LYS:HB3	22:V:81:GLN:C	2.17	0.69
29:c:250:GLU:O	29:c:253:LYS:HG2	1.92	0.69
15:A:92:PRO:HB2	15:A:93:LEU:HD12	1.71	0.69
23:W:123:ARG:HH12	23:W:127:THR:HB	1.56	0.69
24:X:194:ARG:HD2	24:X:210:LEU:HD21	1.74	0.69
27:a:112:ILE:HD12	27:a:113:LEU:N	2.07	0.69
19:F:392:ASN:HB2	19:F:395:GLN:HG3	1.74	0.69
19:F:298:SER:HB3	19:F:299:GLU:HG3	1.75	0.69
21:U:649:ARG:HB3	21:U:675:MET:HE1	1.74	0.69
12:R:8:PHE:HE1	12:R:13:ILE:HG12	1.58	0.69
21:U:447:GLY:HA3	21:U:480:GLY:HA2	1.73	0.69
22:V:379:LEU:HD13	22:V:395:ILE:HG12	1.72	0.69
18:E:47:LEU:HD13	19:F:80:ILE:HG12	1.72	0.69
27:a:50:PHE:O	27:a:86:GLN:NE2	2.25	0.69
32:f:496:LEU:O	32:f:500:LEU:CB	2.41	0.69
7:M:195:LYS:HG3	7:M:196:ILE:HD12	1.75	0.69
15:A:78:TRP:CG	32:f:528:ARG:HH12	2.10	0.69
21:U:341:PHE:HB2	21:U:881:PRO:HD2	1.74	0.69
21:U:770:TRP:CG	29:c:179:SER:HG	2.10	0.69
24:X:255:LEU:HD12	24:X:287:LEU:HD13	1.74	0.69
25:Y:344:HIS:HB3	25:Y:358:ARG:HG2	1.73	0.69
18:E:288:ALA:O	18:E:294:ARG:NH1	2.26	0.69
32:f:433:ASN:O	32:f:437:ASP:HB2	1.93	0.69
17:D:392:TYR:HB2	23:W:135:LYS:HA	1.75	0.68
23:W:409:LEU:HD21	24:X:344:ARG:HG2	1.74	0.68
29:c:188:SER:HA	29:c:189:ILE:HG22	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:487:MET:HB3	32:f:500:LEU:HD22	1.74	0.68
21:U:155:LEU:O	21:U:158:ARG:NH1	2.25	0.68
15:A:170:PRO:HA	15:A:229:VAL:HG12	1.73	0.68
22:V:94:VAL:HG22	22:V:138:PRO:HD3	1.74	0.68
26:Z:105:ASP:HA	26:Z:108:ILE:HD13	1.74	0.68
27:a:71:VAL:HA	28:b:17:ARG:HH12	1.56	0.68
15:A:333:ARG:HH12	15:A:340:LYS:HD3	1.58	0.68
17:D:82:ILE:HD11	20:C:60:ARG:HH21	1.58	0.68
21:U:406:ALA:HA	21:U:445:ALA:HB2	1.75	0.68
7:M:40:ARG:HH11	7:M:148:LEU:HB3	1.58	0.68
16:B:317:ASP:HB3	16:B:318:GLY:HA2	1.73	0.68
12:R:7:LYS:O	12:R:143:TYR:OH	2.10	0.68
17:D:159:LYS:HB3	17:D:160:PRO:HA	1.75	0.68
26:Z:142:GLU:OE2	26:Z:153:LYS:NZ	2.27	0.68
2:H:160:ALA:H	3:I:55:LEU:HD21	1.59	0.68
3:I:122:THR:O	4:J:125:ARG:NH1	2.27	0.68
9:O:38:SER:OG	9:O:40:ASN:OD1	2.12	0.68
13:S:55:SER:HB3	13:S:107:TYR:HB2	1.76	0.68
15:A:157:ILE:HG22	15:A:158:ASP:HB2	1.75	0.68
17:D:67:ASN:HD22	21:U:607:VAL:HG12	1.58	0.68
20:C:248:MET:HE3	20:C:273:MET:HB3	1.76	0.68
25:Y:356:THR:HA	25:Y:357:ASN:CG	2.19	0.68
30:d:203:PRO:HG2	30:d:206:MET:HG2	1.76	0.68
32:f:604:ARG:NH2	32:f:607:GLN:HG3	2.09	0.68
5:K:71:ASP:HB3	5:K:74:ILE:HB	1.75	0.68
1:G:206:LEU:HB3	1:G:208:ILE:HG12	1.75	0.67
22:V:400:HIS:ND1	30:d:144:MET:HB3	2.09	0.67
22:V:479:ARG:NH2	25:Y:374:ASP:OD1	2.27	0.67
29:c:121:TRP:CD1	29:c:192:LEU:HD11	2.28	0.67
16:B:205:LEU:CD2	16:B:206:THR:HG23	2.24	0.67
32:f:662:LEU:H	32:f:664:ALA:HA	1.58	0.67
30:d:3:GLU:HB3	30:d:4:GLN:HA	1.76	0.67
6:L:7:ASP:O	6:L:21:GLN:NE2	2.26	0.67
22:V:466:ILE:HG23	22:V:467:TYR:H	1.58	0.67
8:N:40:ARG:NH1	8:N:180:ALA:O	2.27	0.67
8:N:67:SER:HA	8:N:70:LEU:HD12	1.76	0.67
21:U:885:MET:HB3	21:U:888:GLN:HG3	1.76	0.67
23:W:169:LEU:O	23:W:182:ARG:NH1	2.27	0.67
29:c:209:LYS:HA	29:c:210:ASN:HB2	1.75	0.67
30:d:214:GLY:N	30:d:215:TRP:HB3	2.09	0.67
32:f:190:TYR:CZ	32:f:668:PRO:HB3	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:392:LYS:O	32:f:433:ASN:ND2	2.25	0.67
19:F:291:ILE:HB	19:F:306:VAL:HG11	1.77	0.67
21:U:109:THR:OG1	21:U:156:GLU:O	2.11	0.67
15:A:401:ARG:HH12	15:A:404:ALA:HA	1.60	0.67
22:V:455:LYS:N	22:V:456:GLY:HA2	2.10	0.67
27:a:270:ARG:HH11	27:a:313:LYS:HB3	1.59	0.67
26:Z:262:LEU:HD23	26:Z:265:LEU:HD22	1.76	0.67
15:A:74:PRO:HG2	32:f:521:ARG:NE	1.95	0.67
15:A:218:PRO:HB3	15:A:428:ARG:NH2	2.08	0.67
22:V:282:ASN:O	22:V:315:LYS:NZ	2.28	0.67
22:V:337:LEU:O	22:V:401:ASN:ND2	2.28	0.67
1:G:159:TYR:HB3	2:H:81:PRO:HG3	1.75	0.66
6:L:67:ASP:OD1	6:L:68:ASN:N	2.28	0.66
23:W:331:GLY:HA2	23:W:332:SER:HB3	1.77	0.66
27:a:244:ASN:ND2	27:a:276:CYS:SG	2.68	0.66
27:a:270:ARG:NH1	27:a:310:LEU:O	2.28	0.66
10:P:88:MET:HG3	10:P:124:LEU:HD11	1.77	0.66
15:A:381:THR:OG1	16:B:343:ARG:NH1	2.29	0.66
21:U:35:TRP:HB3	21:U:70:HIS:CG	2.30	0.66
23:W:55:ARG:HH12	23:W:79:GLU:HG3	1.60	0.66
27:a:286:ALA:HA	27:a:288:HIS:HB2	1.76	0.66
25:Y:13:LYS:HG2	25:Y:146:ARG:HD2	1.77	0.66
32:f:142:HIS:HA	32:f:145:PHE:HB3	1.75	0.66
21:U:247:GLN:HE22	21:U:912:ILE:HG22	1.60	0.66
23:W:384:LEU:HD13	23:W:388:GLU:HB3	1.76	0.66
22:V:265:ASP:O	22:V:269:LYS:NZ	2.28	0.66
22:V:336:GLU:HA	22:V:339:LEU:HD12	1.77	0.66
15:A:255:ARG:NH2	19:F:259:MET:SD	2.69	0.66
15:A:380:SER:HB3	15:A:384:GLU:HB3	1.77	0.66
26:Z:43:TRP:HB3	26:Z:90:ARG:HH21	1.60	0.66
1:G:110:PRO:O	1:G:111:VAL:HG12	1.96	0.66
16:B:182:GLU:HB2	16:B:239:VAL:HG21	1.76	0.66
3:I:178:ASP:HB3	3:I:192:LEU:HD11	1.76	0.66
17:D:170:MET:HE2	17:D:333:PHE:HE2	1.61	0.66
17:D:373:ALA:HB3	17:D:375:ILE:HG12	1.78	0.66
11:Q:148:THR:HB	11:Q:151:ILE:HB	1.77	0.66
17:D:287:ARG:HD3	20:C:222:LYS:HE2	1.76	0.66
9:O:63:LEU:HD11	9:O:79:ALA:HB2	1.77	0.66
17:D:283:ARG:HG3	17:D:286:GLN:HE21	1.61	0.66
22:V:345:ARG:HD3	22:V:361:PHE:HD1	1.61	0.66
29:c:278:GLN:HA	29:c:279:ASP:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:147:SER:HB3	30:d:151:VAL:HG23	1.77	0.66
29:c:180:ASN:HB2	29:c:204:THR:HG21	1.78	0.65
32:f:615:GLY:HA2	32:f:619:LEU:H	1.60	0.65
10:P:21:ALA:HB2	10:P:189:ILE:HD13	1.78	0.65
15:A:316:LYS:NZ	15:A:317:VAL:O	2.28	0.65
17:D:389:GLU:HB2	17:D:391:ARG:HB2	1.78	0.65
23:W:48:LEU:HD12	23:W:96:GLN:HE22	1.60	0.65
32:f:154:GLU:HG2	32:f:157:ASP:HB2	1.77	0.65
32:f:629:MET:HE2	32:f:649:ASN:HD21	1.61	0.65
16:B:264:PRO:O	16:B:267:VAL:N	2.28	0.65
17:D:151:ILE:HB	17:D:152:MET:HA	1.78	0.65
19:F:275:ALA:HB1	19:F:326:VAL:HG11	1.77	0.65
22:V:79:VAL:HG13	22:V:80:LYS:H	1.60	0.65
22:V:322:VAL:HG13	22:V:323:GLY:H	1.62	0.65
15:A:420:TYR:CE1	16:B:350:LYS:HG2	2.32	0.65
18:E:193:CYS:SG	18:E:194:ASN:N	2.69	0.65
27:a:135:ILE:HG12	27:a:158:LEU:HD13	1.78	0.65
29:c:157:ILE:HG12	29:c:158:ASP:H	1.60	0.65
1:G:23:TYR:O	1:G:26:GLU:HG2	1.96	0.65
8:N:144:ARG:NH2	8:N:151:GLU:OE1	2.30	0.65
22:V:250:LEU:HA	22:V:253:LEU:HD12	1.77	0.65
21:U:338:HIS:CE1	21:U:785:PRO:HB3	2.31	0.65
24:X:171:LEU:O	24:X:213:GLN:NE2	2.28	0.65
32:f:191:LYS:NZ	32:f:667:GLN:O	2.30	0.65
6:L:46:LEU:HD13	6:L:63:ILE:HD13	1.78	0.65
18:E:174:GLY:HA2	18:E:176:PRO:HD2	1.79	0.65
21:U:742:HIS:O	21:U:883:ARG:NH2	2.29	0.65
12:R:59:LEU:HD22	12:R:83:LEU:HD13	1.79	0.65
19:F:103:ASP:OD2	26:Z:88:ARG:NH2	2.30	0.65
20:C:171:HIS:O	20:C:173:GLU:N	2.30	0.65
30:d:191:PHE:HA	30:d:222:TYR:HE1	1.62	0.65
20:C:170:LYS:HB3	25:Y:95:LEU:HD23	1.79	0.65
32:f:372:ASN:N	32:f:373:GLY:HA2	2.11	0.65
22:V:333:ILE:HD11	22:V:360:TYR:HE2	1.60	0.65
22:V:447:ILE:HG13	22:V:449:ALA:H	1.61	0.65
4:J:36:ARG:HE	4:J:157:LYS:HA	1.62	0.64
16:B:205:LEU:HD23	16:B:206:THR:HG23	1.78	0.64
2:H:231:ALA:H	2:H:232:ALA:C	2.05	0.64
15:A:169:LYS:HG3	32:f:580:ALA:HB3	1.79	0.64
17:D:152:MET:HE1	18:E:61:LEU:O	1.98	0.64
21:U:68:PHE:HB3	21:U:73:ALA:HB3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:600:LEU:O	32:f:604:ARG:CB	2.44	0.64
20:C:19:GLY:HA2	22:V:195:ILE:HD11	1.79	0.64
32:f:578:ASN:ND2	32:f:610:THR:OG1	2.30	0.64
22:V:190:ASP:HA	22:V:200:ARG:HH21	1.63	0.64
26:Z:97:THR:HA	26:Z:124:ILE:HG13	1.80	0.64
32:f:230:LYS:NZ	32:f:666:MET:SD	2.71	0.64
32:f:403:LEU:HD11	32:f:410:LYS:HG2	1.79	0.64
11:Q:13:VAL:HB	11:Q:183:ILE:HB	1.79	0.64
18:E:173:TYR:CZ	18:E:300:HIS:HB3	2.33	0.64
21:U:199:ARG:O	21:U:203:LYS:NZ	2.27	0.64
30:d:103:LEU:HD11	30:d:115:PHE:CD1	2.32	0.64
4:J:22:ALA:HB1	4:J:128:GLY:HA2	1.80	0.64
29:c:191:ALA:O	29:c:194:HIS:ND1	2.26	0.64
7:M:92:ARG:NH2	14:T:73:ASP:OD1	2.30	0.64
15:A:78:TRP:CG	32:f:528:ARG:NH1	2.66	0.64
19:F:373:MET:SD	19:F:373:MET:N	2.71	0.64
26:Z:54:PHE:HB3	26:Z:82:PHE:HE2	1.63	0.64
32:f:221:PHE:CZ	32:f:230:LYS:HD3	2.32	0.64
22:V:228:ARG:O	22:V:232:HIS:ND1	2.31	0.64
32:f:430:SER:O	32:f:434:THR:OG1	2.05	0.64
5:K:69:GLU:O	5:K:93:ARG:NH2	2.30	0.64
22:V:333:ILE:HD11	22:V:360:TYR:CE2	2.32	0.64
26:Z:225:GLN:HG2	26:Z:228:TYR:HE2	1.63	0.64
32:f:414:ILE:HG13	32:f:417:ILE:HD11	1.79	0.64
32:f:399:LEU:HD23	32:f:418:LEU:HD21	1.80	0.64
10:P:169:GLN:O	10:P:173:ASN:ND2	2.24	0.63
15:A:205:GLY:HA2	15:A:206:ILE:HG22	1.79	0.63
20:C:295:THR:HG22	20:C:296:ASN:H	1.63	0.63
32:f:454:LEU:O	32:f:458:SER:OG	2.11	0.63
1:G:52:THR:HG22	1:G:53:GLN:H	1.64	0.63
17:D:241:GLY:O	17:D:245:ARG:NH2	2.31	0.63
22:V:167:LEU:HD11	22:V:171:VAL:HB	1.79	0.63
32:f:298:ASN:H	32:f:329:ALA:HA	1.64	0.63
32:f:567:ILE:HG13	32:f:605:LEU:HD22	1.80	0.63
24:X:90:ARG:HH21	24:X:125:LEU:HA	1.63	0.63
27:a:112:ILE:HD12	27:a:113:LEU:H	1.62	0.63
32:f:270:ILE:HD12	32:f:274:LEU:HD12	1.80	0.63
18:E:178:THR:OG1	33:E:401:ATP:O2A	2.15	0.63
23:W:340:VAL:HG22	23:W:350:ARG:HH11	1.64	0.63
5:K:93:ARG:NH1	12:R:68:LEU:O	2.32	0.63
16:B:205:LEU:HD23	16:B:206:THR:N	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:215:ASN:OD1	21:U:216:VAL:N	2.30	0.63
5:K:108:THR:O	5:K:111:SER:OG	2.16	0.63
17:D:148:ASP:HB3	17:D:149:SER:C	2.23	0.63
32:f:89:LEU:O	32:f:93:ALA:HB2	1.98	0.63
32:f:590:ALA:HB2	32:f:603:VAL:HG11	1.80	0.63
32:f:689:GLN:HA	32:f:692:ASP:HB3	1.78	0.63
1:G:126:THR:HG22	2:H:128:ARG:HH22	1.64	0.63
2:H:65:VAL:HG22	2:H:75:VAL:HG12	1.81	0.63
4:J:96:LEU:HA	11:Q:62:LYS:HE2	1.81	0.63
4:J:108:THR:HG22	4:J:133:ILE:HD13	1.80	0.63
5:K:209:LYS:O	5:K:214:ASN:ND2	2.32	0.63
20:C:175:PHE:CZ	20:C:182:GLN:HA	2.34	0.63
25:Y:356:THR:OG1	25:Y:357:ASN:O	2.14	0.63
32:f:588:GLN:HA	32:f:591:GLN:HB2	1.78	0.63
19:F:86:LEU:HB2	19:F:88:TYR:CE1	2.33	0.63
26:Z:250:TYR:O	26:Z:254:ASN:HB2	1.98	0.63
15:A:429:TYR:O	15:A:433:ASN:ND2	2.31	0.62
16:B:259:TYR:OH	17:D:274:ARG:NH2	2.32	0.62
20:C:66:LEU:HG	20:C:70:GLY:HA2	1.79	0.62
32:f:651:ILE:O	32:f:655:SER:CB	2.46	0.62
23:W:408:ARG:HD2	24:X:346:GLN:HE22	1.64	0.62
28:b:164:ASP:N	28:b:165:GLY:HA2	2.13	0.62
9:O:17:ASP:O	9:O:33:LYS:NZ	2.31	0.62
11:Q:38:MET:O	11:Q:65:GLN:NE2	2.32	0.62
21:U:789:ILE:HG23	21:U:844:LYS:HE2	1.79	0.62
22:V:224:LEU:HD12	22:V:228:ARG:HG3	1.80	0.62
32:f:86:ASN:HA	32:f:89:LEU:HB3	1.80	0.62
17:D:45:LYS:NZ	21:U:156:GLU:OE2	2.32	0.62
17:D:167:ILE:HD12	17:D:167:ILE:O	1.97	0.62
22:V:318:GLN:O	22:V:319:HIS:ND1	2.33	0.62
24:X:409:LYS:HE2	29:c:260:GLU:HB3	1.80	0.62
25:Y:190:ALA:O	25:Y:291:HIS:NE2	2.26	0.62
26:Z:207:ASP:O	26:Z:210:SER:OG	2.11	0.62
6:L:121:GLN:HE22	7:M:131:PHE:HE1	1.47	0.62
25:Y:110:TYR:O	25:Y:113:ARG:HB3	2.00	0.62
26:Z:220:LEU:HB3	26:Z:221:PRO:HA	1.81	0.62
1:G:163:PHE:HD1	2:H:58:ASP:H	1.47	0.62
20:C:286:THR:HG23	20:C:287:LYS:H	1.64	0.62
24:X:346:GLN:HE21	24:X:349:HIS:HB2	1.64	0.62
32:f:301:ASP:OD1	32:f:302:PRO:HD3	1.99	0.62
32:f:626:ARG:O	32:f:630:SER:OG	2.12	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:4:PRO:HB2	14:T:100:ARG:HH21	1.65	0.62
22:V:157:THR:OG1	22:V:158:PRO:HD3	2.00	0.62
26:Z:91:ILE:HD12	26:Z:91:ILE:O	2.00	0.62
1:G:28:ALA:HB2	7:M:14:PHE:HE2	1.65	0.62
3:I:233:VAL:O	3:I:237:ILE:HG13	2.00	0.62
12:R:50:ALA:HB2	13:S:129:SER:HB2	1.81	0.62
25:Y:262:SER:HB3	25:Y:270:VAL:HG11	1.81	0.62
26:Z:144:VAL:HG12	26:Z:145:HIS:H	1.64	0.62
29:c:174:PRO:HB2	29:c:175:ARG:HD3	1.81	0.62
29:c:281:LYS:HB2	29:c:282:ARG:HA	1.80	0.62
3:I:62:SER:OG	3:I:65:ILE:O	2.15	0.62
11:Q:29:LYS:HD3	11:Q:32:HIS:HB2	1.80	0.62
17:D:105:SER:O	17:D:245:ARG:NH1	2.33	0.62
32:f:529:ARG:HD2	32:f:561:GLU:HB3	1.80	0.62
25:Y:357:ASN:HB2	25:Y:358:ARG:HA	1.82	0.62
32:f:675:ASP:OD1	32:f:679:ARG:NH1	2.32	0.62
14:T:27:LEU:HD22	14:T:184:TYR:H	1.65	0.61
15:A:206:ILE:HG13	15:A:207:GLU:H	1.63	0.61
22:V:173:ILE:O	22:V:177:ASN:ND2	2.32	0.61
25:Y:17:LEU:HA	25:Y:150:PHE:HE1	1.64	0.61
27:a:125:ILE:N	27:a:126:GLY:HA2	2.15	0.61
5:K:50:VAL:HG21	5:K:66:LYS:HG2	1.82	0.61
20:C:347:ILE:HD11	20:C:387:VAL:HG21	1.82	0.61
21:U:203:LYS:O	21:U:207:ASN:ND2	2.31	0.61
23:W:219:THR:HG22	23:W:222:LEU:H	1.64	0.61
32:f:167:LEU:O	32:f:171:PHE:CB	2.48	0.61
7:M:8:ASP:O	7:M:22:GLN:NE2	2.29	0.61
7:M:56:LYS:H	7:M:57:LEU:HA	1.65	0.61
7:M:180:GLN:HB2	7:M:184:MET:HG2	1.83	0.61
10:P:190:ILE:HG22	10:P:195:ILE:HG23	1.80	0.61
18:E:120:TYR:OH	19:F:147:PRO:O	2.17	0.61
1:G:17:SER:OG	1:G:21:ARG:N	2.33	0.61
2:H:71:HIS:HA	2:H:218:PHE:H	1.66	0.61
32:f:268:THR:HB	32:f:656:HIS:CD2	2.35	0.61
11:Q:168:GLN:NE2	11:Q:174:ASN:O	2.34	0.61
14:T:92:LEU:HG	14:T:125:VAL:HG11	1.82	0.61
23:W:72:LYS:HZ1	23:W:122:LEU:HB2	1.65	0.61
32:f:532:PRO:HB3	32:f:551:LEU:HD21	1.83	0.61
1:G:111:VAL:HG11	1:G:142:GLY:HA3	1.83	0.61
25:Y:210:SER:HB3	25:Y:213:LEU:HB2	1.82	0.61
26:Z:63:LYS:HB2	26:Z:64:ASP:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:143:LEU:HD12	17:D:252:ARG:HH12	1.66	0.61
22:V:241:ARG:HG3	22:V:242:HIS:H	1.66	0.61
32:f:62:ILE:HA	32:f:65:ASN:HB3	1.83	0.61
32:f:286:LEU:HD13	32:f:316:ASN:HD22	1.66	0.61
32:f:518:HIS:HA	32:f:521:ARG:HG2	1.81	0.61
32:f:685:VAL:HG23	32:f:686:ARG:H	1.66	0.61
2:H:66:GLU:OE2	2:H:91:ARG:NH2	2.34	0.61
7:M:106:ILE:HD12	7:M:107:PRO:HD2	1.81	0.61
22:V:89:LYS:HD3	22:V:92:ARG:HH11	1.64	0.61
26:Z:170:VAL:HG13	29:c:152:LYS:HA	1.83	0.61
32:f:601:PHE:O	32:f:605:LEU:HB3	2.00	0.61
6:L:120:THR:O	7:M:129:ARG:NH1	2.34	0.61
7:M:141:SER:HB3	7:M:144:ASP:HB2	1.82	0.61
15:A:83:ASP:OD1	16:B:137:SER:OG	2.19	0.61
22:V:281:ASN:H	22:V:284:GLU:HB3	1.66	0.61
24:X:384:VAL:HB	25:Y:312:ARG:HH22	1.65	0.61
26:Z:201:LEU:HD13	27:a:361:LYS:HG3	1.83	0.61
32:f:470:LYS:HE3	32:f:496:LEU:HD22	1.83	0.61
2:H:66:GLU:HG3	2:H:91:ARG:HH21	1.65	0.60
17:D:100:THR:HB	17:D:114:ARG:HD2	1.83	0.60
20:C:217:SER:HB3	20:C:218:GLU:CB	2.21	0.60
21:U:353:LEU:HD13	21:U:385:PHE:HZ	1.66	0.60
27:a:235:ASP:OD2	27:a:249:GLN:NE2	2.34	0.60
29:c:100:LYS:HA	29:c:105:PRO:HB3	1.82	0.60
32:f:432:ALA:HB1	32:f:679:ARG:HG2	1.83	0.60
17:D:374:ASP:HA	18:E:291:ARG:NH1	2.16	0.60
20:C:157:GLN:NE2	20:C:316:GLU:O	2.35	0.60
23:W:241:LEU:HA	23:W:244:CYS:SG	2.41	0.60
32:f:679:ARG:HB2	32:f:680:PRO:HD3	1.82	0.60
6:L:204:ASP:HB3	6:L:205:LEU:C	2.26	0.60
11:Q:12:TYR:HB3	11:Q:153:ARG:HH21	1.65	0.60
26:Z:210:SER:O	26:Z:214:LYS:HG2	2.01	0.60
1:G:39:SER:H	1:G:172:GLN:NE2	1.99	0.60
7:M:34:SER:OG	7:M:65:ARG:NH1	2.35	0.60
21:U:505:ASP:HB3	21:U:508:THR:HG22	1.82	0.60
22:V:290:TYR:OH	22:V:294:ARG:NH2	2.35	0.60
26:Z:236:LEU:HD21	27:a:335:TRP:CD1	2.37	0.60
32:f:430:SER:HA	32:f:433:ASN:HB3	1.84	0.60
1:G:138:MET:HB3	1:G:154:CYS:HB3	1.83	0.60
2:H:68:ILE:HG23	2:H:91:ARG:HD3	1.84	0.60
15:A:100:LYS:HZ2	15:A:142:VAL:HB	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:223:ILE:HG13	16:B:346:ARG:HB2	1.84	0.60
16:B:390:LEU:HD23	16:B:394:ASP:HB3	1.84	0.60
18:E:86:GLN:OE1	19:F:117:ARG:NH2	2.34	0.60
21:U:74:PHE:HB3	21:U:103:LYS:HE3	1.83	0.60
32:f:231:LEU:O	32:f:235:ASP:CB	2.36	0.60
1:G:43:ARG:HH11	1:G:150:GLN:HA	1.66	0.60
9:O:35:HIS:NE2	9:O:53:ASP:OD1	2.34	0.60
20:C:117:ARG:HG3	20:C:124:HIS:HB2	1.83	0.60
25:Y:301:ILE:HD12	25:Y:342:ARG:HB3	1.82	0.60
18:E:269:THR:OG1	18:E:271:HIS:ND1	2.34	0.60
20:C:158:ILE:HA	20:C:161:ILE:HG22	1.82	0.60
6:L:66:VAL:HG11	6:L:88:MET:HG3	1.82	0.60
11:Q:38:MET:HA	11:Q:61:GLN:NE2	2.16	0.60
16:B:255:LEU:HD12	16:B:256:ILE:HG12	1.84	0.60
17:D:238:LYS:HA	18:E:208:ILE:HG12	1.84	0.60
11:Q:22:ALA:HB2	11:Q:27:GLN:HA	1.84	0.60
16:B:173:VAL:O	20:C:232:ARG:NH1	2.35	0.60
16:B:191:ASP:HA	16:B:194:ILE:HG22	1.83	0.60
21:U:363:SER:HB3	29:c:173:GLU:HB3	1.84	0.60
29:c:174:PRO:HB2	29:c:175:ARG:HH11	1.66	0.60
32:f:648:ARG:NH2	32:f:692:ASP:OD1	2.33	0.60
5:K:104:ASN:OD1	12:R:57:ARG:NH2	2.31	0.59
16:B:248:LEU:HD21	16:B:270:LEU:HD22	1.84	0.59
17:D:263:PHE:HD1	17:D:308:ILE:HG13	1.67	0.59
19:F:312:GLU:O	19:F:316:GLN:HG3	2.01	0.59
21:U:615:ARG:HH21	21:U:645:ASN:HD21	1.49	0.59
3:I:72:MET:HE1	3:I:105:ILE:HG23	1.84	0.59
12:R:127:SER:HB3	12:R:136:TYR:CE2	2.37	0.59
18:E:65:THR:HG22	18:E:66:GLU:H	1.67	0.59
19:F:359:GLU:HB2	19:F:385:ALA:HB1	1.83	0.59
21:U:252:LEU:HD21	21:U:264:VAL:HG11	1.84	0.59
27:a:122:LYS:HE3	27:a:134:THR:HG21	1.84	0.59
2:H:19:LEU:HD13	2:H:22:ILE:HD12	1.83	0.59
26:Z:22:HIS:HA	26:Z:25:ARG:HG2	1.84	0.59
30:d:215:TRP:CH2	30:d:222:TYR:HB3	2.38	0.59
30:d:233:GLU:CB	30:d:235:THR:HG23	2.32	0.59
15:A:348:LEU:HA	15:A:351:ARG:HH21	1.66	0.59
32:f:294:SER:O	32:f:298:ASN:ND2	2.35	0.59
6:L:65:HIS:HD2	6:L:221:PHE:HD2	1.50	0.59
6:L:85:CYS:SG	6:L:89:ARG:NH1	2.76	0.59
7:M:232:ARG:NH1	7:M:234:GLU:OE1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:56:VAL:HG21	21:U:599:ILE:HG23	1.83	0.59
17:D:285:VAL:HA	17:D:288:ILE:HB	1.83	0.59
19:F:86:LEU:O	19:F:88:TYR:N	2.34	0.59
22:V:97:ALA:HB3	22:V:98:LEU:HA	1.85	0.59
29:c:249:LEU:HD21	29:c:297:VAL:HG11	1.84	0.59
32:f:133:LYS:HG3	32:f:137:PHE:CD2	2.38	0.59
15:A:218:PRO:O	15:A:221:GLY:N	2.29	0.59
15:A:237:PHE:HB2	15:A:271:LEU:HB2	1.84	0.59
19:F:92:ASN:OD1	19:F:93:VAL:N	2.36	0.59
22:V:275:VAL:H	22:V:276:PHE:HA	1.68	0.59
2:H:174:LEU:HD21	2:H:194:THR:HG21	1.84	0.59
15:A:264:ALA:HB1	15:A:315:ILE:HG21	1.85	0.59
15:A:355:PHE:HE1	15:A:385:ILE:HB	1.68	0.59
17:D:152:MET:HE2	18:E:62:LYS:HG3	1.81	0.59
20:C:229:ARG:HH12	20:C:232:ARG:NE	1.97	0.59
26:Z:106:ILE:HD11	26:Z:153:LYS:HB3	1.85	0.59
31:e:58:ALA:HB3	31:e:59:GLU:HA	1.85	0.59
32:f:141:ARG:HB3	32:f:144:VAL:HG12	1.83	0.59
15:A:212:VAL:HG12	15:A:339:ARG:HB3	1.85	0.59
16:B:108:SER:O	16:B:152:LEU:N	2.32	0.59
26:Z:215:VAL:HG11	27:a:346:ILE:HG21	1.85	0.59
32:f:600:LEU:HD13	32:f:600:LEU:H	1.68	0.59
1:G:81:THR:OG1	1:G:137:CYS:HB3	2.03	0.59
16:B:220:LYS:HB2	16:B:346:ARG:CZ	2.33	0.59
21:U:788:VAL:HG13	21:U:884:VAL:HG11	1.84	0.59
25:Y:23:ARG:NH1	25:Y:52:PRO:O	2.35	0.59
17:D:392:TYR:HA	23:W:136:ILE:HG13	1.83	0.59
18:E:61:LEU:HD11	18:E:72:LYS:HB2	1.84	0.59
22:V:224:LEU:HB2	22:V:227:VAL:HB	1.84	0.59
26:Z:256:GLN:HE22	29:c:298:GLN:HB2	1.67	0.59
29:c:243:SER:H	29:c:245:VAL:H	1.50	0.59
32:f:390:GLU:HG3	32:f:395:TYR:HB3	1.85	0.59
1:G:56:VAL:HA	1:G:61:LEU:HD13	1.85	0.58
1:G:102:LYS:HD3	1:G:108:GLU:HA	1.85	0.58
17:D:44:TYR:HA	20:C:25:LEU:HD11	1.84	0.58
21:U:643:SER:O	21:U:649:ARG:NH1	2.37	0.58
22:V:326:GLN:HB3	22:V:353:LEU:HD13	1.85	0.58
23:W:48:LEU:HB2	23:W:96:GLN:OE1	2.03	0.58
32:f:612:LEU:HD13	32:f:660:TYR:CE1	2.37	0.58
17:D:255:LYS:HE2	17:D:299:PHE:HE1	1.68	0.58
18:E:239:GLY:HA2	18:E:257:LEU:HD11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:215:TRP:CG	30:d:216:VAL:H	2.20	0.58
2:H:40:ALA:HB1	2:H:182:LEU:H	1.67	0.58
21:U:14:GLU:O	21:U:20:LYS:NZ	2.36	0.58
21:U:842:LYS:HG2	21:U:882:ALA:HB2	1.84	0.58
23:W:236:HIS:ND1	23:W:237:GLU:OE1	2.36	0.58
26:Z:193:ASN:O	26:Z:196:HIS:ND1	2.19	0.58
29:c:63:ASP:OD1	29:c:66:THR:OG1	2.21	0.58
15:A:345:LEU:HG	15:A:346:PRO:HD2	1.84	0.58
16:B:190:LEU:HD13	16:B:194:ILE:HB	1.85	0.58
22:V:416:ARG:HB3	25:Y:348:ASP:OD1	2.03	0.58
32:f:458:SER:HB2	32:f:461:PHE:HA	1.85	0.58
11:Q:17:SER:OG	11:Q:179:SER:OG	2.21	0.58
15:A:119:ALA:HA	19:F:127:SER:HB3	1.85	0.58
16:B:304:GLU:O	16:B:307:ARG:HG2	2.03	0.58
19:F:357:PRO:O	19:F:362:ARG:NH1	2.35	0.58
23:W:187:LEU:HA	23:W:190:MET:HE3	1.85	0.58
32:f:282:LYS:HZ1	32:f:286:LEU:HD23	1.68	0.58
8:N:7:GLN:HB3	8:N:111:VAL:HG23	1.85	0.58
21:U:96:TYR:O	21:U:100:ILE:HG12	2.03	0.58
25:Y:63:TRP:HB3	25:Y:64:GLN:HB3	1.85	0.58
19:F:165:PRO:HB2	19:F:166:THR:OG1	2.04	0.58
20:C:236:VAL:HG22	20:C:239:ARG:HH12	1.68	0.58
21:U:188:MET:HG2	21:U:194:ARG:HD3	1.86	0.58
29:c:281:LYS:HB3	29:c:283:HIS:CD2	2.38	0.58
4:J:32:ALA:HB3	4:J:161:ILE:HD11	1.85	0.58
11:Q:52:ASP:OD1	12:R:88:TYR:OH	2.20	0.58
11:Q:84:THR:HG21	11:Q:104:LEU:HD11	1.85	0.58
18:E:86:GLN:NE2	18:E:108:MET:O	2.37	0.58
20:C:72:TYR:HB2	20:C:116:LEU:HB3	1.84	0.58
1:G:53:GLN:HA	1:G:215:ILE:HA	1.84	0.58
7:M:136:MET:HE3	7:M:148:LEU:HD11	1.86	0.58
19:F:89:LEU:HG	19:F:153:VAL:HG13	1.85	0.58
31:e:59:GLU:HB3	31:e:63:HIS:CE1	2.39	0.58
32:f:42:GLU:HG3	32:f:43:HIS:CD2	2.39	0.58
3:I:123:GLN:HG3	4:J:125:ARG:NH2	2.18	0.57
15:A:357:ILE:HG23	15:A:358:HIS:HD1	1.68	0.57
21:U:759:SER:HA	21:U:782:ALA:HA	1.86	0.57
7:M:8:ASP:HB3	7:M:21:PHE:HD2	1.68	0.57
11:Q:153:ARG:HH22	11:Q:184:ASP:HB3	1.70	0.57
15:A:277:ILE:HG22	15:A:321:THR:HB	1.85	0.57
28:b:15:TYR:O	28:b:25:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:336:GLU:HG3	32:f:337:ASP:H	1.68	0.57
1:G:211:LYS:NZ	1:G:232:GLU:OE2	2.36	0.57
15:A:237:PHE:HA	15:A:270:CYS:SG	2.45	0.57
17:D:60:TYR:HD1	21:U:603:LEU:HD21	1.68	0.57
17:D:83:GLN:NE2	17:D:140:VAL:HG21	2.10	0.57
20:C:136:SER:HA	20:C:139:MET:HB2	1.87	0.57
22:V:451:ILE:HG13	22:V:458:VAL:HG13	1.85	0.57
26:Z:186:THR:HG23	26:Z:187:LEU:H	1.70	0.57
32:f:119:VAL:O	32:f:123:PHE:HB3	2.04	0.57
1:G:180:GLU:HG2	2:H:56:LEU:HG	1.86	0.57
22:V:279:GLN:HE21	22:V:285:TRP:CD1	2.21	0.57
3:I:83:ALA:O	3:I:86:LEU:N	2.38	0.57
3:I:171:ALA:O	3:I:175:LEU:HG	2.03	0.57
18:E:179:GLY:N	33:E:401:ATP:O2A	2.36	0.57
23:W:45:GLU:HB2	23:W:93:ARG:HG3	1.85	0.57
27:a:97:LEU:HD22	27:a:118:ILE:HG13	1.86	0.57
1:G:11:ARG:O	1:G:24:GLN:NE2	2.32	0.57
3:I:140:ASP:OD1	3:I:144:GLY:N	2.37	0.57
23:W:137:TYR:HB3	23:W:140:ILE:HD12	1.86	0.57
27:a:54:ASP:HA	27:a:57:ILE:HG22	1.86	0.57
29:c:191:ALA:C	29:c:194:HIS:HD1	2.13	0.57
32:f:193:HIS:HA	32:f:195:GLU:HG2	1.87	0.57
18:E:138:LEU:HD22	18:E:140:GLU:HG2	1.86	0.57
25:Y:92:GLU:HA	25:Y:100:ILE:HD13	1.86	0.57
1:G:203:SER:O	1:G:207:SER:N	2.38	0.57
11:Q:22:ALA:CB	11:Q:27:GLN:HA	2.35	0.57
12:R:11:GLY:HA3	12:R:179:VAL:O	2.05	0.57
15:A:281:GLY:O	15:A:326:THR:OG1	2.19	0.57
15:A:309:PHE:CZ	19:F:235:LEU:HG	2.38	0.57
32:f:141:ARG:HG3	32:f:144:VAL:H	1.70	0.57
32:f:333:SER:O	32:f:334:ASN:ND2	2.38	0.57
5:K:16:SER:O	5:K:19:GLY:HA3	2.05	0.57
16:B:211:TYR:OH	16:B:217:LYS:HA	2.05	0.57
20:C:303:SER:O	20:C:307:ARG:N	2.37	0.57
21:U:112:CYS:SG	21:U:159:ARG:NH1	2.78	0.57
22:V:82:LEU:O	22:V:87:SER:OG	2.23	0.57
22:V:148:ARG:HG3	22:V:149:PRO:HD3	1.86	0.57
22:V:411:SER:HB2	22:V:447:ILE:HD13	1.86	0.57
32:f:369:GLY:O	32:f:372:ASN:ND2	2.38	0.57
15:A:428:ARG:O	15:A:431:THR:OG1	2.22	0.57
17:D:389:GLU:HA	17:D:390:ASN:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:79:VAL:O	22:V:80:LYS:NZ	2.27	0.57
22:V:224:LEU:HD13	22:V:227:VAL:HB	1.87	0.57
23:W:416:GLN:HB3	23:W:417:ARG:CA	2.35	0.57
32:f:444:SER:HB3	32:f:476:LYS:HG3	1.87	0.57
32:f:615:GLY:HA2	32:f:619:LEU:N	2.19	0.57
17:D:45:LYS:HG2	21:U:187:LEU:HD13	1.87	0.56
17:D:194:ILE:HD12	17:D:196:ILE:HD13	1.86	0.56
26:Z:195:VAL:HG13	26:Z:199:LYS:HD3	1.87	0.56
30:d:227:SER:C	30:d:229:GLN:HA	2.30	0.56
32:f:155:TYR:HA	32:f:184:LYS:HE2	1.86	0.56
32:f:282:LYS:HE3	32:f:286:LEU:HD23	1.87	0.56
9:O:36:PHE:CD1	9:O:42:TYR:HE1	2.22	0.56
9:O:163:ILE:HG23	9:O:170:GLY:HA2	1.88	0.56
10:P:44:PRO:HA	10:P:50:TYR:HD1	1.70	0.56
16:B:255:LEU:HB3	20:C:229:ARG:HG3	1.87	0.56
17:D:293:LEU:O	17:D:326:ARG:NH1	2.37	0.56
18:E:128:GLY:HA2	18:E:129:ASN:HB2	1.85	0.56
29:c:154:LYS:HB3	29:c:156:VAL:HG22	1.87	0.56
15:A:103:ASN:ND2	19:F:169:ASP:OD1	2.39	0.56
15:A:157:ILE:HG22	15:A:158:ASP:CB	2.34	0.56
27:a:33:LEU:HD13	27:a:36:GLN:HB2	1.87	0.56
28:b:94:HIS:HD2	28:b:136:VAL:HG21	1.71	0.56
30:d:114:GLU:HA	30:d:117:THR:HG22	1.87	0.56
31:e:42:ASN:O	31:e:46:ASP:HB2	2.06	0.56
32:f:436:VAL:HG21	32:f:675:ASP:OD1	2.04	0.56
6:L:50:LYS:HB3	6:L:59:HIS:HB3	1.86	0.56
11:Q:140:LEU:HA	11:Q:143:LEU:HB3	1.88	0.56
15:A:80:LEU:HD23	16:B:137:SER:HB3	1.87	0.56
18:E:84:ARG:HH11	18:E:108:MET:HG3	1.70	0.56
5:K:212:ALA:HA	5:K:234:LEU:HD22	1.87	0.56
20:C:99:VAL:HG13	20:C:100:ASP:C	2.31	0.56
23:W:370:TYR:HA	23:W:371:THR:HB	1.87	0.56
26:Z:212:LEU:HD12	27:a:350:LYS:HD2	1.86	0.56
32:f:291:ILE:HG23	32:f:651:ILE:HD12	1.88	0.56
32:f:301:ASP:OD1	32:f:301:ASP:N	2.38	0.56
3:I:69:ASN:OD1	3:I:70:GLU:N	2.38	0.56
16:B:139:VAL:HA	16:B:140:ASP:HB3	1.88	0.56
18:E:281:ARG:HD3	18:E:387:LYS:NZ	2.21	0.56
20:C:192:PRO:HD3	20:C:296:ASN:CG	2.30	0.56
22:V:200:ARG:HH11	22:V:242:HIS:HB2	1.71	0.56
25:Y:79:ASP:HA	25:Y:82:LYS:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:254:ALA:HA	27:a:261:LEU:HD23	1.88	0.56
4:J:137:ASP:N	4:J:141:THR:O	2.39	0.56
17:D:87:LEU:HB2	18:E:80:VAL:HG23	1.87	0.56
17:D:303:VAL:HA	17:D:304:ASN:HB2	1.88	0.56
20:C:90:HIS:HB2	20:C:91:PRO:HD3	1.86	0.56
23:W:405:LYS:HG3	24:X:342:PHE:HA	1.88	0.56
29:c:227:GLU:OE2	29:c:234:TYR:N	2.39	0.56
32:f:106:ALA:HB1	32:f:107:LEU:HA	1.88	0.56
1:G:50:ILE:O	1:G:218:GLY:N	2.38	0.56
1:G:163:PHE:HB2	1:G:166:THR:OG1	2.05	0.56
2:H:6:TYR:HE2	2:H:126:GLY:HA3	1.71	0.56
3:I:90:LEU:HD12	3:I:114:LEU:HB2	1.87	0.56
6:L:72:ILE:HG22	6:L:134:ILE:HA	1.86	0.56
17:D:283:ARG:HA	17:D:286:GLN:HG2	1.87	0.56
21:U:705:LYS:HA	21:U:708:GLN:HG3	1.88	0.56
23:W:374:THR:HG23	27:a:327:VAL:HA	1.87	0.56
23:W:455:LEU:HD12	23:W:456:GLN:HG2	1.88	0.56
32:f:495:VAL:HA	32:f:498:ILE:HG22	1.88	0.56
32:f:528:ARG:O	32:f:532:PRO:HD3	2.06	0.56
5:K:13:ASN:HD21	6:L:126:ARG:HH11	1.54	0.56
23:W:67:LEU:HD22	23:W:71:VAL:HB	1.88	0.56
27:a:100:THR:HA	27:a:103:LYS:HE2	1.88	0.56
3:I:105:ILE:HD12	3:I:106:PRO:HD2	1.88	0.56
17:D:160:PRO:HG2	17:D:221:HIS:CD2	2.41	0.56
28:b:12:ASN:ND2	28:b:53:THR:OG1	2.39	0.56
32:f:193:HIS:CE1	32:f:408:LEU:HB2	2.41	0.56
16:B:188:GLY:O	33:B:501:ATP:N6	2.39	0.55
18:E:138:LEU:O	18:E:142:ILE:HG13	2.06	0.55
29:c:227:GLU:OE1	29:c:233:ASP:N	2.39	0.55
30:d:6:LYS:HD3	30:d:50:LEU:HG	1.87	0.55
30:d:26:LEU:HD11	30:d:54:ILE:HD12	1.88	0.55
32:f:100:PHE:CG	32:f:109:LEU:HD21	2.41	0.55
32:f:192:THR:HA	32:f:193:HIS:HB2	1.88	0.55
1:G:173:THR:O	1:G:176:THR:OG1	2.24	0.55
22:V:159:LEU:HD13	22:V:178:SER:HB2	1.88	0.55
29:c:28:ALA:HB1	29:c:180:ASN:HD21	1.72	0.55
29:c:152:LYS:HG3	29:c:153:GLY:H	1.70	0.55
2:H:15:PRO:HA	3:I:23:TYR:CD1	2.41	0.55
4:J:36:ARG:HB3	4:J:144:LEU:HD23	1.88	0.55
7:M:83:ASP:HB2	7:M:133:CYS:SG	2.47	0.55
20:C:229:ARG:NH1	20:C:279:GLN:OE1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:65:ARG:HB2	23:W:66:ILE:HB	1.88	0.55
32:f:95:GLY:O	32:f:99:LYS:HG2	2.05	0.55
2:H:45:VAL:HG22	2:H:212:ILE:HG22	1.89	0.55
16:B:222:VAL:HG23	16:B:328:ILE:HG23	1.88	0.55
16:B:294:ARG:HB3	20:C:264:GLY:HA3	1.87	0.55
17:D:181:VAL:O	17:D:306:LYS:NZ	2.39	0.55
17:D:323:ARG:NH1	17:D:324:PRO:O	2.39	0.55
17:D:374:ASP:HA	18:E:291:ARG:HH12	1.70	0.55
21:U:181:LEU:HD11	21:U:201:LEU:HD12	1.89	0.55
21:U:571:CYS:HB2	21:U:601:ARG:HH21	1.71	0.55
24:X:359:ALA:O	24:X:363:ARG:HG3	2.06	0.55
17:D:75:ALA:HB1	20:C:56:VAL:HG21	1.88	0.55
18:E:142:ILE:HG12	18:E:183:LEU:HD11	1.89	0.55
20:C:171:HIS:HB3	20:C:174:LEU:HD21	1.88	0.55
23:W:371:THR:O	23:W:414:ASN:HB2	2.06	0.55
23:W:435:LEU:HD13	29:c:239:LYS:HE3	1.89	0.55
30:d:184:LYS:HB2	30:d:185:ALA:HB2	1.88	0.55
31:e:59:GLU:O	31:e:63:HIS:ND1	2.39	0.55
32:f:551:LEU:HD23	32:f:554:PHE:HD2	1.70	0.55
1:G:76:ILE:HG12	1:G:142:GLY:HA2	1.88	0.55
5:K:143:PHE:HB2	5:K:154:PHE:HB2	1.88	0.55
7:M:174:THR:OG1	18:E:372:ARG:NH1	2.40	0.55
17:D:337:ASP:O	17:D:341:LYS:N	2.35	0.55
22:V:160:LEU:HB2	22:V:161:PRO:HD3	1.88	0.55
22:V:358:MET:HB2	22:V:359:PRO:HD3	1.87	0.55
28:b:50:GLY:H	28:b:64:LEU:HD12	1.72	0.55
32:f:399:LEU:HD21	32:f:414:ILE:HD11	1.88	0.55
32:f:447:VAL:HA	32:f:476:LYS:HE2	1.89	0.55
1:G:127:GLN:OE1	2:H:128:ARG:N	2.38	0.55
17:D:348:ILE:HD11	17:D:352:MET:HE3	1.88	0.55
19:F:164:LEU:HD12	19:F:165:PRO:HD2	1.87	0.55
22:V:90:GLU:OE1	22:V:90:GLU:N	2.38	0.55
22:V:211:TYR:O	22:V:214:HIS:HB2	2.07	0.55
3:I:148:TYR:HA	3:I:158:GLY:HA2	1.89	0.55
11:Q:116:TYR:CE1	11:Q:126:LYS:HD3	2.41	0.55
14:T:44:ARG:HA	14:T:50:MET:HG3	1.89	0.55
17:D:200:ARG:HD2	17:D:296:MET:HE3	1.88	0.55
20:C:328:ILE:HG12	33:C:501:ATP:N1	2.22	0.55
22:V:228:ARG:HH12	22:V:254:LEU:HA	1.71	0.55
22:V:342:ILE:HD12	22:V:343:PRO:HD2	1.87	0.55
23:W:84:ASN:O	23:W:87:ILE:HD12	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:274:VAL:O	23:W:283:GLN:NE2	2.39	0.55
23:W:408:ARG:NH1	24:X:349:HIS:HB3	2.22	0.55
30:d:159:PRO:N	30:d:160:ALA:HA	2.22	0.55
32:f:608:GLY:HA3	32:f:652:LEU:HD21	1.88	0.55
5:K:227:HIS:HA	5:K:228:MET:C	2.30	0.55
8:N:26:ILE:HG21	8:N:29:ARG:HD3	1.88	0.55
13:S:91:MET:O	13:S:95:ILE:HG13	2.06	0.55
15:A:120:LYS:HB2	19:F:90:VAL:HB	1.88	0.55
17:D:96:VAL:HG11	20:C:127:LEU:HD13	1.89	0.55
17:D:390:ASN:O	23:W:135:LYS:HE2	2.07	0.55
22:V:290:TYR:CD1	22:V:328:VAL:HG23	2.41	0.55
30:d:163:TYR:HA	30:d:166:PHE:HD2	1.72	0.55
30:d:241:GLU:HA	30:d:244:LYS:HB2	1.88	0.55
32:f:382:THR:HG22	32:f:386:LYS:NZ	2.22	0.55
32:f:567:ILE:HG12	32:f:602:MET:HA	1.87	0.55
6:L:104:PRO:HD2	6:L:107:ARG:HH11	1.71	0.55
15:A:169:LYS:HG3	32:f:580:ALA:CB	2.36	0.55
26:Z:101:LEU:HD23	26:Z:123:ILE:HD11	1.89	0.55
28:b:68:THR:HA	28:b:71:ILE:HD13	1.89	0.55
32:f:307:LEU:HD22	32:f:322:SER:HA	1.88	0.55
11:Q:47:VAL:HB	11:Q:102:LEU:HG	1.87	0.54
13:S:108:ASN:HB2	13:S:124:PHE:HD2	1.72	0.54
15:A:363:SER:HB2	15:A:403:ILE:HG22	1.89	0.54
17:D:282:ASP:HA	17:D:285:VAL:HG22	1.88	0.54
18:E:252:GLU:O	18:E:255:ARG:HG2	2.07	0.54
18:E:364:GLN:HG2	18:E:367:PHE:HD2	1.72	0.54
19:F:224:LEU:HB3	19:F:351:LYS:HG2	1.88	0.54
25:Y:203:ASP:OD1	25:Y:203:ASP:N	2.36	0.54
32:f:144:VAL:O	32:f:148:LEU:N	2.40	0.54
15:A:323:ARG:HB2	15:A:325:ASP:OD1	2.06	0.54
18:E:56:ILE:HG23	18:E:100:LEU:HB2	1.89	0.54
21:U:428:PRO:HB3	21:U:439:GLU:HB2	1.88	0.54
23:W:5:GLY:HA3	23:W:47:LEU:HD22	1.88	0.54
15:A:75:PRO:O	15:A:79:ASP:HB2	2.08	0.54
19:F:90:VAL:O	19:F:127:SER:OG	2.20	0.54
20:C:168:PRO:HA	20:C:172:PRO:HG3	1.89	0.54
30:d:97:GLN:NE2	30:d:161:GLU:OE2	2.40	0.54
17:D:150:SER:OG	17:D:151:ILE:N	2.32	0.54
21:U:800:VAL:HG21	21:U:914:LEU:HD21	1.90	0.54
22:V:285:TRP:O	22:V:288:TYR:HB3	2.07	0.54
23:W:422:ASN:ND2	26:Z:247:LYS:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:172:LEU:HD12	24:X:175:LYS:HD3	1.89	0.54
25:Y:181:LYS:HA	25:Y:200:LEU:HD12	1.89	0.54
27:a:71:VAL:HA	28:b:17:ARG:NH1	2.20	0.54
32:f:427:PRO:O	32:f:464:LYS:NZ	2.35	0.54
5:K:16:SER:HB3	5:K:20:ARG:H	1.71	0.54
8:N:22:THR:HG22	8:N:27:ALA:HB2	1.90	0.54
9:O:34:ILE:HG12	9:O:44:CYS:SG	2.47	0.54
23:W:328:LEU:HD11	23:W:341:PHE:HE2	1.72	0.54
24:X:174:SER:HA	24:X:177:TYR:HD2	1.73	0.54
31:e:41:ASP:OD1	31:e:42:ASN:N	2.34	0.54
32:f:48:LEU:HA	32:f:51:GLU:HB3	1.89	0.54
32:f:397:ARG:NH2	32:f:432:ALA:HB3	2.22	0.54
32:f:434:THR:HA	32:f:437:ASP:HB3	1.90	0.54
1:G:113:MET:HE3	9:O:70:THR:HA	1.88	0.54
3:I:119:GLN:NE2	4:J:78:ALA:O	2.39	0.54
7:M:228:PRO:HB2	7:M:231:ILE:HG12	1.89	0.54
16:B:224:LEU:HB3	16:B:234:LEU:HD13	1.89	0.54
28:b:16:MET:HA	28:b:25:ARG:HD2	1.88	0.54
4:J:88:ARG:NH2	11:Q:69:MET:HB2	2.17	0.54
6:L:207:THR:HG22	6:L:233:LEU:HD12	1.89	0.54
15:A:427:PRO:HG2	15:A:430:MET:HE2	1.90	0.54
18:E:171:LEU:HB2	18:E:295:LEU:HD22	1.90	0.54
23:W:86:ASN:HB3	23:W:88:MET:HG3	1.90	0.54
28:b:32:ALA:O	28:b:35:ILE:HG13	2.07	0.54
30:d:225:PHE:HB3	30:d:226:ALA:HB2	1.90	0.54
30:d:234:ASP:HB3	30:d:238:PRO:HD3	1.89	0.54
10:P:107:PRO:HG2	10:P:124:LEU:HB2	1.89	0.54
15:A:346:PRO:HB2	15:A:351:ARG:HG2	1.89	0.54
17:D:154:LEU:C	17:D:156:SER:H	2.15	0.54
19:F:70:LYS:O	19:F:73:ILE:HG13	2.08	0.54
20:C:275:GLU:O	20:C:279:GLN:HG3	2.08	0.54
21:U:233:LEU:HD13	21:U:268:LEU:HD21	1.89	0.54
22:V:97:ALA:N	22:V:98:LEU:HB2	2.23	0.54
22:V:475:ALA:O	22:V:479:ARG:HG2	2.08	0.54
23:W:62:SER:HB2	23:W:71:VAL:HG11	1.90	0.54
29:c:216:MET:O	29:c:220:LEU:HD13	2.08	0.54
32:f:52:ILE:HG13	32:f:64:GLU:HG2	1.88	0.54
32:f:383:ILE:HG12	32:f:399:LEU:HD22	1.90	0.54
32:f:414:ILE:HG12	32:f:418:LEU:HD13	1.89	0.54
32:f:608:GLY:HA2	32:f:652:LEU:HD11	1.90	0.54
27:a:245:VAL:HA	27:a:246:GLU:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:117:VAL:HG22	28:b:119:ASP:H	1.72	0.54
1:G:49:VAL:HG22	1:G:219:VAL:HG23	1.90	0.54
5:K:11:GLY:C	5:K:13:ASN:H	2.15	0.54
7:M:10:SER:O	7:M:13:THR:OG1	2.26	0.54
16:B:383:LEU:HB3	16:B:387:LYS:HZ1	1.73	0.54
18:E:90:SER:O	18:E:93:LYS:NZ	2.35	0.54
25:Y:293:ARG:NH1	31:e:49:GLU:OE2	2.40	0.54
25:Y:349:LYS:O	25:Y:350:VAL:HG22	2.08	0.54
26:Z:56:VAL:HA	26:Z:74:TYR:HE2	1.73	0.54
26:Z:102:HIS:CD2	26:Z:104:ASN:HB3	2.43	0.54
29:c:243:SER:CB	29:c:244:VAL:HB	2.37	0.54
30:d:228:GLN:N	30:d:229:GLN:HA	2.22	0.54
32:f:510:GLU:C	32:f:512:ALA:H	2.14	0.54
1:G:86:ASP:HA	7:M:120:HIS:CE1	2.43	0.53
16:B:298:ASN:ND2	18:E:245:GLU:OE1	2.42	0.53
19:F:150:LEU:HB3	19:F:164:LEU:O	2.08	0.53
21:U:382:SER:O	21:U:384:GLN:NE2	2.41	0.53
23:W:416:GLN:HB3	23:W:418:PRO:HD3	1.89	0.53
32:f:320:LEU:HA	32:f:358:VAL:CG1	2.38	0.53
6:L:193:ARG:O	6:L:196:ARG:HG2	2.08	0.53
16:B:402:ALA:HB1	16:B:414:VAL:HG11	1.90	0.53
17:D:54:LEU:HA	17:D:57:GLN:HB2	1.90	0.53
17:D:200:ARG:NH2	17:D:300:ASP:OD1	2.40	0.53
18:E:204:VAL:HG23	18:E:205:ASP:H	1.72	0.53
20:C:42:LEU:O	20:C:45:LEU:HB2	2.08	0.53
21:U:623:GLY:HA2	21:U:659:CYS:HB2	1.90	0.53
25:Y:71:ASN:HA	25:Y:74:LYS:HG2	1.89	0.53
25:Y:349:LYS:HG3	25:Y:350:VAL:HG13	1.90	0.53
27:a:34:TRP:CD1	28:b:19:GLY:H	2.27	0.53
29:c:156:VAL:HG12	29:c:157:ILE:H	1.73	0.53
29:c:270:LEU:HD23	29:c:273:LYS:HE2	1.89	0.53
32:f:327:GLY:O	32:f:331:ALA:HB3	2.08	0.53
32:f:350:LYS:HG2	32:f:356:ALA:HB3	1.89	0.53
2:H:184:LEU:O	2:H:188:ILE:HG13	2.08	0.53
5:K:109:VAL:HG23	5:K:147:ASP:HB3	1.91	0.53
18:E:55:GLN:O	19:F:133:PHE:N	2.35	0.53
18:E:141:GLN:NE2	18:E:300:HIS:O	2.41	0.53
22:V:287:ARG:HD2	31:e:5:LYS:HB2	1.90	0.53
23:W:377:ARG:NH2	27:a:308:GLU:OE2	2.41	0.53
25:Y:381:GLN:HB3	25:Y:385:ARG:NH1	2.23	0.53
29:c:88:ASP:HB3	29:c:91:PHE:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:147:SER:OG	30:d:151:VAL:N	2.31	0.53
30:d:254:GLU:HA	30:d:257:VAL:HG23	1.91	0.53
32:f:335:ARG:N	32:f:336:GLU:HB2	2.24	0.53
32:f:660:TYR:HB2	32:f:663:VAL:N	2.23	0.53
5:K:35:SER:HA	5:K:53:ARG:NH2	2.23	0.53
19:F:370:SER:HA	19:F:373:MET:HG2	1.89	0.53
22:V:79:VAL:HG13	22:V:80:LYS:N	2.22	0.53
32:f:100:PHE:CD2	32:f:109:LEU:HD11	2.43	0.53
32:f:562:VAL:O	32:f:566:SER:HB3	2.07	0.53
2:H:179:ASN:HD21	24:X:159:LYS:HE2	1.74	0.53
3:I:47:ALA:HB1	3:I:64:LYS:HD2	1.91	0.53
7:M:45:VAL:HG11	7:M:138:GLY:HA3	1.90	0.53
15:A:143:ASP:O	15:A:147:TYR:N	2.38	0.53
20:C:243:PRO:HB3	20:C:288:ASN:HB3	1.91	0.53
1:G:73:THR:HB	1:G:76:ILE:HB	1.91	0.53
2:H:71:HIS:CE1	2:H:104:PRO:HB3	2.44	0.53
7:M:66:LEU:HD13	7:M:214:SER:HB2	1.91	0.53
16:B:189:GLY:HA3	16:B:360:THR:HG23	1.91	0.53
17:D:326:ARG:HH21	20:C:141:GLU:HG2	1.74	0.53
24:X:130:GLU:HB3	24:X:153:LEU:HD21	1.90	0.53
24:X:143:TYR:HD2	24:X:144:GLN:HG2	1.72	0.53
25:Y:109:GLU:HG2	25:Y:124:PHE:CE1	2.44	0.53
1:G:61:LEU:HA	7:M:160:TYR:CD1	2.43	0.53
5:K:34:GLY:HA3	5:K:80:GLY:HA2	1.90	0.53
7:M:197:ILE:HA	7:M:200:VAL:HG12	1.90	0.53
16:B:301:GLY:O	16:B:305:ILE:HG13	2.09	0.53
17:D:89:ILE:O	17:D:106:THR:OG1	2.21	0.53
19:F:230:GLY:H	19:F:392:ASN:HB3	1.73	0.53
20:C:155:ASP:OD1	20:C:155:ASP:N	2.42	0.53
32:f:525:PRO:O	32:f:526:THR:HG22	2.09	0.53
15:A:355:PHE:CE1	15:A:385:ILE:HB	2.44	0.53
20:C:373:GLU:HG2	20:C:375:ARG:NH1	2.24	0.53
21:U:61:ALA:HB1	21:U:80:TYR:HB3	1.91	0.53
21:U:844:LYS:HD3	21:U:881:PRO:HD3	1.91	0.53
22:V:284:GLU:HG2	22:V:287:ARG:HE	1.74	0.53
23:W:135:LYS:HB3	23:W:136:ILE:C	2.33	0.53
23:W:405:LYS:HA	24:X:341:PRO:O	2.08	0.53
10:P:66:ARG:O	10:P:69:PHE:HB3	2.09	0.53
13:S:197:ILE:HB	13:S:204:ARG:HB2	1.90	0.53
16:B:393:ALA:HB3	20:C:310:ARG:HD3	1.91	0.53
19:F:313:LEU:O	19:F:317:LEU:HD12	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:359:VAL:O	23:W:363:ILE:HG12	2.09	0.53
28:b:35:ILE:HD13	28:b:184:ILE:HD13	1.90	0.53
32:f:231:LEU:HD23	32:f:249:LEU:HA	1.91	0.53
11:Q:4:LEU:HD22	11:Q:17:SER:HA	1.91	0.53
11:Q:103:LEU:HD23	11:Q:132:HIS:HE1	1.73	0.53
13:S:171:ALA:O	13:S:175:VAL:HG23	2.09	0.53
17:D:373:ALA:HB1	17:D:374:ASP:HB3	1.91	0.53
22:V:213:TYR:HD1	22:V:216:ARG:HD2	1.73	0.53
22:V:490:SER:HA	26:Z:275:LEU:HD21	1.89	0.53
25:Y:170:GLU:N	25:Y:171:GLY:HA3	2.23	0.53
25:Y:326:GLY:HA2	25:Y:329:PHE:HD2	1.74	0.53
27:a:312:MET:HA	27:a:315:LEU:HD12	1.91	0.53
28:b:20:ASP:OD1	28:b:25:ARG:NE	2.39	0.53
32:f:307:LEU:HB3	32:f:322:SER:OG	2.09	0.53
4:J:11:SER:OG	4:J:13:ASP:OD1	2.21	0.52
15:A:140:VAL:HA	15:A:152:PRO:HA	1.91	0.52
15:A:219:GLY:HA3	15:A:381:THR:HB	1.91	0.52
16:B:258:LYS:HA	16:B:296:ASP:HB3	1.90	0.52
19:F:255:GLN:O	19:F:258:GLN:NE2	2.36	0.52
23:W:420:ASP:HB2	23:W:425:LEU:HD12	1.92	0.52
26:Z:176:LEU:HB2	29:c:218:LEU:HD12	1.91	0.52
29:c:37:ALA:O	29:c:41:MET:HG2	2.10	0.52
30:d:215:TRP:CG	30:d:216:VAL:N	2.77	0.52
32:f:220:GLY:O	32:f:224:ALA:CB	2.56	0.52
32:f:462:ASP:C	32:f:464:LYS:H	2.17	0.52
32:f:550:THR:HA	32:f:553:LYS:NZ	2.24	0.52
4:J:87:ALA:HB2	4:J:111:ILE:HD11	1.91	0.52
22:V:440:LYS:NZ	30:d:143:LEU:O	2.42	0.52
23:W:72:LYS:NZ	23:W:119:PRO:O	2.42	0.52
23:W:441:LYS:HA	23:W:444:HIS:CE1	2.43	0.52
24:X:330:LEU:HA	24:X:333:GLN:HB2	1.92	0.52
25:Y:34:ASP:N	25:Y:34:ASP:OD1	2.42	0.52
32:f:90:LEU:HA	32:f:93:ALA:HB3	1.91	0.52
2:H:123:GLN:HB2	3:I:128:ARG:NH2	2.22	0.52
2:H:123:GLN:HG3	3:I:128:ARG:HB3	1.90	0.52
7:M:229:LYS:HZ1	7:M:235:ALA:H	1.57	0.52
17:D:143:LEU:HD13	17:D:144:PRO:HD2	1.91	0.52
17:D:352:MET:HE2	18:E:164:ILE:HA	1.91	0.52
20:C:117:ARG:HD3	20:C:122:THR:OG1	2.10	0.52
20:C:297:ARG:HG3	20:C:298:ILE:H	1.73	0.52
21:U:185:MET:HE3	21:U:628:ARG:HH12	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:269:LYS:HE2	22:V:295:ILE:HG13	1.92	0.52
23:W:135:LYS:HB3	23:W:136:ILE:HB	1.92	0.52
32:f:317:THR:HG23	32:f:689:GLN:CD	2.34	0.52
32:f:434:THR:O	32:f:438:VAL:HG12	2.09	0.52
1:G:14:THR:HG22	1:G:24:GLN:HG3	1.91	0.52
3:I:100:GLN:HG3	11:Q:86:ARG:HG3	1.91	0.52
16:B:343:ARG:HB2	16:B:344:PRO:HD3	1.92	0.52
20:C:271:ARG:O	20:C:275:GLU:HG2	2.10	0.52
20:C:321:ASN:O	20:C:325:ARG:HG3	2.08	0.52
21:U:388:ASP:OD1	21:U:389:ASN:ND2	2.42	0.52
22:V:143:ALA:HB3	22:V:145:LEU:HB3	1.92	0.52
30:d:58:GLY:O	30:d:62:SER:OG	2.19	0.52
17:D:145:PRO:HB2	17:D:146:GLU:HB2	1.90	0.52
20:C:338:LEU:O	25:Y:174:TRP:NE1	2.31	0.52
23:W:247:TYR:O	23:W:250:ILE:HG13	2.09	0.52
31:e:63:HIS:HA	31:e:66:LYS:HE2	1.91	0.52
32:f:662:LEU:N	32:f:663:VAL:HA	2.25	0.52
4:J:198:VAL:O	4:J:201:SER:OG	2.28	0.52
7:M:83:ASP:O	7:M:87:LEU:HG	2.10	0.52
17:D:204:MET:HA	17:D:331:ILE:O	2.10	0.52
21:U:424:ALA:HA	21:U:427:LEU:HD13	1.92	0.52
27:a:28:LEU:HD23	27:a:37:LEU:HA	1.91	0.52
27:a:35:HIS:CE1	28:b:17:ARG:HB2	2.45	0.52
32:f:660:TYR:HB3	32:f:663:VAL:HG23	1.90	0.52
10:P:91:VAL:HG21	10:P:109:ILE:HD11	1.92	0.52
18:E:55:GLN:HB3	18:E:100:LEU:O	2.10	0.52
19:F:421:MET:HA	19:F:424:ILE:HD12	1.91	0.52
21:U:118:LEU:HD21	21:U:123:LYS:HA	1.92	0.52
25:Y:296:VAL:O	25:Y:300:ARG:HG3	2.10	0.52
32:f:314:ASN:HD21	32:f:355:VAL:HG13	1.75	0.52
32:f:436:VAL:O	32:f:440:ALA:CB	2.58	0.52
1:G:61:LEU:HG	1:G:66:VAL:HG21	1.90	0.52
4:J:98:VAL:HG22	12:R:78:ALA:HB1	1.92	0.52
6:L:167:SER:O	6:L:170:THR:OG1	2.25	0.52
15:A:156:LYS:C	15:A:157:ILE:HD13	2.35	0.52
17:D:251:PHE:CE2	17:D:292:LEU:HB2	2.45	0.52
20:C:203:VAL:O	20:C:207:THR:OG1	2.21	0.52
23:W:432:LEU:HD12	29:c:239:LYS:HE2	1.92	0.52
24:X:281:GLY:H	24:X:284:THR:HG22	1.74	0.52
26:Z:225:GLN:HG2	26:Z:228:TYR:CE2	2.43	0.52
32:f:61:ASP:O	32:f:62:ILE:HG22	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:604:ARG:HD2	32:f:649:ASN:HB3	1.92	0.52
32:f:604:ARG:HG2	32:f:645:LEU:HB2	1.92	0.52
2:H:150:ASP:OD1	2:H:154:ALA:N	2.43	0.52
6:L:40:SER:OG	6:L:43:HIS:O	2.28	0.52
15:A:172:VAL:HB	15:A:226:ALA:HB1	1.90	0.52
17:D:326:ARG:NH2	20:C:141:GLU:OE2	2.43	0.52
18:E:85:ARG:HH22	29:c:46:ARG:HG3	1.74	0.52
22:V:349:ARG:HD2	22:V:354:LYS:HD3	1.92	0.52
23:W:373:ILE:HG12	23:W:374:THR:O	2.09	0.52
26:Z:68:TRP:HH2	26:Z:111:LEU:HB2	1.75	0.52
28:b:91:ARG:HH22	28:b:130:ARG:HG2	1.74	0.52
29:c:57:MET:HE1	29:c:141:VAL:HB	1.90	0.52
32:f:285:ALA:HB1	32:f:287:LEU:HB3	1.92	0.52
7:M:43:ASP:OD1	7:M:43:ASP:N	2.42	0.52
16:B:124:SER:HA	16:B:129:SER:O	2.10	0.52
16:B:170:LEU:O	16:B:173:VAL:HG22	2.10	0.52
17:D:337:ASP:O	17:D:341:LYS:HG2	2.10	0.52
19:F:252:ALA:HB3	19:F:255:GLN:HG2	1.92	0.52
20:C:88:LYS:HD2	20:C:94:LYS:HE3	1.90	0.52
20:C:217:SER:CB	20:C:218:GLU:HB3	2.28	0.52
21:U:377:HIS:O	21:U:380:THR:HG22	2.09	0.52
24:X:203:PRO:HB3	24:X:206:LEU:HG	1.92	0.52
5:K:205:VAL:O	15:A:375:ARG:NH2	2.42	0.51
16:B:305:ILE:O	16:B:308:THR:HG22	2.10	0.51
32:f:462:ASP:O	32:f:463:SER:OG	2.26	0.51
32:f:533:LEU:HD21	32:f:565:ASN:HB3	1.92	0.51
10:P:26:ARG:HH21	10:P:38:ASP:HA	1.75	0.51
11:Q:46:CYS:HA	11:Q:102:LEU:HB2	1.92	0.51
16:B:203:LEU:HG	16:B:211:TYR:HD1	1.76	0.51
23:W:148:THR:O	23:W:151:THR:OG1	2.28	0.51
26:Z:9:VAL:HG12	26:Z:48:LEU:HB3	1.92	0.51
29:c:131:GLN:HA	29:c:134:GLU:HG2	1.91	0.51
31:e:62:LYS:HZ3	31:e:66:LYS:HD3	1.75	0.51
32:f:193:HIS:NE2	32:f:408:LEU:HB2	2.25	0.51
32:f:210:ARG:CZ	32:f:212:ASN:HB2	2.41	0.51
32:f:268:THR:HB	32:f:656:HIS:HD2	1.73	0.51
7:M:38:GLY:HA3	7:M:136:MET:HE2	1.92	0.51
20:C:13:GLU:HG2	21:U:141:CYS:SG	2.50	0.51
21:U:31:VAL:HG22	21:U:35:TRP:CD1	2.45	0.51
22:V:275:VAL:HB	22:V:277:PRO:HD3	1.91	0.51
4:J:26:VAL:HG22	4:J:129:ILE:HA	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:79:SER:O	5:K:139:VAL:HG23	2.10	0.51
6:L:107:ARG:NH2	14:T:74:GLU:HG3	2.26	0.51
10:P:189:ILE:HG23	10:P:196:THR:HB	1.91	0.51
15:A:205:GLY:HA2	15:A:206:ILE:CG2	2.39	0.51
16:B:167:THR:OG1	16:B:168:ASP:N	2.44	0.51
16:B:190:LEU:O	16:B:194:ILE:N	2.30	0.51
16:B:294:ARG:HG2	20:C:261:GLY:O	2.11	0.51
20:C:100:ASP:CG	20:C:123:LEU:H	2.18	0.51
21:U:742:HIS:HB2	21:U:883:ARG:HH12	1.75	0.51
22:V:179:LYS:O	22:V:183:GLU:HG3	2.11	0.51
4:J:10:PHE:HA	4:J:16:LEU:HD23	1.91	0.51
4:J:195:LEU:O	4:J:201:SER:OG	2.29	0.51
6:L:121:GLN:HG3	7:M:129:ARG:HG2	1.93	0.51
14:T:57:TYR:HE2	14:T:61:GLN:HE21	1.58	0.51
15:A:104:ALA:H	15:A:112:ILE:HG23	1.75	0.51
15:A:295:VAL:O	15:A:298:THR:OG1	2.20	0.51
16:B:224:LEU:O	16:B:330:ALA:HA	2.10	0.51
17:D:312:ASN:ND2	18:E:242:ARG:HH22	2.05	0.51
18:E:252:GLU:HA	18:E:255:ARG:HE	1.76	0.51
21:U:208:LEU:HD23	21:U:210:LYS:H	1.75	0.51
21:U:596:ASN:O	21:U:599:ILE:HG22	2.11	0.51
25:Y:131:THR:HG21	25:Y:136:HIS:HB2	1.92	0.51
32:f:222:VAL:HG11	32:f:238:LYS:NZ	2.26	0.51
32:f:646:ASP:OD1	32:f:647:VAL:N	2.43	0.51
32:f:661:GLY:N	32:f:662:LEU:HA	2.25	0.51
8:N:144:ARG:H	8:N:147:MET:HE3	1.73	0.51
10:P:135:ASP:N	10:P:135:ASP:OD1	2.41	0.51
17:D:250:VAL:O	17:D:253:LEU:HG	2.10	0.51
18:E:247:THR:OG1	18:E:248:SER:N	2.44	0.51
20:C:269:VAL:O	20:C:272:THR:HB	2.11	0.51
21:U:243:LEU:O	21:U:913:ILE:HG21	2.10	0.51
26:Z:225:GLN:HE22	26:Z:229:GLN:HB2	1.75	0.51
29:c:282:ARG:HD2	29:c:284:LEU:HB3	1.93	0.51
3:I:149:GLN:O	3:I:157:GLY:N	2.40	0.51
16:B:205:LEU:CD2	16:B:206:THR:H	2.24	0.51
17:D:121:ARG:HG3	17:D:122:GLU:OE1	2.10	0.51
19:F:403:ALA:HB1	19:F:415:LEU:HD11	1.92	0.51
29:c:64:ASP:HA	29:c:139:ARG:HE	1.74	0.51
32:f:109:LEU:HB2	32:f:141:ARG:HH12	1.76	0.51
32:f:135:MET:O	32:f:139:LEU:N	2.33	0.51
32:f:281:ILE:HG13	32:f:282:LYS:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:291:ILE:HD12	32:f:294:SER:HB2	1.93	0.51
32:f:326:LEU:HG	32:f:337:ASP:OD2	2.10	0.51
17:D:389:GLU:HB3	17:D:390:ASN:C	2.36	0.51
21:U:16:GLU:OE1	21:U:18:GLN:NE2	2.44	0.51
23:W:312:MET:SD	23:W:361:HIS:ND1	2.73	0.51
25:Y:102:ASP:HA	25:Y:105:MET:HG2	1.92	0.51
27:a:97:LEU:HD11	27:a:117:ALA:HB1	1.93	0.51
32:f:210:ARG:O	32:f:214:ALA:HB2	2.10	0.51
32:f:446:ASN:C	32:f:448:LEU:H	2.18	0.51
1:G:15:ILE:HD12	2:H:21:GLN:HE22	1.76	0.51
5:K:18:GLU:HB2	5:K:19:GLY:HA2	1.92	0.51
15:A:187:LEU:O	15:A:190:VAL:HG12	2.10	0.51
33:D:501:ATP:PG	18:E:294:ARG:HH22	2.33	0.51
20:C:119:ASP:N	20:C:119:ASP:OD1	2.44	0.51
21:U:625:ILE:HG13	21:U:626:LEU:HG	1.92	0.51
25:Y:46:ARG:C	25:Y:48:ASN:H	2.19	0.51
26:Z:252:LYS:HE2	29:c:301:ALA:HB1	1.93	0.51
28:b:95:LEU:HA	28:b:98:LYS:HZ3	1.76	0.51
30:d:40:GLY:HA3	30:d:41:THR:C	2.35	0.51
30:d:213:ARG:HB2	30:d:215:TRP:CD1	2.46	0.51
2:H:93:LEU:HD21	2:H:113:ARG:HB2	1.91	0.51
5:K:16:SER:N	5:K:20:ARG:O	2.44	0.51
6:L:189:LYS:O	6:L:193:ARG:HG3	2.11	0.51
17:D:133:HIS:CE1	17:D:135:HIS:H	2.29	0.51
17:D:167:ILE:HG22	33:D:501:ATP:N6	2.25	0.51
17:D:255:LYS:HE2	17:D:299:PHE:CE1	2.45	0.51
20:C:338:LEU:H	25:Y:174:TRP:CD1	2.29	0.51
21:U:692:ALA:HB1	21:U:736:ILE:HB	1.93	0.51
28:b:20:ASP:OD2	28:b:25:ARG:NH2	2.30	0.51
32:f:238:LYS:HG2	32:f:240:LEU:HG	1.93	0.51
17:D:182:GLU:HG3	17:D:183:LEU:HD12	1.93	0.50
17:D:202:VAL:HB	17:D:308:ILE:HA	1.92	0.50
18:E:174:GLY:C	18:E:176:PRO:HD2	2.36	0.50
25:Y:232:GLU:CD	25:Y:234:PRO:HD2	2.36	0.50
27:a:14:SER:HB2	27:a:18:GLN:HG2	1.93	0.50
30:d:145:GLU:N	30:d:146:GLY:HA2	2.26	0.50
32:f:337:ASP:O	32:f:341:LEU:N	2.44	0.50
1:G:185:LYS:HG3	1:G:187:PHE:H	1.76	0.50
4:J:228:TYR:HA	4:J:231:GLU:HG2	1.92	0.50
7:M:35:THR:HA	7:M:166:GLY:HA3	1.93	0.50
15:A:339:ARG:NH1	19:F:402:GLU:OE2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:E:210:GLU:O	18:E:213:ARG:HG2	2.11	0.50
18:E:260:LEU:HB3	18:E:264:MET:HE2	1.92	0.50
21:U:249:CYS:HB3	21:U:328:ILE:HG21	1.93	0.50
4:J:146:GLN:HG2	4:J:154:HIS:O	2.11	0.50
8:N:114:VAL:HA	8:N:119:MET:O	2.12	0.50
12:R:83:LEU:HD22	12:R:101:ILE:HD11	1.93	0.50
19:F:191:LEU:HG	19:F:194:GLN:NE2	2.22	0.50
19:F:303:ASP:O	19:F:306:VAL:N	2.44	0.50
30:d:140:GLU:HG3	30:d:144:MET:HE3	1.92	0.50
32:f:483:ALA:O	32:f:500:LEU:HD21	2.12	0.50
15:A:316:LYS:HG2	15:A:317:VAL:H	1.76	0.50
16:B:251:VAL:HG22	16:B:285:ASP:H	1.76	0.50
17:D:270:ILE:HA	18:E:251:ARG:HH21	1.77	0.50
33:D:501:ATP:H1'	18:E:291:ARG:HH21	1.77	0.50
18:E:71:VAL:HG11	18:E:107:ILE:HD11	1.93	0.50
26:Z:45:LYS:HG3	26:Z:46:LYS:H	1.76	0.50
32:f:673:THR:O	32:f:677:GLU:HG2	2.11	0.50
5:K:37:ALA:HB2	5:K:50:VAL:HG23	1.93	0.50
15:A:97:ARG:HB2	15:A:98:CYS:SG	2.52	0.50
21:U:692:ALA:HB2	21:U:733:ALA:HB1	1.93	0.50
21:U:808:PRO:HD3	21:U:836:THR:HB	1.93	0.50
22:V:255:LEU:CD2	22:V:291:TYR:HB3	2.39	0.50
23:W:190:MET:HE1	23:W:209:ILE:HG13	1.93	0.50
28:b:122:LYS:O	28:b:125:VAL:HG12	2.12	0.50
1:G:172:GLN:OE1	1:G:172:GLN:N	2.44	0.50
2:H:185:GLU:OE1	2:H:185:GLU:N	2.44	0.50
4:J:65:LEU:HD22	4:J:88:ARG:HG2	1.93	0.50
16:B:395:ILE:HG13	16:B:398:ILE:HD11	1.94	0.50
20:C:39:SER:O	20:C:43:ARG:HG3	2.11	0.50
20:C:214:VAL:HG12	20:C:249:ASP:H	1.76	0.50
21:U:403:THR:HG23	21:U:777:HIS:HE2	1.77	0.50
22:V:89:LYS:HD2	22:V:93:PHE:CE2	2.46	0.50
23:W:61:VAL:O	23:W:64:SER:OG	2.27	0.50
23:W:257:GLN:HB3	23:W:259:GLU:N	2.26	0.50
23:W:377:ARG:HH21	27:a:308:GLU:CD	2.18	0.50
24:X:364:LYS:O	24:X:368:MET:HG2	2.12	0.50
26:Z:214:LYS:HB3	26:Z:222:ILE:HG12	1.94	0.50
29:c:295:ASN:HA	29:c:298:GLN:HG2	1.93	0.50
31:e:62:LYS:NZ	31:e:66:LYS:HD3	2.27	0.50
32:f:251:ALA:O	32:f:334:ASN:ND2	2.45	0.50
32:f:408:LEU:HD23	32:f:443:GLY:HA3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:22:LEU:HD12	1:G:22:LEU:O	2.12	0.50
5:K:11:GLY:O	5:K:12:VAL:HG22	2.12	0.50
7:M:156:VAL:HG12	7:M:158:TYR:HD1	1.77	0.50
8:N:18:SER:HB2	8:N:30:VAL:HA	1.93	0.50
10:P:13:ALA:HB3	10:P:137:VAL:HG23	1.94	0.50
10:P:153:LEU:HB3	10:P:166:THR:HG23	1.94	0.50
14:T:6:VAL:O	14:T:56:ASP:HA	2.11	0.50
14:T:25:ASP:HA	14:T:187:PHE:HA	1.93	0.50
21:U:842:LYS:HA	21:U:843:GLU:CB	2.41	0.50
22:V:81:GLN:HB3	22:V:82:LEU:C	2.37	0.50
25:Y:191:ILE:HG13	25:Y:192:ARG:H	1.77	0.50
26:Z:237:LEU:HB2	26:Z:239:ASP:HB3	1.94	0.50
29:c:188:SER:CA	29:c:189:ILE:HG22	2.42	0.50
30:d:52:ARG:HH22	30:d:92:SER:HB2	1.76	0.50
32:f:529:ARG:HA	32:f:562:VAL:HG12	1.94	0.50
11:Q:178:PHE:HB2	11:Q:194:ILE:HB	1.92	0.50
17:D:43:ARG:HA	17:D:46:LYS:HB2	1.94	0.50
17:D:337:ASP:H	17:D:340:GLN:HB2	1.76	0.50
18:E:174:GLY:CA	18:E:176:PRO:HD2	2.40	0.50
20:C:159:LYS:NZ	20:C:163:GLU:OE2	2.34	0.50
21:U:886:PRO:HA	21:U:889:LEU:HD12	1.93	0.50
23:W:75:TYR:HD1	23:W:78:LYS:HE2	1.76	0.50
23:W:183:VAL:O	23:W:186:ILE:HG22	2.12	0.50
26:Z:267:ARG:HH22	29:c:291:LEU:HD13	1.77	0.50
29:c:295:ASN:OD1	29:c:298:GLN:NE2	2.44	0.50
32:f:83:GLU:O	32:f:87:SER:OG	2.21	0.50
32:f:96:VAL:HG12	32:f:135:MET:HE1	1.94	0.50
32:f:165:VAL:HA	32:f:168:ASN:HB3	1.93	0.50
32:f:194:LEU:HD23	32:f:199:PHE:CD2	2.47	0.50
3:I:119:GLN:HE21	3:I:123:GLN:HE22	1.60	0.50
8:N:44:CYS:SG	8:N:99:ILE:HB	2.52	0.50
15:A:78:TRP:HB2	32:f:528:ARG:HH12	1.72	0.50
17:D:115:ILE:HA	17:D:139:LEU:HB2	1.94	0.50
17:D:185:LEU:HD11	17:D:259:PRO:HB3	1.94	0.50
18:E:83:CYS:HB3	18:E:87:LEU:HD21	1.93	0.50
22:V:26:PRO:O	22:V:29:PRO:HD2	2.12	0.50
3:I:45:LEU:HD11	3:I:137:ILE:HG12	1.93	0.49
16:B:218:PRO:HB2	16:B:346:ARG:HH12	1.77	0.49
19:F:431:LYS:HB2	19:F:432:LYS:HB2	1.93	0.49
20:C:267:SER:HA	20:C:270:GLN:HB2	1.94	0.49
23:W:155:GLN:HG2	23:W:157:GLY:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:151:VAL:HG13	29:c:152:LYS:N	2.25	0.49
32:f:320:LEU:HA	32:f:358:VAL:HG13	1.94	0.49
32:f:450:VAL:HB	32:f:472:LYS:NZ	2.27	0.49
32:f:582:LEU:O	32:f:586:LEU:HG	2.11	0.49
32:f:662:LEU:H	32:f:664:ALA:CA	2.24	0.49
2:H:22:ILE:HD13	2:H:152:SER:HA	1.94	0.49
5:K:191:LEU:O	5:K:195:ILE:HG13	2.12	0.49
15:A:351:ARG:HH11	15:A:378:PRO:HA	1.76	0.49
19:F:436:GLN:C	19:F:438:TYR:H	2.20	0.49
21:U:436:ALA:HB1	21:U:472:ILE:HG12	1.93	0.49
22:V:235:LEU:HD12	22:V:247:GLN:HG3	1.94	0.49
25:Y:349:LYS:C	25:Y:351:ASN:H	2.20	0.49
32:f:135:MET:HA	32:f:138:MET:HB2	1.94	0.49
5:K:141:LEU:HB2	5:K:156:MET:HG2	1.95	0.49
14:T:89:HIS:HA	14:T:112:ILE:HD12	1.93	0.49
14:T:114:GLY:HA2	14:T:192:VAL:HG21	1.93	0.49
15:A:97:ARG:HB3	16:B:131:HIS:HD2	1.77	0.49
15:A:105:ASP:OD1	15:A:105:ASP:N	2.44	0.49
18:E:118:LEU:HD11	18:E:196:LEU:HD11	1.93	0.49
19:F:232:GLY:HA2	33:F:501:ATP:PB	2.52	0.49
20:C:89:VAL:HG12	20:C:91:PRO:HD2	1.94	0.49
20:C:184:LYS:HB3	20:C:277:LEU:HD22	1.93	0.49
21:U:232:ILE:O	21:U:236:LEU:HG	2.12	0.49
21:U:478:SER:OG	21:U:511:ALA:HB1	2.12	0.49
21:U:725:MET:HE1	29:c:182:GLY:HA3	1.94	0.49
22:V:144:ASP:OD1	22:V:150:ARG:NH2	2.31	0.49
22:V:194:LYS:O	22:V:242:HIS:NE2	2.33	0.49
23:W:67:LEU:H	23:W:68:VAL:HA	1.77	0.49
23:W:142:ARG:HH21	23:W:178:GLU:HB2	1.77	0.49
23:W:392:PHE:O	23:W:396:LEU:HG	2.12	0.49
29:c:261:GLU:O	29:c:264:LYS:HG2	2.11	0.49
32:f:123:PHE:HA	32:f:126:CYS:HB2	1.94	0.49
32:f:185:VAL:HG23	32:f:187:ASP:HB2	1.93	0.49
4:J:17:PHE:O	4:J:21:TYR:HB3	2.12	0.49
6:L:155:ASP:HB3	7:M:62:SER:HB2	1.93	0.49
8:N:132:SER:HA	8:N:135:ILE:HG12	1.93	0.49
9:O:51:ASP:O	9:O:55:THR:OG1	2.17	0.49
18:E:216:ARG:NE	18:E:259:GLU:OE1	2.45	0.49
21:U:176:MET:HA	21:U:179:TYR:CD1	2.46	0.49
22:V:108:LEU:HA	22:V:111:TYR:HD2	1.77	0.49
22:V:408:ARG:O	22:V:411:SER:OG	2.23	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:92:LYS:N	23:W:93:ARG:HB3	2.24	0.49
26:Z:136:GLU:OE2	26:Z:157:HIS:ND1	2.46	0.49
27:a:156:TYR:CG	27:a:179:PHE:HB2	2.46	0.49
32:f:370:SER:HB3	32:f:372:ASN:HD22	1.76	0.49
16:B:395:ILE:HA	16:B:398:ILE:HG12	1.95	0.49
17:D:65:GLN:O	20:C:49:ARG:NH2	2.45	0.49
17:D:119:ILE:HG21	17:D:123:LEU:HG	1.93	0.49
18:E:251:ARG:HH12	18:E:255:ARG:CZ	2.26	0.49
19:F:84:LYS:HA	19:F:161:LEU:HD22	1.93	0.49
20:C:36:ASN:O	20:C:40:GLN:HG2	2.12	0.49
22:V:90:GLU:HG3	22:V:158:PRO:HB3	1.94	0.49
26:Z:222:ILE:CG2	26:Z:223:ASN:HB3	2.33	0.49
29:c:174:PRO:CB	29:c:175:ARG:HA	2.42	0.49
29:c:244:VAL:HA	29:c:247:GLU:HB2	1.95	0.49
32:f:617:LEU:N	32:f:618:THR:O	2.46	0.49
5:K:70:ILE:HG23	5:K:93:ARG:HG2	1.93	0.49
5:K:232:GLU:HA	5:K:235:GLU:HG3	1.94	0.49
6:L:160:SER:OG	6:L:165:SER:HB3	2.13	0.49
8:N:34:LEU:HD21	8:N:186:ARG:CZ	2.42	0.49
15:A:380:SER:O	16:B:343:ARG:NH1	2.45	0.49
16:B:249:ARG:HH11	20:C:283:PHE:HE1	1.60	0.49
19:F:205:PRO:O	19:F:209:LYS:HG2	2.12	0.49
19:F:343:LEU:HD22	19:F:351:LYS:HZ3	1.78	0.49
21:U:374:SER:HB2	21:U:410:VAL:HB	1.93	0.49
24:X:205:LYS:HG3	24:X:208:ALA:HB3	1.94	0.49
26:Z:182:THR:N	26:Z:183:THR:HA	2.27	0.49
26:Z:236:LEU:HD21	27:a:335:TRP:HD1	1.77	0.49
32:f:391:LEU:CD1	32:f:392:LYS:H	2.18	0.49
4:J:11:SER:HB3	4:J:17:PHE:CZ	2.47	0.49
8:N:19:ARG:HB3	8:N:171:GLY:C	2.38	0.49
16:B:203:LEU:HG	16:B:211:TYR:CD1	2.47	0.49
17:D:141:ASP:OD1	17:D:142:VAL:N	2.46	0.49
19:F:150:LEU:HD22	19:F:164:LEU:HB3	1.95	0.49
19:F:223:VAL:HG23	19:F:350:ARG:HB2	1.94	0.49
21:U:176:MET:HA	21:U:179:TYR:HD1	1.77	0.49
22:V:281:ASN:N	22:V:284:GLU:HB3	2.27	0.49
1:G:39:SER:H	1:G:172:GLN:HE21	1.59	0.49
4:J:200:GLN:HB2	16:B:358:GLU:OE2	2.13	0.49
5:K:91:LYS:O	5:K:95:GLU:HG3	2.13	0.49
8:N:45:ARG:HD2	8:N:52:THR:OG1	2.12	0.49
11:Q:36:PHE:O	11:Q:44:LEU:N	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:C:99:VAL:HA	20:C:100:ASP:CB	2.37	0.49
20:C:308:PRO:O	20:C:310:ARG:HG3	2.13	0.49
21:U:471:ASP:OD1	21:U:471:ASP:N	2.46	0.49
27:a:211:PHE:HA	27:a:271:LYS:HE3	1.95	0.49
1:G:71:LYS:O	1:G:95:ARG:NH2	2.46	0.49
2:H:49:GLU:HA	2:H:208:ILE:HG22	1.94	0.49
5:K:73:HIS:HA	5:K:226:PHE:CE2	2.48	0.49
13:S:38:ARG:HH12	14:T:151:ARG:HD3	1.78	0.49
16:B:178:LYS:HG3	20:C:283:PHE:HA	1.94	0.49
16:B:294:ARG:NH1	16:B:295:TYR:O	2.45	0.49
21:U:113:VAL:HG22	21:U:158:ARG:HG3	1.94	0.49
21:U:167:ILE:HD12	21:U:204:ILE:HG21	1.94	0.49
21:U:525:ASN:OD1	21:U:526:ALA:N	2.46	0.49
21:U:541:HIS:HB2	21:U:544:ILE:HG22	1.93	0.49
22:V:234:ARG:O	22:V:237:THR:HG22	2.13	0.49
22:V:252:ASN:ND2	22:V:284:GLU:OE2	2.43	0.49
23:W:402:ILE:HG23	23:W:416:GLN:HE22	1.77	0.49
26:Z:197:GLY:HA3	27:a:364:GLU:CD	2.37	0.49
7:M:15:SER:OG	7:M:17:ASP:OD1	2.17	0.49
15:A:348:LEU:HA	15:A:351:ARG:NH2	2.28	0.49
16:B:248:LEU:HD23	16:B:282:VAL:HG22	1.95	0.49
17:D:149:SER:OG	18:E:78:ARG:NH2	2.46	0.49
22:V:47:SER:HA	22:V:50:GLU:HB2	1.94	0.49
25:Y:333:GLU:HA	25:Y:336:ARG:HH21	1.78	0.49
27:a:214:GLY:HA2	27:a:217:LEU:HD13	1.94	0.49
29:c:154:LYS:HG2	29:c:156:VAL:H	1.76	0.49
32:f:371:CYS:C	32:f:373:GLY:HA2	2.38	0.49
32:f:535:LEU:HD22	32:f:569:ALA:HB1	1.95	0.49
32:f:639:THR:O	32:f:642:VAL:HG22	2.13	0.49
1:G:184:LYS:HB2	1:G:185:LYS:O	2.13	0.48
15:A:343:PHE:HA	15:A:344:SER:OG	2.13	0.48
18:E:161:ARG:HD2	23:W:175:GLY:HA2	1.95	0.48
19:F:102:ASN:HA	19:F:103:ASP:HA	1.59	0.48
21:U:73:ALA:HB1	21:U:76:GLU:HB3	1.95	0.48
24:X:406:ASN:HB2	25:Y:376:LEU:HD11	1.94	0.48
30:d:175:ARG:HH21	30:d:205:LYS:NZ	2.10	0.48
32:f:230:LYS:O	32:f:234:ASP:CB	2.50	0.48
16:B:220:LYS:NZ	16:B:317:ASP:O	2.34	0.48
18:E:242:ARG:HD3	18:E:254:GLN:HG3	1.94	0.48
19:F:406:ILE:HG22	19:F:409:ARG:HH11	1.78	0.48
21:U:265:ILE:HG12	21:U:269:ARG:HH11	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:322:VAL:HG13	22:V:323:GLY:N	2.27	0.48
26:Z:219:LYS:HG3	26:Z:220:LEU:HD23	1.94	0.48
28:b:50:GLY:N	28:b:64:LEU:HD12	2.28	0.48
29:c:33:ILE:HD11	29:c:207:TYR:HD1	1.78	0.48
32:f:436:VAL:O	32:f:440:ALA:HB3	2.12	0.48
32:f:644:PHE:HE1	32:f:648:ARG:HH21	1.60	0.48
12:R:101:ILE:HB	12:R:112:TYR:HB2	1.96	0.48
13:S:92:LEU:HD23	13:S:124:PHE:CE2	2.48	0.48
20:C:331:ILE:HD13	20:C:334:ARG:HE	1.78	0.48
22:V:440:LYS:NZ	30:d:146:GLY:HA3	2.29	0.48
23:W:98:LYS:HD3	23:W:138:VAL:HB	1.95	0.48
24:X:223:LYS:HE2	25:Y:244:ALA:HB2	1.95	0.48
26:Z:224:HIS:CB	26:Z:225:GLN:HA	2.35	0.48
28:b:16:MET:O	28:b:25:ARG:HB2	2.14	0.48
32:f:220:GLY:O	32:f:224:ALA:HB3	2.14	0.48
4:J:132:LEU:HG	4:J:146:GLN:HB2	1.95	0.48
5:K:59:MET:HE3	5:K:64:ILE:HD13	1.95	0.48
5:K:191:LEU:HD21	5:K:221:GLN:HE21	1.77	0.48
12:R:7:LYS:HG2	12:R:124:ALA:HA	1.95	0.48
12:R:174:VAL:O	12:R:189:SER:HA	2.14	0.48
16:B:120:HIS:ND1	16:B:134:SER:OG	2.44	0.48
16:B:230:THR:HG21	16:B:353:PHE:CE2	2.48	0.48
17:D:112:TYR:HB3	20:C:71:SER:HB2	1.95	0.48
20:C:11:LEU:HD11	21:U:141:CYS:HA	1.95	0.48
21:U:24:LEU:HD13	21:U:59:PHE:CD2	2.48	0.48
22:V:134:PHE:HA	22:V:137:GLU:OE1	2.14	0.48
22:V:273:LYS:HA	22:V:274:SER:HB2	1.95	0.48
23:W:51:GLU:OE1	23:W:51:GLU:N	2.46	0.48
25:Y:20:ALA:HB2	25:Y:150:PHE:HD1	1.77	0.48
25:Y:78:GLU:OE1	25:Y:81:LEU:HD22	2.13	0.48
30:d:170:LEU:HA	30:d:173:THR:HG22	1.96	0.48
32:f:261:TRP:O	32:f:264:ASP:HB3	2.14	0.48
32:f:603:VAL:O	32:f:607:GLN:HG2	2.14	0.48
3:I:3:ARG:HH21	3:I:8:ARG:NH2	2.12	0.48
6:L:229:VAL:HG12	6:L:233:LEU:HG	1.96	0.48
12:R:20:ALA:HB3	12:R:31:VAL:HG21	1.95	0.48
16:B:166:ASP:HA	16:B:167:THR:OG1	2.14	0.48
17:D:370:ILE:HG23	17:D:371:SER:H	1.77	0.48
20:C:69:GLN:HB2	20:C:118:ASN:HB2	1.94	0.48
21:U:506:ALA:HB2	21:U:541:HIS:HB3	1.96	0.48
22:V:55:THR:HB	22:V:198:GLN:CD	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:139:GLU:HG2	23:W:142:ARG:HB2	1.95	0.48
24:X:406:ASN:HA	24:X:409:LYS:HD3	1.94	0.48
26:Z:228:TYR:O	26:Z:231:GLN:HB3	2.14	0.48
27:a:215:GLU:HG3	27:a:340:VAL:HG22	1.93	0.48
28:b:164:ASP:H	28:b:165:GLY:HA2	1.78	0.48
30:d:48:LEU:O	30:d:52:ARG:HG3	2.13	0.48
30:d:190:LEU:HD23	30:d:191:PHE:H	1.79	0.48
1:G:152:TYR:HA	1:G:162:GLY:HA2	1.96	0.48
7:M:56:LYS:N	7:M:57:LEU:HA	2.26	0.48
9:O:113:ILE:HA	9:O:119:THR:HG22	1.95	0.48
9:O:215:LYS:HB3	10:P:197:THR:HB	1.95	0.48
15:A:333:ARG:O	15:A:337:LEU:N	2.31	0.48
17:D:170:MET:HE2	17:D:333:PHE:CE2	2.44	0.48
17:D:179:GLU:HA	17:D:183:LEU:HD13	1.94	0.48
18:E:184:ALA:HB1	18:E:231:PHE:CZ	2.49	0.48
19:F:85:THR:HA	19:F:86:LEU:HD23	1.94	0.48
20:C:255:GLY:N	20:C:256:SER:HB2	2.28	0.48
21:U:26:LYS:HD2	30:d:34:ASN:ND2	2.29	0.48
23:W:235:GLN:OE1	23:W:243:ILE:HD13	2.13	0.48
25:Y:334:LEU:O	25:Y:338:ILE:HG13	2.14	0.48
26:Z:211:TYR:HD2	27:a:353:LEU:HD21	1.79	0.48
32:f:116:MET:SD	32:f:144:VAL:HB	2.54	0.48
2:H:42:ASN:OD1	2:H:42:ASN:N	2.43	0.48
6:L:44:ALA:N	6:L:137:TYR:OH	2.46	0.48
6:L:172:LEU:O	6:L:175:HIS:N	2.40	0.48
15:A:74:PRO:HG2	32:f:521:ARG:HH21	1.78	0.48
16:B:133:VAL:HG13	16:B:158:ALA:HA	1.96	0.48
19:F:225:MET:HE3	19:F:354:PHE:CZ	2.48	0.48
20:C:13:GLU:N	20:C:14:GLY:HA3	2.27	0.48
21:U:32:ASN:OD1	21:U:33:ASP:N	2.43	0.48
21:U:159:ARG:HB3	21:U:162:VAL:HG12	1.95	0.48
21:U:493:VAL:HG21	21:U:519:VAL:HG11	1.96	0.48
23:W:441:LYS:NZ	26:Z:207:ASP:OD2	2.46	0.48
24:X:318:ILE:HG22	24:X:321:THR:H	1.79	0.48
26:Z:43:TRP:HZ3	26:Z:48:LEU:HD12	1.78	0.48
26:Z:59:ASP:CG	28:b:99:HIS:HE2	2.20	0.48
26:Z:210:SER:HB2	26:Z:214:LYS:NZ	2.29	0.48
32:f:575:SER:HB3	32:f:609:LEU:HG	1.94	0.48
32:f:680:PRO:HG2	32:f:691:VAL:HG21	1.96	0.48
4:J:221:ASN:O	4:J:223:GLU:N	2.37	0.48
6:L:200:PRO:HD2	6:L:203:GLN:HE22	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:261:GLY:HA3	16:B:263:GLY:H	1.79	0.48
17:D:112:TYR:O	20:C:71:SER:HB2	2.14	0.48
17:D:406:VAL:HG23	17:D:407:ILE:HB	1.96	0.48
18:E:173:TYR:OH	18:E:300:HIS:HB3	2.13	0.48
28:b:8:VAL:HA	28:b:110:ILE:HG13	1.96	0.48
29:c:227:GLU:HB2	29:c:230:THR:HA	1.96	0.48
30:d:139:LEU:O	30:d:143:LEU:HD13	2.13	0.48
30:d:201:ASN:N	30:d:201:ASN:OD1	2.46	0.48
6:L:158:ALA:HB3	6:L:176:MET:HE3	1.95	0.48
7:M:40:ARG:NH1	7:M:160:TYR:O	2.47	0.48
7:M:185:THR:O	7:M:189:ILE:HG12	2.14	0.48
7:M:200:VAL:HG22	7:M:201:HIS:H	1.79	0.48
10:P:58:THR:OG1	11:Q:121:LEU:O	2.26	0.48
10:P:106:GLU:HB3	10:P:139:SER:HB3	1.95	0.48
15:A:97:ARG:HA	15:A:98:CYS:HA	1.54	0.48
17:D:384:MET:HA	17:D:387:VAL:HG12	1.95	0.48
19:F:100:ASP:OD1	19:F:100:ASP:N	2.46	0.48
21:U:792:ASN:OD1	21:U:793:LYS:N	2.44	0.48
22:V:31:ALA:HB3	22:V:32:PRO:HD3	1.95	0.48
23:W:35:ALA:HB2	23:W:48:LEU:HD11	1.96	0.48
23:W:397:VAL:HG21	24:X:341:PRO:HA	1.95	0.48
26:Z:191:ILE:O	26:Z:195:VAL:HG23	2.13	0.48
30:d:49:ILE:HD11	30:d:89:LEU:HD22	1.96	0.48
3:I:151:ASP:HB2	3:I:155:ASN:O	2.14	0.48
9:O:67:SER:HB3	9:O:74:PRO:HG3	1.95	0.48
10:P:56:LEU:HD21	10:P:58:THR:HB	1.95	0.48
17:D:92:PHE:HA	17:D:103:VAL:HG23	1.95	0.48
20:C:60:ARG:O	20:C:64:GLN:HG2	2.14	0.48
27:a:197:ALA:HA	27:a:200:LEU:HB3	1.96	0.48
29:c:229:LEU:O	29:c:230:THR:OG1	2.24	0.48
32:f:433:ASN:O	32:f:437:ASP:CB	2.62	0.48
32:f:467:GLU:OE2	32:f:496:LEU:HG	2.14	0.48
2:H:119:GLN:NE2	2:H:152:SER:O	2.47	0.47
6:L:137:TYR:CZ	6:L:142:PRO:HB3	2.50	0.47
11:Q:12:TYR:HB2	11:Q:182:ILE:HD11	1.95	0.47
15:A:74:PRO:CB	32:f:521:ARG:HB3	2.35	0.47
17:D:218:ALA:O	17:D:222:HIS:ND1	2.44	0.47
20:C:248:MET:HG3	20:C:293:MET:SD	2.54	0.47
23:W:100:ALA:O	23:W:104:MET:HG2	2.14	0.47
4:J:118:TYR:HD1	4:J:124:ARG:HH21	1.61	0.47
16:B:191:ASP:N	16:B:191:ASP:OD1	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:261:GLY:HA2	16:B:262:ASP:HB3	1.96	0.47
18:E:193:CYS:SG	18:E:227:PRO:HG2	2.54	0.47
19:F:369:HIS:ND1	19:F:397:LYS:HG2	2.29	0.47
21:U:567:ILE:HD13	21:U:570:LEU:HD12	1.96	0.47
23:W:446:ILE:HG21	26:Z:157:HIS:HB2	1.94	0.47
29:c:156:VAL:HG12	29:c:157:ILE:N	2.29	0.47
32:f:394:THR:OG1	32:f:686:ARG:NH2	2.46	0.47
2:H:50:LYS:NZ	2:H:62:VAL:O	2.48	0.47
17:D:251:PHE:HE2	17:D:292:LEU:HB2	1.79	0.47
24:X:134:VAL:HG13	24:X:172:LEU:HD23	1.97	0.47
26:Z:81:MET:HE1	29:c:94:LYS:HB3	1.96	0.47
28:b:18:ASN:HD21	28:b:25:ARG:NH2	2.13	0.47
32:f:371:CYS:SG	32:f:372:ASN:N	2.86	0.47
32:f:481:LYS:NZ	32:f:505:GLU:OE1	2.29	0.47
6:L:103:LEU:HD22	6:L:107:ARG:HD2	1.96	0.47
14:T:153:VAL:HG21	14:T:168:LEU:HD11	1.96	0.47
18:E:61:LEU:HD12	18:E:70:ILE:HG22	1.97	0.47
19:F:76:ASN:O	19:F:80:ILE:HG13	2.13	0.47
19:F:314:LEU:HD21	19:F:342:LEU:HD23	1.95	0.47
21:U:474:ARG:NH2	21:U:500:ASN:HB2	2.25	0.47
22:V:80:LYS:CE	22:V:86:VAL:HB	2.44	0.47
23:W:423:ASN:N	23:W:423:ASN:OD1	2.46	0.47
32:f:191:LYS:HZ2	32:f:668:PRO:HA	1.79	0.47
32:f:336:GLU:HG3	32:f:337:ASP:N	2.28	0.47
32:f:535:LEU:HD23	32:f:547:ILE:HG23	1.95	0.47
32:f:601:PHE:O	32:f:605:LEU:CB	2.62	0.47
32:f:613:GLY:HA2	32:f:656:HIS:HA	1.97	0.47
3:I:31:ALA:O	3:I:50:ARG:NH2	2.47	0.47
3:I:164:ILE:HA	3:I:165:GLY:HA2	1.69	0.47
19:F:90:VAL:HG13	19:F:150:LEU:HA	1.96	0.47
20:C:85:VAL:C	20:C:96:VAL:HG23	2.38	0.47
21:U:35:TRP:HB3	21:U:70:HIS:CD2	2.49	0.47
22:V:54:LYS:N	22:V:55:THR:OG1	2.47	0.47
22:V:207:ALA:HA	22:V:210:CYS:SG	2.54	0.47
32:f:52:ILE:O	32:f:56:ASP:CB	2.62	0.47
32:f:390:GLU:HB3	32:f:391:LEU:HA	1.97	0.47
32:f:500:LEU:O	32:f:504:GLY:HA3	2.14	0.47
32:f:604:ARG:HH21	32:f:649:ASN:HB3	1.79	0.47
1:G:58:ASP:OD1	1:G:59:LYS:N	2.48	0.47
1:G:138:MET:HE3	1:G:140:LEU:HD11	1.96	0.47
7:M:54:LEU:H	7:M:57:LEU:HD11	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:R:37:ILE:HG23	12:R:60:ALA:HB2	1.96	0.47
12:R:65:ILE:O	12:R:69:ARG:HG3	2.15	0.47
17:D:121:ARG:HD3	29:c:282:ARG:HD3	1.97	0.47
18:E:249:ALA:O	18:E:252:GLU:HG2	2.14	0.47
19:F:299:GLU:HA	19:F:300:LYS:HA	1.67	0.47
19:F:301:ALA:HB3	19:F:304:ARG:HB2	1.95	0.47
20:C:100:ASP:OD1	20:C:122:THR:HB	2.14	0.47
20:C:175:PHE:HD1	20:C:180:ILE:HG23	1.79	0.47
21:U:216:VAL:HG21	21:U:232:ILE:HD13	1.95	0.47
22:V:246:GLY:O	22:V:249:THR:OG1	2.28	0.47
24:X:242:ILE:HG13	24:X:243:ASP:H	1.79	0.47
25:Y:64:GLN:HG2	25:Y:65:ILE:HG22	1.96	0.47
25:Y:343:LEU:HD23	25:Y:343:LEU:O	2.14	0.47
25:Y:357:ASN:CB	25:Y:358:ARG:HA	2.45	0.47
1:G:13:ILE:HB	1:G:129:ALA:HB1	1.97	0.47
4:J:180:ALA:HA	4:J:181:ILE:HA	1.44	0.47
5:K:200:ILE:HA	5:K:203:LYS:NZ	2.29	0.47
7:M:23:VAL:HG12	7:M:27:MET:HE3	1.97	0.47
13:S:35:ILE:O	14:T:151:ARG:NH2	2.47	0.47
13:S:84:THR:O	13:S:88:ILE:HG13	2.15	0.47
13:S:93:SER:OG	13:S:128:GLY:O	2.21	0.47
14:T:146:ALA:O	14:T:150:LEU:HG	2.15	0.47
15:A:102:ILE:HD11	15:A:135:GLU:O	2.15	0.47
16:B:180:PRO:CG	16:B:239:VAL:HG23	2.38	0.47
17:D:300:ASP:HA	17:D:301:GLN:HA	1.49	0.47
17:D:411:GLU:HA	17:D:412:GLN:HB2	1.96	0.47
18:E:145:LEU:HD21	18:E:299:ILE:HD13	1.97	0.47
18:E:312:ILE:HG23	18:E:343:LEU:HD23	1.96	0.47
19:F:229:PRO:HA	19:F:230:GLY:HA2	1.56	0.47
23:W:446:ILE:HD13	26:Z:157:HIS:HB2	1.97	0.47
24:X:80:ILE:HD12	24:X:81:SER:O	2.13	0.47
26:Z:162:ILE:O	29:c:224:SER:OG	2.21	0.47
26:Z:190:ARG:NH2	27:a:375:LEU:HB2	2.30	0.47
27:a:32:LYS:HB2	28:b:20:ASP:HA	1.96	0.47
28:b:97:LEU:HD23	28:b:107:MET:HB3	1.96	0.47
32:f:88:ALA:O	32:f:92:CYS:CB	2.62	0.47
32:f:192:THR:HB	32:f:194:LEU:HB2	1.96	0.47
32:f:210:ARG:NH1	32:f:212:ASN:HD22	2.13	0.47
32:f:393:ASP:HB3	32:f:429:ARG:HG2	1.96	0.47
32:f:398:TRP:HZ2	32:f:690:ALA:O	1.97	0.47
32:f:460:HIS:HB3	32:f:461:PHE:H	1.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:585:MET:HG2	32:f:589:LEU:HD11	1.96	0.47
5:K:225:ASN:HA	5:K:227:HIS:HB3	1.97	0.47
7:M:169:ARG:O	7:M:173:LYS:HG2	2.15	0.47
13:S:6:VAL:HG12	13:S:57:PHE:CD1	2.50	0.47
15:A:391:GLU:HA	15:A:394:MET:HB3	1.95	0.47
16:B:135:ILE:HD12	16:B:135:ILE:O	2.14	0.47
17:D:283:ARG:HG3	17:D:286:GLN:NE2	2.28	0.47
18:E:305:ASN:O	18:E:309:ARG:N	2.42	0.47
21:U:566:LEU:O	21:U:570:LEU:HG	2.13	0.47
21:U:724:VAL:HA	21:U:727:LYS:HG2	1.96	0.47
28:b:146:GLU:HG2	28:b:147:GLU:H	1.80	0.47
32:f:238:LYS:NZ	32:f:249:LEU:HD21	2.30	0.47
32:f:516:PHE:HE1	32:f:534:ALA:HB3	1.80	0.47
5:K:200:ILE:O	5:K:204:GLN:HG3	2.15	0.47
9:O:36:PHE:HD1	9:O:42:TYR:HE1	1.60	0.47
18:E:310:LEU:HD13	18:E:332:VAL:HG21	1.97	0.47
22:V:153:LYS:O	22:V:157:THR:CG2	2.57	0.47
26:Z:239:ASP:OD1	26:Z:239:ASP:N	2.48	0.47
27:a:219:HIS:ND1	27:a:221:VAL:HG22	2.30	0.47
29:c:299:CYS:SG	29:c:300:LEU:N	2.88	0.47
32:f:401:LEU:O	32:f:405:LEU:HD13	2.15	0.47
6:L:164:ARG:HD2	6:L:198:THR:O	2.15	0.47
9:O:211:VAL:HG21	10:P:198:ARG:HD3	1.96	0.47
11:Q:5:ILE:HG22	11:Q:16:ALA:HB3	1.97	0.47
21:U:168:LEU:HD13	21:U:204:ILE:HD11	1.97	0.47
21:U:427:LEU:HD23	21:U:429:LYS:NZ	2.29	0.47
24:X:176:THR:O	24:X:180:LEU:HG	2.14	0.47
28:b:87:CYS:SG	28:b:127:LEU:HD11	2.55	0.47
30:d:233:GLU:HB3	30:d:235:THR:HG23	1.97	0.47
32:f:24:PRO:O	32:f:27:THR:OG1	2.31	0.47
32:f:483:ALA:O	32:f:486:ASP:N	2.45	0.47
32:f:550:THR:HA	32:f:553:LYS:HZ1	1.80	0.47
1:G:148:GLY:O	1:G:150:GLN:NE2	2.48	0.46
3:I:105:ILE:HD11	3:I:109:GLN:HG3	1.97	0.46
13:S:193:LEU:HD23	13:S:208:VAL:HB	1.97	0.46
14:T:186:ARG:HE	14:T:202:PRO:HB2	1.80	0.46
15:A:74:PRO:HG2	32:f:521:ARG:CZ	2.44	0.46
16:B:133:VAL:HG11	16:B:159:VAL:HG12	1.97	0.46
17:D:60:TYR:HE1	21:U:640:LEU:HD21	1.79	0.46
17:D:82:ILE:HA	17:D:83:GLN:HA	1.46	0.46
18:E:265:ASP:OD2	18:E:294:ARG:NH2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:185:MET:HE1	21:U:191:LYS:HE3	1.96	0.46
21:U:521:LEU:HB2	21:U:554:LEU:CD2	2.46	0.46
23:W:56:THR:HG21	23:W:103:LYS:HG2	1.97	0.46
24:X:258:LYS:HD3	24:X:266:ASP:HB2	1.95	0.46
28:b:164:ASP:HB2	28:b:166:THR:HG22	1.96	0.46
32:f:350:LYS:HA	32:f:356:ALA:HB3	1.96	0.46
32:f:562:VAL:O	32:f:566:SER:CB	2.64	0.46
32:f:601:PHE:CZ	32:f:605:LEU:HD13	2.50	0.46
2:H:43:GLY:HA2	2:H:144:PRO:HG3	1.97	0.46
4:J:84:ILE:O	4:J:88:ARG:HG3	2.15	0.46
6:L:179:PHE:CE2	6:L:190:HIS:HB3	2.50	0.46
11:Q:44:LEU:HD21	11:Q:57:ALA:HA	1.96	0.46
14:T:27:LEU:HD13	14:T:184:TYR:HB3	1.96	0.46
15:A:406:GLU:HA	15:A:409:PHE:CE2	2.50	0.46
20:C:168:PRO:HG2	20:C:290:LYS:HE2	1.97	0.46
20:C:215:SER:HA	20:C:216:GLY:HA3	1.54	0.46
21:U:766:PHE:HD1	21:U:776:SER:HA	1.80	0.46
23:W:32:ALA:O	23:W:36:LYS:HG3	2.15	0.46
24:X:406:ASN:HA	24:X:409:LYS:HB2	1.96	0.46
27:a:335:TRP:CG	27:a:336:VAL:H	2.34	0.46
29:c:59:GLY:HA2	29:c:70:ILE:HG22	1.97	0.46
32:f:238:LYS:HZ1	32:f:249:LEU:HD21	1.80	0.46
2:H:6:TYR:CE2	2:H:126:GLY:HA3	2.51	0.46
6:L:45:VAL:HG11	6:L:188:VAL:HA	1.98	0.46
6:L:130:VAL:HG22	6:L:132:LEU:H	1.81	0.46
7:M:213:LEU:O	7:M:226:ILE:HG13	2.15	0.46
11:Q:163:CYS:O	11:Q:167:LEU:HG	2.16	0.46
15:A:103:ASN:HB2	15:A:112:ILE:HG23	1.96	0.46
15:A:176:ASP:HA	15:A:357:ILE:HD12	1.97	0.46
15:A:288:GLY:HA2	15:A:289:ALA:HA	1.69	0.46
18:E:76:GLY:N	18:E:77:PRO:HD2	2.30	0.46
18:E:162:VAL:HB	18:E:164:ILE:HG22	1.97	0.46
20:C:255:GLY:CA	20:C:256:SER:HB2	2.45	0.46
21:U:630:PRO:HA	21:U:659:CYS:SG	2.55	0.46
25:Y:286:TRP:C	25:Y:288:PHE:H	2.23	0.46
29:c:147:PRO:HG2	29:c:148:ILE:HD12	1.96	0.46
30:d:189:ILE:HD13	30:d:194:ALA:HB2	1.96	0.46
32:f:174:LEU:HA	32:f:177:GLU:HG2	1.98	0.46
32:f:370:SER:CB	32:f:372:ASN:HD22	2.28	0.46
2:H:122:THR:HG22	2:H:129:PRO:HB3	1.98	0.46
3:I:3:ARG:HH11	5:K:11:GLY:N	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:229:LYS:NZ	7:M:235:ALA:H	2.14	0.46
15:A:102:ILE:HG22	15:A:113:ILE:HG12	1.96	0.46
15:A:161:VAL:HG21	15:A:256:MET:HE2	1.98	0.46
17:D:240:LEU:HB2	17:D:284:GLU:OE1	2.15	0.46
18:E:191:LEU:HD23	18:E:229:ILE:HD11	1.96	0.46
27:a:214:GLY:O	27:a:241:ASN:ND2	2.48	0.46
32:f:452:GLN:O	32:f:456:ILE:HG22	2.15	0.46
6:L:38:LEU:HD21	6:L:191:GLY:HA2	1.98	0.46
7:M:229:LYS:HD2	7:M:229:LYS:HA	1.48	0.46
18:E:360:ASP:OD1	18:E:360:ASP:N	2.41	0.46
19:F:359:GLU:H	19:F:359:GLU:CD	2.19	0.46
19:F:418:GLU:OE1	19:F:418:GLU:N	2.42	0.46
20:C:214:VAL:HG22	20:C:215:SER:H	1.79	0.46
21:U:350:LEU:HD12	21:U:353:LEU:HD12	1.96	0.46
22:V:62:HIS:HA	22:V:65:ARG:HB3	1.98	0.46
23:W:240:TYR:CD1	23:W:276:LEU:HB3	2.50	0.46
24:X:203:PRO:HB2	24:X:204:PRO:C	2.41	0.46
25:Y:208:PHE:HB3	25:Y:209:THR:H	1.55	0.46
28:b:12:ASN:OD1	28:b:12:ASN:N	2.48	0.46
32:f:180:ILE:HG13	32:f:181:MET:N	2.30	0.46
32:f:436:VAL:HG11	32:f:675:ASP:HA	1.97	0.46
1:G:60:LEU:HD11	7:M:176:ILE:HG21	1.98	0.46
1:G:60:LEU:HB3	7:M:160:TYR:HB3	1.98	0.46
4:J:10:PHE:HD1	5:K:23:GLN:HE21	1.64	0.46
6:L:184:LEU:H	6:L:184:LEU:HD12	1.80	0.46
6:L:204:ASP:HA	6:L:205:LEU:HB3	1.97	0.46
15:A:158:ASP:OD1	15:A:159:PRO:HD2	2.16	0.46
15:A:171:ASP:OD1	15:A:171:ASP:N	2.48	0.46
17:D:130:VAL:HG21	17:D:139:LEU:HD22	1.96	0.46
18:E:70:ILE:HG12	18:E:80:VAL:HG12	1.98	0.46
19:F:181:PRO:HG3	19:F:238:ARG:HG2	1.97	0.46
19:F:265:ALA:O	19:F:269:ARG:HG3	2.16	0.46
20:C:248:MET:HE3	20:C:273:MET:HE2	1.98	0.46
21:U:331:GLY:O	21:U:335:ILE:HG12	2.15	0.46
23:W:86:ASN:HD22	23:W:88:MET:HE2	1.80	0.46
23:W:372:ARG:HG2	23:W:414:ASN:HB3	1.98	0.46
24:X:327:TYR:O	24:X:331:LEU:HD13	2.16	0.46
25:Y:183:TYR:OH	25:Y:212:GLU:HB2	2.15	0.46
25:Y:377:LEU:HA	25:Y:380:VAL:HG22	1.98	0.46
26:Z:12:HIS:ND1	26:Z:168:GLU:OE1	2.49	0.46
26:Z:59:ASP:OD2	28:b:99:HIS:NE2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:78:GLU:O	27:a:82:HIS:ND1	2.36	0.46
32:f:438:VAL:HG13	32:f:472:LYS:HD3	1.98	0.46
1:G:89:SER:HG	7:M:120:HIS:CE1	2.29	0.46
3:I:220:ASN:HA	3:I:221:GLY:HA2	1.46	0.46
6:L:36:VAL:HG22	6:L:160:SER:HB2	1.97	0.46
17:D:412:GLN:HG3	17:D:414:HIS:H	1.80	0.46
33:E:401:ATP:O1G	19:F:347:ARG:NH2	2.41	0.46
21:U:19:LEU:HB2	30:d:27:LYS:NZ	2.30	0.46
21:U:261:LEU:HA	21:U:264:VAL:HG12	1.97	0.46
22:V:133:PRO:O	22:V:137:GLU:HG3	2.15	0.46
27:a:268:LEU:HD23	27:a:271:LYS:HD3	1.98	0.46
32:f:281:ILE:HG13	32:f:282:LYS:N	2.30	0.46
32:f:612:LEU:O	32:f:614:LYS:HG3	2.16	0.46
32:f:653:GLY:O	32:f:656:HIS:NE2	2.49	0.46
1:G:116:LYS:HG2	1:G:160:TYR:CG	2.51	0.46
2:H:22:ILE:HG21	2:H:152:SER:HB3	1.96	0.46
2:H:139:TRP:HA	2:H:144:PRO:HA	1.98	0.46
13:S:197:ILE:HG22	13:S:199:THR:HG23	1.97	0.46
16:B:249:ARG:HE	20:C:283:PHE:HE1	1.59	0.46
16:B:294:ARG:HB3	20:C:264:GLY:CA	2.45	0.46
21:U:243:LEU:HD21	21:U:913:ILE:HD13	1.98	0.46
21:U:699:THR:HG21	21:U:812:ALA:O	2.16	0.46
22:V:59:ALA:HA	22:V:60:ALA:C	2.40	0.46
27:a:129:GLN:HG3	27:a:130:VAL:H	1.81	0.46
30:d:182:ILE:HG21	30:d:213:ARG:HH12	1.81	0.46
31:e:62:LYS:O	31:e:66:LYS:HG3	2.16	0.46
32:f:327:GLY:HA3	32:f:366:ILE:HD13	1.98	0.46
32:f:642:VAL:O	32:f:645:LEU:HG	2.15	0.46
5:K:107:MET:HG2	5:K:111:SER:CB	2.45	0.46
17:D:81:ARG:HD2	29:c:154:LYS:HD2	1.96	0.46
20:C:11:LEU:HG	20:C:13:GLU:HB3	1.98	0.46
22:V:482:PHE:O	22:V:486:ILE:HG13	2.15	0.46
25:Y:19:ILE:O	25:Y:23:ARG:HG2	2.15	0.46
25:Y:367:GLN:OE1	25:Y:371:LYS:HE2	2.16	0.46
29:c:29:GLU:HB2	29:c:203:ILE:HG13	1.97	0.46
29:c:178:THR:HA	29:c:181:LEU:HD23	1.98	0.46
29:c:241:ASN:ND2	29:c:300:LEU:O	2.41	0.46
30:d:35:PHE:HD2	30:d:36:LEU:HD23	1.80	0.46
30:d:160:ALA:H	30:d:161:GLU:HA	1.81	0.46
32:f:234:ASP:O	32:f:238:LYS:N	2.48	0.46
2:H:87:VAL:O	2:H:91:ARG:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:8:ARG:HD3	3:I:11:ILE:HD12	1.98	0.46
7:M:74:GLY:HA3	7:M:224:HIS:CE1	2.50	0.46
15:A:347:ASP:O	15:A:351:ARG:HG3	2.16	0.46
16:B:202:GLU:OE1	16:B:206:THR:OG1	2.31	0.46
19:F:79:LYS:O	19:F:82:VAL:HG22	2.16	0.46
20:C:213:ARG:HH21	20:C:249:ASP:HB2	1.80	0.46
22:V:210:CYS:SG	22:V:211:TYR:N	2.89	0.46
25:Y:233:ARG:NH2	25:Y:264:TYR:O	2.41	0.46
28:b:120:ASN:OD1	28:b:121:GLU:N	2.47	0.46
30:d:44:THR:O	30:d:47:GLN:NE2	2.49	0.46
30:d:236:THR:O	30:d:239:SER:OG	2.34	0.46
32:f:407:HIS:HB2	32:f:410:LYS:HB2	1.97	0.46
32:f:415:GLU:HA	32:f:441:TYR:CZ	2.51	0.46
32:f:537:LEU:HD21	32:f:674:PHE:CZ	2.50	0.46
4:J:219:ILE:H	4:J:219:ILE:HD12	1.80	0.45
6:L:89:ARG:HH21	13:S:77:HIS:HB3	1.80	0.45
10:P:70:ARG:NH2	10:P:97:GLU:OE2	2.40	0.45
15:A:206:ILE:HG13	15:A:207:GLU:N	2.30	0.45
20:C:340:ARG:NH2	25:Y:179:ARG:HE	2.13	0.45
21:U:173:VAL:N	21:U:174:PRO:HD3	2.32	0.45
21:U:380:THR:HG23	21:U:382:SER:H	1.82	0.45
21:U:520:MET:HE2	21:U:525:ASN:HD22	1.81	0.45
22:V:144:ASP:N	22:V:145:LEU:HA	2.31	0.45
24:X:207:GLN:NE2	24:X:211:ASP:OD1	2.45	0.45
25:Y:138:LEU:HD22	25:Y:168:ILE:HD11	1.97	0.45
26:Z:205:LEU:HA	26:Z:208:ILE:HG22	1.98	0.45
27:a:342:ASP:H	27:a:345:GLN:HB2	1.81	0.45
31:e:1:MET:N	31:e:2:SER:HA	2.15	0.45
32:f:87:SER:O	32:f:91:ARG:HG2	2.15	0.45
32:f:293:ASN:HB3	32:f:307:LEU:HD21	1.98	0.45
32:f:330:TYR:HB3	32:f:336:GLU:HG2	1.97	0.45
32:f:528:ARG:HA	32:f:531:VAL:CG2	2.45	0.45
3:I:119:GLN:NE2	4:J:79:ASP:HA	2.31	0.45
7:M:72:HIS:CE1	7:M:105:ASN:HB3	2.50	0.45
15:A:184:ILE:HD12	15:A:187:LEU:HD11	1.97	0.45
16:B:226:GLY:HA3	16:B:353:PHE:HB3	1.98	0.45
17:D:143:LEU:HD22	17:D:144:PRO:HD2	1.98	0.45
19:F:144:LYS:HA	19:F:145:LEU:HA	1.72	0.45
20:C:378:VAL:HG12	20:C:379:THR:H	1.82	0.45
21:U:19:LEU:HB2	30:d:27:LYS:HZ2	1.81	0.45
21:U:510:GLU:OE2	21:U:546:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:259:LEU:HD11	22:V:294:ARG:HD2	1.97	0.45
22:V:296:LYS:HZ1	22:V:308:THR:HG21	1.81	0.45
22:V:350:GLN:HB3	22:V:353:LEU:HB3	1.98	0.45
27:a:4:VAL:HB	27:a:5:PRO:HD3	1.98	0.45
27:a:271:LYS:HA	27:a:274:LEU:HG	1.99	0.45
32:f:83:GLU:HB3	32:f:84:PRO:HD3	1.97	0.45
32:f:656:HIS:C	32:f:658:VAL:H	2.24	0.45
32:f:674:PHE:O	32:f:678:LEU:HG	2.15	0.45
1:G:56:VAL:HG22	1:G:61:LEU:HD22	1.98	0.45
6:L:166:GLN:HA	6:L:169:ARG:HH11	1.81	0.45
10:P:26:ARG:HB3	10:P:37:THR:O	2.16	0.45
15:A:114:ASN:OD1	15:A:115:VAL:N	2.49	0.45
16:B:139:VAL:HA	16:B:140:ASP:CB	2.46	0.45
17:D:249:ASP:HA	17:D:252:ARG:HG2	1.98	0.45
18:E:109:ARG:NH2	19:F:121:CYS:SG	2.89	0.45
18:E:144:GLU:O	18:E:148:VAL:HG23	2.16	0.45
21:U:9:ILE:HD11	21:U:37:GLU:HG3	1.98	0.45
22:V:80:LYS:HE2	22:V:86:VAL:HB	1.98	0.45
23:W:124:LEU:O	23:W:128:LEU:HD23	2.17	0.45
27:a:193:GLN:HA	27:a:196:ARG:HB3	1.97	0.45
27:a:342:ASP:HB2	27:a:345:GLN:HG2	1.98	0.45
29:c:229:LEU:CD2	29:c:231:LEU:HB2	2.47	0.45
32:f:23:GLU:HB3	32:f:24:PRO:HD3	1.99	0.45
32:f:210:ARG:CZ	32:f:212:ASN:HD22	2.29	0.45
32:f:353:MET:HE1	32:f:361:LEU:HB2	1.98	0.45
6:L:139:ASP:H	14:T:81:HIS:HE1	1.64	0.45
15:A:74:PRO:HG2	32:f:521:ARG:NH2	2.31	0.45
15:A:146:LYS:HE2	15:A:146:LYS:HB2	1.80	0.45
15:A:290:GLY:HA2	15:A:291:GLY:HA3	1.66	0.45
16:B:152:LEU:HD23	16:B:157:HIS:HD1	1.81	0.45
20:C:255:GLY:H	20:C:256:SER:HB2	1.81	0.45
21:U:340:GLN:HG3	21:U:880:ASN:HB3	1.97	0.45
23:W:42:GLU:O	23:W:45:GLU:HB3	2.17	0.45
25:Y:118:GLU:O	25:Y:121:LEU:HG	2.17	0.45
25:Y:216:TYR:O	25:Y:220:VAL:HG23	2.16	0.45
26:Z:233:VAL:O	26:Z:236:LEU:HB2	2.17	0.45
32:f:226:PHE:HB2	32:f:368:VAL:CG1	2.46	0.45
6:L:46:LEU:CD1	6:L:63:ILE:HD13	2.45	0.45
13:S:211:ARG:HH21	13:S:213:ASP:CG	2.25	0.45
16:B:108:SER:N	16:B:152:LEU:O	2.30	0.45
20:C:82:LYS:HG3	20:C:84:LYS:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:158:ARG:HD2	21:U:193:PHE:CE1	2.52	0.45
21:U:436:ALA:O	21:U:472:ILE:HD13	2.16	0.45
21:U:757:MET:HG3	21:U:758:PRO:HD3	1.99	0.45
22:V:455:LYS:H	22:V:456:GLY:HA2	1.81	0.45
23:W:33:LYS:O	23:W:37:GLU:HG3	2.17	0.45
23:W:440:ASN:HB3	26:Z:230:LEU:HD11	1.97	0.45
25:Y:237:ARG:HD3	25:Y:264:TYR:CE1	2.52	0.45
25:Y:307:LEU:HD22	25:Y:308:LEU:HD22	1.98	0.45
32:f:112:MET:HE2	32:f:114:ASN:ND2	2.31	0.45
32:f:242:LYS:C	32:f:244:LYS:H	2.24	0.45
12:R:7:LYS:HE2	12:R:124:ALA:HA	1.98	0.45
15:A:357:ILE:HG23	15:A:358:HIS:ND1	2.30	0.45
20:C:184:LYS:NZ	20:C:280:LEU:HB3	2.32	0.45
21:U:62:LEU:O	21:U:66:LYS:HG2	2.17	0.45
24:X:183:LEU:HB3	24:X:184:PRO:HD3	1.97	0.45
24:X:343:SER:HB2	24:X:387:ILE:HB	1.98	0.45
25:Y:39:ASP:OD1	25:Y:39:ASP:N	2.49	0.45
27:a:339:ARG:HD3	27:a:339:ARG:HA	1.75	0.45
28:b:6:THR:HB	28:b:49:VAL:HG22	1.99	0.45
30:d:155:LYS:HA	30:d:158:ILE:HD11	1.97	0.45
30:d:191:PHE:HA	30:d:222:TYR:CE1	2.49	0.45
31:e:40:GLU:N	31:e:41:ASP:HA	2.31	0.45
32:f:282:LYS:CE	32:f:286:LEU:HD23	2.47	0.45
32:f:371:CYS:O	32:f:372:ASN:HB2	2.17	0.45
32:f:664:ALA:HB3	32:f:668:PRO:HG2	1.98	0.45
4:J:31:THR:HG22	4:J:163:ARG:N	2.32	0.45
10:P:125:ASP:HB2	10:P:129:CYS:HB3	1.98	0.45
15:A:312:ARG:HA	15:A:313:GLY:HA2	1.55	0.45
16:B:117:ASP:HB3	32:f:588:GLN:HE22	1.73	0.45
17:D:304:ASN:O	17:D:305:VAL:HB	2.16	0.45
20:C:131:VAL:HG13	20:C:132:ASP:H	1.80	0.45
21:U:460:TYR:HD2	21:U:461:LEU:HD12	1.82	0.45
22:V:80:LYS:HD2	22:V:82:LEU:O	2.17	0.45
23:W:80:TRP:CD1	23:W:84:ASN:HD21	2.34	0.45
23:W:441:LYS:HA	23:W:444:HIS:HE1	1.82	0.45
26:Z:164:ALA:HB3	26:Z:169:GLU:HG3	1.97	0.45
26:Z:176:LEU:HD12	26:Z:178:ASP:H	1.81	0.45
26:Z:208:ILE:HA	26:Z:211:TYR:CD2	2.51	0.45
32:f:191:LYS:NZ	32:f:668:PRO:HA	2.32	0.45
32:f:282:LYS:NZ	32:f:283:SER:O	2.45	0.45
1:G:144:ASP:OD2	1:G:147:GLN:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:66:GLU:HG2	2:H:87:VAL:HG11	1.99	0.45
4:J:33:VAL:O	4:J:44:GLY:N	2.49	0.45
11:Q:107:TYR:HA	11:Q:113:PRO:HA	1.98	0.45
15:A:108:ASP:HB2	15:A:109:PRO:HD3	1.97	0.45
15:A:420:TYR:HE1	16:B:350:LYS:HG2	1.79	0.45
16:B:174:MET:HE3	16:B:175:LYS:HE2	1.98	0.45
17:D:203:LEU:HB3	17:D:330:LYS:HA	1.98	0.45
19:F:120:LYS:HG2	19:F:136:VAL:HG21	1.98	0.45
19:F:181:PRO:HD2	19:F:242:ALA:HB2	1.98	0.45
19:F:187:ASP:HA	19:F:368:ILE:HG21	1.97	0.45
19:F:311:LEU:O	19:F:315:ASN:HB2	2.16	0.45
20:C:170:LYS:C	20:C:172:PRO:HD3	2.42	0.45
20:C:327:ASP:O	20:C:331:ILE:HG12	2.17	0.45
21:U:632:GLN:O	21:U:636:VAL:HG22	2.16	0.45
22:V:197:THR:HG22	22:V:200:ARG:H	1.81	0.45
22:V:319:HIS:HB2	22:V:320:THR:HA	1.99	0.45
32:f:135:MET:HA	32:f:138:MET:SD	2.57	0.45
32:f:293:ASN:HD22	32:f:307:LEU:HG	1.82	0.45
32:f:388:GLU:O	32:f:391:LEU:HB3	2.16	0.45
32:f:663:VAL:HA	32:f:664:ALA:HA	1.59	0.45
16:B:208:PRO:O	16:B:212:GLU:HG2	2.16	0.45
16:B:222:VAL:HA	16:B:346:ARG:HG2	1.97	0.45
16:B:288:ASP:O	16:B:292:THR:HG23	2.17	0.45
16:B:357:ASP:OD1	16:B:360:THR:OG1	2.33	0.45
17:D:175:GLN:NE2	17:D:179:GLU:OE2	2.50	0.45
18:E:172:LEU:HD23	18:E:299:ILE:HB	1.99	0.45
19:F:293:THR:HG23	19:F:337:ILE:HG21	1.99	0.45
22:V:197:THR:C	22:V:199:ASN:H	2.25	0.45
23:W:370:TYR:HA	23:W:371:THR:CB	2.46	0.45
24:X:297:ARG:HB2	24:X:337:ARG:NH1	2.31	0.45
24:X:410:VAL:O	24:X:413:SER:OG	2.30	0.45
25:Y:50:MET:SD	25:Y:74:LYS:HB3	2.57	0.45
27:a:163:TYR:CD1	27:a:172:TYR:HB2	2.52	0.45
27:a:270:ARG:O	27:a:270:ARG:NH2	2.50	0.45
28:b:51:LEU:HD11	28:b:61:LEU:HB2	1.99	0.45
32:f:11:TRP:HB3	32:f:12:GLN:HB3	1.99	0.45
1:G:157:ALA:HB3	1:G:159:TYR:HD1	1.82	0.45
4:J:12:PRO:HG3	5:K:26:TYR:CZ	2.52	0.45
5:K:157:ASP:OD2	5:K:159:SER:OG	2.32	0.45
10:P:15:LYS:HD3	10:P:119:PRO:HG2	1.99	0.45
12:R:21:THR:HG22	12:R:26:ILE:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:125:ASP:N	13:S:125:ASP:OD1	2.49	0.45
15:A:191:VAL:CG2	15:A:316:LYS:HE2	2.44	0.45
15:A:362:MET:HG2	15:A:363:SER:H	1.81	0.45
17:D:41:TYR:CD2	21:U:152:GLY:HA3	2.52	0.45
17:D:303:VAL:HG23	17:D:304:ASN:HB2	1.98	0.45
20:C:80:MET:HB2	20:C:84:LYS:O	2.17	0.45
20:C:89:VAL:HB	20:C:92:GLU:HB2	1.99	0.45
21:U:908:ILE:HG12	21:U:909:GLY:H	1.82	0.45
27:a:304:VAL:O	27:a:307:VAL:HG22	2.17	0.45
29:c:104:ARG:HB3	29:c:106:GLU:OE1	2.17	0.45
5:K:177:ALA:O	5:K:181:LEU:HB2	2.17	0.44
7:M:92:ARG:NH1	7:M:96:SER:OG	2.49	0.44
7:M:110:HIS:NE2	8:N:70:LEU:HA	2.32	0.44
11:Q:128:PRO:HB2	11:Q:147:TYR:OH	2.17	0.44
13:S:6:VAL:HG12	13:S:57:PHE:CE1	2.51	0.44
16:B:255:LEU:CD1	16:B:256:ILE:HG12	2.47	0.44
20:C:167:LEU:HD22	20:C:175:PHE:CE2	2.53	0.44
21:U:59:PHE:HA	21:U:62:LEU:HD13	1.99	0.44
21:U:157:THR:OG1	21:U:159:ARG:NH2	2.50	0.44
21:U:193:PHE:HA	21:U:196:LYS:HD2	1.97	0.44
22:V:76:LYS:HA	22:V:77:GLU:HA	1.74	0.44
22:V:100:MET:HG2	22:V:102:PRO:HD2	1.99	0.44
22:V:443:ARG:NH2	30:d:180:GLY:O	2.49	0.44
24:X:173:GLU:O	24:X:176:THR:HG22	2.17	0.44
26:Z:124:ILE:HA	26:Z:135:THR:HA	1.99	0.44
27:a:307:VAL:O	27:a:311:VAL:HG22	2.17	0.44
28:b:20:ASP:CG	28:b:25:ARG:HE	2.25	0.44
30:d:45:LYS:HG2	30:d:48:LEU:HD12	1.99	0.44
32:f:234:ASP:HA	32:f:237:ASN:HB2	1.98	0.44
32:f:255:LEU:O	32:f:259:LEU:HB2	2.17	0.44
32:f:626:ARG:O	32:f:630:SER:CB	2.65	0.44
6:L:203:GLN:HG2	6:L:204:ASP:O	2.17	0.44
8:N:45:ARG:HB2	8:N:52:THR:HG21	2.00	0.44
16:B:199:GLU:O	16:B:203:LEU:N	2.50	0.44
18:E:203:ILE:HG23	18:E:256:THR:HG21	2.00	0.44
21:U:28:ASN:HD22	21:U:59:PHE:HZ	1.65	0.44
22:V:137:GLU:HA	22:V:140:ASP:HB2	1.98	0.44
22:V:419:LEU:O	22:V:422:ILE:HG22	2.17	0.44
25:Y:387:ILE:HA	25:Y:388:ASN:HA	1.54	0.44
26:Z:21:ASP:OD1	26:Z:22:HIS:N	2.50	0.44
26:Z:225:GLN:NE2	26:Z:229:GLN:HB2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:70:ARG:HG2	28:b:17:ARG:HB3	1.98	0.44
30:d:256:ILE:N	30:d:257:VAL:HA	2.33	0.44
32:f:116:MET:SD	32:f:141:ARG:HG2	2.58	0.44
32:f:383:ILE:HG21	32:f:399:LEU:HD21	2.00	0.44
5:K:79:SER:H	5:K:139:VAL:HG23	1.81	0.44
5:K:154:PHE:HB3	5:K:162:PHE:HE1	1.81	0.44
6:L:7:ASP:OD1	6:L:20:HIS:ND1	2.50	0.44
6:L:172:LEU:O	6:L:173:GLU:C	2.60	0.44
15:A:100:LYS:NZ	15:A:142:VAL:HB	2.32	0.44
18:E:40:TYR:O	18:E:43:SER:OG	2.31	0.44
18:E:195:PHE:CZ	18:E:197:LYS:HB2	2.53	0.44
18:E:210:GLU:O	18:E:213:ARG:N	2.50	0.44
18:E:219:PHE:O	18:E:223:ARG:HG3	2.18	0.44
18:E:240:GLY:HA2	18:E:284:THR:HB	1.99	0.44
19:F:313:LEU:O	19:F:316:GLN:HB2	2.17	0.44
20:C:285:ALA:HB1	20:C:286:THR:HB	2.00	0.44
22:V:80:LYS:HA	22:V:80:LYS:HD3	1.61	0.44
23:W:230:MET:HE2	23:W:246:HIS:CE1	2.52	0.44
23:W:333:LEU:HD12	23:W:333:LEU:O	2.17	0.44
24:X:258:LYS:HE3	24:X:270:LEU:HD11	1.98	0.44
25:Y:109:GLU:HG2	25:Y:124:PHE:HE1	1.82	0.44
28:b:29:GLN:O	28:b:33:VAL:HG23	2.17	0.44
30:d:168:ASP:O	30:d:171:LEU:HB2	2.17	0.44
32:f:207:ASP:OD2	32:f:217:PHE:HD2	2.01	0.44
32:f:476:LYS:NZ	32:f:477:ASP:OD1	2.50	0.44
32:f:660:TYR:CB	32:f:663:VAL:HG23	2.48	0.44
32:f:664:ALA:HB3	32:f:668:PRO:HD2	1.99	0.44
32:f:680:PRO:O	32:f:683:VAL:HB	2.17	0.44
2:H:50:LYS:NZ	2:H:62:VAL:HB	2.32	0.44
3:I:3:ARG:HH21	3:I:8:ARG:HH21	1.66	0.44
4:J:154:HIS:CE1	5:K:59:MET:HG3	2.52	0.44
11:Q:11:ASP:OD1	11:Q:11:ASP:N	2.48	0.44
14:T:23:ALA:HB3	14:T:169:VAL:HG11	1.99	0.44
16:B:224:LEU:HD13	16:B:234:LEU:HB3	1.98	0.44
16:B:283:PHE:CE2	16:B:285:ASP:HB2	2.52	0.44
17:D:374:ASP:OD1	17:D:377:SER:HB2	2.17	0.44
19:F:70:LYS:HG3	19:F:74:LYS:HE3	1.98	0.44
21:U:26:LYS:O	21:U:30:VAL:HG22	2.17	0.44
22:V:161:PRO:O	22:V:164:GLU:HB2	2.17	0.44
23:W:40:LEU:HB2	23:W:41:GLN:CA	2.41	0.44
23:W:144:ARG:HA	23:W:147:LYS:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:366:MET:SD	23:W:378:MET:HE2	2.58	0.44
23:W:408:ARG:HD2	24:X:346:GLN:NE2	2.29	0.44
27:a:206:LEU:HB3	27:a:264:ASN:OD1	2.16	0.44
27:a:320:VAL:HG22	27:a:322:GLY:H	1.81	0.44
30:d:10:ASN:OD1	30:d:11:ARG:N	2.50	0.44
30:d:68:ILE:HB	30:d:69:PRO:HD3	1.99	0.44
32:f:190:TYR:CE2	32:f:668:PRO:HB3	2.53	0.44
32:f:242:LYS:O	32:f:244:LYS:N	2.48	0.44
32:f:382:THR:O	32:f:386:LYS:NZ	2.51	0.44
32:f:528:ARG:HA	32:f:531:VAL:HG23	1.98	0.44
3:I:14:PRO:HA	4:J:21:TYR:CE1	2.52	0.44
4:J:88:ARG:NH2	11:Q:70:ARG:HG3	2.32	0.44
4:J:88:ARG:HH12	11:Q:69:MET:HB2	1.83	0.44
5:K:13:ASN:ND2	6:L:126:ARG:HH11	2.15	0.44
7:M:233:GLU:OE1	7:M:237:LYS:HG2	2.18	0.44
15:A:122:VAL:N	19:F:88:TYR:O	2.30	0.44
15:A:311:PRO:HD2	15:A:313:GLY:HA2	1.99	0.44
16:B:173:VAL:HG12	20:C:232:ARG:HG2	2.00	0.44
16:B:235:LEU:O	16:B:238:ALA:N	2.48	0.44
17:D:200:ARG:HH22	17:D:300:ASP:CG	2.24	0.44
17:D:312:ASN:HD21	18:E:242:ARG:NH2	2.08	0.44
18:E:82:GLY:O	18:E:106:THR:OG1	2.24	0.44
19:F:336:ASP:OD1	19:F:336:ASP:N	2.50	0.44
20:C:187:LEU:HG	20:C:313:ARG:O	2.17	0.44
20:C:338:LEU:HD13	20:C:378:VAL:HB	1.98	0.44
20:C:343:ASN:HB3	20:C:346:LYS:HG2	1.99	0.44
21:U:161:ASP:OD1	21:U:162:VAL:N	2.51	0.44
22:V:59:ALA:N	22:V:60:ALA:HB3	2.31	0.44
22:V:344:ASP:HB3	31:e:43:TRP:NE1	2.33	0.44
23:W:253:THR:HB	23:W:254:PRO:HD3	2.00	0.44
29:c:227:GLU:HG2	29:c:233:ASP:HB2	1.99	0.44
1:G:171:LYS:HB3	1:G:205:VAL:HG11	1.99	0.44
10:P:59:ASP:OD2	10:P:104:TYR:N	2.45	0.44
11:Q:86:ARG:HA	11:Q:86:ARG:HD3	1.76	0.44
16:B:155:LYS:HA	16:B:156:VAL:HA	1.53	0.44
16:B:401:GLU:HG3	16:B:422:SER:HB2	1.98	0.44
22:V:96:ARG:HA	22:V:98:LEU:HD12	1.99	0.44
22:V:428:LEU:HD21	22:V:434:ALA:N	2.33	0.44
25:Y:197:ALA:HB3	25:Y:226:VAL:HG21	1.98	0.44
26:Z:102:HIS:HD2	26:Z:104:ASN:HB3	1.81	0.44
27:a:73:PRO:HG2	27:a:113:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:243:GLY:HA3	27:a:244:ASN:HA	1.78	0.44
27:a:325:ASP:OD1	27:a:327:VAL:HG12	2.18	0.44
28:b:95:LEU:HA	28:b:98:LYS:NZ	2.32	0.44
29:c:88:ASP:HB3	29:c:91:PHE:CB	2.47	0.44
32:f:89:LEU:HD21	32:f:126:CYS:SG	2.57	0.44
32:f:622:TYR:CE1	32:f:654:LYS:HD3	2.52	0.44
1:G:122:SER:HB2	1:G:158:GLY:HA2	1.99	0.44
4:J:51:ALA:C	4:J:53:LEU:H	2.26	0.44
4:J:120:GLN:OE1	5:K:135:ARG:N	2.49	0.44
10:P:142:CYS:O	10:P:146:MET:HG3	2.16	0.44
12:R:64:ARG:O	12:R:68:LEU:HG	2.18	0.44
15:A:119:ALA:HA	19:F:127:SER:CB	2.48	0.44
15:A:174:TYR:CD1	15:A:227:ARG:HD2	2.44	0.44
16:B:363:ARG:O	16:B:367:ILE:HG13	2.18	0.44
19:F:69:MET:HA	19:F:72:LYS:HG2	1.99	0.44
19:F:76:ASN:HD22	19:F:76:ASN:C	2.25	0.44
25:Y:212:GLU:H	25:Y:212:GLU:HG2	1.57	0.44
26:Z:52:ASN:OD1	26:Z:53:SER:N	2.40	0.44
26:Z:262:LEU:HA	26:Z:265:LEU:HD22	2.00	0.44
28:b:140:ILE:O	28:b:170:LEU:HA	2.18	0.44
32:f:108:ARG:HE	32:f:141:ARG:HE	1.66	0.44
32:f:589:LEU:HA	32:f:592:TYR:CE2	2.52	0.44
3:I:139:TRP:HD1	3:I:145:PHE:CE1	2.35	0.44
9:O:195:LYS:NZ	10:P:151:GLU:OE1	2.51	0.44
18:E:75:ASN:HD21	19:F:130:GLN:HA	1.82	0.44
18:E:326:ILE:HD12	18:E:326:ILE:O	2.17	0.44
19:F:295:ARG:CZ	19:F:301:ALA:HA	2.48	0.44
21:U:560:MET:HE2	21:U:589:ALA:O	2.17	0.44
22:V:244:ALA:C	22:V:246:GLY:H	2.26	0.44
22:V:289:LEU:HA	22:V:292:THR:HG22	2.00	0.44
23:W:124:LEU:HA	23:W:127:THR:HG22	1.99	0.44
24:X:378:LEU:HA	24:X:385:LEU:HA	2.00	0.44
26:Z:190:ARG:HG3	26:Z:191:ILE:HD12	1.98	0.44
27:a:73:PRO:O	27:a:77:VAL:HG23	2.18	0.44
27:a:144:ASN:HA	27:a:145:LEU:HA	1.58	0.44
28:b:140:ILE:HB	28:b:170:LEU:HD13	1.99	0.44
28:b:157:VAL:HG21	28:b:170:LEU:HB2	1.98	0.44
30:d:160:ALA:HB3	30:d:161:GLU:HA	2.00	0.44
32:f:197:ASN:CG	32:f:237:ASN:HD21	2.25	0.44
32:f:680:PRO:CG	32:f:691:VAL:HG21	2.47	0.44
2:H:22:ILE:O	2:H:26:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:N:41:ILE:HG12	8:N:76:VAL:HG22	2.00	0.44
13:S:27:THR:HB	13:S:40:SER:H	1.82	0.44
17:D:289:LEU:HD12	17:D:292:LEU:HD11	1.99	0.44
19:F:406:ILE:HG22	19:F:409:ARG:NH1	2.32	0.44
21:U:250:PHE:HA	21:U:253:TYR:HB3	2.00	0.44
24:X:306:LEU:HD11	24:X:313:LEU:HG	2.00	0.44
25:Y:141:VAL:HG13	25:Y:160:ASN:ND2	2.33	0.44
26:Z:59:ASP:HB2	28:b:95:LEU:HD11	2.00	0.44
32:f:222:VAL:HG11	32:f:238:LYS:HZ1	1.82	0.44
32:f:458:SER:OG	32:f:459:GLU:N	2.51	0.44
32:f:604:ARG:CD	32:f:649:ASN:HB3	2.48	0.44
5:K:160:GLY:O	6:L:82:ARG:NH2	2.39	0.43
9:O:52:THR:O	9:O:56:THR:HG22	2.17	0.43
10:P:93:ASN:O	10:P:97:GLU:HG3	2.18	0.43
15:A:351:ARG:NH1	15:A:378:PRO:HA	2.32	0.43
20:C:337:ASN:OD1	25:Y:177:ARG:NH2	2.44	0.43
21:U:474:ARG:HE	21:U:500:ASN:CG	2.26	0.43
22:V:149:PRO:HG3	22:V:203:LEU:HG	2.00	0.43
22:V:279:GLN:NE2	22:V:285:TRP:CD1	2.85	0.43
26:Z:168:GLU:H	26:Z:168:GLU:HG2	1.60	0.43
30:d:40:GLY:HA3	30:d:41:THR:O	2.18	0.43
32:f:98:ARG:O	32:f:102:ARG:NH2	2.51	0.43
32:f:106:ALA:HB1	32:f:107:LEU:CA	2.47	0.43
32:f:282:LYS:NZ	32:f:286:LEU:HD23	2.33	0.43
1:G:43:ARG:HA	1:G:48:ALA:HA	1.99	0.43
2:H:171:LYS:NZ	3:I:55:LEU:HD22	2.33	0.43
4:J:65:LEU:HD11	4:J:87:ALA:HB1	2.00	0.43
5:K:96:THR:HG22	5:K:107:MET:SD	2.58	0.43
6:L:193:ARG:HA	6:L:196:ARG:HD2	2.00	0.43
14:T:86:ARG:HG2	14:T:121:PHE:CE1	2.53	0.43
14:T:136:SER:HB3	14:T:154:LEU:HD11	2.00	0.43
20:C:190:GLY:HA3	20:C:317:PHE:HB3	2.00	0.43
21:U:218:GLN:O	21:U:221:ILE:HG13	2.18	0.43
21:U:630:PRO:HG2	21:U:663:THR:HG21	2.00	0.43
25:Y:293:ARG:HH22	31:e:53:SER:HA	1.84	0.43
26:Z:54:PHE:HB2	26:Z:78:MET:SD	2.58	0.43
26:Z:144:VAL:HG12	26:Z:145:HIS:N	2.30	0.43
27:a:293:PHE:HB3	27:a:329:LYS:O	2.18	0.43
29:c:128:ASN:O	29:c:131:GLN:NE2	2.51	0.43
32:f:255:LEU:O	32:f:259:LEU:CB	2.67	0.43
32:f:327:GLY:O	32:f:331:ALA:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:400:PRO:HG3	32:f:441:TYR:CE1	2.53	0.43
2:H:34:PRO:HA	2:H:163:MET:O	2.18	0.43
3:I:143:TYR:HB2	3:I:146:GLN:NE2	2.33	0.43
4:J:119:THR:OG1	5:K:135:ARG:NH2	2.49	0.43
6:L:175:HIS:HB3	6:L:179:PHE:CE2	2.53	0.43
8:N:21:THR:HA	8:N:27:ALA:H	1.83	0.43
10:P:45:MET:HE3	10:P:71:LEU:HD22	2.00	0.43
11:Q:9:GLY:HA3	11:Q:12:TYR:CZ	2.53	0.43
12:R:160:ILE:O	12:R:164:THR:HG23	2.19	0.43
13:S:46:LEU:HB3	13:S:72:LEU:HD11	2.00	0.43
13:S:111:GLY:HA2	13:S:120:ALA:O	2.17	0.43
16:B:203:LEU:HB3	16:B:204:PRO:HD3	2.01	0.43
16:B:309:MET:O	16:B:312:LEU:HB3	2.17	0.43
17:D:146:GLU:CD	17:D:253:LEU:HB3	2.43	0.43
21:U:707:ASN:O	21:U:711:GLN:HG2	2.17	0.43
22:V:27:PRO:O	22:V:30:PRO:HD2	2.18	0.43
22:V:30:PRO:HA	22:V:33:GLN:HB2	2.00	0.43
23:W:324:TYR:O	23:W:327:GLU:HG2	2.18	0.43
25:Y:377:LEU:O	25:Y:381:GLN:HG3	2.17	0.43
26:Z:118:ASN:N	26:Z:118:ASN:OD1	2.50	0.43
26:Z:182:THR:H	26:Z:183:THR:HA	1.84	0.43
29:c:161:ARG:NH1	29:c:162:LEU:O	2.51	0.43
29:c:273:LYS:HB2	29:c:277:LYS:HE2	2.01	0.43
30:d:52:ARG:HG2	30:d:81:TYR:CD2	2.53	0.43
30:d:213:ARG:C	30:d:215:TRP:HB3	2.43	0.43
32:f:194:LEU:HB3	32:f:195:GLU:H	1.41	0.43
32:f:320:LEU:HD21	32:f:693:VAL:HG23	2.00	0.43
32:f:350:LYS:HZ2	32:f:357:GLY:HA2	1.84	0.43
32:f:449:LYS:O	32:f:453:LEU:HG	2.18	0.43
32:f:560:PRO:HB3	32:f:598:ASN:ND2	2.32	0.43
16:B:162:VAL:O	16:B:163:LEU:HD12	2.18	0.43
17:D:96:VAL:HG23	17:D:97:ASP:OD1	2.18	0.43
17:D:218:ALA:C	17:D:222:HIS:HD1	2.25	0.43
17:D:277:ALA:C	17:D:280:GLY:H	2.25	0.43
17:D:387:VAL:HG21	18:E:159:PHE:CE2	2.54	0.43
20:C:295:THR:HB	20:C:300:ILE:HD11	2.01	0.43
20:C:328:ILE:HD12	20:C:328:ILE:HA	1.84	0.43
22:V:79:VAL:HG12	22:V:161:PRO:HB2	2.01	0.43
22:V:82:LEU:C	22:V:84:LYS:H	2.27	0.43
23:W:87:ILE:O	23:W:88:MET:HB2	2.19	0.43
23:W:122:LEU:HA	23:W:125:ILE:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:328:LEU:HD11	23:W:341:PHE:CE2	2.53	0.43
30:d:192:THR:O	30:d:196:ARG:HG3	2.17	0.43
3:I:143:TYR:HB2	3:I:146:GLN:HE21	1.83	0.43
4:J:68:ASN:HA	4:J:211:MET:HE1	2.00	0.43
4:J:75:GLY:HA3	4:J:129:ILE:HG22	1.99	0.43
5:K:173:ALA:O	5:K:177:ALA:N	2.52	0.43
6:L:4:ASN:HB3	15:A:327:LEU:HD11	2.01	0.43
9:O:161:ALA:O	9:O:165:ASN:ND2	2.38	0.43
9:O:218:PRO:HA	10:P:194:LYS:HA	2.01	0.43
13:S:123:SER:O	13:S:130:TYR:HA	2.18	0.43
15:A:158:ASP:HB3	15:A:162:THR:HG23	2.00	0.43
18:E:126:ASP:HB2	18:E:185:ARG:HG2	2.00	0.43
18:E:331:ILE:HD11	18:E:368:MET:HG2	1.99	0.43
20:C:82:LYS:HE2	20:C:84:LYS:HD3	2.00	0.43
20:C:321:ASN:OD1	20:C:322:GLU:N	2.52	0.43
21:U:710:ARG:HA	21:U:713:TYR:HD2	1.83	0.43
22:V:263:LEU:C	22:V:265:ASP:H	2.26	0.43
22:V:487:HIS:NE2	26:Z:267:ARG:HD3	2.32	0.43
25:Y:14:ASN:HD21	25:Y:214:MET:HA	1.84	0.43
27:a:173:TYR:HE2	27:a:216:LEU:HD22	1.84	0.43
29:c:36:LEU:HD11	29:c:71:ASP:HA	2.00	0.43
29:c:275:VAL:HG13	29:c:276:GLY:H	1.82	0.43
29:c:275:VAL:HG13	29:c:276:GLY:N	2.34	0.43
32:f:22:ARG:HA	32:f:25:LEU:HD12	2.00	0.43
32:f:109:LEU:HA	32:f:110:ALA:HB3	2.00	0.43
32:f:245:ASP:O	32:f:249:LEU:HG	2.18	0.43
32:f:610:THR:HG23	32:f:611:HIS:CD2	2.53	0.43
3:I:237:ILE:O	3:I:241:GLU:HG3	2.18	0.43
11:Q:177:THR:HA	11:Q:194:ILE:O	2.19	0.43
13:S:122:TYR:HE1	13:S:132:ARG:HB2	1.83	0.43
15:A:328:ASP:HB3	15:A:329:PRO:HD3	2.01	0.43
16:B:105:THR:HG21	20:C:120:SER:HA	1.99	0.43
16:B:313:LEU:O	16:B:317:ASP:N	2.51	0.43
16:B:393:ALA:HB2	33:B:501:ATP:H4'	2.00	0.43
20:C:175:PHE:CD2	20:C:182:GLN:HG3	2.53	0.43
20:C:229:ARG:NH2	20:C:232:ARG:HB2	2.33	0.43
22:V:363:LEU:HA	22:V:378:VAL:HG11	1.99	0.43
22:V:433:ASP:OD1	22:V:433:ASP:N	2.50	0.43
23:W:440:ASN:O	23:W:443:THR:OG1	2.18	0.43
25:Y:57:LEU:HD11	25:Y:62:ASP:HA	2.00	0.43
27:a:259:PRO:C	27:a:261:LEU:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:172:HIS:C	29:c:174:PRO:HD3	2.44	0.43
30:d:147:SER:OG	30:d:150:LYS:N	2.51	0.43
31:e:41:ASP:CG	31:e:42:ASN:H	2.23	0.43
5:K:50:VAL:HG11	5:K:66:LYS:HB3	2.01	0.43
7:M:113:ASP:O	7:M:117:MET:HG2	2.18	0.43
15:A:226:ALA:HB2	16:B:319:PHE:HE1	1.83	0.43
17:D:235:PHE:O	17:D:246:MET:HE1	2.18	0.43
20:C:209:CYS:HB3	20:C:243:PRO:HG2	1.99	0.43
20:C:297:ARG:CG	20:C:298:ILE:H	2.31	0.43
21:U:250:PHE:HZ	21:U:333:MET:SD	2.42	0.43
22:V:286:ALA:HB2	22:V:315:LYS:HD3	2.00	0.43
23:W:55:ARG:NH1	23:W:75:TYR:O	2.52	0.43
23:W:90:LEU:HA	23:W:94:ARG:HD2	2.01	0.43
32:f:383:ILE:HD11	32:f:390:GLU:CD	2.43	0.43
32:f:483:ALA:HB3	32:f:484:PRO:HD3	2.00	0.43
1:G:189:TRP:CE3	1:G:193:GLN:HG3	2.53	0.43
2:H:14:SER:OG	2:H:18:LYS:N	2.51	0.43
3:I:219:GLU:H	3:I:223:THR:HA	1.84	0.43
5:K:36:THR:HA	5:K:171:GLY:HA3	2.01	0.43
7:M:215:TRP:CZ3	7:M:219:LEU:HB3	2.53	0.43
10:P:44:PRO:HA	10:P:50:TYR:CD1	2.50	0.43
10:P:54:ALA:HB3	10:P:106:GLU:HB2	1.99	0.43
10:P:141:THR:OG1	10:P:142:CYS:N	2.52	0.43
11:Q:161:ARG:HH12	11:Q:194:ILE:HD12	1.83	0.43
17:D:205:TYR:HD2	17:D:332:GLU:OE1	2.02	0.43
20:C:139:MET:HE1	20:C:213:ARG:HB2	2.01	0.43
21:U:92:ASP:HA	21:U:97:VAL:HG21	2.01	0.43
22:V:80:LYS:HA	22:V:81:GLN:HB2	2.00	0.43
22:V:239:THR:HA	22:V:240:LEU:HA	1.73	0.43
32:f:470:LYS:HG3	32:f:473:LYS:HE3	2.00	0.43
1:G:43:ARG:HD2	1:G:149:PRO:O	2.19	0.43
1:G:152:TYR:CD1	1:G:162:GLY:HA3	2.54	0.43
4:J:221:ASN:C	4:J:223:GLU:H	2.25	0.43
5:K:10:ARG:O	5:K:12:VAL:N	2.52	0.43
5:K:195:ILE:O	5:K:198:SER:OG	2.34	0.43
6:L:65:HIS:CD2	6:L:221:PHE:HD2	2.33	0.43
7:M:137:LEU:O	7:M:148:LEU:HD12	2.18	0.43
8:N:53:GLN:OE1	9:O:118:SER:HA	2.18	0.43
15:A:220:THR:HB	33:A:501:ATP:C8	2.53	0.43
15:A:246:VAL:HG21	16:B:307:ARG:HH21	1.82	0.43
15:A:322:ASN:OD1	15:A:428:ARG:HD2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:178:LYS:HB2	20:C:283:PHE:HA	2.01	0.43
16:B:383:LEU:C	16:B:387:LYS:HZ3	2.27	0.43
19:F:238:ARG:NH1	19:F:250:LYS:HG2	2.29	0.43
20:C:11:LEU:HD13	21:U:144:ASP:HB3	2.00	0.43
20:C:254:ILE:HA	20:C:257:SER:HB3	1.99	0.43
21:U:356:THR:HG22	21:U:717:ILE:HG21	2.01	0.43
21:U:611:ASN:HB3	21:U:614:VAL:CG1	2.44	0.43
23:W:219:THR:HA	23:W:220:GLU:HB3	2.00	0.43
25:Y:143:TYR:HA	25:Y:146:ARG:HG2	2.01	0.43
25:Y:328:GLU:O	25:Y:331:ASP:HB3	2.18	0.43
29:c:33:ILE:HD11	29:c:207:TYR:CD1	2.54	0.43
3:I:68:LEU:HD22	3:I:90:LEU:HD22	2.00	0.43
3:I:148:TYR:HA	3:I:158:GLY:CA	2.48	0.43
3:I:196:VAL:HG12	3:I:197:LEU:HD12	2.00	0.43
9:O:163:ILE:HG12	9:O:170:GLY:HA2	2.00	0.43
12:R:8:PHE:CE1	12:R:13:ILE:HG12	2.47	0.43
14:T:192:VAL:HG12	14:T:197:VAL:HG22	2.01	0.43
17:D:122:GLU:HG2	17:D:123:LEU:N	2.34	0.43
17:D:220:ALA:HA	17:D:227:PHE:CZ	2.54	0.43
18:E:364:GLN:HA	18:E:367:PHE:HB2	2.01	0.43
19:F:215:LEU:HB2	19:F:217:ILE:HG12	2.01	0.43
21:U:172:ASP:HA	21:U:173:VAL:HB	2.00	0.43
32:f:123:PHE:HD1	32:f:134:GLN:HG3	1.84	0.43
32:f:164:ASN:N	32:f:164:ASN:OD1	2.52	0.43
32:f:462:ASP:OD2	32:f:464:LYS:HB3	2.18	0.43
32:f:537:LEU:HA	32:f:537:LEU:HD23	1.81	0.43
1:G:18:PRO:HA	2:H:24:TYR:CE1	2.53	0.42
1:G:208:ILE:HB	1:G:210:PHE:HD1	1.84	0.42
3:I:204:SER:C	3:I:206:LEU:H	2.27	0.42
11:Q:71:ASN:HB3	11:Q:73:TYR:CE2	2.54	0.42
12:R:164:THR:HG21	12:R:192:VAL:HG21	2.01	0.42
15:A:299:MET:O	15:A:302:LEU:HB3	2.18	0.42
20:C:142:LYS:HD2	20:C:142:LYS:HA	1.90	0.42
22:V:171:VAL:O	22:V:175:MET:HG3	2.19	0.42
22:V:299:GLN:HG3	30:d:113:ALA:HB1	2.00	0.42
24:X:142:ARG:HD3	24:X:145:GLU:HG3	1.99	0.42
24:X:360:ASP:HA	24:X:363:ARG:NE	2.33	0.42
25:Y:173:ASP:O	25:Y:177:ARG:NH2	2.42	0.42
26:Z:37:GLY:HA3	26:Z:95:TYR:CZ	2.54	0.42
26:Z:63:LYS:H	26:Z:64:ASP:HB2	1.83	0.42
27:a:333:MET:HE2	27:a:333:MET:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:278:GLN:HB2	29:c:279:ASP:O	2.19	0.42
30:d:60:GLN:O	30:d:64:LEU:HB2	2.19	0.42
32:f:123:PHE:CE2	32:f:127:LYS:HD3	2.54	0.42
1:G:10:ASP:OD1	1:G:10:ASP:N	2.51	0.42
1:G:38:THR:HA	1:G:172:GLN:NE2	2.34	0.42
4:J:130:SER:OG	4:J:149:PRO:HD3	2.19	0.42
7:M:99:ARG:HB3	14:T:69:GLN:HE22	1.84	0.42
14:T:24:ALA:HB1	14:T:41:ARG:NH1	2.34	0.42
15:A:74:PRO:HB2	15:A:75:PRO:HD3	2.00	0.42
15:A:313:GLY:C	15:A:315:ILE:H	2.26	0.42
17:D:109:SER:HA	20:C:91:PRO:HG2	2.00	0.42
19:F:234:THR:OG1	33:F:501:ATP:O1G	2.36	0.42
21:U:12:LEU:HB2	21:U:44:LYS:HE3	2.02	0.42
22:V:368:ARG:HH22	31:e:47:ASN:HD21	1.66	0.42
24:X:398:GLU:O	24:X:402:GLU:HG3	2.19	0.42
26:Z:8:LYS:HG3	26:Z:47:VAL:HG23	2.00	0.42
32:f:660:TYR:HB2	32:f:662:LEU:C	2.44	0.42
6:L:200:PRO:HB2	6:L:203:GLN:OE1	2.19	0.42
16:B:170:LEU:HD21	16:B:270:LEU:HG	2.01	0.42
16:B:246:THR:O	16:B:281:ILE:N	2.47	0.42
16:B:334:ILE:HD12	16:B:337:LEU:HD12	2.00	0.42
17:D:62:LYS:O	17:D:66:LYS:HG3	2.20	0.42
17:D:83:GLN:HG3	17:D:133:HIS:CD2	2.54	0.42
17:D:325:GLY:N	17:D:328:ASP:OD1	2.47	0.42
20:C:171:HIS:HB3	20:C:174:LEU:CD2	2.50	0.42
21:U:127:ASP:O	21:U:131:GLU:HG2	2.19	0.42
23:W:70:VAL:O	23:W:73:MET:HG2	2.18	0.42
23:W:449:GLU:O	23:W:453:HIS:ND1	2.44	0.42
24:X:74:ARG:HH22	24:X:116:TRP:HB2	1.84	0.42
25:Y:42:MET:HE3	25:Y:46:ARG:HH12	1.84	0.42
25:Y:210:SER:HB3	25:Y:213:LEU:CB	2.49	0.42
25:Y:232:GLU:O	25:Y:236:LEU:N	2.43	0.42
26:Z:120:VAL:HG23	26:Z:138:TYR:O	2.19	0.42
26:Z:134:PRO:HG3	29:c:220:LEU:CD1	2.49	0.42
29:c:152:LYS:HG3	29:c:153:GLY:N	2.32	0.42
32:f:379:ILE:CG2	32:f:399:LEU:HD11	2.49	0.42
1:G:189:TRP:CH2	1:G:197:THR:HG21	2.54	0.42
3:I:135:LEU:HD11	3:I:162:THR:HG21	2.01	0.42
4:J:148:ASP:HB3	4:J:152:THR:H	1.84	0.42
4:J:187:THR:O	4:J:190:LEU:HB3	2.19	0.42
6:L:136:GLY:O	6:L:142:PRO:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:N:119:MET:SD	14:T:6:VAL:HG21	2.59	0.42
11:Q:160:LEU:O	11:Q:164:LEU:HD13	2.18	0.42
15:A:98:CYS:HB3	16:B:130:GLU:HB2	2.02	0.42
15:A:344:SER:N	15:A:345:LEU:HB3	2.34	0.42
17:D:185:LEU:HB2	17:D:306:LYS:HZ1	1.84	0.42
17:D:259:PRO:HA	17:D:304:ASN:ND2	2.34	0.42
18:E:143:ARG:O	18:E:147:GLU:HG3	2.19	0.42
18:E:317:ALA:O	18:E:320:ILE:HG22	2.18	0.42
19:F:85:THR:HA	19:F:86:LEU:HA	1.60	0.42
19:F:224:LEU:HD22	19:F:348:LEU:HD13	2.00	0.42
21:U:82:LEU:O	21:U:129:ARG:NE	2.52	0.42
22:V:254:LEU:HG	22:V:258:TYR:HD2	1.84	0.42
26:Z:181:ASP:HA	26:Z:182:THR:HA	1.65	0.42
27:a:34:TRP:CH2	27:a:67:PHE:HE1	2.38	0.42
27:a:139:GLU:HA	27:a:142:LEU:HB3	2.01	0.42
28:b:5:SER:HB3	28:b:64:LEU:HD21	2.02	0.42
29:c:55:GLY:HA3	29:c:112:TYR:CZ	2.55	0.42
31:e:1:MET:HB3	31:e:3:GLU:H	1.84	0.42
32:f:6:GLU:HG2	32:f:8:ALA:H	1.83	0.42
32:f:180:ILE:HG13	32:f:181:MET:H	1.84	0.42
32:f:334:ASN:C	32:f:336:GLU:HB2	2.45	0.42
1:G:49:VAL:O	1:G:50:ILE:HD13	2.19	0.42
9:O:137:VAL:HG13	9:O:141:LYS:HD2	2.02	0.42
11:Q:3:TYR:OH	11:Q:130:ALA:O	2.29	0.42
16:B:217:LYS:C	16:B:219:PRO:HD3	2.44	0.42
16:B:351:ILE:O	16:B:351:ILE:HD12	2.19	0.42
16:B:409:GLU:OE1	16:B:411:ARG:NE	2.44	0.42
20:C:109:THR:HG23	20:C:112:CYS:SG	2.59	0.42
20:C:193:GLY:HA3	20:C:317:PHE:HE2	1.85	0.42
23:W:192:LEU:O	23:W:196:VAL:HG23	2.20	0.42
25:Y:85:ASP:HA	25:Y:88:LEU:CD2	2.50	0.42
26:Z:210:SER:HB2	26:Z:214:LYS:HZ3	1.83	0.42
27:a:112:ILE:HD13	27:a:151:VAL:HG21	2.02	0.42
29:c:53:VAL:HG22	29:c:114:SER:HB2	2.01	0.42
30:d:184:LYS:HA	30:d:185:ALA:HA	1.74	0.42
32:f:245:ASP:O	32:f:248:MET:HG2	2.20	0.42
32:f:510:GLU:C	32:f:512:ALA:N	2.78	0.42
32:f:586:LEU:HD13	32:f:607:GLN:OE1	2.20	0.42
2:H:124:SER:HA	3:I:127:LYS:NZ	2.34	0.42
3:I:180:LYS:HB2	3:I:183:GLU:OE1	2.18	0.42
3:I:245:ALA:O	3:I:249:ARG:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:231:LYS:C	5:K:233:GLU:H	2.26	0.42
6:L:189:LYS:HA	6:L:192:LEU:HG	2.00	0.42
7:M:34:SER:HA	7:M:167:LYS:HZ3	1.84	0.42
11:Q:115:LEU:O	11:Q:126:LYS:HD2	2.19	0.42
15:A:253:GLY:O	15:A:257:VAL:HG12	2.19	0.42
17:D:136:SER:HB3	20:C:67:GLN:HA	2.01	0.42
18:E:113:ARG:HB3	18:E:221:TYR:OH	2.20	0.42
18:E:387:LYS:HA	18:E:387:LYS:HD2	1.88	0.42
22:V:89:LYS:HD2	22:V:93:PHE:HE2	1.83	0.42
22:V:392:TYR:O	22:V:395:ILE:HG22	2.19	0.42
23:W:127:THR:HA	23:W:130:MET:HG2	2.02	0.42
23:W:441:LYS:HD2	23:W:444:HIS:HE1	1.84	0.42
24:X:117:ALA:HB2	24:X:125:LEU:HD23	2.02	0.42
25:Y:53:TYR:CD1	25:Y:53:TYR:C	2.97	0.42
25:Y:267:ARG:HG3	25:Y:270:VAL:HG12	2.02	0.42
29:c:292:MET:O	29:c:296:ILE:HG13	2.20	0.42
32:f:39:HIS:CG	32:f:40:ASN:H	2.37	0.42
32:f:109:LEU:CG	32:f:141:ARG:HH22	2.33	0.42
32:f:294:SER:HA	32:f:325:GLY:CA	2.49	0.42
32:f:472:LYS:O	32:f:475:LYS:HB3	2.18	0.42
3:I:136:TYR:HB2	3:I:148:TYR:HB2	2.02	0.42
5:K:94:VAL:O	5:K:98:ASN:ND2	2.52	0.42
6:L:41:LYS:HG3	6:L:180:MET:HB3	2.00	0.42
15:A:226:ALA:HB2	16:B:319:PHE:CE1	2.54	0.42
16:B:126:SER:HA	16:B:127:VAL:HA	1.50	0.42
16:B:357:ASP:O	16:B:361:LYS:HG3	2.19	0.42
17:D:130:VAL:HA	17:D:142:VAL:HA	2.02	0.42
17:D:336:PRO:HB2	17:D:341:LYS:NZ	2.34	0.42
21:U:396:ALA:HB1	21:U:400:ALA:CB	2.50	0.42
21:U:772:TRP:HB3	21:U:775:LEU:HG	2.01	0.42
22:V:368:ARG:HH22	31:e:47:ASN:ND2	2.17	0.42
27:a:68:GLU:CD	27:a:71:VAL:HG23	2.44	0.42
30:d:135:HIS:HB3	30:d:136:PRO:HD3	2.00	0.42
32:f:21:GLN:O	32:f:24:PRO:HD2	2.19	0.42
32:f:210:ARG:NE	32:f:212:ASN:HB2	2.35	0.42
32:f:270:ILE:HG23	32:f:271:ASP:H	1.85	0.42
2:H:15:PRO:HA	3:I:23:TYR:CE1	2.54	0.42
2:H:106:PRO:HG2	10:P:78:GLU:OE2	2.20	0.42
3:I:228:LEU:HD13	3:I:233:VAL:CG2	2.50	0.42
5:K:225:ASN:HB2	5:K:226:PHE:CG	2.55	0.42
6:L:39:LYS:HD3	6:L:144:ILE:HG12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:157:ARG:HB3	7:M:59:GLU:OE2	2.19	0.42
13:S:73:LYS:O	13:S:77:HIS:ND1	2.41	0.42
17:D:340:GLN:OE1	17:D:340:GLN:N	2.52	0.42
18:E:83:CYS:SG	18:E:107:ILE:HD13	2.60	0.42
22:V:182:LYS:HB3	22:V:182:LYS:HE3	1.83	0.42
23:W:237:GLU:HG2	23:W:238:GLY:H	1.83	0.42
23:W:317:TRP:CD1	23:W:358:VAL:HG21	2.54	0.42
24:X:243:ASP:OD1	24:X:245:PRO:HD2	2.20	0.42
25:Y:138:LEU:HD12	25:Y:141:VAL:HB	2.01	0.42
25:Y:191:ILE:HD12	25:Y:191:ILE:HA	1.93	0.42
25:Y:286:TRP:O	25:Y:287:LEU:HG	2.19	0.42
26:Z:22:HIS:HA	26:Z:25:ARG:CG	2.48	0.42
27:a:186:LYS:NZ	27:a:221:VAL:HB	2.35	0.42
28:b:30:GLN:HG3	28:b:75:LEU:HD13	2.01	0.42
30:d:55:LEU:HD12	30:d:81:TYR:HE2	1.84	0.42
30:d:233:GLU:H	30:d:234:ASP:HA	1.84	0.42
32:f:21:GLN:O	32:f:25:LEU:HG	2.20	0.42
32:f:228:GLN:O	32:f:232:LEU:HB2	2.20	0.42
32:f:357:GLY:HA2	32:f:360:ALA:HB3	2.01	0.42
32:f:454:LEU:O	32:f:458:SER:CB	2.67	0.42
6:L:119:PRO:HB2	6:L:126:ARG:O	2.20	0.42
7:M:42:LYS:HD3	7:M:182:LYS:O	2.20	0.42
10:P:19:CYS:SG	10:P:160:PRO:HG3	2.59	0.42
11:Q:181:ARG:HD3	11:Q:190:ASP:HA	2.02	0.42
13:S:91:MET:HE2	13:S:91:MET:HB3	1.85	0.42
16:B:364:ILE:HG12	33:B:501:ATP:C6	2.55	0.42
17:D:283:ARG:NH2	20:C:218:GLU:OE1	2.53	0.42
21:U:913:ILE:H	21:U:913:ILE:HG13	1.71	0.42
23:W:434:SER:HA	26:Z:237:LEU:HD22	2.01	0.42
24:X:420:LYS:NZ	26:Z:279:LYS:HD2	2.35	0.42
25:Y:319:MET:HA	25:Y:319:MET:HE2	2.01	0.42
27:a:340:VAL:HG12	27:a:341:LEU:N	2.27	0.42
29:c:163:ILE:HG22	29:c:199:HIS:C	2.44	0.42
29:c:250:GLU:HA	29:c:253:LYS:HD3	2.02	0.42
32:f:109:LEU:HB2	32:f:141:ARG:HH22	1.84	0.42
2:H:171:LYS:HZ2	3:I:55:LEU:HD22	1.84	0.42
7:M:54:LEU:HD12	7:M:57:LEU:HD21	2.02	0.42
13:S:13:LEU:HD13	13:S:137:ALA:HB2	2.01	0.42
15:A:83:ASP:HA	15:A:86:THR:HB	2.01	0.42
16:B:346:ARG:HG3	16:B:349:ARG:H	1.85	0.42
19:F:380:ASN:OD1	19:F:417:HIS:NE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:186:LYS:NZ	22:V:234:ARG:HD3	2.35	0.42
25:Y:215:ASP:OD2	25:Y:218:THR:HG23	2.20	0.42
25:Y:297:ARG:HB3	31:e:52:PHE:HZ	1.85	0.42
30:d:45:LYS:O	30:d:49:ILE:HG12	2.20	0.42
32:f:109:LEU:CB	32:f:141:ARG:HH22	2.33	0.42
32:f:324:PHE:CE2	32:f:328:LEU:HD22	2.55	0.42
32:f:397:ARG:HG2	32:f:433:ASN:HA	2.02	0.42
32:f:575:SER:OG	32:f:612:LEU:HD11	2.19	0.42
32:f:612:LEU:HD22	32:f:660:TYR:OH	2.20	0.42
1:G:116:LYS:HG2	1:G:160:TYR:CD1	2.55	0.41
7:M:149:TYR:HA	7:M:159:GLY:HA3	2.02	0.41
7:M:163:CYS:SG	7:M:164:ALA:N	2.93	0.41
10:P:143:ALA:HA	10:P:146:MET:HE2	2.01	0.41
15:A:329:PRO:O	15:A:333:ARG:HG2	2.21	0.41
15:A:410:LEU:HA	15:A:413:VAL:HB	2.02	0.41
16:B:205:LEU:CD2	16:B:206:THR:N	2.81	0.41
16:B:298:ASN:OD1	16:B:298:ASN:N	2.53	0.41
17:D:116:LEU:HB2	17:D:139:LEU:O	2.19	0.41
20:C:275:GLU:HA	20:C:278:ASN:HB2	2.01	0.41
21:U:383:ASP:OD2	21:U:387:ARG:NH2	2.53	0.41
21:U:612:ASP:HB3	21:U:647:HIS:CG	2.55	0.41
22:V:449:ALA:HB1	22:V:459:GLN:O	2.18	0.41
23:W:121:LYS:HG3	23:W:122:LEU:HD12	2.02	0.41
32:f:345:VAL:HG13	32:f:360:ALA:HB2	2.01	0.41
32:f:458:SER:O	32:f:459:GLU:HB2	2.19	0.41
32:f:600:LEU:H	32:f:600:LEU:CD1	2.33	0.41
32:f:617:LEU:N	32:f:618:THR:C	2.78	0.41
6:L:49:LEU:HD21	6:L:199:LEU:HD21	2.01	0.41
6:L:60:GLN:HG2	19:F:439:ALA:HB1	2.01	0.41
10:P:25:ASP:OD1	10:P:25:ASP:N	2.50	0.41
11:Q:59:TYR:O	11:Q:63:ASN:ND2	2.36	0.41
12:R:6:PHE:HA	12:R:124:ALA:O	2.20	0.41
12:R:196:HIS:O	12:R:200:SER:OG	2.27	0.41
14:T:1:THR:N	14:T:105:PRO:O	2.47	0.41
15:A:97:ARG:HB3	16:B:131:HIS:CD2	2.55	0.41
16:B:177:GLU:N	16:B:178:LYS:HA	2.30	0.41
16:B:283:PHE:CZ	16:B:285:ASP:HB2	2.54	0.41
17:D:285:VAL:HA	17:D:288:ILE:HD12	2.02	0.41
17:D:389:GLU:CA	17:D:390:ASN:HB2	2.50	0.41
18:E:111:LEU:HD11	18:E:114:GLU:HG2	2.00	0.41
18:E:172:LEU:CD2	18:E:299:ILE:HB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:C:312:ASP:OD1	20:C:313:ARG:N	2.50	0.41
21:U:682:TYR:HB3	21:U:725:MET:SD	2.59	0.41
21:U:766:PHE:CD1	21:U:776:SER:HA	2.54	0.41
24:X:221:GLU:HB3	24:X:223:LYS:HG2	2.02	0.41
25:Y:51:ALA:HA	25:Y:54:TYR:HD2	1.84	0.41
25:Y:182:VAL:HG11	25:Y:213:LEU:HD22	2.02	0.41
26:Z:241:SER:HB3	26:Z:245:PHE:HB3	2.02	0.41
27:a:35:HIS:HE1	28:b:17:ARG:HB2	1.86	0.41
28:b:116:PRO:HA	28:b:146:GLU:HG3	2.01	0.41
31:e:59:GLU:HB3	31:e:63:HIS:HE1	1.83	0.41
32:f:431:PHE:HB2	32:f:464:LYS:HE2	2.02	0.41
32:f:615:GLY:HA2	32:f:618:THR:O	2.20	0.41
2:H:4:ARG:HH21	7:M:127:ALA:HB2	1.85	0.41
6:L:82:ARG:HA	6:L:85:CYS:HB3	2.03	0.41
12:R:18:SER:OG	12:R:173:ALA:N	2.37	0.41
15:A:383:ALA:HB3	16:B:343:ARG:NH1	2.26	0.41
15:A:429:TYR:HA	15:A:432:TYR:CE2	2.55	0.41
16:B:122:ILE:HA	16:B:131:HIS:O	2.20	0.41
16:B:140:ASP:OD1	16:B:143:LEU:HB3	2.19	0.41
17:D:143:LEU:CD1	17:D:146:GLU:HA	2.51	0.41
17:D:191:TYR:CE2	17:D:198:PRO:HB3	2.55	0.41
17:D:252:ARG:HA	17:D:255:LYS:HE3	2.02	0.41
17:D:258:ALA:HA	17:D:259:PRO:C	2.45	0.41
17:D:313:ARG:HH22	18:E:242:ARG:HG3	1.85	0.41
17:D:384:MET:O	17:D:387:VAL:HG12	2.21	0.41
18:E:204:VAL:HG11	19:F:308:ARG:HH22	1.85	0.41
20:C:147:THR:OG1	20:C:148:TYR:N	2.54	0.41
20:C:193:GLY:H	20:C:355:SER:HB2	1.85	0.41
21:U:388:ASP:OD1	21:U:389:ASN:N	2.48	0.41
25:Y:210:SER:HB3	25:Y:213:LEU:HG	2.02	0.41
29:c:75:MET:HE3	29:c:76:PRO:HD2	2.02	0.41
32:f:241:TYR:CG	32:f:244:LYS:HE3	2.55	0.41
32:f:350:LYS:HB3	32:f:352:SER:O	2.20	0.41
1:G:80:MET:SD	1:G:138:MET:HA	2.61	0.41
3:I:3:ARG:HH11	5:K:11:GLY:H	1.68	0.41
5:K:167:ALA:H	6:L:56:LEU:HD13	1.85	0.41
8:N:11:GLY:HA2	8:N:103:TRP:HD1	1.85	0.41
10:P:58:THR:O	11:Q:85:ARG:NH2	2.53	0.41
10:P:73:LEU:O	10:P:77:LYS:HG3	2.20	0.41
11:Q:2:GLU:HB2	11:Q:18:ASP:OD2	2.20	0.41
16:B:261:GLY:HA3	16:B:263:GLY:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:E:281:ARG:HD3	18:E:387:LYS:CE	2.50	0.41
19:F:154:ASN:O	19:F:157:SER:OG	2.29	0.41
21:U:364:VAL:HG12	21:U:728:PHE:CD1	2.55	0.41
21:U:567:ILE:HD11	21:U:585:THR:HB	2.03	0.41
22:V:98:LEU:HA	22:V:99:ARG:HA	1.68	0.41
22:V:269:LYS:HB3	22:V:273:LYS:NZ	2.36	0.41
22:V:279:GLN:HB2	22:V:285:TRP:CG	2.55	0.41
23:W:436:MET:O	23:W:440:ASN:ND2	2.46	0.41
26:Z:201:LEU:HD11	27:a:364:GLU:HB3	2.02	0.41
27:a:112:ILE:H	27:a:112:ILE:HG13	1.69	0.41
27:a:337:GLN:HE21	27:a:339:ARG:NH1	2.18	0.41
27:a:342:ASP:O	27:a:346:ILE:HD12	2.20	0.41
28:b:48:ASN:OD1	28:b:48:ASN:N	2.52	0.41
30:d:226:ALA:HA	30:d:227:SER:HA	1.66	0.41
32:f:84:PRO:HA	32:f:87:SER:HB2	2.02	0.41
32:f:109:LEU:HG	32:f:141:ARG:HH22	1.85	0.41
32:f:537:LEU:HD22	32:f:669:ARG:CZ	2.49	0.41
5:K:104:ASN:ND2	13:S:130:TYR:OH	2.54	0.41
6:L:62:LYS:HD2	6:L:74:ILE:O	2.20	0.41
8:N:35:THR:HG21	8:N:56:ALA:HB1	2.02	0.41
14:T:136:SER:HB2	14:T:150:LEU:HD13	2.02	0.41
15:A:307:ASP:OD1	15:A:336:ARG:HD2	2.21	0.41
16:B:125:THR:HG22	16:B:129:SER:OG	2.20	0.41
16:B:139:VAL:HB	16:B:141:LYS:N	2.35	0.41
16:B:286:GLU:N	16:B:330:ALA:O	2.54	0.41
17:D:133:HIS:HB3	17:D:136:SER:OG	2.21	0.41
17:D:201:GLY:O	17:D:329:ARG:HB2	2.20	0.41
33:E:401:ATP:H4'	19:F:344:ARG:HE	1.85	0.41
21:U:444:TYR:CE1	21:U:479:LEU:HD23	2.55	0.41
22:V:80:LYS:HG3	22:V:87:SER:HA	2.01	0.41
22:V:99:ARG:HG3	22:V:143:ALA:O	2.20	0.41
22:V:372:LEU:HD13	22:V:426:LEU:O	2.20	0.41
23:W:435:LEU:HD22	29:c:239:LYS:NZ	2.36	0.41
24:X:332:GLU:HA	24:X:335:LEU:HB2	2.02	0.41
24:X:371:ASP:C	24:X:373:LYS:H	2.28	0.41
25:Y:221:THR:O	25:Y:224:VAL:HG12	2.20	0.41
25:Y:330:ILE:HA	25:Y:333:GLU:HB3	2.02	0.41
27:a:148:VAL:C	27:a:150:SER:H	2.28	0.41
27:a:270:ARG:HH22	27:a:274:LEU:N	2.18	0.41
29:c:121:TRP:HB3	29:c:192:LEU:HD21	2.02	0.41
32:f:445:GLY:H	32:f:476:LYS:CG	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:543:PRO:O	32:f:547:ILE:HG12	2.21	0.41
4:J:95:ARG:HH22	4:J:101:PRO:HA	1.86	0.41
5:K:225:ASN:HA	5:K:226:PHE:HA	1.78	0.41
9:O:216:ILE:HG23	10:P:194:LYS:HD2	2.02	0.41
16:B:265:LYS:HA	16:B:268:ARG:HB2	2.02	0.41
16:B:319:PHE:HA	16:B:320:ASP:HA	1.60	0.41
17:D:238:LYS:NZ	18:E:75:ASN:HA	2.36	0.41
17:D:346:SER:O	17:D:349:THR:HG22	2.20	0.41
18:E:85:ARG:HH22	29:c:46:ARG:CG	2.33	0.41
19:F:137:ILE:HB	19:F:138:GLY:C	2.45	0.41
19:F:295:ARG:HB3	19:F:296:PHE:H	1.55	0.41
20:C:118:ASN:OD1	20:C:118:ASN:N	2.41	0.41
20:C:167:LEU:HB3	20:C:168:PRO:HD3	2.01	0.41
20:C:334:ARG:O	25:Y:174:TRP:N	2.54	0.41
21:U:844:LYS:HE3	21:U:844:LYS:HB3	1.93	0.41
23:W:55:ARG:NH1	23:W:79:GLU:HG3	2.31	0.41
23:W:254:PRO:HA	23:W:257:GLN:HB2	2.03	0.41
24:X:126:ARG:HH22	24:X:156:GLU:HG3	1.85	0.41
24:X:331:LEU:HD23	24:X:364:LYS:HG2	2.02	0.41
27:a:33:LEU:HD12	27:a:33:LEU:O	2.21	0.41
30:d:242:LEU:O	30:d:246:VAL:HG23	2.21	0.41
32:f:52:ILE:CG1	32:f:64:GLU:HG2	2.51	0.41
32:f:62:ILE:O	32:f:66:ALA:N	2.53	0.41
32:f:89:LEU:HD11	32:f:126:CYS:SG	2.60	0.41
4:J:143:ARG:O	4:J:143:ARG:HG3	2.21	0.41
15:A:91:GLN:HB2	15:A:92:PRO:HD3	2.02	0.41
15:A:115:VAL:HG13	15:A:117:GLN:H	1.86	0.41
15:A:427:PRO:HA	15:A:429:TYR:CZ	2.55	0.41
18:E:109:ARG:NH1	19:F:133:PHE:HE2	2.18	0.41
18:E:275:MET:HE2	18:E:275:MET:HB3	1.93	0.41
20:C:117:ARG:O	20:C:121:TYR:HA	2.20	0.41
20:C:147:THR:HG21	25:Y:133:ALA:HB2	2.03	0.41
21:U:500:ASN:HA	21:U:503:GLN:HG2	2.02	0.41
21:U:740:GLY:HA3	21:U:744:VAL:HG22	2.01	0.41
22:V:160:LEU:HD22	22:V:213:TYR:CD2	2.56	0.41
25:Y:221:THR:HA	25:Y:224:VAL:HG12	2.03	0.41
26:Z:77:ASN:O	26:Z:81:MET:HG3	2.20	0.41
27:a:77:VAL:HA	27:a:80:ILE:HG22	2.01	0.41
29:c:65:TYR:HD1	29:c:66:THR:HG23	1.85	0.41
30:d:69:PRO:HA	30:d:72:GLU:HG2	2.02	0.41
32:f:33:VAL:CG2	32:f:34:PRO:HD3	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:73:TYR:HD2	32:f:74:LEU:HD12	1.85	0.41
1:G:88:ARG:NH2	7:M:157:SER:O	2.53	0.41
5:K:225:ASN:OD1	5:K:225:ASN:N	2.54	0.41
6:L:40:SER:HA	6:L:180:MET:SD	2.60	0.41
9:O:1:THR:HG23	9:O:33:LYS:HE3	2.03	0.41
10:P:53:LEU:HD13	10:P:60:VAL:HA	2.03	0.41
14:T:99:ARG:CG	14:T:105:PRO:HA	2.42	0.41
16:B:294:ARG:HB3	20:C:264:GLY:C	2.46	0.41
17:D:47:LEU:HD12	20:C:25:LEU:HB3	2.02	0.41
17:D:326:ARG:HH21	20:C:141:GLU:CG	2.33	0.41
19:F:235:LEU:HD13	33:F:501:ATP:H3'	2.02	0.41
20:C:143:VAL:HG22	20:C:144:PRO:O	2.21	0.41
20:C:187:LEU:HA	20:C:293:MET:HB2	2.01	0.41
21:U:208:LEU:HD23	21:U:210:LYS:N	2.36	0.41
22:V:31:ALA:O	22:V:35:VAL:HG22	2.21	0.41
22:V:100:MET:O	22:V:104:THR:HG23	2.20	0.41
22:V:194:LYS:O	22:V:195:ILE:HD13	2.21	0.41
22:V:360:TYR:O	22:V:363:LEU:HB3	2.20	0.41
25:Y:297:ARG:O	25:Y:301:ILE:HG22	2.20	0.41
27:a:320:VAL:HG21	27:a:333:MET:SD	2.61	0.41
30:d:134:LYS:HA	30:d:137:VAL:HG22	2.02	0.41
32:f:192:THR:OG1	32:f:194:LEU:HD22	2.21	0.41
32:f:246:HIS:HA	32:f:249:LEU:HB2	2.03	0.41
1:G:15:ILE:HD12	2:H:21:GLN:NE2	2.36	0.41
3:I:149:GLN:HB3	3:I:157:GLY:O	2.21	0.41
4:J:65:LEU:CD2	4:J:88:ARG:HG2	2.50	0.41
5:K:101:PHE:CE2	12:R:61:ARG:HB2	2.56	0.41
7:M:34:SER:HA	7:M:167:LYS:NZ	2.36	0.41
8:N:3:ILE:HD12	8:N:44:CYS:SG	2.60	0.41
10:P:44:PRO:HB3	10:P:50:TYR:HE1	1.85	0.41
12:R:114:VAL:HA	12:R:119:ASN:O	2.21	0.41
15:A:178:GLY:HA3	33:A:501:ATP:N1	2.36	0.41
15:A:283:ALA:HA	15:A:284:ARG:HA	1.68	0.41
15:A:330:ALA:HA	15:A:333:ARG:HE	1.86	0.41
15:A:409:PHE:O	15:A:413:VAL:HG23	2.19	0.41
16:B:186:ASP:O	16:B:367:ILE:HG21	2.20	0.41
16:B:207:HIS:CE1	16:B:210:TYR:HD2	2.39	0.41
17:D:143:LEU:HB3	17:D:252:ARG:HH22	1.86	0.41
17:D:371:SER:HA	17:D:372:GLY:HA3	1.72	0.41
19:F:295:ARG:NH2	19:F:300:LYS:O	2.54	0.41
19:F:339:ASP:OD2	19:F:341:ALA:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:F:391:PHE:HA	19:F:395:GLN:OE1	2.20	0.41
20:C:157:GLN:NE2	20:C:318:PRO:HD3	2.35	0.41
20:C:165:ILE:O	20:C:168:PRO:HD2	2.20	0.41
20:C:171:HIS:N	20:C:172:PRO:HD3	2.35	0.41
20:C:192:PRO:HA	20:C:193:GLY:HA3	1.82	0.41
20:C:229:ARG:C	20:C:231:VAL:H	2.29	0.41
22:V:186:LYS:HZ3	22:V:234:ARG:HD3	1.85	0.41
22:V:276:PHE:HA	22:V:277:PRO:HD3	1.86	0.41
23:W:200:ILE:O	23:W:204:ILE:HG12	2.21	0.41
23:W:397:VAL:HG11	24:X:341:PRO:HB3	2.03	0.41
24:X:344:ARG:HA	24:X:385:LEU:O	2.21	0.41
25:Y:275:LEU:HD23	25:Y:275:LEU:O	2.21	0.41
26:Z:84:LYS:HE3	29:c:76:PRO:HG3	2.01	0.41
26:Z:190:ARG:O	26:Z:193:ASN:HB2	2.20	0.41
27:a:70:ARG:HA	27:a:70:ARG:HD2	1.97	0.41
29:c:156:VAL:CG1	29:c:157:ILE:H	2.30	0.41
30:d:39:THR:HG23	30:d:86:LYS:HE3	2.03	0.41
30:d:190:LEU:HD23	30:d:191:PHE:N	2.36	0.41
30:d:193:GLU:HA	30:d:196:ARG:HH11	1.86	0.41
32:f:88:ALA:O	32:f:92:CYS:HB3	2.21	0.41
32:f:123:PHE:HA	32:f:126:CYS:SG	2.61	0.41
32:f:289:CYS:HA	32:f:647:VAL:HG21	2.02	0.41
32:f:316:ASN:HB3	32:f:317:THR:H	1.56	0.41
32:f:429:ARG:O	32:f:433:ASN:HB2	2.21	0.41
32:f:468:GLU:HA	32:f:471:ASP:HB2	2.03	0.41
4:J:38:ARG:NH2	4:J:182:GLU:O	2.27	0.41
13:S:168:LEU:O	13:S:172:MET:HG2	2.21	0.41
14:T:85:PRO:HB2	14:T:121:PHE:CD2	2.56	0.41
17:D:384:MET:HE2	18:E:167:PRO:HG3	2.03	0.41
19:F:370:SER:HB3	19:F:400:CYS:SG	2.60	0.41
20:C:42:LEU:HA	20:C:45:LEU:HD13	2.03	0.41
22:V:156:SER:O	22:V:160:LEU:HG	2.21	0.41
27:a:96:PHE:O	27:a:100:THR:HG23	2.20	0.41
29:c:245:VAL:HG22	29:c:248:MET:SD	2.61	0.41
32:f:153:GLU:H	32:f:153:GLU:CD	2.28	0.41
32:f:438:VAL:HG22	32:f:472:LYS:HD3	2.03	0.41
32:f:516:PHE:CE1	32:f:534:ALA:HB3	2.54	0.41
32:f:604:ARG:HH11	32:f:645:LEU:HD13	1.86	0.41
3:I:93:ILE:HA	3:I:96:ARG:HG2	2.01	0.40
7:M:56:LYS:HB3	7:M:57:LEU:C	2.45	0.40
18:E:219:PHE:HA	18:E:222:ALA:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:C:283:PHE:CD2	20:C:284:GLU:HG2	2.56	0.40
21:U:230:SER:HA	21:U:268:LEU:HD11	2.04	0.40
21:U:712:LEU:O	21:U:716:VAL:HG22	2.21	0.40
23:W:86:ASN:CB	23:W:88:MET:HG3	2.51	0.40
23:W:335:SER:OG	23:W:336:PRO:HD3	2.21	0.40
26:Z:41:GLY:HA3	26:Z:92:VAL:HB	2.02	0.40
26:Z:221:PRO:CD	26:Z:222:ILE:HA	2.51	0.40
27:a:341:LEU:HD23	27:a:346:ILE:HG13	2.03	0.40
31:e:6:GLN:N	31:e:7:PRO:HD2	2.36	0.40
32:f:39:HIS:CG	32:f:40:ASN:N	2.88	0.40
32:f:54:GLN:HA	32:f:57:MET:HG2	2.03	0.40
32:f:219:ASN:OD1	32:f:223:ASN:ND2	2.54	0.40
32:f:638:LEU:HA	32:f:639:THR:C	2.46	0.40
1:G:72:ILE:HG12	1:G:78:CYS:SG	2.60	0.40
3:I:239:LYS:NZ	3:I:243:GLU:OE2	2.54	0.40
7:M:40:ARG:NH1	7:M:148:LEU:HB3	2.31	0.40
9:O:76:VAL:HG23	9:O:104:ASP:OD1	2.21	0.40
15:A:290:GLY:H	19:F:295:ARG:HD3	1.87	0.40
15:A:296:GLN:O	15:A:300:LEU:HB2	2.21	0.40
16:B:176:VAL:HA	16:B:177:GLU:HA	1.76	0.40
17:D:164:TYR:HB3	17:D:218:ALA:HB1	2.02	0.40
17:D:315:ASP:OD1	17:D:315:ASP:N	2.54	0.40
18:E:281:ARG:HG3	18:E:283:ASP:OD1	2.20	0.40
18:E:312:ILE:O	18:E:315:ILE:HG13	2.21	0.40
19:F:225:MET:HE3	19:F:354:PHE:CE2	2.57	0.40
19:F:389:ASP:C	19:F:391:PHE:H	2.30	0.40
20:C:163:GLU:O	20:C:167:LEU:HB2	2.20	0.40
20:C:213:ARG:NH2	20:C:249:ASP:HB2	2.36	0.40
21:U:264:VAL:HG22	21:U:268:LEU:HD22	2.02	0.40
21:U:366:HIS:ND1	21:U:396:ALA:HA	2.36	0.40
22:V:63:SER:O	22:V:66:GLU:HB3	2.21	0.40
22:V:275:VAL:N	22:V:276:PHE:HA	2.32	0.40
23:W:268:LYS:HE2	23:W:301:LYS:HE2	2.03	0.40
25:Y:80:GLU:HA	25:Y:83:ARG:HG2	2.02	0.40
26:Z:68:TRP:CE3	26:Z:108:ILE:HG13	2.57	0.40
26:Z:190:ARG:HH22	27:a:374:ILE:HG13	1.86	0.40
29:c:71:ASP:HB2	29:c:104:ARG:NH1	2.35	0.40
32:f:95:GLY:HA2	32:f:98:ARG:HE	1.86	0.40
32:f:211:MET:SD	32:f:240:LEU:HB3	2.61	0.40
32:f:571:GLY:HA2	32:f:605:LEU:HD21	2.03	0.40
2:H:46:LEU:HD13	2:H:75:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:107:CYS:HB2	3:I:146:GLN:OE1	2.20	0.40
4:J:80:ALA:O	4:J:84:ILE:HG13	2.20	0.40
6:L:166:GLN:NE2	6:L:169:ARG:HD2	2.36	0.40
11:Q:19:ARG:NH2	11:Q:31:ASP:O	2.54	0.40
14:T:67:LEU:HD21	14:T:91:TRP:CZ3	2.57	0.40
15:A:95:VAL:HG12	15:A:144:ARG:NH1	2.36	0.40
17:D:406:VAL:HA	17:D:407:ILE:HA	1.80	0.40
18:E:128:GLY:HA3	18:E:131:SER:OG	2.22	0.40
19:F:124:ILE:HD12	19:F:124:ILE:HA	1.96	0.40
19:F:146:LYS:HB2	19:F:147:PRO:HD2	2.04	0.40
19:F:193:LYS:HE3	19:F:193:LYS:HB2	1.80	0.40
19:F:321:GLN:HG3	19:F:322:PRO:HD3	2.02	0.40
21:U:554:LEU:HD23	21:U:554:LEU:C	2.46	0.40
21:U:680:VAL:HB	21:U:683:VAL:HG12	2.04	0.40
23:W:268:LYS:HA	23:W:271:VAL:HG12	2.04	0.40
24:X:53:LEU:O	24:X:57:LEU:HG	2.21	0.40
24:X:391:PRO:HG2	24:X:392:PRO:HD3	2.03	0.40
26:Z:263:ALA:O	26:Z:267:ARG:HG2	2.22	0.40
28:b:53:THR:HG22	28:b:59:GLU:O	2.21	0.40
29:c:213:GLU:HA	29:c:216:MET:HG2	2.03	0.40
32:f:29:VAL:HG12	32:f:33:VAL:HG13	2.03	0.40
32:f:231:LEU:HG	32:f:249:LEU:HD22	2.02	0.40
32:f:524:GLU:HB2	32:f:525:PRO:HD2	2.03	0.40
32:f:563:SER:O	32:f:567:ILE:HG22	2.21	0.40
32:f:680:PRO:O	32:f:683:VAL:N	2.55	0.40
4:J:145:TYR:CE1	4:J:155:ALA:HB2	2.56	0.40
13:S:68:ILE:HD11	13:S:92:LEU:HD13	2.03	0.40
17:D:89:ILE:HB	18:E:78:ARG:HB2	2.03	0.40
17:D:96:VAL:HG22	17:D:101:ALA:HA	2.02	0.40
17:D:119:ILE:HG12	17:D:122:GLU:OE2	2.22	0.40
18:E:92:LEU:HD23	18:E:92:LEU:HA	1.93	0.40
21:U:401:LYS:HB2	21:U:401:LYS:HE2	1.71	0.40
22:V:193:GLN:O	22:V:194:LYS:HB2	2.21	0.40
22:V:363:LEU:O	22:V:367:VAL:HG23	2.20	0.40
26:Z:96:HIS:CE1	26:Z:123:ILE:HG12	2.57	0.40
26:Z:266:ILE:O	26:Z:270:VAL:HG23	2.21	0.40
27:a:252:LYS:HD3	27:a:252:LYS:HA	1.75	0.40
27:a:287:ASN:HA	27:a:288:HIS:C	2.47	0.40
28:b:54:LEU:HD12	28:b:55:ALA:N	2.37	0.40
29:c:41:MET:HE1	29:c:112:TYR:CG	2.56	0.40
32:f:51:GLU:O	32:f:55:VAL:HG22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:89:LEU:O	32:f:89:LEU:HD12	2.21	0.40
32:f:323:ILE:O	32:f:326:LEU:HB3	2.22	0.40
32:f:587:ARG:C	32:f:589:LEU:H	2.29	0.40
2:H:42:ASN:O	2:H:144:PRO:HG3	2.21	0.40
3:I:17:ARG:HD2	3:I:22:GLU:HG3	2.02	0.40
3:I:97:TYR:CG	3:I:105:ILE:HD13	2.57	0.40
3:I:125:GLY:HA2	4:J:3:TYR:CG	2.57	0.40
6:L:135:ALA:HA	6:L:143:HIS:O	2.20	0.40
7:M:67:PHE:HB2	7:M:75:MET:HB2	2.03	0.40
8:N:36:PRO:HA	8:N:42:PHE:CE1	2.56	0.40
17:D:391:ARG:HH21	17:D:395:LEU:HG	1.87	0.40
18:E:208:ILE:C	18:E:210:GLU:H	2.30	0.40
21:U:57:ARG:HG3	21:U:58:GLN:N	2.35	0.40
21:U:397:THR:OG1	21:U:398:ASN:N	2.54	0.40
22:V:275:VAL:HB	22:V:277:PRO:CD	2.52	0.40
22:V:494:MET:HG3	26:Z:278:ASN:ND2	2.27	0.40
23:W:243:ILE:HB	23:W:247:TYR:CD1	2.57	0.40
25:Y:233:ARG:HB3	25:Y:234:PRO:HD3	2.04	0.40
27:a:245:VAL:HG22	27:a:247:ARG:N	2.36	0.40
30:d:175:ARG:HA	30:d:178:ILE:HD13	2.02	0.40
30:d:214:GLY:CA	30:d:215:TRP:HB3	2.51	0.40
32:f:115:ASP:O	32:f:119:VAL:HG22	2.22	0.40
32:f:383:ILE:HD13	32:f:395:TYR:CE2	2.57	0.40
32:f:647:VAL:O	32:f:650:ILE:HG13	2.21	0.40
32:f:648:ARG:HH22	32:f:692:ASP:CG	2.29	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	G	238/245 (97%)	223 (94%)	13 (6%)	2 (1%)	16 52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	230/233 (99%)	216 (94%)	14 (6%)	0	100	100
3	I	248/260 (95%)	230 (93%)	17 (7%)	1 (0%)	30	66
4	J	237/247 (96%)	223 (94%)	12 (5%)	2 (1%)	16	52
5	K	224/240 (93%)	204 (91%)	16 (7%)	4 (2%)	6	33
6	L	236/268 (88%)	218 (92%)	18 (8%)	0	100	100
7	M	238/254 (94%)	219 (92%)	18 (8%)	1 (0%)	30	66
8	N	189/238 (79%)	182 (96%)	7 (4%)	0	100	100
9	O	218/276 (79%)	212 (97%)	6 (3%)	0	100	100
10	P	202/204 (99%)	192 (95%)	10 (5%)	0	100	100
11	Q	197/201 (98%)	185 (94%)	12 (6%)	0	100	100
12	R	199/262 (76%)	191 (96%)	8 (4%)	0	100	100
13	S	211/240 (88%)	203 (96%)	8 (4%)	0	100	100
14	T	213/263 (81%)	207 (97%)	6 (3%)	0	100	100
15	A	359/433 (83%)	317 (88%)	37 (10%)	5 (1%)	9	39
16	B	339/440 (77%)	308 (91%)	27 (8%)	4 (1%)	10	42
17	D	378/418 (90%)	339 (90%)	32 (8%)	7 (2%)	6	32
18	E	351/403 (87%)	321 (92%)	27 (8%)	3 (1%)	14	49
19	F	362/439 (82%)	326 (90%)	33 (9%)	3 (1%)	16	52
20	C	382/398 (96%)	337 (88%)	42 (11%)	3 (1%)	16	52
21	U	798/953 (84%)	762 (96%)	34 (4%)	2 (0%)	36	71
22	V	478/533 (90%)	431 (90%)	39 (8%)	8 (2%)	7	35
23	W	454/456 (100%)	412 (91%)	38 (8%)	4 (1%)	14	49
24	X	378/422 (90%)	363 (96%)	15 (4%)	0	100	100
25	Y	376/389 (97%)	341 (91%)	31 (8%)	4 (1%)	11	45
26	Z	284/324 (88%)	257 (90%)	23 (8%)	4 (1%)	9	39
27	a	371/376 (99%)	343 (92%)	23 (6%)	5 (1%)	9	41
28	b	189/377 (50%)	180 (95%)	8 (4%)	1 (0%)	24	62
29	c	285/309 (92%)	253 (89%)	26 (9%)	6 (2%)	5	29
30	d	255/349 (73%)	227 (89%)	25 (10%)	3 (1%)	10	42
31	e	36/70 (51%)	32 (89%)	3 (8%)	1 (3%)	4	24
32	f	686/749 (92%)	571 (83%)	110 (16%)	5 (1%)	18	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9841/11269 (87%)	9025 (92%)	738 (8%)	78 (1%)	18	52

All (78) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	111	VAL
5	K	12	VAL
21	U	364	VAL
23	W	136	ILE
25	Y	350	VAL
29	c	157	ILE
29	c	244	VAL
32	f	62	ILE
32	f	447	VAL
4	J	199	VAL
15	A	159	PRO
15	A	206	ILE
16	B	218	PRO
16	B	263	GLY
17	D	149	SER
17	D	151	ILE
18	E	247	THR
22	V	82	LEU
27	a	340	VAL
32	f	131	VAL
1	G	185	LYS
3	I	108	GLU
17	D	305	VAL
20	C	219	LEU
20	C	298	ILE
22	V	59	ALA
22	V	96	ARG
25	Y	287	LEU
26	Z	144	VAL
27	a	336	VAL
32	f	281	ILE
16	B	230	THR
17	D	170	MET
17	D	374	ASP
19	F	168	TYR
23	W	40	LEU
23	W	138	VAL

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Mol	Chain	Res	Type
25	Y	64	GLN
25	Y	67	VAL
26	Z	33	LYS
28	b	77	THR
29	c	156	VAL
30	d	213	ARG
32	f	435	LEU
5	K	179	SER
7	M	235	ALA
15	A	268	LYS
17	D	155	THR
18	E	208	ILE
19	F	426	GLU
23	W	427	ASP
27	a	69	HIS
27	a	260	ASP
30	d	214	GLY
31	e	4	LYS
18	E	292	PRO
20	C	68	GLU
22	V	54	LYS
22	V	319	HIS
4	J	98	VAL
15	A	345	LEU
29	c	105	PRO
16	B	227	PRO
17	D	125	LYS
19	F	326	VAL
22	V	464	ILE
26	Z	240	VAL
15	A	172	VAL
21	U	134	VAL
22	V	322	VAL
27	a	166	ILE
29	c	151	VAL
5	K	11	GLY
22	V	317	PRO
5	K	89	ILE
29	c	189	ILE
26	Z	221	PRO
30	d	37	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	193/209 (92%)	193 (100%)	0	100	100
2	H	164/190 (86%)	164 (100%)	0	100	100
3	I	193/220 (88%)	193 (100%)	0	100	100
4	J	152/210 (72%)	152 (100%)	0	100	100
5	K	186/202 (92%)	186 (100%)	0	100	100
6	L	198/229 (86%)	197 (100%)	1 (0%)	81	81
7	M	192/211 (91%)	192 (100%)	0	100	100
8	N	148/180 (82%)	148 (100%)	0	100	100
9	O	177/227 (78%)	177 (100%)	0	100	100
10	P	172/173 (99%)	172 (100%)	0	100	100
11	Q	164/171 (96%)	164 (100%)	0	100	100
12	R	153/201 (76%)	153 (100%)	0	100	100
13	S	174/198 (88%)	174 (100%)	0	100	100
14	T	175/214 (82%)	175 (100%)	0	100	100
15	A	308/372 (83%)	308 (100%)	0	100	100
16	B	298/385 (77%)	298 (100%)	0	100	100
17	D	333/366 (91%)	332 (100%)	1 (0%)	86	84
18	E	308/353 (87%)	308 (100%)	0	100	100
19	F	312/379 (82%)	312 (100%)	0	100	100
20	C	332/346 (96%)	332 (100%)	0	100	100
21	U	685/816 (84%)	685 (100%)	0	100	100
22	V	414/459 (90%)	414 (100%)	0	100	100
23	W	416/416 (100%)	416 (100%)	0	100	100
24	X	327/362 (90%)	327 (100%)	0	100	100
25	Y	334/344 (97%)	334 (100%)	0	100	100
26	Z	257/295 (87%)	257 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	a	333/336 (99%)	333 (100%)	0	100	100
28	b	167/312 (54%)	166 (99%)	1 (1%)	78	80
29	c	252/267 (94%)	252 (100%)	0	100	100
30	d	231/293 (79%)	231 (100%)	0	100	100
31	e	38/63 (60%)	38 (100%)	0	100	100
32	f	582/628 (93%)	577 (99%)	5 (1%)	70	76
All	All	8368/9627 (87%)	8360 (100%)	8 (0%)	87	88

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	L	159	MET
17	D	143	LEU
28	b	97	LEU
32	f	89	LEU
32	f	107	LEU
32	f	526	THR
32	f	600	LEU
32	f	637	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	12	HIS
2	H	71	HIS
2	H	88	HIS
2	H	112	GLN
3	I	119	GLN
3	I	142	HIS
4	J	68	ASN
5	K	23	GLN
5	K	98	ASN
6	L	8	ASN
6	L	53	GLN
6	L	117	GLN
8	N	66	HIS
8	N	154	GLN
8	N	158	ASN
10	P	61	GLN

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Mol	Chain	Res	Type
11	Q	24	ASN
12	R	29	GLN
13	S	58	HIS
13	S	159	GLN
13	S	160	ASN
14	T	147	GLN
15	A	94	GLN
15	A	197	HIS
15	A	314	ASN
15	A	379	ASN
16	B	368	HIS
17	D	91	GLN
17	D	158	GLN
17	D	286	GLN
17	D	412	GLN
18	E	51	GLN
18	E	307	GLN
19	F	116	GLN
19	F	194	GLN
19	F	307	GLN
19	F	392	ASN
19	F	428	GLN
20	C	36	ASN
20	C	40	GLN
20	C	53	ASN
20	C	296	ASN
21	U	18	GLN
21	U	70	HIS
21	U	111	GLN
21	U	338	HIS
21	U	355	ASN
21	U	464	GLN
21	U	718	ASN
21	U	805	ASN
21	U	880	ASN
22	V	33	GLN
22	V	279	GLN
22	V	329	HIS
22	V	401	ASN
23	W	257	GLN
23	W	414	ASN
23	W	426	ASN

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Mol	Chain	Res	Type
24	X	405	GLN
26	Z	77	ASN
26	Z	96	HIS
26	Z	225	GLN
26	Z	243	GLN
27	a	18	GLN
27	a	35	HIS
27	a	164	GLN
27	a	227	ASN
27	a	337	GLN
28	b	142	ASN
29	c	92	GLN
29	c	172	HIS
29	c	210	ASN
29	c	214	GLN
29	c	221	HIS
29	c	283	HIS
29	c	298	GLN
30	d	109	GLN
30	d	149	ASN
30	d	245	GLN
31	e	6	GLN
32	f	39	HIS
32	f	40	ASN
32	f	212	ASN
32	f	228	GLN
32	f	237	ASN
32	f	269	GLN
32	f	314	ASN
32	f	316	ASN
32	f	372	ASN
32	f	406	ASN
32	f	491	GLN
32	f	565	ASN
32	f	578	ASN
32	f	588	GLN
32	f	611	HIS
32	f	623	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
33	ATP	A	501	-	32,33,33	1.29	5 (15%)	48,52,52	1.80	13 (27%)
33	ATP	F	501	-	32,33,33	1.34	4 (12%)	48,52,52	1.78	9 (18%)
33	ATP	B	501	-	32,33,33	1.34	5 (15%)	48,52,52	1.76	12 (25%)
33	ATP	E	401	-	32,33,33	1.30	4 (12%)	48,52,52	1.83	10 (20%)
33	ATP	C	501	-	32,33,33	1.33	5 (15%)	48,52,52	1.76	11 (22%)
33	ATP	D	501	-	32,33,33	1.37	5 (15%)	48,52,52	1.75	10 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	ATP	A	501	-	-	1/22/38/38	0/3/3/3
33	ATP	F	501	-	-	4/22/38/38	0/3/3/3
33	ATP	B	501	-	-	0/22/38/38	0/3/3/3
33	ATP	E	401	-	-	3/22/38/38	0/3/3/3
33	ATP	C	501	-	-	2/22/38/38	0/3/3/3
33	ATP	D	501	-	-	3/22/38/38	0/3/3/3

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	E	401	ATP	C5-C4	4.75	1.47	1.39
33	C	501	ATP	C5-C4	4.64	1.47	1.39
33	D	501	ATP	C5-C4	4.59	1.47	1.39
33	F	501	ATP	C5-C4	4.57	1.47	1.39
33	B	501	ATP	C5-C4	4.56	1.47	1.39
33	A	501	ATP	C5-C4	4.54	1.47	1.39
33	D	501	ATP	C5-C6	2.72	1.48	1.41
33	A	501	ATP	C5-C6	2.68	1.48	1.41
33	B	501	ATP	C5-C6	2.65	1.48	1.41
33	C	501	ATP	C5-C6	2.59	1.48	1.41
33	F	501	ATP	C5-C6	2.58	1.48	1.41
33	E	401	ATP	C5-C6	2.57	1.48	1.41
33	C	501	ATP	C5-N7	-2.42	1.34	1.39
33	E	401	ATP	C5-N7	-2.36	1.34	1.39
33	D	501	ATP	C8-N7	2.34	1.36	1.31
33	B	501	ATP	C5-N7	-2.31	1.34	1.39
33	A	501	ATP	C8-N7	2.30	1.36	1.31
33	F	501	ATP	C5-N7	-2.30	1.34	1.39
33	A	501	ATP	C5-N7	-2.24	1.35	1.39
33	B	501	ATP	C8-N7	2.22	1.35	1.31
33	D	501	ATP	C4-N9	-2.20	1.33	1.37
33	D	501	ATP	C5-N7	-2.18	1.35	1.39
33	F	501	ATP	C8-N7	2.18	1.35	1.31
33	B	501	ATP	C4-N9	-2.17	1.33	1.37
33	C	501	ATP	C8-N7	2.16	1.35	1.31
33	E	401	ATP	C8-N7	2.16	1.35	1.31
33	A	501	ATP	C4-N9	-2.11	1.33	1.37
33	C	501	ATP	C4-N9	-2.11	1.33	1.37

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	E	401	ATP	C5-C4-N3	-5.76	118.79	126.72
33	F	501	ATP	C5-C4-N3	-5.46	119.20	126.72
33	B	501	ATP	C5-C4-N3	-5.42	119.25	126.72
33	A	501	ATP	C5-C4-N3	-5.37	119.32	126.72
33	C	501	ATP	C5-C4-N3	-5.36	119.33	126.72
33	D	501	ATP	C5-C4-N3	-5.25	119.48	126.72
33	E	401	ATP	N3-C4-N9	4.84	135.39	127.17
33	F	501	ATP	N3-C4-N9	4.74	135.24	127.17
33	B	501	ATP	N3-C4-N9	4.49	134.80	127.17
33	C	501	ATP	N3-C4-N9	4.47	134.76	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	A	501	ATP	N3-C4-N9	4.44	134.72	127.17
33	D	501	ATP	N3-C4-N9	4.22	134.35	127.17
33	E	401	ATP	C2-N3-C4	3.63	120.70	111.83
33	A	501	ATP	C2-N3-C4	3.61	120.66	111.83
33	B	501	ATP	C2-N3-C4	3.58	120.57	111.83
33	A	501	ATP	N3-C2-N1	-3.54	123.22	128.58
33	F	501	ATP	C2-N3-C4	3.51	120.41	111.83
33	D	501	ATP	C2-N3-C4	3.49	120.36	111.83
33	F	501	ATP	C4-N9-C8	3.49	109.40	105.74
33	C	501	ATP	C2-N3-C4	3.47	120.31	111.83
33	D	501	ATP	C4-C5-N7	-3.46	106.63	110.58
33	E	401	ATP	N3-C2-N1	-3.41	123.42	128.58
33	B	501	ATP	N3-C2-N1	-3.37	123.48	128.58
33	A	501	ATP	C4-C5-N7	-3.33	106.77	110.58
33	B	501	ATP	C4-C5-N7	-3.30	106.81	110.58
33	C	501	ATP	N3-C2-N1	-3.29	123.61	128.58
33	D	501	ATP	N3-C2-N1	-3.29	123.61	128.58
33	A	501	ATP	C4-N9-C8	3.27	109.17	105.74
33	F	501	ATP	N3-C2-N1	-3.26	123.65	128.58
33	C	501	ATP	C4-C5-N7	-3.25	106.86	110.58
33	E	401	ATP	C4-C5-N7	-3.24	106.88	110.58
33	D	501	ATP	C4-N9-C8	3.20	109.09	105.74
33	F	501	ATP	C4-C5-N7	-3.19	106.94	110.58
33	B	501	ATP	C4-N9-C8	3.18	109.07	105.74
33	C	501	ATP	C4-N9-C8	3.05	108.94	105.74
33	E	401	ATP	C4-N9-C8	2.90	108.78	105.74
33	C	501	ATP	C2'-C1'-N9	-2.71	106.57	113.30
33	E	401	ATP	C3'-C2'-C1'	2.69	106.55	101.46
33	F	501	ATP	C5-N7-C8	2.56	107.48	103.45
33	D	501	ATP	C5-N7-C8	2.55	107.46	103.45
33	A	501	ATP	C5-N7-C8	2.51	107.39	103.45
33	E	401	ATP	C5-N7-C8	2.50	107.38	103.45
33	C	501	ATP	C5-N7-C8	2.47	107.34	103.45
33	B	501	ATP	C5-N7-C8	2.45	107.31	103.45
33	A	501	ATP	C3'-C2'-C1'	2.37	105.95	101.46
33	F	501	ATP	N9-C8-N7	-2.34	110.62	113.94
33	D	501	ATP	N9-C8-N7	-2.32	110.65	113.94
33	C	501	ATP	C3'-C2'-C1'	2.28	105.78	101.46
33	A	501	ATP	N9-C8-N7	-2.27	110.71	113.94
33	A	501	ATP	C2-N1-C6	2.24	122.42	118.73
33	B	501	ATP	C3'-C2'-C1'	2.23	105.69	101.46
33	D	501	ATP	C6-C5-N7	2.22	136.38	132.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	B	501	ATP	C2'-C1'-N9	-2.21	107.81	113.30
33	A	501	ATP	C6-C5-N7	2.20	136.34	132.09
33	C	501	ATP	C2-N1-C6	2.20	122.34	118.73
33	E	401	ATP	C2-N1-C6	2.17	122.30	118.73
33	B	501	ATP	N9-C8-N7	-2.16	110.87	113.94
33	C	501	ATP	N9-C8-N7	-2.10	110.95	113.94
33	A	501	ATP	C2'-C1'-N9	-2.10	108.09	113.30
33	B	501	ATP	C6-C5-N7	2.10	136.13	132.09
33	D	501	ATP	C2-N1-C6	2.08	122.15	118.73
33	A	501	ATP	O3G-PG-O2G	2.05	115.50	107.80
33	F	501	ATP	C2-N1-C6	2.04	122.07	118.73
33	B	501	ATP	C2-N1-C6	2.03	122.06	118.73
33	E	401	ATP	O3G-PG-O2G	2.02	115.39	107.80

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
33	A	501	ATP	C5'-O5'-PA-O1A
33	F	501	ATP	C5'-O5'-PA-O3A
33	F	501	ATP	PA-O3A-PB-O2B
33	D	501	ATP	C2'-C1'-N9-C8
33	E	401	ATP	C5'-O5'-PA-O1A
33	E	401	ATP	C5'-O5'-PA-O2A
33	E	401	ATP	C5'-O5'-PA-O3A
33	F	501	ATP	C5'-O5'-PA-O1A
33	D	501	ATP	PB-O3A-PA-O2A
33	C	501	ATP	PB-O3A-PA-O1A
33	D	501	ATP	O4'-C1'-N9-C8
33	F	501	ATP	PA-O3A-PB-O1B
33	C	501	ATP	PB-O3A-PA-O2A

There are no ring outliers.

6 monomers are involved in 16 short contacts:

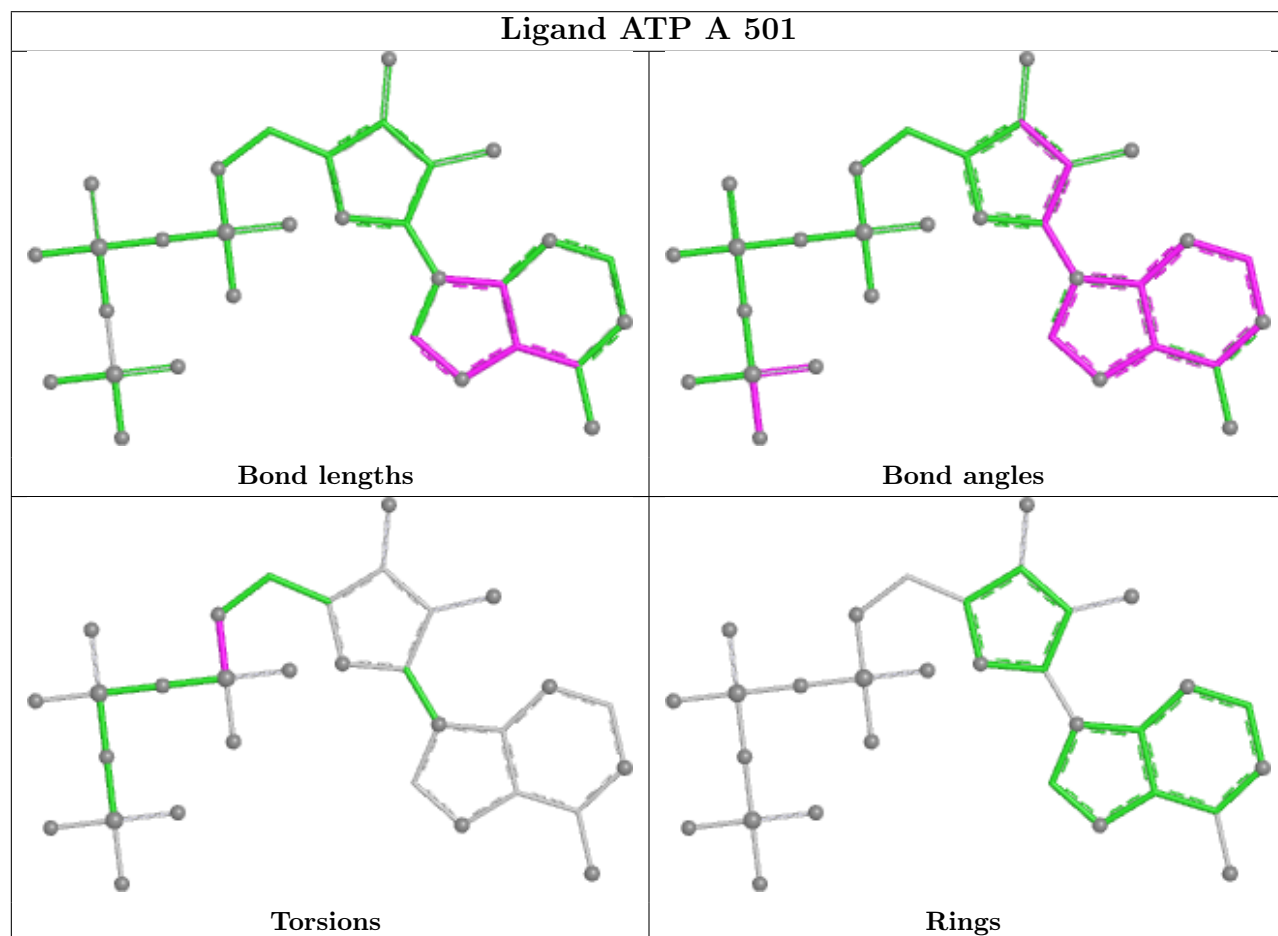
Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	A	501	ATP	2	0
33	F	501	ATP	3	0
33	B	501	ATP	3	0
33	E	401	ATP	4	0
33	C	501	ATP	1	0

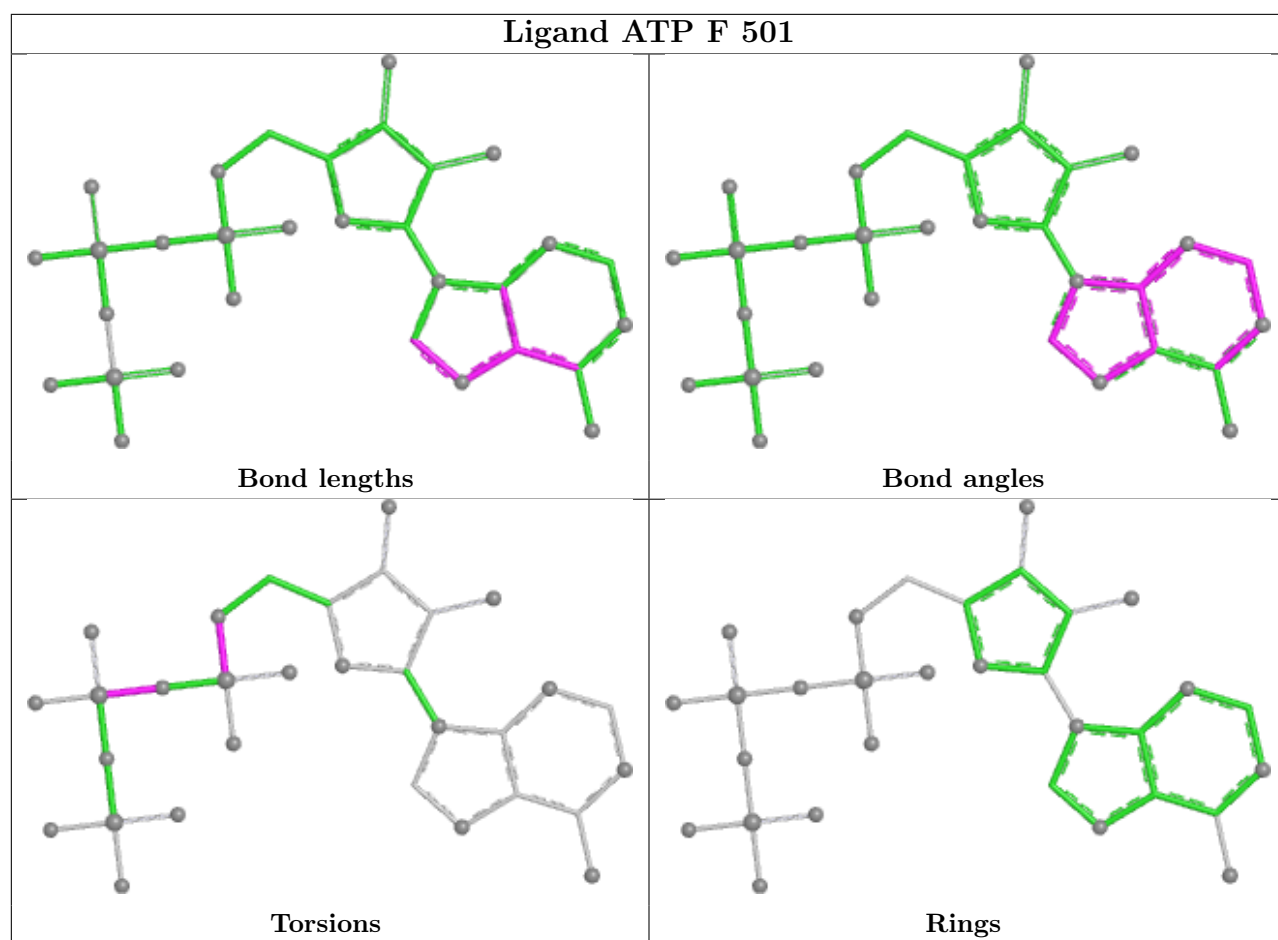
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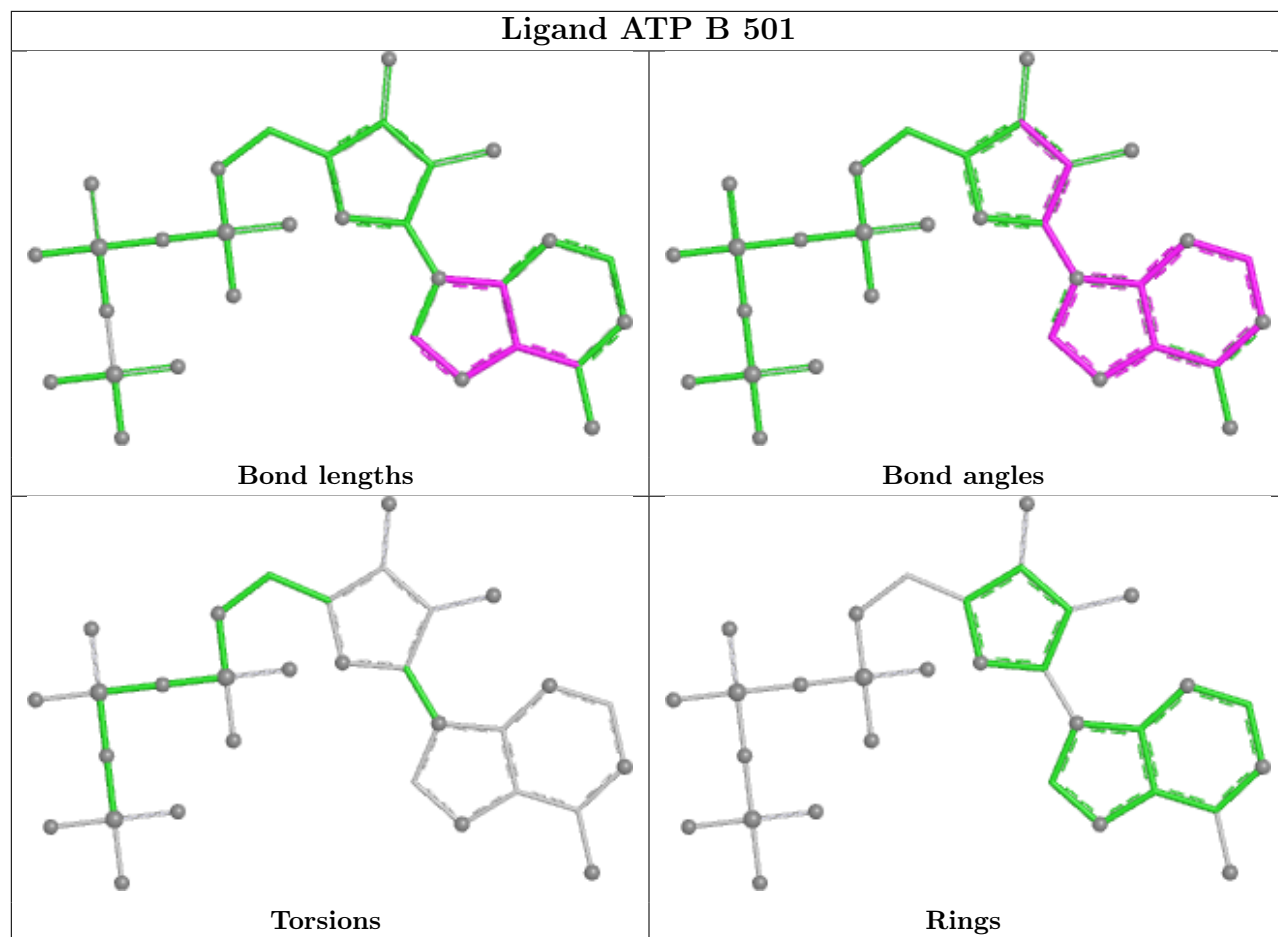
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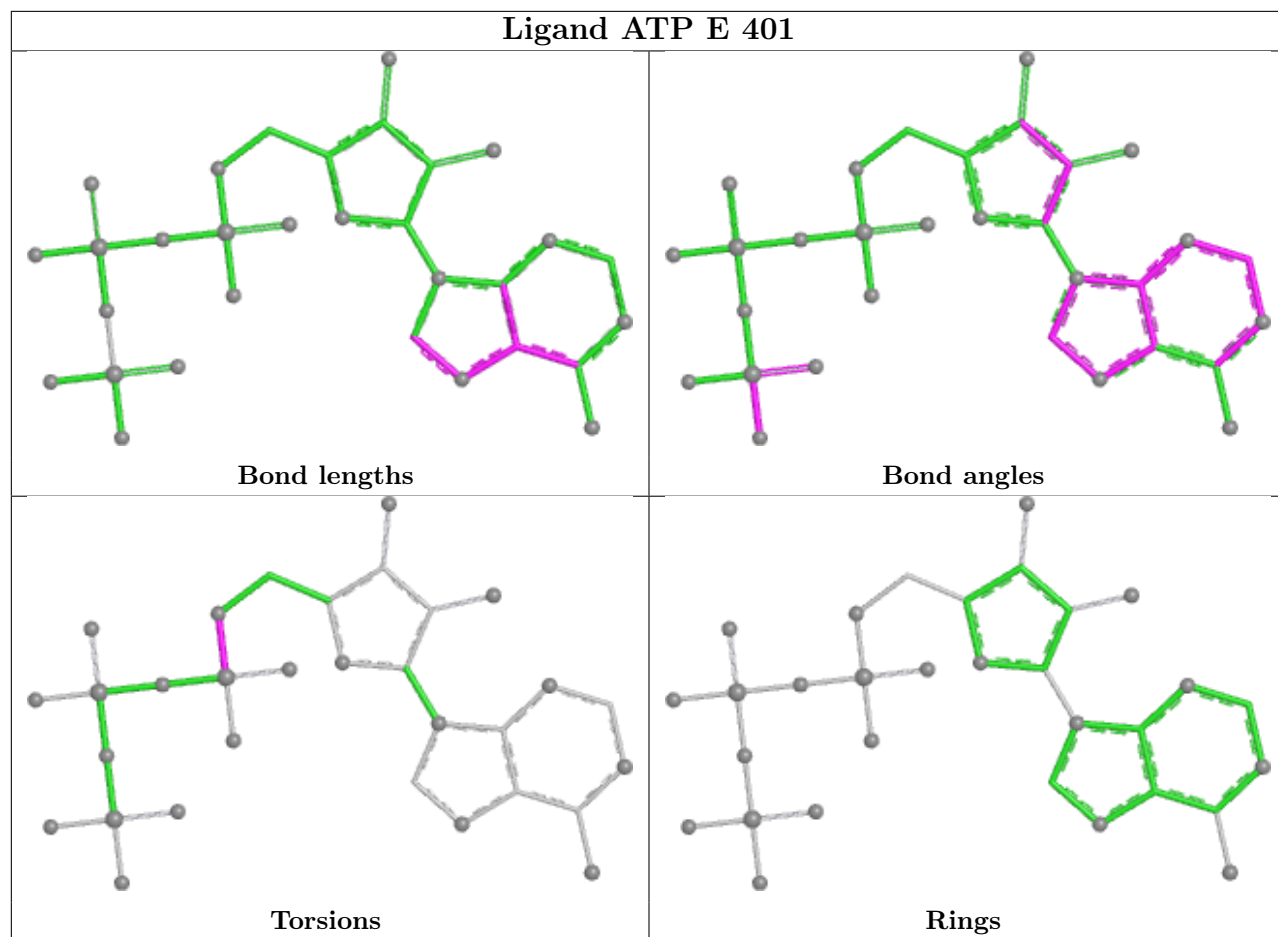
Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	D	501	ATP	3	0

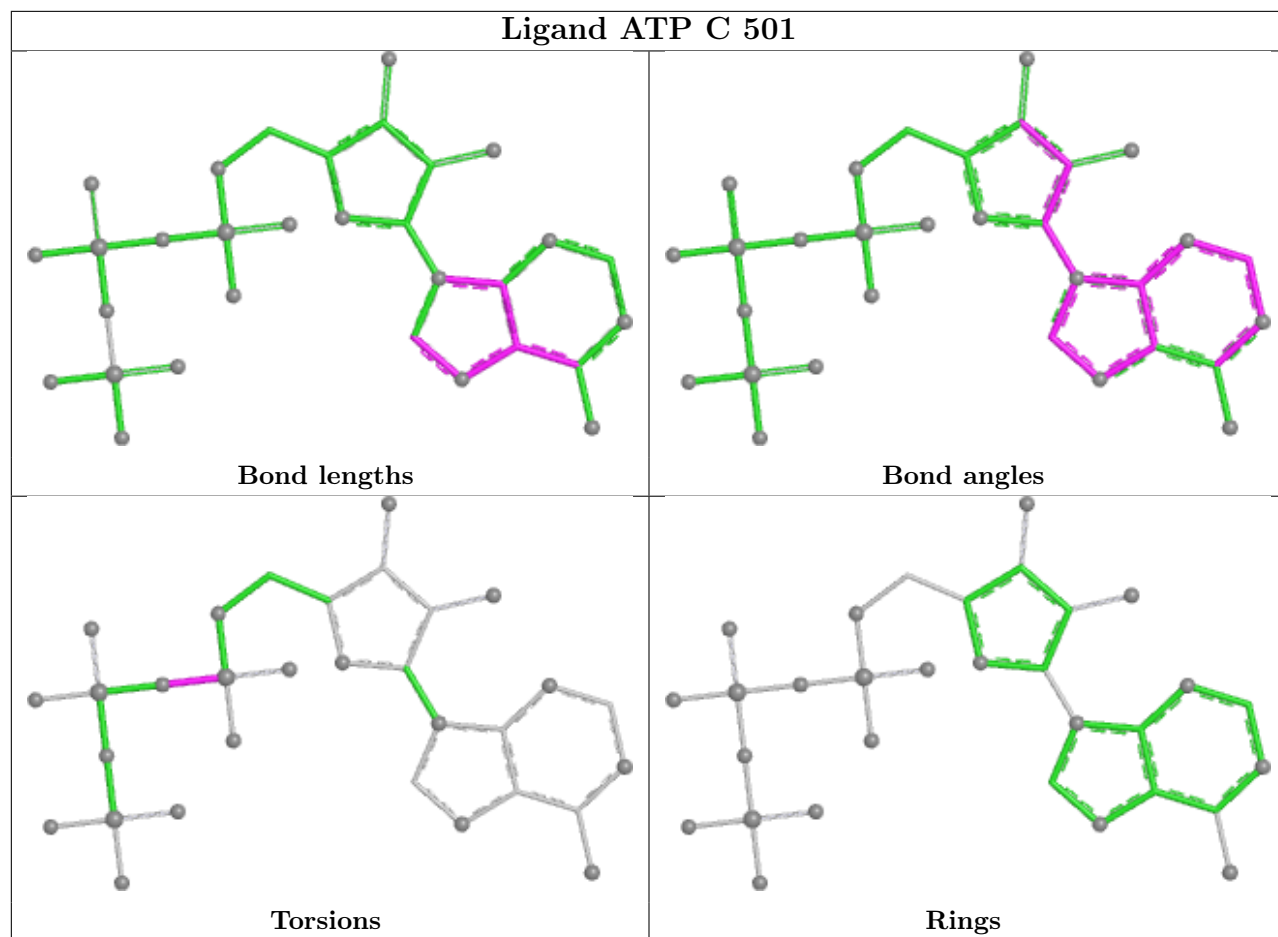
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

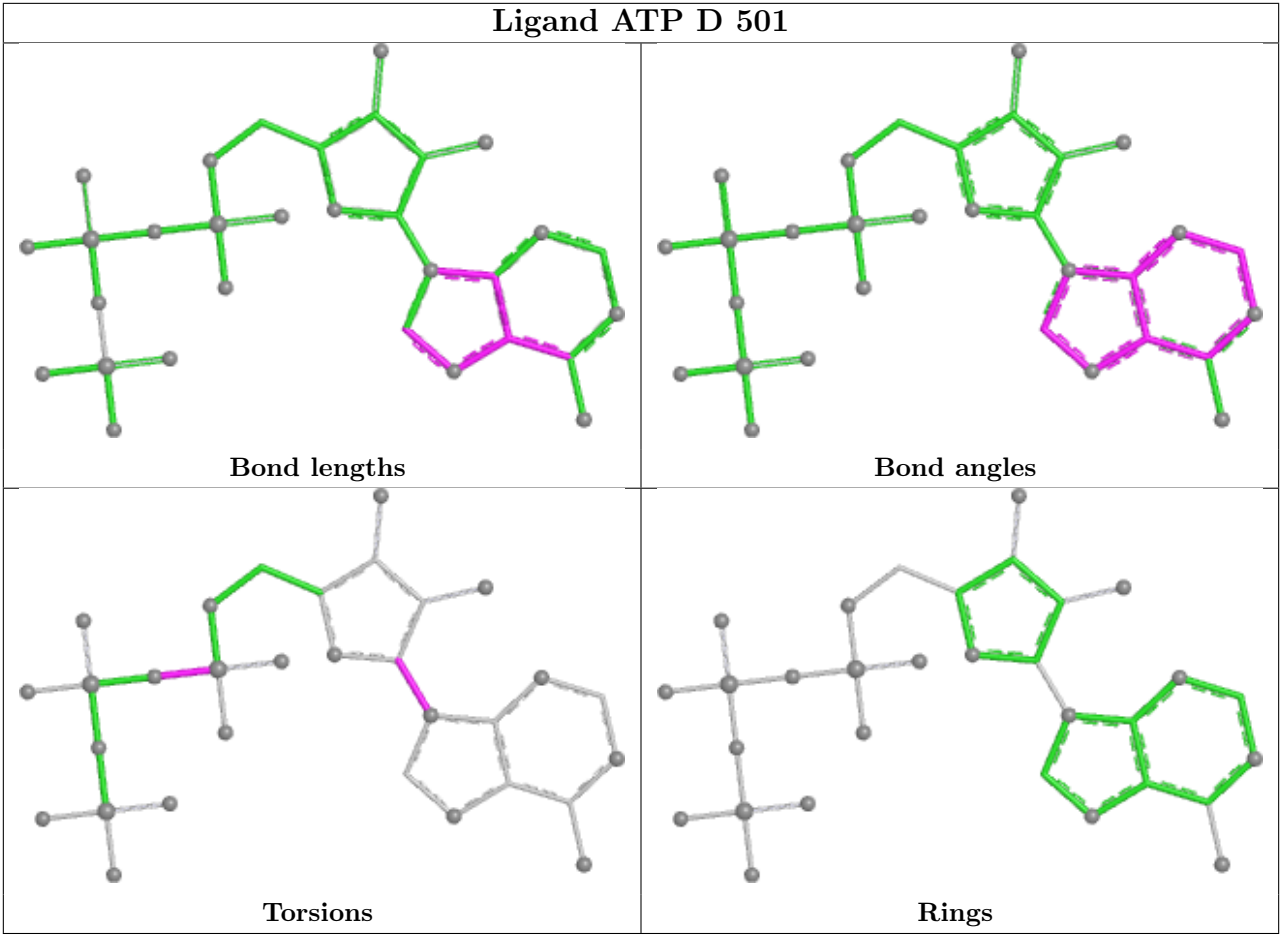












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	f	3
2	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	f	110:ALA	C	111:LEU	N	9.72
1	f	79:ASN	C	80:TYR	N	7.23
1	f	348:ASP	C	349:SER	N	5.88
1	H	2:ALA	C	3:GLU	N	5.52

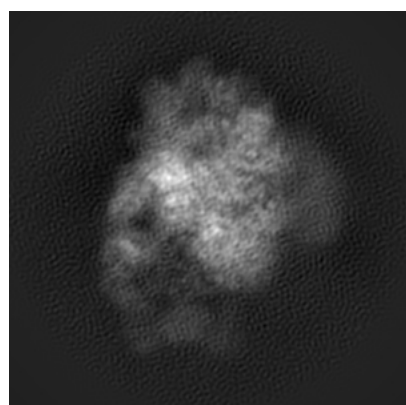
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8334. These allow visual inspection of the internal detail of the map and identification of artifacts.

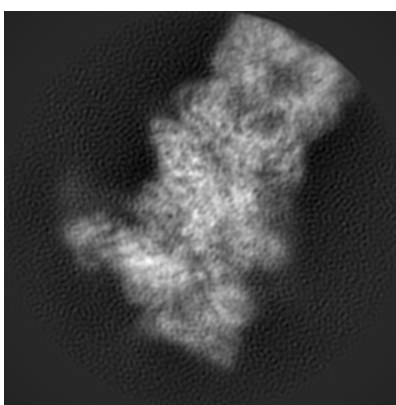
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

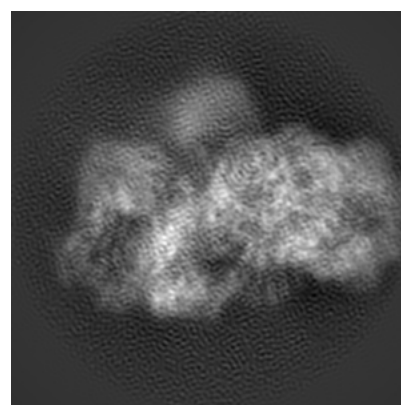
6.1.1 Primary map



X



Y

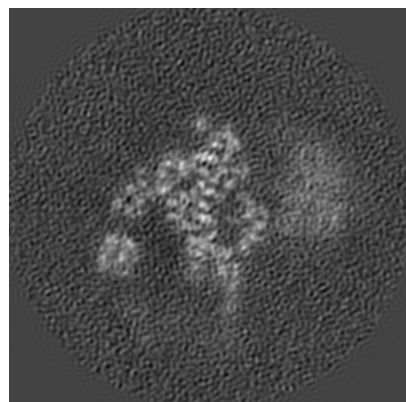


Z

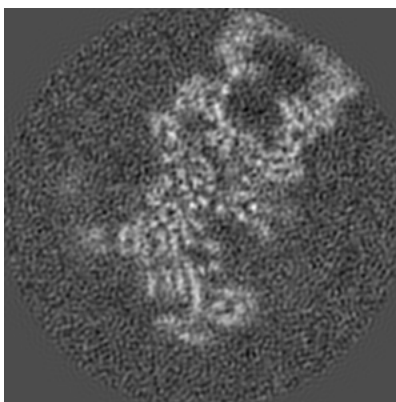
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

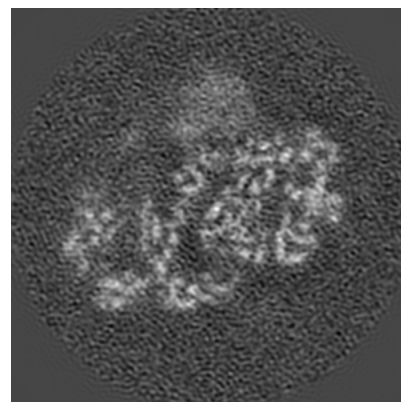
6.2.1 Primary map



X Index: 180



Y Index: 180

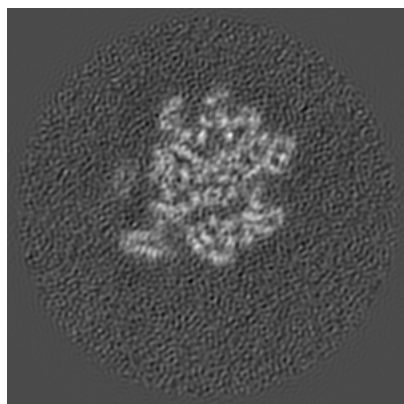


Z Index: 180

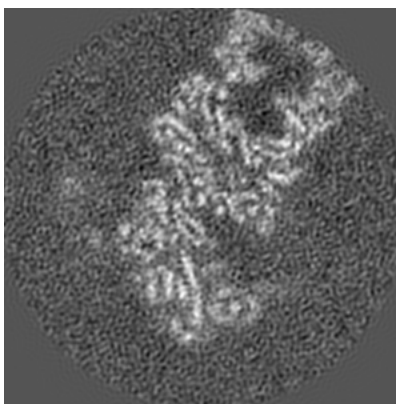
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

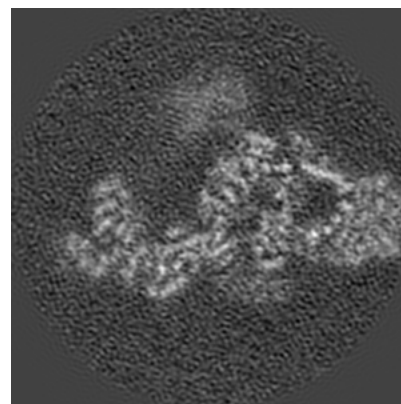
6.3.1 Primary map



X Index: 244



Y Index: 183

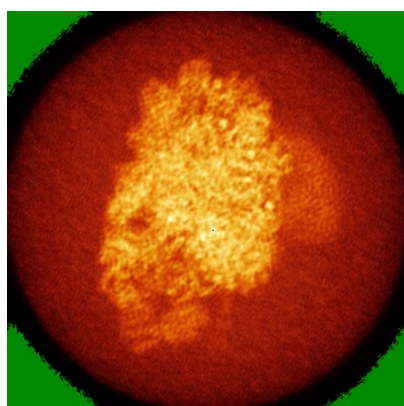


Z Index: 208

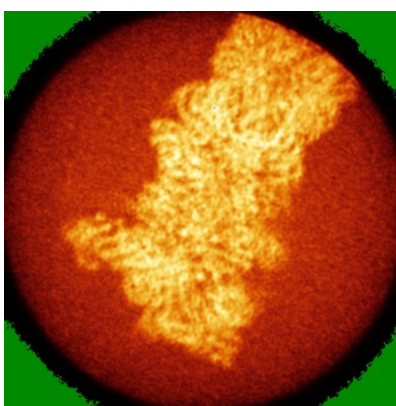
The images above show the largest variance slices of the map in three orthogonal directions.

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

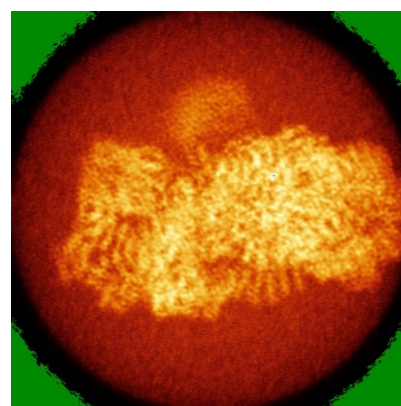
6.4.1 Primary map



X



Y

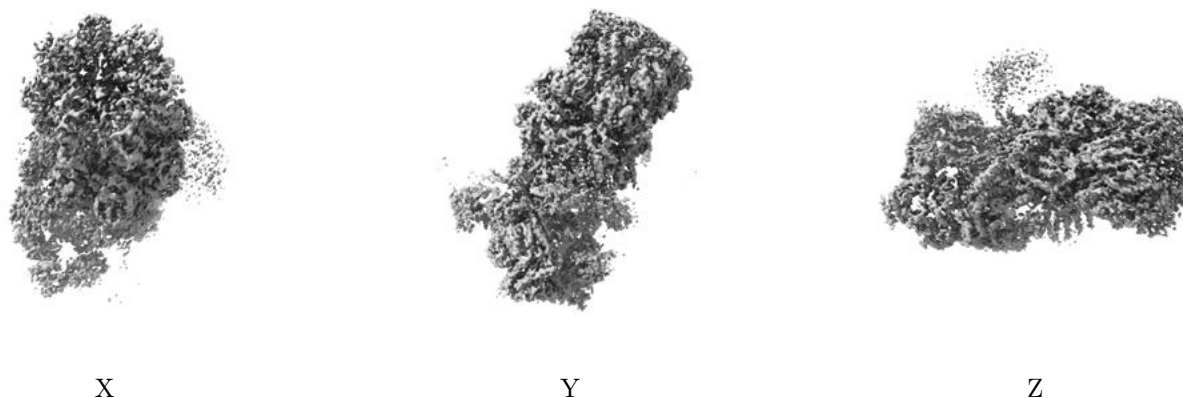


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0033. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

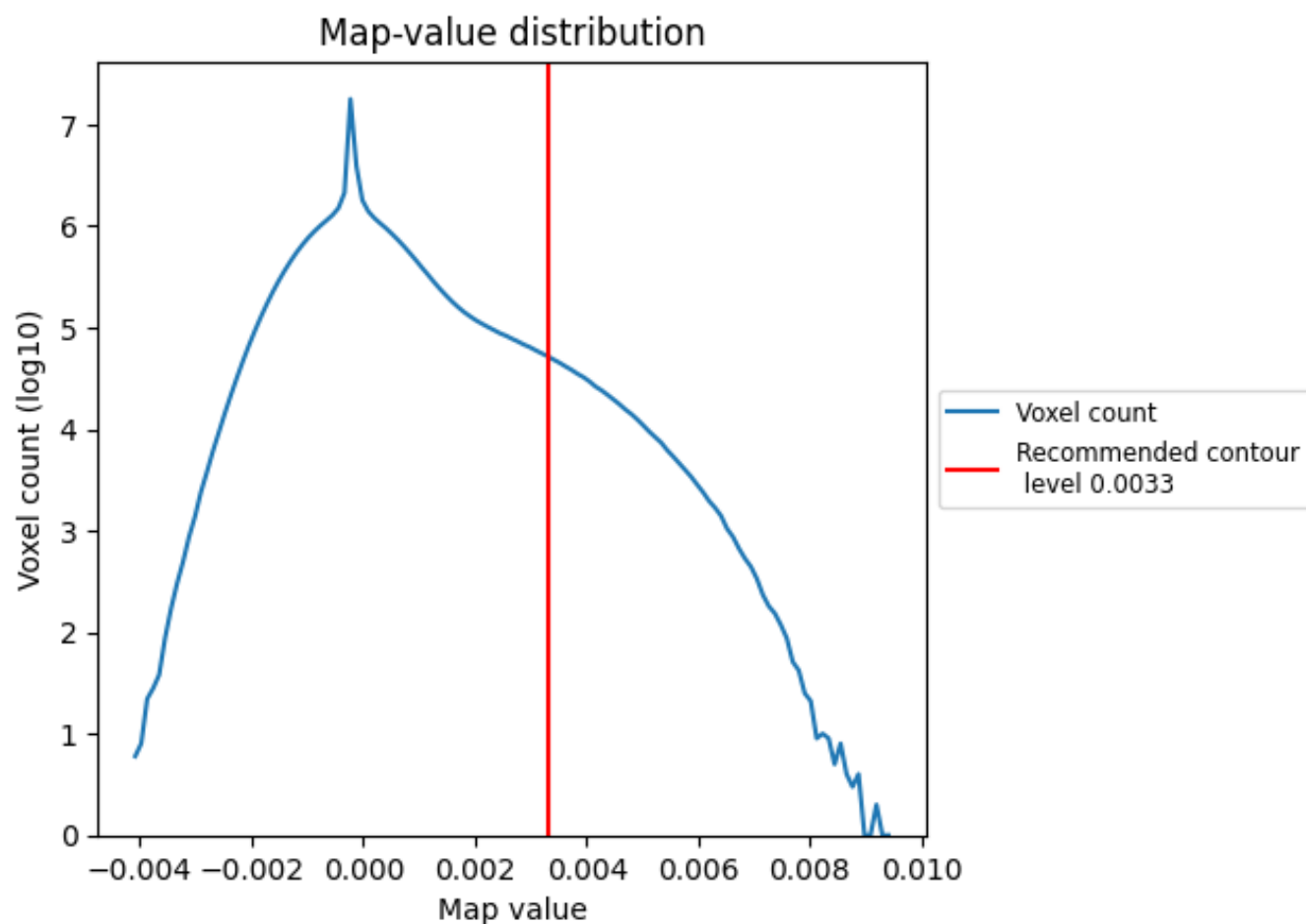
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

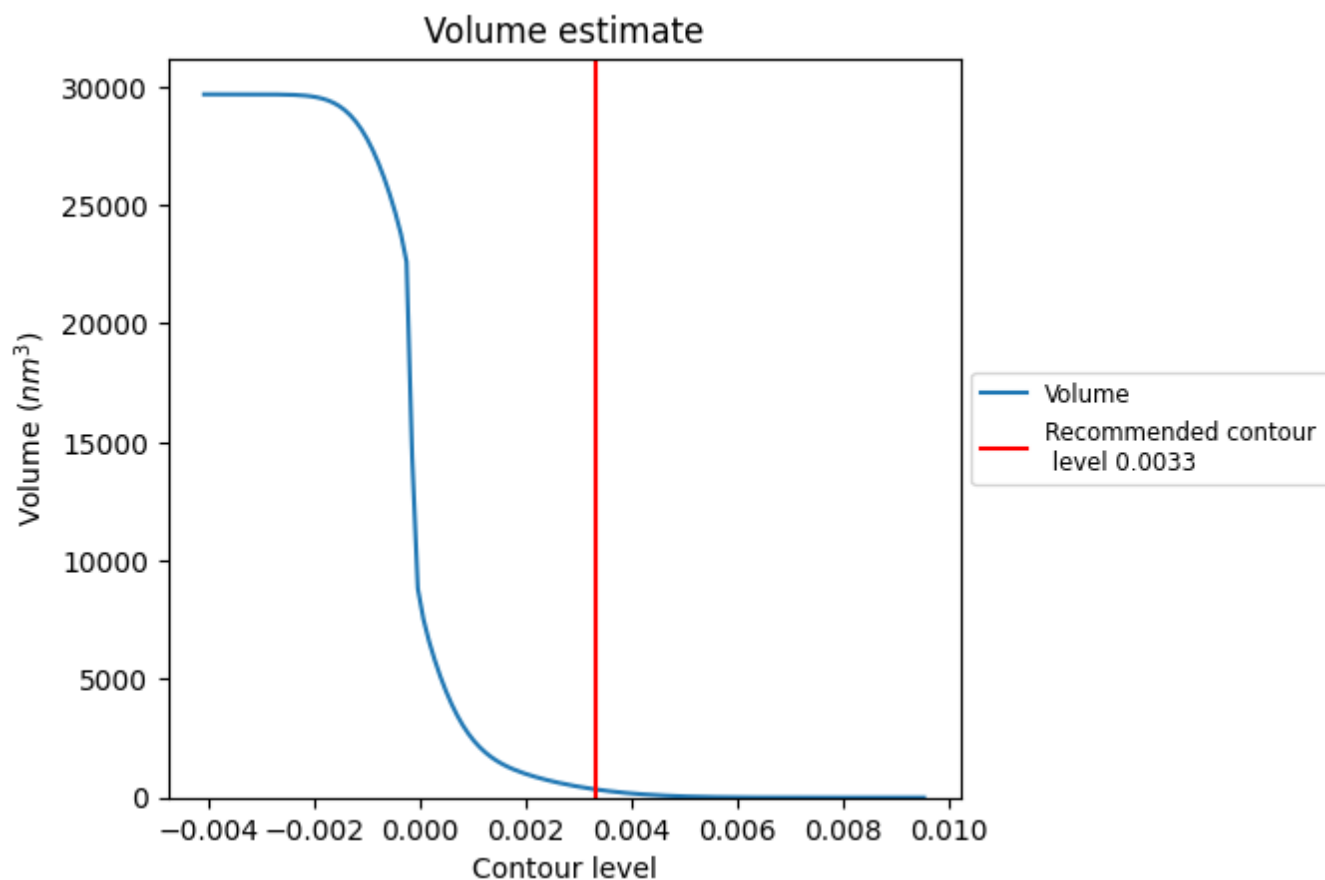
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

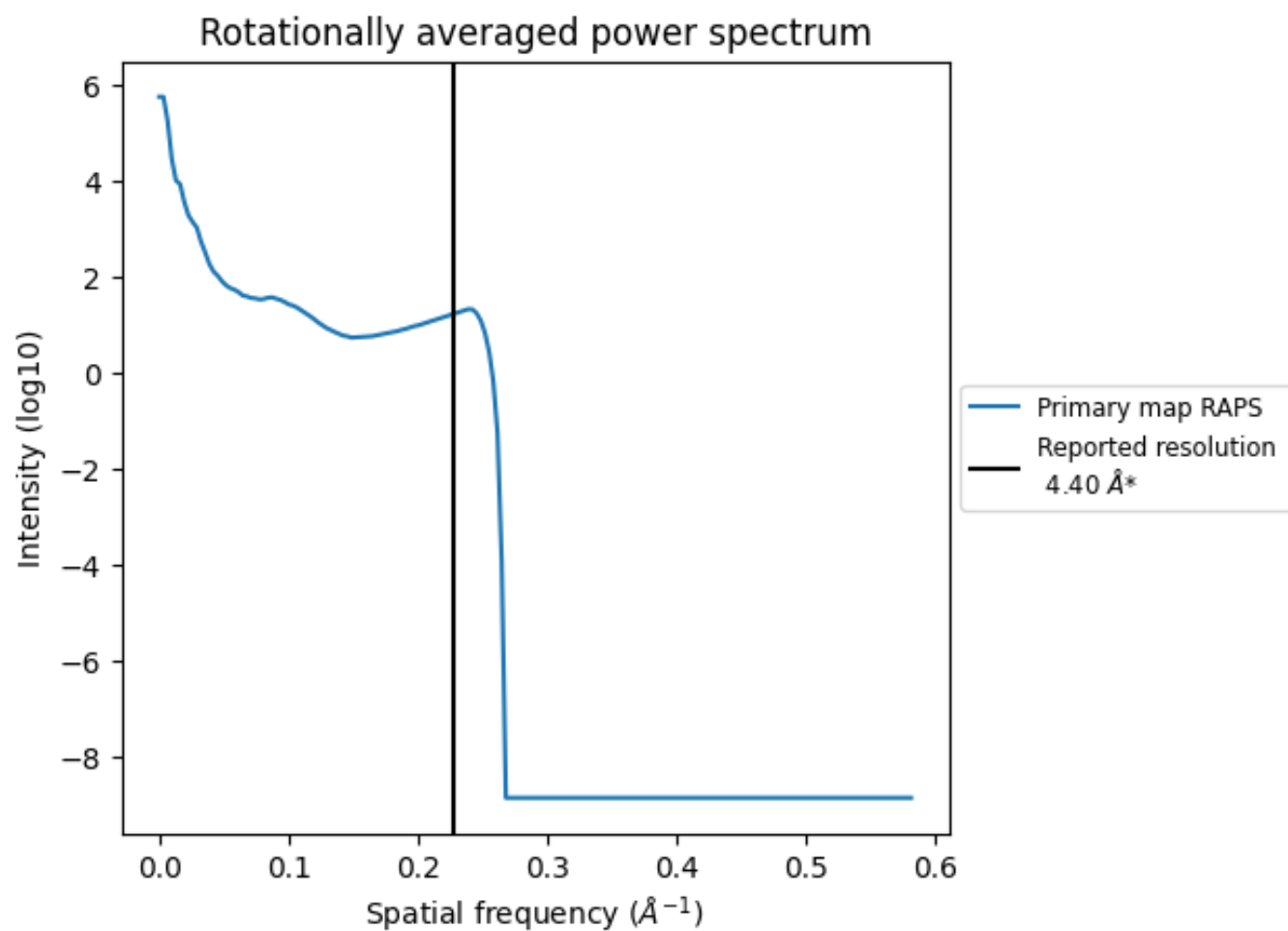
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 349 nm³; this corresponds to an approximate mass of 316 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 0.227 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

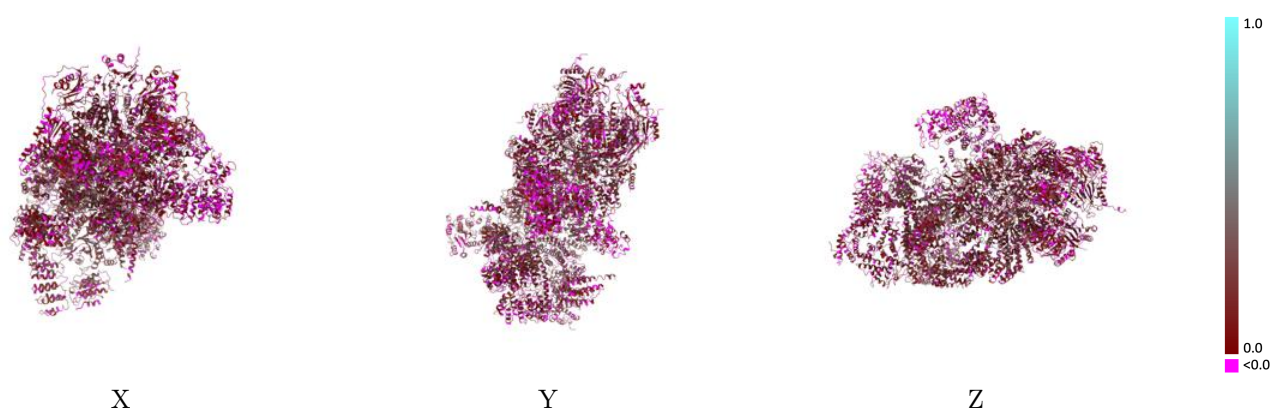
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-8334 and PDB model 5T0G. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay ⓘ

This section was not generated.

9.2 Q-score mapped to coordinate model ⓘ

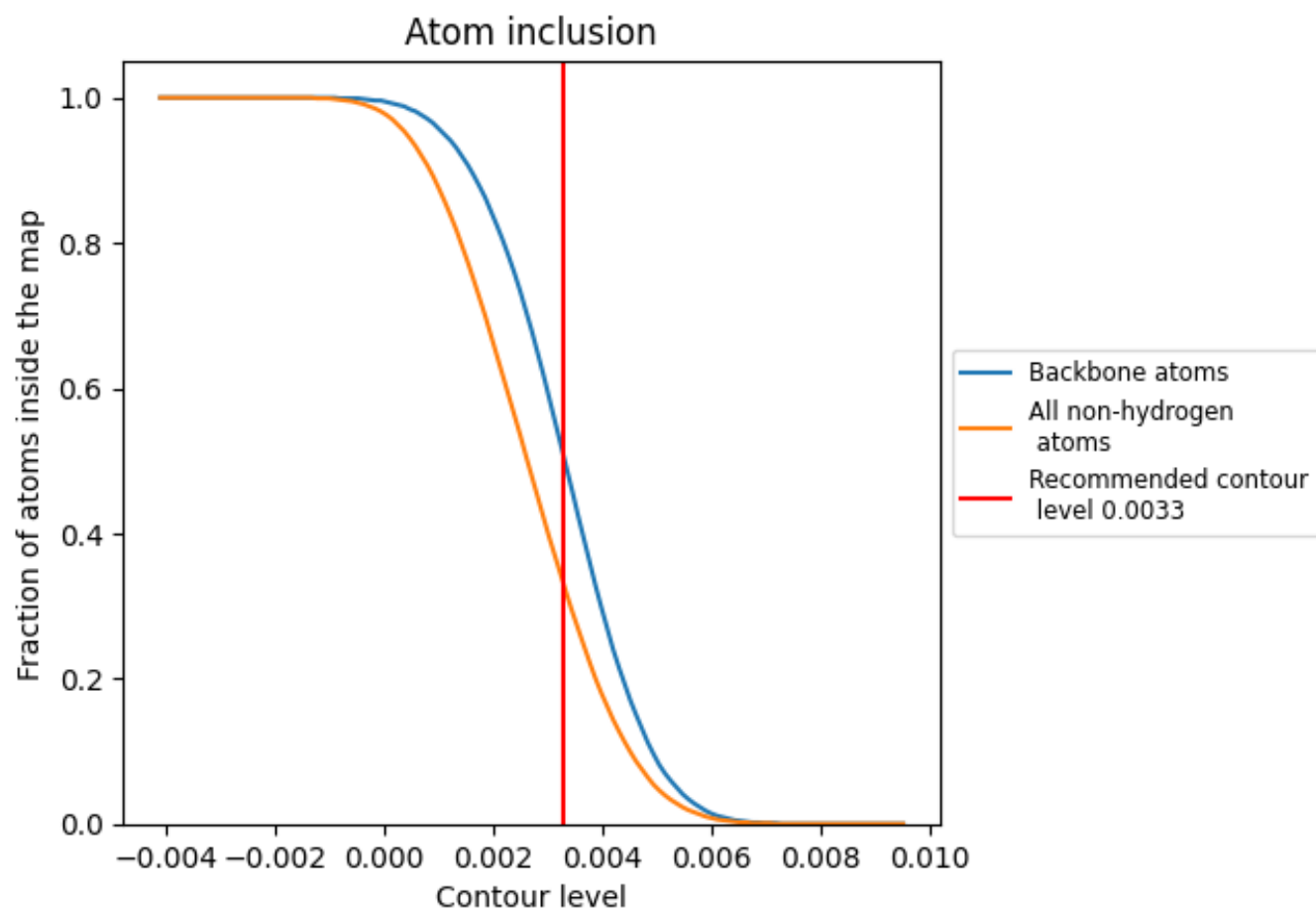


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 51% of all backbone atoms, 33% 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 (0.0033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3290	 0.1320
A	 0.3820	 0.1430
B	 0.3680	 0.1620
C	 0.3960	 0.1710
D	 0.4190	 0.1900
E	 0.4210	 0.1890
F	 0.3710	 0.1510
G	 0.4490	 0.1720
H	 0.4650	 0.1990
I	 0.4510	 0.1800
J	 0.4350	 0.1630
K	 0.3780	 0.1360
L	 0.3860	 0.1190
M	 0.3910	 0.1290
N	 0.3160	 0.1070
O	 0.3010	 0.1110
P	 0.3730	 0.1180
Q	 0.3170	 0.1040
R	 0.3260	 0.1060
S	 0.2770	 0.0860
T	 0.3160	 0.1110
U	 0.3590	 0.1160
V	 0.3080	 0.1200
W	 0.3120	 0.1420
X	 0.1420	 0.1390
Y	 0.3900	 0.1430
Z	 0.3480	 0.1620
a	 0.3270	 0.1380
b	 0.2040	 0.1080
c	 0.3830	 0.1510
d	 0.3040	 0.0980
e	 0.2670	 0.1470
f	 0.0080	 0.0170

