



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 04:30 PM UTC

PDB ID : 9SZV / pdb_00009szv
EMDB ID : EMD-52194
Title : Co-chaperone Bag1-bound human 26S proteasome in SBAG1.3 state
Authors : Cheng, T.C.; Sakata, E.; Muntaner, J.; Maestro-Lopez, M.; Cuellar, J.; Valpuesta, J.M.
Deposited on : 2025-10-15
Resolution : 3.60 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

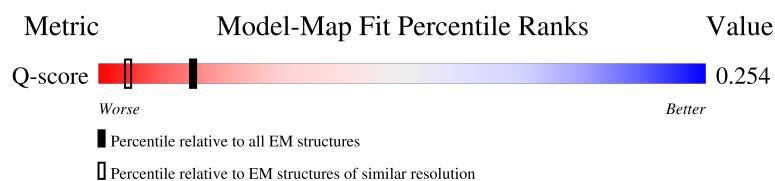
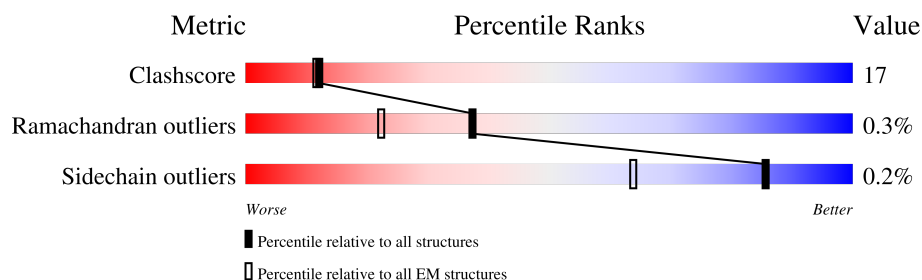
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	G	246	
1	g	246	
2	H	234	
2	h	234	

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Mol	Chain	Length	Quality of chain
3	I	261	
3	i	261	
4	J	248	
4	j	248	
5	L	269	
5	l	269	
6	M	255	
6	m	255	
7	K	241	
7	k	241	
8	N	239	
8	n	239	
9	O	277	
9	o	277	
10	P	205	
10	p	205	
11	Q	201	
11	q	201	
12	R	263	
12	r	263	
13	S	241	
13	s	241	
14	T	264	
14	t	264	
15	f	908	

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Mol	Chain	Length	Quality of chain
16	x	230	
17	a	376	
18	b	377	
19	c	310	
20	d	350	
21	e	70	
22	U	953	
23	V	534	
24	X	422	
25	Y	389	
26	Z	324	
27	W	456	
28	A	433	
29	B	440	
30	C	398	
31	D	418	
32	E	403	
33	F	439	

2 Entry composition [i](#)

There are 35 unique types of molecules in this entry. The entry contains 104040 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	237	Total	C	N	O	S	0	0
			1841	1168	307	353	13		
1	g	243	Total	C	N	O	S	0	0
			1885	1194	316	362	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	226	Total	C	N	O	S	0	0
			1749	1116	297	330	6		
2	h	232	Total	C	N	O	S	0	0
			1809	1156	306	341	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	247	Total	C	N	O	S	0	0
			1927	1219	327	372	9		
3	i	250	Total	C	N	O	S	0	0
			1971	1245	339	377	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	237	Total	C	N	O	S	0	0
			1865	1169	332	359	5		
4	j	238	Total	C	N	O	S	0	0
			1878	1178	333	362	5		

- Molecule 5 is a protein called Isoform Long of Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	237	Total	C	N	O	S	0	0
			1864	1167	335	351	11		
5	l	237	Total	C	N	O	S	0	0
			1864	1167	335	351	11		

- Molecule 6 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	238	Total	C	N	O	S	0	0
			1862	1180	318	353	11		
6	m	240	Total	C	N	O	S	0	0
			1881	1193	321	356	11		

- Molecule 7 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	222	Total	C	N	O	S	0	0
			1694	1066	280	338	10		
7	k	234	Total	C	N	O	S	0	0
			1789	1125	295	358	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	n	202	Total	C	N	O	S	0	0
			1514	949	258	295	12		
8	N	203	Total	C	N	O	S	0	0
			1521	954	259	296	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
			1659	1044	283	320	12		
9	O	220	Total	C	N	O	S	0	0
			1659	1044	283	320	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
			1591	1013	265	294	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	P	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	q	196	Total	C	N	O	S	0	0
			1571	1006	267	289	9		
11	Q	196	Total	C	N	O	S	0	0
			1571	1006	267	289	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
			1559	982	274	294	9		
12	R	201	Total	C	N	O	S	0	0
			1559	982	274	294	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
			1654	1047	284	313	10		
13	S	212	Total	C	N	O	S	0	0
			1643	1041	280	312	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	t	216	Total	C	N	O	S	0	0
			1687	1064	291	320	12		
14	T	216	Total	C	N	O	S	0	0
			1687	1064	291	320	12		

- Molecule 15 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	f	823	Total	C	N	O	S	0	0
			6292	3963	1077	1208	44		

- Molecule 16 is a protein called BAG family molecular chaperone regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	x	85	Total	C	N	O	S	0	0
			635	397	110	125	3		

- Molecule 17 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	373	Total	C	N	O	S	0	0
			2969	1887	510	557	15		

- Molecule 18 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

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

- Molecule 19 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	287	Total	C	N	O	S	0	0
			2224	1398	388	419	19		

- Molecule 20 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	252	Total	C	N	O	S	0	0
			2063	1338	335	382	8		

- Molecule 21 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	e	50	Total	C	N	O	0	0
			407	244	63	100		

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	859	Total	C	N	O	S	0	0
			6648	4199	1136	1269	44		

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	444	Total	C	N	O	S	0	0
			3600	2289	645	653	13		

- 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
			3002	1912	509	569	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	380	Total	C	N	O	S	0	0
			3021	1904	530	570	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
			2248	1427	392	424	5		

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	444	Total	C	N	O	S	0	0
			3570	2250	616	680	24		

- Molecule 28 is a protein called 26S protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A	403	Total	C	N	O	S	0	0
			3119	1958	548	596	17		

- Molecule 29 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B	400	Total	C	N	O	S	0	0
			3060	1918	527	601	14		

- Molecule 30 is a protein called Isoform 2 of 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	C	368	Total	C	N	O	S	0	0
			2839	1766	518	537	18		

- Molecule 31 is a protein called 26S protease regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	D	372	Total	C	N	O	S	0	0
			2904	1827	506	560	11		

- Molecule 32 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	E	361	Total	C	N	O	S	0	0
			2776	1734	500	526	16		

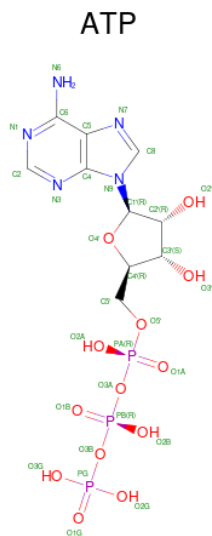
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	246	ALA	GLY	conflict	UNP A0A087X2I1

- Molecule 33 is a protein called 26S protease regulatory subunit 6A.

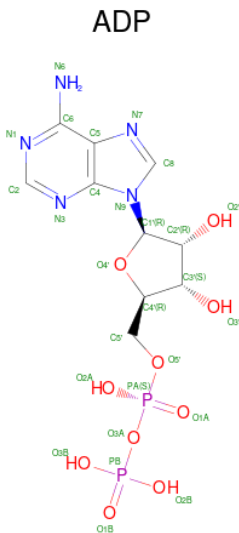
Mol	Chain	Residues	Atoms					AltConf	Trace
33	F	354	Total	C	N	O	S	0	0
			2694	1696	463	518	17		

- Molecule 34 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
34	A	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$) (labeled as "Ligand of Interest" by depositor).



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

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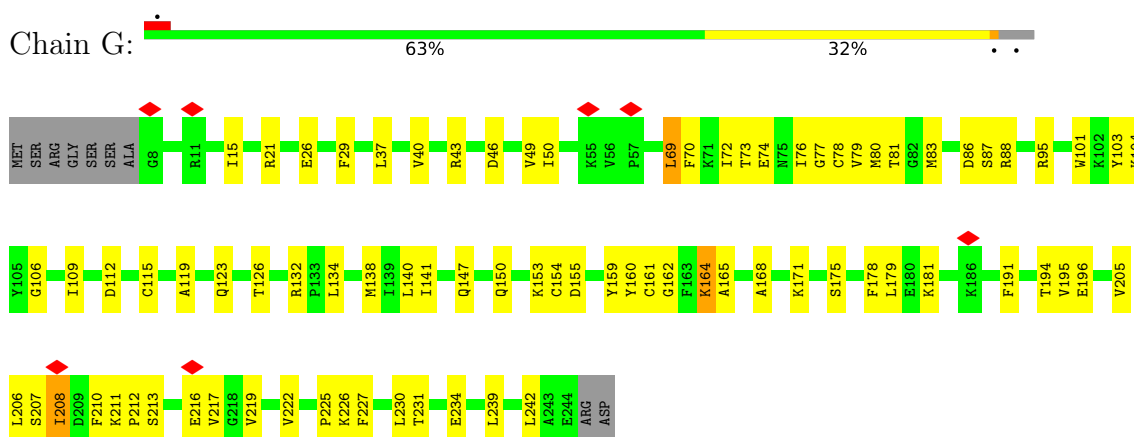
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Mol	Chain	Residues	Atoms					AltConf
35	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

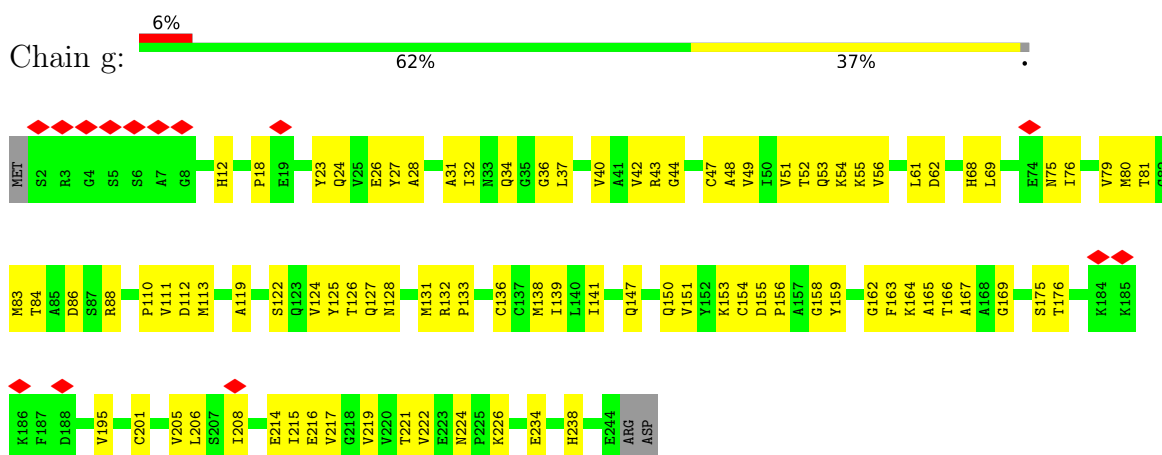
3 Residue-property plots

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

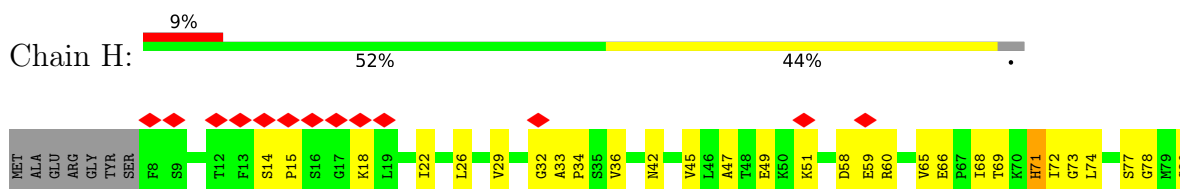
- Molecule 1: Proteasome subunit alpha type-6

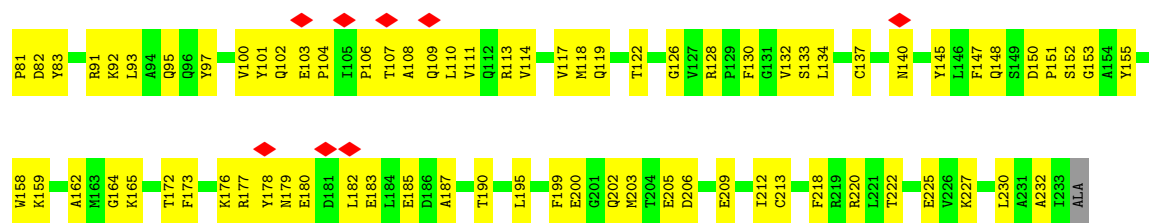


- Molecule 1: Proteasome subunit alpha type-6

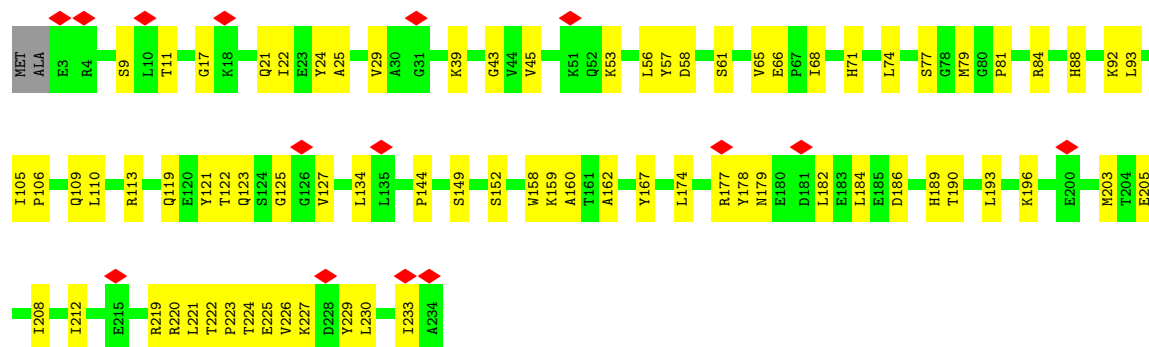


- Molecule 2: Proteasome subunit alpha type-2

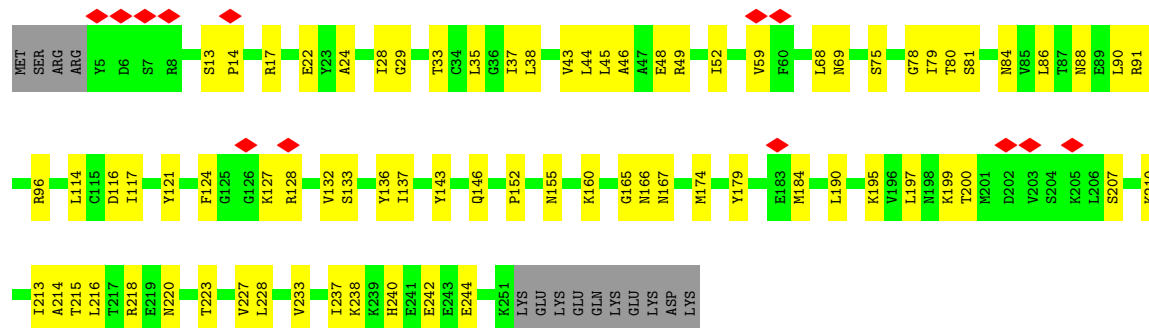




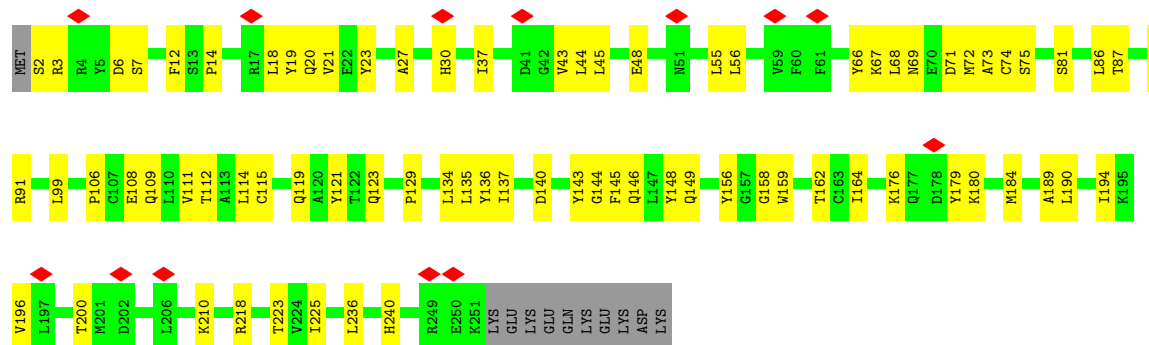
• Molecule 2: Proteasome subunit alpha type-2



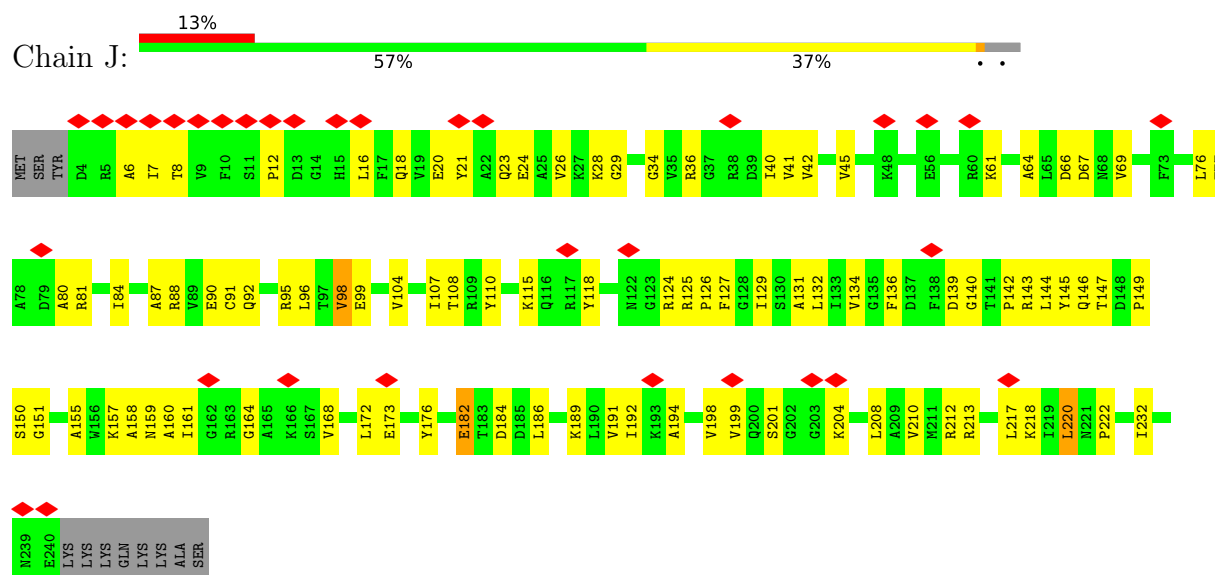
• Molecule 3: Proteasome subunit alpha type-4



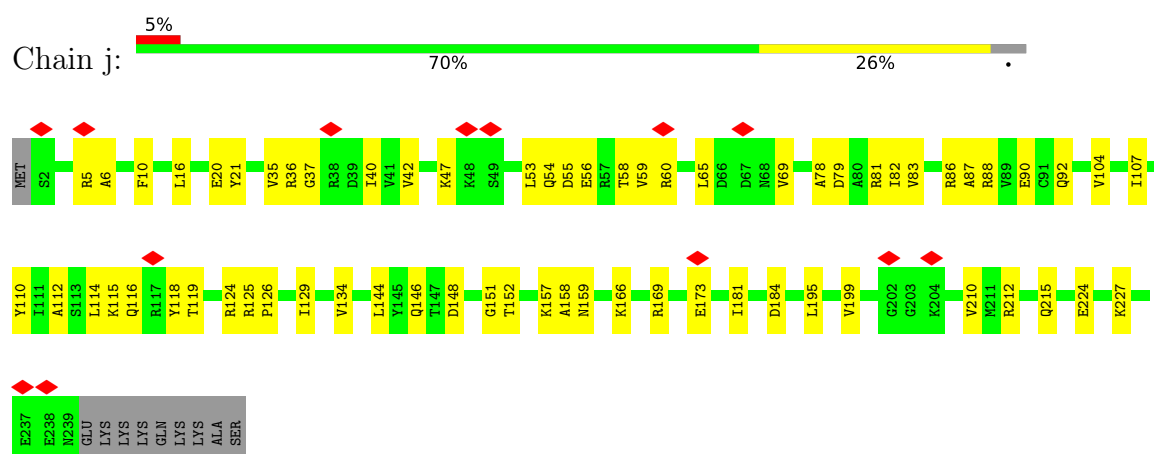
• Molecule 3: Proteasome subunit alpha type-4



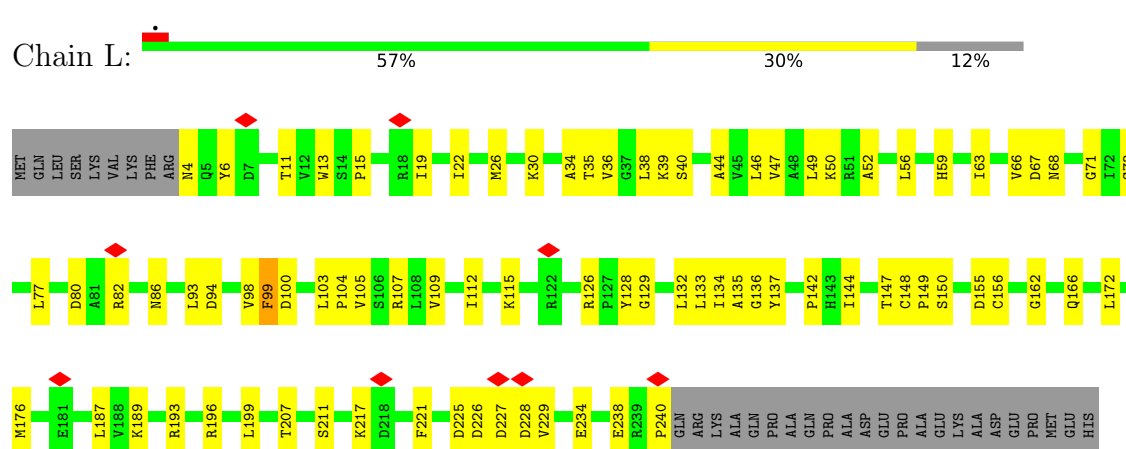
- Molecule 4: Proteasome subunit alpha type-7



- Molecule 4: Proteasome subunit alpha type-7

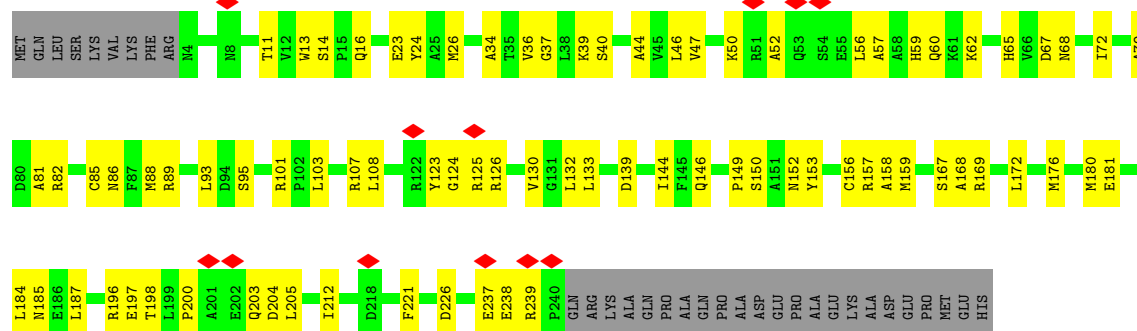


- Molecule 5: Isoform Long of Proteasome subunit alpha type-1



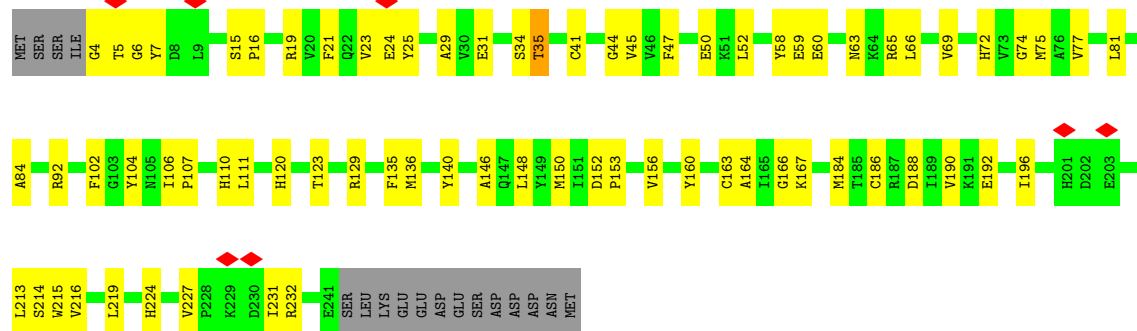
- Molecule 5: Isoform Long of Proteasome subunit alpha type-1

Chain L: 



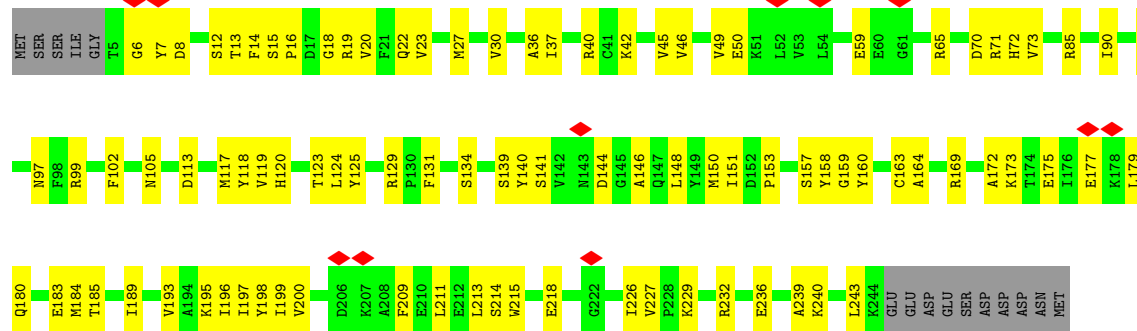
• Molecule 6: Proteasome subunit alpha type-3

Chain M: 



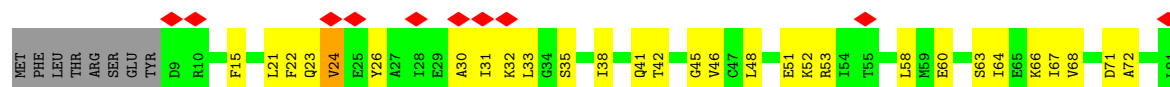
• Molecule 6: Proteasome subunit alpha type-3

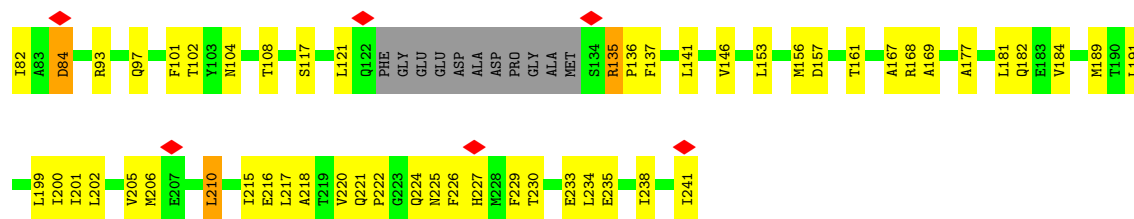
Chain m: 



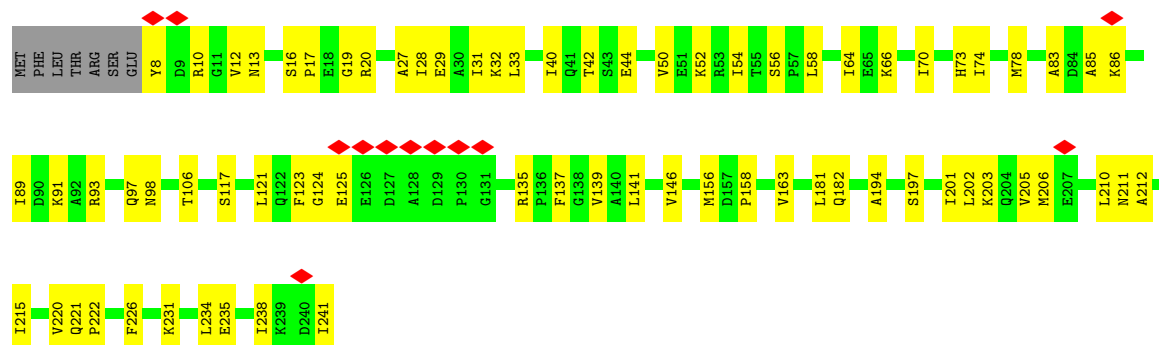
• Molecule 7: Proteasome subunit alpha type-5

Chain K: 

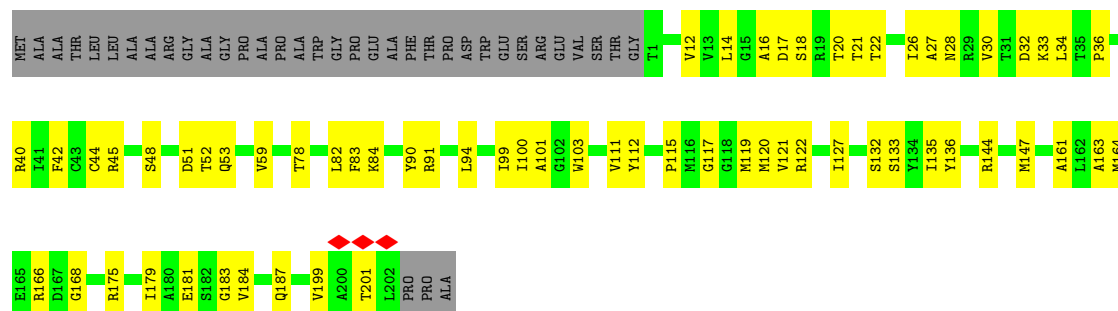




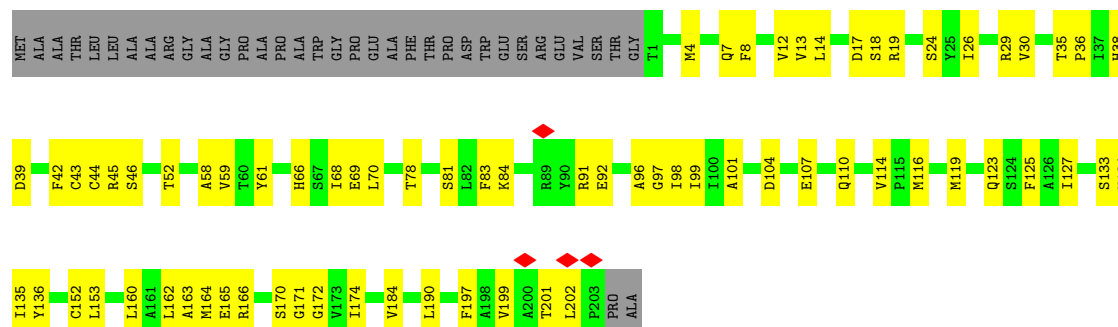
• Molecule 7: Proteasome subunit alpha type-5



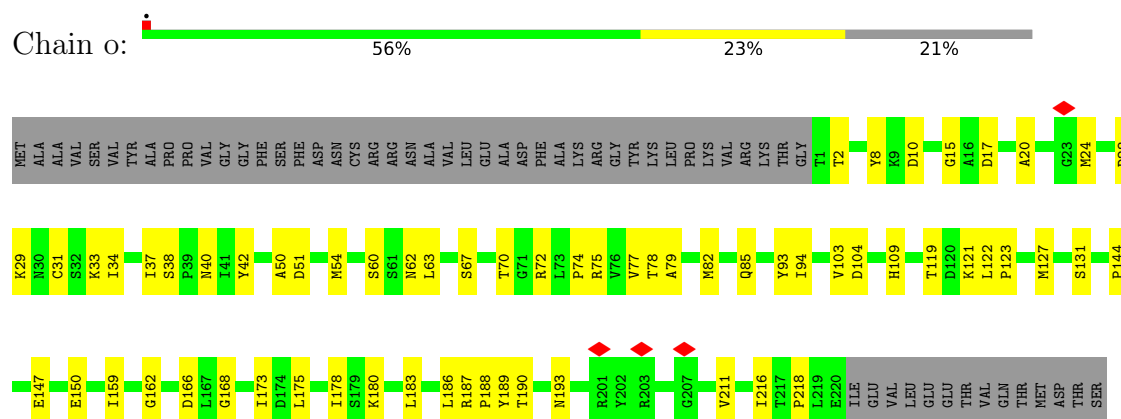
• Molecule 8: Proteasome subunit beta type-6



• Molecule 8: Proteasome subunit beta type-6



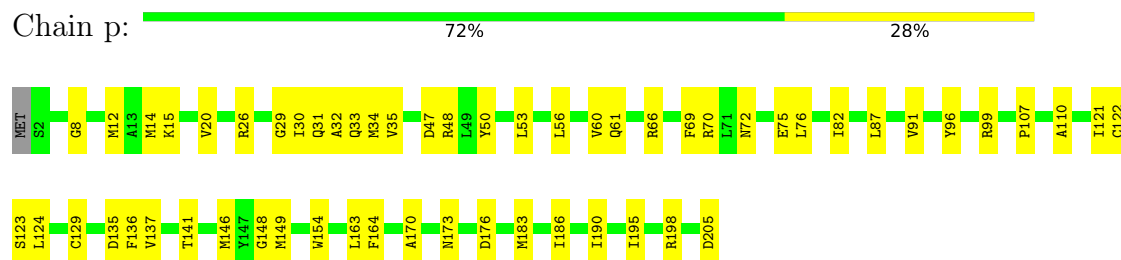
- Molecule 9: Proteasome subunit beta type-7



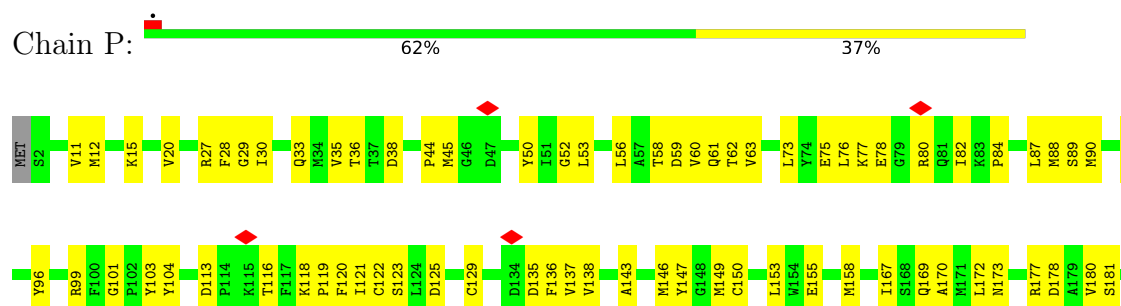
- Molecule 9: Proteasome subunit beta type-7

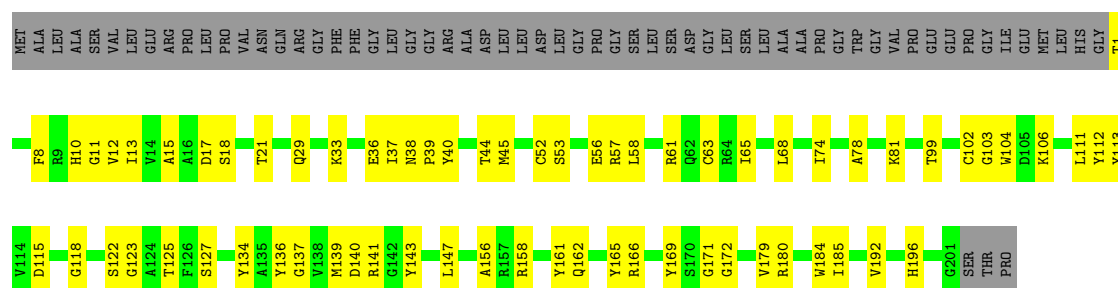


- Molecule 10: Proteasome subunit beta type-3

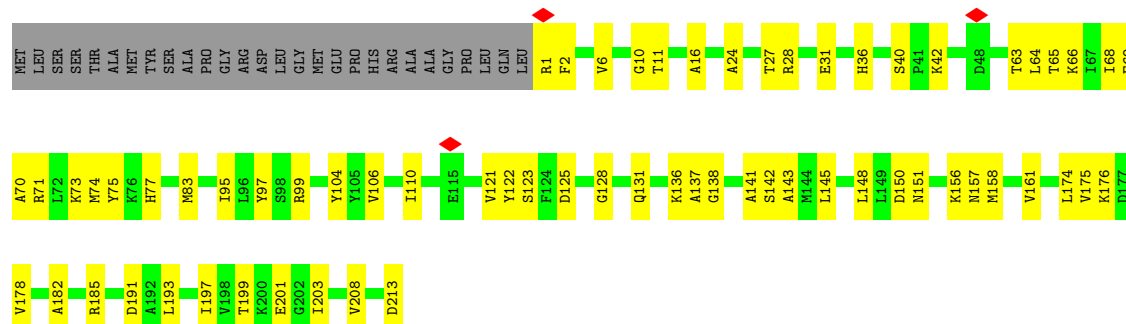


- Molecule 10: Proteasome subunit beta type-3

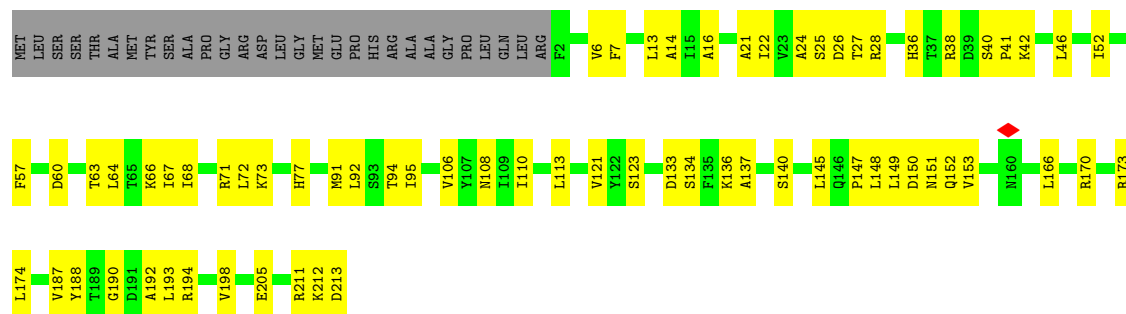




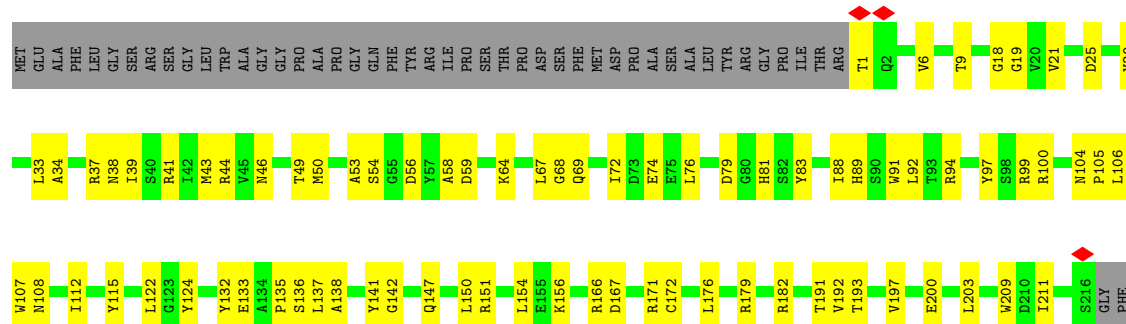
• Molecule 13: Proteasome subunit beta type-1



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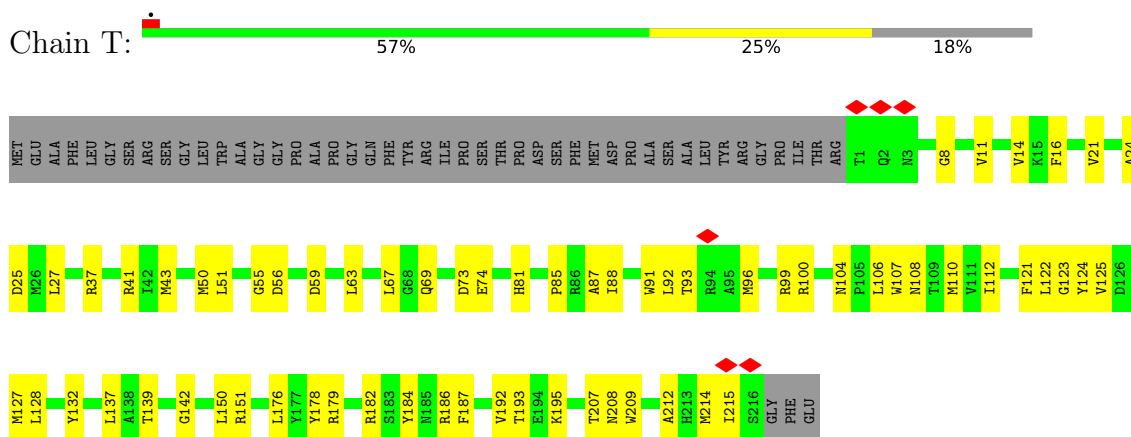
• Molecule 14: Proteasome subunit beta type-4



GLU

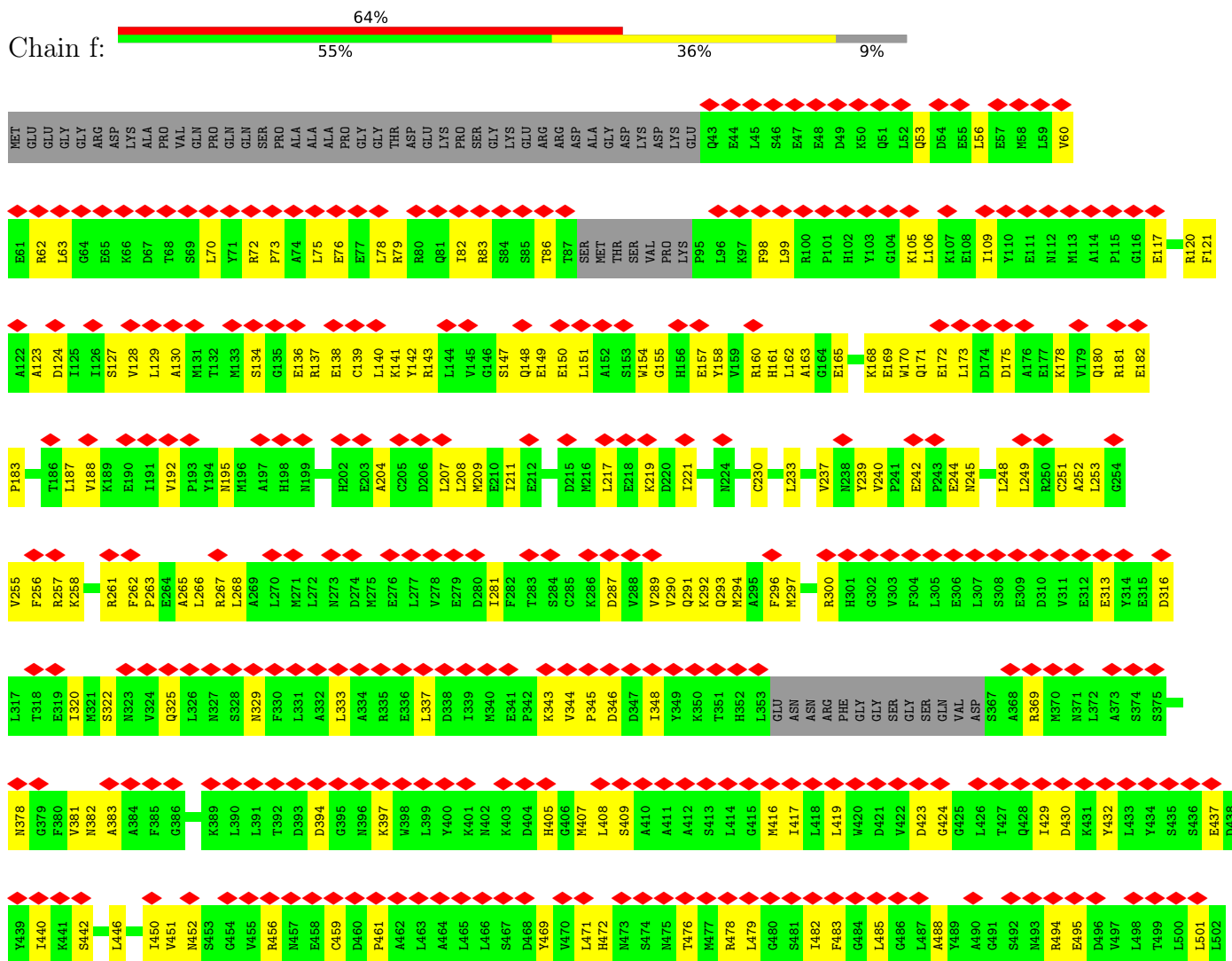
• Molecule 14: Proteasome subunit beta type-4

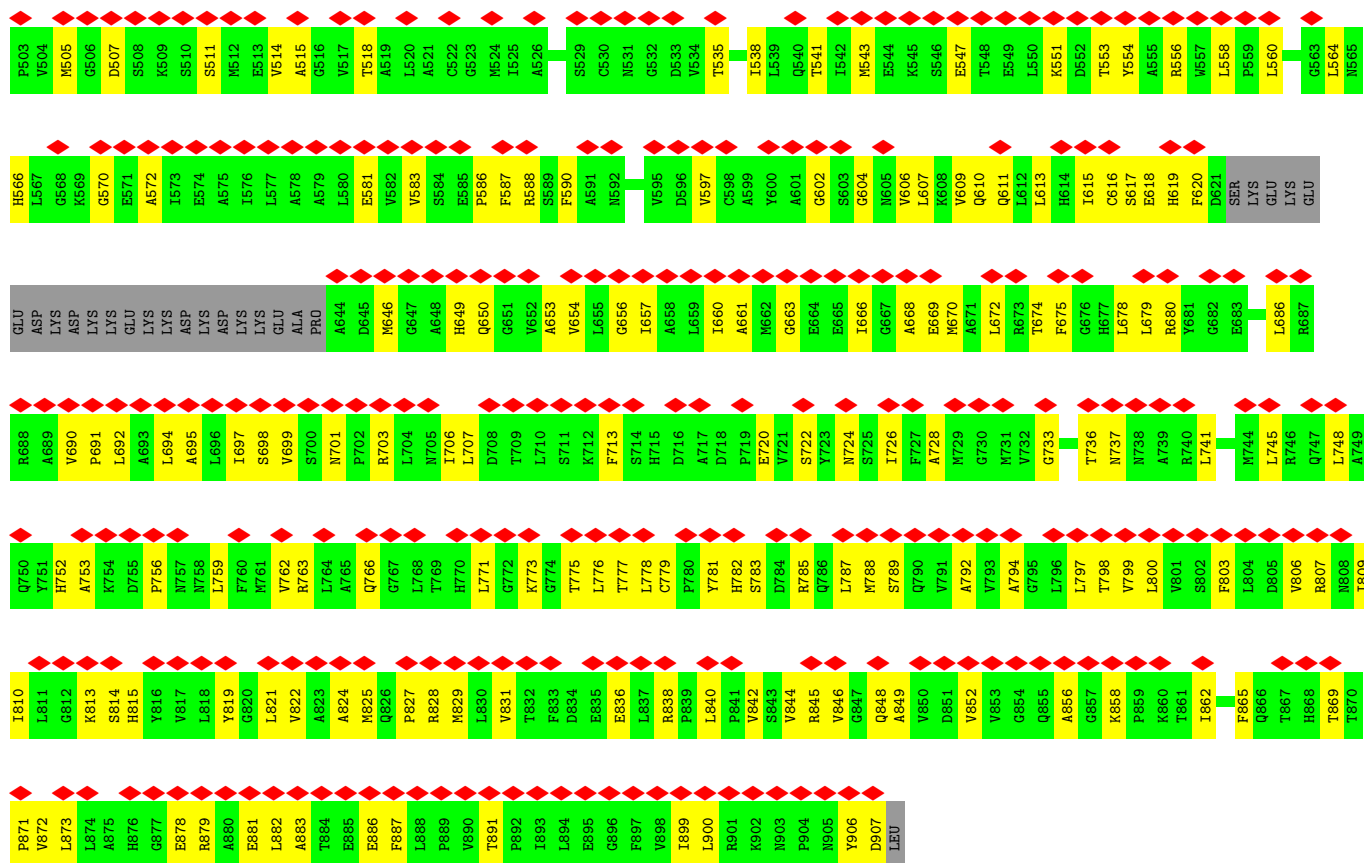
Chain T:



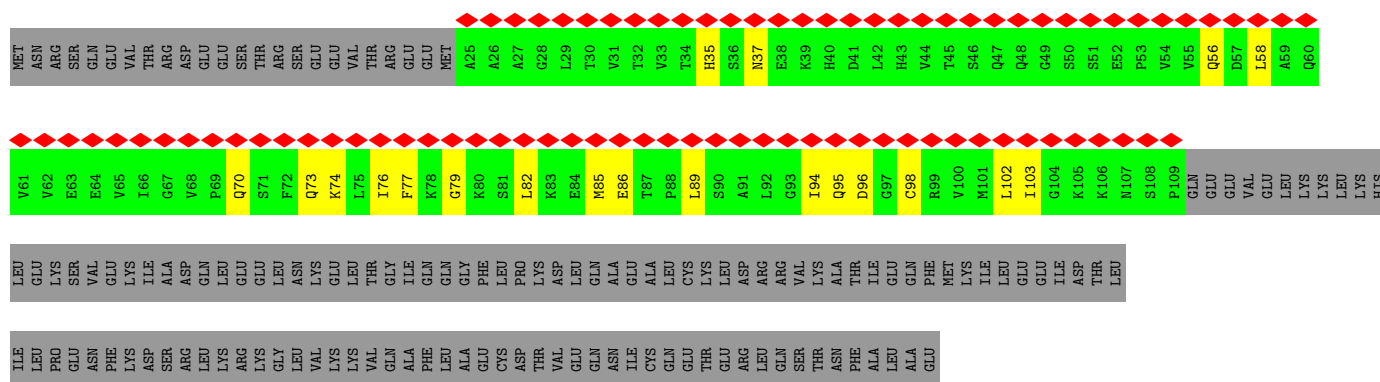
• Molecule 15: 26S proteasome non-ATPase regulatory subunit 2

Chain f:



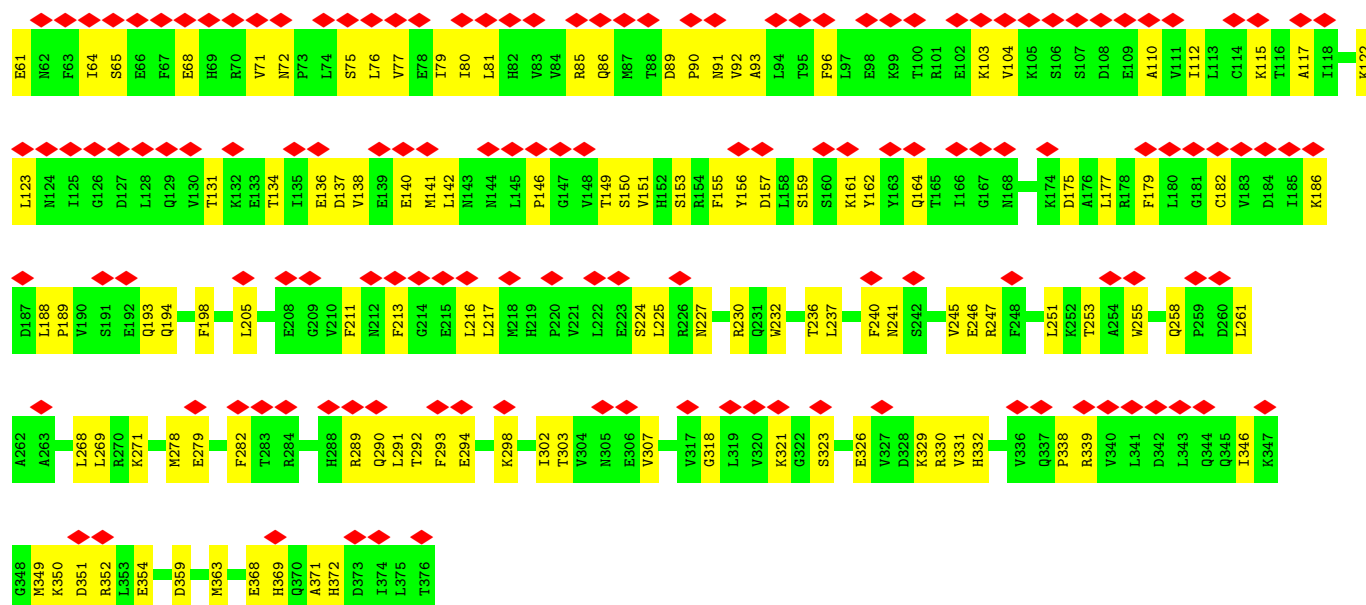


• Molecule 16: BAG family molecular chaperone regulator 1

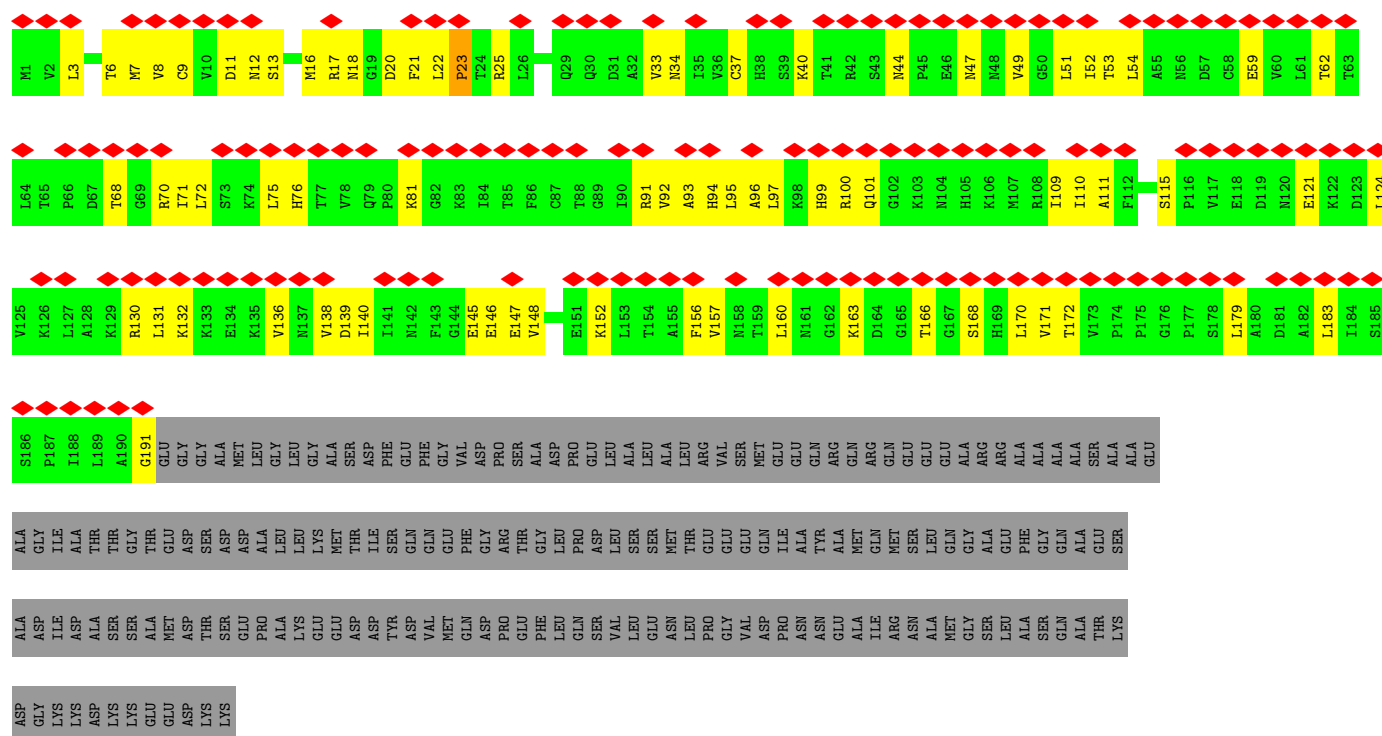
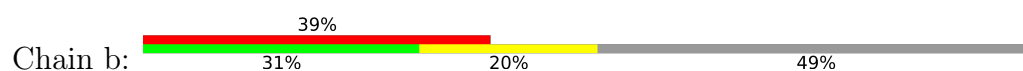


• Molecule 17: 26S proteasome non-ATPase regulatory subunit 13



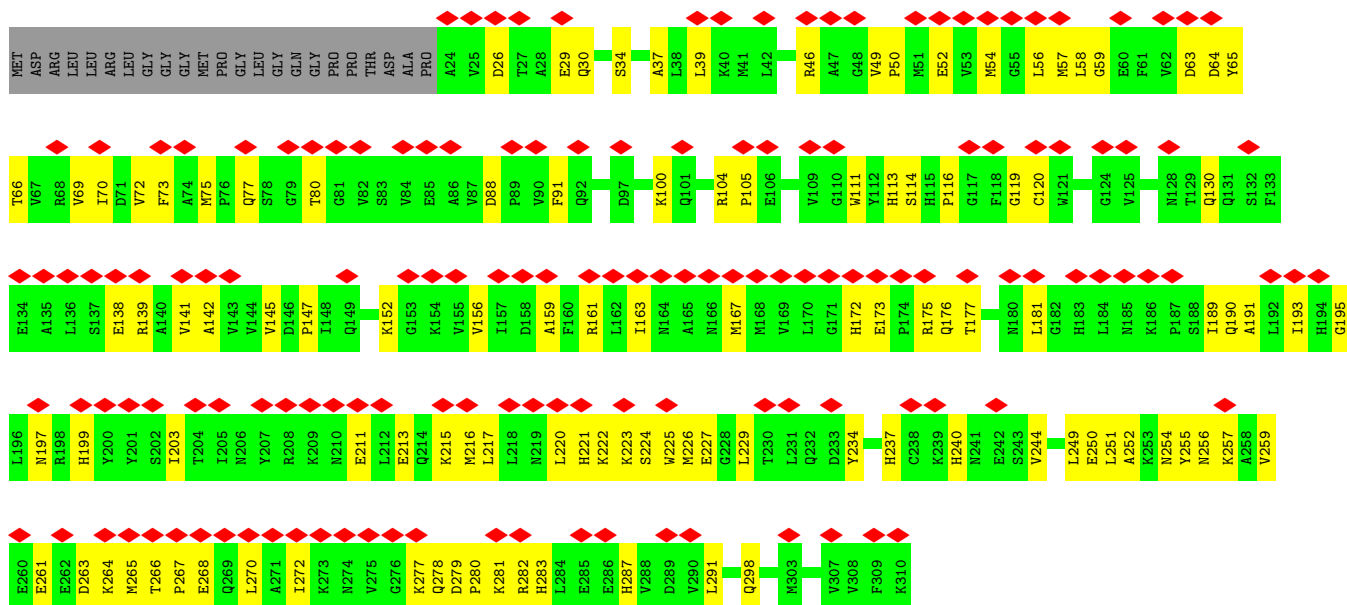


• Molecule 18: 26S proteasome non-ATPase regulatory subunit 4

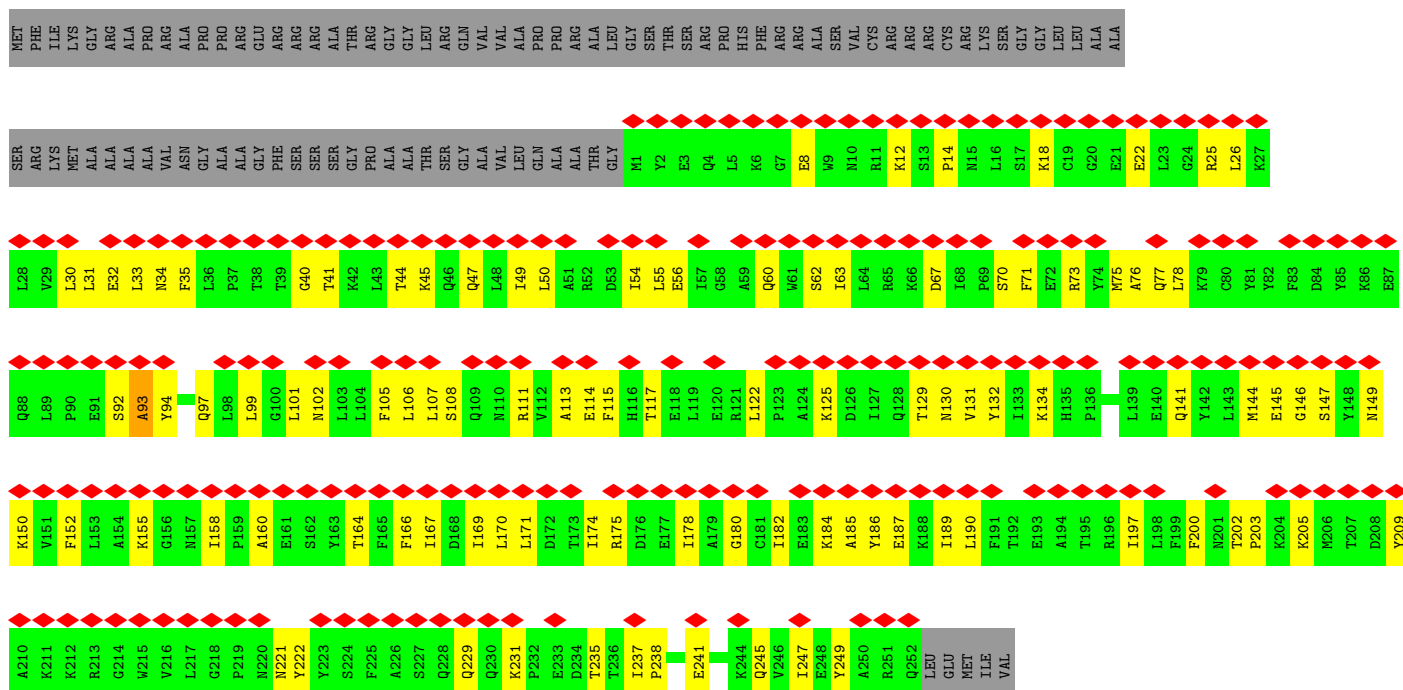


• Molecule 19: 26S proteasome non-ATPase regulatory subunit 14

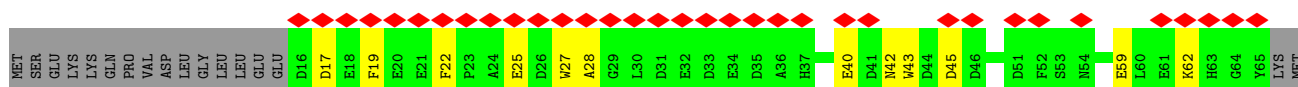




• Molecule 20: 26S proteasome non-ATPase regulatory subunit 8



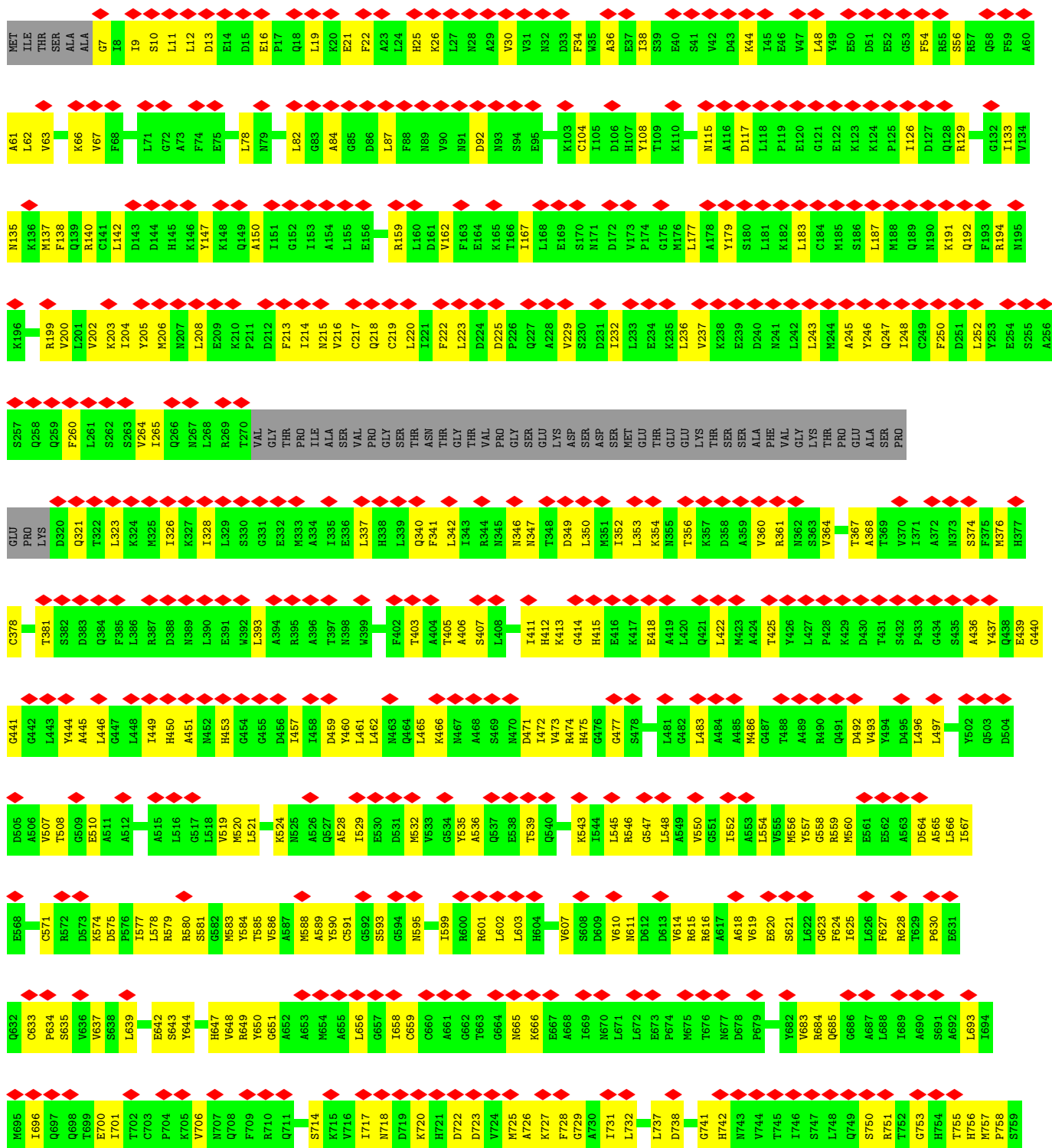
• Molecule 21: 26S proteasome complex subunit SEM1

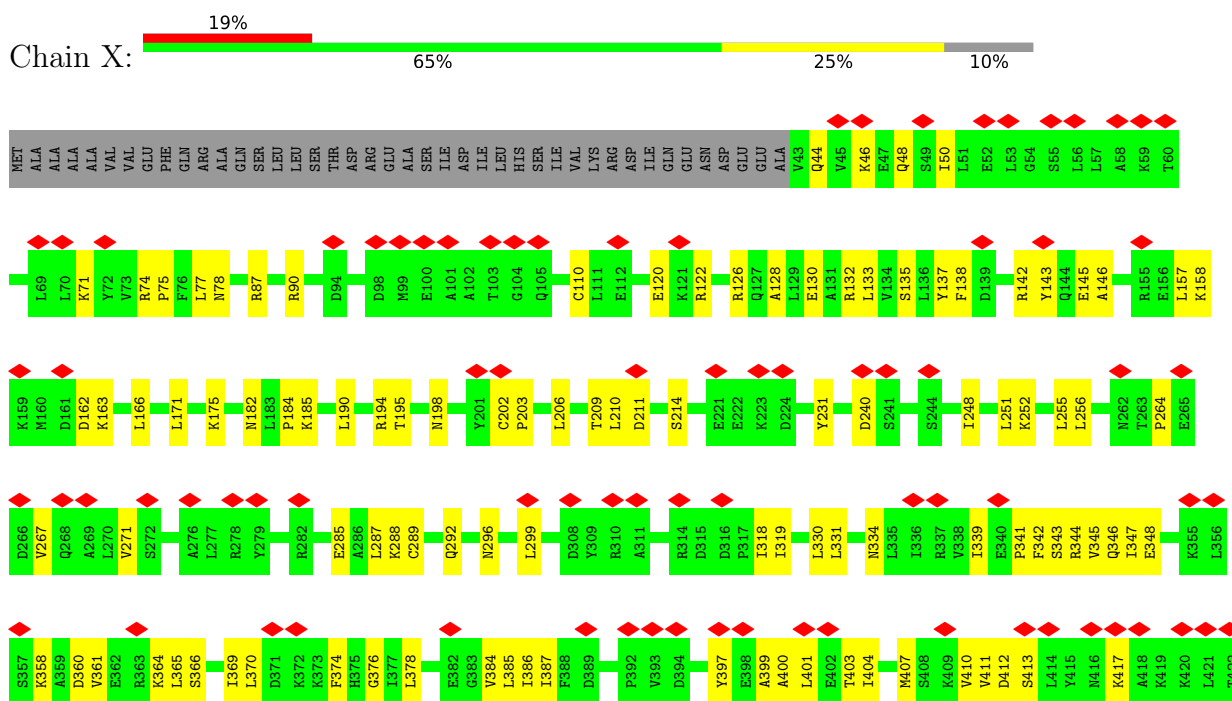


GLU
THR
SER

• Molecule 22: 26S proteasome non-ATPase regulatory subunit 1

Chain U: 

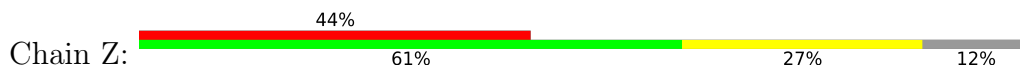


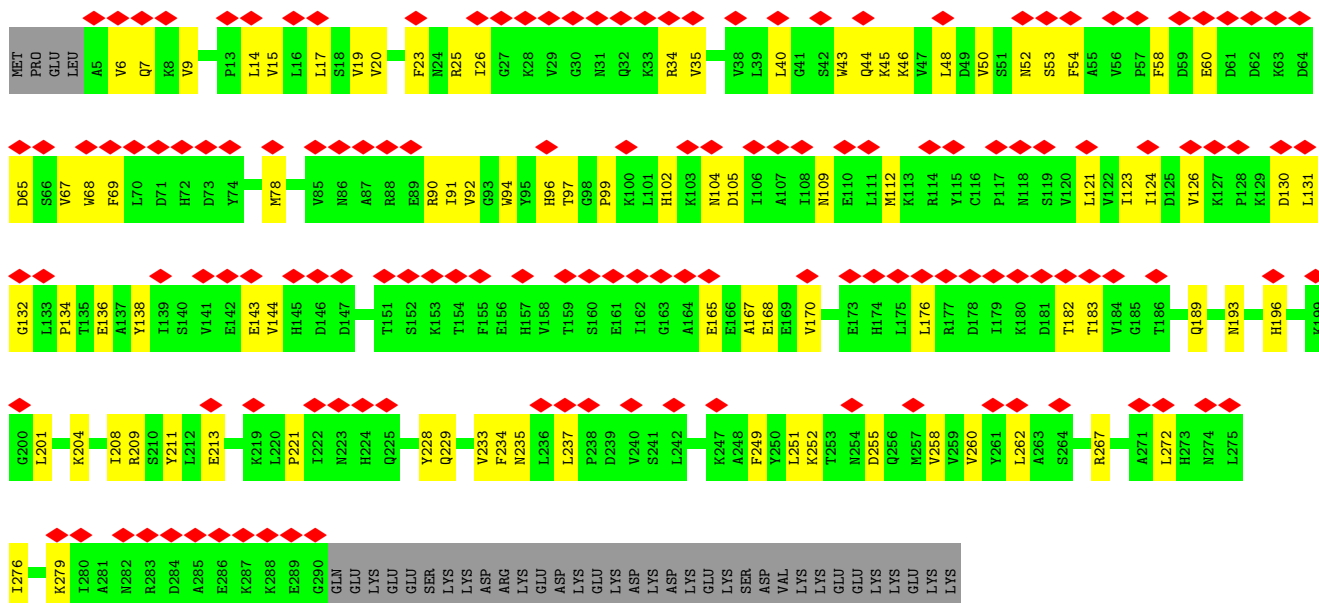


- Molecule 25: 26S proteasome non-ATPase regulatory subunit 6



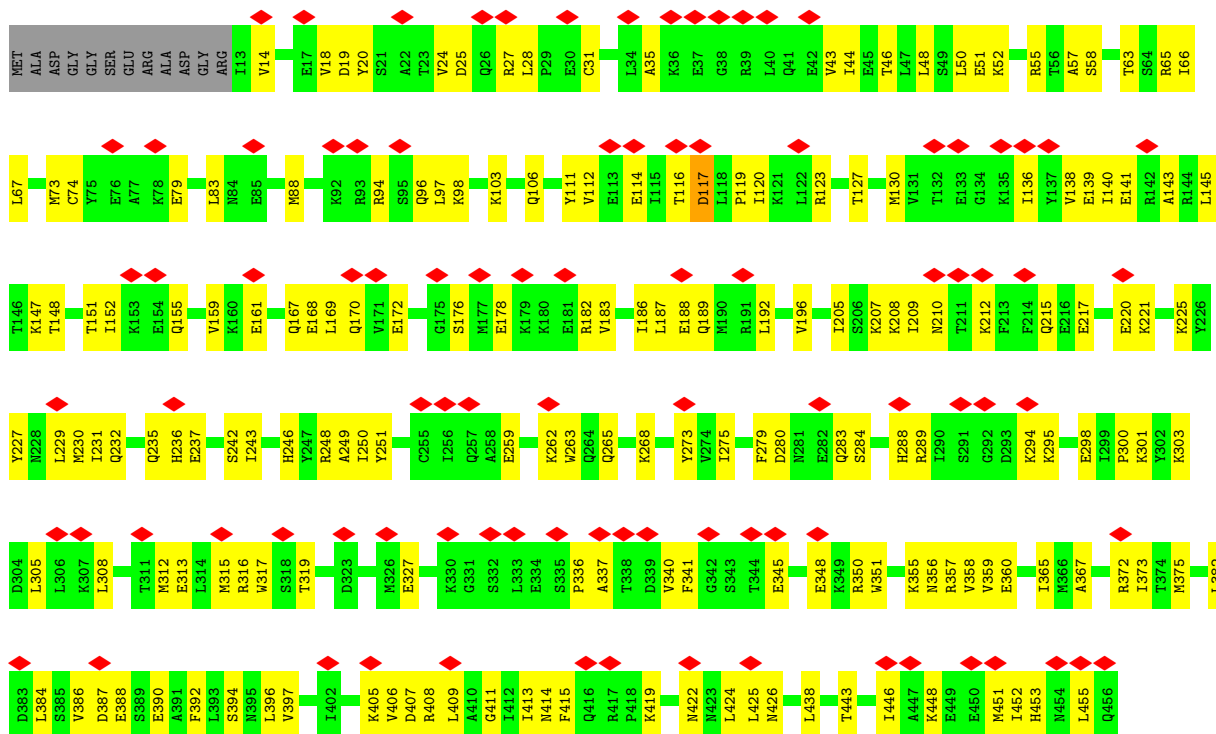
- Molecule 26: 26S proteasome non-ATPase regulatory subunit 7





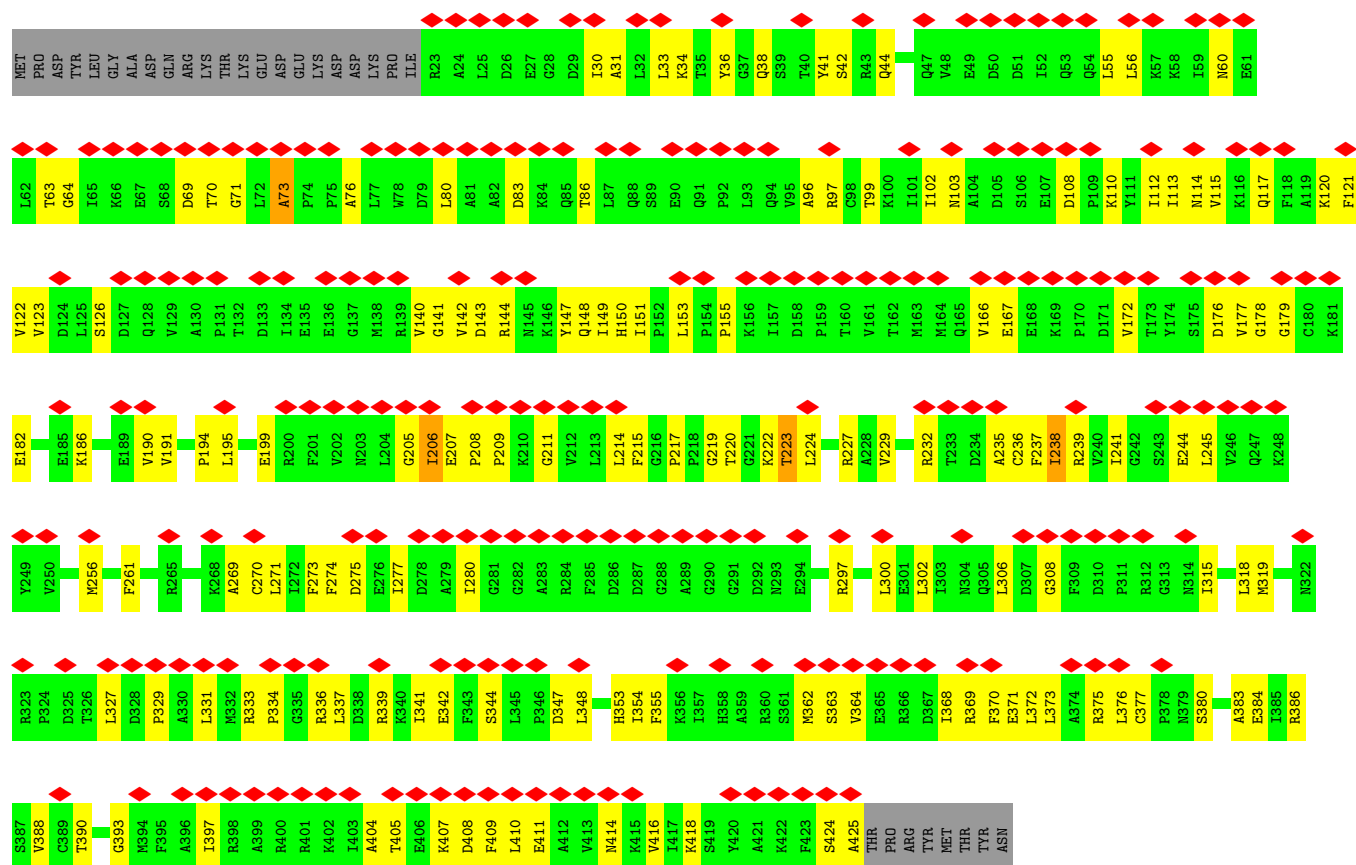
• Molecule 27: 26S proteasome non-ATPase regulatory subunit 12

Chain W: 20% 58% 39%

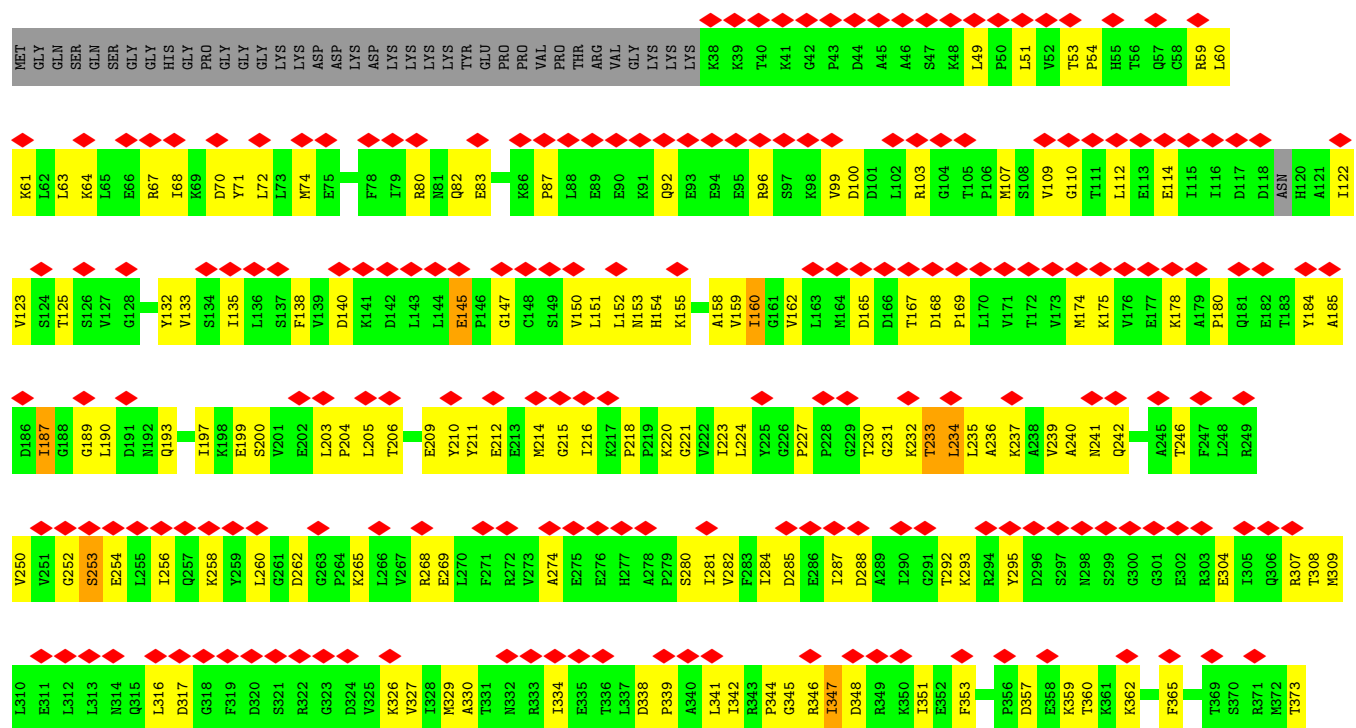


• Molecule 28: 26S protease regulatory subunit 7

Chain A: 54% 57% 35% 7%



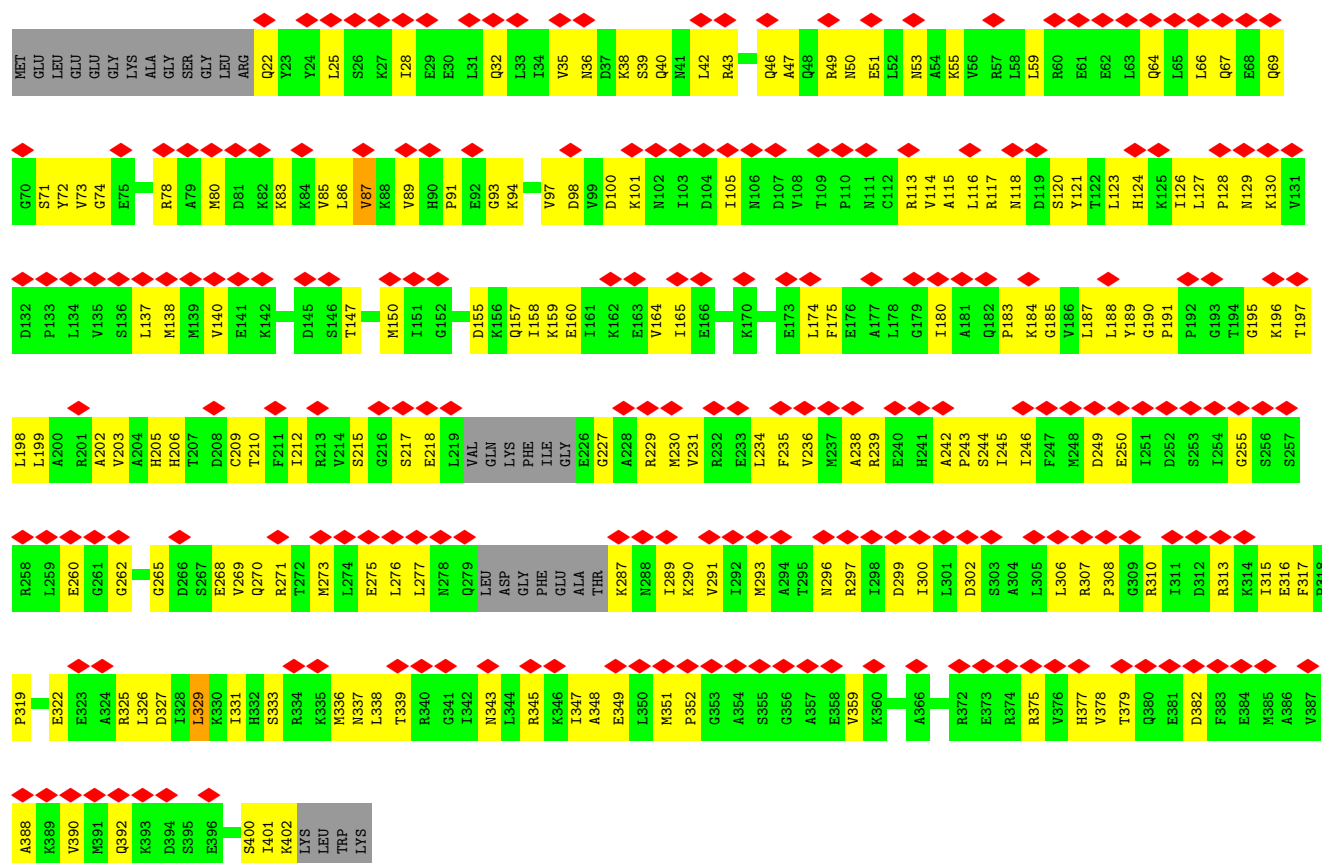
• Molecule 29: 26S protease regulatory subunit 4





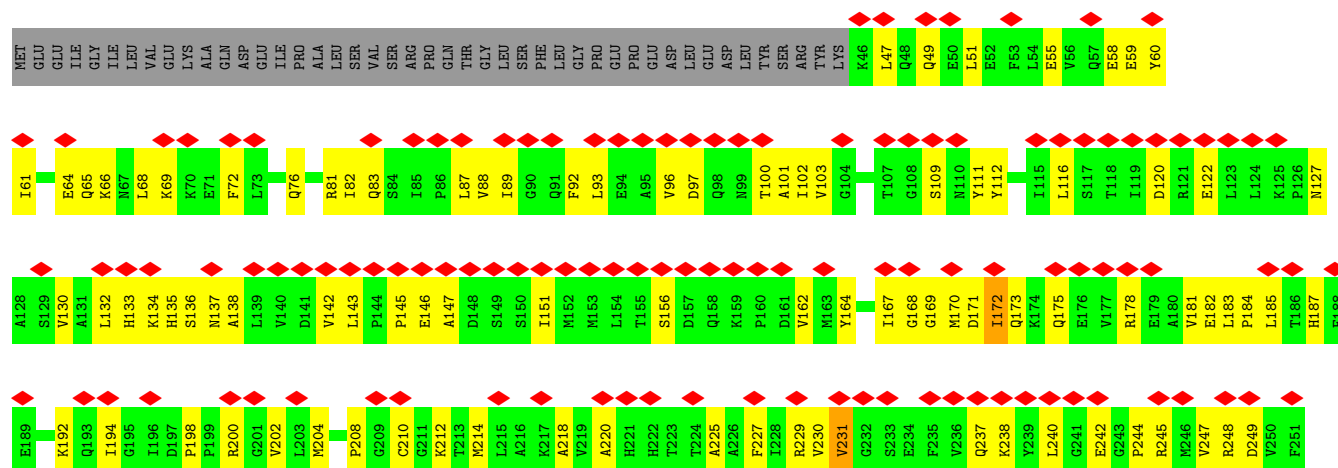
- Molecule 30: Isoform 2 of 26S proteasome regulatory subunit 8

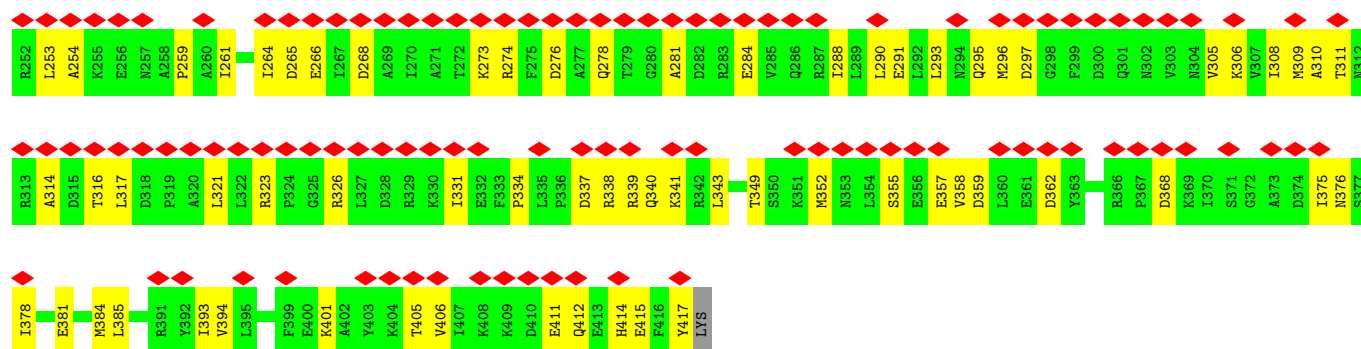
Chain C:



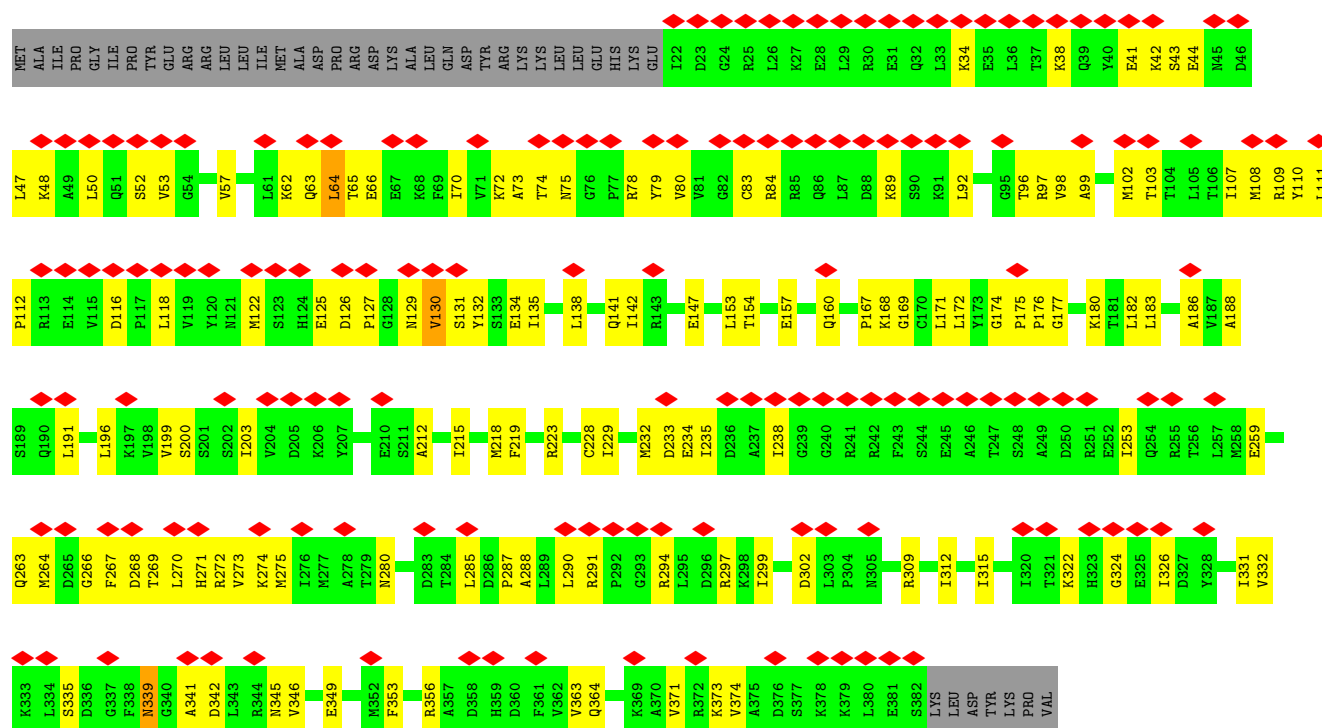
- Molecule 31: 26S protease regulatory subunit 6B

Chain D:

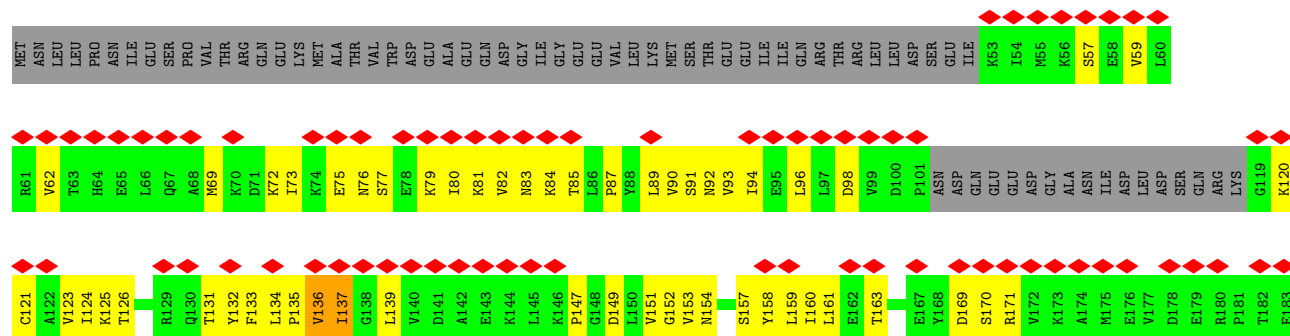
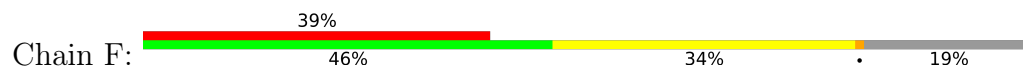


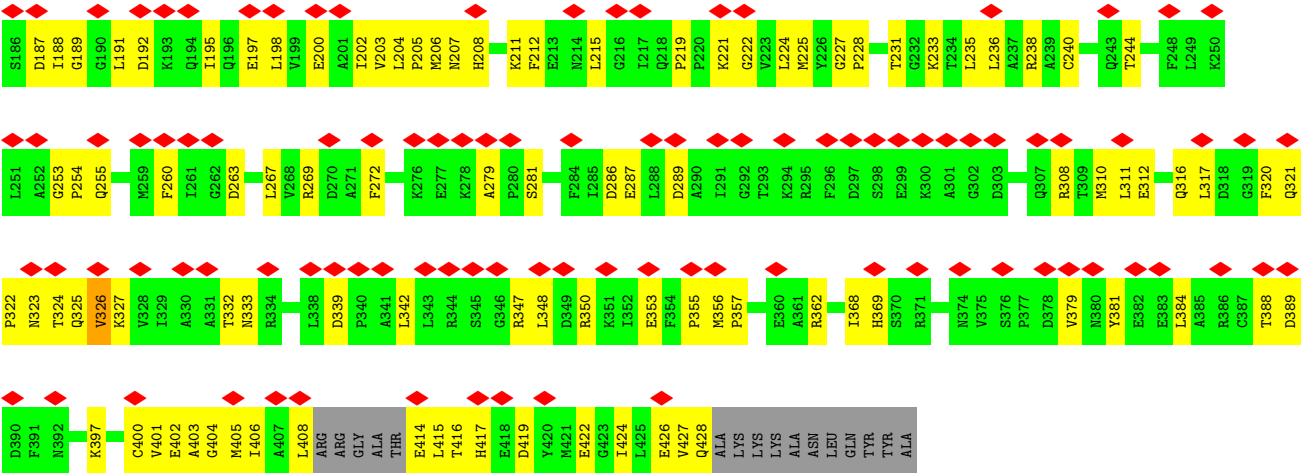


• Molecule 32: 26S proteasome regulatory subunit 10B



• Molecule 33: 26S protease regulatory subunit 6A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19267	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.285	Depositor
Minimum map value	-1.034	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.105	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	423.9, 423.9, 423.9	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.413, 1.413, 1.413	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	G	0.11	0/1873	0.33	1/2533 (0.0%)
1	g	0.13	0/1918	0.34	0/2592
2	H	0.13	0/1784	0.38	0/2416
2	h	0.11	0/1848	0.31	0/2502
3	I	0.12	0/1956	0.32	0/2637
3	i	0.12	0/2001	0.33	0/2694
4	J	0.15	0/1890	0.40	0/2550
4	j	0.11	0/1904	0.30	0/2569
5	L	0.12	0/1899	0.31	0/2567
5	l	0.10	0/1899	0.30	0/2567
6	M	0.12	0/1897	0.33	0/2555
6	m	0.13	0/1916	0.34	0/2580
7	K	0.13	0/1718	0.41	1/2319 (0.0%)
7	k	0.09	0/1817	0.27	0/2455
8	N	0.10	0/1548	0.27	0/2097
8	n	0.11	0/1540	0.30	0/2085
9	O	0.12	0/1686	0.32	0/2282
9	o	0.11	0/1686	0.30	0/2282
10	P	0.11	0/1620	0.33	0/2184
10	p	0.11	0/1620	0.30	0/2184
11	Q	0.12	0/1603	0.35	0/2168
11	q	0.11	0/1603	0.33	0/2168
12	R	0.09	0/1590	0.27	0/2147
12	r	0.14	0/1590	0.27	0/2147
13	S	0.12	0/1673	0.34	0/2254
13	s	0.11	0/1684	0.31	0/2268
14	T	0.09	0/1720	0.25	0/2328
14	t	0.10	0/1720	0.29	0/2328
15	f	0.12	0/6385	0.33	0/8637
16	x	0.07	0/643	0.26	0/868
17	a	0.11	0/3023	0.32	0/4093
18	b	0.11	0/1478	0.35	0/2001

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	c	0.12	0/2260	0.37	0/3052
20	d	0.11	0/2109	0.33	0/2851
21	e	0.11	0/415	0.36	0/563
22	U	0.11	0/6750	0.32	0/9116
23	V	0.11	0/3667	0.30	0/4951
24	X	0.10	0/3045	0.28	0/4104
25	Y	0.11	0/3063	0.34	0/4123
26	Z	0.11	0/2286	0.33	0/3099
27	W	0.12	0/3610	0.36	0/4853
28	A	0.14	0/3165	0.36	0/4273
29	B	0.18	0/3100	0.52	2/4189 (0.0%)
30	C	0.16	0/2865	0.42	0/3851
31	D	0.14	0/2945	0.39	0/3979
32	E	0.13	0/2811	0.38	0/3791
33	F	0.13	0/2726	0.38	0/3682
All	All	0.12	0/105549	0.34	4/142534 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	B	233	THR	N-CA-C	-12.27	98.79	113.88
29	B	234	LEU	N-CA-C	-11.70	98.11	112.38
7	K	24	VAL	N-CA-C	-6.75	106.21	112.96
1	G	208	ILE	N-CA-C	-5.28	107.58	112.43

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1841	0	1848	63	0
1	g	1885	0	1891	74	0
2	H	1749	0	1750	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	h	1809	0	1800	63	0
3	I	1927	0	1936	66	0
3	i	1971	0	1992	72	0
4	J	1865	0	1887	77	0
4	j	1878	0	1899	59	0
5	L	1864	0	1852	59	0
5	l	1864	0	1852	71	0
6	M	1862	0	1842	58	0
6	m	1881	0	1868	78	0
7	K	1694	0	1691	66	0
7	k	1789	0	1773	61	0
8	N	1521	0	1494	58	0
8	n	1514	0	1487	59	0
9	O	1659	0	1681	43	0
9	o	1659	0	1681	49	0
10	P	1591	0	1609	78	0
10	p	1591	0	1609	46	0
11	Q	1571	0	1573	61	0
11	q	1571	0	1573	63	0
12	R	1559	0	1523	51	0
12	r	1559	0	1523	53	0
13	S	1643	0	1640	52	0
13	s	1654	0	1656	50	0
14	T	1687	0	1666	50	0
14	t	1687	0	1666	68	0
15	f	6292	0	6314	252	0
16	x	635	0	652	15	0
17	a	2969	0	2984	98	0
18	b	1458	0	1505	66	0
19	c	2224	0	2240	105	0
20	d	2063	0	2078	79	0
21	e	407	0	312	15	0
22	U	6648	0	6715	257	0
23	V	3600	0	3668	146	0
24	X	3002	0	3106	89	0
25	Y	3021	0	3022	115	0
26	Z	2248	0	2277	82	0
27	W	3570	0	3696	146	0
28	A	3119	0	3162	123	0
29	B	3060	0	3090	164	0
30	C	2839	0	2942	169	0
31	D	2904	0	2925	139	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	E	2776	0	2816	133	0
33	F	2694	0	2736	136	0
34	A	31	0	12	2	0
35	B	27	0	12	5	0
35	C	27	0	12	5	0
35	D	27	0	12	3	0
35	E	27	0	12	1	0
35	F	27	0	12	3	0
All	All	104040	0	104574	3585	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (3585) 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)
6:M:186:CYS:SG	6:M:219:LEU:HD13	1.90	1.12
22:U:633:CYS:SG	22:U:634:PRO:HD3	2.02	0.99
15:f:803:PHE:HA	15:f:806:VAL:HG13	1.47	0.97
33:F:154:ASN:HB2	33:F:159:LEU:H	1.34	0.93
26:Z:252:LYS:HG3	26:Z:255:ASP:HB2	1.54	0.90
29:B:114:GLU:HB3	29:B:122:ILE:HB	1.52	0.90
12:r:166:ARG:HH21	11:Q:140:LEU:HD13	1.37	0.89
33:F:381:TYR:HA	33:F:384:LEU:HD13	1.54	0.89
22:U:630:PRO:O	22:U:633:CYS:SG	2.31	0.88
29:B:234:LEU:HD13	29:B:330:ALA:HB1	1.54	0.88
22:U:554:LEU:HD13	22:U:761:VAL:HG21	1.57	0.86
22:U:685:GLN:HB2	22:U:729:GLY:HA3	1.57	0.86
11:q:145:ARG:HG2	12:R:158:ARG:HE	1.41	0.85
2:H:71:HIS:HB2	2:H:107:THR:HG21	1.57	0.84
1:G:88:ARG:HG3	6:M:156:VAL:HG21	1.58	0.84
22:U:583:MET:HE3	22:U:618:ALA:HA	1.58	0.84
16:x:82:LEU:HD11	16:x:89:LEU:HD21	1.59	0.83
25:Y:101:ARG:NH1	25:Y:105:MET:SD	2.52	0.83
23:V:353:LEU:HB3	23:V:357:LEU:HD23	1.61	0.83
28:A:140:VAL:HG11	28:A:149:ILE:HG23	1.59	0.83
14:T:63:LEU:HD21	14:T:106:LEU:HD13	1.59	0.82
5:L:13:TRP:HA	5:L:19:ILE:HG22	1.60	0.82
23:V:302:TYR:HB3	23:V:339:LEU:HD21	1.59	0.82
4:J:88:ARG:HH11	11:Q:70:ARG:HA	1.45	0.82
22:U:521:LEU:HD13	22:U:554:LEU:HD12	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:186:CYS:SG	6:M:219:LEU:CD1	2.69	0.81
4:J:40:ILE:HD11	4:J:210:VAL:HG13	1.64	0.80
1:g:52:THR:HG21	1:g:79:VAL:HG21	1.63	0.80
6:M:41:CYS:SG	6:M:186:CYS:HB3	2.22	0.80
3:I:22:GLU:HG2	29:B:435:PRO:HG2	1.64	0.79
2:h:121:TYR:HD1	2:h:127:VAL:HG21	1.47	0.79
6:M:47:PHE:HB2	6:M:214:SER:HB3	1.64	0.79
20:d:122:LEU:HB3	20:d:125:LYS:HB3	1.63	0.79
22:U:880:ASN:OD1	22:U:881:PRO:HD3	1.83	0.79
15:f:538:ILE:HG23	15:f:558:LEU:HD12	1.65	0.79
5:l:126:ARG:HB3	7:k:13:ASN:HB3	1.65	0.78
28:A:33:LEU:HA	28:A:36:TYR:HB2	1.65	0.78
31:D:376:ASN:ND2	35:D:501:ADP:N3	2.30	0.78
22:U:619:VAL:HG23	22:U:651:GLY:HA3	1.64	0.78
30:C:59:LEU:HG	31:D:116:LEU:HD12	1.63	0.78
20:d:203:PRO:HG2	20:d:205:LYS:HB3	1.64	0.78
19:c:211:GLU:HB3	19:c:215:LYS:HE3	1.66	0.78
26:Z:99:PRO:HA	26:Z:123:ILE:HD13	1.65	0.78
3:I:38:LEU:HA	3:I:43:VAL:HG23	1.65	0.78
23:V:399:ARG:HH21	23:V:402:VAL:HG11	1.49	0.78
22:U:583:MET:HE1	22:U:621:SER:HB2	1.66	0.78
30:C:67:GLN:HA	31:D:136:SER:HA	1.65	0.77
2:H:92:LYS:HG2	9:O:65:LEU:HD11	1.66	0.77
5:L:226:ASP:OD1	5:L:227:ASP:N	2.18	0.77
15:f:720:GLU:HB2	15:f:807:ARG:HD3	1.66	0.77
32:E:322:LYS:HE2	33:F:215:LEU:HD22	1.65	0.77
6:M:190:VAL:HG21	6:M:215:TRP:HE1	1.50	0.77
31:D:168:GLY:H	35:D:501:ADP:HN62	1.32	0.77
33:F:235:LEU:HD11	35:F:501:ADP:H2'	1.66	0.77
19:c:141:VAL:HG12	19:c:161:ARG:HE	1.48	0.76
19:c:88:ASP:HB3	19:c:91:PHE:HB3	1.66	0.76
13:s:27:THR:HB	13:s:40:SER:H	1.49	0.76
31:D:411:GLU:HG2	31:D:412:GLN:H	1.49	0.76
13:s:158:MET:SD	10:P:169:GLN:NE2	2.59	0.76
12:R:161:TYR:HH	12:R:196:HIS:HD1	1.30	0.76
7:K:230:THR:HG22	7:K:233:GLU:HB2	1.66	0.76
5:l:125:ARG:HH21	5:l:126:ARG:HG2	1.51	0.76
33:F:369:HIS:ND1	33:F:400:CYS:SG	2.58	0.76
9:o:193:ASN:HD21	13:S:211:ARG:HB3	1.48	0.75
20:d:155:LYS:HD3	20:d:170:LEU:HD22	1.68	0.75
6:m:198:TYR:HB3	6:m:243:LEU:HD21	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:b:3:LEU:HD11	18:b:44:ASN:HD22	1.51	0.75
31:D:264:ILE:HB	31:D:309:MET:HG3	1.68	0.75
12:R:125:THR:OG1	12:R:139:MET:SD	2.44	0.75
31:D:244:PRO:HB3	31:D:291:GLU:HG3	1.68	0.75
15:f:604:GLY:HA2	15:f:661:ALA:HB2	1.68	0.75
26:Z:34:ARG:NH1	26:Z:97:THR:O	2.20	0.75
31:D:358:VAL:HG23	31:D:394:VAL:HB	1.69	0.75
22:U:610:VAL:HA	22:U:615:ARG:HE	1.51	0.75
26:Z:102:HIS:HE1	26:Z:104:ASN:HB3	1.52	0.74
3:I:133:SER:HB2	3:I:152:PRO:HD3	1.67	0.74
5:l:81:ALA:HB2	5:l:130:VAL:HG21	1.69	0.74
30:C:73:VAL:H	31:D:111:TYR:HA	1.52	0.74
17:a:352:ARG:HH12	26:Z:235:ASN:HB3	1.51	0.74
29:B:51:LEU:O	29:B:64:LYS:NZ	2.21	0.74
15:f:461:PRO:HA	16:x:76:ILE:HG21	1.70	0.74
23:V:340:GLY:HA3	23:V:408:ARG:HH12	1.50	0.74
6:M:63:ASN:HB2	6:M:81:LEU:HD21	1.69	0.74
6:M:77:VAL:HG23	6:M:135:PHE:HB3	1.70	0.74
11:Q:85:ARG:NH2	10:P:58:THR:O	2.20	0.74
15:f:160:ARG:HH12	29:B:413:LYS:HE3	1.50	0.74
22:U:12:LEU:HB3	22:U:48:LEU:HD21	1.69	0.74
24:X:182:ASN:HD21	25:Y:248:GLU:HB2	1.53	0.74
22:U:202:VAL:HG21	22:U:223:LEU:HD22	1.68	0.74
26:Z:90:ARG:HE	26:Z:91:ILE:H	1.33	0.74
22:U:571:CYS:SG	22:U:601:ARG:NH1	2.61	0.74
2:H:26:LEU:HA	2:H:29:VAL:HG12	1.70	0.74
23:V:215:ALA:HB3	23:V:253:LEU:HD22	1.69	0.74
33:F:353:GLU:HG3	33:F:355:PRO:HD3	1.70	0.73
29:B:421:LYS:O	29:B:425:ASN:ND2	2.21	0.73
5:L:129:GLY:HA2	5:L:149:PRO:HB3	1.70	0.73
8:n:122:ARG:HH22	8:N:202:LEU:HB2	1.51	0.73
22:U:637:VAL:HG21	22:U:656:LEU:HD11	1.69	0.73
28:A:229:VAL:HG21	28:A:237:PHE:HD2	1.53	0.73
13:s:185:ARG:HG3	10:P:147:TYR:HB3	1.69	0.73
27:W:360:GLU:HG3	27:W:396:LEU:HD21	1.70	0.73
30:C:322:GLU:HB2	30:C:349:GLU:HG2	1.71	0.73
9:o:104:ASP:O	9:o:180:LYS:NZ	2.21	0.73
12:r:8:PHE:HE1	12:r:13:ILE:HG12	1.52	0.73
15:f:369:ARG:HH12	15:f:756:PRO:HB2	1.52	0.73
13:S:57:PHE:HD1	13:S:60:ASP:H	1.36	0.73
24:X:255:LEU:HD11	24:X:267:VAL:HG13	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:237:ARG:HA	25:Y:241:ILE:HB	1.70	0.72
26:Z:20:VAL:HG13	26:Z:126:VAL:HG13	1.71	0.72
30:C:64:GLN:OE1	30:C:67:GLN:NE2	2.22	0.72
20:d:131:VAL:HA	20:d:134:LYS:HG2	1.70	0.72
24:X:142:ARG:NH2	24:X:145:GLU:OE1	2.22	0.72
11:Q:101:ASN:HB3	11:Q:132:HIS:CE1	2.25	0.72
10:P:59:ASP:HA	10:P:62:THR:HG22	1.72	0.72
5:l:123:TYR:HH	3:i:2:SER:N	1.87	0.72
10:p:15:LYS:HE3	10:p:121:ILE:HG12	1.70	0.72
14:T:43:MET:HE1	14:T:67:LEU:HD23	1.72	0.72
28:A:190:VAL:HG13	28:A:209:PRO:HB2	1.71	0.72
29:B:233:THR:N	35:B:501:ADP:O1A	2.22	0.72
8:n:121:VAL:HG21	14:t:39:ILE:HG22	1.71	0.72
15:f:672:LEU:HD11	15:f:706:ILE:HG12	1.71	0.72
17:a:205:LEU:HB3	17:a:268:LEU:HD11	1.70	0.72
20:d:117:THR:HG21	23:V:265:ASP:HB3	1.72	0.72
22:U:237:VAL:HG13	22:U:321:GLN:H	1.53	0.72
27:W:178:GLU:H	27:W:182:ARG:HB2	1.54	0.72
28:A:97:ARG:HG3	28:A:144:ARG:H	1.54	0.72
22:U:205:TYR:HB3	22:U:215:ASN:HB2	1.72	0.72
27:W:48:LEU:HD23	27:W:51:GLU:OE2	1.88	0.72
8:n:30:VAL:HG21	14:T:212:ALA:HA	1.72	0.71
26:Z:94:TRP:HB3	26:Z:112:MET:HE3	1.71	0.71
16:x:74:LYS:HB2	16:x:103:ILE:HB	1.72	0.71
28:A:333:ARG:O	28:A:337:LEU:N	2.23	0.71
21:e:27:TRP:NE1	23:V:351:PRO:O	2.22	0.71
26:Z:193:ASN:HA	26:Z:196:HIS:CE1	2.25	0.71
32:E:234:GLU:OE2	32:E:280:ASN:ND2	2.23	0.71
1:G:49:VAL:HG12	1:G:219:VAL:HG22	1.72	0.71
1:g:163:PHE:HA	2:h:58:ASP:H	1.55	0.71
19:c:234:TYR:HA	19:c:237:HIS:HB2	1.72	0.71
14:T:122:LEU:HG	14:T:137:LEU:HD12	1.72	0.71
31:D:355:SER:HB3	31:D:358:VAL:HB	1.72	0.71
32:E:34:LYS:HD3	33:F:62:VAL:HG22	1.72	0.71
8:n:12:VAL:HG11	8:n:101:ALA:HB1	1.73	0.71
28:A:56:LEU:O	28:A:60:ASN:ND2	2.22	0.71
9:O:41:ILE:HG22	9:O:102:GLY:HA3	1.70	0.71
18:b:37:CYS:HG	18:b:68:THR:HG1	1.34	0.71
4:j:92:GLN:HB3	11:q:62:LYS:HD2	1.73	0.71
14:t:43:MET:HE1	14:t:67:LEU:HD23	1.70	0.71
21:e:27:TRP:HA	23:V:355:ARG:HE	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A:102:ILE:HA	28:A:113:ILE:HG23	1.70	0.71
30:C:89:VAL:HG12	30:C:91:PRO:HD2	1.72	0.71
1:G:43:ARG:HB3	1:G:164:LYS:HA	1.71	0.70
27:W:117:ASP:HB3	27:W:120:ILE:HG12	1.72	0.70
8:n:119:MET:HE3	14:t:58:ALA:HB2	1.73	0.70
22:U:616:ARG:HB3	22:U:647:HIS:HB2	1.73	0.70
29:B:110:GLY:HA3	29:B:125:THR:HA	1.73	0.70
33:F:379:VAL:HG22	33:F:416:THR:HG23	1.72	0.70
1:G:49:VAL:HG22	1:G:194:THR:HG22	1.71	0.70
15:f:344:VAL:HG12	15:f:346:ASP:H	1.57	0.70
27:W:186:ILE:HG21	27:W:209:ILE:HG21	1.71	0.70
4:J:67:ASP:HB3	11:Q:69:MET:HE1	1.71	0.70
3:i:180:LYS:H	3:i:184:MET:HE2	1.56	0.70
15:f:408:LEU:HB3	15:f:815:HIS:HE1	1.57	0.70
15:f:809:ILE:HG12	15:f:814:SER:HB3	1.74	0.70
5:l:52:ALA:HB1	5:l:57:ALA:HB3	1.73	0.70
17:a:71:VAL:HG21	17:a:76:LEU:HD22	1.73	0.70
2:H:159:LYS:NZ	2:H:180:GLU:O	2.22	0.70
4:J:158:ALA:HB3	7:K:58:LEU:HD13	1.74	0.70
13:S:27:THR:HB	13:S:40:SER:H	1.55	0.70
17:a:177:LEU:HD11	17:a:216:LEU:HD23	1.74	0.70
32:E:309:ARG:HE	32:E:332:VAL:HG13	1.55	0.70
32:E:177:GLY:HA2	32:E:339:ASN:HB2	1.74	0.70
13:s:110:ILE:HB	13:s:122:TYR:HB2	1.74	0.69
19:c:216:MET:HG2	19:c:220:LEU:HD12	1.73	0.69
12:r:97:MET:H	12:r:116:SER:HB3	1.55	0.69
13:s:24:ALA:HB1	13:s:193:LEU:HD11	1.74	0.69
13:S:28:ARG:NH1	13:S:187:VAL:O	2.25	0.69
22:U:159:ARG:HB3	22:U:162:VAL:HB	1.74	0.69
23:V:315:LYS:HA	25:Y:385:ARG:HG3	1.74	0.69
12:r:63:CYS:HB2	12:r:74:ILE:HG21	1.74	0.69
19:c:63:ASP:OD2	22:U:543:LYS:NZ	2.25	0.69
29:B:211:TYR:HA	29:B:214:MET:HB2	1.75	0.69
22:U:633:CYS:SG	22:U:634:PRO:CD	2.78	0.69
4:J:134:VAL:HG12	4:J:144:LEU:HD13	1.73	0.69
2:h:11:THR:HB	2:h:21:GLN:HE21	1.57	0.69
9:o:62:ASN:ND2	9:o:82:MET:SD	2.66	0.69
6:M:35:THR:HA	6:M:166:GLY:HA3	1.74	0.69
6:m:214:SER:HB3	6:m:226:ILE:HD12	1.75	0.69
18:b:109:ILE:HB	18:b:138:VAL:HG22	1.73	0.69
33:F:134:LEU:HD21	33:F:160:ILE:HG12	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:201:ILE:O	7:K:205:VAL:HG23	1.92	0.69
15:f:668:ALA:HB1	15:f:697:ILE:HG23	1.74	0.69
19:c:255:TYR:HD1	19:c:280:PRO:HG3	1.58	0.69
22:U:619:VAL:HG11	22:U:648:VAL:HG13	1.74	0.69
23:V:367:VAL:HA	23:V:402:VAL:HG23	1.75	0.69
32:E:131:SER:O	32:E:135:ILE:HG12	1.93	0.69
10:P:78:GLU:HG2	10:P:80:ARG:H	1.58	0.69
15:f:836:GLU:HG3	15:f:838:ARG:HG2	1.73	0.69
27:W:152:ILE:HD13	27:W:161:GLU:HB3	1.75	0.69
27:W:183:VAL:HG11	27:W:215:GLN:HE22	1.57	0.69
28:A:232:ARG:HH22	28:A:271:LEU:HB3	1.58	0.69
31:D:412:GLN:HE22	31:D:415:GLU:HB3	1.58	0.69
4:J:108:THR:HG21	4:J:145:TYR:HB2	1.75	0.69
22:U:342:LEU:O	22:U:346:ASN:HB2	1.93	0.69
2:H:74:LEU:HD11	2:H:134:LEU:HD12	1.75	0.68
11:q:169:LYS:O	11:Q:27:GLN:NE2	2.26	0.68
19:c:58:LEU:HD13	19:c:73:PHE:HE2	1.57	0.68
29:B:220:LYS:NZ	29:B:345:GLY:O	2.24	0.68
3:I:80:THR:HG22	30:C:401:ILE:HA	1.75	0.68
6:M:59:GLU:HG2	6:M:60:GLU:H	1.57	0.68
22:U:619:VAL:HG21	22:U:648:VAL:HA	1.75	0.68
23:V:191:LEU:HD21	23:V:210:CYS:HB3	1.75	0.68
11:q:26:VAL:HG11	12:r:136:TYR:HE2	1.56	0.68
19:c:54:MET:HG2	19:c:113:HIS:HD2	1.58	0.68
20:d:129:THR:HG22	20:d:130:ASN:H	1.58	0.68
24:X:343:SER:HB2	27:W:405:LYS:HB3	1.74	0.68
25:Y:157:ILE:HG22	25:Y:186:LEU:HD12	1.76	0.68
27:W:390:GLU:OE1	27:W:408:ARG:NH1	2.26	0.68
3:I:28:ILE:HG21	3:I:133:SER:HB3	1.75	0.68
7:k:52:LYS:NZ	7:k:64:ILE:O	2.26	0.68
15:f:456:ARG:NH2	15:f:488:ALA:O	2.27	0.68
17:a:33:LEU:HD21	18:b:145:GLU:HG3	1.75	0.68
30:C:202:ALA:O	30:C:205:HIS:ND1	2.26	0.68
14:t:209:TRP:HB2	8:N:190:LEU:HD12	1.76	0.68
7:K:235:GLU:HA	7:K:238:ILE:HG12	1.76	0.68
9:O:187:ARG:HB3	9:O:188:PRO:HD2	1.75	0.68
17:a:72:ASN:HA	18:b:17:ARG:HH22	1.59	0.68
29:B:216:ILE:HG13	29:B:218:PRO:HD3	1.75	0.68
3:i:18:LEU:HD12	3:i:20:GLN:HE22	1.58	0.68
13:S:68:ILE:HD11	13:S:92:LEU:HD13	1.75	0.68
19:c:220:LEU:HB3	26:Z:134:PRO:HB3	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:C:270:GLN:NE2	30:C:273:MET:SD	2.67	0.68
2:H:110:LEU:HD12	2:H:113:ARG:HB2	1.75	0.68
25:Y:256:VAL:HA	25:Y:259:TYR:CE2	2.29	0.68
26:Z:102:HIS:CE1	26:Z:104:ASN:HB3	2.29	0.68
27:W:248:ARG:HH12	27:W:289:ARG:HD2	1.59	0.68
15:f:505:MET:SD	15:f:518:THR:OG1	2.51	0.68
25:Y:23:ARG:NH2	25:Y:52:PRO:O	2.26	0.68
30:C:325:ARG:NH2	30:C:351:MET:O	2.27	0.67
33:F:81:LYS:HA	33:F:84:LYS:HB3	1.76	0.67
9:o:63:LEU:HD11	9:o:79:ALA:HB2	1.77	0.67
17:a:251:LEU:HG	17:a:255:TRP:HE1	1.58	0.67
28:A:269:ALA:HB1	28:A:315:ILE:HG12	1.76	0.67
14:t:122:LEU:HG	14:t:137:LEU:HD12	1.75	0.67
22:U:347:ASN:ND2	22:U:741:GLY:O	2.25	0.67
22:U:643:SER:O	22:U:649:ARG:NE	2.23	0.67
31:D:202:VAL:HB	31:D:308:ILE:HG12	1.76	0.67
4:J:104:VAL:HG21	4:J:143:ARG:HB2	1.76	0.67
5:l:85:CYS:SG	5:l:89:ARG:NH2	2.68	0.67
14:t:91:TRP:HE3	14:t:92:LEU:HD22	1.60	0.67
9:O:13:VAL:HG22	9:O:177:VAL:HG12	1.75	0.67
6:m:236:GLU:OE2	6:m:240:LYS:NZ	2.27	0.67
22:U:475:HIS:NE2	22:U:507:VAL:O	2.28	0.67
25:Y:247:LEU:O	25:Y:251:HIS:ND1	2.26	0.67
29:B:233:THR:C	29:B:235:LEU:N	2.45	0.67
4:J:12:PRO:HG3	7:K:26:TYR:CE2	2.30	0.67
13:s:36:HIS:O	14:t:151:ARG:NH1	2.28	0.67
1:g:176:THR:HG23	2:h:56:LEU:HD21	1.76	0.67
7:k:146:VAL:HG11	7:k:222:PRO:HA	1.75	0.67
27:W:243:ILE:HA	27:W:246:HIS:CE1	2.29	0.67
10:p:149:MET:HG2	10:p:170:ALA:HA	1.77	0.67
22:U:265:ILE:HD11	22:U:326:ILE:HA	1.77	0.67
26:Z:60:GLU:OE2	26:Z:102:HIS:NE2	2.28	0.67
4:J:95:ARG:HG3	11:Q:62:LYS:HZ1	1.60	0.67
27:W:167:GLN:O	27:W:170:GLN:NE2	2.27	0.67
32:E:172:LEU:HG	32:E:299:ILE:HD11	1.76	0.67
1:G:208:ILE:HD13	32:E:287:PRO:HG2	1.77	0.66
3:i:48:GLU:OE2	3:i:210:LYS:NZ	2.28	0.66
19:c:163:ILE:HD12	19:c:167:MET:HB2	1.77	0.66
33:F:206:MET:HE2	33:F:327:LYS:HG2	1.76	0.66
4:J:87:ALA:HB1	4:J:107:ILE:HD11	1.77	0.66
5:L:67:ASP:OD1	5:L:68:ASN:N	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:R:103:GLY:HA2	12:R:179:VAL:HG11	1.76	0.66
19:c:130:GLN:HG3	19:c:142:ALA:HB2	1.77	0.66
29:B:53:THR:H	29:B:64:LYS:HZ3	1.41	0.66
29:B:253:SER:OG	29:B:254:GLU:N	2.26	0.66
2:H:148:GLN:OE1	2:H:158:TRP:NE1	2.26	0.66
5:l:107:ARG:HH12	14:t:83:TYR:HE1	1.44	0.66
2:h:68:ILE:HG21	2:h:110:LEU:HD11	1.78	0.66
6:m:70:ASP:OD1	6:m:99:ARG:NH2	2.28	0.66
10:P:15:LYS:HB2	10:P:121:ILE:HD13	1.77	0.66
3:i:111:VAL:HG22	3:i:136:TYR:HD2	1.59	0.66
23:V:219:GLU:OE1	23:V:256:ARG:NH1	2.29	0.66
1:G:153:LYS:HZ1	1:G:168:ALA:HB2	1.61	0.66
2:H:34:PRO:HA	2:H:164:GLY:HA3	1.77	0.66
14:T:99:ARG:NH2	14:T:104:ASN:OD1	2.25	0.66
29:B:232:LYS:NZ	30:C:308:PRO:HG3	2.11	0.66
1:g:61:LEU:HA	6:m:160:TYR:HA	1.76	0.66
7:k:50:VAL:HG11	7:k:66:LYS:HB2	1.78	0.66
22:U:376:MET:HE2	22:U:738:ASP:HB3	1.78	0.66
23:V:307:ARG:O	23:V:311:ASN:ND2	2.27	0.66
32:E:48:LYS:HB2	33:F:76:ASN:ND2	2.11	0.66
27:W:242:SER:O	27:W:246:HIS:ND1	2.28	0.66
3:I:84:ASN:O	3:I:88:ASN:ND2	2.25	0.66
14:T:25:ASP:HA	14:T:187:PHE:HA	1.76	0.66
15:f:482:ILE:HD13	15:f:518:THR:HG22	1.77	0.66
24:X:182:ASN:HA	25:Y:244:ALA:HB1	1.77	0.66
29:B:125:THR:HG21	29:B:152:LEU:HD22	1.77	0.66
3:i:109:GLN:OE1	11:q:71:ASN:ND2	2.29	0.65
11:Q:35:MET:HG3	11:Q:181:ARG:HH11	1.60	0.65
2:H:104:PRO:HD2	2:H:106:PRO:HD3	1.77	0.65
14:T:25:ASP:O	14:T:41:ARG:NH1	2.30	0.65
22:U:13:ASP:OD2	22:U:44:LYS:NZ	2.30	0.65
30:C:234:LEU:HD23	30:C:238:ALA:HB3	1.78	0.65
30:C:250:GLU:HG3	30:C:296:ASN:H	1.62	0.65
3:I:116:ASP:OD1	4:J:81:ARG:NH1	2.29	0.65
22:U:367:THR:HB	22:U:403:THR:HG21	1.78	0.65
2:H:93:LEU:HD13	2:H:117:VAL:HG12	1.77	0.65
4:J:40:ILE:HD12	4:J:212:ARG:HG2	1.76	0.65
11:q:173:LEU:HA	11:Q:173:LEU:HA	1.77	0.65
13:s:66:LYS:HG3	14:t:94:ARG:NH2	2.12	0.65
15:f:469:TYR:HA	15:f:472:HIS:HB2	1.77	0.65
30:C:91:PRO:HD3	31:D:109:SER:HA	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:D:237:GLN:HG2	31:D:238:LYS:H	1.61	0.65
5:l:200:PRO:O	5:l:239:ARG:NH1	2.28	0.65
9:o:121:LYS:NZ	14:T:215:ILE:O	2.29	0.65
28:A:369:ARG:HB3	28:A:372:LEU:HD13	1.77	0.65
33:F:260:PHE:HB3	33:F:263:ASP:HB2	1.79	0.65
25:Y:291:HIS:HA	25:Y:295:TYR:CZ	2.32	0.65
28:A:76:ALA:HA	28:A:80:LEU:HB2	1.78	0.65
32:E:131:SER:HA	32:E:134:GLU:HB2	1.79	0.65
2:h:160:ALA:HB3	3:i:55:LEU:HD22	1.79	0.65
4:j:116:GLN:OE1	7:k:135:ARG:NH2	2.29	0.65
11:q:172:ILE:HG23	11:q:173:LEU:HD12	1.78	0.65
8:N:98:ILE:HB	8:N:114:VAL:HG23	1.79	0.65
23:V:338:LEU:HD11	23:V:397:ARG:HD2	1.78	0.65
24:X:404:ILE:HG12	26:Z:262:LEU:HD21	1.79	0.65
6:m:46:VAL:HG12	6:m:215:TRP:HB3	1.78	0.65
9:o:211:VAL:HG21	10:p:198:ARG:HD3	1.79	0.65
12:R:44:THR:H	12:R:99:THR:HG23	1.60	0.65
15:f:151:LEU:HD12	15:f:158:TYR:HE2	1.60	0.65
26:Z:15:VAL:HG11	26:Z:50:VAL:HG12	1.79	0.65
27:W:236:HIS:ND1	27:W:237:GLU:OE2	2.29	0.65
31:D:185:LEU:O	31:D:187:HIS:ND1	2.29	0.65
2:H:95:GLN:HG3	9:O:61:SER:HB3	1.79	0.65
13:S:27:THR:HG22	13:S:41:PRO:HA	1.79	0.65
25:Y:250:LEU:HB3	25:Y:257:ARG:HB2	1.77	0.65
33:F:84:LYS:HA	33:F:161:LEU:HD13	1.77	0.65
19:c:29:GLU:OE1	19:c:161:ARG:NH2	2.29	0.65
19:c:46:ARG:HH21	26:Z:167:ALA:HB2	1.62	0.65
23:V:212:TYR:HA	23:V:253:LEU:HD11	1.78	0.65
24:X:195:THR:HA	31:D:170:MET:HE3	1.79	0.65
7:K:42:THR:HG23	7:K:45:GLY:H	1.62	0.64
1:g:12:HIS:O	1:g:24:GLN:NE2	2.30	0.64
22:U:792:ASN:HB3	22:U:914:LEU:HB3	1.78	0.64
28:A:397:ILE:HD13	29:B:211:TYR:HB3	1.79	0.64
31:D:130:VAL:HG12	31:D:142:VAL:HG13	1.80	0.64
7:K:35:SER:HB2	7:K:66:LYS:HE2	1.79	0.64
9:o:70:THR:HG23	9:o:72:ARG:H	1.62	0.64
15:f:852:VAL:HG22	29:B:185:ALA:HB1	1.79	0.64
13:S:60:ASP:OD1	14:T:100:ARG:NH2	2.30	0.64
15:f:781:TYR:O	15:f:785:ARG:NH1	2.27	0.64
22:U:62:LEU:HD12	22:U:87:LEU:HB3	1.77	0.64
27:W:265:GLN:HB2	27:W:336:PRO:HD3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:180:GLU:OE1	2:H:182:LEU:N	2.30	0.64
12:r:167:ASP:OD1	12:r:168:ALA:N	2.29	0.64
25:Y:117:LYS:NZ	25:Y:153:ASP:OD2	2.31	0.64
31:D:127:ASN:HB3	31:D:248:ARG:HD3	1.80	0.64
18:b:18:ASN:HD21	18:b:25:ARG:HH12	1.46	0.64
33:F:200:GLU:HA	33:F:204:LEU:HD23	1.78	0.64
2:h:79:MET:HG3	2:h:81:PRO:HD2	1.80	0.64
11:Q:19:ARG:NH2	11:Q:31:ASP:OD1	2.30	0.64
17:a:34:TRP:HB3	17:a:71:VAL:HA	1.80	0.64
19:c:119:GLY:HA3	19:c:190:GLN:HE21	1.61	0.64
26:Z:90:ARG:HH21	26:Z:91:ILE:HG13	1.63	0.64
13:s:28:ARG:NH2	13:s:213:ASP:O	2.31	0.64
19:c:63:ASP:OD1	19:c:64:ASP:N	2.28	0.64
26:Z:105:ASP:O	26:Z:109:ASN:ND2	2.30	0.64
33:F:357:PRO:O	33:F:362:ARG:NE	2.31	0.64
7:k:85:ALA:HB2	7:k:139:VAL:HG21	1.79	0.64
22:U:446:LEU:O	22:U:450:HIS:ND1	2.20	0.64
2:H:68:ILE:HD11	2:H:74:LEU:HD22	1.79	0.64
2:H:205:GLU:HB3	2:H:227:LYS:HB2	1.79	0.64
3:I:78:GLY:HA3	3:I:132:VAL:HA	1.79	0.64
1:g:49:VAL:HG21	1:g:195:VAL:HG12	1.79	0.64
1:g:88:ARG:NH2	6:m:157:SER:O	2.30	0.64
22:U:21:GLU:HG3	22:U:25:HIS:CE1	2.33	0.64
23:V:314:ARG:NH1	25:Y:378:ASN:OD1	2.31	0.64
26:Z:121:LEU:HB2	26:Z:138:TYR:HB2	1.78	0.64
1:g:31:ALA:HA	1:g:34:GLN:HG2	1.79	0.64
11:Q:138:LEU:HD21	11:Q:170:ARG:HB2	1.80	0.64
23:V:464:ILE:HG23	23:V:468:SER:HB3	1.80	0.64
5:l:79:ALA:HB3	7:k:121:LEU:HD23	1.80	0.63
11:q:78:THR:O	11:q:82:ASN:ND2	2.31	0.63
12:r:113:TYR:CE1	12:r:128:VAL:HG21	2.32	0.63
15:f:886:GLU:HB3	15:f:906:TYR:HD2	1.61	0.63
19:c:152:LYS:HG3	31:D:83:GLN:HG2	1.80	0.63
22:U:347:ASN:HB2	22:U:741:GLY:HA3	1.81	0.63
22:U:529:ILE:HG12	22:U:566:LEU:HD21	1.79	0.63
31:D:147:ALA:HB2	31:D:253:LEU:HD22	1.79	0.63
9:O:182:LYS:HD2	9:O:184:ASP:HB2	1.81	0.63
23:V:371:ASN:O	23:V:399:ARG:NH2	2.30	0.63
28:A:277:ILE:HG13	28:A:280:ILE:HD11	1.80	0.63
4:J:29:GLY:HA2	29:B:438:LEU:HD22	1.79	0.63
4:J:132:LEU:HD22	4:J:159:ASN:HD22	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:r:81:LYS:NZ	12:r:85:ASN:OD1	2.30	0.63
12:R:17:ASP:OD2	12:R:171:GLY:N	2.31	0.63
15:f:120:ARG:HD3	15:f:147:SER:HB3	1.81	0.63
15:f:707:LEU:HD22	15:f:741:LEU:HD13	1.79	0.63
30:C:199:LEU:HA	30:C:202:ALA:HB3	1.79	0.63
6:m:141:SER:HB2	6:m:144:ASP:HB3	1.80	0.63
19:c:254:ASN:HB3	19:c:278:GLN:HB3	1.81	0.63
30:C:195:GLY:N	35:C:501:ADP:O2A	2.31	0.63
2:H:102:GLN:N	10:P:89:SER:OG	2.26	0.63
5:L:148:CYS:SG	5:L:150:SER:OG	2.56	0.63
6:m:93:GLU:OE2	6:m:97:ASN:ND2	2.32	0.63
6:m:183:GLU:OE1	6:m:183:GLU:N	2.32	0.63
10:P:143:ALA:HA	10:P:146:MET:HE2	1.80	0.63
13:S:36:HIS:HB3	14:T:132:TYR:CZ	2.34	0.63
14:T:16:PHE:HE2	14:T:21:VAL:HG23	1.64	0.63
18:b:13:SER:OG	18:b:16:MET:SD	2.56	0.63
19:c:175:ARG:HB3	19:c:181:LEU:HD11	1.80	0.63
22:U:583:MET:HA	22:U:586:VAL:HG12	1.80	0.63
32:E:47:LEU:HD22	33:F:139:LEU:HA	1.78	0.63
14:T:124:TYR:HB2	14:T:137:LEU:HD13	1.81	0.63
22:U:644:TYR:N	30:C:50:ASN:OD1	2.31	0.63
25:Y:164:ALA:HA	25:Y:168:ILE:HB	1.81	0.63
25:Y:259:TYR:HB3	25:Y:274:SER:HB2	1.81	0.63
20:d:12:LYS:HG2	20:d:14:PRO:HD3	1.80	0.63
22:U:524:LYS:HA	22:U:556:MET:HE2	1.81	0.63
23:V:296:LYS:HB3	23:V:301:GLU:HB2	1.81	0.63
24:X:413:SER:HB3	25:Y:379:ARG:HH22	1.61	0.63
5:L:82:ARG:O	5:L:86:ASN:ND2	2.31	0.63
5:L:193:ARG:HG2	5:L:196:ARG:HH21	1.64	0.63
7:K:146:VAL:HG21	7:K:222:PRO:HA	1.80	0.63
13:s:123:SER:HB3	13:s:136:LYS:HG2	1.80	0.63
24:X:203:PRO:HB2	24:X:206:LEU:HB3	1.80	0.63
25:Y:137:ARG:HD2	25:Y:168:ILE:HD12	1.80	0.63
28:A:167:GLU:HG3	28:A:239:ARG:HB3	1.81	0.63
31:D:297:ASP:OD2	31:D:326:ARG:NH1	2.32	0.63
7:k:40:ILE:HD11	7:k:181:LEU:HD11	1.79	0.63
25:Y:94:ASN:ND2	25:Y:99:GLU:OE2	2.32	0.63
33:F:231:THR:OG1	33:F:233:LYS:NZ	2.31	0.63
3:i:190:LEU:HD11	3:i:236:LEU:HD21	1.80	0.62
10:p:176:ASP:O	12:R:29:GLN:NE2	2.32	0.62
19:c:56:LEU:HA	19:c:111:TRP:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:104:MET:HE2	25:Y:127:THR:HB	1.80	0.62
30:C:150:MET:N	30:C:150:MET:SD	2.73	0.62
31:D:337:ASP:O	31:D:340:GLN:N	2.32	0.62
15:f:409:SER:HB2	15:f:815:HIS:ND1	2.13	0.62
22:U:229:VAL:HA	22:U:232:ILE:HG12	1.81	0.62
27:W:52:LYS:HD3	27:W:55:ARG:HH21	1.64	0.62
1:g:132:ARG:NH2	6:m:123:THR:O	2.32	0.62
8:n:22:THR:HG23	8:n:27:ALA:HB2	1.81	0.62
14:T:69:GLN:NE2	14:T:73:ASP:OD1	2.32	0.62
15:f:378:ASN:OD1	15:f:382:ASN:ND2	2.33	0.62
17:a:368:GLU:O	17:a:372:HIS:ND1	2.32	0.62
24:X:74:ARG:O	24:X:78:ASN:ND2	2.33	0.62
30:C:50:ASN:HB2	31:D:72:PHE:HE2	1.64	0.62
2:H:15:PRO:HG2	2:H:18:LYS:HB2	1.78	0.62
4:J:45:VAL:HG11	4:J:61:LYS:HG2	1.79	0.62
6:M:120:HIS:HA	6:M:123:THR:HG22	1.81	0.62
1:g:86:ASP:OD1	6:m:120:HIS:NE2	2.32	0.62
18:b:171:VAL:HG11	18:b:183:LEU:HD22	1.79	0.62
11:q:27:GLN:NE2	11:Q:169:LYS:O	2.32	0.62
15:f:494:ARG:HH21	15:f:495:GLU:HG2	1.64	0.62
33:F:89:LEU:HD22	33:F:126:THR:HB	1.81	0.62
14:t:99:ARG:HG2	14:t:106:LEU:HG	1.82	0.62
30:C:191:PRO:HG3	30:C:319:PRO:HG3	1.81	0.62
30:C:306:LEU:HG	30:C:308:PRO:HD2	1.81	0.62
6:m:40:ARG:HD2	6:m:148:LEU:HB3	1.80	0.62
15:f:856:ALA:HB3	15:f:858:LYS:HE3	1.80	0.62
18:b:139:ASP:HB3	18:b:168:SER:HB3	1.82	0.62
19:c:172:HIS:CG	19:c:173:GLU:H	2.18	0.62
19:c:244:VAL:HG13	19:c:291:LEU:HD13	1.82	0.62
22:U:247:GLN:NE2	22:U:911:ILE:O	2.32	0.62
22:U:802:TYR:HA	22:U:895:PRO:HG3	1.81	0.62
30:C:187:LEU:HD22	30:C:189:TYR:HD1	1.65	0.62
6:m:179:LEU:HD21	6:m:189:ILE:HD12	1.82	0.62
15:f:581:GLU:HA	15:f:588:ARG:HD2	1.81	0.62
20:d:235:THR:HG23	20:d:238:PRO:HG2	1.82	0.62
28:A:229:VAL:HG21	28:A:237:PHE:CD2	2.34	0.62
28:A:355:PHE:CZ	28:A:373:LEU:HD12	2.35	0.62
31:D:349:THR:HG23	31:D:355:SER:HB2	1.81	0.62
33:F:81:LYS:O	33:F:85:THR:N	2.30	0.62
33:F:416:THR:HG22	33:F:417:HIS:CD2	2.34	0.62
3:I:49:ARG:HB3	3:I:52:ILE:HD11	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:40:SER:HB3	5:L:187:LEU:HD22	1.81	0.62
3:i:159:TRP:HA	4:j:54:GLN:HA	1.82	0.62
10:P:113:ASP:OD2	10:P:116:THR:N	2.31	0.62
16:x:35:HIS:HB3	16:x:102:LEU:HB3	1.80	0.62
19:c:254:ASN:O	19:c:278:GLN:NE2	2.33	0.62
20:d:32:GLU:HG3	20:d:33:LEU:H	1.64	0.62
22:U:21:GLU:HB2	22:U:54:PHE:HZ	1.65	0.62
23:V:228:ARG:NH1	23:V:258:TYR:OH	2.33	0.62
23:V:372:LEU:O	23:V:376:ASN:ND2	2.31	0.62
7:K:168:ARG:NH1	7:K:169:ALA:O	2.33	0.62
3:i:12:PHE:HE2	4:j:126:PRO:HD2	1.64	0.62
26:Z:252:LYS:O	26:Z:255:ASP:N	2.33	0.62
32:E:135:ILE:HD12	32:E:142:ILE:HD13	1.81	0.62
6:M:69:VAL:HA	6:M:92:ARG:HG2	1.82	0.61
7:K:221:GLN:HB2	7:K:224:GLN:HB2	1.80	0.61
14:t:166:ARG:NH1	14:t:200:GLU:OE1	2.32	0.61
19:c:52:GLU:O	19:c:77:GLN:NE2	2.33	0.61
27:W:24:VAL:HG12	27:W:50:LEU:HD21	1.80	0.61
5:L:132:LEU:HB2	5:L:147:THR:HB	1.82	0.61
1:g:24:GLN:NE2	6:m:13:THR:OG1	2.33	0.61
10:p:14:MET:HG3	10:p:163:LEU:HD11	1.82	0.61
22:U:536:ALA:HB1	22:U:578:LEU:HD21	1.82	0.61
32:E:154:THR:O	32:E:272:ARG:NH2	2.32	0.61
1:g:68:HIS:NE2	1:g:80:MET:O	2.33	0.61
15:f:452:ASN:ND2	15:f:452:ASN:O	2.33	0.61
28:A:393:GLY:HA2	29:B:214:MET:HE2	1.81	0.61
30:C:78:ARG:HE	30:C:80:MET:HE3	1.65	0.61
9:o:122:LEU:HD12	9:o:123:PRO:HD2	1.82	0.61
13:S:52:ILE:HG22	13:S:110:ILE:HG12	1.82	0.61
28:A:112:ILE:HA	28:A:122:VAL:HG22	1.83	0.61
31:D:314:ALA:HA	31:D:317:LEU:HD13	1.82	0.61
31:D:341:LYS:NZ	31:D:368:ASP:O	2.31	0.61
6:M:45:VAL:HG23	6:M:146:ALA:HB1	1.82	0.61
8:N:17:ASP:OD1	8:N:18:SER:N	2.32	0.61
12:R:33:LYS:HG3	12:R:45:MET:HB2	1.80	0.61
22:U:453:HIS:HB3	22:U:457:ILE:HG13	1.82	0.61
25:Y:245:GLU:OE1	25:Y:245:GLU:N	2.31	0.61
33:F:189:GLY:H	35:F:501:ADP:HN62	1.46	0.61
3:I:33:THR:HA	3:I:165:GLY:HA3	1.81	0.61
4:J:42:VAL:HG23	4:J:191:VAL:HG21	1.83	0.61
18:b:11:ASP:HA	18:b:54:LEU:HD21	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:172:GLU:HB2	27:W:182:ARG:HH21	1.65	0.61
4:J:95:ARG:HG3	11:Q:62:LYS:NZ	2.14	0.61
4:J:140:GLY:HA2	4:J:213:ARG:HH12	1.66	0.61
5:L:107:ARG:NH2	14:T:74:GLU:OE2	2.33	0.61
8:n:91:ARG:NH1	14:t:59:ASP:OD1	2.33	0.61
19:c:63:ASP:CG	19:c:64:ASP:H	2.08	0.61
20:d:241:GLU:OE1	20:d:245:GLN:NE2	2.34	0.61
31:D:143:LEU:HG	31:D:145:PRO:HD2	1.81	0.61
33:F:81:LYS:O	33:F:85:THR:HG23	2.00	0.61
2:H:65:VAL:O	2:H:220:ARG:NH1	2.32	0.61
2:h:208:ILE:HD12	2:h:230:LEU:HD21	1.81	0.61
15:f:289:VAL:HA	15:f:292:LYS:HE2	1.82	0.61
26:Z:204:LYS:HD2	27:W:443:THR:HG21	1.83	0.61
30:C:137:LEU:HD11	31:D:326:ARG:HH12	1.65	0.61
10:p:20:VAL:HG11	10:p:110:ALA:HB1	1.83	0.61
10:p:34:MET:O	12:R:166:ARG:NH1	2.32	0.61
10:P:135:ASP:OD1	10:P:136:PHE:N	2.34	0.61
15:f:849:ALA:HB3	15:f:879:ARG:HD3	1.82	0.61
18:b:132:LYS:HD2	18:b:163:LYS:HD3	1.81	0.61
22:U:575:ASP:HB2	22:U:578:LEU:HD23	1.83	0.61
6:M:190:VAL:CG2	6:M:215:TRP:HE1	2.11	0.61
8:n:14:LEU:HD21	8:n:101:ALA:HB3	1.83	0.61
14:t:89:HIS:HA	14:t:112:ILE:HD12	1.82	0.61
9:O:37:ILE:HB	9:O:41:ILE:HG13	1.82	0.61
9:O:43:CYS:SG	9:O:98:LEU:HD12	2.40	0.61
15:f:560:LEU:HD21	15:f:798:THR:HA	1.83	0.61
22:U:215:ASN:OD1	22:U:216:VAL:N	2.34	0.61
27:W:55:ARG:HH11	27:W:96:GLN:HG3	1.65	0.61
30:C:255:GLY:N	30:C:302:ASP:O	2.30	0.61
1:G:49:VAL:HG11	1:G:195:VAL:HG22	1.81	0.60
5:l:196:ARG:NH1	5:l:237:GLU:O	2.34	0.60
4:j:87:ALA:HA	4:j:90:GLU:HG2	1.82	0.60
8:n:83:PHE:CD2	8:n:100:ILE:HG12	2.36	0.60
22:U:564:ASP:OD1	22:U:565:ALA:N	2.33	0.60
23:V:375:PHE:HA	23:V:378:VAL:HG22	1.83	0.60
29:B:220:LYS:HB3	29:B:348:ASP:H	1.66	0.60
30:C:190:GLY:HA3	30:C:317:PHE:HB2	1.82	0.60
3:i:158:GLY:O	4:j:55:ASP:N	2.34	0.60
11:q:4:LEU:HD11	11:q:45:LEU:HB3	1.82	0.60
15:f:138:GLU:HA	15:f:141:LYS:HG2	1.83	0.60
22:U:471:ASP:HB2	22:U:472:ILE:HD12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A:237:PHE:HE1	28:A:239:ARG:HB2	1.66	0.60
20:d:189:ILE:O	20:d:222:TYR:N	2.30	0.60
24:X:157:LEU:HB3	24:X:166:LEU:HD21	1.83	0.60
30:C:215:SER:HA	30:C:249:ASP:HB2	1.83	0.60
31:D:261:ILE:HG22	31:D:306:LYS:HB3	1.84	0.60
33:F:134:LEU:HB2	33:F:159:LEU:HD12	1.82	0.60
8:n:59:VAL:HG13	8:n:82:LEU:HD22	1.84	0.60
18:b:20:ASP:OD1	18:b:21:PHE:N	2.32	0.60
19:c:54:MET:HG2	19:c:113:HIS:CD2	2.36	0.60
15:f:720:GLU:O	15:f:724:ASN:ND2	2.33	0.60
22:U:183:LEU:HD22	22:U:187:LEU:HD22	1.82	0.60
22:U:218:GLN:HG3	22:U:222:PHE:HE2	1.67	0.60
23:V:357:LEU:HA	23:V:360:TYR:HB2	1.84	0.60
28:A:69:ASP:HB3	29:B:138:PHE:HE2	1.67	0.60
30:C:73:VAL:HG23	31:D:112:TYR:N	2.17	0.60
1:G:50:ILE:HG23	1:G:141:ILE:HD13	1.84	0.60
6:m:164:ALA:O	6:m:173:LYS:NZ	2.35	0.60
17:a:33:LEU:HD13	18:b:18:ASN:HD22	1.65	0.60
29:B:103:ARG:HG2	29:B:160:ILE:HB	1.82	0.60
2:H:100:VAL:HG13	10:P:93:ASN:HD22	1.67	0.60
5:L:82:ARG:NH2	7:K:117:SER:OG	2.35	0.60
14:t:54:SER:O	14:t:108:ASN:ND2	2.34	0.60
11:Q:154:GLU:OE1	11:Q:154:GLU:N	2.35	0.60
15:f:675:PHE:HB3	15:f:690:VAL:HG13	1.83	0.60
23:V:473:GLN:HB2	26:Z:260:VAL:HG21	1.81	0.60
24:X:410:VAL:HG23	24:X:411:VAL:HG13	1.84	0.60
8:n:127:ILE:HG22	8:n:132:SER:HB2	1.82	0.60
13:S:26:ASP:OD1	13:S:27:THR:N	2.32	0.60
26:Z:9:VAL:HG12	26:Z:48:LEU:HB3	1.82	0.60
31:D:132:LEU:HB3	31:D:137:ASN:HA	1.83	0.60
1:g:12:HIS:C	1:g:24:GLN:HE21	2.08	0.60
9:o:15:GLY:HA3	9:o:159:ILE:HD11	1.84	0.60
22:U:620:GLU:HB3	22:U:651:GLY:HA2	1.82	0.60
31:D:220:ALA:HB2	31:D:261:ILE:HD11	1.84	0.60
3:I:22:GLU:OE2	29:B:434:THR:OG1	2.20	0.59
9:o:193:ASN:ND2	13:S:213:ASP:OD1	2.35	0.59
12:r:42:LEU:HD21	12:r:184:TRP:HB3	1.83	0.59
30:C:235:PHE:HD2	30:C:276:LEU:HD12	1.66	0.59
30:C:260:GLU:HG2	30:C:262:GLY:H	1.66	0.59
31:D:218:ALA:O	31:D:220:ALA:N	2.35	0.59
1:g:37:LEU:HG	1:g:53:GLN:HE21	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:m:214:SER:HA	6:m:227:VAL:HG23	1.84	0.59
8:n:122:ARG:NH1	8:N:202:LEU:O	2.35	0.59
9:o:37:ILE:HG23	9:o:60:SER:HA	1.83	0.59
15:f:606:VAL:HG11	29:B:70:ASP:HB3	1.82	0.59
25:Y:67:VAL:O	25:Y:71:ASN:ND2	2.29	0.59
27:W:96:GLN:HG2	27:W:97:LEU:H	1.67	0.59
29:B:258:LYS:O	29:B:307:ARG:NH1	2.34	0.59
7:K:181:LEU:HA	7:K:184:VAL:HG22	1.84	0.59
2:h:121:TYR:CD1	2:h:127:VAL:HG21	2.34	0.59
4:j:36:ARG:HH21	4:j:157:LYS:HG2	1.66	0.59
11:q:35:MET:HE2	11:q:43:LEU:HD21	1.83	0.59
15:f:806:VAL:HA	15:f:809:ILE:HG22	1.85	0.59
19:c:217:LEU:HD21	26:Z:17:LEU:HD13	1.84	0.59
27:W:18:VAL:H	27:W:57:ALA:HB1	1.66	0.59
29:B:412:MET:HB2	29:B:415:THR:HA	1.82	0.59
1:g:141:ILE:HG22	1:g:151:VAL:HG22	1.83	0.59
15:f:485:LEU:HD13	15:f:501:LEU:HD21	1.83	0.59
22:U:510:GLU:HA	22:U:547:GLY:HA3	1.84	0.59
22:U:799:LYS:HB2	22:U:923:GLU:HB3	1.84	0.59
28:A:245:LEU:HA	28:A:256:MET:HE3	1.85	0.59
6:M:140:TYR:HB3	6:M:216:VAL:HG22	1.83	0.59
11:q:26:VAL:HG11	12:r:136:TYR:CE2	2.38	0.59
31:D:375:ILE:HG12	31:D:378:ILE:HG12	1.83	0.59
32:E:288:ALA:O	32:E:294:ARG:NE	2.34	0.59
33:F:92:ASN:HB3	33:F:125:LYS:HB3	1.85	0.59
5:l:44:ALA:HB1	5:l:144:ILE:HD11	1.83	0.59
10:p:135:ASP:OD1	10:p:136:PHE:N	2.32	0.59
19:c:26:ASP:H	19:c:176:GLN:HE21	1.49	0.59
30:C:89:VAL:O	30:C:93:GLY:N	2.35	0.59
22:U:187:LEU:HD23	31:D:49:GLN:HB3	1.85	0.59
27:W:340:VAL:HA	27:W:350:ARG:HH11	1.66	0.59
30:C:338:LEU:HA	30:C:378:VAL:H	1.68	0.59
32:E:153:LEU:HD23	32:E:191:LEU:HG	1.84	0.59
6:M:214:SER:OG	6:M:224:HIS:NE2	2.33	0.59
5:l:153:TYR:H	6:m:85:ARG:HH12	1.51	0.59
2:h:159:LYS:N	3:i:55:LEU:O	2.29	0.59
6:m:213:LEU:HG	6:m:227:VAL:HG21	1.84	0.59
11:Q:93:ARG:HH22	10:P:103:TYR:HA	1.68	0.59
13:S:13:LEU:HD11	13:S:149:LEU:HD13	1.84	0.59
13:S:25:SER:HB2	13:S:42:LYS:HB2	1.85	0.59
18:b:16:MET:SD	18:b:115:SER:OG	2.59	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:356:ASN:OD1	27:W:357:ARG:N	2.35	0.59
30:C:113:ARG:HE	30:C:130:LYS:H	1.51	0.59
30:C:199:LEU:O	30:C:203:VAL:HG22	2.03	0.59
1:G:106:GLY:HA3	9:O:77:VAL:HG12	1.85	0.59
4:J:34:GLY:N	4:J:159:ASN:OD1	2.36	0.59
5:l:146:GLN:HG3	5:l:159:MET:HG2	1.85	0.59
1:g:54:LYS:N	1:g:214:GLU:O	2.34	0.59
15:f:208:LEU:HD23	15:f:211:ILE:HD11	1.85	0.59
19:c:39:LEU:HD13	26:Z:14:LEU:HD12	1.84	0.59
22:U:405:THR:HG21	22:U:441:GLY:HA2	1.85	0.59
28:A:383:ALA:HB1	29:B:346:ARG:HH21	1.68	0.59
30:C:157:GLN:HE21	30:C:315:ILE:HG22	1.67	0.59
32:E:38:LYS:HE2	32:E:42:LYS:HE3	1.84	0.59
32:E:346:VAL:HG22	32:E:374:VAL:HG21	1.85	0.59
13:S:13:LEU:HD22	13:S:145:LEU:HD21	1.84	0.59
20:d:25:ARG:HH21	20:d:50:LEU:HB2	1.68	0.59
2:H:122:THR:OG1	2:H:152:SER:HA	2.03	0.58
4:J:92:GLN:HG3	11:Q:66:LEU:HB2	1.85	0.58
5:l:72:ILE:HG21	5:l:88:MET:HE1	1.85	0.58
2:h:106:PRO:HB2	2:h:109:GLN:HG2	1.84	0.58
2:h:193:LEU:HA	2:h:196:LYS:HE3	1.84	0.58
20:d:41:THR:HG22	20:d:44:THR:H	1.68	0.58
8:n:166:ARG:HH11	14:T:37:ARG:HD3	1.68	0.58
11:q:19:ARG:HB2	11:q:177:THR:HG23	1.85	0.58
13:s:158:MET:HE3	13:s:161:VAL:HG21	1.84	0.58
10:P:30:ILE:HG12	10:P:33:GLN:HG2	1.85	0.58
15:f:157:GLU:O	15:f:161:HIS:ND1	2.23	0.58
22:U:177:LEU:O	22:U:205:TYR:OH	2.21	0.58
23:V:225:ASP:HB3	23:V:261:TYR:HE2	1.67	0.58
29:B:190:LEU:HG	29:B:193:GLN:HB2	1.84	0.58
10:P:125:ASP:OD1	10:P:129:CYS:N	2.30	0.58
15:f:313:GLU:HG3	15:f:316:ASP:HB2	1.85	0.58
25:Y:387:ILE:HD13	26:Z:276:ILE:HG22	1.84	0.58
33:F:235:LEU:HD23	33:F:238:ARG:HH21	1.68	0.58
1:G:208:ILE:HG23	1:G:210:PHE:H	1.67	0.58
4:J:77:THR:OG1	29:B:438:LEU:HD12	2.04	0.58
4:J:80:ALA:O	4:J:84:ILE:HG12	2.04	0.58
3:i:123:GLN:NE2	4:j:125:ARG:O	2.37	0.58
8:n:40:ARG:HG2	8:n:103:TRP:HE3	1.69	0.58
9:O:112:SER:OG	9:O:120:ASP:OD1	2.21	0.58
15:f:325:GLN:O	15:f:329:ASN:ND2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:f:419:LEU:HA	15:f:451:VAL:HA	1.84	0.58
24:X:184:PRO:HD2	25:Y:244:ALA:HB2	1.85	0.58
25:Y:155:ASP:OD1	25:Y:156:LEU:N	2.36	0.58
25:Y:250:LEU:HD21	25:Y:260:LEU:HD13	1.85	0.58
29:B:54:PRO:HG2	29:B:61:LYS:HB2	1.84	0.58
33:F:153:VAL:HG22	33:F:160:ILE:HD13	1.86	0.58
4:J:118:TYR:HA	4:J:124:ARG:HE	1.69	0.58
9:o:93:TYR:O	10:p:99:ARG:NH2	2.35	0.58
11:Q:93:ARG:NH1	10:P:101:GLY:O	2.37	0.58
22:U:545:LEU:HB3	22:U:577:ILE:HG21	1.86	0.58
23:V:207:ALA:HB1	23:V:211:TYR:CZ	2.38	0.58
23:V:440:LYS:HE3	23:V:443:ARG:HH21	1.69	0.58
24:X:412:ASP:OD1	24:X:413:SER:N	2.36	0.58
29:B:107:MET:HG2	29:B:151:LEU:HD13	1.85	0.58
15:f:535:THR:HG21	15:f:566:HIS:HE1	1.67	0.58
18:b:124:LEU:HD13	18:b:152:LYS:HB3	1.85	0.58
1:G:205:VAL:HG12	1:G:206:LEU:HG	1.86	0.58
7:k:98:ASN:OD1	12:r:61:ARG:NH1	2.37	0.58
15:f:782:HIS:CD2	15:f:789:SER:HB3	2.38	0.58
15:f:846:VAL:HG11	15:f:872:VAL:HG11	1.85	0.58
28:A:33:LEU:HB2	29:B:411:ARG:HE	1.68	0.58
29:B:165:ASP:O	29:B:167:THR:N	2.35	0.58
30:C:100:ASP:OD1	30:C:101:LYS:N	2.37	0.58
5:l:56:LEU:HD21	7:k:182:GLN:HB2	1.86	0.58
7:K:52:LYS:NZ	7:K:64:ILE:O	2.36	0.58
4:j:90:GLU:OE1	4:j:110:TYR:HD2	1.87	0.58
10:p:30:ILE:HG22	10:p:33:GLN:HG2	1.86	0.58
12:R:17:ASP:OD1	12:R:18:SER:N	2.37	0.58
18:b:34:ASN:HB3	18:b:72:LEU:HD11	1.86	0.58
30:C:244:SER:HB2	30:C:289:ILE:HG13	1.86	0.58
4:J:6:ALA:O	4:J:18:GLN:NE2	2.37	0.58
10:P:56:LEU:HD13	10:P:104:TYR:HB2	1.86	0.58
15:f:771:LEU:HD22	15:f:778:LEU:HD21	1.86	0.58
30:C:327:ASP:O	30:C:331:ILE:HG12	2.02	0.58
31:D:208:PRO:HB2	31:D:375:ILE:HD12	1.85	0.58
1:G:50:ILE:HD13	1:G:79:VAL:HB	1.85	0.57
1:G:69:LEU:HD11	1:G:216:GLU:HG2	1.86	0.57
6:M:15:SER:OG	6:M:19:ARG:N	2.37	0.57
1:g:40:VAL:HG23	1:g:167:ALA:HB2	1.85	0.57
1:g:111:VAL:HG21	1:g:150:GLN:HB2	1.86	0.57
12:r:127:SER:HB3	12:r:136:TYR:CE1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Q:85:ARG:HA	11:Q:118:MET:HE1	1.84	0.57
10:P:138:VAL:HG11	10:P:146:MET:HB3	1.85	0.57
13:S:26:ASP:OD2	13:S:190:GLY:N	2.28	0.57
15:f:720:GLU:HG2	15:f:724:ASN:HD21	1.69	0.57
15:f:775:THR:HA	15:f:873:LEU:HD11	1.85	0.57
21:e:19:PHE:HB2	23:V:321:ALA:HA	1.85	0.57
23:V:110:HIS:HB2	23:V:138:PRO:HD3	1.86	0.57
23:V:167:LEU:O	23:V:171:VAL:HG23	2.05	0.57
24:X:292:GLN:O	24:X:296:ASN:ND2	2.35	0.57
28:A:306:LEU:O	28:A:336:ARG:NE	2.37	0.57
7:K:68:VAL:HG11	7:K:93:ARG:HH22	1.68	0.57
5:l:157:ARG:HG3	6:m:59:GLU:OE2	2.03	0.57
2:h:65:VAL:O	2:h:220:ARG:NH2	2.37	0.57
7:k:52:LYS:HE3	7:k:54:ILE:HD11	1.86	0.57
13:s:16:ALA:HB2	13:s:121:VAL:HG23	1.86	0.57
14:t:34:ALA:O	8:N:166:ARG:NH1	2.37	0.57
19:c:57:MET:H	19:c:111:TRP:HA	1.69	0.57
19:c:57:MET:HA	19:c:72:VAL:HG23	1.86	0.57
20:d:106:LEU:HG	20:d:111:ARG:HB3	1.85	0.57
5:L:100:ASP:OD2	13:S:66:LYS:NZ	2.30	0.57
8:n:53:GLN:NE2	9:o:119:THR:O	2.38	0.57
8:n:59:VAL:HG11	8:n:83:PHE:CZ	2.39	0.57
12:R:38:ASN:HB2	12:R:39:PRO:HD2	1.85	0.57
14:T:11:VAL:HG23	14:T:24:ALA:HB2	1.87	0.57
15:f:60:VAL:O	15:f:105:LYS:NZ	2.31	0.57
15:f:143:ARG:NE	15:f:158:TYR:OH	2.35	0.57
15:f:845:ARG:NH2	15:f:882:LEU:O	2.37	0.57
22:U:789:ILE:HB	22:U:911:ILE:HG13	1.86	0.57
33:F:222:GLY:HA3	33:F:348:LEU:HA	1.85	0.57
7:k:73:HIS:CE1	7:k:106:THR:HB	2.40	0.57
13:s:75:TYR:CD1	13:s:83:MET:HG2	2.39	0.57
22:U:571:CYS:HA	22:U:579:ARG:HA	1.85	0.57
30:C:231:VAL:HG21	30:C:269:VAL:HG22	1.87	0.57
3:i:45:LEU:HG	3:i:137:ILE:HD13	1.86	0.57
19:c:263:ASP:OD1	19:c:264:LYS:N	2.37	0.57
23:V:490:SER:O	23:V:494:MET:HG2	2.04	0.57
28:A:102:ILE:HB	28:A:113:ILE:HG12	1.87	0.57
33:F:312:GLU:O	33:F:316:GLN:HG3	2.03	0.57
4:J:28:LYS:HD2	4:J:28:LYS:C	2.29	0.57
1:g:42:VAL:HG23	1:g:165:ALA:HB2	1.87	0.57
8:n:28:ASN:HD21	9:o:122:LEU:HD13	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:N:135:ILE:HD13	8:N:163:ALA:HB2	1.86	0.57
14:T:8:GLY:N	14:T:55:GLY:O	2.27	0.57
15:f:407:MET:HB3	15:f:440:ILE:HG12	1.87	0.57
17:a:258:GLN:CD	17:a:258:GLN:H	2.12	0.57
25:Y:300:ARG:NH1	25:Y:333:GLU:OE2	2.37	0.57
30:C:38:LYS:O	30:C:42:LEU:HD13	2.04	0.57
31:D:146:GLU:HB3	31:D:249:ASP:HB3	1.87	0.57
32:E:130:VAL:HA	32:E:132:TYR:CZ	2.40	0.57
7:K:101:PHE:HD1	12:R:57:ARG:HG2	1.70	0.57
10:p:66:ARG:HH12	10:p:70:ARG:HB3	1.68	0.57
9:O:51:ASP:OD2	10:P:99:ARG:NH2	2.34	0.57
17:a:205:LEU:O	17:a:271:LYS:NZ	2.37	0.57
19:c:49:VAL:HG11	32:E:103:THR:HG21	1.85	0.57
23:V:313:LEU:HD13	23:V:328:VAL:HG11	1.87	0.57
25:Y:231:LEU:HD11	25:Y:236:LEU:HD13	1.87	0.57
29:B:223:ILE:HD11	29:B:347:ILE:HB	1.87	0.57
30:C:86:LEU:HB3	30:C:94:LYS:NZ	2.20	0.57
6:M:66:LEU:HD13	6:M:214:SER:HB2	1.87	0.57
3:i:37:ILE:HD12	3:i:189:ALA:HB1	1.86	0.57
6:m:40:ARG:NH2	6:m:146:ALA:O	2.23	0.57
10:P:27:ARG:NH1	10:P:180:VAL:O	2.38	0.57
16:x:89:LEU:HB3	16:x:94:ILE:HD12	1.87	0.57
22:U:352:ILE:HG21	22:U:376:MET:HE1	1.85	0.57
22:U:835:ILE:HD12	22:U:838:LYS:HB3	1.87	0.57
23:V:225:ASP:HB3	23:V:261:TYR:CE2	2.39	0.57
30:C:140:VAL:HG12	30:C:212:ILE:HG23	1.86	0.57
7:K:84:ASP:OD1	7:K:84:ASP:N	2.38	0.57
5:l:14:SER:OG	5:l:16:GLN:OE1	2.22	0.57
3:i:218:ARG:NH1	3:i:223:THR:OG1	2.37	0.57
28:A:229:VAL:HG22	28:A:232:ARG:CZ	2.34	0.57
28:A:362:MET:HB2	28:A:364:VAL:HG22	1.86	0.57
31:D:204:MET:HG3	31:D:310:ALA:HA	1.86	0.57
2:h:22:ILE:HD13	2:h:152:SER:HA	1.86	0.57
9:o:70:THR:O	9:o:72:ARG:NH1	2.38	0.57
11:q:5:ILE:HD11	11:q:143:LEU:HD11	1.87	0.57
14:T:51:LEU:HD11	14:T:110:MET:HE2	1.85	0.57
27:W:25:ASP:HA	27:W:65:ARG:HH22	1.70	0.57
27:W:284:SER:O	27:W:288:HIS:ND1	2.36	0.57
29:B:109:VAL:HB	30:C:94:LYS:HD3	1.87	0.57
31:D:162:VAL:HG21	31:D:214:MET:HE1	1.86	0.57
2:H:202:GLN:HB2	24:X:202:CYS:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:m:15:SER:HB3	6:m:19:ARG:H	1.69	0.56
8:n:119:MET:HE2	14:t:6:VAL:HG22	1.86	0.56
23:V:86:VAL:HG21	23:V:160:LEU:HD13	1.86	0.56
28:A:390:THR:HG23	29:B:216:ILE:HB	1.87	0.56
2:H:14:SER:OG	3:I:128:ARG:NH2	2.38	0.56
2:H:66:GLU:OE1	2:H:91:ARG:NH2	2.38	0.56
5:l:82:ARG:O	5:l:86:ASN:ND2	2.34	0.56
3:i:86:LEU:O	3:i:90:LEU:HD23	2.06	0.56
22:U:360:VAL:HG11	22:U:393:LEU:HD21	1.87	0.56
22:U:611:ASN:HB3	22:U:614:VAL:HG12	1.87	0.56
25:Y:27:SER:HB3	25:Y:59:LYS:HD3	1.86	0.56
26:Z:109:ASN:HD21	26:Z:121:LEU:HD21	1.70	0.56
33:F:362:ARG:HD2	33:F:388:THR:HG22	1.87	0.56
1:G:21:ARG:NH1	1:G:26:GLU:OE1	2.39	0.56
2:H:51:LYS:HE2	2:H:200:GLU:HG3	1.88	0.56
2:H:106:PRO:HB2	2:H:110:LEU:HB2	1.88	0.56
4:J:160:ALA:HB1	4:J:168:VAL:HG13	1.87	0.56
7:K:42:THR:OG1	7:K:189:MET:O	2.23	0.56
7:K:104:ASN:OD1	12:R:57:ARG:NH2	2.38	0.56
5:l:50:LYS:HB2	5:l:59:HIS:HB3	1.86	0.56
4:j:173:GLU:HA	7:k:58:LEU:HD21	1.87	0.56
14:t:19:GLY:HA3	14:t:193:THR:HG22	1.87	0.56
14:T:88:ILE:HG22	14:T:112:ILE:HD13	1.86	0.56
14:T:112:ILE:O	14:T:123:GLY:N	2.36	0.56
15:f:669:GLU:OE2	15:f:670:MET:HG3	2.05	0.56
15:f:692:LEU:HB3	15:f:800:LEU:HD12	1.86	0.56
17:a:61:GLU:OE2	17:a:65:SER:OG	2.22	0.56
17:a:91:ASN:OD1	17:a:92:VAL:N	2.39	0.56
17:a:138:VAL:O	17:a:142:LEU:HG	2.06	0.56
20:d:158:ILE:HD11	20:d:167:ILE:HG23	1.87	0.56
22:U:607:VAL:HB	31:D:68:LEU:HD21	1.87	0.56
22:U:790:GLY:HA3	22:U:800:VAL:HG21	1.86	0.56
24:X:137:TYR:HB3	24:X:146:ALA:HB2	1.87	0.56
25:Y:286:TRP:CD1	25:Y:286:TRP:H	2.22	0.56
28:A:362:MET:HG2	29:B:214:MET:O	2.04	0.56
29:B:218:PRO:HB2	29:B:220:LYS:HD3	1.85	0.56
29:B:309:MET:N	29:B:309:MET:SD	2.78	0.56
32:E:98:VAL:HA	32:E:110:TYR:HA	1.87	0.56
33:F:357:PRO:HB2	33:F:362:ARG:HG3	1.86	0.56
33:F:416:THR:HG22	33:F:417:HIS:HD2	1.71	0.56
15:f:666:ILE:HD11	29:B:68:ILE:HG12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:799:LYS:HG2	22:U:925:VAL:HB	1.87	0.56
5:L:46:LEU:HD21	5:L:135:ALA:HB2	1.87	0.56
5:l:95:SER:HB2	5:l:103:LEU:HD12	1.87	0.56
14:t:1:THR:N	14:t:105:PRO:O	2.33	0.56
18:b:138:VAL:HB	18:b:160:LEU:HD13	1.87	0.56
22:U:78:LEU:HD11	22:U:104:CYS:HB2	1.86	0.56
22:U:546:ARG:HE	22:U:771:PHE:HB3	1.70	0.56
25:Y:128:TYR:HB2	25:Y:140:ILE:HD13	1.87	0.56
28:A:235:ALA:HB1	28:A:270:CYS:HA	1.86	0.56
32:E:266:GLY:O	32:E:271:HIS:ND1	2.39	0.56
6:m:14:PHE:HB3	6:m:18:GLY:HA2	1.88	0.56
15:f:337:LEU:HD21	15:f:871:PRO:HB2	1.88	0.56
15:f:479:LEU:HD21	15:f:514:VAL:HA	1.87	0.56
15:f:679:LEU:HG	15:f:690:VAL:HG11	1.87	0.56
20:d:30:LEU:HA	20:d:47:GLN:HE22	1.71	0.56
27:W:205:ILE:HA	27:W:208:LYS:HG2	1.86	0.56
29:B:236:ALA:O	29:B:239:VAL:HG22	2.05	0.56
32:E:102:MET:HG2	33:F:158:TYR:HE2	1.71	0.56
1:G:196:GLU:HB3	1:G:242:LEU:HD13	1.88	0.56
4:J:158:ALA:HB1	4:J:172:LEU:HD13	1.86	0.56
16:x:56:GLN:HE22	16:x:86:GLU:HA	1.71	0.56
17:a:146:PRO:HB3	26:Z:143:GLU:HG3	1.88	0.56
19:c:256:ASN:O	19:c:259:VAL:HG12	2.05	0.56
20:d:249:TYR:HB3	23:V:480:ILE:HG12	1.87	0.56
24:X:401:LEU:HB2	25:Y:365:GLN:HE22	1.70	0.56
28:A:219:GLY:N	34:A:501:ATP:O2G	2.39	0.56
32:E:287:PRO:HA	32:E:290:LEU:HD23	1.88	0.56
4:J:41:VAL:HG13	4:J:142:PRO:HB2	1.86	0.56
3:i:73:ALA:HB2	3:i:225:ILE:HD13	1.88	0.56
12:r:35:ILE:HD11	12:r:45:MET:HE3	1.88	0.56
10:P:59:ASP:O	10:P:62:THR:HG22	2.05	0.56
22:U:440:GLY:HA3	22:U:472:ILE:HG22	1.87	0.56
25:Y:234:PRO:C	25:Y:236:LEU:H	2.13	0.56
27:W:316:ARG:HG2	27:W:319:THR:HG23	1.88	0.56
30:C:273:MET:HE2	30:C:277:LEU:HD12	1.88	0.56
31:D:229:ARG:O	31:D:231:VAL:N	2.39	0.56
31:D:230:VAL:HG11	31:D:264:ILE:HG12	1.87	0.56
4:J:115:LYS:HD3	4:J:149:PRO:HA	1.88	0.56
6:m:99:ARG:NH1	14:t:69:GLN:OE1	2.37	0.56
13:S:24:ALA:HB1	13:S:193:LEU:HD11	1.88	0.56
19:c:281:LYS:HZ2	19:c:282:ARG:HD3	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:d:132:TYR:HD1	20:d:160:ALA:HA	1.71	0.56
21:e:40:GLU:O	25:Y:293:ARG:NH1	2.39	0.56
22:U:179:TYR:O	22:U:183:LEU:HG	2.05	0.56
25:Y:173:ASP:OD1	25:Y:174:TRP:N	2.34	0.56
26:Z:209:ARG:NH1	26:Z:213:GLU:OE1	2.39	0.56
28:A:241:ILE:HG22	28:A:244:GLU:H	1.71	0.56
29:B:292:THR:HA	29:B:309:MET:HE3	1.88	0.56
31:D:381:GLU:O	31:D:385:LEU:HG	2.06	0.56
33:F:169:ASP:O	33:F:171:ARG:N	2.38	0.56
9:O:38:SER:HB3	9:O:41:ILE:HG12	1.88	0.56
9:O:146:MET:HE2	9:O:151:ALA:HA	1.87	0.56
15:f:151:LEU:HD12	15:f:158:TYR:CE2	2.41	0.56
22:U:466:LYS:HZ2	22:U:496:LEU:HD22	1.70	0.56
22:U:602:LEU:HD22	22:U:603:LEU:HD22	1.88	0.56
24:X:370:LEU:HD21	25:Y:306:GLN:HE21	1.71	0.56
25:Y:294:TYR:HD1	25:Y:298:GLU:HB2	1.71	0.56
27:W:248:ARG:HA	27:W:251:TYR:HB3	1.88	0.56
32:E:66:GLU:HA	32:E:89:LYS:HD2	1.88	0.56
32:E:176:PRO:O	32:E:339:ASN:ND2	2.39	0.56
32:E:188:ALA:HA	32:E:191:LEU:HB2	1.87	0.56
33:F:94:ILE:HB	33:F:123:VAL:HB	1.88	0.56
4:J:64:ALA:HB2	4:J:217:LEU:HD12	1.88	0.55
1:g:53:GLN:HA	1:g:215:ILE:HG22	1.88	0.55
4:j:116:GLN:OE1	4:j:119:THR:OG1	2.24	0.55
15:f:472:HIS:O	15:f:478:ARG:NE	2.39	0.55
21:e:25:GLU:N	23:V:326:GLN:OE1	2.39	0.55
28:A:410:LEU:O	28:A:414:ASN:ND2	2.38	0.55
29:B:362:LYS:HG3	29:B:380:LEU:HD21	1.88	0.55
2:H:72:ILE:HG13	2:H:107:THR:HG23	1.86	0.55
5:l:203:GLN:O	5:l:239:ARG:NH1	2.39	0.55
14:t:41:ARG:NH1	14:t:53:ALA:O	2.38	0.55
15:f:56:LEU:HD12	15:f:98:PHE:HD2	1.71	0.55
17:a:291:LEU:HB2	17:a:331:VAL:HB	1.88	0.55
19:c:237:HIS:HA	19:c:240:HIS:HB3	1.88	0.55
2:H:109:GLN:NE2	10:P:78:GLU:OE2	2.39	0.55
4:J:28:LYS:HZ1	29:B:438:LEU:HB3	1.72	0.55
5:L:11:THR:HG23	6:M:129:ARG:HB3	1.88	0.55
1:g:224:ASN:O	1:g:226:LYS:N	2.40	0.55
6:m:50:GLU:OE2	6:m:209:PHE:HB2	2.05	0.55
8:n:144:ARG:H	8:n:147:MET:HE3	1.70	0.55
14:t:192:VAL:HG22	14:t:197:VAL:HG12	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:O:111:TYR:CE2	9:O:121:LYS:HB2	2.41	0.55
11:Q:124:LEU:O	10:P:61:GLN:NE2	2.33	0.55
10:P:84:PRO:HB2	10:P:120:PHE:CD2	2.41	0.55
15:f:230:CYS:HA	15:f:233:LEU:HD12	1.87	0.55
22:U:218:GLN:HG3	22:U:222:PHE:CE2	2.40	0.55
23:V:265:ASP:OD1	23:V:266:GLN:N	2.39	0.55
29:B:288:ASP:OD2	29:B:330:ALA:N	2.40	0.55
2:H:232:ALA:HB1	24:X:87:ARG:HG3	1.86	0.55
3:I:17:ARG:NE	29:B:434:THR:HG21	2.22	0.55
4:J:28:LYS:HZ1	29:B:438:LEU:CB	2.20	0.55
7:K:229:PHE:O	7:K:234:LEU:HB3	2.07	0.55
13:s:174:LEU:O	13:s:178:VAL:HG13	2.06	0.55
11:Q:85:ARG:HH22	10:P:62:THR:N	2.03	0.55
20:d:171:LEU:HA	20:d:174:ILE:HG22	1.89	0.55
22:U:650:TYR:HB2	22:U:683:VAL:HA	1.89	0.55
26:Z:255:ASP:HA	26:Z:258:VAL:HG22	1.86	0.55
28:A:376:LEU:HD11	28:A:416:VAL:HG23	1.88	0.55
29:B:175:LYS:HG2	29:B:178:LYS:HD3	1.88	0.55
30:C:229:ARG:O	30:C:231:VAL:N	2.38	0.55
2:H:107:THR:HB	2:H:140:ASN:HB2	1.88	0.55
4:J:155:ALA:HB3	7:K:63:SER:HB2	1.89	0.55
8:n:90:TYR:HB3	8:n:94:LEU:HD23	1.89	0.55
14:t:25:ASP:OD1	14:t:41:ARG:NH2	2.39	0.55
14:t:37:ARG:NH1	8:N:165:GLU:OE1	2.39	0.55
23:V:245:ASP:OD1	23:V:246:GLY:N	2.38	0.55
26:Z:130:ASP:OD1	26:Z:131:LEU:N	2.36	0.55
33:F:93:VAL:HB	33:F:147:PRO:HA	1.88	0.55
1:g:110:PRO:HG2	1:g:113:MET:HB2	1.88	0.55
2:h:134:LEU:HB2	2:h:149:SER:OG	2.07	0.55
7:k:203:LYS:HG3	7:k:210:LEU:HD21	1.89	0.55
11:q:183:ILE:HD12	11:q:188:ILE:HG12	1.89	0.55
14:T:91:TRP:HE3	14:T:92:LEU:HD22	1.71	0.55
22:U:524:LYS:HD3	22:U:559:ARG:HE	1.71	0.55
22:U:628:ARG:NH1	22:U:753:GLY:O	2.33	0.55
23:V:321:ALA:HB1	23:V:324:PHE:HB3	1.89	0.55
27:W:451:MET:O	27:W:455:LEU:HG	2.07	0.55
28:A:404:ALA:HA	28:A:407:LYS:HB2	1.89	0.55
31:D:156:SER:HB3	31:D:227:PHE:HB3	1.89	0.55
3:I:37:ILE:HD11	3:I:184:MET:HE1	1.89	0.55
3:I:121:TYR:HA	3:I:127:LYS:HD2	1.89	0.55
6:M:35:THR:N	6:M:50:GLU:OE2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:84:ASP:HB3	7:K:137:PHE:HD2	1.71	0.55
12:r:33:LYS:HG3	12:r:45:MET:HG3	1.89	0.55
13:S:170:ARG:HA	13:S:173:ARG:HE	1.71	0.55
14:T:67:LEU:HD11	14:T:88:ILE:HD12	1.86	0.55
15:f:616:CYS:HA	15:f:650:GLN:HG2	1.88	0.55
28:A:80:LEU:HD11	29:B:99:VAL:HB	1.89	0.55
29:B:400:THR:HG22	30:C:180:ILE:HD12	1.88	0.55
32:E:83:CYS:HA	32:E:107:ILE:HB	1.87	0.55
33:F:389:ASP:OD1	33:F:389:ASP:N	2.39	0.55
2:H:107:THR:HB	2:H:140:ASN:CB	2.37	0.55
8:n:101:ALA:HB2	8:n:111:VAL:HG13	1.88	0.55
12:R:36:GLU:OE1	12:R:36:GLU:N	2.40	0.55
17:a:194:GLN:NE2	17:a:225:LEU:O	2.37	0.55
23:V:219:GLU:HA	23:V:224:LEU:HB3	1.88	0.55
24:X:74:ARG:CG	24:X:75:PRO:HD3	2.37	0.55
24:X:299:LEU:HD22	24:X:331:LEU:HD12	1.88	0.55
24:X:360:ASP:OD1	24:X:361:VAL:N	2.40	0.55
25:Y:191:ILE:HD12	25:Y:293:ARG:HD2	1.88	0.55
29:B:123:VAL:HG21	29:B:159:VAL:HG21	1.89	0.55
3:I:35:LEU:HG	3:I:46:ALA:HB3	1.88	0.55
7:K:200:ILE:HG22	7:K:241:ILE:HG23	1.89	0.55
2:h:177:ARG:HG3	2:h:190:THR:HG22	1.89	0.55
6:m:72:HIS:ND1	6:m:139:SER:OG	2.30	0.55
14:t:44:ARG:HG3	14:t:197:VAL:HG21	1.89	0.55
13:S:153:VAL:HG22	13:S:166:LEU:HD21	1.87	0.55
17:a:338:PRO:HG3	26:Z:233:VAL:HG23	1.89	0.55
20:d:8:GLU:HB3	20:d:18:LYS:HZ1	1.72	0.55
28:A:386:ARG:O	28:A:390:THR:OG1	2.21	0.55
11:q:16:ALA:HB2	11:q:160:LEU:HD11	1.89	0.55
11:Q:102:LEU:HD12	11:Q:118:MET:HE2	1.89	0.55
18:b:96:ALA:O	18:b:99:HIS:ND1	2.40	0.55
19:c:163:ILE:HG23	19:c:199:HIS:HB3	1.88	0.55
23:V:482:PHE:O	23:V:486:ILE:HG12	2.07	0.55
27:W:227:TYR:O	27:W:231:ILE:HG23	2.07	0.55
31:D:89:ILE:HB	32:E:78:ARG:HG2	1.89	0.55
5:l:126:ARG:HH12	7:k:121:LEU:HD11	1.72	0.54
3:i:66:TYR:HB2	3:i:74:CYS:SG	2.47	0.54
7:k:235:GLU:HA	7:k:238:ILE:HG22	1.88	0.54
9:o:186:LEU:HD23	9:o:189:TYR:HD1	1.72	0.54
12:r:144:SER:HB3	12:r:147:LEU:HG	1.88	0.54
10:P:138:VAL:HG21	10:P:146:MET:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:c:251:LEU:HD22	19:c:279:ASP:HB2	1.89	0.54
19:c:277:LYS:HD2	19:c:282:ARG:HG2	1.88	0.54
22:U:685:GLN:HG2	22:U:725:MET:HG3	1.89	0.54
28:A:217:PRO:HD2	28:A:344:SER:HB2	1.89	0.54
31:D:172:ILE:HD12	31:D:334:PRO:HD2	1.89	0.54
6:M:184:MET:HB3	6:M:188:ASP:OD1	2.07	0.54
10:P:149:MET:HG2	10:P:170:ALA:HA	1.90	0.54
25:Y:79:ASP:HB3	25:Y:83:ARG:HH21	1.72	0.54
29:B:284:ILE:HB	29:B:287:ILE:HG22	1.89	0.54
29:B:285:ASP:HA	29:B:330:ALA:O	2.08	0.54
32:E:97:ARG:NH2	32:E:112:PRO:O	2.40	0.54
6:M:59:GLU:HG2	6:M:60:GLU:N	2.20	0.54
10:P:122:CYS:SG	10:P:123:SER:N	2.80	0.54
24:X:132:ARG:NH1	24:X:135:SER:OG	2.39	0.54
24:X:271:VAL:HB	24:X:288:LYS:HE2	1.89	0.54
25:Y:268:TYR:HA	25:Y:271:PHE:HB3	1.88	0.54
26:Z:94:TRP:CZ3	26:Z:96:HIS:HB3	2.43	0.54
27:W:112:VAL:HG21	27:W:147:LYS:HE2	1.89	0.54
30:C:209:CYS:HA	30:C:243:PRO:HB2	1.89	0.54
30:C:379:THR:HG23	30:C:382:ASP:H	1.71	0.54
3:I:155:ASN:HD21	29:B:438:LEU:C	2.15	0.54
3:i:6:ASP:OD1	3:i:7:SER:N	2.40	0.54
15:f:157:GLU:OE1	15:f:157:GLU:N	2.36	0.54
23:V:225:ASP:OD1	23:V:226:VAL:N	2.41	0.54
25:Y:62:ASP:OD1	25:Y:63:TRP:N	2.40	0.54
28:A:205:GLY:O	28:A:207:GLU:N	2.40	0.54
30:C:196:LYS:N	35:C:501:ADP:O1B	2.40	0.54
32:E:129:ASN:C	32:E:131:SER:H	2.16	0.54
33:F:59:VAL:HA	33:F:62:VAL:HB	1.90	0.54
3:I:49:ARG:CB	3:I:52:ILE:HD11	2.36	0.54
3:I:79:ILE:HA	30:C:401:ILE:O	2.08	0.54
4:J:96:LEU:HA	11:Q:62:LYS:HE3	1.90	0.54
4:J:125:ARG:HG2	4:J:126:PRO:HD2	1.89	0.54
1:g:131:MET:HE2	6:m:125:TYR:HE1	1.72	0.54
3:i:108:GLU:HA	3:i:148:TYR:HE2	1.72	0.54
6:m:8:ASP:O	6:m:22:GLN:NE2	2.36	0.54
12:r:13:ILE:HG13	12:r:152:ALA:HB1	1.89	0.54
14:t:43:MET:HE2	14:t:64:LYS:HA	1.88	0.54
10:P:203:ARG:NH2	10:P:205:ASP:OD2	2.41	0.54
12:R:1:THR:N	12:R:169:TYR:O	2.40	0.54
22:U:580:ARG:HD3	22:U:771:PHE:CZ	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:633:CYS:HB3	22:U:659:CYS:SG	2.47	0.54
29:B:153:ASN:HB3	29:B:160:ILE:HD12	1.90	0.54
29:B:180:PRO:HD2	29:B:242:GLN:HB3	1.90	0.54
32:E:172:LEU:HD21	32:E:183:LEU:HD23	1.89	0.54
6:M:34:SER:OG	6:M:65:ARG:NH1	2.39	0.54
6:m:164:ALA:HB3	6:m:173:LYS:HZ2	1.72	0.54
15:f:237:VAL:O	15:f:245:ASN:ND2	2.39	0.54
15:f:450:ILE:HG23	15:f:822:VAL:HG11	1.89	0.54
15:f:803:PHE:HA	15:f:806:VAL:CG1	2.32	0.54
20:d:200:PHE:CG	20:d:205:LYS:HG2	2.43	0.54
22:U:519:VAL:HG23	22:U:520:MET:SD	2.48	0.54
24:X:171:LEU:HD13	24:X:210:LEU:HD13	1.89	0.54
31:D:254:ALA:HB1	31:D:305:VAL:HG11	1.89	0.54
32:E:138:LEU:O	32:E:142:ILE:HD12	2.07	0.54
33:F:197:GLU:OE2	33:F:350:ARG:NH2	2.40	0.54
7:K:71:ASP:OD1	7:K:72:ALA:N	2.35	0.54
10:P:59:ASP:HA	10:P:62:THR:CG2	2.37	0.54
18:b:95:LEU:HB3	26:Z:69:PHE:CD1	2.42	0.54
19:c:261:GLU:HB3	19:c:270:LEU:HD21	1.89	0.54
22:U:567:ILE:HG13	22:U:586:VAL:HB	1.89	0.54
25:Y:156:LEU:O	25:Y:160:ASN:ND2	2.41	0.54
27:W:55:ARG:NH1	27:W:96:GLN:HG3	2.23	0.54
31:D:192:LYS:O	31:D:194:ILE:N	2.39	0.54
32:E:125:GLU:HB2	32:E:127:PRO:HD2	1.88	0.54
3:I:90:LEU:HD13	3:I:114:LEU:HD22	1.90	0.54
5:L:50:LYS:HD2	5:L:211:SER:HB2	1.89	0.54
5:l:157:ARG:NE	5:l:176:MET:SD	2.80	0.54
15:f:405:HIS:CE1	15:f:813:LYS:HE2	2.43	0.54
20:d:190:LEU:HA	20:d:221:ASN:HA	1.89	0.54
22:U:925:VAL:HG13	22:U:927:PRO:HD3	1.90	0.54
29:B:189:GLY:HA3	29:B:360:THR:HG23	1.90	0.54
29:B:317:ASP:OD1	29:B:346:ARG:NH1	2.41	0.54
30:C:83:LYS:HG2	30:C:105:ILE:HG12	1.90	0.54
31:D:88:VAL:HA	32:E:79:TYR:HA	1.90	0.54
5:l:34:ALA:O	5:l:62:LYS:NZ	2.41	0.54
4:j:212:ARG:HB2	4:j:215:GLN:HB2	1.90	0.54
9:O:163:ILE:HG12	9:O:170:GLY:HA2	1.90	0.54
15:f:209:MET:HE3	29:B:59:ARG:HG2	1.90	0.54
17:a:41:VAL:HG12	17:a:79:ILE:HG21	1.89	0.54
20:d:105:PHE:HE1	20:d:169:ILE:HG12	1.72	0.54
22:U:36:ALA:HB2	23:V:270:LEU:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:98:LYS:H	27:W:98:LYS:HD2	1.72	0.54
27:W:212:LYS:NZ	27:W:215:GLN:OE1	2.40	0.54
29:B:107:MET:HB3	29:B:151:LEU:HD22	1.90	0.54
32:E:84:ARG:NE	32:E:108:MET:O	2.40	0.54
32:E:175:PRO:HB2	32:E:176:PRO:HD3	1.90	0.54
33:F:154:ASN:N	33:F:159:LEU:O	2.29	0.54
7:k:117:SER:HB2	7:k:156:MET:HE1	1.89	0.54
11:q:142:ILE:HD12	12:R:141:ARG:HG3	1.89	0.54
8:N:92:GLU:OE1	8:N:92:GLU:N	2.32	0.54
11:Q:35:MET:SD	11:Q:45:LEU:HD21	2.48	0.54
17:a:51:ALA:O	17:a:86:GLN:NE2	2.38	0.54
19:c:234:TYR:C	27:W:426:ASN:HD21	2.15	0.54
22:U:108:TYR:OH	22:U:159:ARG:NH1	2.41	0.54
22:U:742:HIS:O	22:U:883:ARG:NE	2.41	0.54
5:L:44:ALA:HB1	5:L:144:ILE:HD11	1.90	0.53
6:M:106:ILE:HG12	6:M:111:LEU:HB2	1.91	0.53
4:j:56:GLU:OE2	4:j:60:ARG:NH2	2.41	0.53
7:k:83:ALA:HA	7:k:86:LYS:HE3	1.89	0.53
13:s:175:VAL:HA	13:s:178:VAL:HG22	1.89	0.53
17:a:193:GLN:HB3	17:a:225:LEU:HD13	1.90	0.53
22:U:483:LEU:HD11	22:U:781:LEU:HD13	1.90	0.53
27:W:94:ARG:HD2	27:W:94:ARG:O	2.08	0.53
27:W:152:ILE:HA	27:W:155:GLN:HE21	1.73	0.53
29:B:282:VAL:HG12	29:B:284:ILE:HG23	1.91	0.53
30:C:73:VAL:N	31:D:111:TYR:HA	2.23	0.53
30:C:86:LEU:HB3	30:C:94:LYS:HZ1	1.73	0.53
30:C:138:MET:HG3	31:D:290:LEU:HD11	1.90	0.53
1:G:73:THR:HG22	1:G:76:ILE:HB	1.90	0.53
5:l:152:ASN:HA	6:m:85:ARG:HH12	1.73	0.53
6:m:173:LYS:O	6:m:177:GLU:HG2	2.07	0.53
11:Q:56:PHE:HE2	11:Q:102:LEU:HD11	1.73	0.53
22:U:457:ILE:HA	22:U:460:TYR:CE1	2.42	0.53
23:V:212:TYR:O	23:V:216:ARG:HG2	2.07	0.53
25:Y:298:GLU:OE2	25:Y:302:HIS:NE2	2.40	0.53
27:W:308:LEU:HD22	27:W:315:MET:HE3	1.90	0.53
33:F:402:GLU:HA	33:F:405:MET:HE2	1.89	0.53
3:I:24:ALA:O	3:I:28:ILE:HG12	2.08	0.53
2:h:93:LEU:HD13	2:h:113:ARG:HB3	1.91	0.53
13:s:1:ARG:HH11	13:s:2:PHE:H	1.56	0.53
14:t:99:ARG:NH1	14:t:104:ASN:OD1	2.40	0.53
10:P:155:GLU:HB2	10:P:158:MET:HE3	1.88	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:b:111:ALA:HB3	18:b:140:ILE:HG13	1.91	0.53
23:V:339:LEU:O	23:V:408:ARG:NH1	2.41	0.53
25:Y:16:ASP:HB3	25:Y:150:PHE:CE1	2.43	0.53
27:W:169:LEU:O	27:W:182:ARG:NH2	2.41	0.53
28:A:274:PHE:HB2	28:A:319:MET:HG2	1.89	0.53
29:B:230:THR:HG23	29:B:391:SER:HB2	1.89	0.53
30:C:35:VAL:HG11	31:D:59:GLU:HA	1.91	0.53
30:C:195:GLY:HA2	35:C:501:ADP:O3B	2.08	0.53
31:D:87:LEU:HB2	32:E:80:VAL:HB	1.90	0.53
31:D:88:VAL:HG13	31:D:134:LYS:HA	1.90	0.53
33:F:401:VAL:O	33:F:405:MET:HG3	2.09	0.53
3:I:38:LEU:HD23	3:I:160:LYS:HG2	1.90	0.53
3:I:213:ILE:HG13	3:I:228:LEU:HB2	1.90	0.53
8:n:199:VAL:HG13	8:n:201:THR:HG23	1.89	0.53
15:f:553:THR:HG23	15:f:554:TYR:CD1	2.43	0.53
15:f:806:VAL:O	15:f:810:ILE:HG22	2.08	0.53
18:b:91:ARG:NH1	18:b:130:ARG:HD3	2.23	0.53
25:Y:46:ARG:NH1	25:Y:46:ARG:HA	2.23	0.53
5:l:82:ARG:NH1	7:k:117:SER:OG	2.41	0.53
4:j:83:VAL:HG21	4:j:129:ILE:HD11	1.90	0.53
10:p:91:VAL:HG13	10:p:124:LEU:HD11	1.90	0.53
15:f:669:GLU:HG2	29:B:49:LEU:HD23	1.90	0.53
26:Z:138:TYR:HE1	27:W:448:LYS:HD3	1.72	0.53
29:B:133:VAL:HG11	29:B:158:ALA:HB1	1.89	0.53
32:E:109:ARG:HD2	32:E:111:LEU:HD11	1.90	0.53
33:F:134:LEU:HD22	33:F:160:ILE:H	1.72	0.53
33:F:342:LEU:HB3	33:F:348:LEU:HD12	1.91	0.53
1:G:175:SER:HB3	1:G:205:VAL:HG21	1.91	0.53
2:H:222:THR:N	2:H:225:GLU:OE1	2.41	0.53
5:L:56:LEU:HD13	7:K:167:ALA:HB3	1.91	0.53
9:o:24:MET:HE2	13:S:188:TYR:CZ	2.43	0.53
10:P:45:MET:HG3	10:P:87:LEU:HD11	1.91	0.53
14:T:193:THR:HG23	14:T:195:LYS:H	1.72	0.53
17:a:134:THR:O	17:a:138:VAL:HG23	2.08	0.53
21:e:42:ASN:OD1	21:e:43:TRP:N	2.42	0.53
22:U:21:GLU:O	22:U:25:HIS:ND1	2.41	0.53
28:A:103:ASN:HB2	28:A:114:ASN:H	1.73	0.53
28:A:347:ASP:OD1	28:A:348:LEU:N	2.37	0.53
29:B:232:LYS:N	35:B:501:ADP:O1A	2.41	0.53
33:F:120:LYS:O	33:F:136:VAL:HA	2.08	0.53
33:F:134:LEU:HD22	33:F:159:LEU:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:F:310:MET:HE3	33:F:342:LEU:HG	1.90	0.53
5:L:93:LEU:HD21	13:S:73:LYS:HG2	1.91	0.53
6:M:136:MET:HB3	6:M:148:LEU:HD11	1.90	0.53
1:g:36:GLY:O	1:g:55:LYS:NZ	2.41	0.53
6:m:119:VAL:HG13	6:m:131:PHE:HD2	1.74	0.53
11:Q:58:GLU:O	11:Q:62:LYS:HG2	2.09	0.53
12:R:58:LEU:HD12	12:R:61:ARG:HD3	1.90	0.53
15:f:886:GLU:HB3	15:f:906:TYR:CD2	2.43	0.53
22:U:347:ASN:HB3	22:U:813:TYR:CD1	2.44	0.53
25:Y:359:PRO:HG2	25:Y:364:TRP:HD1	1.74	0.53
26:Z:165:GLU:HB3	26:Z:168:GLU:HG2	1.90	0.53
27:W:317:TRP:HB3	27:W:358:VAL:HG21	1.91	0.53
28:A:38:GLN:HB3	28:A:42:SER:OG	2.08	0.53
32:E:188:ALA:HA	32:E:191:LEU:HD22	1.91	0.53
1:G:80:MET:HE2	1:G:87:SER:HA	1.91	0.53
8:n:48:SER:HB2	8:n:51:ASP:HB2	1.91	0.53
9:o:104:ASP:OD2	9:o:109:HIS:ND1	2.42	0.53
13:s:176:LYS:HE2	13:s:208:VAL:HG21	1.89	0.53
9:O:54:MET:HG2	10:P:96:TYR:CE1	2.44	0.53
10:P:12:MET:HE3	10:P:150:CYS:SG	2.49	0.53
15:f:602:GLY:HA3	15:f:788:MET:HE1	1.91	0.53
15:f:619:HIS:HA	29:B:87:PRO:HA	1.90	0.53
18:b:124:LEU:HD21	18:b:156:PHE:HB2	1.90	0.53
28:A:69:ASP:CB	29:B:138:PHE:HE2	2.21	0.53
28:A:327:LEU:HB3	28:A:329:PRO:HD2	1.91	0.53
7:K:35:SER:HB3	7:K:51:GLU:OE2	2.09	0.53
2:h:222:THR:N	2:h:225:GLU:OE2	2.41	0.53
3:i:69:ASN:ND2	3:i:71:ASP:OD1	2.34	0.53
3:i:112:THR:HG23	4:j:81:ARG:HD2	1.91	0.53
6:m:169:ARG:HB2	6:m:173:LYS:HZ3	1.74	0.53
9:o:144:PRO:HB3	14:T:214:MET:HE3	1.91	0.53
15:f:844:VAL:HG12	15:f:882:LEU:HD13	1.91	0.53
17:a:240:PHE:HE2	17:a:271:LYS:HE2	1.74	0.53
22:U:492:ASP:OD1	22:U:493:VAL:N	2.42	0.53
23:V:121:PHE:CZ	23:V:167:LEU:HD22	2.43	0.53
27:W:217:GLU:N	27:W:217:GLU:OE1	2.41	0.53
28:A:63:THR:OG1	28:A:64:GLY:N	2.42	0.53
30:C:128:PRO:HG2	30:C:130:LYS:HZ1	1.74	0.53
30:C:130:LYS:HE2	31:D:102:ILE:HG21	1.91	0.53
31:D:311:THR:HG21	31:D:317:LEU:HD11	1.91	0.53
9:o:38:SER:HB2	9:o:74:PRO:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:O:215:LYS:HE2	9:O:215:LYS:HA	1.91	0.53
19:c:172:HIS:CD2	19:c:173:GLU:H	2.27	0.53
19:c:257:LYS:O	19:c:261:GLU:HG2	2.09	0.53
23:V:125:ASN:HD22	23:V:159:LEU:HG	1.74	0.53
27:W:27:ARG:NH2	27:W:46:THR:OG1	2.41	0.53
28:A:214:LEU:HB3	28:A:318:LEU:HD21	1.91	0.53
1:G:78:CYS:SG	1:G:140:LEU:HB3	2.49	0.52
1:G:112:ASP:OD2	9:O:72:ARG:NH2	2.36	0.52
4:J:173:GLU:HA	7:K:58:LEU:HD21	1.89	0.52
5:L:103:LEU:HD12	5:L:104:PRO:HD2	1.91	0.52
12:R:15:ALA:HB2	12:R:156:ALA:HB1	1.92	0.52
15:f:792:ALA:HB1	15:f:824:ALA:HA	1.90	0.52
16:x:58:LEU:HD12	16:x:89:LEU:HD12	1.91	0.52
24:X:397:TYR:HB3	25:Y:365:GLN:OE1	2.09	0.52
25:Y:141:VAL:HG21	25:Y:168:ILE:HG21	1.91	0.52
32:E:182:LEU:HD22	35:E:501:ADP:H2'	1.92	0.52
33:F:91:SER:O	33:F:149:ASP:HA	2.08	0.52
4:J:76:LEU:HA	29:B:437:GLY:O	2.08	0.52
1:g:122:SER:OG	1:g:156:PRO:O	2.27	0.52
6:m:134:SER:HB2	6:m:153:PRO:HD3	1.91	0.52
11:q:103:LEU:HG	11:q:132:HIS:CD2	2.44	0.52
15:f:423:ASP:OD1	15:f:424:GLY:N	2.41	0.52
29:B:224:LEU:HD13	29:B:234:LEU:HD22	1.91	0.52
29:B:262:ASP:H	29:B:265:LYS:NZ	2.06	0.52
29:B:415:THR:HG22	29:B:417:GLU:H	1.74	0.52
2:H:36:VAL:HG12	2:H:162:ALA:HB2	1.91	0.52
4:J:159:ASN:OD1	4:J:159:ASN:N	2.30	0.52
6:M:186:CYS:HG	6:M:219:LEU:HD13	1.73	0.52
6:M:190:VAL:HG21	6:M:215:TRP:NE1	2.20	0.52
2:h:39:LYS:HD3	2:h:159:LYS:HA	1.90	0.52
10:p:30:ILE:HG23	10:p:32:ALA:H	1.75	0.52
33:F:91:SER:HA	33:F:124:ILE:HG23	1.90	0.52
1:G:153:LYS:NZ	1:G:168:ALA:HB2	2.25	0.52
2:H:107:THR:O	2:H:111:VAL:N	2.43	0.52
2:H:113:ARG:O	2:H:117:VAL:HG23	2.10	0.52
1:g:44:GLY:N	1:g:47:CYS:O	2.34	0.52
10:P:12:MET:HA	10:P:138:VAL:HG12	1.90	0.52
10:P:149:MET:HE2	10:P:173:ASN:ND2	2.24	0.52
15:f:239:TYR:CZ	29:B:64:LYS:HG2	2.44	0.52
19:c:114:SER:HB2	19:c:147:PRO:HG3	1.90	0.52
19:c:234:TYR:O	27:W:422:ASN:ND2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:d:34:ASN:OD1	20:d:35:PHE:N	2.39	0.52
23:V:168:GLN:NE2	23:V:190:ASP:OD2	2.37	0.52
27:W:138:VAL:HG12	27:W:139:GLU:HG2	1.92	0.52
27:W:263:TRP:CZ2	27:W:295:LYS:HB3	2.43	0.52
27:W:359:VAL:HG13	27:W:382:LEU:HD22	1.91	0.52
30:C:49:ARG:O	30:C:53:ASN:ND2	2.34	0.52
32:E:353:PHE:HZ	32:E:373:LYS:HD2	1.75	0.52
7:K:229:PHE:HD2	7:K:234:LEU:HB2	1.74	0.52
15:f:862:ILE:HG23	15:f:865:PHE:HE1	1.75	0.52
19:c:250:GLU:OE2	19:c:254:ASN:ND2	2.41	0.52
22:U:135:ASN:HA	22:U:138:PHE:CE2	2.44	0.52
22:U:265:ILE:HD11	22:U:326:ILE:HG12	1.90	0.52
22:U:360:VAL:O	22:U:361:ARG:NH1	2.34	0.52
22:U:580:ARG:NE	22:U:584:TYR:OH	2.41	0.52
30:C:160:GLU:OE1	30:C:313:ARG:NH2	2.41	0.52
30:C:329:LEU:HD22	30:C:359:VAL:HG13	1.91	0.52
30:C:375:ARG:HG2	30:C:377:HIS:H	1.74	0.52
11:q:14:LEU:HD13	11:q:182:ILE:HG12	1.92	0.52
8:N:8:PHE:HE2	8:N:13:VAL:HG23	1.75	0.52
10:P:12:MET:SD	10:P:167:ILE:HG13	2.50	0.52
14:T:124:TYR:HE1	14:T:139:THR:HG22	1.75	0.52
22:U:82:LEU:O	22:U:129:ARG:HD2	2.09	0.52
23:V:392:TYR:HA	23:V:395:ILE:HB	1.91	0.52
24:X:285:GLU:HA	24:X:288:LYS:HD2	1.92	0.52
27:W:52:LYS:HD3	27:W:55:ARG:NH2	2.24	0.52
27:W:367:ALA:HA	27:W:415:PHE:CD2	2.44	0.52
30:C:72:TYR:O	30:C:116:LEU:N	2.37	0.52
31:D:168:GLY:N	35:D:501:ADP:HN62	2.03	0.52
32:E:57:VAL:CG2	33:F:133:PHE:HB2	2.39	0.52
33:F:414:GLU:HG3	33:F:415:LEU:HG	1.90	0.52
14:t:56:ASP:N	14:t:107:TRP:O	2.38	0.52
12:R:102:CYS:HB3	12:R:111:LEU:HG	1.91	0.52
15:f:244:GLU:O	15:f:248:LEU:HG	2.09	0.52
15:f:698:SER:HB2	15:f:703:ARG:HH21	1.74	0.52
15:f:799:VAL:HG21	15:f:821:LEU:HD12	1.92	0.52
26:Z:34:ARG:HH21	26:Z:102:HIS:HE2	1.57	0.52
28:A:195:LEU:HD13	28:A:232:ARG:HD2	1.91	0.52
32:E:57:VAL:HG22	33:F:133:PHE:HB2	1.90	0.52
32:E:74:THR:OG1	32:E:75:ASN:OD1	2.23	0.52
32:E:99:ALA:HB3	32:E:109:ARG:HG3	1.91	0.52
2:H:22:ILE:HD12	2:H:152:SER:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:i:90:LEU:HD21	3:i:114:LEU:HD22	1.92	0.52
9:o:166:ASP:OD1	9:o:168:GLY:N	2.42	0.52
12:R:11:GLY:HA2	12:R:104:TRP:HZ3	1.75	0.52
15:f:777:THR:HB	15:f:828:ARG:HD3	1.92	0.52
17:a:293:PHE:HB2	17:a:329:LYS:HG2	1.90	0.52
20:d:30:LEU:HD13	20:d:54:ILE:HD11	1.91	0.52
23:V:82:LEU:HD11	23:V:166:TYR:HE2	1.74	0.52
28:A:151:ILE:HG22	28:A:153:LEU:HG	1.91	0.52
29:B:338:ASP:HB3	29:B:341:LEU:HD23	1.91	0.52
4:J:98:VAL:HG13	12:R:78:ALA:HB1	1.90	0.52
7:k:70:ILE:HD11	7:k:89:ILE:HD12	1.91	0.52
9:o:147:GLU:HG3	9:o:150:GLU:H	1.75	0.52
20:d:175:ARG:HH21	20:d:205:LYS:HD2	1.74	0.52
22:U:16:GLU:HB2	22:U:19:LEU:HB2	1.92	0.52
22:U:439:GLU:HB2	22:U:473:VAL:HG12	1.92	0.52
22:U:557:TYR:HA	22:U:589:ALA:HA	1.91	0.52
26:Z:52:ASN:OD1	26:Z:53:SER:N	2.42	0.52
29:B:96:ARG:HA	29:B:100:ASP:HB3	1.91	0.52
31:D:412:GLN:O	31:D:412:GLN:NE2	2.42	0.52
32:E:109:ARG:HH22	33:F:135:PRO:HB3	1.74	0.52
1:G:123:GLN:HA	1:G:126:THR:HG22	1.91	0.52
5:l:167:SER:HB2	5:l:197:GLU:HG2	1.92	0.52
8:n:20:THR:O	8:n:27:ALA:N	2.42	0.52
10:p:173:ASN:ND2	13:S:151:ASN:HD22	2.07	0.52
11:q:101:ASN:OD1	11:q:120:TYR:N	2.43	0.52
11:Q:147:TYR:HA	11:Q:151:ILE:HD11	1.91	0.52
16:x:70:GLN:HA	16:x:73:GLN:HG2	1.92	0.52
28:A:418:LYS:NZ	29:B:348:ASP:OD1	2.30	0.52
29:B:112:LEU:HD22	29:B:145:GLU:O	2.10	0.52
29:B:114:GLU:HB3	29:B:122:ILE:CB	2.34	0.52
32:E:102:MET:HG2	33:F:158:TYR:CE2	2.45	0.52
32:E:326:ILE:HG22	32:E:326:ILE:O	2.10	0.52
33:F:281:SER:H	33:F:326:VAL:HG22	1.75	0.52
33:F:427:VAL:HG23	33:F:428:GLN:HG3	1.91	0.52
7:K:199:LEU:HD11	7:K:215:ILE:HG21	1.92	0.51
11:q:16:ALA:HB2	11:q:180:VAL:HG12	1.91	0.51
13:s:28:ARG:HH21	13:s:191:ASP:HB3	1.75	0.51
28:A:55:LEU:HB2	29:B:72:LEU:HD23	1.93	0.51
29:B:209:GLU:HA	29:B:212:GLU:HB3	1.92	0.51
30:C:127:LEU:HD11	31:D:96:VAL:HG21	1.91	0.51
32:E:168:LYS:NZ	32:E:264:MET:HA	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:E:339:ASN:ND2	32:E:341:ALA:H	2.07	0.51
3:I:44:LEU:HD22	3:I:190:LEU:HD23	1.92	0.51
3:I:45:LEU:HD13	3:I:75:SER:OG	2.09	0.51
3:I:46:ALA:HA	3:I:213:ILE:HG22	1.90	0.51
3:i:67:LYS:HE2	3:i:225:ILE:HD12	1.91	0.51
17:a:26:GLU:HA	17:a:29:TYR:CE2	2.46	0.51
17:a:290:GLN:HG2	17:a:290:GLN:O	2.09	0.51
20:d:8:GLU:HB3	20:d:18:LYS:NZ	2.26	0.51
22:U:552:ILE:O	22:U:585:THR:OG1	2.26	0.51
23:V:314:ARG:NH1	25:Y:378:ASN:O	2.43	0.51
31:D:240:LEU:HD13	31:D:284:GLU:HB3	1.93	0.51
32:E:309:ARG:HG2	32:E:332:VAL:HG22	1.91	0.51
5:l:60:GLN:CD	7:k:163:VAL:HA	2.35	0.51
3:i:99:LEU:HD12	10:p:69:PHE:HB2	1.91	0.51
9:O:109:HIS:HB3	9:O:111:TYR:HE1	1.75	0.51
13:S:106:VAL:HG23	13:S:108:ASN:HD21	1.75	0.51
20:d:31:LEU:HD11	22:U:19:LEU:HD12	1.91	0.51
22:U:635:SER:O	30:C:43:ARG:NH1	2.43	0.51
25:Y:234:PRO:O	25:Y:236:LEU:N	2.37	0.51
28:A:176:ASP:HA	28:A:227:ARG:HG2	1.91	0.51
4:J:150:SER:OG	4:J:151:GLY:N	2.43	0.51
5:L:126:ARG:HD2	7:K:15:PHE:HE1	1.75	0.51
6:M:192:GLU:O	6:M:196:ILE:HG12	2.10	0.51
8:n:179:ILE:HG13	8:n:184:VAL:HG23	1.92	0.51
11:Q:59:TYR:HE2	11:Q:87:ASN:HD21	1.57	0.51
15:f:748:LEU:O	15:f:752:HIS:ND1	2.27	0.51
15:f:887:PHE:HB3	15:f:900:LEU:HB3	1.92	0.51
20:d:26:LEU:HD22	20:d:30:LEU:HD22	1.93	0.51
22:U:82:LEU:HG	22:U:129:ARG:HG3	1.92	0.51
29:B:262:ASP:HA	29:B:265:LYS:HB2	1.92	0.51
2:H:179:ASN:OD1	2:H:180:GLU:N	2.41	0.51
5:L:155:ASP:OD1	5:L:156:CYS:N	2.43	0.51
11:q:29:LYS:HG2	11:q:31:ASP:H	1.76	0.51
14:t:136:SER:HB3	14:t:154:LEU:HD12	1.91	0.51
15:f:437:GLU:HB2	15:f:440:ILE:HG13	1.92	0.51
17:a:77:VAL:HA	17:a:80:ILE:HG12	1.91	0.51
22:U:550:VAL:HG22	22:U:768:GLN:HE22	1.76	0.51
27:W:79:GLU:O	27:W:79:GLU:HG2	2.10	0.51
28:A:215:PHE:CE1	28:A:342:GLU:HB3	2.45	0.51
29:B:200:SER:O	29:B:326:LYS:NZ	2.44	0.51
30:C:197:THR:O	30:C:198:LEU:HG	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:F:212:PHE:CD2	33:F:219:PRO:HG3	2.45	0.51
33:F:310:MET:HE1	33:F:339:ASP:OD1	2.11	0.51
4:J:192:ILE:C	4:J:194:ALA:H	2.18	0.51
7:k:70:ILE:HA	7:k:93:ARG:HG2	1.92	0.51
6:m:185:THR:O	6:m:189:ILE:HG12	2.11	0.51
6:m:215:TRP:CE3	6:m:227:VAL:HG22	2.46	0.51
18:b:52:ILE:HG13	18:b:93:ALA:HA	1.92	0.51
19:c:100:LYS:HA	19:c:105:PRO:HG3	1.91	0.51
20:d:93:ALA:O	20:d:97:GLN:NE2	2.43	0.51
21:e:22:PHE:HZ	23:V:287:ARG:HG2	1.76	0.51
22:U:405:THR:OG1	22:U:445:ALA:HB2	2.10	0.51
23:V:376:ASN:ND2	23:V:399:ARG:HD3	2.26	0.51
25:Y:13:LYS:HA	25:Y:16:ASP:HB2	1.91	0.51
25:Y:39:ASP:HA	25:Y:42:MET:HE3	1.93	0.51
7:K:82:ILE:H	7:K:82:ILE:HD12	1.75	0.51
5:l:126:ARG:HH22	7:k:121:LEU:HG	1.75	0.51
7:k:141:LEU:HB2	7:k:156:MET:HB3	1.93	0.51
11:Q:19:ARG:HD3	11:Q:177:THR:HG23	1.93	0.51
15:f:239:TYR:HB2	29:B:63:LEU:HG	1.92	0.51
20:d:187:GLU:OE1	23:V:452:ASN:ND2	2.43	0.51
22:U:474:ARG:HB3	22:U:508:THR:HG21	1.93	0.51
22:U:580:ARG:HD3	22:U:771:PHE:HZ	1.74	0.51
25:Y:296:VAL:HB	25:Y:300:ARG:HH21	1.74	0.51
27:W:448:LYS:O	27:W:452:ILE:HG12	2.10	0.51
30:C:36:ASN:O	30:C:40:GLN:HG2	2.10	0.51
1:G:178:PHE:HA	1:G:181:LYS:HE2	1.92	0.51
5:L:36:VAL:HG22	5:L:47:VAL:HB	1.92	0.51
2:h:43:GLY:HA3	2:h:184:LEU:HD21	1.93	0.51
10:p:190:ILE:HA	10:p:195:ILE:HG22	1.91	0.51
12:r:97:MET:O	12:r:116:SER:N	2.42	0.51
15:f:78:LEU:O	15:f:82:ILE:HG12	2.11	0.51
15:f:127:SER:HA	15:f:139:CYS:HA	1.93	0.51
15:f:165:GLU:HA	15:f:168:LYS:HD2	1.93	0.51
18:b:131:LEU:HD22	18:b:136:VAL:HG21	1.93	0.51
19:c:195:GLY:O	19:c:199:HIS:N	2.43	0.51
23:V:258:TYR:O	23:V:263:LEU:N	2.44	0.51
23:V:264:TYR:HD2	23:V:295:ILE:HG13	1.76	0.51
27:W:327:GLU:HG2	27:W:337:ALA:HB1	1.92	0.51
29:B:293:LYS:C	29:B:295:TYR:H	2.18	0.51
31:D:273:LYS:HE3	31:D:276:ASP:HB2	1.92	0.51
1:G:70:PHE:HB3	1:G:95:ARG:HH12	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:200:ILE:HG23	7:K:241:ILE:HD12	1.92	0.51
8:N:17:ASP:OD2	8:N:171:GLY:N	2.44	0.51
15:f:423:ASP:HB2	16:x:37:ASN:H	1.76	0.51
15:f:745:LEU:HA	15:f:748:LEU:HD12	1.93	0.51
19:c:281:LYS:HG2	19:c:282:ARG:HH11	1.74	0.51
29:B:224:LEU:HD23	29:B:351:ILE:HB	1.93	0.51
1:G:147:GLN:HB3	1:G:150:GLN:HE21	1.77	0.51
4:J:90:GLU:HG3	4:J:110:TYR:CE1	2.47	0.51
8:N:133:SER:HA	8:N:136:TYR:CZ	2.46	0.51
11:Q:35:MET:HG3	11:Q:181:ARG:HD2	1.92	0.51
10:P:36:THR:OG1	10:P:38:ASP:OD1	2.28	0.51
15:f:219:LYS:HD3	15:f:258:LYS:NZ	2.26	0.51
19:c:120:CYS:O	19:c:197:ASN:ND2	2.44	0.51
22:U:465:LEU:HD21	22:U:477:GLY:HA3	1.93	0.51
22:U:798:PRO:HB2	22:U:800:VAL:HG23	1.92	0.51
28:A:73:ALA:HA	28:A:76:ALA:HB3	1.93	0.51
2:H:33:ALA:N	31:D:417:TYR:OH	2.32	0.50
6:M:186:CYS:O	6:M:190:VAL:HG23	2.10	0.50
8:N:116:MET:SD	8:N:116:MET:N	2.83	0.50
15:f:840:LEU:HB3	15:f:842:VAL:HG23	1.93	0.50
20:d:76:ALA:O	22:U:7:GLY:N	2.44	0.50
20:d:175:ARG:HE	20:d:205:LYS:HD3	1.76	0.50
28:A:408:ASP:OD1	28:A:409:PHE:N	2.44	0.50
31:D:411:GLU:HG2	31:D:412:GLN:N	2.23	0.50
32:E:126:ASP:OD1	32:E:127:PRO:HD3	2.10	0.50
4:J:42:VAL:HG12	4:J:210:VAL:HG22	1.91	0.50
4:J:204:LYS:HD2	4:J:222:PRO:HB3	1.93	0.50
5:l:24:TYR:HB3	7:k:19:GLY:HA2	1.93	0.50
8:N:81:SER:HA	8:N:84:LYS:HG2	1.92	0.50
27:W:123:ARG:NH1	27:W:123:ARG:O	2.44	0.50
29:B:230:THR:HA	35:B:501:ADP:O2A	2.11	0.50
29:B:246:THR:OG1	29:B:280:SER:HB2	2.11	0.50
29:B:316:LEU:HD13	29:B:347:ILE:HD12	1.94	0.50
30:C:155:ASP:O	30:C:159:LYS:HG3	2.11	0.50
33:F:134:LEU:HD11	33:F:137:ILE:HA	1.93	0.50
3:I:214:ALA:HB2	3:I:227:VAL:HG12	1.92	0.50
4:j:37:GLY:HA2	4:j:181:ILE:HD12	1.94	0.50
12:r:102:CYS:HB3	12:r:111:LEU:HD13	1.93	0.50
13:s:150:ASP:OD2	10:P:177:ARG:NE	2.40	0.50
9:O:8:TYR:CD1	9:O:13:VAL:HG23	2.46	0.50
15:f:674:THR:O	15:f:678:LEU:HG	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:e:27:TRP:HB2	23:V:355:ARG:HB3	1.93	0.50
23:V:111:TYR:CE2	23:V:115:LYS:HE2	2.46	0.50
23:V:176:MET:HG3	23:V:217:VAL:HG22	1.94	0.50
28:A:115:VAL:HG12	28:A:117:GLN:H	1.76	0.50
29:B:250:VAL:HB	29:B:284:ILE:HG22	1.94	0.50
30:C:198:LEU:HD13	35:C:501:ADP:H5'2	1.92	0.50
5:L:66:VAL:C	13:S:77:HIS:HE2	2.20	0.50
6:m:140:TYR:CZ	6:m:218:GLU:HB3	2.47	0.50
12:r:59:LEU:HD22	12:r:83:LEU:HD22	1.93	0.50
14:t:124:TYR:HB2	14:t:137:LEU:HD13	1.93	0.50
14:t:138:ALA:HB3	14:t:147:GLN:HB2	1.94	0.50
11:Q:16:ALA:HB2	11:Q:160:LEU:HD11	1.91	0.50
15:f:887:PHE:HB3	15:f:900:LEU:HD12	1.93	0.50
19:c:37:ALA:HA	19:c:72:VAL:HG12	1.93	0.50
22:U:9:ILE:HB	22:U:44:LYS:HE3	1.92	0.50
22:U:413:LYS:HA	22:U:449:ILE:HA	1.93	0.50
22:U:457:ILE:HA	22:U:460:TYR:HE1	1.76	0.50
22:U:802:TYR:CD1	22:U:892:LEU:HD11	2.47	0.50
23:V:109:ASN:O	23:V:113:LEU:HD23	2.11	0.50
31:D:58:GLU:HA	31:D:61:ILE:HG12	1.91	0.50
31:D:381:GLU:O	31:D:384:MET:HG3	2.12	0.50
33:F:75:GLU:O	33:F:79:LYS:HG2	2.11	0.50
1:G:165:ALA:HB1	1:G:179:LEU:HD13	1.92	0.50
2:H:32:GLY:HA2	2:H:165:LYS:HB3	1.92	0.50
11:q:142:ILE:HD11	12:R:137:GLY:C	2.37	0.50
12:r:103:GLY:HA2	12:r:179:VAL:HG11	1.92	0.50
15:f:680:ARG:HE	28:A:64:GLY:H	1.60	0.50
24:X:71:LYS:O	24:X:74:ARG:NH1	2.42	0.50
30:C:236:VAL:HA	30:C:239:ARG:HE	1.77	0.50
32:E:268:ASP:OD1	32:E:269:THR:N	2.44	0.50
8:N:66:HIS:CE1	8:N:70:LEU:HD11	2.47	0.50
9:O:161:ALA:O	9:O:165:ASN:ND2	2.45	0.50
13:S:194:ARG:NH1	13:S:205:GLU:OE1	2.44	0.50
22:U:701:ILE:HD13	22:U:809:SER:HA	1.93	0.50
23:V:131:LEU:HD11	23:V:171:VAL:HG21	1.93	0.50
24:X:413:SER:O	24:X:417:LYS:HB2	2.11	0.50
25:Y:236:LEU:HG	25:Y:240:VAL:HG22	1.94	0.50
31:D:247:VAL:HG12	31:D:295:GLN:HG3	1.94	0.50
32:E:50:LEU:HD23	32:E:52:SER:H	1.76	0.50
33:F:134:LEU:CD1	33:F:137:ILE:HA	2.42	0.50
2:H:213:CYS:HB2	2:H:218:PHE:HD1	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:163:PHE:CE2	1:g:166:THR:HG22	2.46	0.50
2:h:219:ARG:NH1	2:h:221:LEU:HA	2.27	0.50
7:k:210:LEU:HD23	7:k:210:LEU:H	1.76	0.50
6:m:73:VAL:HG22	6:m:139:SER:HB2	1.93	0.50
11:q:9:GLY:HA3	11:q:12:TYR:CZ	2.46	0.50
9:O:45:GLY:HA2	9:O:98:LEU:HD13	1.94	0.50
11:Q:118:MET:HE3	11:Q:122:ALA:HA	1.93	0.50
15:f:846:VAL:HG21	15:f:872:VAL:HG21	1.92	0.50
16:x:70:GLN:NE2	16:x:85:MET:SD	2.81	0.50
17:a:350:LYS:HE2	26:Z:213:GLU:HA	1.94	0.50
27:W:300:PRO:HA	27:W:303:LYS:HE2	1.92	0.50
27:W:375:MET:HE3	27:W:408:ARG:NH2	2.27	0.50
28:A:220:THR:O	28:A:223:THR:OG1	2.30	0.50
33:F:192:ASP:HA	33:F:195:ILE:HG12	1.92	0.50
7:K:38:ILE:HD11	7:K:177:ALA:HB1	1.92	0.50
1:g:127:GLN:HG3	2:h:127:VAL:HG23	1.94	0.50
8:N:123:GLN:NE2	8:N:125:PHE:O	2.44	0.50
15:f:160:ARG:HH12	29:B:413:LYS:CE	2.20	0.50
15:f:240:VAL:HB	15:f:244:GLU:HG3	1.94	0.50
15:f:471:LEU:O	15:f:471:LEU:HD23	2.11	0.50
15:f:570:GLY:O	15:f:572:ALA:N	2.43	0.50
19:c:50:PRO:HG2	32:E:53:VAL:HG11	1.93	0.50
19:c:222:LYS:HE3	26:Z:176:LEU:HD11	1.93	0.50
19:c:259:VAL:HG11	24:X:411:VAL:HG12	1.94	0.50
20:d:144:MET:C	23:V:440:LYS:HZ1	2.20	0.50
22:U:208:LEU:HD12	22:U:215:ASN:ND2	2.27	0.50
22:U:558:GLY:H	22:U:589:ALA:HA	1.77	0.50
27:W:220:GLU:OE1	27:W:220:GLU:N	2.45	0.50
29:B:274:ALA:HB1	29:B:280:SER:HB3	1.94	0.50
30:C:42:LEU:O	30:C:46:GLN:HG2	2.11	0.50
30:C:86:LEU:O	30:C:87:VAL:HG12	2.12	0.50
30:C:271:ARG:O	30:C:275:GLU:HG2	2.12	0.50
32:E:43:SER:O	32:E:47:LEU:HG	2.11	0.50
2:H:150:ASP:OD1	2:H:153:GLY:N	2.31	0.50
5:l:180:MET:HG3	5:l:181:GLU:HG3	1.94	0.50
8:n:33:LYS:HD3	8:n:45:ARG:HE	1.75	0.50
11:q:8:GLN:NE2	11:q:113:PRO:O	2.45	0.50
11:Q:35:MET:HB3	11:Q:43:LEU:HD11	1.94	0.50
10:P:28:PHE:HD2	10:P:36:THR:HG22	1.77	0.50
12:R:52:CYS:O	12:R:56:GLU:HG2	2.12	0.50
14:T:50:MET:HE3	14:T:192:VAL:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:b:70:ARG:HG3	18:b:71:ILE:HD12	1.94	0.50
22:U:368:ALA:HB1	22:U:731:ILE:HB	1.94	0.50
24:X:339:ILE:HD11	24:X:387:ILE:HD11	1.94	0.50
27:W:148:THR:OG1	27:W:168:GLU:OE1	2.27	0.50
27:W:407:ASP:O	27:W:411:GLY:N	2.45	0.50
29:B:211:TYR:CE2	29:B:218:PRO:HD2	2.47	0.50
32:E:324:GLY:HA2	32:E:363:VAL:HA	1.94	0.50
33:F:224:LEU:HD11	33:F:332:THR:HG22	1.94	0.50
4:J:64:ALA:O	4:J:88:ARG:NH2	2.45	0.49
4:J:88:ARG:NH1	11:Q:70:ARG:HA	2.19	0.49
15:f:86:THR:HB	15:f:155:GLY:HA3	1.94	0.49
15:f:333:LEU:HD13	15:f:871:PRO:HB3	1.94	0.49
18:b:146:GLU:HG2	18:b:147:GLU:N	2.27	0.49
20:d:55:LEU:HD13	20:d:78:LEU:HA	1.93	0.49
24:X:74:ARG:HG2	24:X:75:PRO:HD3	1.94	0.49
24:X:271:VAL:HG11	24:X:288:LYS:HG2	1.94	0.49
27:W:14:VAL:HG23	27:W:58:SER:HB3	1.93	0.49
27:W:44:ILE:O	27:W:48:LEU:HG	2.11	0.49
30:C:352:PRO:HD2	30:C:390:VAL:HG11	1.94	0.49
32:E:167:PRO:HB3	32:E:297:ARG:HH21	1.75	0.49
3:I:124:PHE:O	3:I:127:LYS:NZ	2.41	0.49
10:p:122:CYS:SG	10:p:123:SER:N	2.85	0.49
12:r:19:ARG:NH1	12:r:168:ALA:O	2.45	0.49
14:t:133:GLU:OE1	14:t:133:GLU:N	2.46	0.49
10:P:59:ASP:CA	10:P:62:THR:HG22	2.41	0.49
12:R:8:PHE:CE2	12:R:10:HIS:HB2	2.47	0.49
13:S:27:THR:OG1	13:S:192:ALA:HB3	2.11	0.49
17:a:123:LEU:HD12	17:a:162:TYR:CD1	2.47	0.49
19:c:161:ARG:NE	19:c:203:ILE:HD11	2.27	0.49
21:e:28:ALA:H	23:V:355:ARG:HE	1.60	0.49
23:V:180:ARG:NH1	23:V:183:GLU:OE1	2.45	0.49
28:A:411:GLU:HA	28:A:414:ASN:HD21	1.76	0.49
30:C:113:ARG:O	30:C:127:LEU:N	2.45	0.49
30:C:140:VAL:HG11	30:C:234:LEU:HD22	1.94	0.49
3:i:190:LEU:O	3:i:194:ILE:HG13	2.13	0.49
13:s:10:GLY:HA3	13:s:42:LYS:HE2	1.93	0.49
14:t:46:ASN:OD1	14:t:49:THR:N	2.43	0.49
11:Q:157:VAL:HG12	11:Q:161:ARG:HH12	1.77	0.49
15:f:83:ARG:HD2	15:f:83:ARG:O	2.12	0.49
15:f:478:ARG:NH1	15:f:507:ASP:OD2	2.41	0.49
16:x:56:GLN:NE2	16:x:85:MET:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:240:LEU:HG	23:V:241:ARG:HE	1.78	0.49
24:X:190:LEU:HD21	24:X:214:SER:HA	1.94	0.49
25:Y:359:PRO:HB2	25:Y:364:TRP:HB2	1.94	0.49
31:D:210:CYS:N	31:D:376:ASN:OD1	2.45	0.49
32:E:48:LYS:HD3	33:F:76:ASN:HB2	1.94	0.49
7:K:191:LEU:HD22	7:K:221:GLN:NE2	2.27	0.49
1:g:83:MET:HE3	1:g:84:THR:H	1.77	0.49
1:g:206:LEU:HD23	1:g:208:ILE:HD13	1.92	0.49
6:m:229:LYS:O	6:m:232:ARG:HB3	2.11	0.49
10:p:82:ILE:HG12	10:p:87:LEU:HB2	1.95	0.49
11:q:166:GLU:CD	12:R:137:GLY:HA2	2.37	0.49
11:Q:56:PHE:CD2	11:Q:100:VAL:HG21	2.47	0.49
18:b:145:GLU:H	18:b:145:GLU:CD	2.20	0.49
19:c:225:TRP:N	19:c:227:GLU:OE1	2.46	0.49
22:U:374:SER:OG	22:U:407:SER:HB2	2.12	0.49
24:X:78:ASN:HB3	24:X:122:ARG:HH22	1.77	0.49
25:Y:235:ASP:O	25:Y:239:LYS:HG2	2.12	0.49
27:W:231:ILE:HG22	27:W:246:HIS:NE2	2.28	0.49
27:W:263:TRP:CH2	27:W:295:LYS:HB3	2.48	0.49
28:A:34:LYS:HD3	30:C:174:LEU:HB3	1.94	0.49
3:I:240:HIS:O	3:I:244:GLU:HG2	2.12	0.49
1:g:163:PHE:HA	2:h:58:ASP:N	2.23	0.49
2:h:196:LYS:HB3	2:h:203:MET:SD	2.52	0.49
15:f:99:LEU:HD23	15:f:106:LEU:HD11	1.94	0.49
32:E:72:LYS:NZ	32:E:73:ALA:O	2.45	0.49
32:E:263:GLN:O	32:E:266:GLY:N	2.43	0.49
33:F:98:ASP:HB3	33:F:121:CYS:SG	2.53	0.49
2:h:45:VAL:HG22	2:h:212:ILE:HG22	1.94	0.49
6:m:151:ILE:HG12	6:m:157:SER:HB2	1.94	0.49
11:q:85:ARG:HB2	11:q:118:MET:HE1	1.94	0.49
12:R:8:PHE:CE1	12:R:13:ILE:HG12	2.47	0.49
12:R:158:ARG:O	12:R:162:GLN:HG2	2.12	0.49
17:a:103:LYS:HG3	17:a:104:VAL:HG23	1.94	0.49
17:a:224:SER:HA	17:a:227:ASN:HB2	1.94	0.49
20:d:105:PHE:HD1	20:d:169:ILE:HG21	1.77	0.49
22:U:717:ILE:HG13	22:U:731:ILE:HG12	1.94	0.49
23:V:449:ALA:HA	23:V:458:VAL:HG13	1.93	0.49
27:W:117:ASP:CG	27:W:119:PRO:HD2	2.37	0.49
30:C:117:ARG:HD2	30:C:120:SER:OG	2.12	0.49
31:D:411:GLU:CG	31:D:412:GLN:H	2.23	0.49
32:E:92:LEU:O	32:E:96:THR:OG1	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:E:126:ASP:CG	32:E:127:PRO:HD3	2.38	0.49
1:g:175:SER:HA	1:g:205:VAL:HG21	1.95	0.49
2:h:223:PRO:HA	2:h:226:VAL:HB	1.93	0.49
3:i:194:ILE:HG12	3:i:236:LEU:HD23	1.94	0.49
4:j:169:ARG:NH2	7:k:56:SER:OG	2.37	0.49
13:s:148:LEU:HD23	13:s:178:VAL:HG12	1.95	0.49
12:R:21:THR:HG21	12:R:169:TYR:HD1	1.76	0.49
15:f:170:TRP:O	15:f:181:ARG:NH1	2.45	0.49
15:f:252:ALA:HB1	15:f:268:LEU:HD13	1.94	0.49
17:a:156:TYR:HB3	17:a:179:PHE:HB2	1.95	0.49
19:c:220:LEU:HD13	26:Z:134:PRO:HA	1.93	0.49
19:c:298:GLN:HB2	26:Z:252:LYS:NZ	2.27	0.49
22:U:202:VAL:HG12	22:U:219:CYS:HB2	1.95	0.49
22:U:642:GLU:OE2	30:C:47:ALA:HA	2.13	0.49
24:X:194:ARG:HH21	24:X:214:SER:HB2	1.77	0.49
27:W:413:ILE:HD12	27:W:415:PHE:CZ	2.47	0.49
3:I:91:ARG:HD3	10:P:76:LEU:HB3	1.95	0.49
1:g:88:ARG:NH1	6:m:113:ASP:OD1	2.46	0.49
8:n:168:GLY:HA3	14:T:182:ARG:HH21	1.75	0.49
11:Q:81:ALA:HA	11:Q:104:LEU:HD13	1.95	0.49
11:Q:101:ASN:HB3	11:Q:132:HIS:NE2	2.26	0.49
11:Q:102:LEU:HB2	11:Q:118:MET:HG3	1.93	0.49
10:P:149:MET:HE2	10:P:173:ASN:HD22	1.78	0.49
15:f:703:ARG:HB3	15:f:706:ILE:HG13	1.94	0.49
18:b:136:VAL:HG12	18:b:138:VAL:HG23	1.94	0.49
22:U:341:PHE:HD1	22:U:881:PRO:HB2	1.78	0.49
23:V:171:VAL:HB	23:V:187:ILE:HG21	1.95	0.49
24:X:185:LYS:NZ	25:Y:244:ALA:HB3	2.27	0.49
28:A:121:PHE:CE1	28:A:123:VAL:HB	2.48	0.49
29:B:227:PRO:HD2	29:B:353:PHE:HD2	1.78	0.49
29:B:232:LYS:HZ3	30:C:308:PRO:HG3	1.74	0.49
6:M:35:THR:HG22	6:M:167:LYS:HB3	1.93	0.49
6:m:215:TRP:CZ3	6:m:227:VAL:HG22	2.47	0.49
10:p:148:GLY:C	13:S:148:LEU:HD11	2.38	0.49
14:T:85:PRO:HB2	14:T:121:PHE:HD2	1.78	0.49
15:f:136:GLU:HG3	15:f:137:ARG:H	1.78	0.49
15:f:137:ARG:HH22	15:f:172:GLU:HG3	1.77	0.49
15:f:208:LEU:HA	15:f:211:ILE:HG12	1.95	0.49
15:f:666:ILE:HD12	15:f:669:GLU:OE2	2.13	0.49
15:f:869:THR:HG23	15:f:871:PRO:HD2	1.94	0.49
23:V:475:ALA:O	23:V:478:GLN:NE2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:E:285:LEU:O	32:E:285:LEU:HG	2.12	0.49
2:H:58:ASP:OD1	2:H:60:ARG:HG2	2.13	0.49
4:j:88:ARG:CZ	11:q:70:ARG:HA	2.43	0.49
13:s:64:LEU:O	13:s:68:ILE:HG12	2.13	0.49
10:P:82:ILE:HG12	10:P:87:LEU:HB2	1.95	0.49
18:b:92:VAL:HG12	26:Z:68:TRP:H	1.78	0.49
20:d:44:THR:HA	20:d:47:GLN:HB3	1.95	0.49
22:U:179:TYR:CZ	22:U:183:LEU:HD11	2.48	0.49
22:U:532:MET:HB3	22:U:548:LEU:HD11	1.95	0.49
23:V:268:GLU:HB3	23:V:295:ILE:HD11	1.95	0.49
23:V:372:LEU:HA	23:V:399:ARG:CZ	2.42	0.49
25:Y:46:ARG:HA	25:Y:46:ARG:CZ	2.43	0.49
27:W:148:THR:O	27:W:152:ILE:HG12	2.12	0.49
28:A:148:GLN:HB2	28:A:150:HIS:CE1	2.48	0.49
30:C:115:ALA:O	30:C:124:HIS:N	2.41	0.49
30:C:215:SER:OG	30:C:218:GLU:OE2	2.26	0.49
30:C:217:SER:O	31:D:274:ARG:NE	2.46	0.49
32:E:331:ILE:HG23	32:E:371:VAL:HG21	1.93	0.49
2:H:45:VAL:HG22	2:H:212:ILE:HG22	1.94	0.48
3:I:114:LEU:O	3:I:117:ILE:HG22	2.13	0.48
7:K:121:LEU:HD23	7:K:136:PRO:HB3	1.95	0.48
10:P:118:LYS:HD3	10:P:119:PRO:HD2	1.95	0.48
17:a:186:LYS:HA	17:a:193:GLN:HE22	1.78	0.48
18:b:25:ARG:NH1	18:b:145:GLU:OE2	2.46	0.48
20:d:78:LEU:HD22	20:d:102:ASN:ND2	2.28	0.48
22:U:685:GLN:HB3	22:U:726:ALA:HA	1.95	0.48
23:V:466:ILE:HG22	23:V:470:ARG:HH12	1.77	0.48
30:C:66:LEU:O	30:C:69:GLN:N	2.46	0.48
30:C:117:ARG:H	30:C:121:TYR:HA	1.77	0.48
30:C:140:VAL:HB	30:C:212:ILE:HG12	1.95	0.48
5:L:13:TRP:HE1	6:M:129:ARG:HD2	1.78	0.48
5:L:56:LEU:HD11	7:K:182:GLN:HA	1.95	0.48
2:h:11:THR:OG1	2:h:122:THR:O	2.27	0.48
9:o:173:ILE:HD11	9:o:190:THR:HB	1.93	0.48
9:O:173:ILE:HD12	9:O:190:THR:HB	1.94	0.48
17:a:211:PHE:O	17:a:339:ARG:NH1	2.46	0.48
17:a:236:THR:HG21	17:a:253:THR:HG21	1.95	0.48
19:c:104:ARG:HB2	26:Z:25:ARG:HD2	1.95	0.48
22:U:461:LEU:O	22:U:465:LEU:HD23	2.12	0.48
22:U:720:LYS:HA	22:U:727:LYS:HD2	1.95	0.48
23:V:407:VAL:HG21	23:V:437:ILE:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:111:TYR:O	27:W:114:GLU:HG3	2.13	0.48
30:C:155:ASP:HA	30:C:158:ILE:HG12	1.95	0.48
30:C:218:GLU:HA	31:D:274:ARG:HE	1.77	0.48
32:E:200:SER:OG	32:E:232:MET:SD	2.71	0.48
32:E:215:ILE:CD1	32:E:259:GLU:HB3	2.43	0.48
32:E:228:CYS:C	32:E:229:ILE:HD13	2.38	0.48
2:H:42:ASN:HB2	2:H:185:GLU:HB2	1.94	0.48
2:H:101:TYR:HE1	10:P:90:MET:HE2	1.78	0.48
2:h:71:HIS:NE2	2:h:105:ILE:O	2.36	0.48
2:h:88:HIS:CD2	2:h:92:LYS:HE2	2.49	0.48
6:m:37:ILE:HD11	6:m:193:VAL:HG13	1.95	0.48
6:m:71:ARG:HH11	6:m:105:ASN:HB3	1.78	0.48
11:q:19:ARG:O	11:q:32:HIS:N	2.44	0.48
9:O:147:GLU:OE1	9:O:149:GLU:N	2.45	0.48
15:f:292:LYS:HE3	15:f:899:ILE:HD13	1.94	0.48
17:a:77:VAL:HG21	17:a:110:ALA:HB1	1.94	0.48
22:U:700:GLU:HA	22:U:706:VAL:HB	1.95	0.48
25:Y:348:ASP:O	25:Y:352:GLU:N	2.45	0.48
27:W:220:GLU:HG2	27:W:221:LYS:H	1.78	0.48
29:B:223:ILE:HA	29:B:329:MET:O	2.13	0.48
29:B:241:ASN:ND2	29:B:281:ILE:HG21	2.28	0.48
1:G:37:LEU:HD11	1:G:81:THR:HA	1.95	0.48
2:H:102:GLN:H	10:P:89:SER:HG	1.56	0.48
4:J:7:ILE:HG22	4:J:8:THR:H	1.79	0.48
11:q:37:LYS:HD3	11:q:188:ILE:HD12	1.96	0.48
9:O:159:ILE:HG21	9:O:173:ILE:HG23	1.95	0.48
15:f:162:LEU:HD21	15:f:187:LEU:HD21	1.94	0.48
15:f:551:LYS:HD2	15:f:586:PRO:HB2	1.95	0.48
19:c:211:GLU:C	19:c:213:GLU:H	2.21	0.48
20:d:147:SER:HB3	20:d:150:LYS:HB2	1.95	0.48
24:X:248:ILE:HD13	24:X:251:LEU:HD21	1.94	0.48
25:Y:177:ARG:HA	25:Y:180:LEU:HD22	1.95	0.48
25:Y:310:SER:H	25:Y:358:ARG:NH1	2.11	0.48
27:W:35:ALA:HB3	27:W:73:MET:HE1	1.95	0.48
27:W:236:HIS:HD1	27:W:237:GLU:CD	2.20	0.48
28:A:182:GLU:O	28:A:186:LYS:HG2	2.14	0.48
29:B:221:GLY:H	29:B:326:LYS:HE2	1.76	0.48
29:B:357:ASP:OD1	29:B:359:LYS:N	2.44	0.48
1:G:101:TRP:CG	1:G:109:ILE:HB	2.49	0.48
12:r:182:ASP:OD1	12:r:183:GLY:N	2.45	0.48
13:s:99:ARG:HG3	13:s:104:TYR:CZ	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:R:8:PHE:HE1	12:R:13:ILE:HG12	1.79	0.48
15:f:446:LEU:HD13	15:f:483:PHE:HB3	1.96	0.48
20:d:105:PHE:O	20:d:108:SER:OG	2.21	0.48
23:V:314:ARG:HH12	25:Y:381:GLN:HB2	1.78	0.48
26:Z:94:TRP:HE1	26:Z:109:ASN:CG	2.20	0.48
29:B:174:MET:HA	30:C:271:ARG:HH22	1.78	0.48
29:B:199:GLU:O	29:B:203:LEU:HG	2.13	0.48
29:B:232:LYS:O	29:B:235:LEU:HB3	2.14	0.48
32:E:153:LEU:CD2	32:E:229:ILE:HD11	2.43	0.48
5:L:99:PHE:HB2	14:T:87:ALA:HB1	1.95	0.48
7:K:199:LEU:HD12	7:K:210:LEU:HD22	1.96	0.48
2:h:21:GLN:HG2	2:h:22:ILE:N	2.28	0.48
4:j:65:LEU:HD13	4:j:88:ARG:HG3	1.95	0.48
7:k:206:MET:HG3	7:k:210:LEU:HB3	1.96	0.48
14:t:79:ASP:OD2	14:t:81:HIS:ND1	2.46	0.48
10:P:73:LEU:O	10:P:77:LYS:HG2	2.13	0.48
15:f:140:LEU:HD22	15:f:169:GLU:HG3	1.95	0.48
15:f:827:PRO:HB2	15:f:829:MET:SD	2.54	0.48
19:c:225:TRP:HA	26:Z:196:HIS:HD2	1.77	0.48
22:U:217:CYS:SG	22:U:248:ILE:HG23	2.54	0.48
22:U:693:LEU:HD12	22:U:696:ILE:HD13	1.95	0.48
24:X:330:LEU:O	24:X:334:ASN:ND2	2.25	0.48
24:X:369:ILE:HD12	24:X:374:PHE:HD2	1.78	0.48
24:X:378:LEU:HD23	25:Y:311:TYR:CE2	2.48	0.48
29:B:140:ASP:OD1	29:B:140:ASP:N	2.46	0.48
30:C:85:VAL:HG11	30:C:123:LEU:HD21	1.94	0.48
30:C:189:TYR:CG	30:C:300:ILE:HD11	2.48	0.48
31:D:133:HIS:CE1	31:D:135:HIS:H	2.31	0.48
32:E:41:GLU:OE1	33:F:69:MET:HB3	2.13	0.48
33:F:339:ASP:OD1	33:F:339:ASP:N	2.46	0.48
1:G:40:VAL:HG13	1:G:179:LEU:HD11	1.96	0.48
1:G:119:ALA:HB2	1:G:160:TYR:HB3	1.96	0.48
4:J:20:GLU:O	4:J:24:GLU:HG2	2.14	0.48
5:L:4:ASN:O	5:L:6:TYR:N	2.44	0.48
2:h:119:GLN:HB2	3:i:81:SER:OG	2.14	0.48
2:h:221:LEU:HD22	2:h:225:GLU:HG3	1.95	0.48
6:m:180:GLN:O	6:m:184:MET:HG2	2.14	0.48
6:m:195:LYS:O	6:m:199:ILE:HD12	2.13	0.48
8:n:26:ILE:O	14:T:179:ARG:NH1	2.44	0.48
14:t:38:ASN:ND2	8:N:201:THR:OG1	2.45	0.48
15:f:99:LEU:HD22	15:f:129:LEU:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:a:136:GLU:O	17:a:140:GLU:HG3	2.14	0.48
19:c:52:GLU:HG2	19:c:116:PRO:HD2	1.94	0.48
19:c:152:LYS:HG3	31:D:83:GLN:CG	2.42	0.48
20:d:101:LEU:HD23	20:d:166:PHE:CE1	2.48	0.48
21:e:59:GLU:HA	21:e:62:LYS:NZ	2.28	0.48
22:U:92:ASP:OD2	22:U:140:ARG:NH2	2.46	0.48
25:Y:127:THR:HG23	25:Y:140:ILE:HD12	1.96	0.48
25:Y:312:ARG:HA	25:Y:356:THR:HG22	1.96	0.48
26:Z:58:PHE:CE1	26:Z:68:TRP:HB2	2.49	0.48
30:C:73:VAL:HG21	31:D:102:ILE:HG13	1.94	0.48
30:C:183:PRO:O	30:C:290:LYS:HD2	2.13	0.48
32:E:57:VAL:HB	33:F:131:THR:OG1	2.14	0.48
3:I:43:VAL:CG1	3:I:137:ILE:HB	2.44	0.48
6:M:190:VAL:HG13	6:M:213:LEU:HD23	1.94	0.48
7:K:23:GLN:HA	7:K:26:TYR:CD2	2.49	0.48
7:K:51:GLU:OE1	7:K:53:ARG:HB2	2.13	0.48
8:n:30:VAL:HG22	8:n:175:ARG:NH2	2.29	0.48
11:q:102:LEU:HB2	11:q:118:MET:HB3	1.96	0.48
17:a:90:PRO:HA	17:a:93:ALA:HB3	1.95	0.48
18:b:51:LEU:HD11	18:b:71:ILE:HG23	1.96	0.48
23:V:407:VAL:HG22	23:V:422:ILE:HD11	1.94	0.48
25:Y:157:ILE:HA	25:Y:160:ASN:HD21	1.77	0.48
26:Z:189:GLN:HE22	26:Z:193:ASN:HD21	1.61	0.48
27:W:387:ASP:O	27:W:390:GLU:HG2	2.13	0.48
29:B:232:LYS:N	35:B:501:ADP:O2B	2.47	0.48
31:D:120:ASP:N	31:D:122:GLU:OE2	2.43	0.48
32:E:212:ALA:HB2	32:E:259:GLU:HG2	1.95	0.48
33:F:187:ASP:HA	33:F:368:ILE:HG21	1.96	0.48
2:H:65:VAL:N	2:H:209:GLU:OE2	2.34	0.48
7:K:46:VAL:HB	7:K:220:VAL:HB	1.96	0.48
3:i:196:VAL:O	3:i:200:THR:HG22	2.14	0.48
6:m:158:TYR:HB2	6:m:160:TYR:HE1	1.79	0.48
11:q:77:PRO:HB3	11:q:106:GLY:HA3	1.95	0.48
11:q:106:GLY:O	11:q:114:ALA:N	2.39	0.48
11:Q:51:GLY:HA3	12:R:118:GLY:HA3	1.96	0.48
10:P:62:THR:HG23	10:P:63:VAL:N	2.29	0.48
15:f:459:CYS:O	16:x:79:GLY:N	2.47	0.48
22:U:633:CYS:CB	22:U:659:CYS:SG	3.02	0.48
23:V:211:TYR:OH	23:V:234:ARG:NH2	2.45	0.48
23:V:442:ILE:HD12	23:V:450:SER:HA	1.96	0.48
24:X:342:PHE:HB3	24:X:345:VAL:HB	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:387:ILE:HD11	26:Z:279:LYS:HG3	1.96	0.48
29:B:184:TYR:CE2	29:B:240:ALA:HB1	2.48	0.48
30:C:287:LYS:C	30:C:289:ILE:H	2.22	0.48
1:G:95:ARG:NH2	8:N:68:ILE:O	2.32	0.48
3:I:179:TYR:CE2	3:I:184:MET:HE1	2.49	0.48
5:L:238:GLU:HG2	5:L:240:PRO:HD3	1.96	0.48
6:m:175:GLU:OE1	6:m:196:ILE:HD13	2.14	0.48
13:s:138:GLY:HA2	13:s:142:SER:HB3	1.96	0.48
8:N:39:ASP:OD1	8:N:39:ASP:N	2.45	0.48
8:N:91:ARG:NH2	14:T:56:ASP:OD2	2.36	0.48
14:T:207:THR:OG1	14:T:209:TRP:NE1	2.46	0.48
15:f:776:LEU:HA	15:f:827:PRO:HA	1.95	0.48
22:U:206:MET:SD	22:U:220:LEU:HD21	2.54	0.48
25:Y:288:PHE:HB2	25:Y:295:TYR:OH	2.14	0.48
28:A:179:GLY:H	28:A:353:HIS:CE1	2.31	0.48
28:A:232:ARG:HH21	28:A:236:CYS:HA	1.79	0.48
29:B:53:THR:OG1	29:B:54:PRO:HD3	2.14	0.48
30:C:78:ARG:HB3	30:C:86:LEU:HD22	1.96	0.48
31:D:204:MET:HB2	31:D:212:LYS:HE3	1.95	0.48
33:F:272:PHE:HE2	33:F:320:PHE:HE2	1.62	0.48
5:L:172:LEU:O	5:L:176:MET:HB3	2.14	0.47
1:g:122:SER:O	1:g:126:THR:HG23	2.14	0.47
8:n:199:VAL:HG11	14:T:186:ARG:HH22	1.79	0.47
9:o:50:ALA:HB2	10:p:129:CYS:HB2	1.96	0.47
15:f:242:GLU:OE1	15:f:242:GLU:N	2.42	0.47
15:f:678:LEU:HD13	15:f:686:LEU:HD11	1.95	0.47
20:d:105:PHE:HB2	20:d:166:PHE:CD2	2.49	0.47
22:U:436:ALA:HB1	22:U:472:ILE:HD13	1.95	0.47
22:U:607:VAL:O	22:U:615:ARG:NH2	2.47	0.47
24:X:346:GLN:HA	24:X:384:VAL:HA	1.96	0.47
28:A:355:PHE:HZ	28:A:373:LEU:HD12	1.79	0.47
30:C:236:VAL:HA	30:C:239:ARG:NE	2.29	0.47
30:C:297:ARG:O	30:C:299:ASP:N	2.45	0.47
33:F:203:VAL:HG12	33:F:207:ASN:ND2	2.29	0.47
4:J:157:LYS:HB3	4:J:176:TYR:CZ	2.49	0.47
5:L:66:VAL:O	13:S:77:HIS:NE2	2.47	0.47
7:K:15:PHE:CD1	7:K:21:LEU:HB3	2.49	0.47
8:n:133:SER:HA	8:n:136:TYR:CE2	2.49	0.47
8:n:135:ILE:HD13	8:n:163:ALA:HB2	1.96	0.47
9:o:8:TYR:CE2	9:o:10:ASP:HB2	2.49	0.47
13:s:1:ARG:NH1	13:s:2:PHE:H	2.11	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:s:11:THR:HG22	13:s:141:ALA:H	1.79	0.47
8:N:19:ARG:HB2	8:N:171:GLY:O	2.13	0.47
14:T:92:LEU:O	14:T:96:MET:HG2	2.14	0.47
17:a:138:VAL:HG11	17:a:155:PHE:HB2	1.96	0.47
17:a:164:GLN:OE1	17:a:164:GLN:N	2.43	0.47
18:b:18:ASN:ND2	18:b:25:ARG:HH12	2.10	0.47
18:b:148:VAL:HG23	18:b:172:THR:HG23	1.96	0.47
19:c:251:LEU:HD21	19:c:283:HIS:CG	2.49	0.47
20:d:62:SER:HB3	20:d:71:PHE:HB2	1.95	0.47
22:U:649:ARG:HB2	22:U:683:VAL:HG21	1.95	0.47
24:X:240:ASP:OD1	24:X:240:ASP:N	2.47	0.47
29:B:423:LYS:O	29:B:426:VAL:HG12	2.13	0.47
30:C:117:ARG:HG2	30:C:118:ASN:H	1.77	0.47
30:C:343:ASN:O	30:C:347:ILE:HG12	2.14	0.47
31:D:88:VAL:O	31:D:132:LEU:N	2.27	0.47
31:D:293:LEU:HA	31:D:296:MET:HG2	1.97	0.47
32:E:99:ALA:N	32:E:109:ARG:O	2.45	0.47
2:H:77:SER:OG	2:H:78:GLY:N	2.47	0.47
2:H:114:VAL:O	2:H:118:MET:HG2	2.14	0.47
2:H:152:SER:O	3:I:81:SER:OG	2.30	0.47
4:J:99:GLU:HG3	12:R:81:LYS:HG2	1.96	0.47
5:L:115:LYS:HE3	5:L:128:TYR:HE2	1.78	0.47
5:l:89:ARG:NH1	13:s:77:HIS:HB3	2.30	0.47
8:n:32:ASP:O	8:n:45:ARG:NH2	2.43	0.47
13:s:71:ARG:HD2	13:s:95:ILE:HD11	1.95	0.47
14:T:93:THR:HA	14:T:125:VAL:HG21	1.96	0.47
15:f:117:GLU:OE1	15:f:120:ARG:NH2	2.46	0.47
15:f:128:VAL:HG11	15:f:154:TRP:CD1	2.49	0.47
15:f:515:ALA:O	15:f:518:THR:OG1	2.32	0.47
19:c:255:TYR:CD1	19:c:280:PRO:HG3	2.45	0.47
22:U:507:VAL:HA	22:U:543:LYS:HD2	1.95	0.47
22:U:639:LEU:O	22:U:643:SER:OG	2.27	0.47
22:U:722:ASP:OD1	22:U:723:ASP:N	2.44	0.47
27:W:98:LYS:HB3	27:W:139:GLU:HG3	1.96	0.47
29:B:239:VAL:HA	29:B:242:GLN:HB2	1.96	0.47
32:E:331:ILE:O	32:E:335:SER:OG	2.30	0.47
7:K:210:LEU:HD21	7:K:241:ILE:HG21	1.95	0.47
1:g:18:PRO:HA	2:h:24:TYR:CE1	2.50	0.47
2:h:205:GLU:HB3	2:h:227:LYS:HB3	1.97	0.47
4:j:87:ALA:O	4:j:90:GLU:HG2	2.13	0.47
13:S:7:PHE:HZ	13:S:140:SER:HB2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:28:ARG:NH2	13:S:213:ASP:O	2.47	0.47
13:S:38:ARG:HH12	13:S:212:LYS:HG3	1.80	0.47
15:f:105:LYS:HZ3	15:f:109:ILE:HD11	1.79	0.47
22:U:486:MET:HE1	22:U:758:PRO:HG3	1.96	0.47
23:V:350:GLN:HG2	23:V:353:LEU:HD23	1.97	0.47
28:A:96:ALA:HB1	29:B:132:TYR:H	1.79	0.47
28:A:362:MET:HE3	28:A:364:VAL:HG21	1.96	0.47
29:B:265:LYS:HB3	29:B:268:ARG:NH2	2.29	0.47
33:F:151:VAL:HG13	33:F:163:THR:HA	1.97	0.47
1:G:165:ALA:HB1	1:G:179:LEU:HB3	1.94	0.47
4:J:23:GLN:O	4:J:26:VAL:HG12	2.14	0.47
5:L:49:LEU:HD21	5:L:199:LEU:HD21	1.97	0.47
3:i:91:ARG:HD3	10:p:76:LEU:HB3	1.96	0.47
11:q:21:ALA:O	11:q:28:MET:N	2.47	0.47
8:N:162:LEU:HD11	8:N:197:PHE:CD1	2.49	0.47
15:f:551:LYS:HG2	15:f:587:PHE:HB2	1.95	0.47
20:d:205:LYS:HZ1	20:d:209:TYR:HB2	1.79	0.47
22:U:552:ILE:HB	22:U:581:SER:OG	2.14	0.47
25:Y:19:ILE:O	25:Y:23:ARG:HG3	2.15	0.47
26:Z:48:LEU:HD11	26:Z:92:VAL:HB	1.95	0.47
27:W:48:LEU:CD2	27:W:51:GLU:OE2	2.58	0.47
31:D:278:GLN:H	31:D:278:GLN:CD	2.22	0.47
32:E:302:ASP:N	32:E:302:ASP:OD1	2.47	0.47
2:H:108:ALA:O	2:H:111:VAL:HG12	2.15	0.47
2:H:147:PHE:HD2	2:H:155:TYR:HB2	1.79	0.47
2:H:150:ASP:CG	2:H:153:GLY:H	2.19	0.47
3:I:44:LEU:HB2	3:I:215:THR:HG22	1.95	0.47
5:L:105:VAL:HG21	5:L:136:GLY:HA3	1.96	0.47
5:l:56:LEU:HD11	7:k:182:GLN:HB2	1.95	0.47
8:n:187:GLN:OE1	8:n:187:GLN:N	2.48	0.47
9:o:34:ILE:HG22	9:o:42:TYR:HD2	1.78	0.47
13:s:125:ASP:OD1	13:s:128:GLY:N	2.32	0.47
12:R:180:ARG:HH11	12:R:185:ILE:HG21	1.80	0.47
17:a:159:SER:OG	17:a:175:ASP:OD2	2.28	0.47
17:a:279:GLU:HA	17:a:282:PHE:CE2	2.48	0.47
19:c:225:TRP:CZ3	19:c:226:MET:HE3	2.49	0.47
19:c:255:TYR:CD2	24:X:411:VAL:HG11	2.49	0.47
20:d:146:GLY:N	23:V:440:LYS:HZ3	2.12	0.47
21:e:27:TRP:HA	23:V:355:ARG:NE	2.24	0.47
22:U:30:VAL:HG12	22:U:34:PHE:HB2	1.96	0.47
22:U:243:LEU:HD21	22:U:915:LYS:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:49:ASN:HA	25:Y:52:PRO:HG2	1.96	0.47
27:W:231:ILE:O	27:W:235:GLN:HG2	2.14	0.47
27:W:259:GLU:OE2	27:W:262:LYS:HD3	2.13	0.47
29:B:53:THR:HG23	29:B:64:LYS:NZ	2.29	0.47
30:C:147:THR:HA	30:C:205:HIS:CE1	2.50	0.47
31:D:352:MET:O	31:D:355:SER:N	2.48	0.47
33:F:221:LYS:HG3	33:F:320:PHE:HE1	1.79	0.47
33:F:286:ASP:OD1	33:F:287:GLU:N	2.47	0.47
33:F:403:ALA:HA	33:F:406:ILE:HG22	1.94	0.47
3:I:218:ARG:NH1	3:I:223:THR:OG1	2.47	0.47
3:I:220:ASN:N	3:I:220:ASN:OD1	2.48	0.47
4:J:69:VAL:HG22	4:J:104:VAL:HG12	1.95	0.47
4:J:139:ASP:OD1	12:R:106:LYS:HD3	2.14	0.47
5:L:26:MET:O	5:L:30:LYS:HG2	2.15	0.47
5:l:67:ASP:OD1	5:l:68:ASN:N	2.48	0.47
5:l:130:VAL:C	5:l:149:PRO:HG3	2.40	0.47
1:g:155:ASP:OD2	1:g:158:GLY:N	2.46	0.47
2:h:203:MET:HB2	2:h:208:ILE:HD11	1.96	0.47
7:k:42:THR:HG21	7:k:194:ALA:HB2	1.96	0.47
7:k:202:LEU:O	7:k:206:MET:HG2	2.15	0.47
10:p:50:TYR:HD2	10:p:190:ILE:HD11	1.80	0.47
10:p:72:ASN:HA	10:p:75:GLU:HG2	1.96	0.47
10:p:149:MET:HE2	13:S:148:LEU:HD12	1.96	0.47
11:q:174:ASN:N	11:Q:172:ILE:O	2.37	0.47
11:Q:116:TYR:HB3	11:Q:124:LEU:HD11	1.96	0.47
15:f:287:ASP:O	15:f:291:GLN:HG2	2.14	0.47
15:f:698:SER:OG	15:f:701:ASN:HB3	2.15	0.47
16:x:77:PHE:HE1	16:x:98:CYS:HB3	1.79	0.47
17:a:34:TRP:CZ3	17:a:68:GLU:HB2	2.50	0.47
19:c:268:GLU:O	19:c:272:ILE:HG12	2.14	0.47
22:U:378:CYS:SG	22:U:783:TYR:OH	2.62	0.47
22:U:593:SER:OG	22:U:595:ASN:OD1	2.32	0.47
22:U:843:GLU:HA	22:U:846:LYS:HG2	1.95	0.47
24:X:365:LEU:HD21	24:X:385:LEU:HD13	1.97	0.47
25:Y:379:ARG:O	25:Y:383:LEU:HG	2.15	0.47
26:Z:44:GLN:HG2	26:Z:45:LYS:N	2.29	0.47
26:Z:182:THR:HG22	26:Z:183:THR:H	1.78	0.47
27:W:136:ILE:O	27:W:141:GLU:HB3	2.15	0.47
27:W:141:GLU:OE1	27:W:141:GLU:N	2.48	0.47
27:W:375:MET:HG3	27:W:386:VAL:HG22	1.97	0.47
28:A:300:LEU:HD21	33:F:255:GLN:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:C:25:LEU:HD11	31:D:47:LEU:HB3	1.96	0.47
30:C:174:LEU:HD12	30:C:175:PHE:N	2.29	0.47
31:D:245:ARG:HA	31:D:248:ARG:HD2	1.96	0.47
32:E:122:MET:HE3	32:E:196:LEU:HB2	1.97	0.47
32:E:288:ALA:HA	32:E:291:ARG:HE	1.79	0.47
33:F:123:VAL:HG22	33:F:133:PHE:CD2	2.50	0.47
33:F:132:TYR:CD2	33:F:158:TYR:HB3	2.50	0.47
33:F:171:ARG:HH11	33:F:267:LEU:HD11	1.79	0.47
2:H:72:ILE:CG1	2:H:107:THR:HG23	2.45	0.47
2:H:100:VAL:HG13	10:P:93:ASN:ND2	2.30	0.47
5:l:144:ILE:HB	5:l:156:CYS:O	2.15	0.47
3:i:179:TYR:CD2	4:j:53:LEU:HD22	2.50	0.47
4:j:79:ASP:HA	4:j:82:ILE:HG12	1.97	0.47
12:r:8:PHE:HE2	12:r:10:HIS:HB2	1.78	0.47
10:P:30:ILE:CG1	10:P:33:GLN:HG2	2.44	0.47
12:R:179:VAL:HA	12:R:184:TRP:HA	1.97	0.47
13:S:113:LEU:HD23	13:S:198:VAL:HG12	1.97	0.47
15:f:75:LEU:HD21	15:f:121:PHE:HB3	1.96	0.47
15:f:617:SER:HA	29:B:82:GLN:HG2	1.97	0.47
19:c:59:GLY:HA3	19:c:69:VAL:HG22	1.96	0.47
22:U:696:ILE:HG22	22:U:737:LEU:HA	1.97	0.47
26:Z:193:ASN:HA	26:Z:196:HIS:HE1	1.79	0.47
28:A:120:LYS:HB2	33:F:90:VAL:HG12	1.97	0.47
29:B:233:THR:O	29:B:234:LEU:C	2.57	0.47
30:C:260:GLU:HG2	30:C:262:GLY:N	2.30	0.47
7:K:93:ARG:HD3	12:R:68:LEU:HB3	1.97	0.47
12:r:113:TYR:O	12:r:120:ARG:HA	2.15	0.47
8:N:14:LEU:HD21	8:N:101:ALA:HB3	1.97	0.47
11:Q:29:LYS:HE3	11:Q:32:HIS:HA	1.95	0.47
10:P:53:LEU:HB2	10:P:60:VAL:HG13	1.95	0.47
17:a:81:LEU:O	17:a:85:ARG:HG2	2.15	0.47
17:a:188:LEU:HD11	17:a:193:GLN:HG3	1.96	0.47
23:V:344:ASP:HB3	23:V:346:LEU:HD23	1.96	0.47
27:W:356:ASN:O	27:W:359:VAL:N	2.48	0.47
29:B:373:THR:O	29:B:414:VAL:HG12	2.15	0.47
29:B:398:ILE:HD12	29:B:426:VAL:HG23	1.97	0.47
30:C:388:ALA:O	30:C:392:GLN:NE2	2.45	0.47
32:E:129:ASN:ND2	32:E:130:VAL:H	2.13	0.47
33:F:356:MET:N	33:F:356:MET:SD	2.86	0.47
3:i:119:GLN:NE2	4:j:79:ASP:OD1	2.46	0.47
7:k:29:GLU:O	7:k:33:LEU:HG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:k:73:HIS:CD2	7:k:74:ILE:HG13	2.50	0.47
7:k:121:LEU:HD12	7:k:123:PHE:CE1	2.50	0.47
6:m:120:HIS:NE2	6:m:124:LEU:HD21	2.30	0.47
8:n:14:LEU:HD23	8:n:44:CYS:SG	2.55	0.47
14:t:167:ASP:O	14:t:171:ARG:HG3	2.15	0.47
15:f:430:ASP:OD1	16:x:74:LYS:NZ	2.41	0.47
15:f:661:ALA:HB3	29:B:71:TYR:OH	2.15	0.47
15:f:679:LEU:HD13	15:f:713:PHE:CD2	2.50	0.47
15:f:783:SER:HB2	15:f:787:LEU:HD13	1.95	0.47
15:f:849:ALA:HA	15:f:862:ILE:HA	1.96	0.47
18:b:94:HIS:CE1	18:b:136:VAL:HG22	2.50	0.47
20:d:149:ASN:HA	20:d:152:PHE:CD2	2.49	0.47
22:U:54:PHE:CE2	22:U:56:SER:HB3	2.50	0.47
23:V:348:PHE:HE1	23:V:357:LEU:HD12	1.80	0.47
24:X:341:PRO:HB3	27:W:397:VAL:HG21	1.97	0.47
24:X:347:ILE:HG13	24:X:358:LYS:NZ	2.30	0.47
25:Y:220:VAL:HG11	25:Y:249:VAL:HG21	1.96	0.47
26:Z:17:LEU:HD23	26:Z:17:LEU:H	1.78	0.47
27:W:19:ASP:OD1	27:W:20:TYR:N	2.48	0.47
27:W:294:LYS:HD3	27:W:294:LYS:N	2.29	0.47
27:W:372:ARG:NH1	27:W:414:ASN:HB3	2.30	0.47
28:A:302:LEU:O	28:A:306:LEU:HG	2.14	0.47
28:A:368:ILE:HG23	28:A:370:PHE:HD2	1.80	0.47
30:C:297:ARG:O	30:C:297:ARG:HG3	2.15	0.47
33:F:317:LEU:HB2	33:F:347:ARG:HH11	1.80	0.47
3:i:3:ARG:HA	4:j:5:ARG:HH22	1.80	0.46
7:k:97:GLN:HB3	12:r:61:ARG:HG2	1.97	0.46
13:s:141:ALA:O	13:s:145:LEU:HD23	2.15	0.46
14:t:99:ARG:HG3	14:t:104:ASN:O	2.14	0.46
14:T:107:TRP:O	14:T:108:ASN:ND2	2.48	0.46
15:f:63:LEU:HG	15:f:109:ILE:HD13	1.96	0.46
22:U:422:LEU:O	22:U:425:THR:OG1	2.34	0.46
23:V:166:TYR:HE1	23:V:206:VAL:HG13	1.80	0.46
28:A:194:PRO:HB3	28:A:208:PRO:HG3	1.97	0.46
28:A:331:LEU:C	28:A:334:PRO:HD2	2.40	0.46
31:D:317:LEU:HB3	31:D:321:LEU:HD11	1.97	0.46
1:G:69:LEU:HD21	1:G:216:GLU:HB3	1.98	0.46
2:H:200:GLU:HB3	31:D:339:ARG:HD3	1.96	0.46
3:I:207:SER:O	3:I:210:LYS:HG2	2.15	0.46
6:M:102:PHE:HB3	8:N:78:THR:HG23	1.96	0.46
3:i:111:VAL:HG22	3:i:136:TYR:CD2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:i:119:GLN:HB2	4:j:78:ALA:HB1	1.97	0.46
7:k:212:ALA:HB1	7:k:231:LYS:HD2	1.97	0.46
10:p:107:PRO:HD2	10:p:124:LEU:HB2	1.97	0.46
13:s:185:ARG:HA	9:O:26:VAL:HB	1.98	0.46
12:R:122:SER:OG	12:R:123:GLY:N	2.48	0.46
15:f:656:GLY:O	15:f:660:ILE:HG12	2.15	0.46
29:B:109:VAL:HG22	29:B:151:LEU:HD23	1.96	0.46
29:B:265:LYS:O	29:B:269:GLU:HG3	2.16	0.46
32:E:112:PRO:HD2	33:F:96:LEU:HD21	1.96	0.46
32:E:130:VAL:HG12	32:E:132:TYR:OH	2.15	0.46
33:F:414:GLU:O	33:F:416:THR:N	2.47	0.46
5:L:52:ALA:HA	5:L:59:HIS:HA	1.97	0.46
5:l:103:LEU:HD22	5:l:108:LEU:HB2	1.97	0.46
5:l:158:ALA:HB1	5:l:172:LEU:HD22	1.98	0.46
2:h:160:ALA:HB1	2:h:174:LEU:HD13	1.98	0.46
3:i:134:LEU:HD12	3:i:136:TYR:HE1	1.80	0.46
4:j:40:ILE:HG22	4:j:212:ARG:HG3	1.98	0.46
8:n:16:ALA:HB1	8:n:33:LYS:HB2	1.97	0.46
9:o:54:MET:HG2	10:p:96:TYR:CE1	2.50	0.46
14:t:30:TYR:N	14:t:33:LEU:O	2.45	0.46
11:Q:193:ASN:OD1	11:Q:193:ASN:N	2.49	0.46
14:T:96:MET:HE3	14:T:127:MET:HA	1.98	0.46
15:f:143:ARG:O	15:f:148:GLN:NE2	2.46	0.46
15:f:560:LEU:HD11	15:f:797:LEU:HG	1.97	0.46
15:f:666:ILE:HD13	29:B:49:LEU:HG	1.96	0.46
19:c:190:GLN:HA	19:c:193:ILE:HG22	1.98	0.46
22:U:658:ILE:HG12	22:U:763:VAL:HG11	1.98	0.46
22:U:751:ARG:H	22:U:751:ARG:HD2	1.81	0.46
25:Y:377:LEU:HA	25:Y:380:VAL:HG22	1.97	0.46
29:B:154:HIS:CG	29:B:155:LYS:H	2.33	0.46
30:C:80:MET:HE2	30:C:80:MET:HA	1.97	0.46
30:C:185:GLY:HA2	30:C:291:VAL:O	2.15	0.46
32:E:131:SER:HB3	32:E:186:ALA:HB2	1.97	0.46
1:G:70:PHE:HZ	1:G:88:ARG:NH1	2.14	0.46
7:K:41:GLN:HB2	7:K:153:LEU:HB2	1.98	0.46
7:K:97:GLN:HG3	12:R:65:ILE:HG13	1.98	0.46
5:l:133:LEU:HD21	5:l:159:MET:HB3	1.98	0.46
11:q:103:LEU:HG	11:q:132:HIS:HD2	1.79	0.46
10:P:78:GLU:OE2	10:P:80:ARG:HB2	2.16	0.46
13:S:64:LEU:HD21	13:S:92:LEU:HD11	1.97	0.46
17:a:89:ASP:HB3	17:a:92:VAL:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:b:13:SER:O	18:b:16:MET:HG2	2.15	0.46
23:V:181:TYR:HB3	23:V:221:LEU:HD21	1.98	0.46
27:W:145:LEU:HD21	27:W:172:GLU:CD	2.40	0.46
27:W:227:TYR:HA	27:W:230:MET:HG3	1.97	0.46
28:A:80:LEU:HA	28:A:83:ASP:HB3	1.97	0.46
28:A:110:LYS:HE3	33:F:85:THR:HG22	1.96	0.46
30:C:198:LEU:HD13	35:C:501:ADP:C5'	2.46	0.46
31:D:273:LYS:HA	31:D:316:THR:HB	1.97	0.46
1:G:74:GLU:O	1:G:226:LYS:HA	2.14	0.46
5:L:225:ASP:O	5:L:229:VAL:N	2.44	0.46
6:M:69:VAL:HG11	6:M:75:MET:HE3	1.98	0.46
4:j:86:ARG:HG2	4:j:114:LEU:HD22	1.98	0.46
6:m:172:ALA:HB2	6:m:200:VAL:HG11	1.97	0.46
14:t:43:MET:HG3	14:t:64:LYS:HG3	1.97	0.46
14:t:91:TRP:CE3	14:t:92:LEU:HD22	2.46	0.46
8:N:4:MET:HB3	8:N:160:LEU:HD21	1.97	0.46
22:U:813:TYR:CE2	22:U:815:ALA:HB2	2.51	0.46
23:V:306:ARG:HA	23:V:309:MET:HG2	1.96	0.46
23:V:482:PHE:HA	23:V:485:ASP:OD2	2.15	0.46
25:Y:250:LEU:HD23	25:Y:257:ARG:HA	1.97	0.46
28:A:205:GLY:H	33:F:404:GLY:CA	2.28	0.46
28:A:229:VAL:HG21	28:A:237:PHE:HB3	1.98	0.46
30:C:164:VAL:HG21	30:C:313:ARG:HG3	1.98	0.46
31:D:173:GLN:C	31:D:175:GLN:H	2.23	0.46
31:D:240:LEU:HD22	31:D:284:GLU:HG3	1.98	0.46
32:E:215:ILE:HA	32:E:218:MET:HG2	1.97	0.46
33:F:154:ASN:OD1	33:F:159:LEU:HB3	2.16	0.46
33:F:422:GLU:O	33:F:426:GLU:HG3	2.15	0.46
3:I:174:MET:HE3	3:I:199:LYS:HG3	1.97	0.46
1:g:56:VAL:HG23	1:g:56:VAL:O	2.16	0.46
3:i:99:LEU:HD21	11:q:86:ARG:HE	1.81	0.46
4:j:90:GLU:OE2	4:j:107:ILE:HG23	2.16	0.46
6:m:193:VAL:HA	6:m:196:ILE:HG22	1.97	0.46
10:p:205:ASP:HB3	12:R:165:TYR:HA	1.98	0.46
12:r:149:VAL:HG12	12:r:178:HIS:HE1	1.79	0.46
22:U:881:PRO:HG2	22:U:927:PRO:HB2	1.98	0.46
22:U:889:LEU:HD23	22:U:892:LEU:HD13	1.96	0.46
24:X:198:ASN:HB3	31:D:170:MET:HE2	1.96	0.46
24:X:347:ILE:HG13	24:X:358:LYS:HZ3	1.79	0.46
28:A:142:VAL:HB	28:A:147:TYR:HA	1.98	0.46
31:D:183:LEU:HD11	31:D:198:PRO:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:83:MET:HE1	1:G:132:ARG:HH21	1.80	0.46
4:J:127:PHE:O	4:J:129:ILE:N	2.45	0.46
4:J:136:PHE:HA	4:J:142:PRO:HA	1.97	0.46
5:L:34:ALA:HA	5:L:162:GLY:HA3	1.97	0.46
2:h:17:GLY:HA3	3:i:27:ALA:HB2	1.97	0.46
2:h:29:VAL:HG13	2:h:77:SER:O	2.16	0.46
3:i:123:GLN:NE2	4:j:125:ARG:HG3	2.30	0.46
4:j:36:ARG:HB2	4:j:144:LEU:HB2	1.97	0.46
14:t:209:TRP:CZ3	8:N:29:ARG:HD2	2.50	0.46
8:N:59:VAL:HG11	8:N:83:PHE:CE2	2.51	0.46
15:f:266:LEU:HD22	15:f:294:MET:SD	2.56	0.46
15:f:344:VAL:O	15:f:348:ILE:HG12	2.16	0.46
17:a:150:SER:O	17:a:153:SER:OG	2.29	0.46
20:d:107:LEU:HD21	20:d:115:PHE:HB2	1.98	0.46
25:Y:268:TYR:OH	25:Y:303:ALA:O	2.33	0.46
26:Z:40:LEU:HG	26:Z:91:ILE:HG12	1.96	0.46
26:Z:182:THR:HG22	26:Z:183:THR:N	2.31	0.46
28:A:30:ILE:O	29:B:411:ARG:NH2	2.48	0.46
30:C:71:SER:HB2	30:C:115:ALA:HB1	1.97	0.46
30:C:89:VAL:N	30:C:93:GLY:O	2.46	0.46
31:D:323:ARG:HD3	31:D:326:ARG:HH21	1.81	0.46
32:E:160:GLN:HB2	32:E:269:THR:HG21	1.96	0.46
32:E:167:PRO:HB3	32:E:297:ARG:NH2	2.31	0.46
33:F:233:LYS:HE2	33:F:332:THR:O	2.16	0.46
1:G:212:PRO:HB3	1:G:239:LEU:HD12	1.98	0.46
2:H:173:PHE:CE1	2:H:177:ARG:HG3	2.51	0.46
5:L:71:GLY:HA3	5:L:221:PHE:CZ	2.50	0.46
12:r:127:SER:HB2	12:r:139:MET:HE1	1.98	0.46
11:Q:56:PHE:O	11:Q:60:ILE:HG12	2.16	0.46
10:P:53:LEU:CB	10:P:60:VAL:HG13	2.46	0.46
15:f:267:ARG:HG3	15:f:787:LEU:HD11	1.98	0.46
15:f:564:LEU:HD13	15:f:794:ALA:HB1	1.97	0.46
17:a:369:HIS:HA	17:a:372:HIS:CE1	2.51	0.46
19:c:65:TYR:OH	22:U:543:LYS:HD3	2.16	0.46
19:c:226:MET:HE2	26:Z:201:LEU:HA	1.97	0.46
20:d:158:ILE:HD12	20:d:164:THR:HA	1.98	0.46
20:d:182:ILE:HG22	20:d:186:TYR:HE2	1.81	0.46
20:d:237:ILE:CG2	20:d:238:PRO:HD3	2.46	0.46
22:U:236:LEU:HB3	22:U:245:ALA:HB2	1.97	0.46
22:U:260:PHE:O	22:U:264:VAL:HG23	2.15	0.46
28:A:232:ARG:NH2	28:A:271:LEU:HB3	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:C:46:GLN:HE22	31:D:69:LYS:N	2.13	0.46
32:E:353:PHE:HA	32:E:356:ARG:HG2	1.98	0.46
1:g:112:ASP:OD2	9:o:72:ARG:NH2	2.40	0.46
10:p:61:GLN:OE1	11:q:85:ARG:HD2	2.16	0.46
8:N:42:PHE:CE1	8:N:184:VAL:HG21	2.51	0.46
11:Q:56:PHE:CE2	11:Q:102:LEU:HD11	2.50	0.46
14:T:142:GLY:HA2	14:T:176:LEU:HD21	1.98	0.46
17:a:64:ILE:HG22	17:a:68:GLU:OE2	2.16	0.46
21:e:27:TRP:HB2	23:V:355:ARG:H	1.81	0.46
22:U:200:VAL:O	22:U:204:ILE:HG22	2.16	0.46
27:W:336:PRO:O	27:W:340:VAL:HG23	2.16	0.46
30:C:114:VAL:HG21	30:C:123:LEU:HD22	1.98	0.46
30:C:117:ARG:HG2	30:C:118:ASN:N	2.31	0.46
31:D:89:ILE:HD11	32:E:70:ILE:HD12	1.98	0.46
33:F:308:ARG:O	33:F:312:GLU:HG2	2.15	0.46
2:H:111:VAL:HA	2:H:114:VAL:HG12	1.98	0.46
6:M:150:MET:HG3	6:M:163:CYS:SG	2.56	0.46
5:l:36:VAL:HG13	5:l:172:LEU:HD11	1.98	0.46
1:g:132:ARG:HB2	6:m:12:SER:HA	1.97	0.46
2:h:88:HIS:NE2	2:h:92:LYS:HE2	2.31	0.46
7:k:29:GLU:O	7:k:32:LYS:HG2	2.16	0.46
11:q:160:LEU:HA	11:q:163:CYS:SG	2.56	0.46
12:R:12:VAL:HB	12:R:179:VAL:HB	1.97	0.46
22:U:243:LEU:HA	22:U:913:ILE:HG21	1.97	0.46
23:V:228:ARG:HD3	23:V:257:ASN:ND2	2.31	0.46
25:Y:228:MET:SD	25:Y:263:LEU:HD13	2.56	0.46
28:A:329:PRO:C	28:A:333:ARG:HE	2.24	0.46
7:K:220:VAL:HA	7:K:226:PHE:CD1	2.51	0.45
2:h:174:LEU:O	2:h:178:TYR:HB2	2.17	0.45
8:N:19:ARG:HD3	8:N:26:ILE:HD12	1.99	0.45
10:P:33:GLN:O	10:P:33:GLN:HG3	2.15	0.45
13:S:46:LEU:HD12	13:S:72:LEU:HD12	1.96	0.45
15:f:163:ALA:HB1	15:f:207:LEU:HD22	1.98	0.45
15:f:178:LYS:HA	15:f:181:ARG:HG3	1.98	0.45
15:f:650:GLN:O	15:f:654:VAL:HG23	2.16	0.45
15:f:776:LEU:HD22	15:f:825:MET:HG2	1.99	0.45
26:Z:23:PHE:HD2	26:Z:97:THR:HG21	1.80	0.45
28:A:176:ASP:H	28:A:227:ARG:HE	1.63	0.45
32:E:157:GLU:H	32:E:157:GLU:CD	2.25	0.45
33:F:225:MET:SD	33:F:233:LYS:HB3	2.56	0.45
5:L:166:GLN:H	5:L:166:GLN:CD	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:l:72:ILE:HD13	5:l:88:MET:HE1	1.97	0.45
1:g:51:VAL:HG23	1:g:217:VAL:HG22	1.97	0.45
4:j:148:ASP:OD2	4:j:152:THR:OG1	2.35	0.45
8:n:40:ARG:HG2	8:n:103:TRP:CE3	2.49	0.45
8:n:112:TYR:CE2	8:n:122:ARG:HB2	2.51	0.45
12:r:71:LYS:O	12:r:71:LYS:HG2	2.16	0.45
8:N:66:HIS:O	8:N:69:GLU:HG2	2.16	0.45
9:O:164:PHE:HZ	9:O:192:PRO:HB2	1.81	0.45
15:f:535:THR:HG21	15:f:566:HIS:CE1	2.49	0.45
17:a:11:SER:HB3	17:a:22:TRP:CZ2	2.51	0.45
23:V:285:TRP:CD1	23:V:315:LYS:HD2	2.51	0.45
23:V:285:TRP:HD1	23:V:315:LYS:HD2	1.81	0.45
25:Y:101:ARG:NH2	25:Y:136:HIS:HB3	2.32	0.45
26:Z:65:ASP:OD2	26:Z:102:HIS:HB2	2.15	0.45
27:W:268:LYS:HA	27:W:301:LYS:HG3	1.98	0.45
29:B:220:LYS:HZ1	29:B:345:GLY:C	2.18	0.45
30:C:265:GLY:O	30:C:268:GLU:HG3	2.16	0.45
33:F:76:ASN:O	33:F:80:ILE:HG12	2.16	0.45
33:F:123:VAL:HG22	33:F:133:PHE:HD2	1.81	0.45
33:F:134:LEU:C	33:F:134:LEU:HD12	2.41	0.45
33:F:191:LEU:O	33:F:195:ILE:HG23	2.15	0.45
33:F:202:ILE:C	33:F:205:PRO:HD2	2.41	0.45
33:F:203:VAL:O	33:F:207:ASN:ND2	2.50	0.45
3:I:28:ILE:HG13	3:I:152:PRO:HG2	1.97	0.45
3:I:233:VAL:O	3:I:237:ILE:HG13	2.16	0.45
4:J:131:ALA:HB3	4:J:147:THR:OG1	2.15	0.45
1:g:47:CYS:SG	1:g:221:THR:HG22	2.56	0.45
7:k:27:ALA:O	7:k:31:ILE:HG12	2.16	0.45
6:m:189:ILE:O	6:m:193:VAL:HG23	2.16	0.45
9:o:17:ASP:OD2	9:o:33:LYS:NZ	2.50	0.45
9:O:20:ALA:HB3	9:O:28:ASP:HB3	1.98	0.45
15:f:53:GLN:HB2	15:f:98:PHE:CE1	2.51	0.45
15:f:137:ARG:NE	15:f:169:GLU:OE2	2.37	0.45
17:a:318:GLY:HA2	17:a:321:LYS:HD3	1.97	0.45
20:d:76:ALA:HB3	22:U:10:SER:HB2	1.97	0.45
22:U:591:CYS:SG	22:U:755:THR:HG21	2.57	0.45
24:X:285:GLU:OE2	24:X:288:LYS:NZ	2.45	0.45
27:W:151:THR:O	27:W:155:GLN:HG3	2.16	0.45
28:A:211:GLY:HA3	28:A:337:LEU:HA	1.99	0.45
30:C:195:GLY:O	30:C:296:ASN:ND2	2.47	0.45
32:E:339:ASN:OD1	32:E:342:ASP:N	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:F:134:LEU:HD22	33:F:160:ILE:N	2.31	0.45
33:F:208:HIS:HB3	33:F:211:LYS:CG	2.46	0.45
1:G:191:PHE:CZ	1:G:219:VAL:HG11	2.52	0.45
3:I:197:LEU:HA	3:I:200:THR:HG22	1.97	0.45
4:J:36:ARG:NH2	7:K:60:GLU:OE2	2.49	0.45
4:J:189:LYS:HG3	4:J:232:ILE:HG12	1.98	0.45
5:l:124:GLY:O	7:k:13:ASN:ND2	2.45	0.45
5:l:168:ALA:HB2	5:l:198:THR:OG1	2.17	0.45
2:h:9:SER:HA	2:h:125:GLY:HA2	1.97	0.45
7:k:12:VAL:HG21	7:k:124:GLY:HA2	1.99	0.45
8:n:17:ASP:OD1	8:n:18:SER:N	2.49	0.45
9:o:67:SER:HB3	9:o:74:PRO:HG3	1.97	0.45
10:p:26:ARG:HH11	10:p:186:ILE:HB	1.81	0.45
15:f:180:GLN:C	15:f:183:PRO:HD2	2.41	0.45
15:f:343:LYS:HB3	15:f:381:VAL:HG11	1.97	0.45
15:f:547:GLU:HB3	15:f:551:LYS:HZ2	1.82	0.45
15:f:619:HIS:HB2	29:B:87:PRO:O	2.16	0.45
17:a:177:LEU:HD21	17:a:216:LEU:HB3	1.98	0.45
18:b:53:THR:OG1	18:b:59:GLU:N	2.48	0.45
22:U:347:ASN:ND2	22:U:813:TYR:HB2	2.32	0.45
22:U:415:HIS:NE2	22:U:418:GLU:HB2	2.31	0.45
28:A:229:VAL:O	28:A:232:ARG:HG2	2.16	0.45
29:B:71:TYR:O	29:B:74:MET:HG2	2.17	0.45
31:D:68:LEU:HD13	31:D:72:PHE:CE1	2.52	0.45
5:L:156:CYS:HA	6:M:58:TYR:HA	1.98	0.45
5:l:150:SER:O	5:l:152:ASN:ND2	2.49	0.45
6:m:36:ALA:HB2	6:m:49:VAL:HG23	1.97	0.45
8:n:36:PRO:HB3	8:n:42:PHE:CZ	2.51	0.45
8:n:45:ARG:HB2	8:n:52:THR:HB	1.99	0.45
11:q:116:TYR:HB3	11:q:124:LEU:HD11	1.98	0.45
12:r:39:PRO:HA	12:r:184:TRP:HE1	1.81	0.45
8:N:164:MET:HA	8:N:170:SER:HB2	1.98	0.45
15:f:149:GLU:OE1	15:f:150:GLU:N	2.50	0.45
15:f:296:PHE:HE2	15:f:899:ILE:HG13	1.80	0.45
15:f:560:LEU:O	15:f:564:LEU:HG	2.16	0.45
15:f:663:GLY:HA2	15:f:781:TYR:CZ	2.52	0.45
17:a:47:ASP:O	17:a:49:CYS:N	2.46	0.45
18:b:157:VAL:HG21	18:b:170:LEU:HB2	1.98	0.45
22:U:117:ASP:OD1	22:U:192:GLN:HG3	2.17	0.45
23:V:362:LEU:HD23	23:V:378:VAL:HG11	1.98	0.45
26:Z:7:GLN:HB3	26:Z:46:LYS:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A:41:TYR:HB2	28:A:44:GLN:HB3	1.98	0.45
29:B:193:GLN:O	29:B:197:ILE:HG22	2.17	0.45
29:B:338:ASP:O	29:B:342:ILE:N	2.48	0.45
33:F:79:LYS:O	33:F:83:ASN:ND2	2.50	0.45
1:G:103:TYR:HB2	8:N:61:TYR:CD1	2.51	0.45
4:J:146:GLN:HG3	4:J:161:ILE:HG13	1.97	0.45
1:g:112:ASP:OD1	1:g:113:MET:N	2.50	0.45
3:i:27:ALA:HA	3:i:30:HIS:ND1	2.31	0.45
4:j:35:VAL:HG12	4:j:42:VAL:HB	1.97	0.45
7:k:141:LEU:HD12	7:k:156:MET:HG2	1.98	0.45
9:o:216:ILE:HG22	9:o:218:PRO:HD3	1.98	0.45
11:q:86:ARG:NH1	11:q:90:ASP:HB3	2.31	0.45
8:N:46:SER:OG	8:N:97:GLY:O	2.33	0.45
10:P:138:VAL:HG22	10:P:147:TYR:CE1	2.52	0.45
15:f:173:LEU:O	15:f:181:ARG:NH2	2.50	0.45
15:f:698:SER:OG	15:f:701:ASN:O	2.34	0.45
15:f:806:VAL:HB	15:f:810:ILE:CG2	2.46	0.45
17:a:54:ASP:OD1	17:a:54:ASP:N	2.50	0.45
18:b:33:VAL:HG11	18:b:71:ILE:HG21	1.97	0.45
18:b:179:LEU:O	18:b:183:LEU:HG	2.16	0.45
22:U:465:LEU:HD11	22:U:477:GLY:HA3	1.98	0.45
23:V:134:PHE:HD2	23:V:187:ILE:HD11	1.81	0.45
23:V:391:THR:HA	23:V:394:LEU:HD13	1.98	0.45
29:B:400:THR:HA	30:C:180:ILE:HG13	1.98	0.45
30:C:187:LEU:HD22	30:C:189:TYR:CD1	2.49	0.45
32:E:232:MET:SD	32:E:234:GLU:N	2.90	0.45
4:J:45:VAL:HG11	4:J:61:LYS:CG	2.46	0.45
1:g:43:ARG:HG2	1:g:164:LYS:O	2.16	0.45
4:j:42:VAL:HG22	4:j:210:VAL:HG23	1.99	0.45
6:m:90:ILE:HG21	6:m:118:TYR:CE2	2.52	0.45
6:m:150:MET:HG3	6:m:163:CYS:SG	2.56	0.45
6:m:169:ARG:HB2	6:m:173:LYS:NZ	2.32	0.45
10:p:56:LEU:O	10:p:60:VAL:HG23	2.16	0.45
12:r:184:TRP:HZ3	12:r:186:ARG:HG3	1.81	0.45
12:r:188:SER:OG	12:r:190:ASP:OD1	2.32	0.45
11:Q:38:MET:HE1	11:Q:60:ILE:HG22	1.99	0.45
12:R:45:MET:HE2	12:R:53:SER:HB2	1.98	0.45
13:S:91:MET:O	13:S:95:ILE:HG12	2.16	0.45
13:S:166:LEU:HG	13:S:170:ARG:HH11	1.81	0.45
15:f:72:ARG:HB3	15:f:73:PRO:HD3	1.98	0.45
15:f:239:TYR:HA	29:B:67:ARG:NH2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:f:316:ASP:O	15:f:320:ILE:HG12	2.16	0.45
18:b:40:LYS:O	18:b:47:ASN:ND2	2.45	0.45
22:U:560:MET:HA	22:U:590:TYR:CE2	2.51	0.45
23:V:91:PRO:O	23:V:94:VAL:HB	2.16	0.45
25:Y:213:LEU:HD12	25:Y:219:PHE:HD1	1.82	0.45
25:Y:367:GLN:O	25:Y:371:LYS:HG2	2.16	0.45
27:W:127:THR:HG21	27:W:147:LYS:NZ	2.32	0.45
28:A:224:LEU:H	28:A:224:LEU:HD22	1.81	0.45
29:B:304:GLU:O	29:B:308:THR:N	2.50	0.45
30:C:306:LEU:O	30:C:310:ARG:NE	2.49	0.45
32:E:174:GLY:O	32:E:180:LYS:NZ	2.49	0.45
5:L:104:PRO:HG2	5:L:107:ARG:HD2	1.98	0.45
7:K:48:LEU:HB2	7:K:218:ALA:HB3	1.98	0.45
5:l:196:ARG:HG3	5:l:239:ARG:HE	1.82	0.45
3:i:12:PHE:CE2	4:j:125:ARG:HB2	2.51	0.45
3:i:87:THR:O	3:i:91:ARG:HG3	2.17	0.45
3:i:194:ILE:HG21	3:i:240:HIS:HB2	1.99	0.45
7:k:215:ILE:HD11	7:k:234:LEU:HD21	1.99	0.45
12:r:100:MET:HB2	12:r:111:LEU:HD11	1.99	0.45
10:P:29:GLY:HA2	10:P:35:VAL:HG23	1.99	0.45
15:f:257:ARG:HH21	15:f:281:ILE:HA	1.81	0.45
15:f:611:GLN:O	15:f:615:ILE:HG23	2.17	0.45
17:a:217:LEU:HB3	17:a:241:ASN:HB2	1.99	0.45
22:U:714:SER:O	22:U:718:ASN:ND2	2.50	0.45
24:X:343:SER:N	27:W:406:VAL:O	2.49	0.45
25:Y:291:HIS:HA	25:Y:295:TYR:CE2	2.51	0.45
30:C:189:TYR:CZ	30:C:316:GLU:HB3	2.51	0.45
31:D:204:MET:HA	31:D:331:ILE:O	2.17	0.45
32:E:219:PHE:O	32:E:223:ARG:HG3	2.16	0.45
1:G:49:VAL:CG2	1:G:194:THR:HG22	2.44	0.45
2:H:72:ILE:HA	2:H:137:CYS:O	2.17	0.45
6:M:160:TYR:CD1	6:M:163:CYS:HB2	2.52	0.45
7:K:217:LEU:HD23	7:K:229:PHE:CD2	2.52	0.45
1:g:27:TYR:CZ	6:m:16:PRO:HA	2.51	0.45
3:i:18:LEU:HD12	3:i:20:GLN:NE2	2.29	0.45
4:j:195:LEU:O	4:j:199:VAL:HG12	2.17	0.45
6:m:45:VAL:HG23	6:m:146:ALA:HB1	1.98	0.45
12:r:174:VAL:O	12:r:189:SER:HA	2.17	0.45
8:N:13:VAL:HG11	8:N:153:LEU:HA	1.99	0.45
8:N:38:HIS:CG	8:N:39:ASP:H	2.35	0.45
9:O:159:ILE:O	9:O:163:ILE:HG13	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:147:PRO:HA	13:S:150:ASP:OD1	2.16	0.45
15:f:182:GLU:HB2	15:f:183:PRO:HD3	1.99	0.45
15:f:233:LEU:O	15:f:237:VAL:HG23	2.16	0.45
19:c:119:GLY:HA3	19:c:190:GLN:NE2	2.30	0.45
22:U:378:CYS:HA	22:U:411:ILE:HA	1.99	0.45
22:U:750:SER:OG	22:U:751:ARG:N	2.50	0.45
24:X:90:ARG:HE	24:X:128:ALA:HB1	1.82	0.45
29:B:135:ILE:HD12	29:B:159:VAL:HG12	1.99	0.45
30:C:43:ARG:HH11	31:D:65:GLN:HE22	1.63	0.45
31:D:170:MET:HB3	31:D:171:ASP:H	1.65	0.45
32:E:44:GLU:HG2	33:F:73:ILE:HG12	1.98	0.45
32:E:135:ILE:HD12	32:E:142:ILE:CD1	2.46	0.45
32:E:169:GLY:HA3	32:E:275:MET:O	2.17	0.45
5:L:94:ASP:O	5:L:98:VAL:HG22	2.16	0.45
5:l:184:LEU:HD12	5:l:185:ASN:N	2.32	0.45
3:i:134:LEU:HD12	3:i:136:TYR:CE1	2.52	0.45
9:o:75:ARG:HB2	9:o:78:THR:HG22	1.99	0.45
9:o:187:ARG:HB3	9:o:188:PRO:HD3	1.97	0.45
10:p:61:GLN:NE2	11:q:124:LEU:O	2.44	0.45
14:t:209:TRP:CH2	8:N:172:GLY:HA2	2.53	0.45
11:Q:49:GLU:O	11:Q:53:THR:HG23	2.17	0.45
15:f:297:MET:HB3	15:f:300:ARG:HH21	1.82	0.45
15:f:442:SER:OG	15:f:476:THR:O	2.32	0.45
15:f:669:GLU:CG	29:B:49:LEU:HD23	2.46	0.45
17:a:232:TRP:CE3	17:a:253:THR:HA	2.52	0.45
17:a:278:MET:HE3	17:a:339:ARG:HD3	1.99	0.45
18:b:92:VAL:HG12	26:Z:67:VAL:HA	1.98	0.45
19:c:191:ALA:HB1	19:c:197:ASN:HB2	1.98	0.45
22:U:78:LEU:O	22:U:82:LEU:HB2	2.16	0.45
25:Y:64:GLN:CD	25:Y:64:GLN:H	2.25	0.45
27:W:187:LEU:HB3	27:W:225:LYS:HZ2	1.82	0.45
29:B:109:VAL:CG2	30:C:94:LYS:HD3	2.47	0.45
30:C:66:LEU:HB3	31:D:136:SER:O	2.17	0.45
31:D:92:PHE:CD1	31:D:103:VAL:HG12	2.52	0.45
31:D:357:GLU:O	31:D:393:ILE:HG23	2.17	0.45
32:E:63:GLN:O	32:E:65:THR:N	2.50	0.45
1:G:159:TYR:CZ	1:G:161:CYS:HB3	2.52	0.44
1:G:208:ILE:HD13	32:E:287:PRO:CG	2.46	0.44
4:J:66:ASP:HB3	4:J:95:ARG:NH2	2.32	0.44
7:k:91:LYS:HZ3	7:k:137:PHE:HZ	1.65	0.44
9:O:211:VAL:HG21	10:P:198:ARG:HD3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:f:62:ARG:HD2	15:f:70:LEU:HB3	2.00	0.44
15:f:175:ASP:O	15:f:178:LYS:NZ	2.46	0.44
15:f:290:VAL:O	15:f:294:MET:HG2	2.17	0.44
15:f:394:ASP:HB2	15:f:397:LYS:HE3	1.98	0.44
17:a:198:PHE:CZ	17:a:230:ARG:HD2	2.51	0.44
18:b:8:VAL:HA	18:b:110:ILE:O	2.18	0.44
18:b:100:ARG:HE	18:b:101:GLN:N	2.15	0.44
19:c:138:GLU:OE1	19:c:139:ARG:NH1	2.50	0.44
20:d:71:PHE:O	20:d:75:MET:HG2	2.16	0.44
21:e:22:PHE:CD2	23:V:324:PHE:HB2	2.52	0.44
23:V:148:ARG:HD2	23:V:148:ARG:O	2.16	0.44
23:V:440:LYS:HA	23:V:443:ARG:HG2	1.99	0.44
24:X:126:ARG:O	24:X:130:GLU:HG3	2.16	0.44
25:Y:316:LEU:HA	25:Y:319:MET:HG2	1.97	0.44
27:W:394:SER:HA	27:W:397:VAL:HG22	1.99	0.44
30:C:113:ARG:HG2	30:C:130:LYS:HB2	1.97	0.44
33:F:388:THR:HG22	33:F:388:THR:O	2.16	0.44
4:J:182:GLU:HB2	4:J:186:LEU:HD12	1.99	0.44
7:K:67:ILE:HG21	7:K:218:ALA:HB2	1.99	0.44
1:g:147:GLN:HG3	1:g:150:GLN:OE1	2.17	0.44
2:h:224:THR:O	2:h:227:LYS:HG3	2.17	0.44
12:r:98:GLY:HA2	12:r:115:ASP:HA	1.99	0.44
15:f:262:PHE:N	15:f:263:PRO:HD2	2.33	0.44
15:f:296:PHE:CE1	15:f:320:ILE:HD12	2.52	0.44
19:c:57:MET:HG2	19:c:69:VAL:HG11	1.98	0.44
22:U:483:LEU:HD13	22:U:778:PHE:CZ	2.52	0.44
27:W:298:GLU:OE1	27:W:298:GLU:N	2.42	0.44
27:W:345:GLU:O	27:W:348:GLU:HG2	2.18	0.44
28:A:199:GLU:OE1	33:F:408:LEU:HB3	2.17	0.44
29:B:204:PRO:O	29:B:206:THR:N	2.50	0.44
30:C:188:LEU:HB3	30:C:317:PHE:CE2	2.52	0.44
3:I:43:VAL:HG12	3:I:216:LEU:HB3	2.00	0.44
2:h:158:TRP:CD1	3:i:56:LEU:HD13	2.52	0.44
2:h:162:ALA:O	2:h:167:TYR:HB2	2.18	0.44
8:N:107:GLU:HB2	8:N:110:GLN:NE2	2.32	0.44
10:P:56:LEU:O	10:P:60:VAL:HG23	2.18	0.44
15:f:188:VAL:O	15:f:192:VAL:HG23	2.17	0.44
15:f:419:LEU:HD22	15:f:822:VAL:HG12	2.00	0.44
18:b:8:VAL:HG13	18:b:51:LEU:HD23	1.99	0.44
18:b:91:ARG:HH12	18:b:130:ARG:HD3	1.82	0.44
20:d:202:THR:N	20:d:203:PRO:HD3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:550:VAL:O	22:U:554:LEU:HD23	2.16	0.44
23:V:489:MET:HE1	25:Y:388:ASN:HA	2.00	0.44
25:Y:337:PHE:HB2	25:Y:343:LEU:HD22	1.98	0.44
26:Z:26:ILE:HD11	26:Z:35:VAL:HG22	1.99	0.44
29:B:344:PRO:HA	29:B:347:ILE:O	2.17	0.44
30:C:326:LEU:HD13	30:C:345:ARG:HA	1.99	0.44
1:G:15:ILE:HD12	1:G:15:ILE:HA	1.88	0.44
6:M:150:MET:HE3	6:M:150:MET:HB3	1.91	0.44
5:l:24:TYR:CE1	7:k:17:PRO:HA	2.52	0.44
1:g:28:ALA:O	1:g:32:ILE:HG12	2.18	0.44
2:h:66:GLU:O	2:h:74:LEU:HD23	2.17	0.44
3:i:14:PRO:HA	4:j:21:TYR:CE1	2.52	0.44
8:n:166:ARG:NH1	14:T:37:ARG:HD3	2.32	0.44
12:r:194:ASP:HA	12:r:197:GLU:HG2	1.98	0.44
13:s:156:LYS:HB2	13:s:156:LYS:HE3	1.83	0.44
10:P:178:ASP:OD2	10:P:181:SER:HB2	2.18	0.44
19:c:57:MET:HE3	19:c:69:VAL:HG21	1.98	0.44
22:U:133:ILE:O	22:U:137:MET:HG2	2.17	0.44
22:U:381:THR:HA	22:U:412:HIS:CE1	2.51	0.44
23:V:394:LEU:HG	23:V:397:ARG:NH2	2.32	0.44
24:X:401:LEU:HB2	25:Y:365:GLN:NE2	2.30	0.44
25:Y:217:LYS:HE3	25:Y:253:LEU:HD21	1.99	0.44
25:Y:362:LYS:HZ1	26:Z:249:PHE:HE2	1.61	0.44
27:W:188:GLU:O	27:W:192:LEU:HD23	2.18	0.44
30:C:25:LEU:HG	31:D:51:LEU:HD12	1.99	0.44
31:D:66:LYS:O	31:D:69:LYS:HG2	2.18	0.44
31:D:337:ASP:HB2	31:D:340:GLN:HB3	2.00	0.44
32:E:97:ARG:HH12	33:F:123:VAL:HG21	1.82	0.44
33:F:269:ARG:N	33:F:316:GLN:HE22	2.16	0.44
2:H:83:TYR:HB2	2:H:132:VAL:HG21	2.00	0.44
2:H:126:GLY:O	2:H:128:ARG:N	2.51	0.44
5:L:109:VAL:HG22	5:L:134:ILE:HD12	1.99	0.44
12:r:1:THR:N	12:r:169:TYR:O	2.50	0.44
15:f:845:ARG:N	15:f:881:GLU:O	2.45	0.44
17:a:157:ASP:OD2	17:a:161:LYS:NZ	2.47	0.44
19:c:63:ASP:CG	19:c:64:ASP:N	2.75	0.44
22:U:204:ILE:O	22:U:208:LEU:HG	2.18	0.44
22:U:684:ARG:HH11	22:U:726:ALA:HB1	1.81	0.44
27:W:28:LEU:HD12	27:W:66:ILE:HD13	1.99	0.44
27:W:88:MET:HA	27:W:130:MET:SD	2.57	0.44
27:W:341:PHE:HB3	27:W:351:TRP:NE1	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A:380:SER:O	28:A:384:GLU:HB2	2.17	0.44
31:D:170:MET:SD	31:D:343:LEU:HD21	2.57	0.44
33:F:321:GLN:HB3	33:F:322:PRO:HD3	1.99	0.44
33:F:424:ILE:O	33:F:427:VAL:HG22	2.18	0.44
4:j:115:LYS:O	4:j:119:THR:HG23	2.17	0.44
8:n:84:LYS:HB2	8:n:120:MET:HB2	1.99	0.44
11:q:3:TYR:OH	11:q:5:ILE:HD12	2.17	0.44
12:r:8:PHE:CE2	12:r:10:HIS:HB2	2.52	0.44
14:t:9:THR:HB	14:t:182:ARG:HB3	1.98	0.44
9:O:45:GLY:HA3	9:O:52:THR:HG21	2.00	0.44
14:T:51:LEU:HD13	14:T:112:ILE:HG12	1.99	0.44
15:f:383:ALA:HA	15:f:417:ILE:HA	2.00	0.44
15:f:678:LEU:HB3	15:f:686:LEU:HD11	2.00	0.44
17:a:326:GLU:CD	27:W:373:ILE:HG13	2.42	0.44
18:b:91:ARG:HD2	18:b:91:ARG:HA	1.70	0.44
20:d:99:LEU:HD23	20:d:122:LEU:HD11	2.00	0.44
23:V:464:ILE:HG21	23:V:469:THR:HG23	2.00	0.44
29:B:168:ASP:N	29:B:169:PRO:HD3	2.32	0.44
30:C:114:VAL:HG23	30:C:126:ILE:HA	1.99	0.44
31:D:93:LEU:HD23	31:D:102:ILE:HD13	1.98	0.44
31:D:242:GLU:OE2	32:E:78:ARG:NH1	2.51	0.44
3:I:143:TYR:HB2	3:I:146:GLN:NE2	2.33	0.44
5:l:196:ARG:HB2	5:l:205:LEU:HD13	1.99	0.44
3:i:43:VAL:HG21	3:i:137:ILE:HB	1.99	0.44
3:i:72:MET:HG3	3:i:137:ILE:O	2.18	0.44
8:N:59:VAL:HG11	8:N:83:PHE:CZ	2.52	0.44
11:Q:39:SER:OG	11:Q:40:GLU:N	2.50	0.44
13:S:36:HIS:O	14:T:151:ARG:NH2	2.51	0.44
15:f:175:ASP:N	15:f:175:ASP:OD1	2.50	0.44
15:f:597:VAL:HA	15:f:660:ILE:HD11	1.98	0.44
15:f:691:PRO:HA	15:f:694:LEU:HD12	2.00	0.44
17:a:25:LEU:HG	17:a:37:LEU:HD11	2.00	0.44
18:b:76:HIS:ND1	33:F:57:SER:OG	2.43	0.44
19:c:75:MET:HG2	19:c:91:PHE:HE2	1.83	0.44
20:d:114:GLU:HA	20:d:117:THR:HG22	1.99	0.44
22:U:599:ILE:HG22	31:D:60:TYR:OH	2.17	0.44
23:V:182:LYS:O	23:V:185:GLN:HG2	2.18	0.44
28:A:122:VAL:HB	33:F:87:PRO:HD2	2.00	0.44
29:B:260:LEU:HD23	29:B:260:LEU:H	1.82	0.44
32:E:153:LEU:HD22	32:E:229:ILE:HD11	1.99	0.44
32:E:345:ASN:O	32:E:349:GLU:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:16:LEU:O	4:J:20:GLU:HG2	2.17	0.44
3:i:111:VAL:HG21	3:i:148:TYR:HD2	1.82	0.44
10:p:53:LEU:HB3	10:p:60:VAL:HG13	2.00	0.44
8:N:52:THR:HG22	8:N:96:ALA:HB1	2.00	0.44
9:O:214:GLU:OE1	10:P:198:ARG:NE	2.42	0.44
12:R:40:TYR:OH	12:R:74:ILE:HG22	2.18	0.44
12:R:143:TYR:HA	12:R:147:LEU:HD11	2.00	0.44
15:f:256:PHE:HB3	15:f:265:ALA:HB2	2.00	0.44
15:f:653:ALA:O	15:f:657:ILE:HG12	2.18	0.44
17:a:81:LEU:HD11	17:a:117:ALA:HB2	2.00	0.44
23:V:330:LYS:HG2	23:V:360:TYR:HE2	1.81	0.44
24:X:182:ASN:ND2	25:Y:244:ALA:O	2.51	0.44
26:Z:19:VAL:HG11	26:Z:124:ILE:HD13	2.00	0.44
30:C:345:ARG:O	30:C:349:GLU:HG3	2.18	0.44
32:E:53:VAL:HA	33:F:157:SER:O	2.18	0.44
33:F:419:ASP:OD1	33:F:419:ASP:N	2.43	0.44
1:G:171:LYS:HD2	1:G:206:LEU:HD21	1.99	0.44
1:G:211:LYS:O	1:G:213:SER:N	2.44	0.44
5:l:176:MET:HE3	5:l:176:MET:HB3	1.91	0.44
3:i:19:TYR:HB3	3:i:23:TYR:CZ	2.52	0.44
4:j:69:VAL:HG22	4:j:104:VAL:HG22	1.98	0.44
9:o:28:ASP:OD1	9:o:29:LYS:N	2.51	0.44
14:t:1:THR:OG1	14:t:59:ASP:OD2	2.33	0.44
11:Q:131:ALA:H	11:Q:140:LEU:HD21	1.82	0.44
13:S:71:ARG:NH1	13:S:95:ILE:HD11	2.33	0.44
13:S:133:ASP:OD1	13:S:134:SER:N	2.51	0.44
13:S:152:GLN:HG2	13:S:174:LEU:HD11	2.00	0.44
16:x:95:GLN:HG2	16:x:96:ASP:H	1.83	0.44
17:a:188:LEU:HB2	17:a:189:PRO:HD2	2.00	0.44
19:c:177:THR:HG23	22:U:364:VAL:HG23	1.99	0.44
20:d:155:LYS:HB3	20:d:167:ILE:HB	2.00	0.44
23:V:225:ASP:OD1	23:V:226:VAL:HG23	2.18	0.44
25:Y:163:LYS:O	25:Y:168:ILE:HG12	2.17	0.44
29:B:395:ILE:HD13	29:B:398:ILE:HD11	2.00	0.44
33:F:240:CYS:O	33:F:244:THR:HG23	2.18	0.44
6:M:160:TYR:CG	6:M:163:CYS:HB2	2.53	0.43
7:K:220:VAL:HG13	7:K:226:PHE:CZ	2.53	0.43
5:l:65:HIS:HA	5:l:221:PHE:HE2	1.83	0.43
1:g:222:VAL:O	1:g:222:VAL:HG13	2.18	0.43
10:p:53:LEU:HD23	10:p:60:VAL:HA	2.00	0.43
12:r:42:LEU:HD21	12:r:184:TRP:CB	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:f:261:ARG:HH21	15:f:263:PRO:CG	2.30	0.43
15:f:322:SER:HA	15:f:456:ARG:HB2	2.00	0.43
19:c:287:HIS:O	19:c:291:LEU:HG	2.17	0.43
20:d:34:ASN:ND2	22:U:26:LYS:HE3	2.33	0.43
20:d:141:GLN:HE22	20:d:145:GLU:HB2	1.82	0.43
23:V:111:TYR:HE2	23:V:115:LYS:HE2	1.83	0.43
23:V:216:ARG:NH1	23:V:253:LEU:HD23	2.33	0.43
23:V:302:TYR:CB	23:V:339:LEU:HD21	2.40	0.43
25:Y:50:MET:HB2	25:Y:70:LEU:CD2	2.47	0.43
27:W:246:HIS:HA	27:W:249:ALA:HB3	1.99	0.43
27:W:280:ASP:OD1	27:W:283:GLN:N	2.37	0.43
30:C:74:GLY:O	30:C:114:VAL:N	2.47	0.43
30:C:86:LEU:HD23	30:C:94:LYS:HZ1	1.83	0.43
30:C:339:THR:HG22	30:C:377:HIS:HB3	2.00	0.43
31:D:167:ILE:HG12	31:D:169:GLY:H	1.83	0.43
7:K:35:SER:CB	7:K:66:LYS:HE2	2.46	0.43
4:j:210:VAL:HG13	4:j:212:ARG:HH11	1.83	0.43
7:k:137:PHE:O	7:k:158:PRO:HB3	2.18	0.43
10:p:30:ILE:HG13	10:p:31:GLN:H	1.82	0.43
10:p:164:PHE:CE1	10:p:198:ARG:HD2	2.53	0.43
11:q:41:LYS:NZ	11:q:185:LYS:O	2.51	0.43
11:q:111:GLU:N	11:q:111:GLU:OE1	2.51	0.43
12:r:161:TYR:OH	12:r:196:HIS:ND1	2.31	0.43
14:t:49:THR:HG21	14:t:88:ILE:HG13	2.00	0.43
14:t:154:LEU:HD23	14:t:154:LEU:HA	1.83	0.43
10:P:59:ASP:C	10:P:62:THR:HG22	2.43	0.43
15:f:416:MET:HE3	15:f:416:MET:HB3	1.89	0.43
15:f:494:ARG:HE	15:f:495:GLU:H	1.65	0.43
15:f:695:ALA:HB2	15:f:728:ALA:HA	2.00	0.43
15:f:848:GLN:OE1	15:f:878:GLU:HB3	2.17	0.43
17:a:292:THR:HA	17:a:329:LYS:O	2.18	0.43
17:a:338:PRO:HB2	26:Z:229:GLN:HA	2.00	0.43
19:c:224:SER:O	26:Z:196:HIS:NE2	2.51	0.43
22:U:727:LYS:O	22:U:731:ILE:HG13	2.18	0.43
23:V:476:PHE:O	23:V:479:ARG:HG2	2.18	0.43
24:X:369:ILE:HD11	24:X:376:GLY:H	1.84	0.43
25:Y:320:ALA:HB1	25:Y:330:ILE:HD13	1.99	0.43
27:W:28:LEU:HD13	27:W:65:ARG:HE	1.82	0.43
27:W:74:CYS:CB	27:W:83:LEU:HD13	2.48	0.43
27:W:308:LEU:HA	27:W:313:GLU:OE2	2.18	0.43
29:B:112:LEU:O	29:B:147:GLY:N	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:B:218:PRO:HB2	29:B:220:LYS:HG2	2.00	0.43
30:C:138:MET:HA	31:D:290:LEU:HD21	2.00	0.43
32:E:129:ASN:C	32:E:131:SER:N	2.74	0.43
1:G:86:ASP:OD1	1:G:86:ASP:N	2.51	0.43
1:G:225:PRO:O	1:G:226:LYS:HB2	2.18	0.43
2:H:180:GLU:HB3	2:H:183:GLU:HG2	2.00	0.43
5:L:13:TRP:NE1	6:M:129:ARG:HD2	2.33	0.43
6:M:215:TRP:CG	6:M:227:VAL:HG12	2.52	0.43
7:K:38:ILE:HD12	7:K:202:LEU:HD22	2.00	0.43
5:l:23:GLU:O	5:l:26:MET:HG2	2.18	0.43
1:g:43:ARG:HA	1:g:48:ALA:HA	1.99	0.43
2:h:177:ARG:HG3	2:h:177:ARG:O	2.17	0.43
4:j:146:GLN:OE1	4:j:159:ASN:ND2	2.51	0.43
13:s:65:THR:O	13:s:69:GLU:HG2	2.17	0.43
13:s:145:LEU:HD21	13:s:182:ALA:HB2	2.00	0.43
13:s:151:ASN:HD21	10:P:169:GLN:NE2	2.17	0.43
11:Q:11:ASP:N	11:Q:11:ASP:OD1	2.50	0.43
10:P:11:VAL:HG11	10:P:52:GLY:HA3	1.99	0.43
15:f:511:SER:HB3	15:f:514:VAL:HG23	2.00	0.43
15:f:762:VAL:O	15:f:766:GLN:HG3	2.18	0.43
15:f:907:ASP:N	15:f:907:ASP:OD1	2.51	0.43
18:b:7:MET:HB2	18:b:97:LEU:HD22	2.00	0.43
20:d:132:TYR:CD1	20:d:160:ALA:HA	2.53	0.43
22:U:138:PHE:O	22:U:142:LEU:HG	2.18	0.43
22:U:639:LEU:HD23	22:U:639:LEU:H	1.83	0.43
23:V:82:LEU:HD11	23:V:166:TYR:CE2	2.54	0.43
23:V:391:THR:O	23:V:395:ILE:N	2.49	0.43
24:X:74:ARG:HA	24:X:77:LEU:HD12	2.00	0.43
28:A:30:ILE:HG13	28:A:31:ALA:N	2.34	0.43
28:A:371:GLU:O	28:A:375:ARG:HG3	2.19	0.43
28:A:377:CYS:HB3	28:A:380:SER:HB3	1.98	0.43
28:A:384:GLU:O	28:A:388:VAL:HG23	2.19	0.43
29:B:224:LEU:HB2	29:B:330:ALA:HA	2.00	0.43
30:C:113:ARG:HH21	30:C:129:ASN:HA	1.84	0.43
31:D:200:ARG:HH22	31:D:326:ARG:HA	1.83	0.43
31:D:237:GLN:CG	31:D:238:LYS:H	2.29	0.43
32:E:97:ARG:NH1	33:F:123:VAL:HG21	2.34	0.43
33:F:323:ASN:OD1	33:F:325:GLN:HG2	2.17	0.43
2:H:113:ARG:HH21	10:P:77:LYS:HB3	1.83	0.43
3:I:90:LEU:HD22	3:I:114:LEU:HD22	2.01	0.43
6:M:59:GLU:CG	6:M:60:GLU:H	2.28	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:102:THR:HA	13:S:94:THR:HG21	2.00	0.43
5:l:86:ASN:HA	5:l:89:ARG:HG2	1.99	0.43
5:l:226:ASP:OD1	5:l:226:ASP:N	2.51	0.43
1:g:81:THR:HG21	1:g:169:GLY:HA2	1.99	0.43
2:h:189:HIS:HA	2:h:233:ILE:HD13	2.00	0.43
3:i:75:SER:OG	3:i:135:LEU:HB3	2.19	0.43
3:i:140:ASP:OD1	3:i:144:GLY:N	2.52	0.43
4:j:184:ASP:OD1	4:j:184:ASP:N	2.51	0.43
9:o:2:THR:HG21	9:o:162:GLY:HA3	2.00	0.43
11:q:4:LEU:HD23	11:q:132:HIS:HD2	1.83	0.43
11:Q:4:LEU:HD22	11:Q:45:LEU:HB3	2.00	0.43
10:P:169:GLN:O	10:P:173:ASN:ND2	2.51	0.43
15:f:134:SER:OG	15:f:136:GLU:O	2.31	0.43
15:f:136:GLU:HG3	15:f:137:ARG:N	2.32	0.43
15:f:514:VAL:O	15:f:518:THR:HG23	2.17	0.43
18:b:140:ILE:HB	18:b:170:LEU:HD12	2.01	0.43
19:c:30:GLN:NE2	19:c:66:THR:HG22	2.34	0.43
19:c:172:HIS:CG	19:c:173:GLU:N	2.83	0.43
19:c:265:MET:O	19:c:266:THR:OG1	2.36	0.43
20:d:92:SER:O	20:d:94:TYR:N	2.51	0.43
22:U:349:ASP:O	22:U:353:LEU:HG	2.19	0.43
22:U:356:THR:HG22	22:U:717:ILE:HD11	2.01	0.43
22:U:627:PHE:CE1	22:U:755:THR:HG22	2.54	0.43
23:V:81:GLN:HG2	23:V:93:PHE:CZ	2.53	0.43
23:V:117:VAL:HG13	23:V:121:PHE:CE2	2.53	0.43
24:X:206:LEU:O	24:X:209:THR:OG1	2.26	0.43
26:Z:228:TYR:HE1	26:Z:229:GLN:HE21	1.65	0.43
27:W:116:THR:OG1	27:W:117:ASP:N	2.49	0.43
29:B:123:VAL:HG12	29:B:125:THR:HG23	2.00	0.43
29:B:237:LYS:HZ1	29:B:353:PHE:HB2	1.82	0.43
29:B:339:PRO:HA	29:B:342:ILE:HB	2.00	0.43
33:F:198:LEU:HD21	33:F:236:LEU:HD21	2.00	0.43
4:J:41:VAL:CG1	4:J:142:PRO:HB2	2.48	0.43
5:L:77:LEU:CD2	5:L:80:ASP:H	2.31	0.43
5:L:109:VAL:HA	5:L:112:ILE:HD12	2.01	0.43
5:L:225:ASP:O	5:L:228:ASP:N	2.52	0.43
5:l:11:THR:HA	6:m:129:ARG:HD3	2.01	0.43
8:n:103:TRP:CZ2	8:n:181:GLU:HG3	2.53	0.43
8:n:133:SER:O	8:N:134:TYR:HA	2.18	0.43
13:s:36:HIS:HB3	14:t:132:TYR:CZ	2.54	0.43
8:N:19:ARG:CZ	8:N:171:GLY:HA3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:N:44:CYS:HB2	8:N:99:ILE:HB	1.99	0.43
11:Q:3:TYR:HE1	11:Q:5:ILE:HB	1.84	0.43
13:S:21:ALA:HB3	13:S:198:VAL:HB	2.01	0.43
15:f:609:VAL:O	15:f:613:LEU:HG	2.19	0.43
15:f:646:MET:O	15:f:649:HIS:ND1	2.49	0.43
15:f:669:GLU:CD	15:f:670:MET:HG3	2.43	0.43
17:a:351:ASP:O	17:a:354:GLU:HG2	2.18	0.43
17:a:371:ALA:HA	20:d:247:ILE:HG21	2.00	0.43
19:c:152:LYS:C	26:Z:170:VAL:HG22	2.42	0.43
26:Z:136:GLU:HB3	27:W:448:LYS:NZ	2.33	0.43
29:B:211:TYR:HB2	29:B:216:ILE:HG12	1.99	0.43
29:B:239:VAL:HA	29:B:242:GLN:CD	2.44	0.43
30:C:22:GLN:O	30:C:25:LEU:HB3	2.17	0.43
32:E:97:ARG:HB3	32:E:111:LEU:O	2.17	0.43
32:E:267:PHE:HB2	32:E:271:HIS:CE1	2.53	0.43
33:F:152:GLY:O	33:F:161:LEU:N	2.48	0.43
4:J:210:VAL:N	4:J:218:LYS:O	2.45	0.43
1:g:52:THR:OG1	1:g:216:GLU:HG3	2.19	0.43
7:k:66:LYS:HA	7:k:78:MET:HE2	2.00	0.43
6:m:117:MET:HE3	6:m:117:MET:HB3	1.91	0.43
9:o:20:ALA:HB2	9:o:31:CYS:HB2	1.99	0.43
12:r:115:ASP:OD1	12:r:119:ASN:N	2.45	0.43
14:t:135:PRO:HB2	14:t:154:LEU:HD13	2.01	0.43
9:O:147:GLU:CD	9:O:150:GLU:H	2.26	0.43
14:T:25:ASP:OD1	14:T:25:ASP:N	2.49	0.43
14:T:59:ASP:O	14:T:63:LEU:HD23	2.18	0.43
15:f:263:PRO:HB2	15:f:891:THR:HB	1.99	0.43
15:f:409:SER:O	15:f:819:TYR:OH	2.32	0.43
19:c:195:GLY:HA3	19:c:199:HIS:CE1	2.53	0.43
22:U:583:MET:CE	22:U:618:ALA:HA	2.38	0.43
22:U:599:ILE:O	31:D:60:TYR:OH	2.34	0.43
22:U:603:LEU:HB3	31:D:64:GLU:CD	2.42	0.43
22:U:732:LEU:HD12	22:U:766:PHE:HZ	1.84	0.43
24:X:400:ALA:O	24:X:403:THR:OG1	2.30	0.43
24:X:417:LYS:HD3	24:X:417:LYS:HA	1.77	0.43
25:Y:138:LEU:HD23	25:Y:168:ILE:HG22	2.01	0.43
26:Z:221:PRO:HD2	27:W:453:HIS:HB3	2.01	0.43
27:W:143:ALA:O	27:W:147:LYS:HG2	2.19	0.43
27:W:340:VAL:HA	27:W:350:ARG:NH1	2.33	0.43
27:W:384:LEU:HB3	27:W:388:GLU:HB2	2.00	0.43
29:B:434:THR:O	29:B:435:PRO:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:C:250:GLU:OE2	30:C:296:ASN:ND2	2.51	0.43
30:C:400:SER:O	30:C:400:SER:OG	2.30	0.43
32:E:200:SER:HA	32:E:203:ILE:HG22	1.99	0.43
2:H:80:GLY:N	2:H:81:PRO:HD2	2.33	0.43
5:L:13:TRP:HZ3	6:M:29:ALA:HB2	1.83	0.43
5:L:189:LYS:HE2	5:L:234:GLU:O	2.18	0.43
2:h:119:GLN:HE21	3:i:81:SER:CB	2.31	0.43
3:i:115:CYS:SG	3:i:156:TYR:HB3	2.58	0.43
6:m:197:ILE:HA	6:m:200:VAL:HG22	2.00	0.43
8:n:14:LEU:HD13	8:n:179:ILE:HD13	1.99	0.43
10:p:8:GLY:HA2	10:p:141:THR:HG21	2.01	0.43
13:s:36:HIS:HB3	14:t:132:TYR:CE2	2.53	0.43
13:s:63:THR:HG21	14:t:97:TYR:CG	2.53	0.43
14:t:209:TRP:HZ3	8:N:29:ARG:HD2	1.83	0.43
10:P:20:VAL:HG12	10:P:121:ILE:HD11	2.01	0.43
10:P:123:SER:HB2	10:P:137:VAL:HB	2.00	0.43
15:f:123:ALA:HB1	15:f:142:TYR:O	2.19	0.43
15:f:217:LEU:O	15:f:221:ILE:HG12	2.19	0.43
17:a:32:LYS:O	18:b:18:ASN:HB2	2.18	0.43
18:b:166:THR:HG22	18:b:191:GLY:HA2	2.00	0.43
19:c:80:THR:HA	33:F:82:VAL:HG11	2.00	0.43
20:d:22:GLU:O	20:d:26:LEU:HG	2.17	0.43
22:U:191:LYS:HA	22:U:194:ARG:HB3	2.00	0.43
22:U:437:TYR:HA	22:U:472:ILE:HG21	1.99	0.43
22:U:451:ALA:HB2	22:U:483:LEU:HD21	2.01	0.43
22:U:583:MET:HE3	22:U:618:ALA:CA	2.38	0.43
23:V:168:GLN:HB3	23:V:191:LEU:HB2	2.01	0.43
23:V:357:LEU:HD13	23:V:360:TYR:HD2	1.84	0.43
24:X:46:LYS:O	24:X:50:ILE:HG12	2.18	0.43
27:W:159:VAL:HG12	27:W:196:VAL:HG22	2.01	0.43
27:W:207:LYS:HA	27:W:210:ASN:ND2	2.34	0.43
27:W:231:ILE:HG13	27:W:232:GLN:N	2.33	0.43
28:A:83:ASP:O	28:A:86:THR:HG22	2.19	0.43
33:F:77:SER:O	33:F:81:LYS:N	2.50	0.43
6:M:5:THR:OG1	6:M:6:GLY:N	2.52	0.43
5:l:159:MET:SD	5:l:169:ARG:NH1	2.90	0.43
10:p:12:MET:HB3	10:p:146:MET:CE	2.48	0.43
10:p:66:ARG:NH1	10:p:70:ARG:HB3	2.33	0.43
13:s:157:ASN:HD21	10:P:172:LEU:HD13	1.84	0.43
14:t:88:ILE:O	14:t:92:LEU:HD23	2.18	0.43
11:Q:52:ASP:OD2	11:Q:99:HIS:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:P:149:MET:HE3	10:P:153:LEU:HD21	2.00	0.43
15:f:76:GLU:CD	15:f:79:ARG:HH22	2.26	0.43
15:f:553:THR:HA	15:f:556:ARG:HH12	1.84	0.43
17:a:112:ILE:HG22	17:a:151:VAL:HG21	2.00	0.43
19:c:145:VAL:HA	19:c:156:VAL:O	2.19	0.43
19:c:217:LEU:HD23	19:c:221:HIS:CE1	2.54	0.43
20:d:113:ALA:HB2	23:V:299:GLN:HG3	2.00	0.43
21:e:17:ASP:N	21:e:17:ASP:OD1	2.51	0.43
22:U:350:LEU:HG	22:U:354:LYS:HE2	2.01	0.43
22:U:521:LEU:HG	22:U:557:TYR:HE2	1.83	0.43
22:U:756:HIS:CE1	22:U:758:PRO:HB2	2.54	0.43
22:U:800:VAL:HB	22:U:880:ASN:HB3	2.01	0.43
23:V:483:CYS:SG	26:Z:267:ARG:HG2	2.59	0.43
24:X:44:GLN:OE1	24:X:48:GLN:NE2	2.36	0.43
25:Y:275:LEU:HG	25:Y:296:VAL:HG12	2.01	0.43
26:Z:6:VAL:HG12	26:Z:43:TRP:CE2	2.53	0.43
26:Z:23:PHE:CD2	26:Z:97:THR:HG21	2.54	0.43
28:A:99:THR:HA	28:A:141:GLY:HA2	2.01	0.43
28:A:206:ILE:HG22	28:A:207:GLU:HG2	2.01	0.43
30:C:97:VAL:HG21	30:C:121:TYR:C	2.43	0.43
30:C:287:LYS:HG3	30:C:287:LYS:O	2.18	0.43
31:D:81:ARG:O	31:D:83:GLN:N	2.52	0.43
31:D:237:GLN:HG2	31:D:238:LYS:N	2.30	0.43
7:K:156:MET:SD	7:K:157:ASP:N	2.92	0.43
1:g:206:LEU:HG	1:g:208:ILE:HG23	2.00	0.43
2:h:109:GLN:O	2:h:113:ARG:HG2	2.19	0.43
3:i:43:VAL:HG23	3:i:137:ILE:HD12	1.99	0.43
3:i:68:LEU:HD12	3:i:72:MET:HG2	2.01	0.43
8:n:40:ARG:NH1	8:n:183:GLY:HA2	2.34	0.43
9:o:51:ASP:OD2	10:p:99:ARG:NH1	2.52	0.43
13:s:197:ILE:O	13:s:203:ILE:HA	2.19	0.43
8:N:45:ARG:HB3	8:N:52:THR:HB	2.00	0.43
13:S:14:ALA:HA	13:S:22:ILE:O	2.19	0.43
22:U:213:PHE:CG	22:U:214:ILE:N	2.86	0.43
22:U:493:VAL:O	22:U:497:LEU:HD13	2.19	0.43
23:V:131:LEU:HD11	23:V:171:VAL:CG2	2.49	0.43
27:W:83:LEU:HD23	27:W:123:ARG:HD3	2.01	0.43
27:W:187:LEU:HB3	27:W:225:LYS:NZ	2.33	0.43
30:C:210:THR:HB	30:C:212:ILE:HG13	2.00	0.43
32:E:129:ASN:O	32:E:131:SER:N	2.45	0.43
32:E:212:ALA:O	32:E:215:ILE:HG12	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:29:GLY:O	3:I:166:ASN:HA	2.18	0.43
3:I:114:LEU:HD23	3:I:136:TYR:OH	2.19	0.43
5:l:50:LYS:HB2	5:l:50:LYS:HE3	1.84	0.43
4:j:47:LYS:NZ	4:j:59:VAL:HG13	2.33	0.43
4:j:134:VAL:HG12	4:j:144:LEU:HD13	2.01	0.43
4:j:166:LYS:HA	4:j:169:ARG:HG2	2.01	0.43
7:k:121:LEU:HD12	7:k:123:PHE:HE1	1.83	0.43
11:q:19:ARG:HH21	11:q:31:ASP:HB3	1.84	0.43
9:O:11:GLY:HA2	9:O:108:PRO:HB3	2.01	0.43
12:R:63:CYS:HB2	12:R:74:ILE:HG21	2.01	0.43
12:R:127:SER:HB3	12:R:136:TYR:CE2	2.53	0.43
15:f:543:MET:HE1	15:f:583:VAL:HG22	2.01	0.43
19:c:34:SER:OG	19:c:70:ILE:HA	2.19	0.43
22:U:199:ARG:O	22:U:203:LYS:HG3	2.18	0.43
22:U:414:GLY:N	22:U:449:ILE:O	2.43	0.43
22:U:591:CYS:HA	22:U:625:ILE:HA	2.00	0.43
25:Y:66:ASP:OD2	25:Y:70:LEU:HB2	2.18	0.43
28:A:143:ASP:O	28:A:147:TYR:N	2.33	0.43
32:E:64:LEU:HD12	32:E:70:ILE:HD11	2.00	0.43
1:G:46:ASP:HB2	1:G:222:VAL:HG12	2.01	0.42
1:G:231:THR:OG1	1:G:234:GLU:OE1	2.32	0.42
2:H:49:GLU:CD	2:H:199:PHE:HD2	2.27	0.42
4:J:80:ALA:HB2	4:J:129:ILE:CD1	2.49	0.42
6:M:231:ILE:HD12	6:M:231:ILE:HA	1.86	0.42
5:l:37:GLY:HA3	5:l:46:LEU:HD23	2.01	0.42
3:i:148:TYR:CE1	4:j:58:THR:HG21	2.54	0.42
9:o:51:ASP:HB3	9:o:94:ILE:HG23	2.01	0.42
11:q:62:LYS:HB2	11:q:62:LYS:HE2	1.89	0.42
11:q:170:ARG:HH21	12:R:140:ASP:CG	2.26	0.42
12:r:1:THR:O	12:r:130:SER:N	2.52	0.42
15:f:219:LYS:HD3	15:f:258:LYS:HZ1	1.83	0.42
24:X:344:ARG:HG3	24:X:386:ILE:HA	2.01	0.42
24:X:399:ALA:O	24:X:403:THR:HG23	2.19	0.42
27:W:340:VAL:HG12	27:W:341:PHE:CD1	2.54	0.42
28:A:277:ILE:HG23	28:A:280:ILE:HG13	2.01	0.42
29:B:262:ASP:H	29:B:265:LYS:HZ2	1.65	0.42
30:C:97:VAL:HG22	30:C:98:ASP:H	1.83	0.42
31:D:88:VAL:N	31:D:132:LEU:O	2.24	0.42
31:D:281:ALA:HA	31:D:284:GLU:HG2	2.01	0.42
3:I:33:THR:HB	3:I:48:GLU:HB3	2.00	0.42
4:J:198:VAL:O	4:J:201:SER:OG	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:72:HIS:H	6:M:72:HIS:CD2	2.38	0.42
4:j:6:ALA:H	7:k:125:GLU:HG2	1.83	0.42
4:j:118:TYR:OH	4:j:124:ARG:NH2	2.52	0.42
8:n:117:GLY:HA3	8:n:119:MET:HE1	2.02	0.42
9:o:75:ARG:HD2	9:o:104:ASP:HB2	2.01	0.42
14:t:21:VAL:HG23	14:t:191:THR:HG22	2.01	0.42
14:t:74:GLU:HG3	14:t:83:TYR:CZ	2.54	0.42
14:T:178:TYR:OH	14:T:208:ASN:N	2.46	0.42
15:f:124:ASP:OD1	15:f:143:ARG:NH1	2.47	0.42
17:a:18:GLN:N	17:a:19:PRO:HD2	2.34	0.42
17:a:359:ASP:O	17:a:363:MET:HG2	2.18	0.42
18:b:51:LEU:HB2	18:b:62:THR:OG1	2.18	0.42
19:c:29:GLU:HA	19:c:65:TYR:HB2	2.01	0.42
19:c:223:LYS:HD2	26:Z:132:GLY:O	2.19	0.42
19:c:223:LYS:HZ3	19:c:225:TRP:HE1	1.67	0.42
19:c:266:THR:O	19:c:268:GLU:N	2.52	0.42
20:d:67:ASP:OD1	20:d:67:ASP:N	2.47	0.42
23:V:360:TYR:O	23:V:364:THR:HG23	2.19	0.42
25:Y:268:TYR:OH	25:Y:307:LEU:HB2	2.20	0.42
25:Y:294:TYR:CD1	25:Y:298:GLU:HB2	2.54	0.42
27:W:275:ILE:HD11	27:W:305:LEU:HA	2.00	0.42
27:W:313:GLU:OE1	27:W:313:GLU:N	2.45	0.42
27:W:359:VAL:HG11	27:W:392:PHE:HD2	1.84	0.42
28:A:191:VAL:C	28:A:194:PRO:HD2	2.44	0.42
29:B:434:THR:O	29:B:434:THR:HG23	2.19	0.42
32:E:141:GLN:OE1	32:E:299:ILE:HB	2.19	0.42
1:G:208:ILE:C	1:G:210:PHE:H	2.27	0.42
3:I:37:ILE:HG23	3:I:44:LEU:HG	2.01	0.42
5:L:52:ALA:HB2	5:L:59:HIS:ND1	2.33	0.42
5:L:77:LEU:HD23	5:L:80:ASP:H	1.83	0.42
7:K:225:ASN:HB2	7:K:227:HIS:CE1	2.54	0.42
5:l:47:VAL:HG13	5:l:212:ILE:HG22	2.02	0.42
5:l:168:ALA:O	5:l:172:LEU:HG	2.20	0.42
1:g:37:LEU:HG	1:g:53:GLN:NE2	2.31	0.42
3:i:176:LYS:HA	4:j:53:LEU:HD11	2.02	0.42
6:m:7:TYR:HB2	6:m:15:SER:HA	2.01	0.42
12:r:6:PHE:HB2	12:r:125:THR:HG22	2.01	0.42
9:O:164:PHE:CZ	9:O:192:PRO:HB2	2.54	0.42
17:a:137:ASP:O	17:a:141:MET:HG2	2.19	0.42
17:a:261:LEU:HD12	17:a:261:LEU:HA	1.86	0.42
20:d:63:ILE:HG12	20:d:166:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:904:LYS:HD3	22:U:912:ILE:HG13	2.01	0.42
23:V:357:LEU:O	23:V:361:PHE:N	2.42	0.42
28:A:178:GLY:HA3	28:A:354:ILE:HG12	2.00	0.42
28:A:239:ARG:NH1	28:A:275:ASP:OD2	2.52	0.42
29:B:233:THR:C	29:B:235:LEU:H	2.24	0.42
30:C:91:PRO:CD	31:D:109:SER:HA	2.46	0.42
31:D:183:LEU:HB2	31:D:184:PRO:HD3	2.00	0.42
32:E:228:CYS:O	32:E:273:VAL:HA	2.19	0.42
33:F:254:PRO:HD3	33:F:287:GLU:HG3	2.01	0.42
1:G:217:VAL:HG13	1:G:230:LEU:HB2	2.01	0.42
2:H:47:ALA:HB1	2:H:195:LEU:HD11	2.01	0.42
2:H:109:GLN:O	2:H:113:ARG:HG2	2.19	0.42
3:I:14:PRO:HA	4:J:21:TYR:CE1	2.54	0.42
3:I:43:VAL:HG13	3:I:137:ILE:HB	1.99	0.42
5:L:207:THR:HB	5:L:226:ASP:HA	2.02	0.42
1:g:18:PRO:HA	2:h:24:TYR:CZ	2.54	0.42
1:g:139:ILE:HG12	1:g:153:LYS:HG3	2.01	0.42
2:h:182:LEU:HB2	2:h:186:ASP:HB3	2.01	0.42
3:i:184:MET:HG3	3:i:189:ALA:HB2	2.01	0.42
7:k:8:TYR:O	7:k:10:ARG:N	2.52	0.42
10:p:33:GLN:HB3	12:R:134:TYR:OH	2.19	0.42
13:s:64:LEU:HD13	13:s:106:VAL:HG21	2.01	0.42
8:N:8:PHE:CE2	8:N:13:VAL:HG23	2.55	0.42
8:N:8:PHE:HB3	8:N:152:CYS:SG	2.59	0.42
10:P:30:ILE:HG12	10:P:33:GLN:CG	2.47	0.42
12:R:112:TYR:CE2	12:R:122:SER:HB2	2.54	0.42
22:U:38:ILE:HG22	22:U:67:VAL:HG22	2.01	0.42
22:U:535:TYR:CZ	22:U:539:THR:HG21	2.54	0.42
22:U:602:LEU:HD11	22:U:621:SER:O	2.19	0.42
23:V:91:PRO:O	23:V:95:LEU:HG	2.18	0.42
28:A:126:SER:OG	28:A:149:ILE:O	2.30	0.42
30:C:49:ARG:NH1	31:D:76:GLN:OE1	2.51	0.42
30:C:184:LYS:HD2	30:C:277:LEU:HB3	2.02	0.42
33:F:227:GLY:O	33:F:333:ASN:HA	2.19	0.42
1:G:161:CYS:SG	1:G:162:GLY:N	2.86	0.42
5:L:35:THR:HG21	5:L:73:SER:HB3	2.02	0.42
7:K:141:LEU:CD2	7:K:156:MET:HE2	2.49	0.42
4:j:16:LEU:O	4:j:20:GLU:HG2	2.20	0.42
4:j:56:GLU:HA	4:j:59:VAL:HG12	2.02	0.42
9:o:82:MET:HA	9:o:85:GLN:NE2	2.35	0.42
12:r:61:ARG:O	12:r:65:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:t:72:ILE:O	14:t:76:LEU:HG	2.18	0.42
15:f:607:LEU:O	15:f:610:GLN:HG3	2.19	0.42
17:a:232:TRP:CZ3	17:a:253:THR:HA	2.54	0.42
20:d:92:SER:OG	20:d:93:ALA:N	2.51	0.42
20:d:229:GLN:HG3	20:d:231:LYS:HB2	2.00	0.42
24:X:211:ASP:O	24:X:231:TYR:HB3	2.20	0.42
28:A:190:VAL:HG21	28:A:339:ARG:HG2	2.01	0.42
29:B:133:VAL:HG11	29:B:158:ALA:CB	2.49	0.42
31:D:132:LEU:HB3	31:D:137:ASN:C	2.44	0.42
31:D:225:ALA:HA	31:D:259:PRO:HB2	2.00	0.42
32:E:312:ILE:HA	32:E:315:ILE:HG12	2.01	0.42
32:E:353:PHE:CZ	32:E:373:LYS:HD2	2.54	0.42
1:G:207:SER:H	32:E:291:ARG:NH2	2.17	0.42
2:H:69:THR:HG22	2:H:72:ILE:HB	2.01	0.42
4:J:66:ASP:OD1	4:J:92:GLN:NE2	2.53	0.42
5:L:133:LEU:HD23	5:L:133:LEU:HA	1.84	0.42
7:K:32:LYS:HE3	28:A:424:SER:OG	2.20	0.42
7:K:157:ASP:C	7:K:157:ASP:OD1	2.62	0.42
1:g:138:MET:HB3	1:g:154:CYS:SG	2.59	0.42
6:m:71:ARG:NH1	6:m:99:ARG:HE	2.18	0.42
9:o:37:ILE:HG21	9:o:63:LEU:HD12	2.02	0.42
12:r:87:VAL:HG11	12:r:116:SER:HA	2.01	0.42
13:s:148:LEU:CD2	13:s:178:VAL:HG12	2.48	0.42
8:N:164:MET:SD	8:N:174:ILE:HG12	2.59	0.42
15:f:143:ARG:NE	15:f:151:LEU:HD11	2.35	0.42
22:U:376:MET:HG2	22:U:738:ASP:O	2.20	0.42
22:U:414:GLY:HA2	22:U:453:HIS:HE1	1.85	0.42
25:Y:215:ASP:HB3	25:Y:218:THR:H	1.84	0.42
27:W:225:LYS:O	27:W:229:LEU:HD23	2.19	0.42
28:A:261:PHE:HZ	28:A:306:LEU:HB3	1.85	0.42
30:C:209:CYS:O	30:C:210:THR:HG23	2.19	0.42
30:C:227:GLY:HA3	30:C:265:GLY:HA3	2.00	0.42
30:C:290:LYS:HA	30:C:290:LYS:HD3	1.72	0.42
32:E:229:ILE:HD12	32:E:274:LYS:HB2	2.01	0.42
33:F:228:PRO:HG2	33:F:356:MET:SD	2.59	0.42
4:J:220:LEU:HD12	4:J:220:LEU:HA	1.79	0.42
6:M:4:GLY:O	6:M:6:GLY:N	2.53	0.42
6:M:77:VAL:HG21	6:M:84:ALA:HB1	2.00	0.42
6:M:152:ASP:HB3	6:M:153:PRO:HD2	2.02	0.42
1:g:159:TYR:CG	1:g:159:TYR:O	2.72	0.42
2:h:159:LYS:HB3	2:h:178:TYR:OH	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:224:GLU:HA	4:j:227:LYS:HG2	2.01	0.42
8:n:103:TRP:NE1	8:n:181:GLU:OE2	2.52	0.42
9:o:175:LEU:HD12	9:o:189:TYR:CD1	2.54	0.42
13:s:6:VAL:HG21	13:s:31:GLU:OE2	2.20	0.42
15:f:130:ALA:O	15:f:134:SER:HB2	2.20	0.42
18:b:22:LEU:HB2	18:b:23:PRO:HD3	2.02	0.42
19:c:252:ALA:CB	24:X:407:MET:HB2	2.49	0.42
20:d:77:GLN:HE21	22:U:11:LEU:HD23	1.85	0.42
22:U:601:ARG:NH2	22:U:602:LEU:HA	2.34	0.42
23:V:160:LEU:HB2	23:V:163:VAL:HG12	2.01	0.42
23:V:173:ILE:HG22	23:V:213:TYR:CE2	2.55	0.42
24:X:110:CYS:HB2	24:X:133:LEU:HD21	2.02	0.42
27:W:148:THR:O	27:W:151:THR:OG1	2.31	0.42
27:W:186:ILE:O	27:W:189:GLN:NE2	2.50	0.42
28:A:373:LEU:HD22	28:A:376:LEU:HD22	2.01	0.42
29:B:221:GLY:HA2	29:B:326:LYS:HG3	2.02	0.42
32:E:130:VAL:HG23	32:E:134:GLU:HG2	2.01	0.42
33:F:84:LYS:O	33:F:87:PRO:HD3	2.19	0.42
3:I:17:ARG:HE	29:B:434:THR:HG21	1.85	0.42
4:J:12:PRO:HG3	7:K:26:TYR:CZ	2.55	0.42
5:l:39:LYS:HA	5:l:44:ALA:HA	2.02	0.42
1:g:86:ASP:HB3	1:g:136:CYS:SG	2.60	0.42
1:g:122:SER:HA	1:g:125:TYR:CD2	2.55	0.42
2:h:225:GLU:O	2:h:229:TYR:HD1	2.02	0.42
14:t:182:ARG:N	14:t:182:ARG:HD2	2.35	0.42
10:P:118:LYS:HD3	10:P:118:LYS:HA	1.84	0.42
10:P:138:VAL:HG11	10:P:146:MET:CB	2.50	0.42
15:f:607:LEU:H	15:f:607:LEU:HD12	1.84	0.42
17:a:326:GLU:OE1	27:W:373:ILE:HG13	2.20	0.42
18:b:6:THR:OG1	18:b:49:VAL:HG22	2.20	0.42
20:d:70:SER:HA	20:d:73:ARG:HE	1.84	0.42
22:U:528:ALA:O	22:U:532:MET:HG3	2.20	0.42
22:U:792:ASN:OD1	22:U:793:LYS:N	2.53	0.42
23:V:408:ARG:HA	23:V:447:ILE:HG21	2.01	0.42
23:V:423:ALA:HB2	23:V:434:ALA:HB2	2.01	0.42
25:Y:234:PRO:C	25:Y:236:LEU:N	2.74	0.42
25:Y:263:LEU:HD12	25:Y:271:PHE:CE1	2.55	0.42
27:W:355:LYS:O	27:W:359:VAL:HG23	2.20	0.42
28:A:239:ARG:HA	28:A:273:PHE:HD2	1.85	0.42
30:C:28:ILE:HD13	30:C:28:ILE:HA	1.96	0.42
30:C:127:LEU:HD12	30:C:128:PRO:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:D:58:GLU:CD	31:D:61:ILE:HD11	2.44	0.42
31:D:92:PHE:CE1	31:D:101:ALA:HB1	2.55	0.42
32:E:47:LEU:HD22	33:F:139:LEU:HD12	2.01	0.42
32:E:126:ASP:O	32:E:127:PRO:C	2.63	0.42
32:E:171:LEU:C	32:E:172:LEU:HD12	2.45	0.42
2:H:133:SER:HB2	2:H:151:PRO:HD3	2.02	0.42
3:I:92:LEU:HD21	3:I:96:ARG:HH22	1.85	0.42
5:L:107:ARG:HH12	14:T:81:HIS:HB2	1.84	0.42
7:K:30:ALA:O	7:K:33:LEU:HG	2.20	0.42
7:K:157:ASP:OD2	7:K:161:THR:HB	2.19	0.42
5:l:13:TRP:H	6:m:22:GLN:HE22	1.67	0.42
5:l:204:ASP:OD1	5:l:205:LEU:N	2.52	0.42
3:i:119:GLN:OE1	4:j:82:ILE:HG21	2.20	0.42
3:i:121:TYR:CE2	3:i:129:PRO:HA	2.54	0.42
6:m:239:ALA:O	6:m:243:LEU:HG	2.20	0.42
10:p:34:MET:HG3	10:p:183:MET:SD	2.59	0.42
13:s:199:THR:HG23	13:s:201:GLU:H	1.85	0.42
14:t:136:SER:HB2	14:t:150:LEU:HB3	2.02	0.42
14:t:141:TYR:CZ	8:N:24:SER:HB2	2.54	0.42
9:O:187:ARG:HB3	9:O:188:PRO:CD	2.48	0.42
13:S:16:ALA:HB2	13:S:121:VAL:HG23	2.02	0.42
13:S:148:LEU:O	13:S:151:ASN:OD1	2.38	0.42
14:T:100:ARG:HD3	14:T:128:LEU:HA	2.02	0.42
15:f:127:SER:OG	15:f:143:ARG:NH2	2.53	0.42
15:f:556:ARG:HG2	15:f:590:PHE:CE2	2.54	0.42
17:a:149:THR:HG23	17:a:182:CYS:HB2	2.01	0.42
20:d:45:LYS:O	20:d:49:ILE:HG13	2.20	0.42
20:d:105:PHE:HB2	20:d:166:PHE:HD2	1.84	0.42
22:U:63:VAL:HA	22:U:66:LYS:HB2	2.00	0.42
22:U:524:LYS:HA	22:U:556:MET:HB3	2.02	0.42
22:U:904:LYS:HB3	22:U:912:ILE:HG23	2.01	0.42
24:X:344:ARG:HH21	27:W:409:LEU:HB3	1.85	0.42
25:Y:56:ALA:HA	25:Y:59:LYS:NZ	2.35	0.42
33:F:397:LYS:O	33:F:401:VAL:HG12	2.20	0.42
1:G:29:PHE:CZ	1:G:155:ASP:HB2	2.55	0.42
1:g:12:HIS:CD2	6:m:6:GLY:HA3	2.55	0.42
1:g:40:VAL:HG21	1:g:201:CYS:SG	2.59	0.42
4:j:47:LYS:HZ3	4:j:59:VAL:HG13	1.85	0.42
4:j:65:LEU:HB2	4:j:69:VAL:HG12	2.02	0.42
7:k:44:GLU:HG2	7:k:44:GLU:O	2.20	0.42
11:q:20:VAL:HG13	11:q:27:GLN:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:t:97:TYR:HA	14:t:100:ARG:HG2	2.02	0.42
10:P:75:GLU:OE2	10:P:82:ILE:N	2.53	0.42
15:f:293:GLN:O	15:f:297:MET:HG3	2.20	0.42
15:f:618:GLU:HB2	15:f:620:PHE:CD2	2.55	0.42
15:f:733:GLY:O	15:f:736:THR:OG1	2.35	0.42
17:a:302:ILE:HD12	17:a:302:ILE:HA	1.94	0.42
18:b:17:ARG:NE	18:b:81:LYS:HE2	2.35	0.42
19:c:255:TYR:HE2	24:X:411:VAL:HG21	1.85	0.42
20:d:180:GLY:O	20:d:184:LYS:HG2	2.20	0.42
22:U:147:TYR:HA	22:U:150:ALA:HB3	2.01	0.42
22:U:229:VAL:HG21	22:U:252:LEU:HD13	2.02	0.42
22:U:368:ALA:HB2	22:U:728:PHE:CD1	2.55	0.42
22:U:557:TYR:CE1	22:U:757:MET:HE3	2.55	0.42
24:X:120:GLU:HB3	24:X:122:ARG:HH21	1.85	0.42
25:Y:101:ARG:HG2	25:Y:136:HIS:CE1	2.55	0.42
26:Z:233:VAL:O	26:Z:237:LEU:HG	2.19	0.42
28:A:178:GLY:HA3	34:A:501:ATP:N1	2.35	0.42
29:B:187:ILE:HA	35:B:501:ADP:C2	2.55	0.42
29:B:231:GLY:O	29:B:234:LEU:HB2	2.20	0.42
31:D:178:ARG:HA	31:D:181:VAL:HG12	2.01	0.42
32:E:72:LYS:HA	32:E:78:ARG:HA	2.02	0.42
32:E:175:PRO:HB3	32:E:280:ASN:HB3	2.02	0.42
32:E:322:LYS:HD3	32:E:322:LYS:HA	1.82	0.42
33:F:254:PRO:HD3	33:F:287:GLU:HB2	2.02	0.42
5:L:15:PRO:HA	6:M:25:TYR:CG	2.55	0.41
6:M:7:TYR:CZ	6:M:16:PRO:HG3	2.55	0.41
1:g:49:VAL:HG13	1:g:219:VAL:HG12	2.01	0.41
2:h:119:GLN:NE2	3:i:81:SER:HB3	2.35	0.41
9:o:175:LEU:HD12	9:o:189:TYR:CE1	2.55	0.41
14:t:74:GLU:HG3	14:t:83:TYR:CE1	2.54	0.41
14:t:156:LYS:HA	14:t:156:LYS:HE3	2.01	0.41
8:N:127:ILE:HD12	8:N:136:TYR:CD1	2.55	0.41
18:b:11:ASP:O	18:b:16:MET:HG3	2.20	0.41
22:U:167:ILE:HD12	22:U:204:ILE:HG12	2.01	0.41
22:U:223:LEU:HD23	22:U:225:ASP:OD2	2.20	0.41
22:U:838:LYS:NZ	22:U:842:LYS:HE3	2.35	0.41
25:Y:17:LEU:HD22	25:Y:214:MET:HG2	2.02	0.41
25:Y:220:VAL:HG11	25:Y:249:VAL:CG2	2.51	0.41
28:A:143:ASP:OD1	28:A:148:GLN:N	2.53	0.41
30:C:209:CYS:HB3	30:C:244:SER:CA	2.49	0.41
30:C:333:SER:HA	30:C:336:MET:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:D:401:LYS:O	31:D:405:THR:HG22	2.20	0.41
33:F:253:GLY:N	33:F:254:PRO:HD2	2.35	0.41
3:I:28:ILE:HG21	3:I:133:SER:CB	2.47	0.41
6:M:41:CYS:N	6:M:44:GLY:O	2.53	0.41
7:k:16:SER:N	7:k:20:ARG:O	2.54	0.41
7:k:86:LYS:HE2	7:k:86:LYS:HB3	1.92	0.41
7:k:197:SER:O	7:k:201:ILE:HG12	2.20	0.41
11:q:118:MET:HE2	11:q:118:MET:HB2	1.89	0.41
12:r:127:SER:HB3	12:r:136:TYR:HE1	1.82	0.41
12:r:168:ALA:HB2	10:P:27:ARG:NH2	2.35	0.41
14:t:203:LEU:HD23	14:t:203:LEU:HA	1.95	0.41
10:P:44:PRO:HB3	10:P:50:TYR:CE2	2.55	0.41
14:T:27:LEU:HD22	14:T:184:TYR:HB2	2.01	0.41
15:f:429:ILE:HD12	15:f:432:TYR:HB2	2.00	0.41
22:U:202:VAL:HG11	22:U:223:LEU:HB2	2.02	0.41
22:U:524:LYS:HE3	22:U:524:LYS:HB3	1.96	0.41
22:U:665:ASN:O	22:U:666:LYS:HB3	2.20	0.41
23:V:471:GLU:N	23:V:472:PRO:HD2	2.34	0.41
25:Y:26:LEU:HB3	25:Y:59:LYS:HD2	2.02	0.41
26:Z:234:PHE:HB2	27:W:438:LEU:HD23	2.02	0.41
27:W:279:PHE:HA	27:W:283:GLN:OE1	2.20	0.41
28:A:333:ARG:HB3	28:A:337:LEU:HB3	2.02	0.41
29:B:252:GLY:O	29:B:253:SER:C	2.64	0.41
2:H:203:MET:SD	2:H:230:LEU:HD21	2.61	0.41
5:l:65:HIS:CD2	13:s:77:HIS:HE1	2.38	0.41
2:h:179:ASN:O	2:h:182:LEU:HD22	2.19	0.41
3:i:145:PHE:O	3:i:146:GLN:NE2	2.54	0.41
4:j:35:VAL:HG23	4:j:158:ALA:HB2	2.01	0.41
11:q:90:ASP:OD1	11:q:91:CYS:N	2.53	0.41
8:N:58:ALA:O	8:N:61:TYR:HB3	2.20	0.41
15:f:237:VAL:HG11	15:f:249:LEU:HD21	2.01	0.41
15:f:261:ARG:HG3	15:f:261:ARG:O	2.20	0.41
15:f:333:LEU:HD11	15:f:831:VAL:HG22	2.01	0.41
15:f:737:ASN:HD21	15:f:773:LYS:C	2.25	0.41
18:b:9:CYS:HA	18:b:52:ILE:O	2.21	0.41
22:U:832:VAL:HB	22:U:836:THR:OG1	2.20	0.41
23:V:403:ILE:HG21	23:V:428:LEU:HD21	2.02	0.41
24:X:138:PHE:CZ	24:X:175:LYS:HB3	2.55	0.41
24:X:162:ASP:OD1	24:X:163:LYS:N	2.54	0.41
26:Z:54:PHE:CB	26:Z:78:MET:HE2	2.50	0.41
28:A:166:VAL:HA	28:A:238:ILE:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:B:54:PRO:HG3	29:B:60:LEU:HD23	2.01	0.41
29:B:211:TYR:HB2	29:B:216:ILE:CG1	2.50	0.41
30:C:329:LEU:HD23	30:C:348:ALA:HB2	2.01	0.41
31:D:97:ASP:HB2	31:D:100:THR:HG22	2.01	0.41
31:D:268:ASP:OD1	31:D:316:THR:OG1	2.34	0.41
32:E:116:ASP:OD1	32:E:118:LEU:HD23	2.20	0.41
2:H:145:TYR:CE2	3:I:59:VAL:HG21	2.56	0.41
2:H:172:THR:O	2:H:176:LYS:HG2	2.20	0.41
3:I:52:ILE:HG22	3:I:52:ILE:O	2.20	0.41
3:I:174:MET:SD	3:I:195:LYS:NZ	2.93	0.41
5:l:152:ASN:HA	6:m:85:ARG:NH1	2.34	0.41
1:g:68:HIS:HE2	1:g:80:MET:C	2.25	0.41
3:i:20:GLN:HG2	3:i:21:VAL:N	2.36	0.41
6:m:119:VAL:O	6:m:123:THR:HG23	2.20	0.41
8:n:44:CYS:HB2	8:n:99:ILE:HB	2.03	0.41
8:n:53:GLN:CD	9:o:119:THR:H	2.29	0.41
11:q:44:LEU:HD12	11:q:104:LEU:HD11	2.02	0.41
13:s:136:LYS:NZ	13:s:137:ALA:O	2.50	0.41
11:Q:145:ARG:O	11:Q:145:ARG:NH1	2.48	0.41
12:R:172:GLY:O	12:R:192:VAL:HG22	2.20	0.41
13:S:63:THR:O	13:S:67:ILE:HG13	2.20	0.41
15:f:753:ALA:HA	15:f:759:LEU:HD22	2.02	0.41
15:f:846:VAL:HG11	15:f:872:VAL:HG21	2.02	0.41
23:V:375:PHE:O	23:V:379:LEU:HG	2.20	0.41
27:W:192:LEU:O	27:W:196:VAL:HG23	2.20	0.41
29:B:92:GLN:OE1	29:B:96:ARG:HB2	2.19	0.41
30:C:39:SER:O	30:C:43:ARG:HG3	2.20	0.41
33:F:289:ASP:OD1	33:F:289:ASP:N	2.52	0.41
1:G:115:CYS:SG	1:G:160:TYR:HB2	2.61	0.41
3:I:78:GLY:O	30:C:402:LYS:HE3	2.20	0.41
4:J:210:VAL:HB	4:J:218:LYS:HB3	2.03	0.41
5:L:19:ILE:HD11	5:L:22:ILE:HG12	2.02	0.41
6:M:31:GLU:O	6:M:167:LYS:HA	2.19	0.41
1:g:23:TYR:HA	1:g:26:GLU:HG2	2.02	0.41
1:g:234:GLU:O	1:g:238:HIS:ND1	2.54	0.41
2:h:53:LYS:HG2	2:h:57:TYR:CE2	2.56	0.41
3:i:14:PRO:HA	4:j:21:TYR:CZ	2.55	0.41
6:m:197:ILE:HG12	6:m:211:LEU:HD11	2.02	0.41
8:n:34:LEU:O	8:n:34:LEU:HD12	2.20	0.41
9:o:40:ASN:ND2	9:o:103:VAL:O	2.43	0.41
10:p:29:GLY:HA2	10:p:35:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:r:19:ARG:NH2	10:P:205:ASP:OD2	2.54	0.41
12:r:91:LYS:HE3	12:r:91:LYS:HB2	1.91	0.41
13:S:123:SER:HB2	13:S:136:LYS:HG2	2.01	0.41
15:f:195:ASN:HD22	15:f:204:ALA:HB2	1.85	0.41
22:U:337:LEU:HG	22:U:340:GLN:HE21	1.86	0.41
23:V:325:LYS:HG2	23:V:329:HIS:NE2	2.36	0.41
23:V:383:GLY:HA2	23:V:386:PHE:CD2	2.56	0.41
25:Y:19:ILE:HD12	25:Y:19:ILE:HA	1.92	0.41
27:W:103:LYS:O	27:W:106:GLN:N	2.54	0.41
27:W:172:GLU:CD	27:W:172:GLU:H	2.29	0.41
27:W:243:ILE:HG22	27:W:273:TYR:CD2	2.55	0.41
27:W:419:LYS:HG3	27:W:424:LEU:HB2	2.03	0.41
28:A:214:LEU:HD12	28:A:341:ILE:HG13	2.01	0.41
28:A:308:GLY:HA3	28:A:336:ARG:NH1	2.35	0.41
28:A:363:SER:O	28:A:405:THR:N	2.53	0.41
30:C:242:ALA:HB3	30:C:243:PRO:HD3	2.02	0.41
31:D:338:ARG:HA	31:D:341:LYS:HB3	2.02	0.41
32:E:199:VAL:HA	32:E:233:ASP:HB3	2.03	0.41
1:G:138:MET:HB3	1:G:154:CYS:SG	2.61	0.41
2:H:58:ASP:OD1	2:H:60:ARG:N	2.53	0.41
2:H:147:PHE:CD2	2:H:155:TYR:HB2	2.55	0.41
5:L:137:TYR:CE2	5:L:217:LYS:HA	2.55	0.41
5:l:93:LEU:HD11	13:s:73:LYS:HG3	2.03	0.41
1:g:62:ASP:N	6:m:159:GLY:O	2.46	0.41
1:g:68:HIS:H	1:g:216:GLU:CD	2.29	0.41
3:i:37:ILE:HD11	3:i:44:LEU:HD12	2.02	0.41
6:m:20:VAL:HG23	6:m:20:VAL:O	2.20	0.41
6:m:42:LYS:HB3	6:m:183:GLU:HA	2.03	0.41
8:n:133:SER:HA	8:n:136:TYR:HE2	1.86	0.41
14:t:50:MET:HE2	14:t:50:MET:HB3	1.93	0.41
9:O:18:THR:OG1	9:O:172:ASN:HB2	2.21	0.41
10:P:88:MET:HG3	10:P:122:CYS:SG	2.60	0.41
13:S:6:VAL:H	13:S:57:PHE:HD2	1.68	0.41
15:f:505:MET:HE3	15:f:541:THR:HG21	2.01	0.41
18:b:121:GLU:CD	18:b:152:LYS:HG3	2.45	0.41
19:c:189:ILE:HD13	30:C:117:ARG:HD3	2.03	0.41
19:c:251:LEU:HD21	19:c:283:HIS:ND1	2.36	0.41
22:U:115:ASN:HD22	22:U:126:ILE:HD11	1.86	0.41
22:U:208:LEU:HD12	22:U:215:ASN:HD22	1.85	0.41
22:U:623:GLY:CA	22:U:659:CYS:HB3	2.50	0.41
23:V:209:LYS:HA	23:V:212:TYR:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:263:LEU:HG	23:V:266:GLN:HB3	2.03	0.41
23:V:326:GLN:O	23:V:330:LYS:HG3	2.20	0.41
23:V:337:LEU:HD21	23:V:364:THR:HG22	2.02	0.41
24:X:74:ARG:HG3	24:X:75:PRO:HD3	2.02	0.41
25:Y:16:ASP:O	25:Y:19:ILE:HG22	2.20	0.41
27:W:176:SER:HB3	32:E:147:GLU:OE2	2.20	0.41
28:A:205:GLY:N	33:F:404:GLY:O	2.52	0.41
29:B:211:TYR:O	29:B:215:GLY:N	2.53	0.41
30:C:51:GLU:O	30:C:55:LYS:HG3	2.20	0.41
31:D:102:ILE:HA	31:D:112:TYR:HA	2.02	0.41
31:D:265:ASP:OD1	31:D:266:GLU:N	2.54	0.41
32:E:267:PHE:HB3	32:E:270:LEU:HB2	2.02	0.41
33:F:76:ASN:C	33:F:76:ASN:OD1	2.63	0.41
2:H:59:GLU:HG2	2:H:206:ASP:HB2	2.01	0.41
2:H:73:GLY:HA3	2:H:218:PHE:CE1	2.55	0.41
2:H:82:ASP:CG	2:H:128:ARG:HH22	2.28	0.41
4:J:134:VAL:CG1	4:J:144:LEU:HD13	2.46	0.41
6:M:163:CYS:SG	6:M:164:ALA:N	2.93	0.41
7:K:206:MET:HE3	7:K:206:MET:HB2	1.92	0.41
7:K:220:VAL:HG22	7:K:226:PHE:CE2	2.56	0.41
5:l:85:CYS:HA	5:l:88:MET:HE2	2.03	0.41
1:g:124:VAL:O	1:g:128:ASN:ND2	2.36	0.41
7:k:202:LEU:HA	7:k:205:VAL:HG22	2.02	0.41
9:o:178:ILE:HG12	9:o:183:LEU:HD13	2.03	0.41
10:p:123:SER:HB2	10:p:137:VAL:HB	2.02	0.41
12:r:134:TYR:HE1	11:Q:140:LEU:HB2	1.85	0.41
8:N:104:ASP:OD1	8:N:110:GLN:NE2	2.54	0.41
15:f:809:ILE:HG12	15:f:814:SER:CB	2.45	0.41
17:a:58:LYS:HE2	17:a:96:PHE:CE2	2.56	0.41
17:a:346:ILE:O	17:a:349:MET:HG2	2.21	0.41
20:d:26:LEU:HD13	22:U:19:LEU:HD21	2.03	0.41
22:U:61:ALA:HB3	22:U:84:ALA:HB2	2.02	0.41
22:U:811:PHE:HB2	22:U:883:ARG:HH22	1.86	0.41
23:V:215:ALA:O	23:V:219:GLU:HG3	2.20	0.41
23:V:486:ILE:HG21	26:Z:272:LEU:HA	2.02	0.41
24:X:143:TYR:CZ	25:Y:252:SER:HB3	2.55	0.41
24:X:366:SER:HA	24:X:369:ILE:HG22	2.02	0.41
30:C:165:ILE:HD13	30:C:165:ILE:HA	1.89	0.41
30:C:260:GLU:OE1	30:C:260:GLU:N	2.47	0.41
30:C:326:LEU:HD12	30:C:326:LEU:HA	1.80	0.41
32:E:232:MET:HE3	32:E:232:MET:HB3	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:E:363:VAL:HG12	32:E:364:GLN:N	2.36	0.41
33:F:188:ILE:HA	35:F:501:ADP:N1	2.36	0.41
2:H:104:PRO:HG2	2:H:106:PRO:HB3	2.03	0.41
3:I:167:ASN:OD1	3:I:167:ASN:N	2.53	0.41
4:J:132:LEU:CD2	4:J:159:ASN:HD22	2.30	0.41
5:l:95:SER:OG	5:l:101:ARG:NH1	2.53	0.41
6:m:23:VAL:O	6:m:27:MET:HG3	2.21	0.41
11:q:49:GLU:O	11:q:53:THR:HG23	2.21	0.41
11:q:107:TYR:HA	11:q:113:PRO:HA	2.03	0.41
12:r:31:VAL:HA	13:s:131:GLN:OE1	2.21	0.41
14:t:68:GLY:O	14:t:72:ILE:HG12	2.20	0.41
14:t:172:CYS:O	14:t:176:LEU:HD23	2.21	0.41
8:N:114:VAL:HA	8:N:119:MET:O	2.20	0.41
8:N:199:VAL:O	8:N:199:VAL:HG23	2.21	0.41
9:O:55:THR:O	9:O:59:ILE:HG12	2.20	0.41
11:Q:85:ARG:NH2	10:P:61:GLN:HB2	2.35	0.41
14:T:14:VAL:HG11	14:T:150:LEU:HD22	2.02	0.41
17:a:36:GLN:O	17:a:40:GLN:HG2	2.20	0.41
17:a:213:PHE:O	17:a:216:LEU:HG	2.20	0.41
17:a:323:SER:H	17:a:332:HIS:HB3	1.84	0.41
18:b:3:LEU:HD11	18:b:44:ASN:ND2	2.29	0.41
18:b:100:ARG:NH2	18:b:101:GLN:O	2.37	0.41
19:c:39:LEU:CD1	26:Z:17:LEU:HD21	2.51	0.41
20:d:40:GLY:O	20:d:45:LYS:NZ	2.52	0.41
22:U:524:LYS:HD3	22:U:559:ARG:NE	2.36	0.41
23:V:361:PHE:O	23:V:364:THR:OG1	2.29	0.41
24:X:397:TYR:CE2	25:Y:362:LYS:HG2	2.56	0.41
25:Y:101:ARG:HH21	25:Y:136:HIS:HB3	1.85	0.41
27:W:63:THR:O	27:W:67:LEU:HG	2.21	0.41
28:A:70:THR:HG22	28:A:71:GLY:N	2.36	0.41
28:A:232:ARG:HH12	28:A:271:LEU:HD13	1.85	0.41
28:A:237:PHE:CD1	28:A:237:PHE:C	2.99	0.41
32:E:171:LEU:O	32:E:299:ILE:HG13	2.20	0.41
33:F:322:PRO:C	33:F:324:THR:H	2.28	0.41
1:G:104:LYS:HE3	1:G:104:LYS:HB3	1.77	0.41
2:H:32:GLY:N	31:D:417:TYR:OH	2.54	0.41
2:H:97:TYR:CD1	2:H:110:LEU:HD13	2.56	0.41
2:H:117:VAL:C	2:H:119:GLN:H	2.29	0.41
3:I:92:LEU:HG	3:I:96:ARG:HH12	1.85	0.41
4:J:40:ILE:HD13	4:J:184:ASP:OD1	2.20	0.41
7:K:52:LYS:HD2	7:K:216:GLU:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:l:72:ILE:HD12	5:l:132:LEU:HD22	2.03	0.41
5:l:139:ASP:N	5:l:139:ASP:OD1	2.53	0.41
1:g:75:ASN:OD1	1:g:76:ILE:HG13	2.21	0.41
1:g:119:ALA:HB1	2:h:84:ARG:NH2	2.35	0.41
3:i:106:PRO:HB2	3:i:109:GLN:HG2	2.03	0.41
3:i:149:GLN:HB2	3:i:162:THR:HG21	2.02	0.41
4:j:82:ILE:HG13	4:j:83:VAL:N	2.36	0.41
8:n:115:PRO:HD2	8:n:119:MET:SD	2.61	0.41
10:p:47:ASP:OD1	10:p:48:ARG:N	2.53	0.41
11:q:2:GLU:OE1	11:q:2:GLU:N	2.41	0.41
11:q:7:ILE:HD11	11:q:14:LEU:HD23	2.02	0.41
11:q:172:ILE:HD12	11:Q:22:ALA:CB	2.51	0.41
11:q:184:ASP:OD1	11:q:184:ASP:N	2.54	0.41
13:s:70:ALA:O	13:s:74:MET:HG3	2.21	0.41
9:O:76:VAL:HG23	9:O:104:ASP:OD1	2.21	0.41
15:f:249:LEU:O	15:f:253:LEU:HD23	2.21	0.41
15:f:829:MET:HA	15:f:872:VAL:O	2.20	0.41
17:a:9:GLN:O	17:a:12:GLN:HG2	2.21	0.41
17:a:115:LYS:HE3	17:a:115:LYS:HB3	1.90	0.41
17:a:245:VAL:HG23	17:a:246:GLU:N	2.36	0.41
17:a:247:ARG:NH1	17:a:269:LEU:HD23	2.36	0.41
17:a:303:THR:O	17:a:307:VAL:HG23	2.21	0.41
18:b:91:ARG:HE	18:b:95:LEU:CD1	2.33	0.41
19:c:229:LEU:HD11	26:Z:201:LEU:HB2	2.03	0.41
20:d:185:ALA:HB3	23:V:442:ILE:HD11	2.01	0.41
22:U:250:PHE:CE1	22:U:328:ILE:HD12	2.55	0.41
22:U:405:THR:HG23	22:U:444:TYR:HD2	1.86	0.41
22:U:406:ALA:HB2	22:U:444:TYR:HE2	1.85	0.41
22:U:532:MET:O	22:U:548:LEU:HD21	2.21	0.41
22:U:761:VAL:HA	22:U:764:LEU:HD12	2.03	0.41
22:U:766:PHE:CD1	22:U:779:LEU:HD22	2.56	0.41
23:V:115:LYS:HZ3	23:V:147:PHE:HZ	1.69	0.41
23:V:254:LEU:HD21	23:V:270:LEU:HD13	2.03	0.41
23:V:258:TYR:CE1	23:V:263:LEU:HD23	2.56	0.41
23:V:290:TYR:OH	23:V:327:THR:HB	2.21	0.41
23:V:292:THR:O	23:V:296:LYS:HG2	2.21	0.41
24:X:256:LEU:HD13	24:X:319:ILE:HD13	2.02	0.41
24:X:264:PRO:HA	24:X:267:VAL:HG23	2.03	0.41
25:Y:179:ARG:HD3	25:Y:182:VAL:HG23	2.02	0.41
25:Y:231:LEU:HD21	25:Y:236:LEU:HD13	2.02	0.41
26:Z:251:LEU:HB2	27:W:425:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:246:HIS:O	27:W:250:ILE:HG23	2.20	0.41
28:A:153:LEU:O	28:A:155:PRO:HD3	2.21	0.41
28:A:425:ALA:HB3	29:B:342:ILE:HG23	2.02	0.41
29:B:235:LEU:O	29:B:239:VAL:HG13	2.21	0.41
31:D:132:LEU:HA	31:D:138:ALA:O	2.21	0.41
31:D:240:LEU:HA	31:D:288:ILE:HD11	2.03	0.41
31:D:290:LEU:HD23	31:D:290:LEU:HA	1.84	0.41
31:D:359:ASP:OD1	31:D:362:ASP:HB3	2.21	0.41
32:E:62:LYS:HB3	32:E:70:ILE:HB	2.03	0.41
1:G:72:ILE:HG13	1:G:78:CYS:SG	2.61	0.41
2:H:103:GLU:N	2:H:104:PRO:HD3	2.36	0.41
5:L:39:LYS:HG3	5:L:142:PRO:HG2	2.02	0.41
6:M:21:PHE:HA	6:M:24:GLU:HB2	2.01	0.41
6:m:49:VAL:HG21	6:m:65:ARG:HB2	2.03	0.41
12:r:25:TYR:CZ	13:s:143:ALA:HA	2.56	0.41
9:O:8:TYR:HE2	9:O:10:ASP:HB2	1.86	0.41
14:T:99:ARG:NH1	14:T:106:LEU:HD21	2.36	0.41
15:f:345:PRO:O	15:f:763:ARG:NH2	2.53	0.41
17:a:217:LEU:HD12	17:a:237:LEU:O	2.20	0.41
18:b:8:VAL:HG23	18:b:110:ILE:HG23	2.03	0.41
19:c:223:LYS:HE2	19:c:225:TRP:CD1	2.56	0.41
20:d:182:ILE:HG22	20:d:186:TYR:CE2	2.55	0.41
21:e:45:ASP:CG	25:Y:293:ARG:HB3	2.46	0.41
22:U:475:HIS:HE2	22:U:507:VAL:C	2.27	0.41
22:U:584:TYR:O	22:U:588:MET:HG2	2.21	0.41
22:U:722:ASP:HB3	22:U:727:LYS:HG3	2.02	0.41
22:U:845:GLU:O	22:U:848:LYS:HG2	2.20	0.41
23:V:440:LYS:HG2	23:V:443:ARG:HE	1.86	0.41
25:Y:24:PHE:CE2	25:Y:286:TRP:HA	2.56	0.41
27:W:31:CYS:HB3	27:W:43:VAL:CG2	2.51	0.41
27:W:169:LEU:HA	27:W:182:ARG:HH22	1.85	0.41
27:W:183:VAL:O	27:W:187:LEU:HG	2.21	0.41
30:C:46:GLN:HE22	31:D:69:LYS:CA	2.34	0.41
30:C:337:ASN:OD1	30:C:338:LEU:N	2.54	0.41
32:E:235:ILE:HD11	32:E:253:ILE:HG23	2.03	0.41
2:H:22:ILE:HD13	2:H:22:ILE:HA	1.91	0.40
2:H:130:PHE:O	2:H:151:PRO:HB3	2.21	0.40
2:H:178:TYR:O	2:H:180:GLU:HB2	2.22	0.40
3:I:114:LEU:HD12	3:I:114:LEU:HA	1.84	0.40
6:M:74:GLY:HA3	6:M:224:HIS:CE1	2.57	0.40
6:M:107:PRO:HG2	6:M:110:HIS:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:53:GLN:HE22	1:g:55:LYS:HG3	1.86	0.40
1:g:162:GLY:HA3	2:h:61:SER:HB3	2.01	0.40
2:h:25:ALA:O	2:h:29:VAL:HG23	2.21	0.40
3:i:164:ILE:HD12	3:i:164:ILE:HA	1.93	0.40
4:j:10:PHE:CE2	7:k:135:ARG:HB2	2.56	0.40
4:j:112:ALA:HB1	4:j:151:GLY:O	2.21	0.40
7:k:211:ASN:CG	7:k:212:ALA:H	2.29	0.40
11:q:15:VAL:HG11	11:q:105:ALA:HB2	2.02	0.40
11:q:39:SER:OG	11:q:40:GLU:N	2.53	0.40
14:t:179:ARG:HA	8:N:26:ILE:HB	2.04	0.40
8:N:7:GLN:HA	8:N:12:VAL:HG12	2.02	0.40
8:N:35:THR:OG1	8:N:43:CYS:HB3	2.20	0.40
8:N:36:PRO:HB3	8:N:42:PHE:CZ	2.56	0.40
9:O:34:ILE:HG12	9:O:44:CYS:SG	2.61	0.40
11:Q:108:ASP:HB3	11:Q:111:GLU:HG3	2.02	0.40
12:R:37:ILE:HD11	12:R:56:GLU:HB3	2.02	0.40
13:S:13:LEU:HD13	13:S:137:ALA:HB2	2.03	0.40
15:f:322:SER:HB3	15:f:456:ARG:O	2.21	0.40
15:f:679:LEU:HB3	15:f:713:PHE:CE2	2.56	0.40
15:f:722:SER:O	15:f:726:ILE:HG12	2.22	0.40
18:b:12:ASN:HD21	18:b:75:LEU:HD11	1.86	0.40
18:b:71:ILE:HD12	18:b:71:ILE:H	1.86	0.40
22:U:459:ASP:O	22:U:462:LEU:HG	2.21	0.40
22:U:624:PHE:CD1	22:U:760:VAL:HG13	2.55	0.40
23:V:322:VAL:O	23:V:326:GLN:HG3	2.21	0.40
23:V:481:SER:O	23:V:484:LEU:HG	2.21	0.40
24:X:158:LYS:HE3	24:X:158:LYS:HB2	1.96	0.40
24:X:162:ASP:O	24:X:166:LEU:HD23	2.20	0.40
24:X:289:CYS:O	24:X:292:GLN:HG2	2.21	0.40
24:X:331:LEU:HB3	24:X:364:LYS:HE3	2.04	0.40
24:X:341:PRO:O	27:W:406:VAL:HG12	2.21	0.40
29:B:80:ARG:O	29:B:83:GLU:HG2	2.21	0.40
29:B:133:VAL:HG21	29:B:158:ALA:HA	2.03	0.40
30:C:188:LEU:HB2	30:C:293:MET:O	2.21	0.40
32:E:48:LYS:HE2	33:F:72:LYS:HD2	2.03	0.40
1:G:77:GLY:HA3	1:G:227:PHE:CD1	2.56	0.40
3:I:13:SER:OG	3:I:17:ARG:N	2.39	0.40
3:I:86:LEU:HD12	3:I:86:LEU:HA	1.81	0.40
3:I:238:LYS:O	3:I:242:GLU:HG3	2.21	0.40
4:J:191:VAL:HG11	4:J:208:LEU:HD21	2.03	0.40
6:M:232:ARG:HA	6:M:232:ARG:HD3	1.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:l:238:GLU:HG3	5:l:239:ARG:H	1.86	0.40
1:g:132:ARG:HA	1:g:133:PRO:HD3	1.93	0.40
1:g:158:GLY:O	2:h:84:ARG:NH2	2.54	0.40
7:k:32:LYS:HE2	7:k:32:LYS:HB3	1.87	0.40
6:m:102:PHE:HB3	8:n:78:THR:HG23	2.02	0.40
8:n:21:THR:HG22	8:n:26:ILE:HA	2.02	0.40
8:n:161:ALA:HA	8:n:164:MET:HG2	2.03	0.40
10:p:30:ILE:CG2	10:p:33:GLN:HG2	2.49	0.40
14:t:142:GLY:HA2	14:t:176:LEU:HD11	2.04	0.40
9:O:76:VAL:H	9:O:104:ASP:CG	2.26	0.40
9:O:76:VAL:N	9:O:104:ASP:OD2	2.38	0.40
12:R:166:ARG:HD3	12:R:166:ARG:HA	1.87	0.40
14:T:176:LEU:HD23	14:T:176:LEU:HA	1.96	0.40
17:a:44:PHE:HE2	17:a:57:ILE:HG12	1.86	0.40
18:b:18:ASN:OD1	18:b:25:ARG:NH1	2.54	0.40
18:b:109:ILE:O	18:b:138:VAL:HA	2.21	0.40
20:d:56:GLU:O	20:d:60:GLN:HG3	2.22	0.40
20:d:178:ILE:O	20:d:182:ILE:HG12	2.20	0.40
22:U:246:TYR:O	22:U:250:PHE:HD1	2.04	0.40
22:U:323:LEU:H	22:U:323:LEU:HD12	1.85	0.40
23:V:394:LEU:H	23:V:394:LEU:HD12	1.85	0.40
24:X:252:LYS:HG3	24:X:287:LEU:HD11	2.02	0.40
25:Y:48:ASN:HB3	25:Y:74:LYS:HE3	2.02	0.40
28:A:205:GLY:H	33:F:404:GLY:C	2.29	0.40
29:B:150:VAL:HG12	29:B:162:VAL:HG23	2.04	0.40
30:C:32:GLN:OE1	31:D:55:GLU:HA	2.22	0.40
30:C:97:VAL:HG22	30:C:98:ASP:N	2.36	0.40
30:C:189:TYR:O	30:C:317:PHE:N	2.49	0.40
31:D:172:ILE:HG23	31:D:334:PRO:HD2	2.02	0.40
32:E:97:ARG:HH21	32:E:111:LEU:HB3	1.85	0.40
33:F:325:GLN:OE1	33:F:326:VAL:HG23	2.22	0.40
1:G:49:VAL:CG1	1:G:219:VAL:HG22	2.48	0.40
1:G:191:PHE:CE1	1:G:219:VAL:HG11	2.56	0.40
7:K:22:PHE:C	7:K:24:VAL:H	2.28	0.40
5:l:40:SER:HB3	5:l:187:LEU:HD22	2.03	0.40
1:g:69:LEU:HD23	1:g:79:VAL:HB	2.02	0.40
2:h:119:GLN:O	2:h:123:GLN:HG2	2.21	0.40
11:Q:36:PHE:HB2	11:Q:44:LEU:HB3	2.03	0.40
13:S:46:LEU:HB3	13:S:72:LEU:HD11	2.04	0.40
15:f:72:ARG:O	15:f:76:GLU:HG2	2.21	0.40
15:f:237:VAL:HG13	15:f:245:ASN:OD1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:f:300:ARG:HH12	15:f:782:HIS:CE1	2.39	0.40
15:f:699:VAL:HG13	15:f:779:CYS:HA	2.03	0.40
17:a:75:SER:O	17:a:79:ILE:HG12	2.21	0.40
17:a:290:GLN:HA	17:a:330:ARG:HG3	2.02	0.40
19:c:249:LEU:HB2	24:X:403:THR:HG22	2.03	0.40
22:U:246:TYR:CD2	22:U:913:ILE:HD12	2.57	0.40
22:U:615:ARG:O	22:U:619:VAL:HG22	2.21	0.40
22:U:773:PHE:N	22:U:774:PRO:HD2	2.37	0.40
27:W:27:ARG:HG2	27:W:31:CYS:SG	2.61	0.40
27:W:48:LEU:HA	27:W:51:GLU:HG2	2.03	0.40
27:W:373:ILE:HG22	27:W:413:ILE:HD11	2.03	0.40
29:B:282:VAL:HB	29:B:327:VAL:HG13	2.03	0.40
30:C:307:ARG:N	30:C:308:PRO:HD2	2.36	0.40
31:D:178:ARG:O	31:D:182:GLU:HG2	2.21	0.40
33:F:308:ARG:O	33:F:311:LEU:HD12	2.21	0.40
1:G:86:ASP:HB3	1:G:134:LEU:HB3	2.04	0.40
1:G:164:LYS:HB3	1:G:164:LYS:HE2	1.88	0.40
2:H:108:ALA:HB3	2:H:140:ASN:C	2.47	0.40
3:I:33:THR:HA	3:I:165:GLY:CA	2.49	0.40
4:J:164:GLY:O	4:J:168:VAL:HG12	2.22	0.40
3:i:143:TYR:HB2	3:i:146:GLN:HG3	2.02	0.40
7:k:28:ILE:O	7:k:31:ILE:HB	2.20	0.40
7:k:220:VAL:HG22	7:k:226:PHE:HD1	1.87	0.40
7:k:221:GLN:OE1	7:k:221:GLN:N	2.54	0.40
6:m:184:MET:HB3	6:m:189:ILE:HD11	2.02	0.40
8:n:28:ASN:ND2	9:o:122:LEU:HD13	2.36	0.40
10:p:135:ASP:HA	10:p:154:TRP:CZ2	2.57	0.40
11:q:29:LYS:HD2	12:r:122:SER:O	2.22	0.40
11:q:172:ILE:O	11:Q:174:ASN:N	2.48	0.40
14:t:18:GLY:HA2	14:t:115:TYR:CE1	2.56	0.40
14:t:211:ILE:HG13	8:N:30:VAL:HG11	2.03	0.40
12:R:113:TYR:CZ	12:R:115:ASP:HB2	2.57	0.40
15:f:686:LEU:O	15:f:690:VAL:HG23	2.21	0.40
17:a:4:VAL:HB	17:a:5:PRO:HD3	2.04	0.40
17:a:122:LYS:HB3	17:a:131:THR:HG22	2.03	0.40
17:a:241:ASN:HA	17:a:339:ARG:NH2	2.37	0.40
17:a:289:ARG:HD2	17:a:332:HIS:ND1	2.37	0.40
19:c:142:ALA:O	19:c:159:ALA:HA	2.22	0.40
19:c:263:ASP:O	19:c:267:PRO:HG3	2.21	0.40
20:d:197:ILE:H	20:d:197:ILE:HD12	1.87	0.40
22:U:21:GLU:OE1	22:U:56:SER:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:22:PHE:HA	22:U:25:HIS:ND1	2.36	0.40
23:V:110:HIS:CB	23:V:138:PRO:HD3	2.50	0.40
23:V:167:LEU:HD12	23:V:168:GLN:N	2.36	0.40
26:Z:204:LYS:O	26:Z:208:ILE:HG13	2.21	0.40
27:W:268:LYS:HB3	27:W:301:LYS:NZ	2.36	0.40
2:H:108:ALA:HA	2:H:111:VAL:HG12	2.03	0.40
2:H:187:ALA:O	2:H:190:THR:OG1	2.27	0.40
2:H:230:LEU:HD23	2:H:230:LEU:HA	1.93	0.40
3:I:68:LEU:HD12	3:I:69:ASN:CB	2.52	0.40
7:K:135:ARG:H	7:K:135:ARG:HG3	1.58	0.40
2:h:39:LYS:HZ1	2:h:144:PRO:C	2.29	0.40
2:h:219:ARG:HH11	2:h:221:LEU:HD23	1.87	0.40
7:k:241:ILE:HD13	7:k:241:ILE:HA	1.96	0.40
6:m:27:MET:HA	6:m:30:VAL:HG12	2.03	0.40
8:n:144:ARG:O	8:n:147:MET:HG3	2.22	0.40
9:o:75:ARG:HB3	9:o:77:VAL:HG22	2.02	0.40
9:o:127:MET:C	9:o:131:SER:HB2	2.47	0.40
12:r:51:ASP:HA	13:s:97:TYR:HE2	1.86	0.40
11:Q:160:LEU:HA	11:Q:163:CYS:SG	2.62	0.40
15:f:171:GLN:HE21	22:U:838:LYS:CE	2.34	0.40
15:f:251:CYS:O	15:f:255:VAL:HG23	2.21	0.40
15:f:845:ARG:HE	15:f:883:ALA:HA	1.87	0.40
17:a:38:THR:HG21	17:a:75:SER:OG	2.22	0.40
17:a:294:GLU:O	17:a:298:LYS:HG3	2.21	0.40
22:U:574:LYS:O	22:U:579:ARG:NH1	2.53	0.40
22:U:607:VAL:HB	31:D:68:LEU:HD11	2.03	0.40
24:X:185:LYS:HZ1	25:Y:244:ALA:HB3	1.86	0.40
24:X:346:GLN:HG3	24:X:348:GLU:OE2	2.21	0.40
25:Y:23:ARG:HH22	25:Y:52:PRO:HB2	1.87	0.40
26:Z:211:TYR:CD1	27:W:446:ILE:HB	2.57	0.40
27:W:312:MET:HG3	27:W:365:ILE:HG22	2.04	0.40
30:C:203:VAL:HA	30:C:206:HIS:HB2	2.03	0.40
30:C:209:CYS:HB2	30:C:245:ILE:HG23	2.02	0.40
33:F:225:MET:HE2	33:F:225:MET:HB3	1.95	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	235/246 (96%)	216 (92%)	18 (8%)	1 (0%)	30	61
1	g	241/246 (98%)	229 (95%)	12 (5%)	0	100	100
2	H	224/234 (96%)	191 (85%)	33 (15%)	0	100	100
2	h	230/234 (98%)	220 (96%)	10 (4%)	0	100	100
3	I	245/261 (94%)	230 (94%)	15 (6%)	0	100	100
3	i	248/261 (95%)	237 (96%)	11 (4%)	0	100	100
4	J	235/248 (95%)	201 (86%)	31 (13%)	3 (1%)	9	39
4	j	236/248 (95%)	226 (96%)	10 (4%)	0	100	100
5	L	235/269 (87%)	225 (96%)	9 (4%)	1 (0%)	30	61
5	l	235/269 (87%)	226 (96%)	9 (4%)	0	100	100
6	M	236/255 (92%)	221 (94%)	14 (6%)	1 (0%)	30	61
6	m	238/255 (93%)	231 (97%)	7 (3%)	0	100	100
7	K	218/241 (90%)	207 (95%)	11 (5%)	0	100	100
7	k	232/241 (96%)	223 (96%)	9 (4%)	0	100	100
8	N	201/239 (84%)	197 (98%)	4 (2%)	0	100	100
8	n	200/239 (84%)	194 (97%)	6 (3%)	0	100	100
9	O	218/277 (79%)	212 (97%)	5 (2%)	1 (0%)	24	57
9	o	218/277 (79%)	210 (96%)	8 (4%)	0	100	100
10	P	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	p	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
11	Q	194/201 (96%)	190 (98%)	4 (2%)	0	100	100
11	q	194/201 (96%)	189 (97%)	5 (3%)	0	100	100
12	R	199/263 (76%)	194 (98%)	5 (2%)	0	100	100
12	r	199/263 (76%)	195 (98%)	4 (2%)	0	100	100
13	S	210/241 (87%)	205 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	s	211/241 (88%)	200 (95%)	11 (5%)	0	100	100
14	T	214/264 (81%)	207 (97%)	7 (3%)	0	100	100
14	t	214/264 (81%)	208 (97%)	6 (3%)	0	100	100
15	f	815/908 (90%)	775 (95%)	40 (5%)	0	100	100
16	x	83/230 (36%)	82 (99%)	1 (1%)	0	100	100
17	a	371/376 (99%)	343 (92%)	28 (8%)	0	100	100
18	b	189/377 (50%)	178 (94%)	10 (5%)	1 (0%)	24	57
19	c	285/310 (92%)	249 (87%)	36 (13%)	0	100	100
20	d	250/350 (71%)	215 (86%)	34 (14%)	1 (0%)	30	61
21	e	48/70 (69%)	43 (90%)	5 (10%)	0	100	100
22	U	853/953 (90%)	797 (93%)	56 (7%)	0	100	100
23	V	442/534 (83%)	424 (96%)	18 (4%)	0	100	100
24	X	378/422 (90%)	364 (96%)	13 (3%)	1 (0%)	36	65
25	Y	378/389 (97%)	342 (90%)	34 (9%)	2 (0%)	24	57
26	Z	284/324 (88%)	257 (90%)	26 (9%)	1 (0%)	30	61
27	W	442/456 (97%)	413 (93%)	27 (6%)	2 (0%)	24	57
28	A	401/433 (93%)	349 (87%)	47 (12%)	5 (1%)	10	41
29	B	398/440 (90%)	337 (85%)	56 (14%)	5 (1%)	9	39
30	C	362/398 (91%)	314 (87%)	45 (12%)	3 (1%)	16	49
31	D	370/418 (88%)	309 (84%)	55 (15%)	6 (2%)	7	36
32	E	359/403 (89%)	319 (89%)	37 (10%)	3 (1%)	16	49
33	F	348/439 (79%)	314 (90%)	29 (8%)	5 (1%)	9	38
All	All	13220/15118 (87%)	12297 (93%)	881 (7%)	42 (0%)	37	65

All (42) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	164	LYS
4	J	199	VAL
6	M	104	TYR
29	B	256	ILE
29	B	435	PRO
30	C	87	VAL
33	F	170	SER

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Mol	Chain	Res	Type
4	J	182	GLU
9	O	187	ARG
20	d	93	ALA
26	Z	144	VAL
28	A	73	ALA
28	A	172	VAL
28	A	206	ILE
29	B	205	LEU
29	B	253	SER
30	C	230	MET
30	C	246	ILE
31	D	164	TYR
31	D	172	ILE
32	E	130	VAL
25	Y	212	GLU
27	W	117	ASP
28	A	108	ASP
31	D	151	ILE
27	W	140	ILE
31	D	82	ILE
31	D	231	VAL
33	F	137	ILE
33	F	326	VAL
32	E	64	LEU
32	E	238	ILE
5	L	63	ILE
18	b	23	PRO
29	B	145	GLU
31	D	406	VAL
24	X	318	ILE
25	Y	234	PRO
28	A	177	VAL
33	F	279	ALA
4	J	98	VAL
33	F	136	VAL

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	201/210 (96%)	200 (100%)	1 (0%)	81	80
1	g	206/210 (98%)	206 (100%)	0	100	100
2	H	184/191 (96%)	183 (100%)	1 (0%)	81	80
2	h	189/191 (99%)	189 (100%)	0	100	100
3	I	204/221 (92%)	204 (100%)	0	100	100
3	i	210/221 (95%)	210 (100%)	0	100	100
4	J	200/211 (95%)	198 (99%)	2 (1%)	68	75
4	j	202/211 (96%)	202 (100%)	0	100	100
5	L	203/230 (88%)	201 (99%)	2 (1%)	68	75
5	l	203/230 (88%)	203 (100%)	0	100	100
6	M	195/212 (92%)	192 (98%)	3 (2%)	57	70
6	m	198/212 (93%)	198 (100%)	0	100	100
7	K	187/203 (92%)	182 (97%)	5 (3%)	39	61
7	k	196/203 (97%)	196 (100%)	0	100	100
8	N	158/181 (87%)	158 (100%)	0	100	100
8	n	157/181 (87%)	157 (100%)	0	100	100
9	O	181/228 (79%)	181 (100%)	0	100	100
9	o	181/228 (79%)	181 (100%)	0	100	100
10	P	173/174 (99%)	173 (100%)	0	100	100
10	p	173/174 (99%)	173 (100%)	0	100	100
11	Q	167/171 (98%)	166 (99%)	1 (1%)	78	79
11	q	167/171 (98%)	167 (100%)	0	100	100
12	R	156/202 (77%)	156 (100%)	0	100	100
12	r	156/202 (77%)	156 (100%)	0	100	100
13	S	177/199 (89%)	177 (100%)	0	100	100
13	s	178/199 (89%)	178 (100%)	0	100	100
14	T	179/215 (83%)	179 (100%)	0	100	100
14	t	179/215 (83%)	179 (100%)	0	100	100
15	f	682/763 (89%)	682 (100%)	0	100	100
16	x	73/207 (35%)	73 (100%)	0	100	100
17	a	329/336 (98%)	329 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	b	167/312 (54%)	167 (100%)	0	100	100
19	c	247/268 (92%)	247 (100%)	0	100	100
20	d	224/294 (76%)	224 (100%)	0	100	100
21	e	42/63 (67%)	42 (100%)	0	100	100
22	U	727/816 (89%)	727 (100%)	0	100	100
23	V	388/460 (84%)	388 (100%)	0	100	100
24	X	326/362 (90%)	326 (100%)	0	100	100
25	Y	320/344 (93%)	320 (100%)	0	100	100
26	Z	252/295 (85%)	252 (100%)	0	100	100
27	W	402/416 (97%)	402 (100%)	0	100	100
28	A	338/372 (91%)	334 (99%)	4 (1%)	63	73
29	B	333/385 (86%)	327 (98%)	6 (2%)	51	68
30	C	313/346 (90%)	312 (100%)	1 (0%)	86	83
31	D	314/366 (86%)	313 (100%)	1 (0%)	86	83
32	E	299/353 (85%)	298 (100%)	1 (0%)	86	83
33	F	290/379 (76%)	290 (100%)	0	100	100
All	All	11226/12833 (88%)	11198 (100%)	28 (0%)	85	85

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	69	LEU
2	H	71	HIS
4	J	91	CYS
4	J	220	LEU
5	L	38	LEU
5	L	99	PHE
6	M	23	VAL
6	M	35	THR
6	M	52	LEU
7	K	31	ILE
7	K	84	ASP
7	K	108	THR
7	K	135	ARG
7	K	210	LEU
11	Q	193	ASN

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Mol	Chain	Res	Type
28	A	222	LYS
28	A	223	THR
28	A	238	ILE
28	A	297	ARG
29	B	160	ILE
29	B	187	ILE
29	B	210	TYR
29	B	334	ILE
29	B	347	ILE
29	B	365	PHE
30	C	329	LEU
31	D	414	HIS
32	E	339	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (120) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	128	ASN
2	H	42	ASN
2	H	119	GLN
2	H	123	GLN
2	H	166	ASN
2	H	207	ASN
3	I	30	HIS
3	I	40	ASN
3	I	102	GLN
3	I	155	ASN
4	J	92	GLN
5	L	86	ASN
5	L	117	GLN
7	K	23	GLN
7	K	178	GLN
7	K	221	GLN
5	l	117	GLN
1	g	53	GLN
1	g	147	GLN
1	g	193	GLN
2	h	95	GLN
2	h	119	GLN
2	h	189	HIS
3	i	109	GLN
4	j	18	GLN

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Mol	Chain	Res	Type
7	k	23	GLN
6	m	105	ASN
9	o	62	ASN
9	o	193	ASN
10	p	93	ASN
10	p	173	ASN
11	q	27	GLN
11	q	71	ASN
11	q	87	ASN
11	q	101	ASN
11	q	132	HIS
11	q	174	ASN
12	r	119	ASN
12	r	151	GLN
13	s	77	HIS
13	s	151	ASN
13	s	157	ASN
14	t	188	GLN
8	N	110	GLN
8	N	123	GLN
8	N	158	ASN
9	O	66	HIS
10	P	93	ASN
10	P	145	GLN
10	P	173	ASN
13	S	80	ASN
14	T	188	GLN
15	f	148	GLN
15	f	171	GLN
15	f	323	ASN
15	f	473	ASN
15	f	566	HIS
15	f	605	ASN
15	f	724	ASN
15	f	815	HIS
16	x	56	GLN
17	a	10	GLN
17	a	143	ASN
17	a	249	GLN
17	a	337	GLN
18	b	12	ASN
18	b	47	ASN

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Mol	Chain	Res	Type
18	b	101	GLN
19	c	113	HIS
19	c	237	HIS
20	d	10	ASN
20	d	47	GLN
20	d	97	GLN
20	d	141	GLN
20	d	221	ASN
20	d	230	GLN
22	U	89	ASN
22	U	107	HIS
22	U	373	ASN
22	U	389	ASN
22	U	718	ASN
22	U	768	GLN
22	U	874	ASN
23	V	64	GLN
23	V	185	GLN
23	V	329	HIS
23	V	350	GLN
23	V	365	GLN
23	V	376	ASN
23	V	400	HIS
24	X	182	ASN
24	X	416	ASN
25	Y	48	ASN
25	Y	306	GLN
26	Z	189	GLN
26	Z	229	GLN
26	Z	235	ASN
26	Z	282	ASN
27	W	99	GLN
27	W	156	ASN
27	W	395	ASN
27	W	426	ASN
29	B	314	ASN
29	B	425	ASN
30	C	46	GLN
30	C	67	GLN
30	C	157	GLN
30	C	206	HIS
30	C	270	GLN

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Mol	Chain	Res	Type
31	D	99	ASN
31	D	135	HIS
31	D	193	GLN
31	D	295	GLN
31	D	353	ASN
31	D	414	HIS
32	E	129	ASN
32	E	300	HIS
32	E	345	ASN
33	F	208	HIS
33	F	417	HIS

5.3.3 RNA [i](#)

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](#)

6 ligands are modelled in this entry.

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
35	ADP	E	501	-	28,29,29	1.42	4 (14%)	43,45,45	1.84	9 (20%)
35	ADP	F	501	-	28,29,29	1.45	4 (14%)	43,45,45	1.87	9 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	ADP	C	501	-	28,29,29	1.47	5 (17%)	43,45,45	1.87	10 (23%)
35	ADP	D	501	-	28,29,29	1.41	4 (14%)	43,45,45	1.92	8 (18%)
35	ADP	B	501	-	28,29,29	1.45	5 (17%)	43,45,45	1.83	10 (23%)
34	ATP	A	501	-	32,33,33	0.27	0	48,52,52	0.30	0

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
35	ADP	E	501	-	-	4/16/32/32	0/3/3/3
35	ADP	F	501	-	-	3/16/32/32	0/3/3/3
35	ADP	C	501	-	-	6/16/32/32	0/3/3/3
35	ADP	D	501	-	-	7/16/32/32	0/3/3/3
35	ADP	B	501	-	-	3/16/32/32	0/3/3/3
34	ATP	A	501	-	-	6/22/38/38	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	F	501	ADP	C5-C4	4.90	1.47	1.39
35	C	501	ADP	C5-C4	4.82	1.47	1.39
35	E	501	ADP	C5-C4	4.71	1.47	1.39
35	B	501	ADP	C5-C4	4.69	1.47	1.39
35	D	501	ADP	C5-C4	4.66	1.47	1.39
35	F	501	ADP	C5-C6	2.86	1.49	1.41
35	C	501	ADP	C5-C6	2.73	1.48	1.41
35	B	501	ADP	C5-C6	2.72	1.48	1.41
35	C	501	ADP	PA-O3A	2.70	1.62	1.59
35	E	501	ADP	C5-C6	2.70	1.48	1.41
35	D	501	ADP	C5-C6	2.69	1.48	1.41
35	B	501	ADP	PA-O3A	2.50	1.62	1.59
35	F	501	ADP	C8-N7	2.36	1.36	1.31
35	E	501	ADP	C8-N7	2.29	1.36	1.31
35	D	501	ADP	C8-N7	2.29	1.36	1.31
35	B	501	ADP	C5-N7	-2.29	1.34	1.39
35	E	501	ADP	C5-N7	-2.28	1.34	1.39
35	C	501	ADP	C8-N7	2.28	1.36	1.31
35	D	501	ADP	C5-N7	-2.27	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	B	501	ADP	C8-N7	2.26	1.36	1.31
35	C	501	ADP	C5-N7	-2.25	1.35	1.39
35	F	501	ADP	C5-N7	-2.23	1.35	1.39

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	F	501	ADP	C5-C4-N3	-6.29	118.06	126.72
35	D	501	ADP	C5-C4-N3	-6.20	118.18	126.72
35	C	501	ADP	C5-C4-N3	-5.98	118.49	126.72
35	E	501	ADP	C5-C4-N3	-5.83	118.69	126.72
35	B	501	ADP	C5-C4-N3	-5.61	118.99	126.72
35	D	501	ADP	N3-C4-N9	4.93	135.54	127.17
35	C	501	ADP	N3-C4-N9	4.76	135.27	127.17
35	F	501	ADP	N3-C4-N9	4.76	135.27	127.17
35	E	501	ADP	N3-C4-N9	4.73	135.22	127.17
35	B	501	ADP	N3-C4-N9	4.49	134.80	127.17
35	D	501	ADP	C2-N3-C4	3.85	121.23	111.83
35	F	501	ADP	C2-N3-C4	3.81	121.13	111.83
35	F	501	ADP	C4-C5-N7	-3.71	106.34	110.58
35	E	501	ADP	C2-N3-C4	3.70	120.86	111.83
35	C	501	ADP	C2-N3-C4	3.69	120.85	111.83
35	B	501	ADP	C2-N3-C4	3.58	120.58	111.83
35	B	501	ADP	C4-C5-N7	-3.39	106.70	110.58
35	C	501	ADP	C4-C5-N7	-3.39	106.71	110.58
35	E	501	ADP	C4-C5-N7	-3.36	106.74	110.58
35	D	501	ADP	C4-C5-N7	-3.35	106.75	110.58
35	D	501	ADP	O4'-C1'-N9	3.33	114.48	108.09
35	E	501	ADP	N3-C2-N1	-3.26	123.65	128.58
35	D	501	ADP	N3-C2-N1	-3.24	123.67	128.58
35	C	501	ADP	N3-C2-N1	-3.13	123.85	128.58
35	B	501	ADP	N3-C2-N1	-3.11	123.88	128.58
35	F	501	ADP	N3-C2-N1	-3.08	123.92	128.58
35	F	501	ADP	C3'-C2'-C1'	2.83	106.82	101.46
35	E	501	ADP	C4-N9-C8	2.80	108.68	105.74
35	B	501	ADP	C4-N9-C8	2.72	108.59	105.74
35	F	501	ADP	C5-N7-C8	2.56	107.48	103.45
35	E	501	ADP	C5-N7-C8	2.49	107.36	103.45
35	B	501	ADP	C5-N7-C8	2.48	107.34	103.45
35	C	501	ADP	C5-N7-C8	2.47	107.33	103.45
35	D	501	ADP	C4-N9-C8	2.47	108.33	105.74
35	D	501	ADP	C5-N7-C8	2.46	107.32	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	C	501	ADP	C4-N9-C8	2.44	108.30	105.74
35	E	501	ADP	C3'-C2'-C1'	2.44	106.07	101.46
35	B	501	ADP	C3'-C2'-C1'	2.34	105.89	101.46
35	C	501	ADP	C3'-C2'-C1'	2.23	105.68	101.46
35	C	501	ADP	O5'-C5'-C4'	2.19	116.46	108.99
35	C	501	ADP	C2'-C1'-N9	-2.19	107.86	113.30
35	B	501	ADP	C2'-C1'-N9	-2.12	108.04	113.30
35	B	501	ADP	C6-C5-N7	2.07	136.09	132.09
35	F	501	ADP	C4-N9-C8	2.06	107.90	105.74
35	F	501	ADP	C6-C5-N7	2.02	135.98	132.09
35	E	501	ADP	C6-C5-N7	2.02	135.98	132.09

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	B	501	ADP	C5'-O5'-PA-O1A
35	B	501	ADP	C5'-O5'-PA-O2A
35	C	501	ADP	C5'-O5'-PA-O2A
35	D	501	ADP	C5'-O5'-PA-O2A
35	D	501	ADP	C5'-O5'-PA-O3A
35	E	501	ADP	C5'-O5'-PA-O1A
35	E	501	ADP	C5'-O5'-PA-O3A
35	E	501	ADP	O4'-C4'-C5'-O5'
35	F	501	ADP	C5'-O5'-PA-O2A
35	F	501	ADP	C5'-O5'-PA-O3A
34	A	501	ATP	O4'-C4'-C5'-O5'
35	D	501	ADP	O4'-C4'-C5'-O5'
35	D	501	ADP	C2'-C1'-N9-C4
35	D	501	ADP	C2'-C1'-N9-C8
35	D	501	ADP	C3'-C4'-C5'-O5'
35	E	501	ADP	C3'-C4'-C5'-O5'
34	A	501	ATP	C3'-C4'-C5'-O5'
35	C	501	ADP	C2'-C1'-N9-C8
35	B	501	ADP	C5'-O5'-PA-O3A
35	C	501	ADP	C5'-O5'-PA-O1A
35	C	501	ADP	C5'-O5'-PA-O3A
35	D	501	ADP	C5'-O5'-PA-O1A
35	F	501	ADP	C5'-O5'-PA-O1A
34	A	501	ATP	PG-O3B-PB-O1B
34	A	501	ATP	PB-O3A-PA-O2A
35	C	501	ADP	C3'-C4'-C5'-O5'

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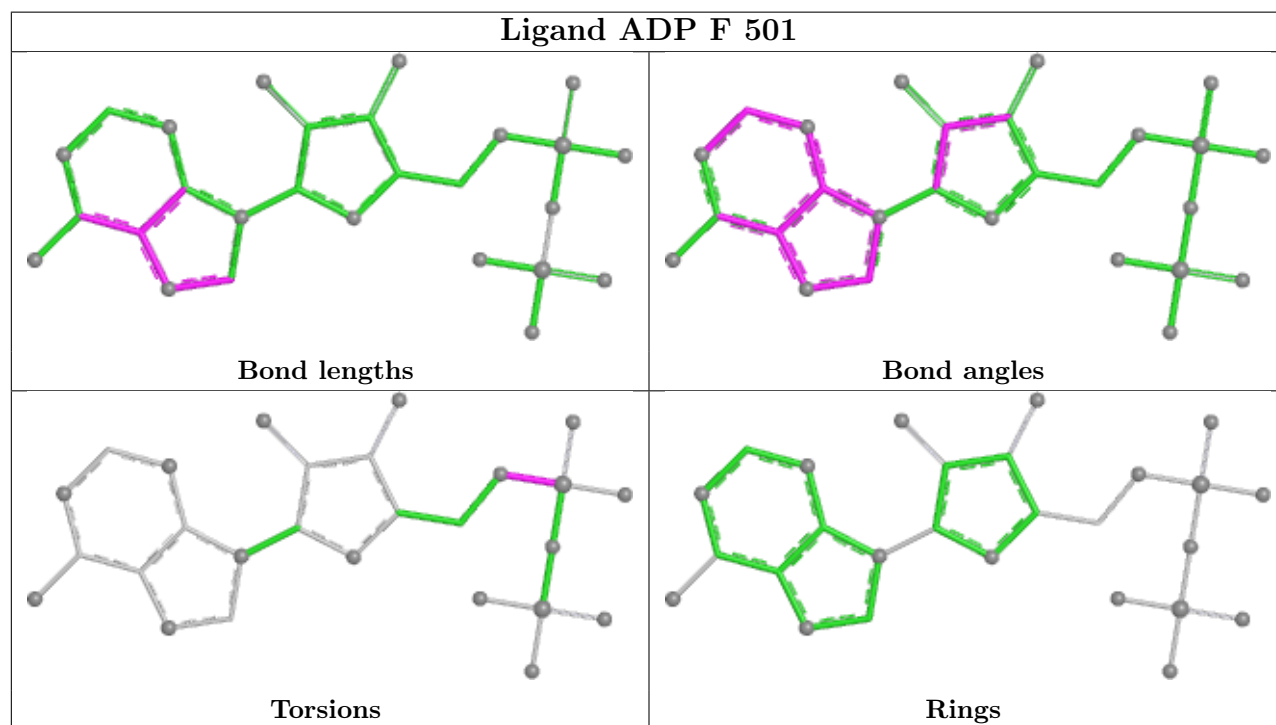
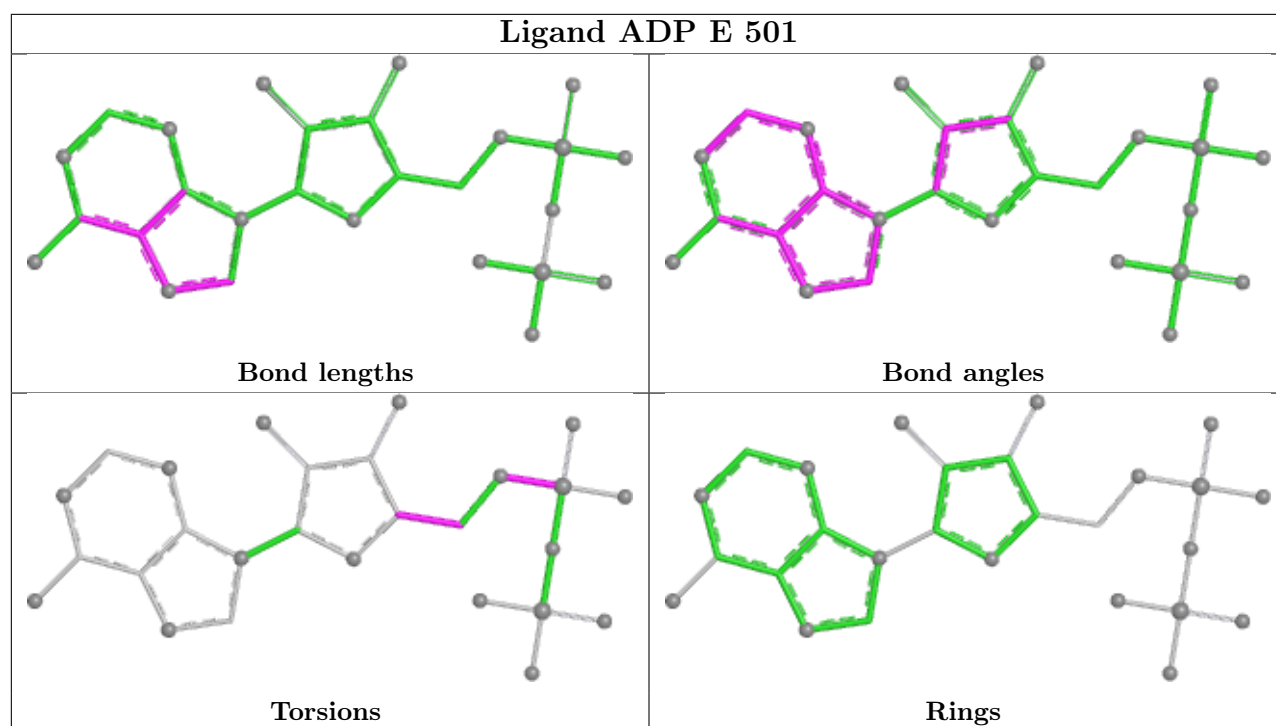
Mol	Chain	Res	Type	Atoms
35	C	501	ADP	O4'-C4'-C5'-O5'
34	A	501	ATP	PB-O3A-PA-O1A
34	A	501	ATP	PG-O3B-PB-O3A

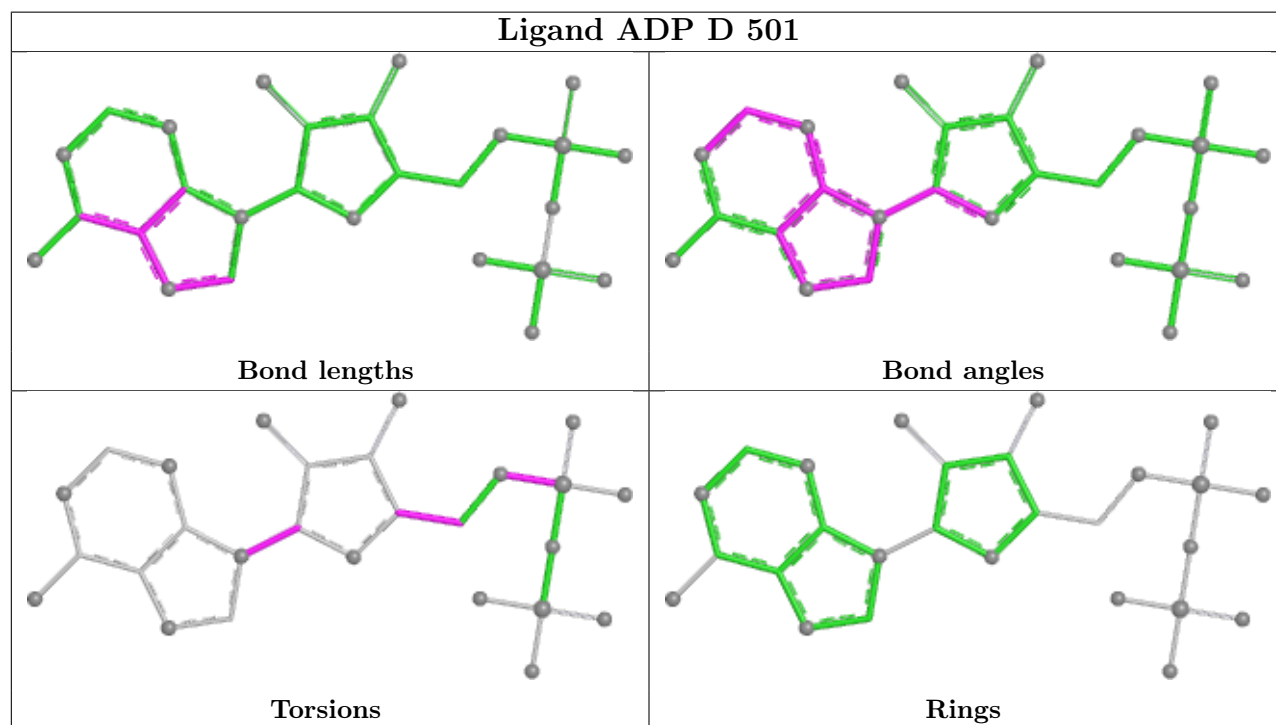
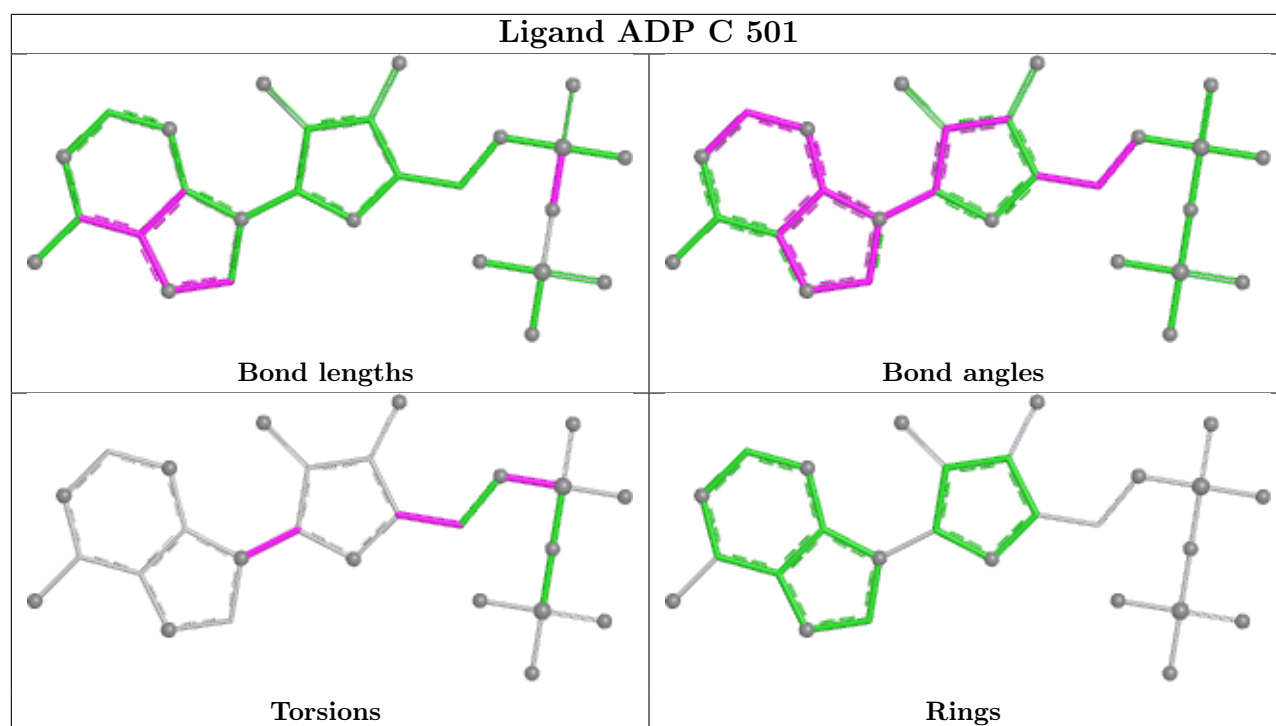
There are no ring outliers.

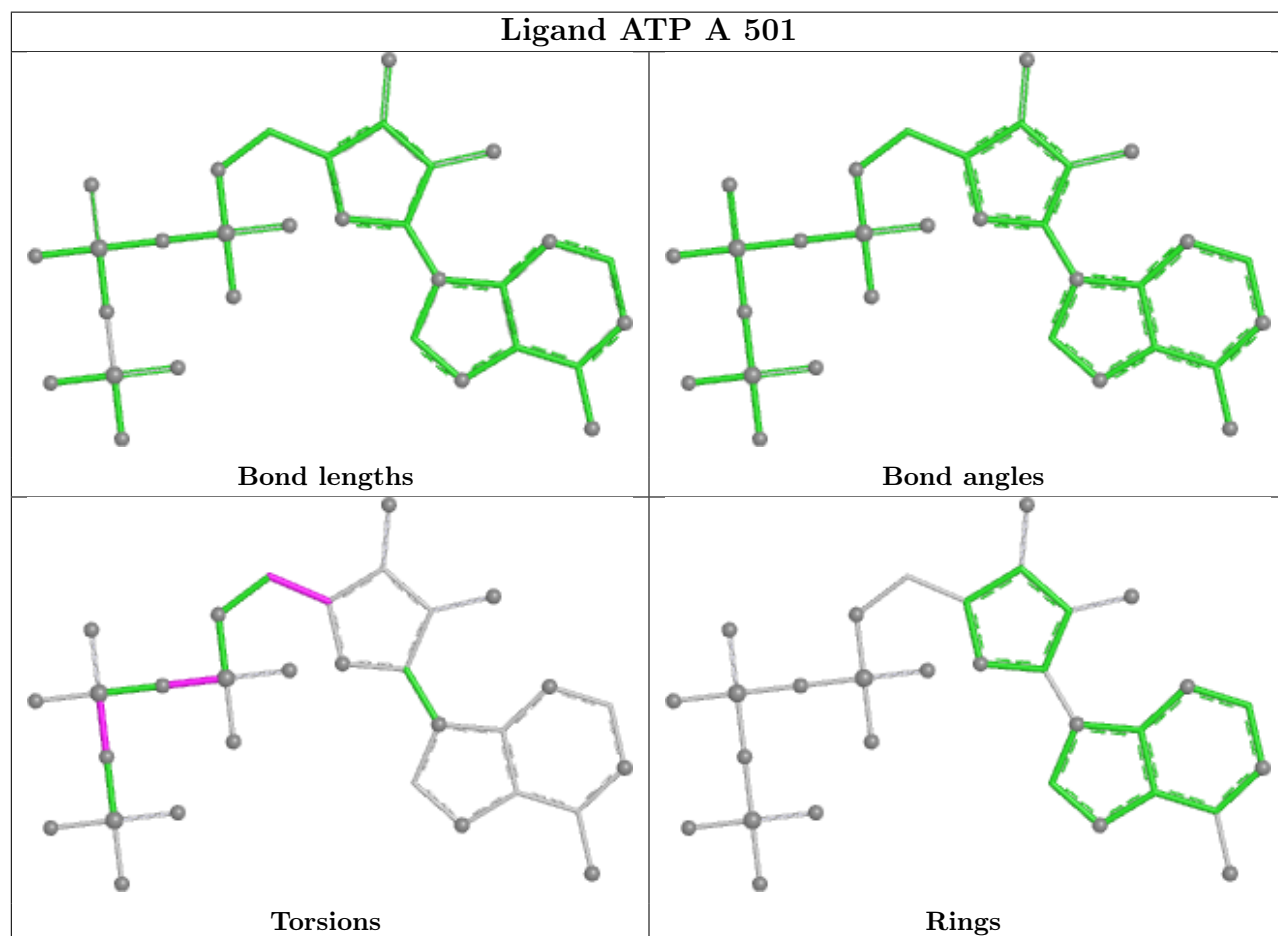
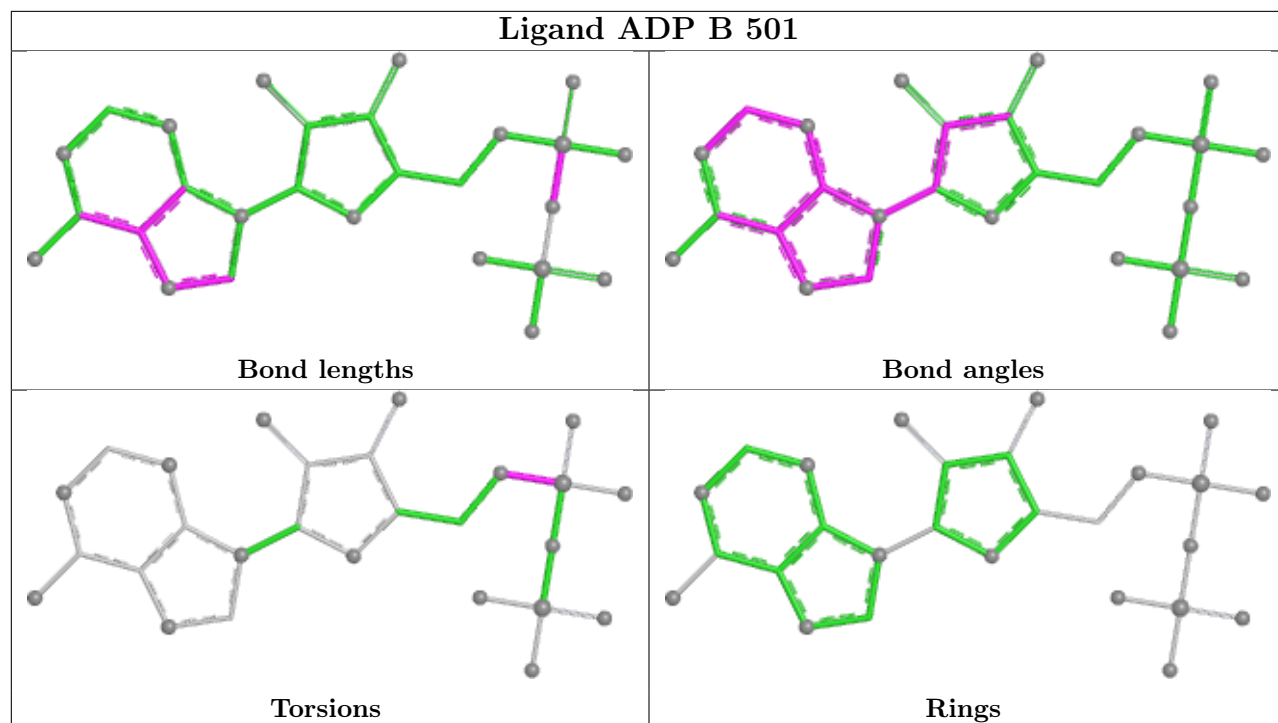
6 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	E	501	ADP	1	0
35	F	501	ADP	3	0
35	C	501	ADP	5	0
35	D	501	ADP	3	0
35	B	501	ADP	5	0
34	A	501	ATP	2	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](#)

There are no chain breaks in this entry.

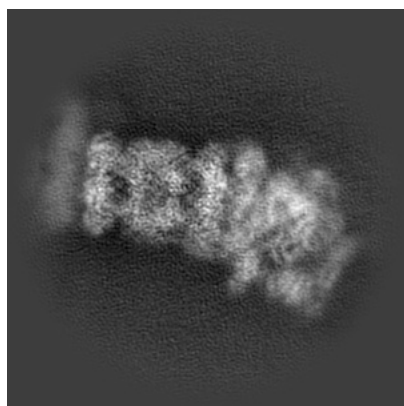
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52194. These allow visual inspection of the internal detail of the map and identification of artifacts.

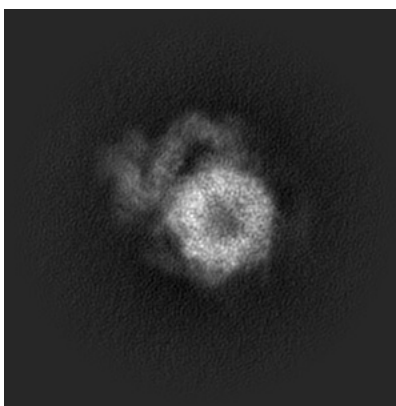
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

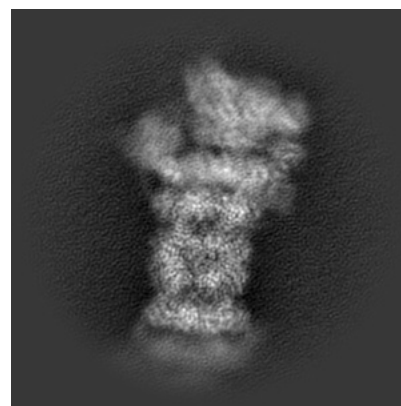
6.1.1 Primary map



X

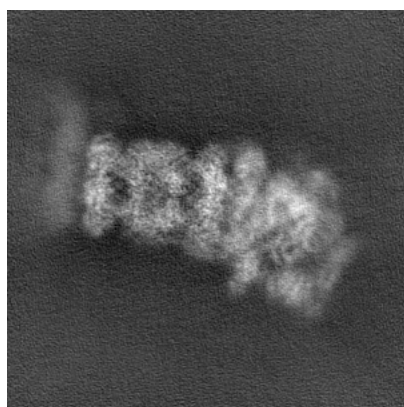


Y

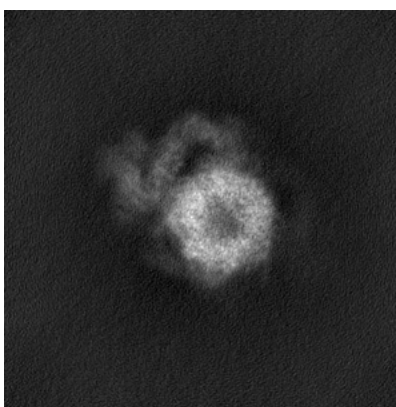


Z

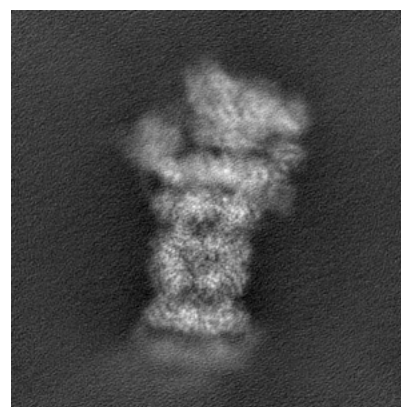
6.1.2 Raw map



X



Y

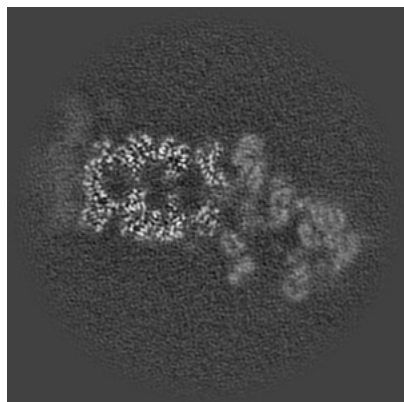


Z

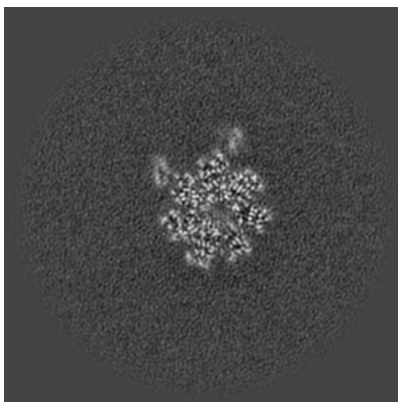
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

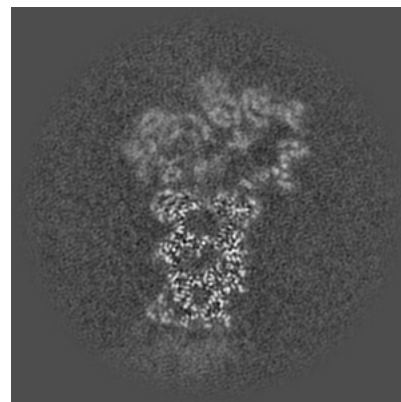
6.2.1 Primary map



X Index: 150

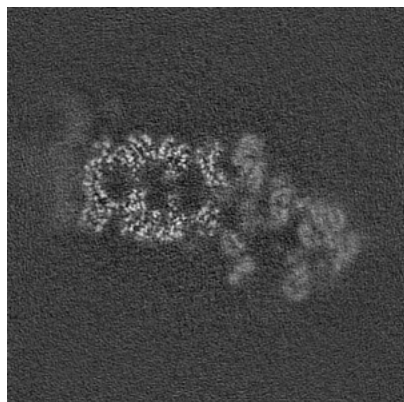


Y Index: 150

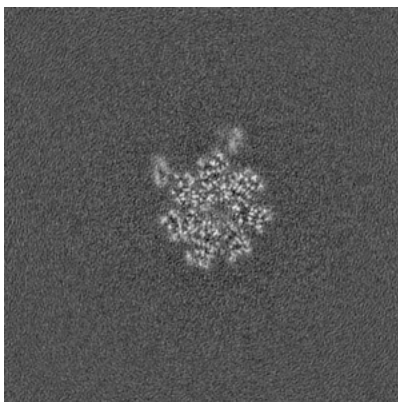


Z Index: 150

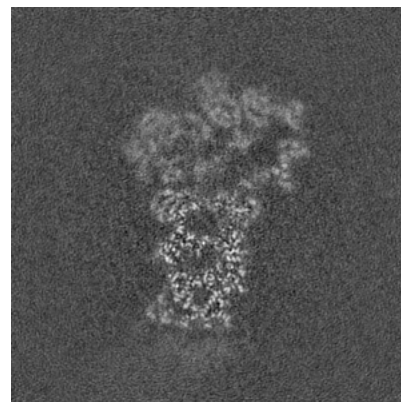
6.2.2 Raw map



X Index: 150



Y Index: 150

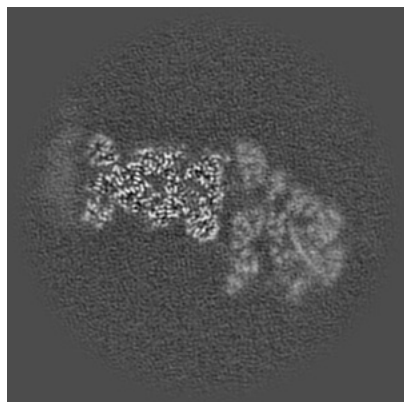


Z Index: 150

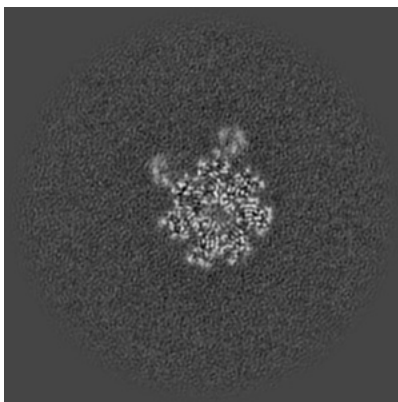
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

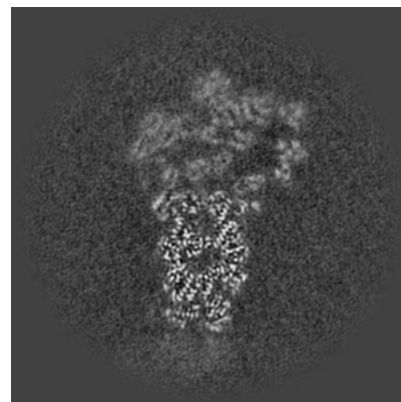
6.3.1 Primary map



X Index: 161

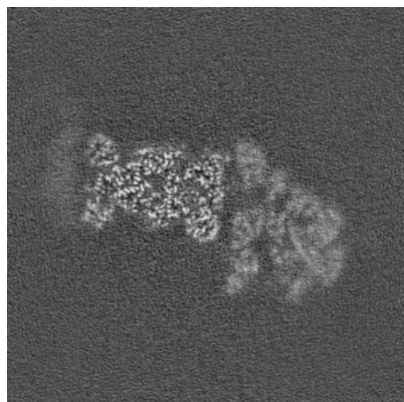


Y Index: 152

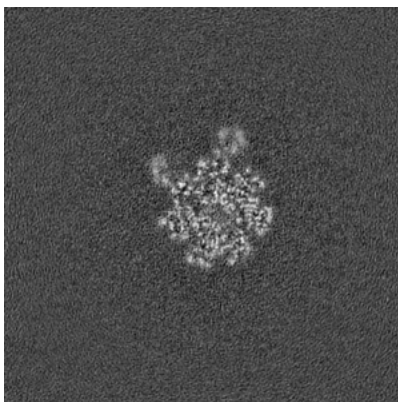


Z Index: 147

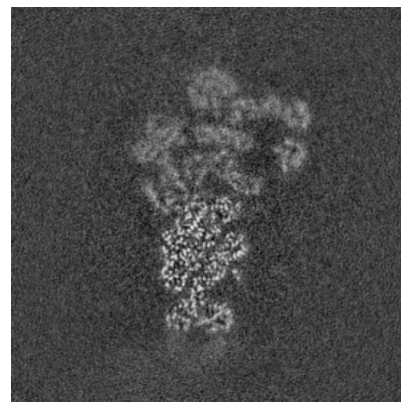
6.3.2 Raw map



X Index: 161



Y Index: 152

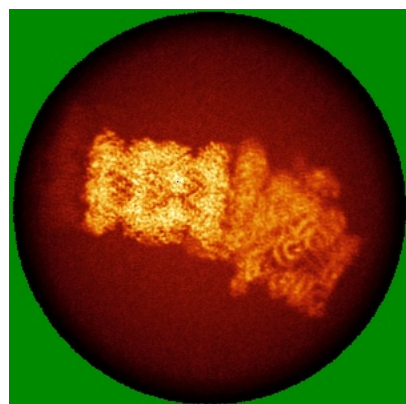


Z Index: 142

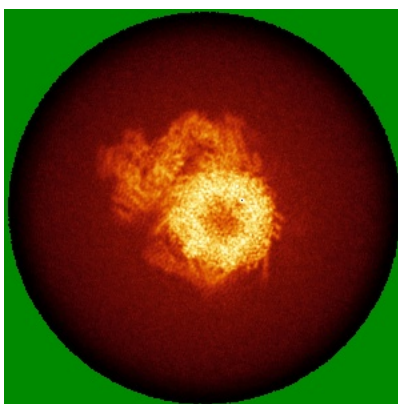
The images above show the largest variance slices of the map in three orthogonal directions.

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

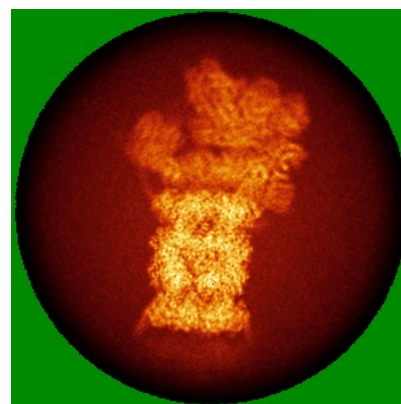
6.4.1 Primary map



X

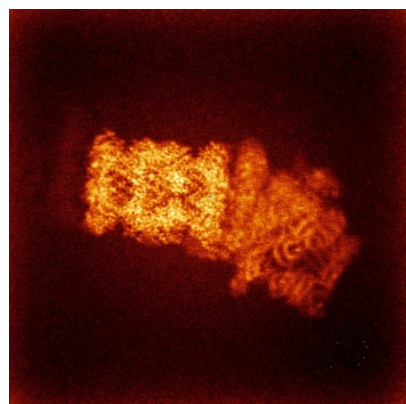


Y

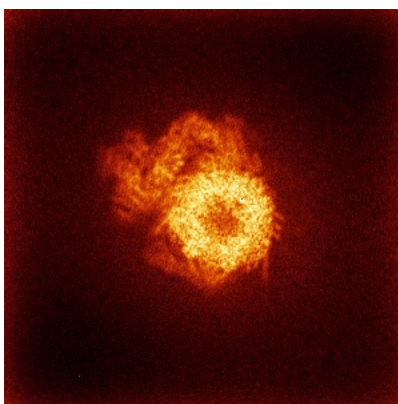


Z

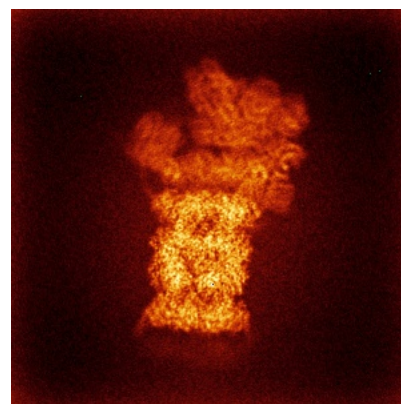
6.4.2 Raw map



X



Y

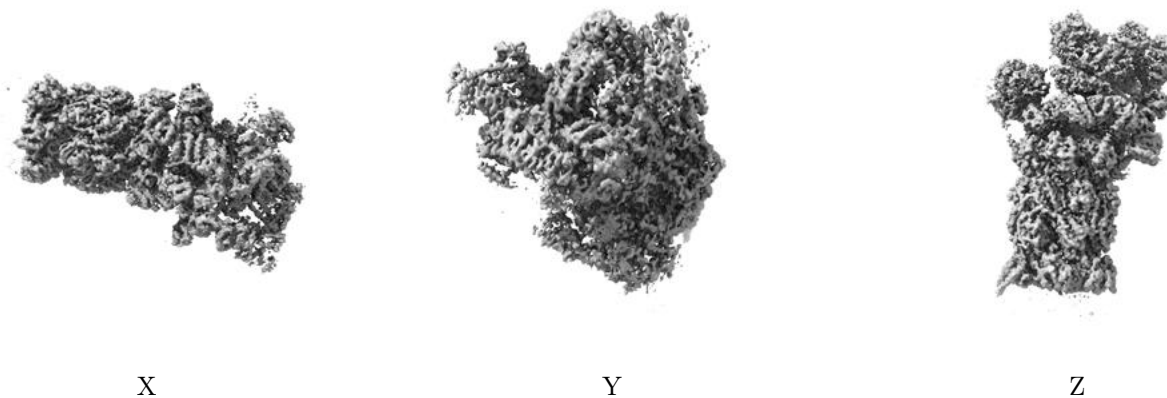


Z

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

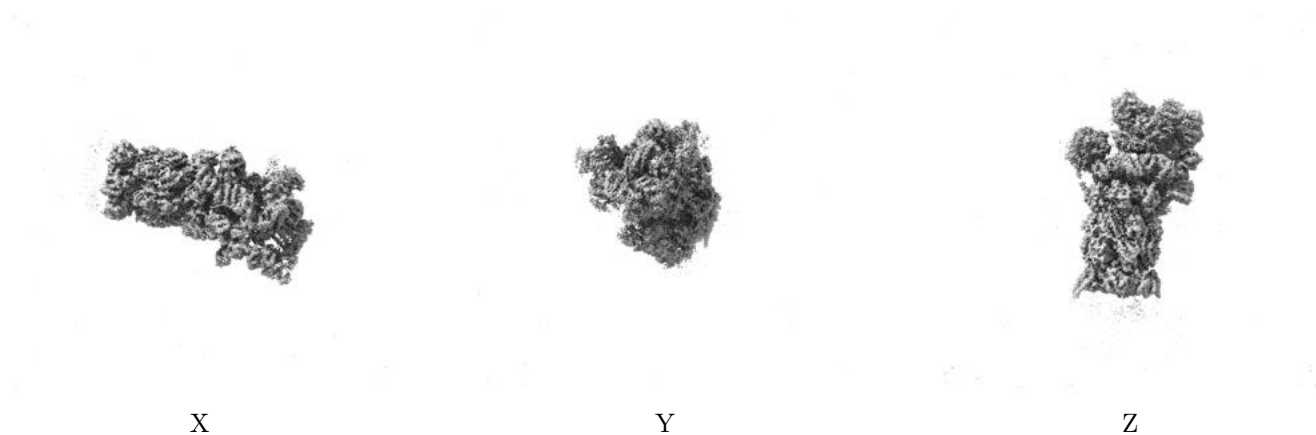
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

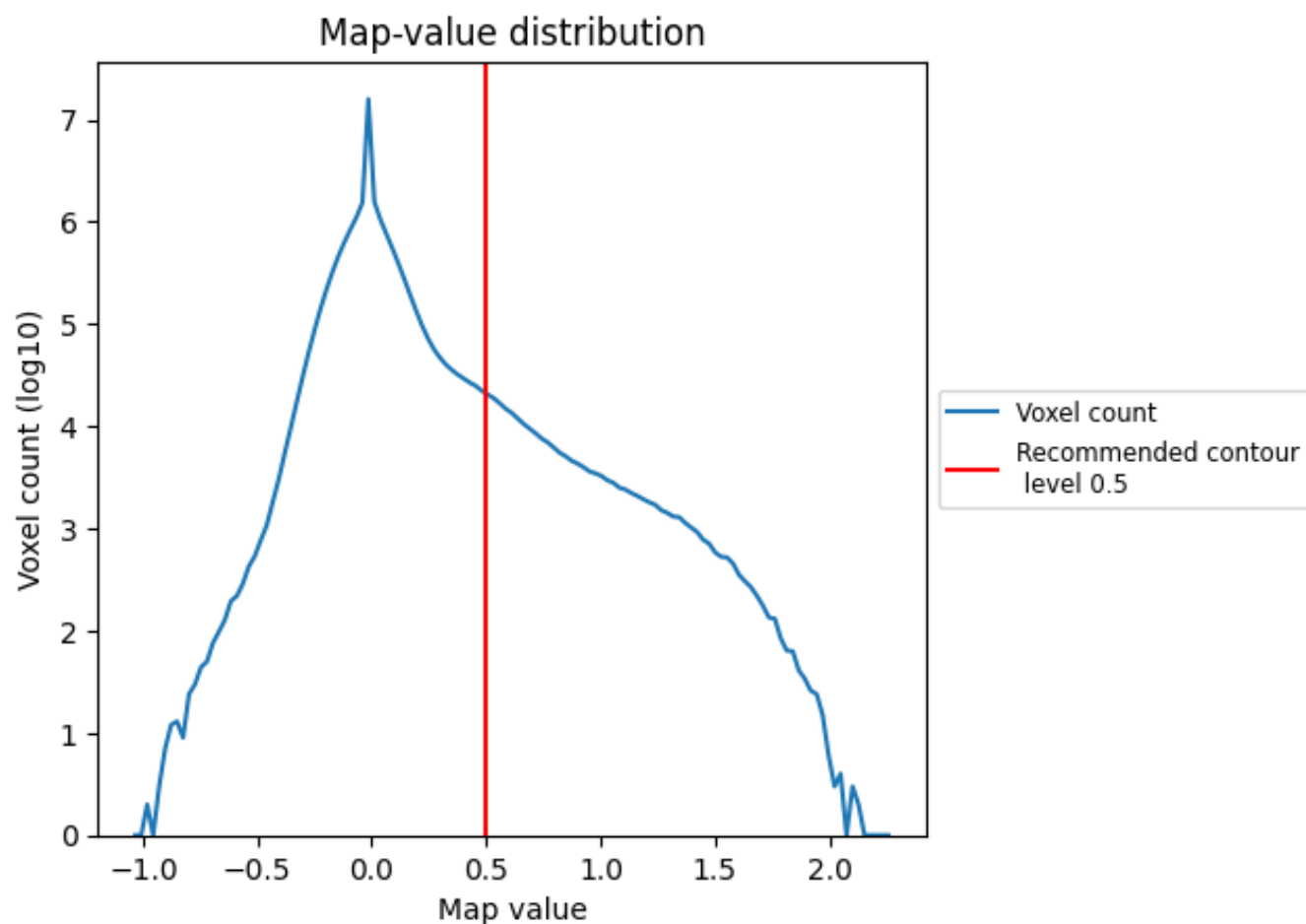
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

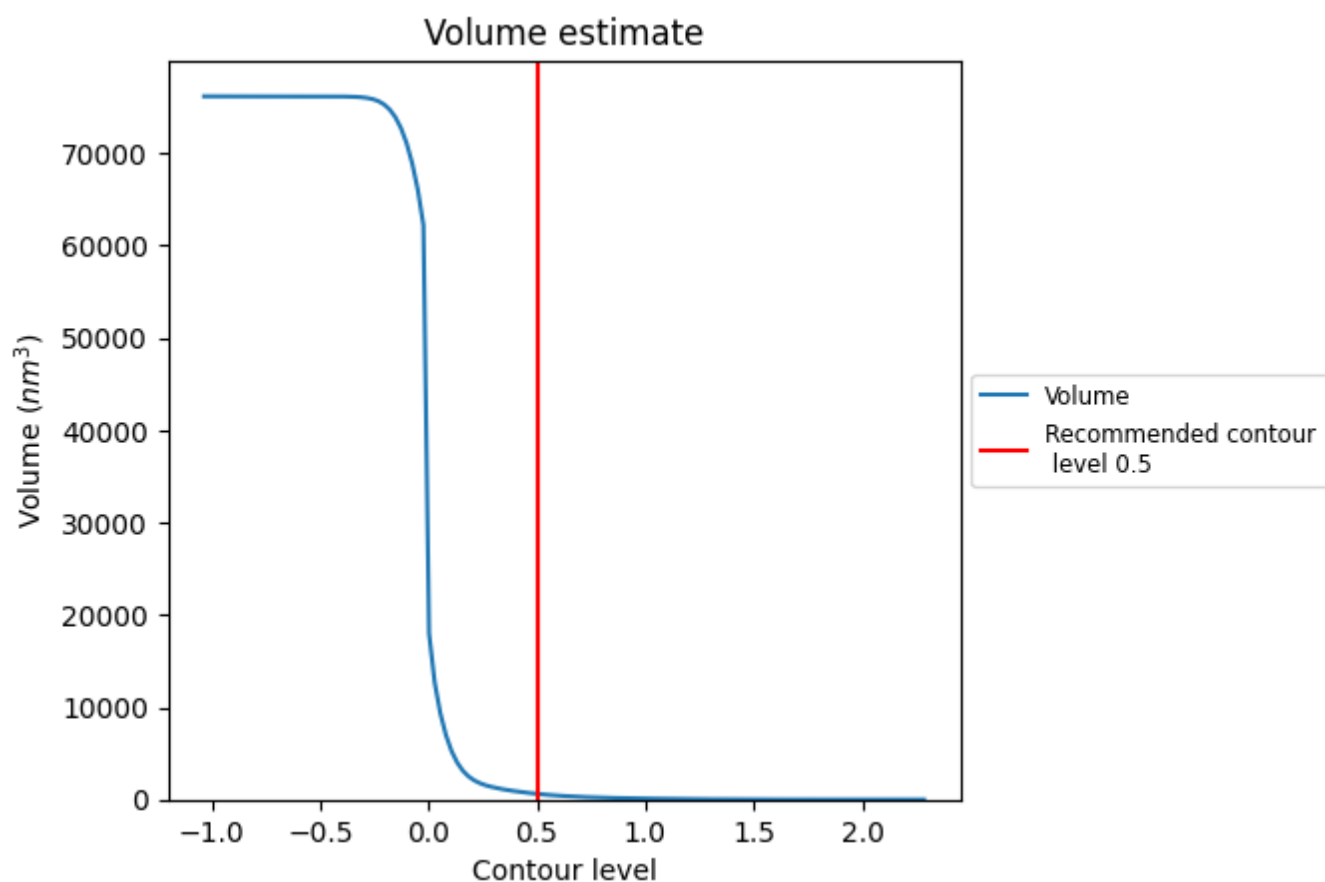
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

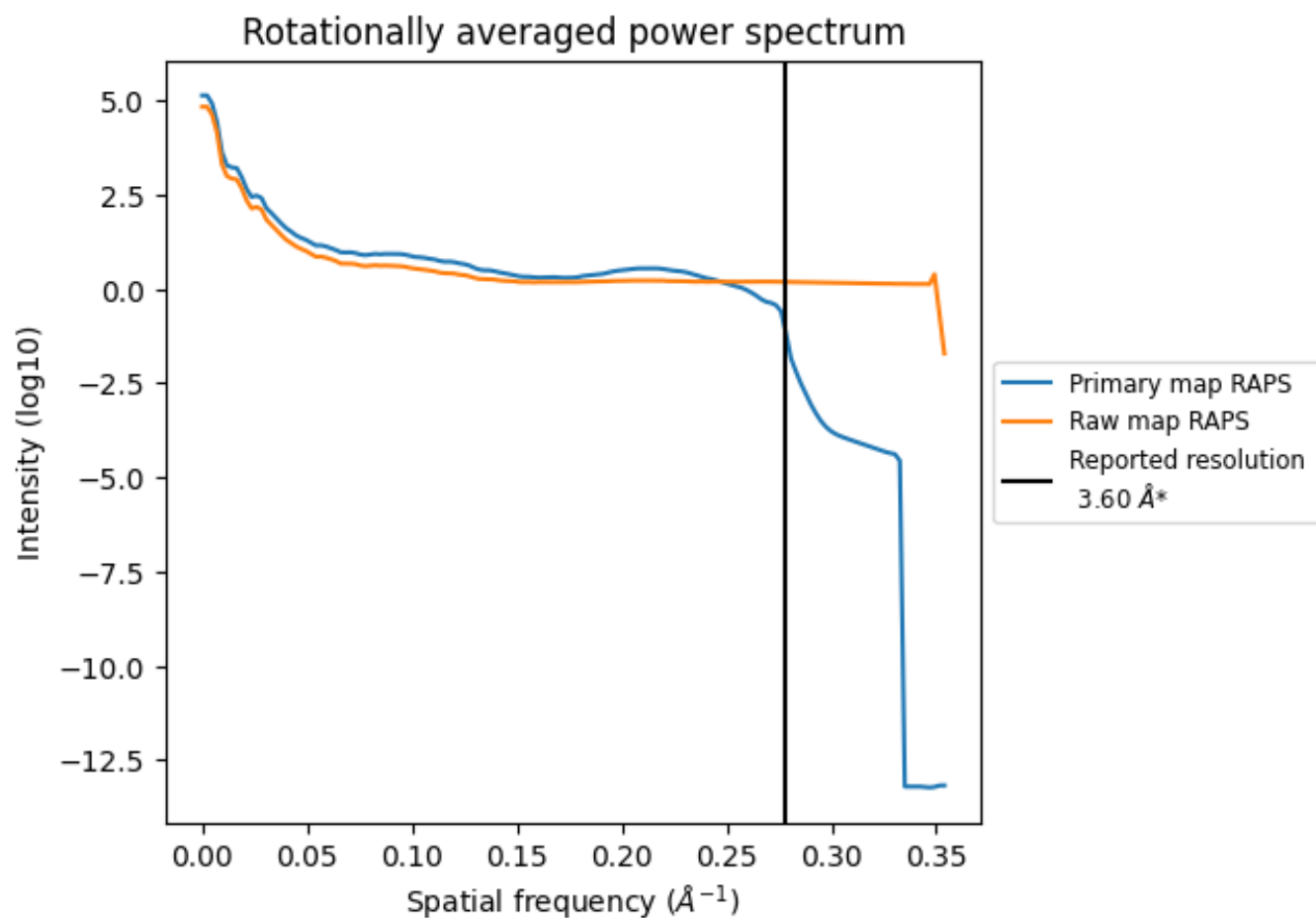
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 621 nm³; this corresponds to an approximate mass of 561 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 ⓘ

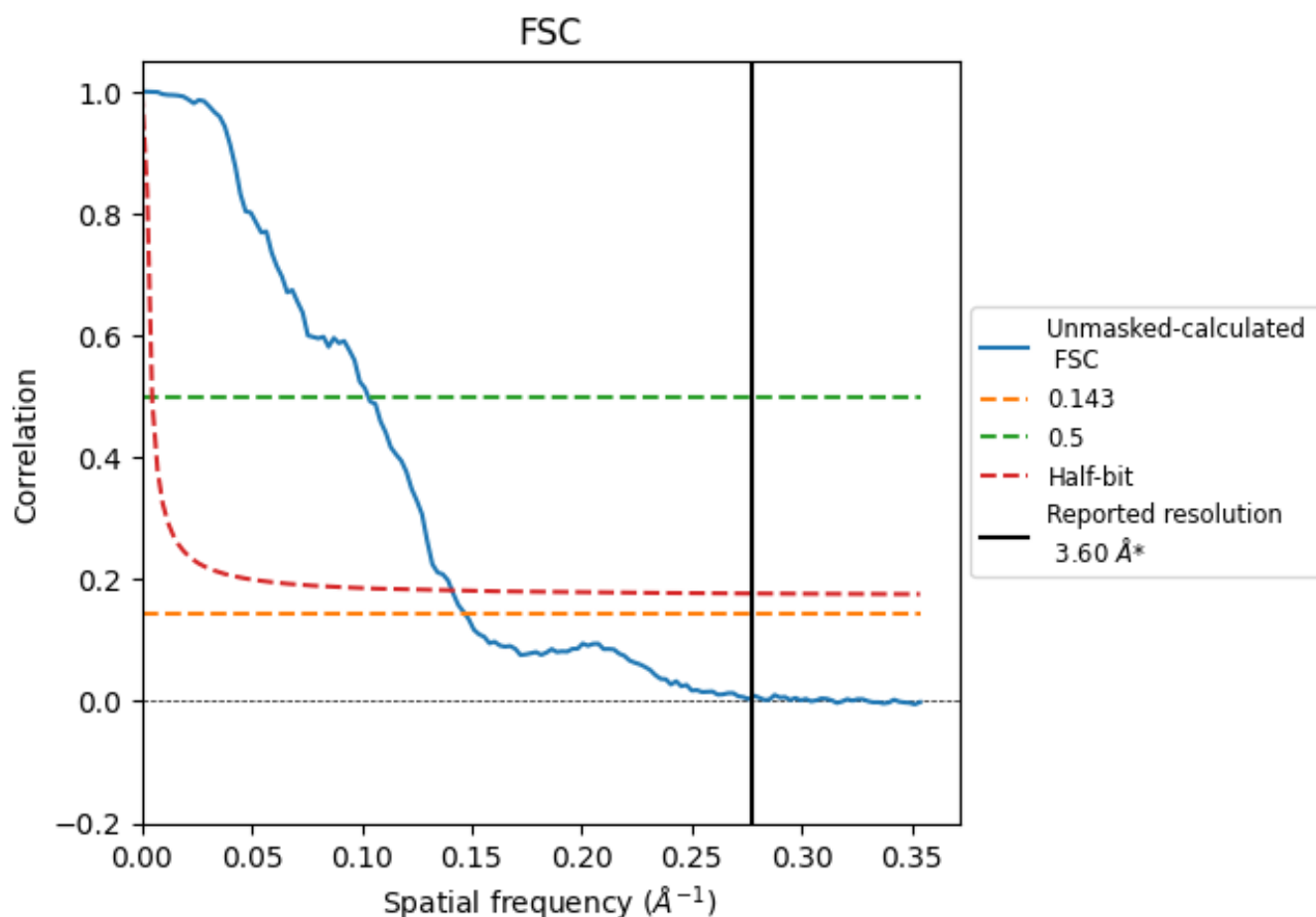


*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

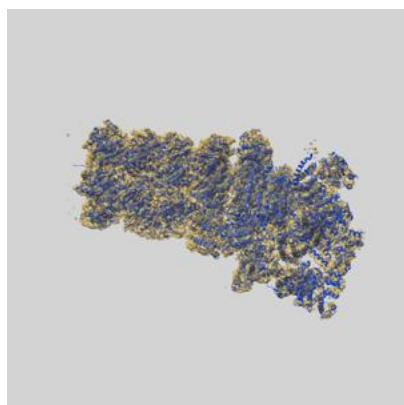
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.80	9.72	7.09

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.80 differs from the reported value 3.6 by more than 10 %

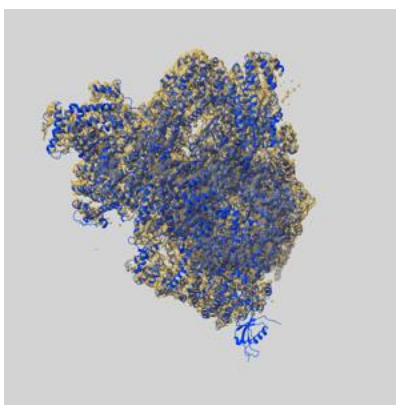
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52194 and PDB model 9SZV. Per-residue inclusion information can be found in section [3](#) on page [13](#).

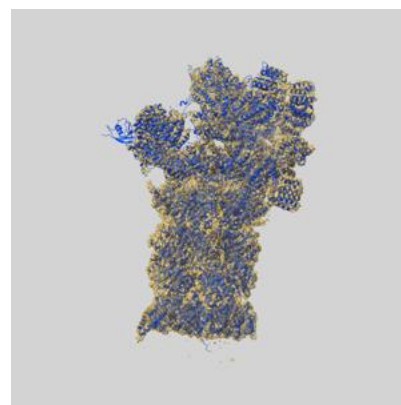
9.1 Map-model overlay [i](#)



X



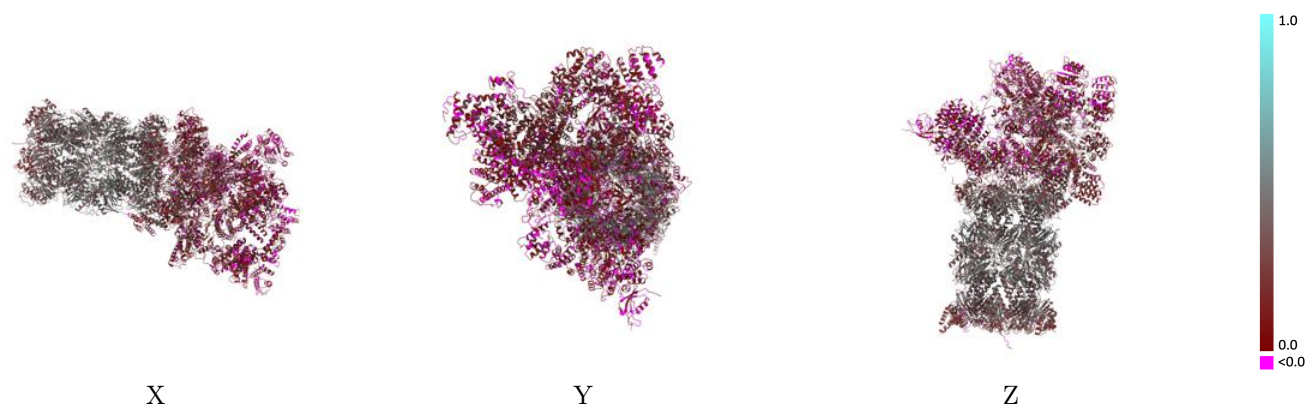
Y



Z

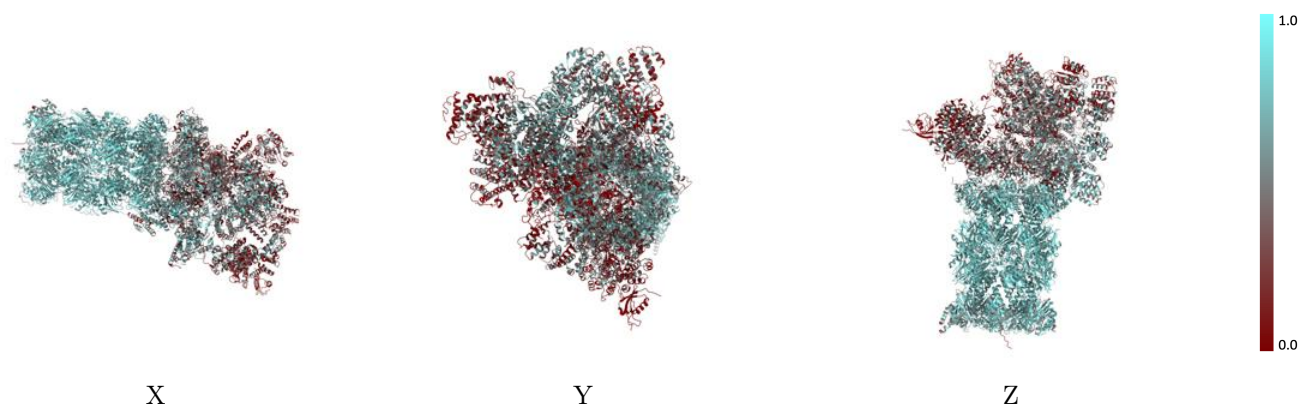
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



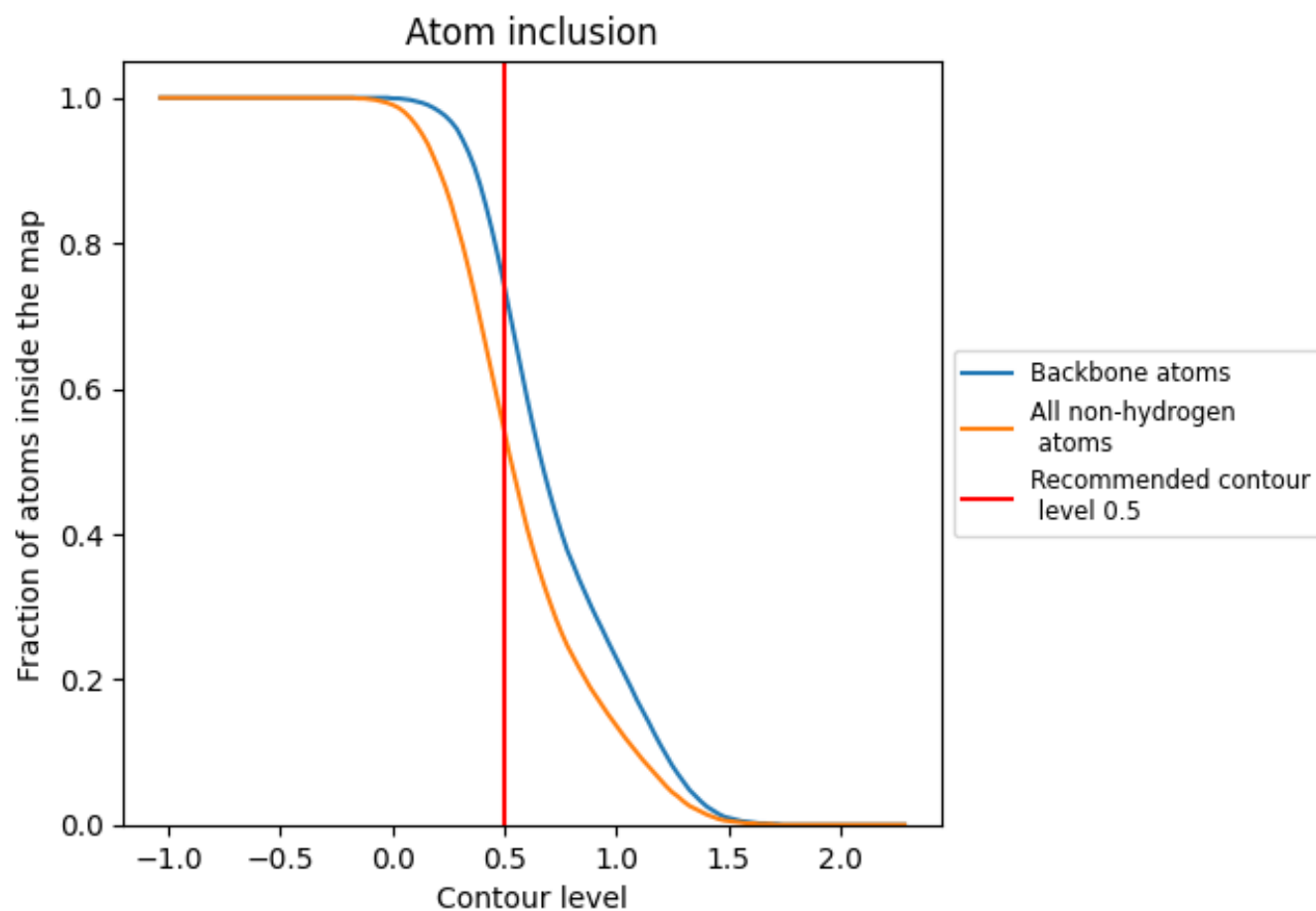
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 54% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5400	 0.2540
A	 0.3570	 0.1330
B	 0.3450	 0.1560
C	 0.3660	 0.1530
D	 0.3500	 0.1760
E	 0.4440	 0.2050
F	 0.3920	 0.1510
G	 0.7310	 0.3910
H	 0.7020	 0.3680
I	 0.7090	 0.3650
J	 0.6220	 0.2950
K	 0.6690	 0.3360
L	 0.7410	 0.3890
M	 0.7250	 0.3720
N	 0.7770	 0.4220
O	 0.7800	 0.4210
P	 0.7870	 0.4230
Q	 0.7980	 0.4220
R	 0.8050	 0.4260
S	 0.7730	 0.4140
T	 0.7810	 0.4190
U	 0.3080	 0.1020
V	 0.3390	 0.1400
W	 0.5720	 0.2010
X	 0.5620	 0.2460
Y	 0.5170	 0.1730
Z	 0.3970	 0.1410
a	 0.4100	 0.1290
b	 0.2470	 0.0820
c	 0.3860	 0.1340
d	 0.2150	 0.0980
e	 0.2730	 0.1390
f	 0.2850	 0.1030
g	 0.6770	 0.3290
h	 0.6810	 0.3410



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Chain	Atom inclusion	Q-score
i	 0.6610	 0.3210
j	 0.6760	 0.3300
k	 0.6870	 0.3480
l	 0.7110	 0.3530
m	 0.6900	 0.3360
n	 0.7750	 0.4120
o	 0.7710	 0.3980
p	 0.7680	 0.4130
q	 0.7870	 0.4170
r	 0.7900	 0.4180
s	 0.7740	 0.4160
t	 0.7680	 0.4080
x	 0.0000	 0.0120