



Full wwPDB EM Validation Report ⓘ

Apr 10, 2026 – 12:30 PM UTC

PDB ID : 9E8O / pdb_00009e8o
EMDB ID : EMD-47726
Title : Nub1/Fat10-processing human 26S proteasome bound to Txnl1 with Rpt2 at top of spiral staircase and partially unfolded Eos
Authors : Arkinson, C.; Gee, C.L.; Martin, A.
Deposited on : 2024-11-05
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

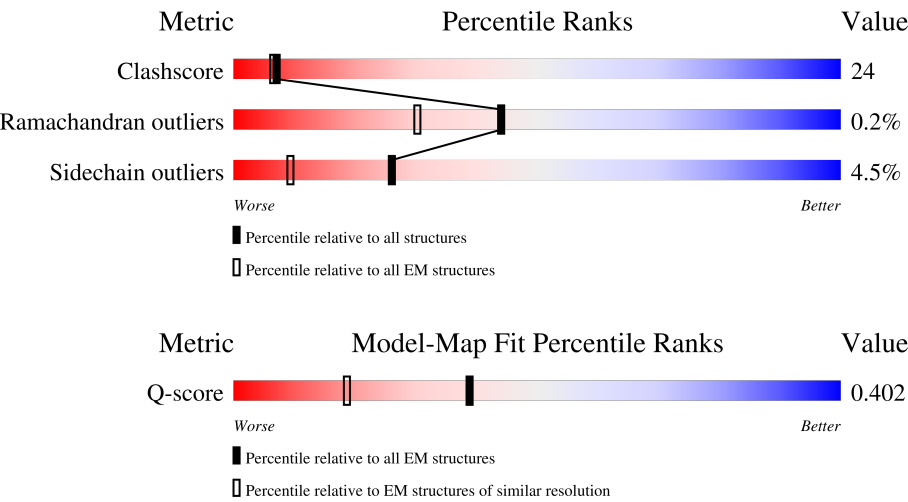
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	B	440	
2	C	406	
3	D	418	
4	c	424	

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Mol	Chain	Length	Quality of chain
5	G	246	
6	H	234	
7	I	261	
8	J	248	
9	K	241	
10	L	263	
11	M	255	
12	N	239	
13	O	277	
14	P	205	
15	Q	201	
16	R	263	
17	S	241	
18	T	264	
19	X	422	
20	Y	389	
21	Z	324	
22	a	376	
23	b	377	
24	d	350	
25	f	908	
26	W	456	
27	V	534	
28	e	70	
29	A	433	

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Mol	Chain	Length	Quality of chain
30	F	439	
31	E	389	
32	U	953	
33	g	390	
34	u	300	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
37	ADP	F	501	-	-	X	-

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 83181 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	397	Total	C	N	O	S	0	0
			3124	1968	530	611	15		

- Molecule 2 is a protein called 26S protease regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	386	Total	C	N	O	S	0	0
			3053	1921	547	567	18		

- Molecule 3 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	377	Total	C	N	O	S	0	0
			3015	1908	521	573	13		

- Molecule 4 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	c	280	Total	C	N	O	S	0	0
			2204	1395	378	412	19		

There are 114 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	311	LEU	-	expression tag	UNP O00487
c	312	ILE	-	expression tag	UNP O00487
c	313	ASN	-	expression tag	UNP O00487
c	314	HIS	-	expression tag	UNP O00487
c	315	HIS	-	expression tag	UNP O00487
c	316	HIS	-	expression tag	UNP O00487
c	317	HIS	-	expression tag	UNP O00487
c	318	HIS	-	expression tag	UNP O00487
c	319	HIS	-	expression tag	UNP O00487

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Chain	Residue	Modelled	Actual	Comment	Reference
c	320	ASP	-	expression tag	UNP O00487
c	321	TYR	-	expression tag	UNP O00487
c	322	ASP	-	expression tag	UNP O00487
c	323	ILE	-	expression tag	UNP O00487
c	324	PRO	-	expression tag	UNP O00487
c	325	THR	-	expression tag	UNP O00487
c	326	THR	-	expression tag	UNP O00487
c	327	ALA	-	expression tag	UNP O00487
c	328	SER	-	expression tag	UNP O00487
c	329	GLU	-	expression tag	UNP O00487
c	330	ASN	-	expression tag	UNP O00487
c	331	LEU	-	expression tag	UNP O00487
c	332	TYR	-	expression tag	UNP O00487
c	333	PHE	-	expression tag	UNP O00487
c	334	GLN	-	expression tag	UNP O00487
c	335	GLY	-	expression tag	UNP O00487
c	336	GLU	-	expression tag	UNP O00487
c	337	LEU	-	expression tag	UNP O00487
c	338	GLY	-	expression tag	UNP O00487
c	339	MET	-	expression tag	UNP O00487
c	340	ARG	-	expression tag	UNP O00487
c	341	GLY	-	expression tag	UNP O00487
c	342	SER	-	expression tag	UNP O00487
c	343	ALA	-	expression tag	UNP O00487
c	344	GLY	-	expression tag	UNP O00487
c	345	LYS	-	expression tag	UNP O00487
c	346	ALA	-	expression tag	UNP O00487
c	347	GLY	-	expression tag	UNP O00487
c	348	GLU	-	expression tag	UNP O00487
c	349	GLY	-	expression tag	UNP O00487
c	350	GLU	-	expression tag	UNP O00487
c	351	ILE	-	expression tag	UNP O00487
c	352	PRO	-	expression tag	UNP O00487
c	353	ALA	-	expression tag	UNP O00487
c	354	PRO	-	expression tag	UNP O00487
c	355	LEU	-	expression tag	UNP O00487
c	356	ALA	-	expression tag	UNP O00487
c	357	GLY	-	expression tag	UNP O00487
c	358	THR	-	expression tag	UNP O00487
c	359	VAL	-	expression tag	UNP O00487
c	360	SER	-	expression tag	UNP O00487
c	361	LYS	-	expression tag	UNP O00487

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Chain	Residue	Modelled	Actual	Comment	Reference
c	362	ILE	-	expression tag	UNP O00487
c	363	LEU	-	expression tag	UNP O00487
c	364	VAL	-	expression tag	UNP O00487
c	365	LYS	-	expression tag	UNP O00487
c	366	GLU	-	expression tag	UNP O00487
c	367	GLY	-	expression tag	UNP O00487
c	368	ASP	-	expression tag	UNP O00487
c	369	THR	-	expression tag	UNP O00487
c	370	VAL	-	expression tag	UNP O00487
c	371	LYS	-	expression tag	UNP O00487
c	372	ALA	-	expression tag	UNP O00487
c	373	GLY	-	expression tag	UNP O00487
c	374	GLN	-	expression tag	UNP O00487
c	375	THR	-	expression tag	UNP O00487
c	376	VAL	-	expression tag	UNP O00487
c	377	LEU	-	expression tag	UNP O00487
c	378	VAL	-	expression tag	UNP O00487
c	379	LEU	-	expression tag	UNP O00487
c	380	GLU	-	expression tag	UNP O00487
c	381	ALA	-	expression tag	UNP O00487
c	382	MET	-	expression tag	UNP O00487
c	383	LYS	-	expression tag	UNP O00487
c	384	MET	-	expression tag	UNP O00487
c	385	GLU	-	expression tag	UNP O00487
c	386	THR	-	expression tag	UNP O00487
c	387	GLU	-	expression tag	UNP O00487
c	388	ILE	-	expression tag	UNP O00487
c	389	ASN	-	expression tag	UNP O00487
c	390	ALA	-	expression tag	UNP O00487
c	391	PRO	-	expression tag	UNP O00487
c	392	THR	-	expression tag	UNP O00487
c	393	ASP	-	expression tag	UNP O00487
c	394	GLY	-	expression tag	UNP O00487
c	395	LYS	-	expression tag	UNP O00487
c	396	VAL	-	expression tag	UNP O00487
c	397	GLU	-	expression tag	UNP O00487
c	398	LYS	-	expression tag	UNP O00487
c	399	VAL	-	expression tag	UNP O00487
c	400	LEU	-	expression tag	UNP O00487
c	401	VAL	-	expression tag	UNP O00487
c	402	LYS	-	expression tag	UNP O00487
c	403	GLU	-	expression tag	UNP O00487

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Chain	Residue	Modelled	Actual	Comment	Reference
c	404	ARG	-	expression tag	UNP O00487
c	405	ASP	-	expression tag	UNP O00487
c	406	ALA	-	expression tag	UNP O00487
c	407	VAL	-	expression tag	UNP O00487
c	408	GLN	-	expression tag	UNP O00487
c	409	GLY	-	expression tag	UNP O00487
c	410	GLY	-	expression tag	UNP O00487
c	411	GLN	-	expression tag	UNP O00487
c	412	GLY	-	expression tag	UNP O00487
c	413	LEU	-	expression tag	UNP O00487
c	414	ILE	-	expression tag	UNP O00487
c	415	LYS	-	expression tag	UNP O00487
c	416	ILE	-	expression tag	UNP O00487
c	417	GLY	-	expression tag	UNP O00487
c	418	VAL	-	expression tag	UNP O00487
c	419	HIS	-	expression tag	UNP O00487
c	420	HIS	-	expression tag	UNP O00487
c	421	HIS	-	expression tag	UNP O00487
c	422	HIS	-	expression tag	UNP O00487
c	423	HIS	-	expression tag	UNP O00487
c	424	HIS	-	expression tag	UNP O00487

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	241	Total	C	N	O	S	0	0
			1873	1190	313	357	13		

- Molecule 6 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	232	Total	C	N	O	S	0	0
			1805	1152	305	342	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	248	Total	C	N	O	S	0	0
			1933	1222	330	371	10		

- Molecule 8 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	239	Total	C	N	O	S	0	0
			1861	1166	327	363	5		

- Molecule 9 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	238	Total	C	N	O	S	0	0
			1813	1139	302	361	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	240	Total	C	N	O	S	0	0
			1876	1175	338	352	11		

- Molecule 11 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	242	Total	C	N	O	S	0	0
			1890	1200	323	356	11		

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	195	Total	C	N	O	S	0	0
			1462	913	250	287	12		

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	220	Total	C	N	O	S	0	0
			1645	1035	278	320	12		

- Molecule 14 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	204	Total	C	N	O	S	0	0
			1587	1010	264	294	19		

- Molecule 15 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	199	Total	C	N	O	S	0	0
			1588	1017	270	292	9		

- Molecule 16 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	201	Total	C	N	O	S	0	0
			1559	982	274	294	9		

- Molecule 17 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	213	Total	C	N	O	S	0	0
			1641	1041	281	309	10		

- Molecule 18 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	216	Total	C	N	O	S	0	0
			1683	1062	291	318	12		

- Molecule 19 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	379	Total	C	N	O	S	0	0
			3001	1914	508	567	12		

- Molecule 20 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

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

- Molecule 21 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Z	286	Total	C	N	O	S	0	0
			2277	1454	391	427	5		

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

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

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

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

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	d	250	Total	C	N	O	S	0	0
			2048	1331	335	373	9		

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	884	Total	C	N	O	S	0	0
			6836	4298	1169	1323	46		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	437	Total	C	N	O	S	0	0
			3564	2258	609	674	23		

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	432	Total	C	N	O	S	0	0
			3527	2252	628	634	13		

- Molecule 28 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	e	50	Total	C	N	O	0	0
			425	260	65	100		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A	398	Total	C	N	O	S	0	0
			3138	1978	552	590	18		

- Molecule 30 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	359	Total	C	N	O	S	0	0
			2803	1774	483	529	17		

- Molecule 31 is a protein called 26S protease regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	E	364	Total	C	N	O	S	0	0
			2887	1814	515	542	16		

- Molecule 32 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	U	829	Total	C	N	O	S	0	0
			6459	4098	1098	1218	45		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	320	ASN	ASP	conflict	UNP Q99460

- Molecule 33 is a protein called FAT10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	200	Total	C	N	O	S	0	0
			1622	1044	274	292	12		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	176	LYS	ASN	conflict	UNP Q5S6Z9
g	228	CR8	HIS	conflict	UNP Q5S6Z9
g	?	-	TYR	deletion	UNP Q5S6Z9
g	?	-	GLY	deletion	UNP Q5S6Z9
g	235	LYS	GLU	conflict	UNP Q5S6Z9
g	239	ASN	HIS	conflict	UNP Q5S6Z9
g	267	ASN	ILE	conflict	UNP Q5S6Z9

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Chain	Residue	Modelled	Actual	Comment	Reference
g	286	TYR	HIS	conflict	UNP Q5S6Z9
g	288	THR	VAL	conflict	UNP Q5S6Z9
g	323	GLU	THR	conflict	UNP Q5S6Z9
g	354	ALA	TYR	conflict	UNP Q5S6Z9
g	392	TYR	-	expression tag	UNP Q5S6Z9

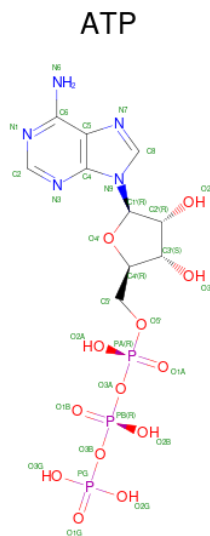
- Molecule 34 is a protein called Thioredoxin-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	u	155	Total	C	N	O	S	0	0
			1240	783	199	250	8		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	-10	GLY	-	expression tag	UNP O43396
u	-9	HIS	-	expression tag	UNP O43396
u	-8	MET	-	expression tag	UNP O43396
u	-7	ASP	-	expression tag	UNP O43396
u	-6	TYR	-	expression tag	UNP O43396
u	-5	LYS	-	expression tag	UNP O43396
u	-4	ASP	-	expression tag	UNP O43396
u	-3	ASP	-	expression tag	UNP O43396
u	-2	ASP	-	expression tag	UNP O43396
u	-1	ASP	-	expression tag	UNP O43396
u	0	LYS	-	expression tag	UNP O43396

- Molecule 35 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

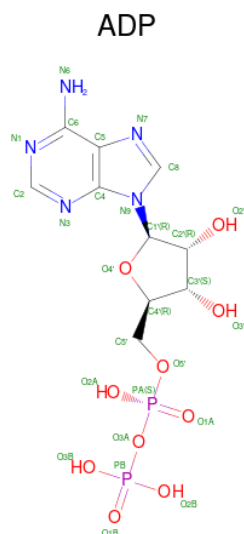


Mol	Chain	Residues	Atoms					AltConf
35	B	1	Total 31	C 10	N 5	O 13	P 3	0
35	C	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
36	B	1	Total Mg 1 1	0
36	C	1	Total Mg 1 1	0
36	D	1	Total Mg 1 1	0

- Molecule 37 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
37	D	1	Total 27	C 10	N 5	O 10	P 2	0
37	A	1	Total 27	C 10	N 5	O 10	P 2	0
37	F	1	Total 27	C 10	N 5	O 10	P 2	0
37	E	1	Total 27	C 10	N 5	O 10	P 2	0

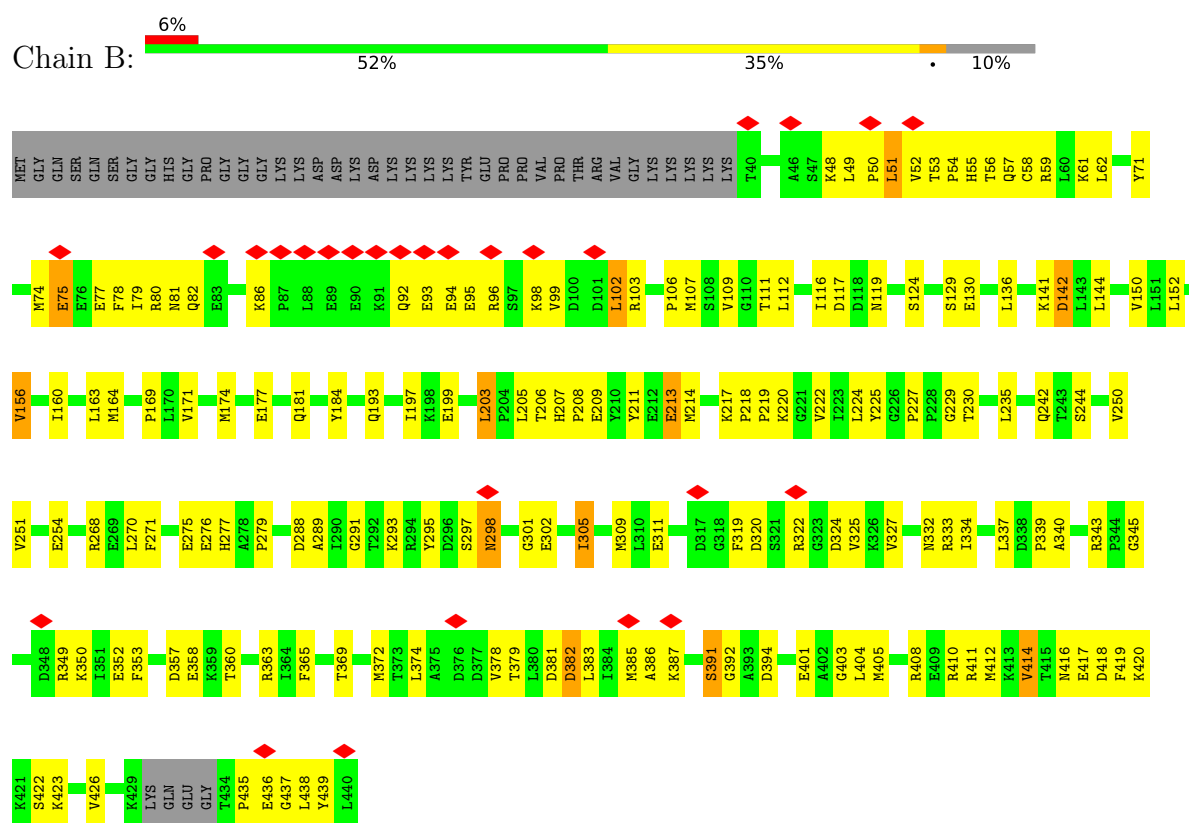
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

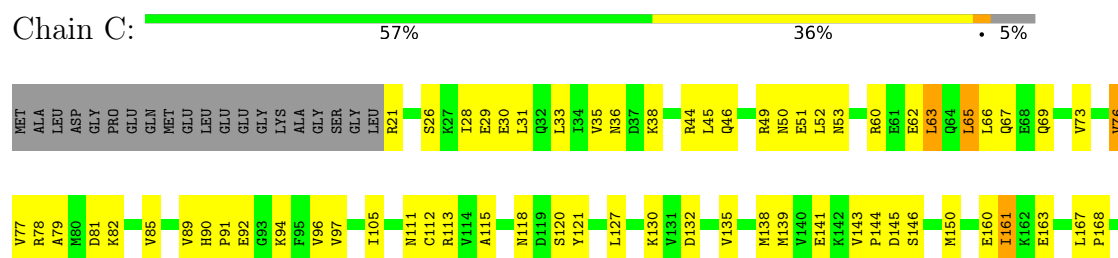
3 Residue-property plots

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: 26S proteasome regulatory subunit 4



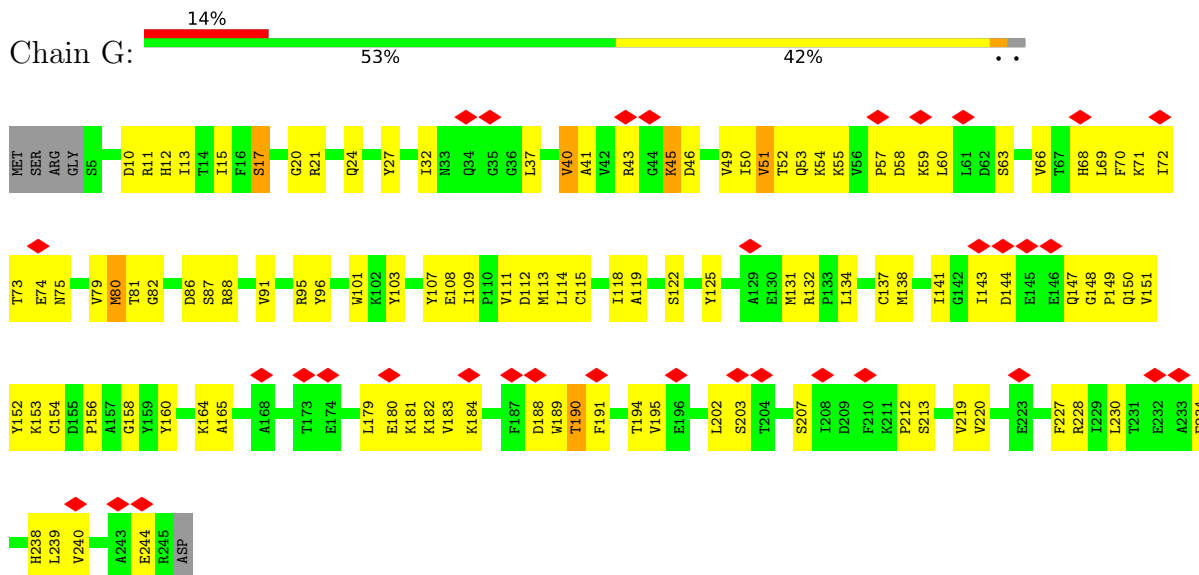
• Molecule 2: 26S protease regulatory subunit 8



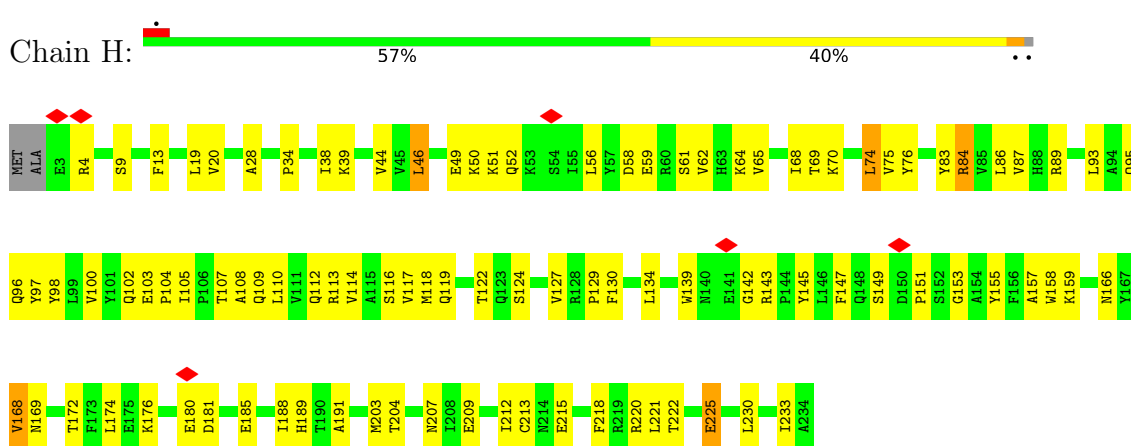


LYS VAL SER ARG GLY LYS GLU ARG ASP ALA VAL GLN GLY GLN GLY ILE LYS ILE GLY VAL HIS HIS HIS HIS

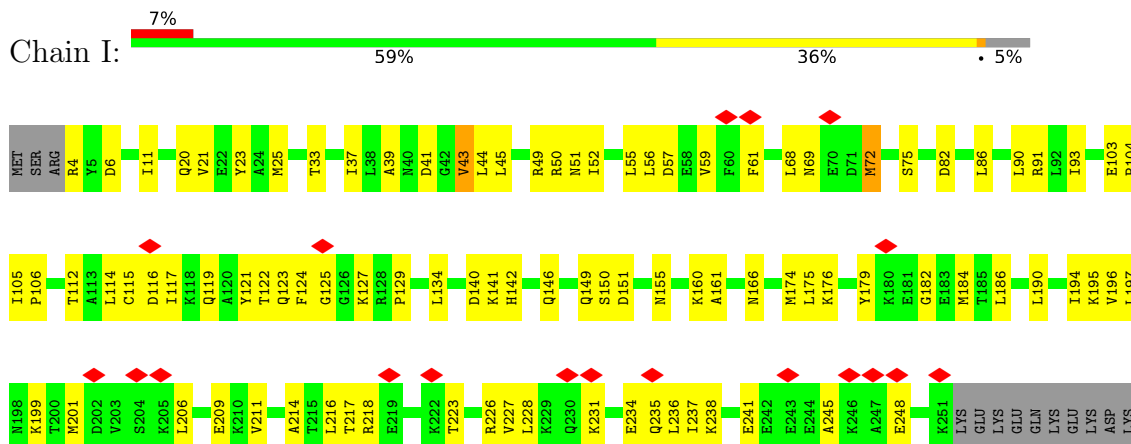
• Molecule 5: Proteasome subunit alpha type-6



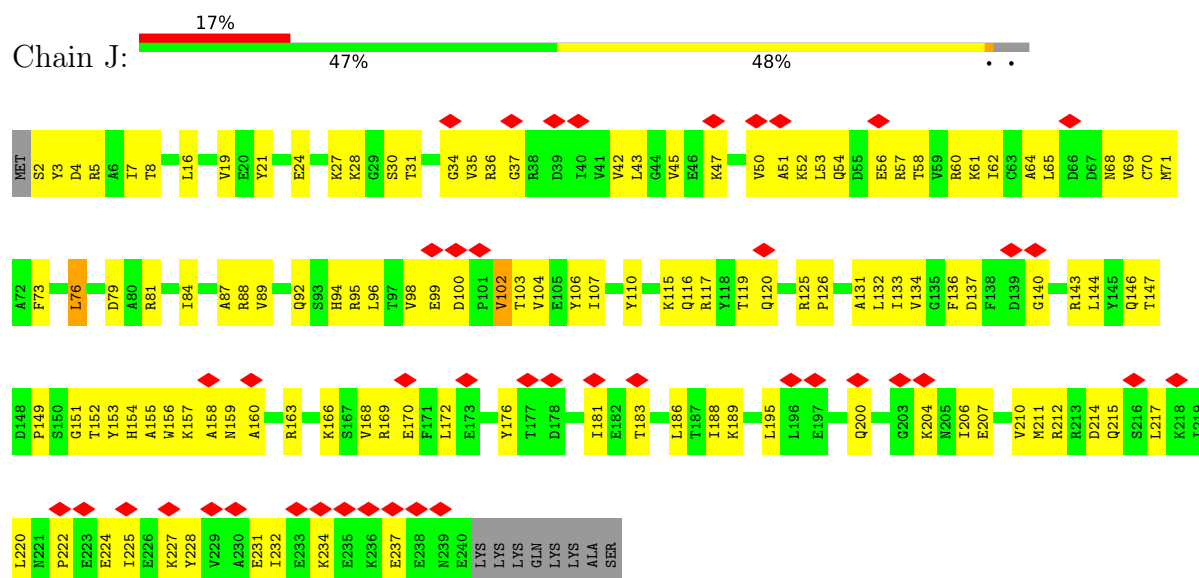
• Molecule 6: Proteasome subunit alpha type-2



• Molecule 7: Proteasome subunit alpha type-4



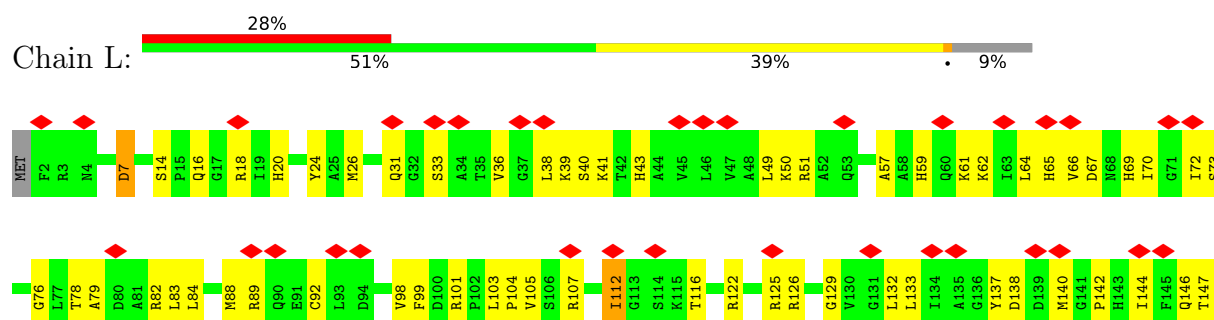
- Molecule 8: Proteasome subunit alpha type-7

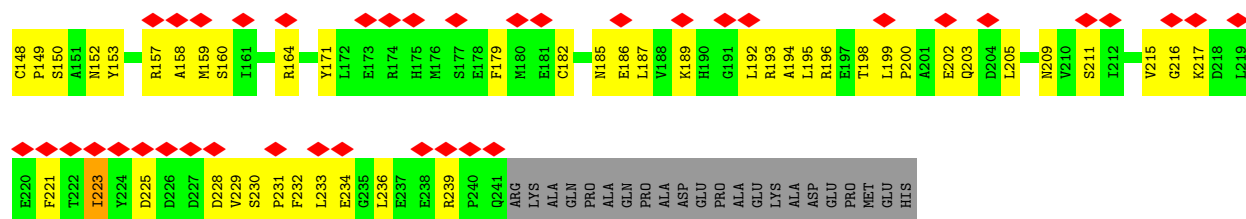


- Molecule 9: Proteasome subunit alpha type-5

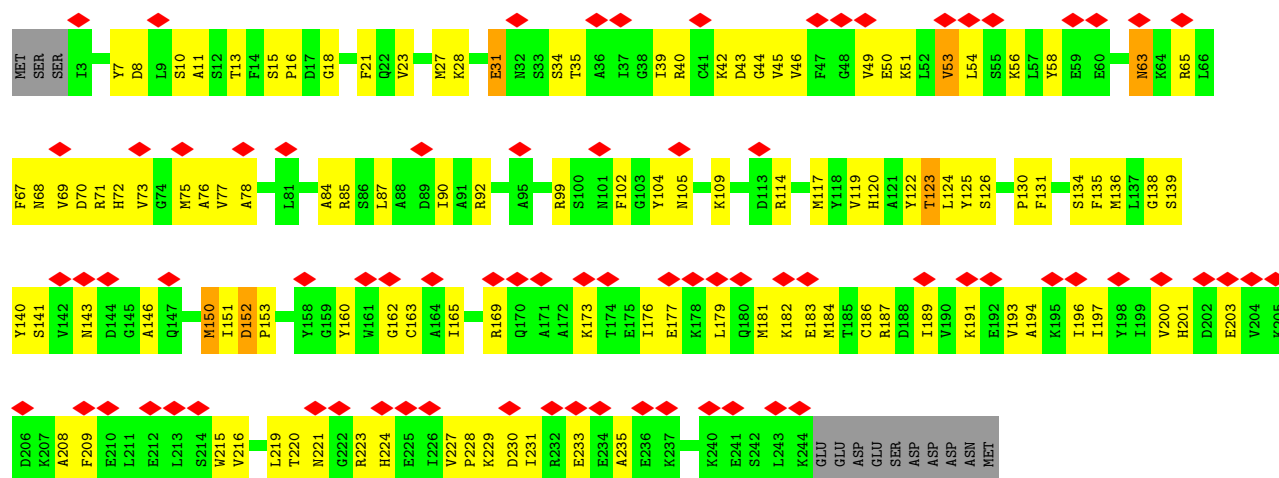


- Molecule 10: Proteasome subunit alpha type-1

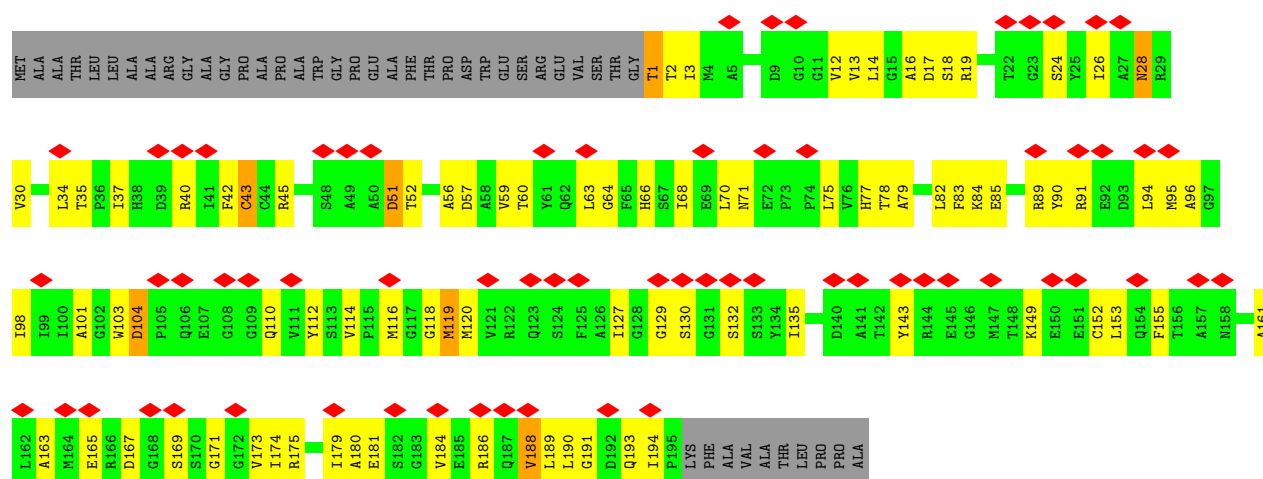




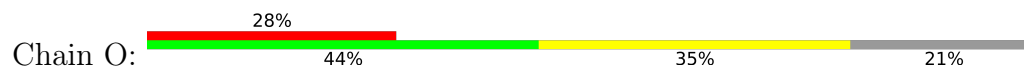
• Molecule 11: Proteasome subunit alpha type-3

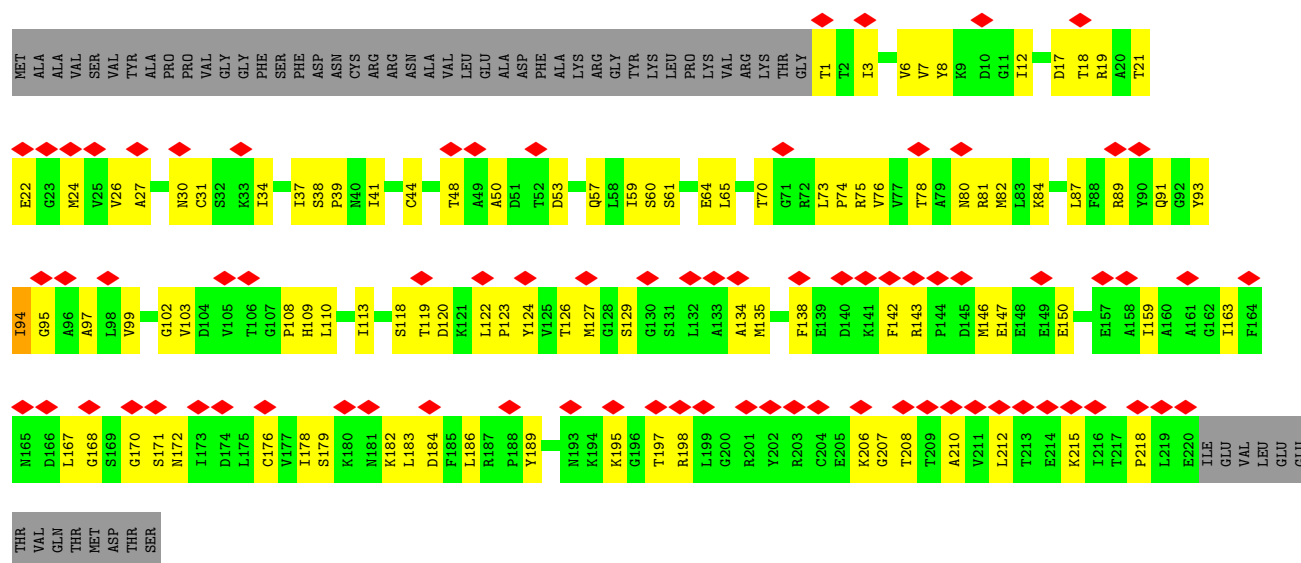


• Molecule 12: Proteasome subunit beta type-6

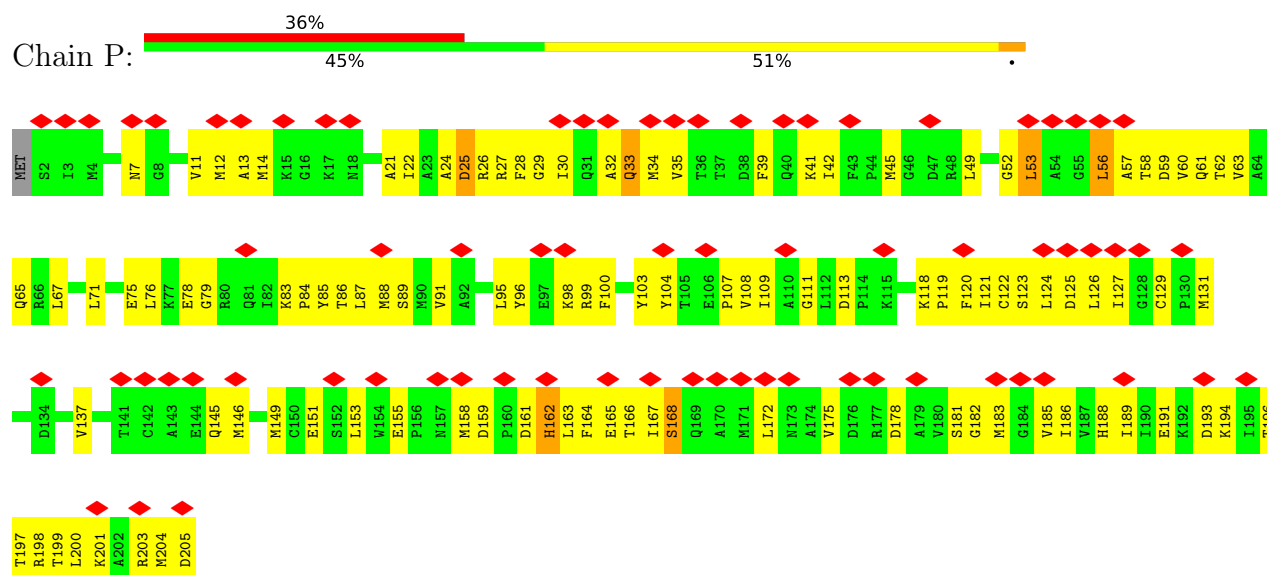


• Molecule 13: Proteasome subunit beta type-7



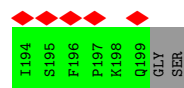


Chain P:

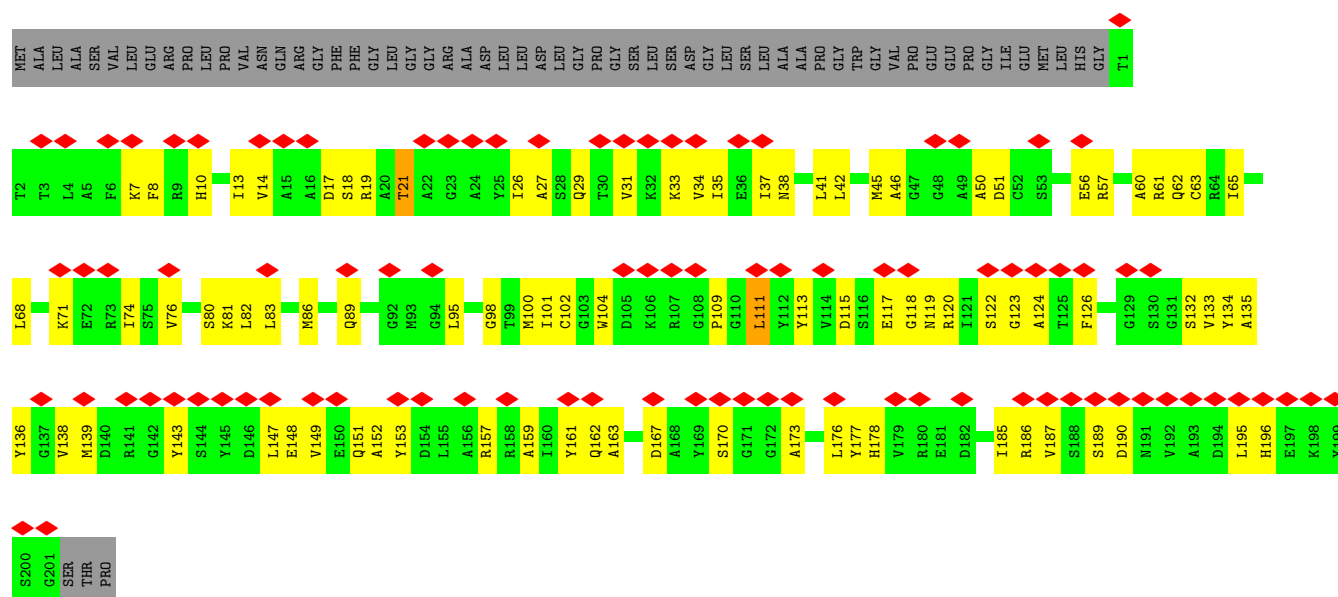


Chain Q:

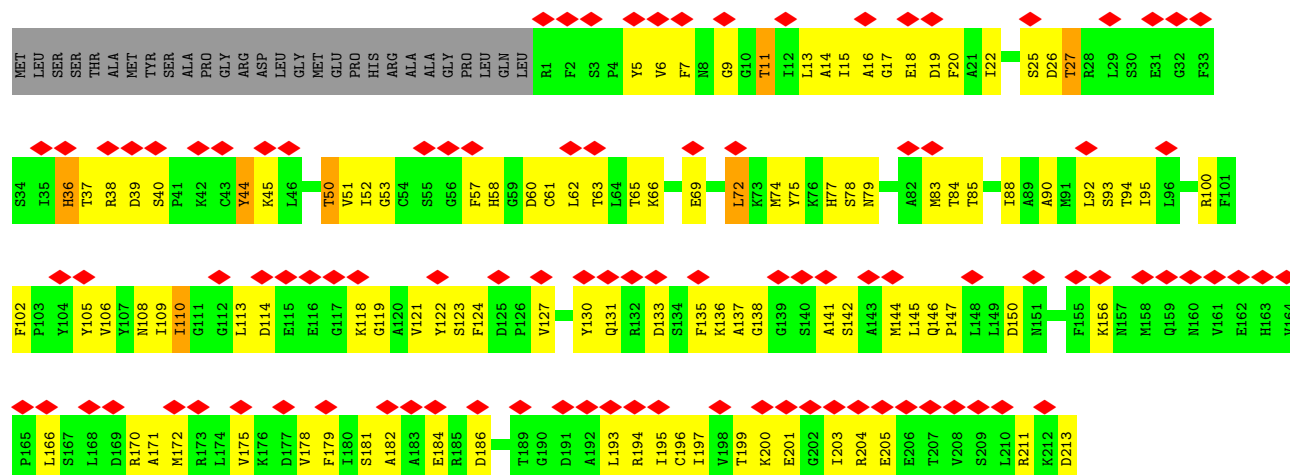
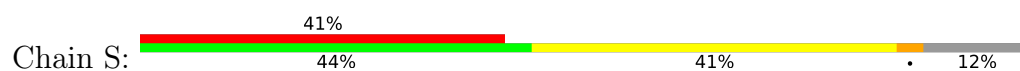




• Molecule 16: Proteasome subunit beta type-5

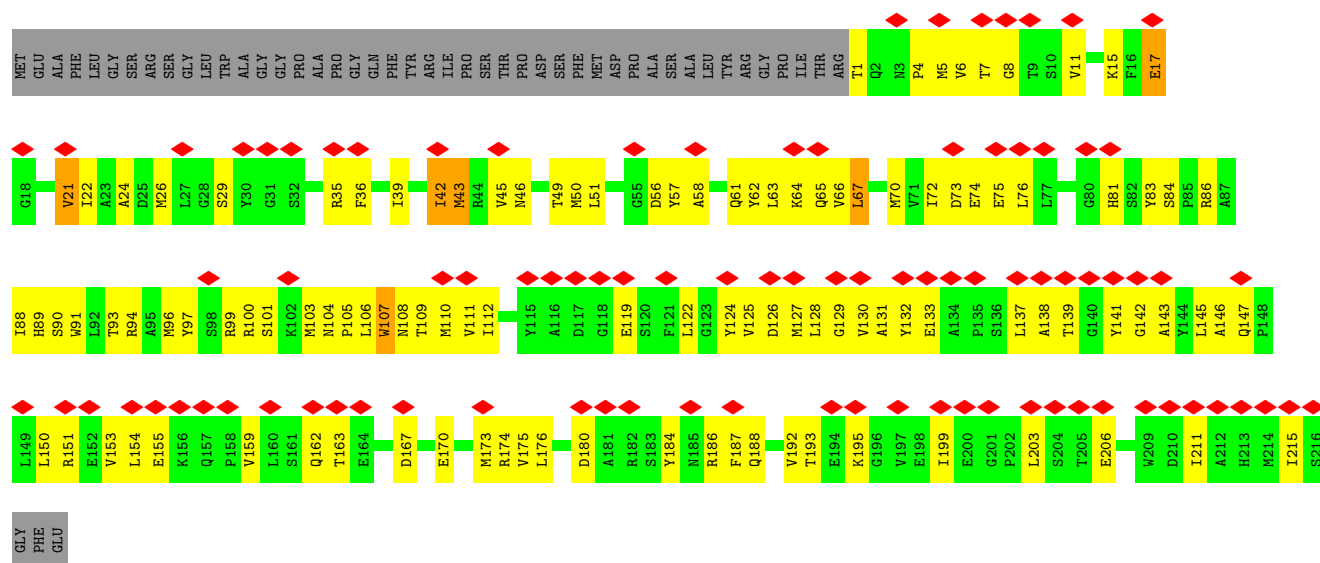


• Molecule 17: Proteasome subunit beta type-1

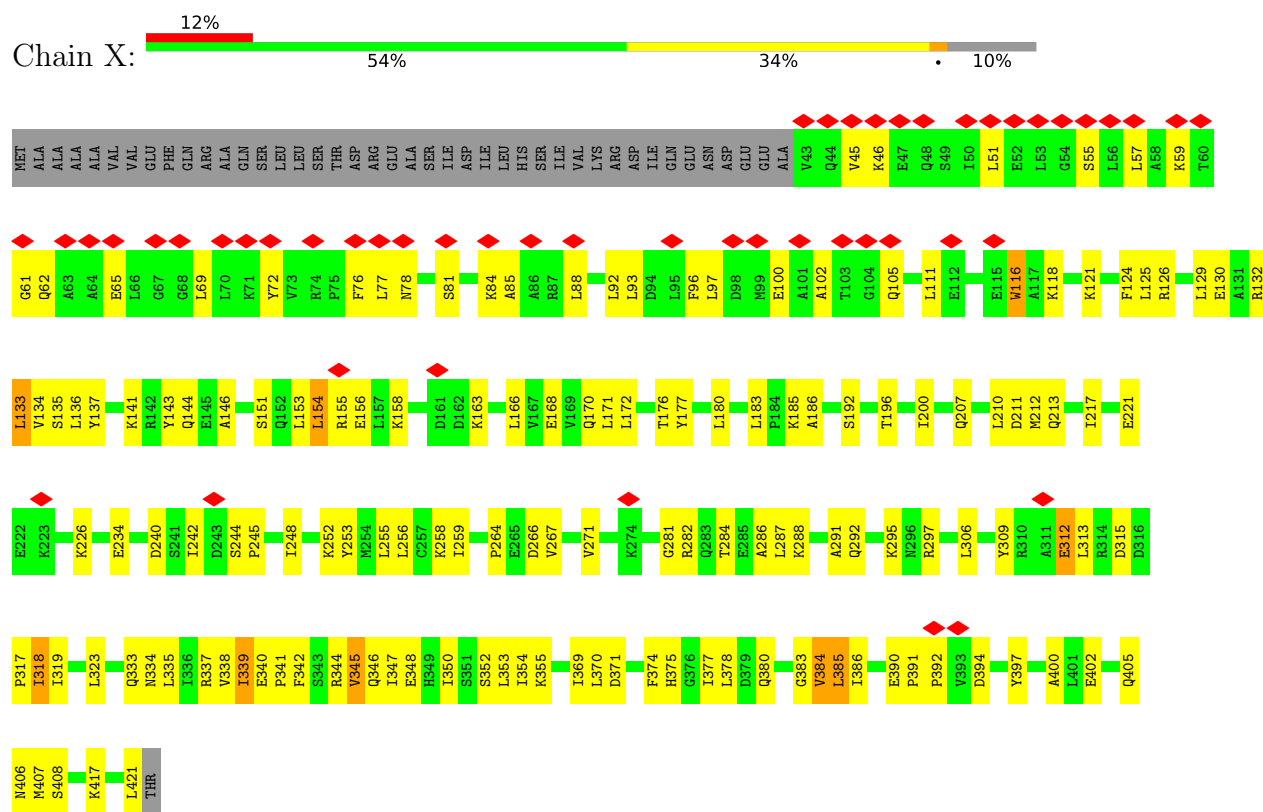


• Molecule 18: Proteasome subunit beta type-4

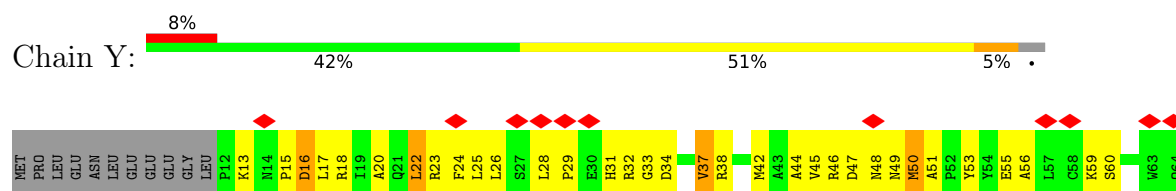


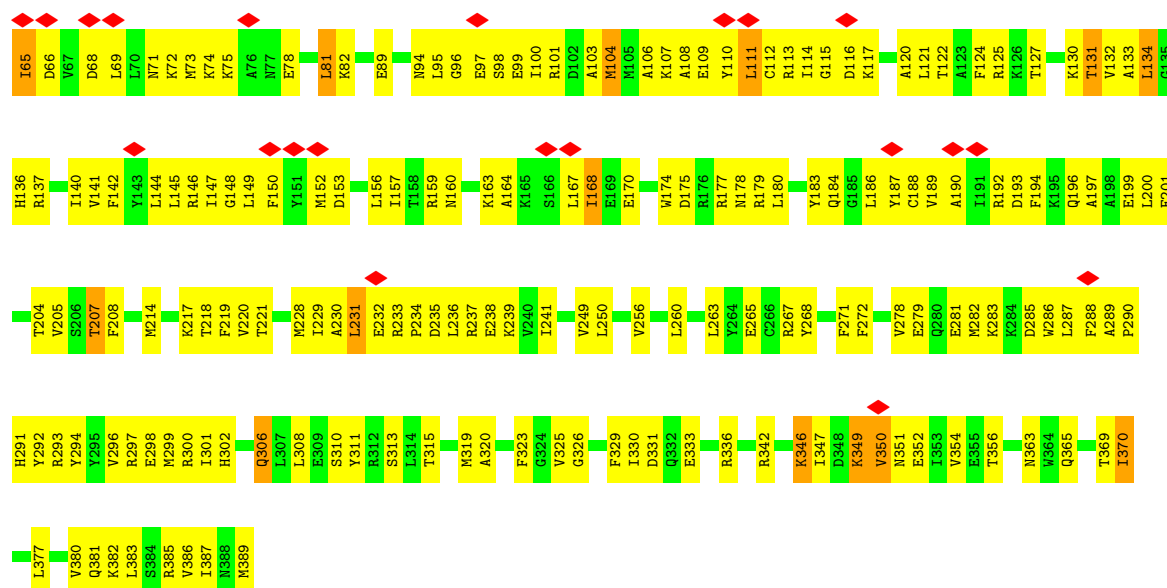


- Molecule 19: 26S proteasome non-ATPase regulatory subunit 11

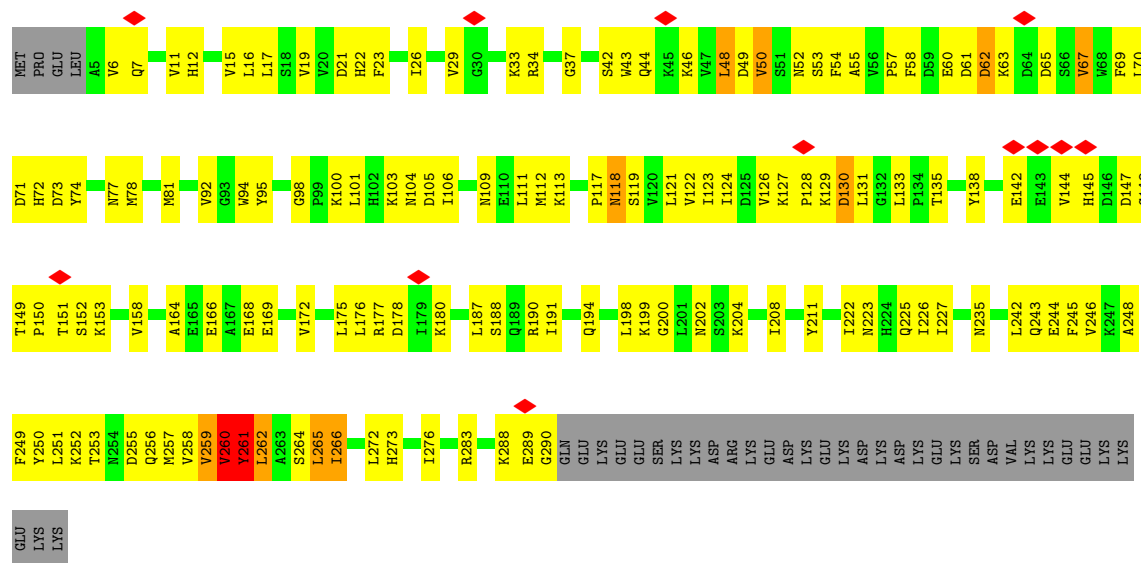


- Molecule 20: 26S proteasome non-ATPase regulatory subunit 6

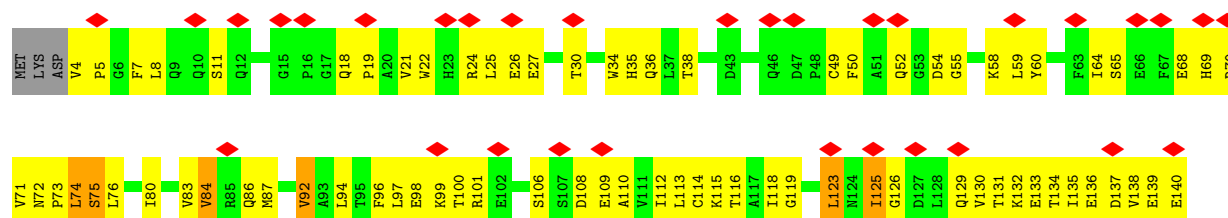


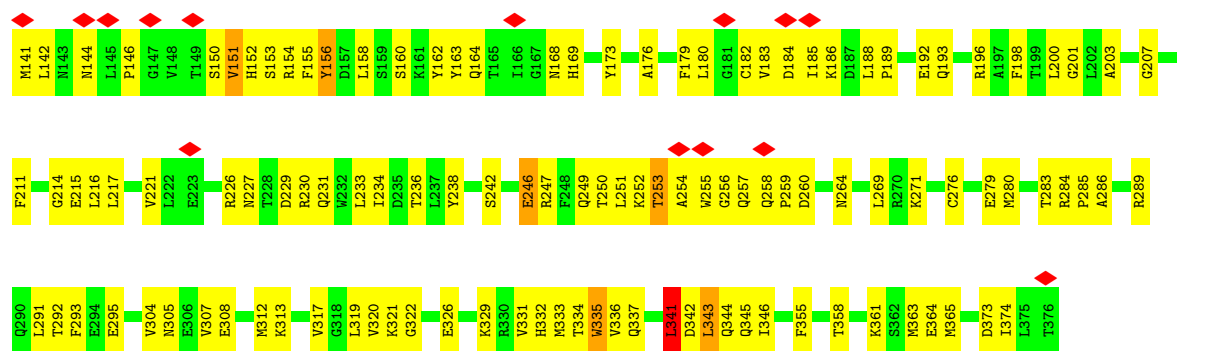


• Molecule 21: 26S proteasome non-ATPase regulatory subunit 7

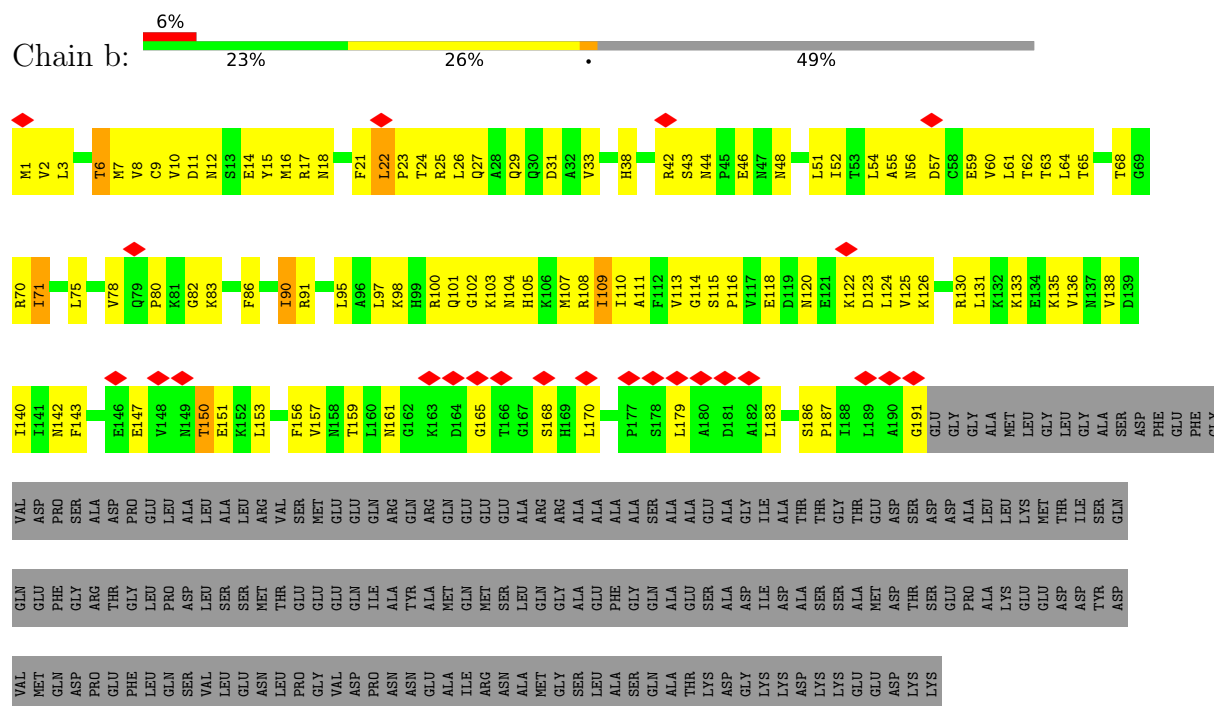


• Molecule 22: 26S proteasome non-ATPase regulatory subunit 13

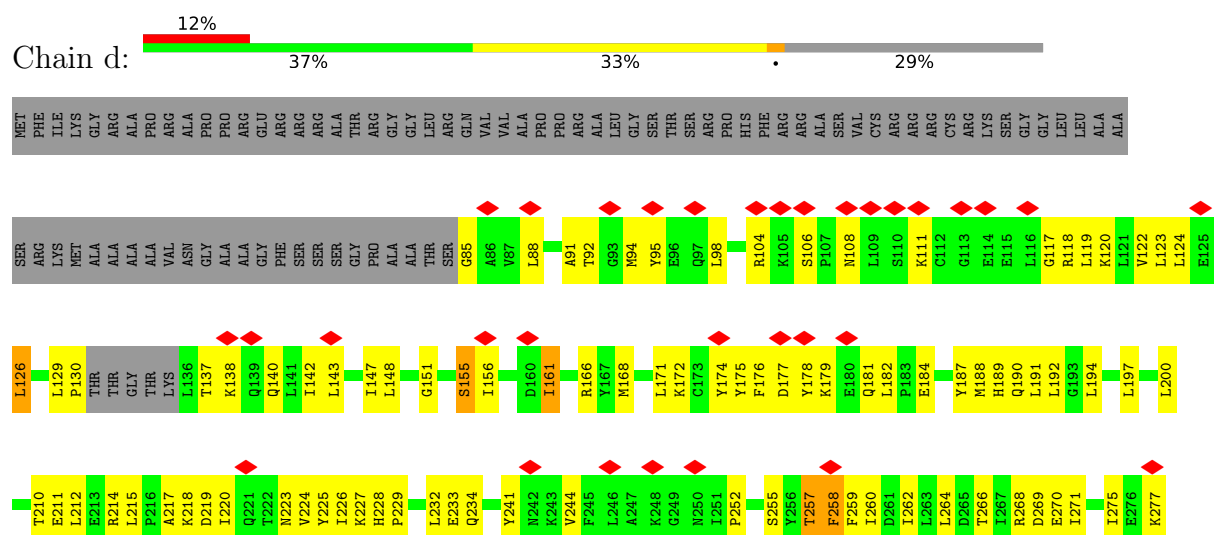


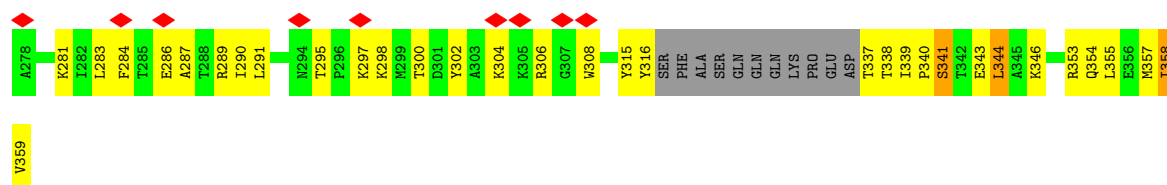


• Molecule 23: 26S proteasome non-ATPase regulatory subunit 4

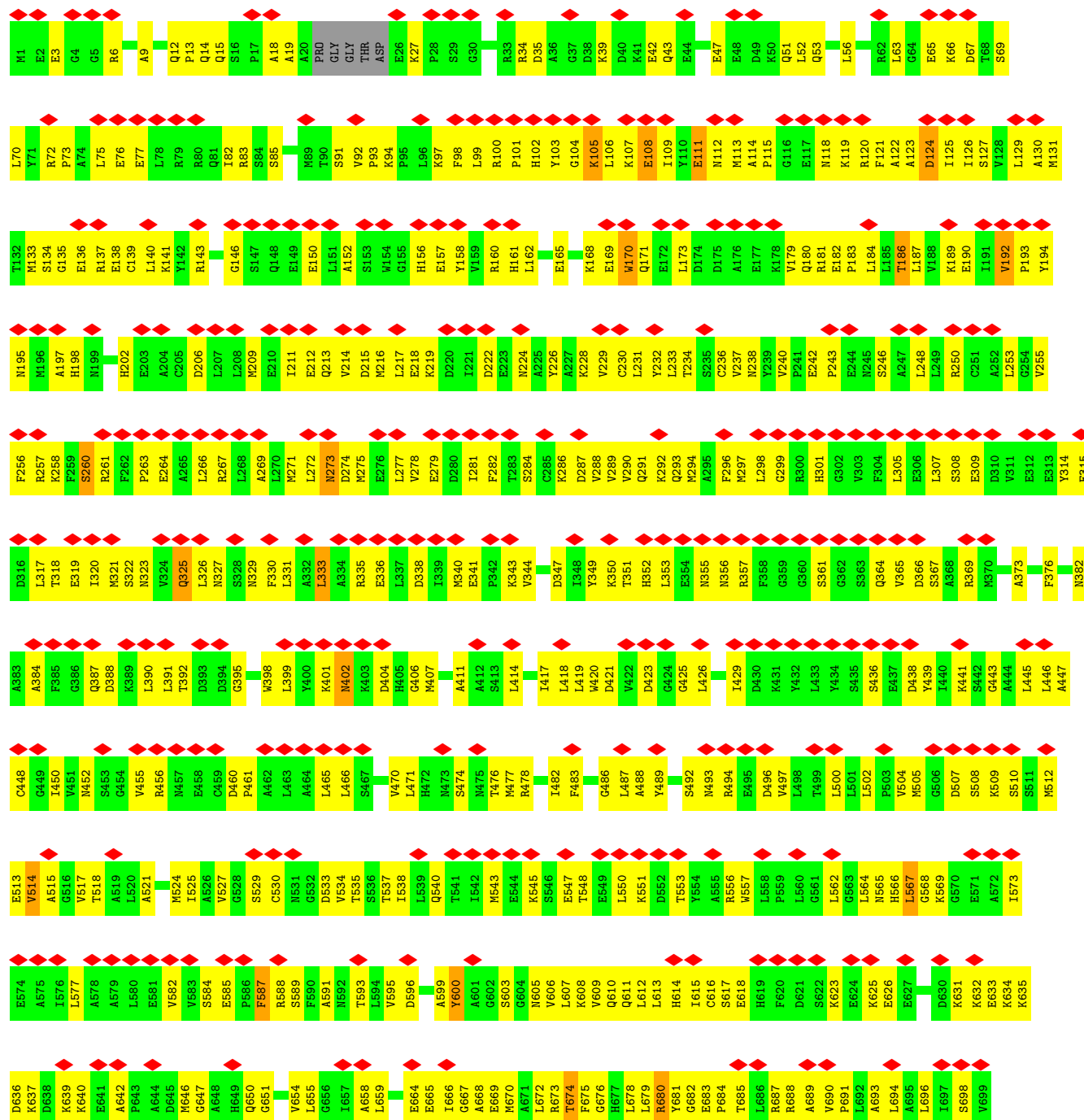


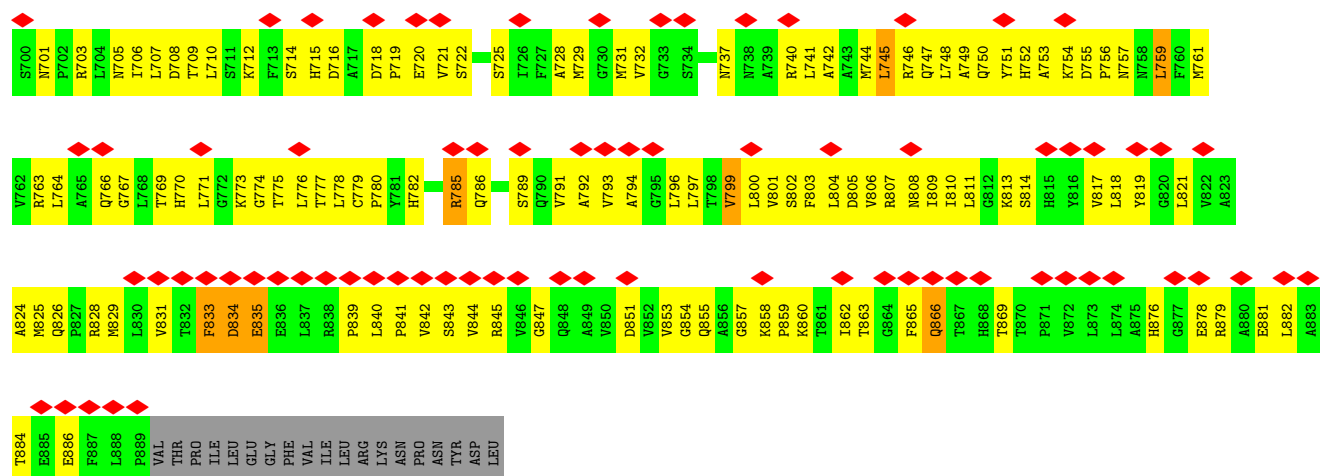
• Molecule 24: 26S proteasome non-ATPase regulatory subunit 8



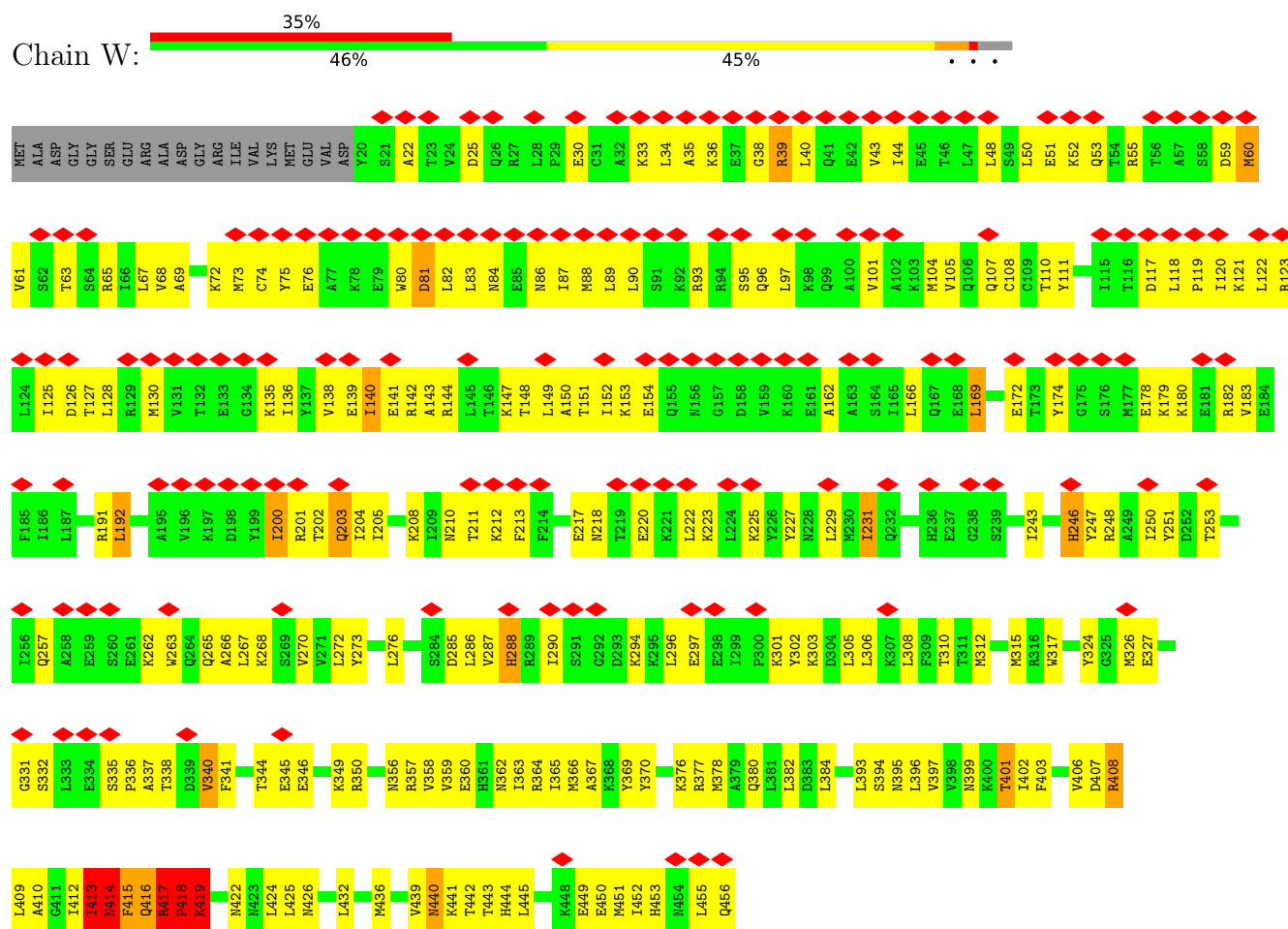


- Molecule 25: 26S proteasome non-ATPase regulatory subunit 2

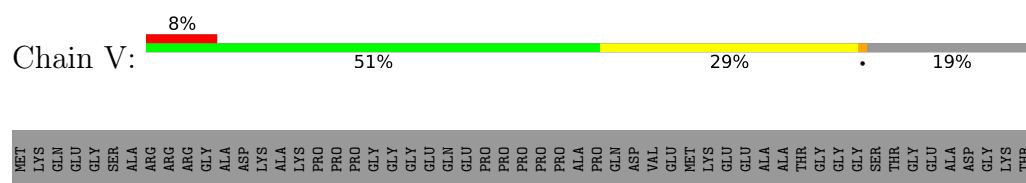


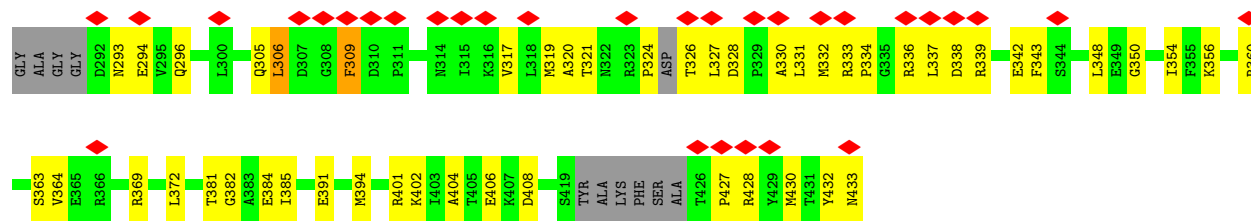


• Molecule 26: 26S proteasome non-ATPase regulatory subunit 12

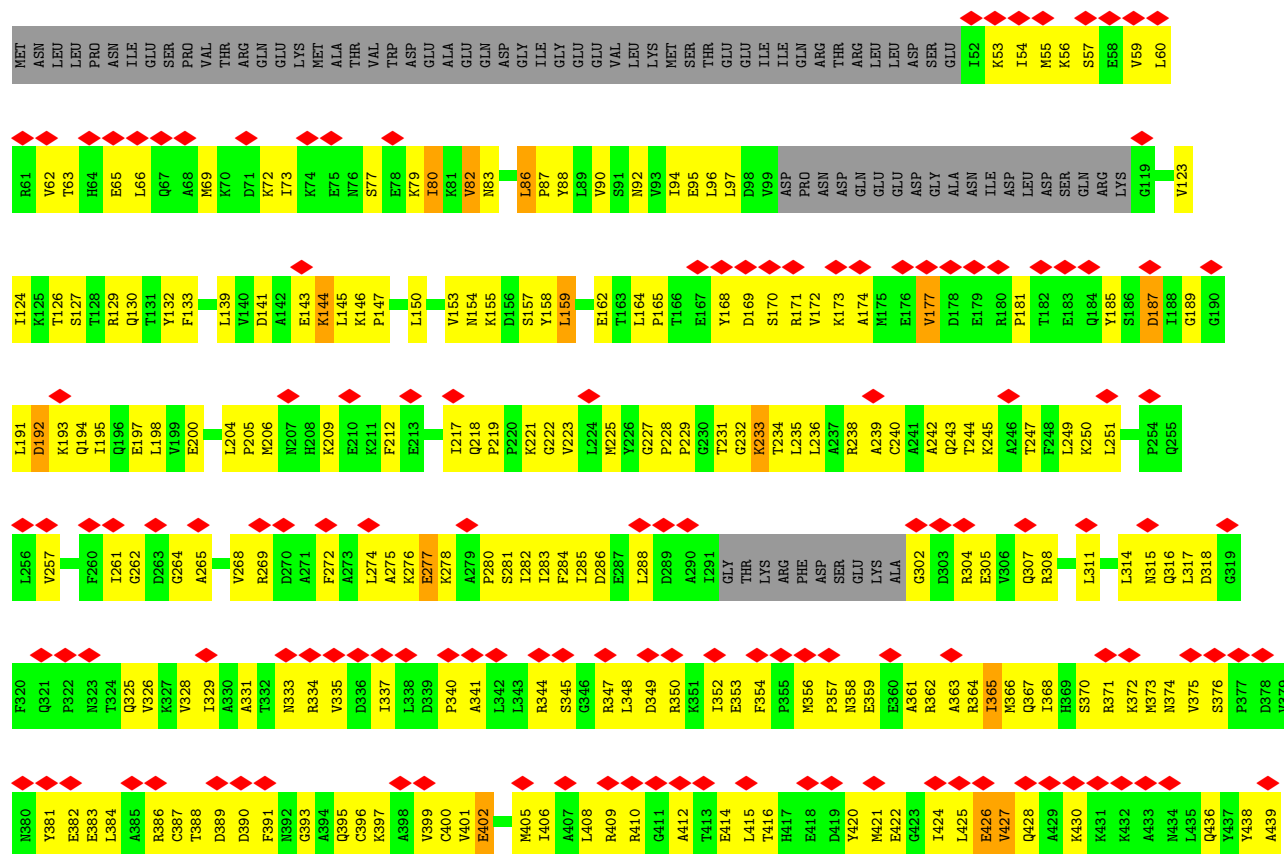


• Molecule 27: 26S proteasome non-ATPase regulatory subunit 3

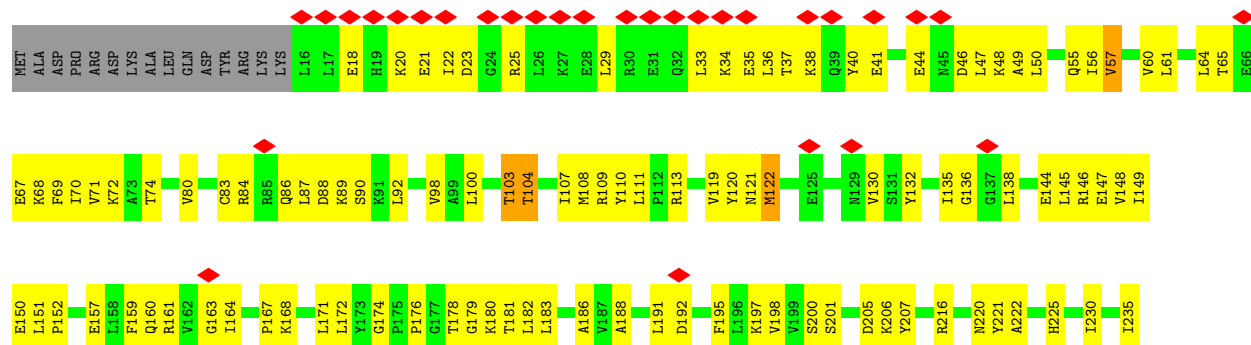


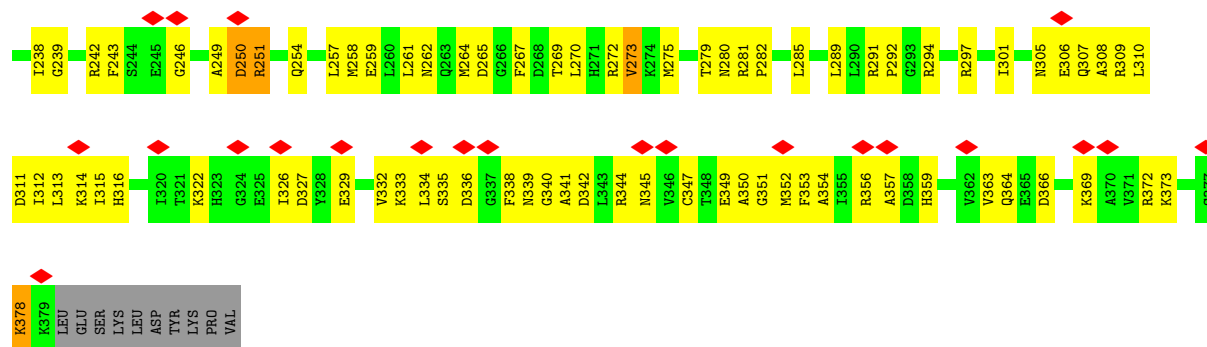


• Molecule 30: 26S proteasome regulatory subunit 6A



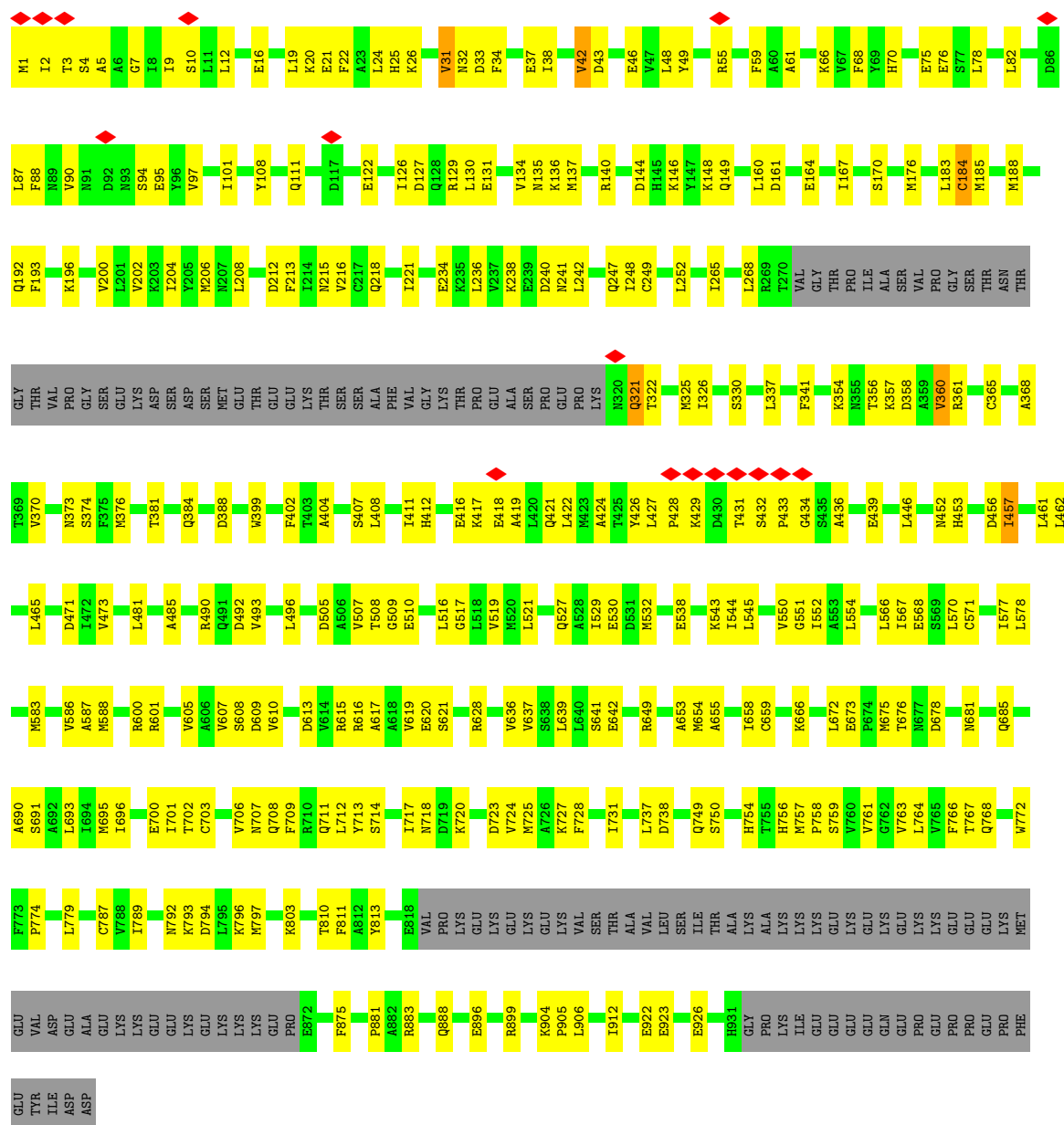
• Molecule 31: 26S protease regulatory subunit 10B



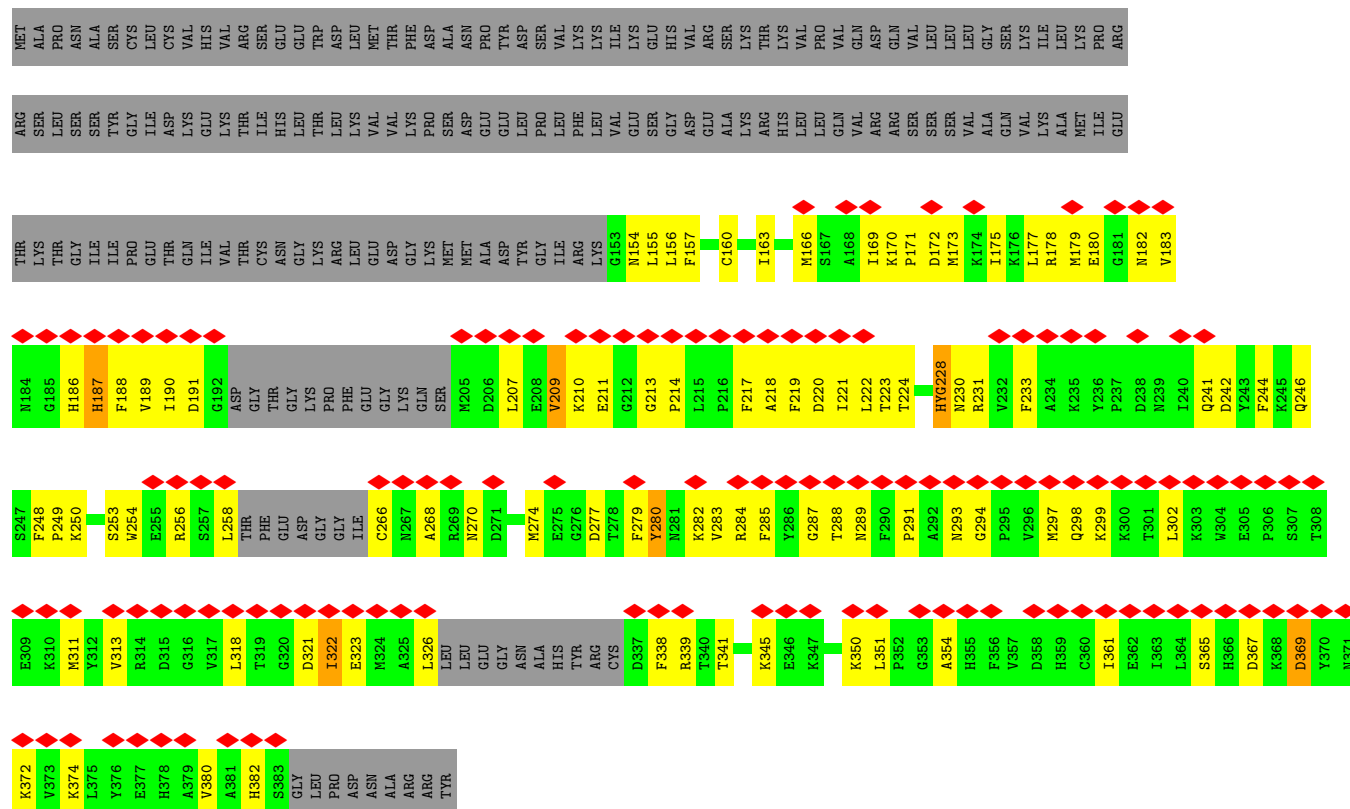
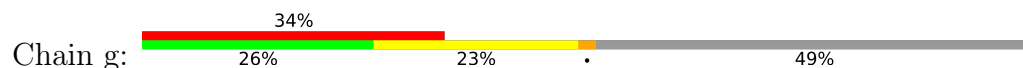


• Molecule 32: 26S proteasome non-ATPase regulatory subunit 1

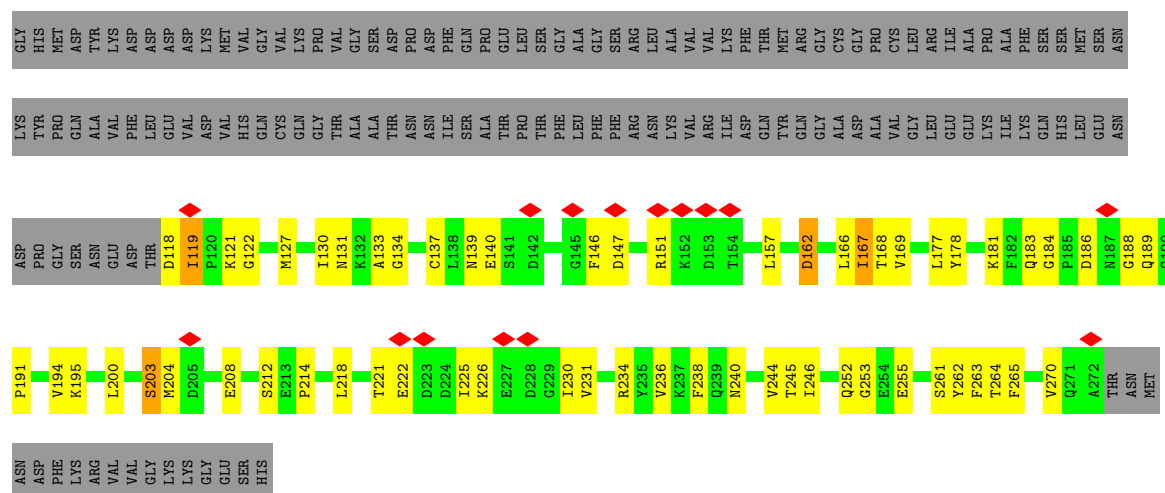
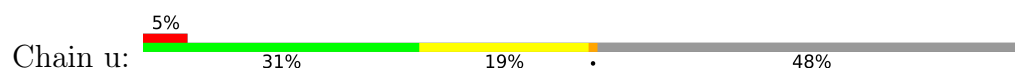
Chain U: 56% 30% 13%



- Molecule 33: FAT10



- Molecule 34: Thioredoxin-like protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73136	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.216	Depositor
Minimum map value	-0.584	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	356.32, 356.32, 356.32	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.048, 1.048, 1.048	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, ATP, ZN, CR8

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	B	0.23	0/3170	0.40	0/4278
2	C	0.28	0/3094	0.37	0/4158
3	D	0.28	0/3064	0.35	0/4131
4	c	0.31	0/2246	0.42	0/3037
5	G	0.16	0/1907	0.37	0/2580
6	H	0.18	0/1844	0.33	0/2499
7	I	0.17	0/1963	0.35	0/2650
8	J	0.17	0/1887	0.40	0/2553
9	K	0.16	0/1841	0.39	0/2486
10	L	0.14	0/1911	0.35	0/2584
11	M	0.14	0/1925	0.39	0/2592
12	N	0.15	0/1487	0.42	0/2013
13	O	0.15	0/1672	0.39	0/2267
14	P	0.17	0/1616	0.46	0/2180
15	Q	0.14	0/1621	0.38	0/2194
16	R	0.15	0/1590	0.43	0/2147
17	S	0.14	0/1671	0.39	0/2252
18	T	0.16	0/1716	0.44	1/2323 (0.0%)
19	X	0.22	0/3045	0.38	0/4105
20	Y	0.30	0/3173	0.58	1/4273 (0.0%)
21	Z	0.33	0/2320	0.57	1/3146 (0.0%)
22	a	0.20	0/3053	0.45	0/4133
23	b	0.22	0/1478	0.45	0/2001
24	d	0.21	0/2090	0.46	1/2820 (0.0%)
25	f	0.20	0/6948	0.51	0/9387
26	W	0.25	0/3612	0.52	1/4858 (0.0%)
27	V	0.22	0/3595	0.38	0/4851
28	e	0.31	0/437	0.47	0/595
29	A	0.20	0/3186	0.45	1/4298 (0.0%)
30	F	0.22	0/2840	0.52	0/3828
31	E	0.25	0/2931	0.43	0/3947
32	U	0.26	0/6574	0.36	1/8899 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.18	0/1635	0.42	0/2197
34	u	0.19	0/1265	0.36	0/1711
All	All	0.22	0/84407	0.43	7/113973 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
20	Y	0	1
22	a	0	1
26	W	0	1
31	E	0	1
All	All	0	4

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	Z	260	VAL	N-CA-CB	-10.76	93.48	111.23
32	U	31	VAL	N-CA-C	-6.66	107.38	113.71
20	Y	50	MET	CA-CB-CG	6.57	127.23	114.10
26	W	413	ILE	N-CA-C	-5.44	107.44	112.83
18	T	67	LEU	CA-CB-CG	5.26	134.71	116.30
24	d	126	LEU	CA-CB-CG	5.04	133.96	116.30
29	A	162	THR	CB-CA-C	-5.00	109.83	115.79

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	E	272	ARG	Sidechain
26	W	417	ARG	Sidechain
20	Y	349	LYS	Peptide
22	a	341	LEU	Peptide

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	B	3124	0	3188	143	0
2	C	3053	0	3173	135	0
3	D	3015	0	3053	119	0
4	c	2204	0	2208	112	0
5	G	1873	0	1872	97	0
6	H	1805	0	1784	70	0
7	I	1933	0	1923	70	0
8	J	1861	0	1846	112	0
9	K	1813	0	1796	110	0
10	L	1876	0	1856	100	0
11	M	1890	0	1880	98	0
12	N	1462	0	1428	74	0
13	O	1645	0	1648	76	0
14	P	1587	0	1598	111	0
15	Q	1588	0	1584	91	0
16	R	1559	0	1523	77	0
17	S	1641	0	1639	88	0
18	T	1683	0	1662	107	0
19	X	3001	0	3106	131	0
20	Y	3115	0	3120	252	0
21	Z	2277	0	2301	148	0
22	a	2995	0	3012	164	0
23	b	1458	0	1505	95	0
24	d	2048	0	2082	106	0
25	f	6836	0	6841	485	0
26	W	3564	0	3685	194	0
27	V	3527	0	3595	142	0
28	e	425	0	328	38	0
29	A	3138	0	3213	155	0
30	F	2803	0	2896	206	0
31	E	2887	0	2952	175	0
32	U	6459	0	6484	211	0
33	g	1622	0	1565	75	0
34	u	1240	0	1189	42	0
35	B	31	0	12	3	0
35	C	31	0	12	4	0
36	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	C	1	0	0	0	0
36	D	1	0	0	0	0
37	A	27	0	12	4	0
37	D	27	0	12	1	0
37	E	27	0	12	8	0
37	F	27	0	12	12	0
38	c	1	0	0	0	0
All	All	83181	0	83607	3980	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 24.

All (3980) 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)
3:D:201:GLY:HA2	3:D:307:VAL:O	1.58	1.01
25:f:104:GLY:HA2	25:f:107:LYS:HD2	1.49	0.95
34:u:168:THR:HG1	34:u:245:THR:HG1	1.14	0.94
20:Y:141:VAL:HG22	20:Y:160:ASN:HB3	1.48	0.94
25:f:682:GLY:HA2	25:f:688:ARG:HH12	1.31	0.93
25:f:825:MET:HE2	25:f:862:ILE:HB	1.50	0.92
8:J:158:ALA:H	9:K:58:LEU:HD21	1.34	0.92
20:Y:111:LEU:HA	20:Y:114:ILE:HB	1.49	0.92
20:Y:134:LEU:HD12	20:Y:168:ILE:HG23	1.49	0.92
30:F:234:THR:HG23	30:F:284:PHE:HE2	1.36	0.89
29:A:145:ASN:HD22	33:g:170:LYS:HE3	1.33	0.89
30:F:66:LEU:HD22	31:E:33:LEU:HD13	1.54	0.89
25:f:294:MET:HE3	25:f:294:MET:H	1.37	0.88
25:f:676:GLY:HA2	25:f:714:SER:HB3	1.54	0.88
27:V:175:MET:HE3	27:V:184:ALA:HA	1.55	0.88
4:c:292:MET:HA	21:Z:259:VAL:HG23	1.52	0.88
9:K:195:ILE:HD11	9:K:217:LEU:HD21	1.56	0.87
21:Z:260:VAL:HG12	21:Z:261:TYR:H	1.37	0.87
9:K:93:ARG:HD2	16:R:68:LEU:HD13	1.56	0.87
20:Y:180:LEU:HD13	20:Y:200:LEU:HB2	1.57	0.87
24:d:308:TRP:HE1	24:d:316:TYR:HB3	1.38	0.86
29:A:274:PHE:HB2	29:A:319:MET:HE1	1.57	0.86
21:Z:259:VAL:HG22	21:Z:260:VAL:H	1.40	0.86
20:Y:133:ALA:HB3	20:Y:136:HIS:HE1	1.40	0.85
25:f:771:LEU:HG	25:f:774:GLY:H	1.40	0.85
20:Y:189:VAL:HG22	28:e:39:TRP:CD1	2.11	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:647:GLY:HA2	25:f:650:GLN:HE22	1.41	0.85
8:J:88:ARG:HE	15:Q:69:MET:HE1	1.41	0.85
17:S:63:THR:HA	18:T:94:ARG:HH22	1.41	0.85
1:B:305:ILE:HG13	2:C:224:ILE:HD11	1.57	0.85
14:P:12:MET:HG3	14:P:167:ILE:HD11	1.59	0.85
8:J:99:GLU:HB3	16:R:81:LYS:HG3	1.59	0.84
21:Z:260:VAL:HG13	27:V:480:ILE:HD11	1.60	0.84
1:B:208:PRO:HD2	25:f:722:SER:HB2	1.57	0.84
22:a:74:LEU:HD11	22:a:109:GLU:HG2	1.60	0.84
25:f:670:MET:O	25:f:673:ARG:NH1	2.11	0.83
5:G:183:VAL:HA	5:G:189:TRP:HH2	1.43	0.83
20:Y:106:ALA:O	20:Y:110:TYR:N	2.12	0.83
25:f:689:ALA:O	25:f:693:ALA:HB3	1.78	0.83
30:F:198:LEU:HD21	30:F:240:CYS:HB2	1.60	0.83
20:Y:107:LYS:HZ1	20:Y:120:ALA:N	1.76	0.83
8:J:71:MET:HB3	8:J:133:ILE:HD12	1.58	0.82
28:e:54:ASN:ND2	28:e:55:GLN:OE1	2.12	0.82
32:U:1:MET:HE2	32:U:2:ILE:HG22	1.62	0.82
33:g:311:MET:O	33:g:354:ALA:HA	1.78	0.82
22:a:312:MET:HE1	26:W:369:TYR:HD2	1.45	0.81
5:G:179:LEU:HB3	6:H:56:LEU:HD21	1.61	0.81
21:Z:127:LYS:O	21:Z:129:LYS:NZ	2.13	0.81
14:P:25:ASP:HA	14:P:185:VAL:HG12	1.62	0.81
25:f:333:LEU:HD21	25:f:810:ILE:HG21	1.63	0.81
21:Z:260:VAL:CA	27:V:480:ILE:HD11	2.10	0.81
32:U:509:GLY:HA3	32:U:544:ILE:HG12	1.62	0.80
20:Y:189:VAL:HG22	28:e:39:TRP:HD1	1.46	0.80
20:Y:164:ALA:HA	20:Y:168:ILE:HB	1.62	0.80
25:f:637:LYS:HE3	25:f:655:LEU:HD22	1.61	0.80
25:f:281:ILE:H	25:f:286:LYS:HZ1	1.27	0.80
14:P:13:ALA:HB3	14:P:137:VAL:HG23	1.64	0.80
4:c:253:LYS:HG3	19:X:406:ASN:HD21	1.47	0.79
25:f:789:SER:H	25:f:793:VAL:HB	1.48	0.79
15:Q:92:LEU:HD11	15:Q:121:LEU:HD12	1.63	0.79
24:d:166:ARG:HB2	32:U:10:SER:HB2	1.64	0.79
26:W:247:TYR:HB3	26:W:270:VAL:HG22	1.66	0.78
1:B:156:VAL:HG23	29:A:92:PRO:HD3	1.65	0.78
3:D:203:LEU:HB2	3:D:327:LEU:HD13	1.65	0.78
17:S:136:LYS:HE3	17:S:136:LYS:HA	1.66	0.78
25:f:349:TYR:OH	25:f:751:TYR:O	2.00	0.77
29:A:212:VAL:HG12	29:A:339:ARG:HB2	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:159:MET:HE3	10:L:160:SER:H	1.48	0.77
3:D:144:PRO:HG2	3:D:147:ALA:HB2	1.66	0.77
10:L:88:MET:SD	10:L:112:ILE:HD11	2.23	0.77
30:F:344:ARG:HH22	31:E:344:ARG:HD2	1.48	0.77
19:X:338:VAL:HG13	19:X:339:ILE:HG23	1.67	0.77
25:f:318:THR:HA	25:f:321:MET:HE3	1.66	0.77
35:B:501:ATP:O1G	2:C:310:ARG:NH2	2.17	0.77
8:J:95:ARG:HB3	15:Q:62:LYS:HE2	1.65	0.77
25:f:505:MET:O	25:f:540:GLN:NE2	2.17	0.77
23:b:3:LEU:HD22	23:b:44:ASN:HD21	1.49	0.77
25:f:192:VAL:HG13	25:f:193:PRO:HD3	1.65	0.77
31:E:135:ILE:O	37:E:501:ADP:N6	2.16	0.77
26:W:150:ALA:HA	26:W:153:LYS:HE2	1.64	0.77
25:f:486:GLY:HA2	25:f:525:ILE:HD11	1.67	0.77
8:J:71:MET:HE1	8:J:73:PHE:HD2	1.48	0.76
25:f:672:LEU:HD11	25:f:707:LEU:HG	1.66	0.76
25:f:271:MET:HE3	25:f:271:MET:O	1.86	0.76
31:E:37:THR:O	31:E:40:TYR:HB3	1.86	0.76
19:X:81:SER:H	19:X:84:LYS:HE2	1.50	0.76
20:Y:300:ARG:NH1	20:Y:333:GLU:OE2	2.18	0.76
32:U:757:MET:HE3	32:U:758:PRO:HD3	1.67	0.76
29:A:364:VAL:HG12	29:A:404:ALA:HB3	1.67	0.76
32:U:16:GLU:HB3	32:U:19:LEU:HD12	1.67	0.76
4:c:128:ASN:O	33:g:231:ARG:NH2	2.19	0.76
20:Y:23:ARG:HH21	20:Y:59:LYS:HE2	1.51	0.76
15:Q:38:MET:HB3	15:Q:42:ILE:HG23	1.67	0.76
14:P:149:MET:O	14:P:153:LEU:HB3	1.85	0.76
29:A:213:LEU:HD23	29:A:319:MET:HG3	1.66	0.75
19:X:312:GLU:HB2	19:X:313:LEU:HD22	1.67	0.75
2:C:340:ARG:HH12	20:Y:174:TRP:HB2	1.52	0.75
21:Z:260:VAL:HA	27:V:480:ILE:HD11	1.69	0.75
22:a:50:PHE:O	22:a:86:GLN:NE2	2.20	0.75
25:f:250:ARG:HG2	25:f:253:LEU:HG	1.69	0.75
2:C:217:SER:OG	3:D:291:GLU:OE1	2.05	0.75
28:e:40:GLU:N	28:e:40:GLU:OE2	2.19	0.75
33:g:210:LYS:HG3	33:g:211:GLU:HG3	1.67	0.75
10:L:189:LYS:NZ	10:L:232:PHE:O	2.20	0.75
12:N:84:LYS:HB2	12:N:120:MET:HB2	1.68	0.75
21:Z:144:VAL:HG23	21:Z:145:HIS:H	1.52	0.75
13:O:94:ILE:HA	14:P:99:ARG:HH12	1.53	0.74
29:A:211:GLY:O	29:A:338:ASP:N	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:148:THR:O	26:W:151:THR:OG1	2.05	0.74
31:E:83:CYS:HA	31:E:107:ILE:HB	1.70	0.74
22:a:321:LYS:HZ1	22:a:336:VAL:HG13	1.53	0.74
25:f:612:LEU:HG	25:f:632:LYS:HG2	1.68	0.74
1:B:209:GLU:O	1:B:213:GLU:HB2	1.88	0.74
12:N:118:GLY:O	18:T:61:GLN:NE2	2.21	0.74
20:Y:319:MET:HG2	20:Y:330:ILE:HD13	1.70	0.74
7:I:119:GLN:NE2	8:J:79:ASP:OD1	2.21	0.74
9:K:207:GLU:HA	29:A:372:LEU:HD11	1.67	0.74
21:Z:69:PHE:HB2	23:b:95:LEU:HD11	1.70	0.74
23:b:15:TYR:HD1	23:b:116:PRO:HD2	1.52	0.74
15:Q:42:ILE:HD11	15:Q:104:LEU:HG	1.70	0.73
30:F:191:LEU:HB3	30:F:194:GLN:HB2	1.70	0.73
23:b:46:GLU:N	23:b:46:GLU:OE2	2.20	0.73
5:G:131:MET:HA	5:G:131:MET:HE2	1.69	0.73
27:V:105:SER:HB2	27:V:173:ILE:HG21	1.69	0.73
8:J:136:PHE:HB3	8:J:140:GLY:HA2	1.70	0.73
12:N:75:LEU:O	12:N:78:THR:OG1	2.06	0.73
21:Z:260:VAL:CG1	27:V:480:ILE:HD11	2.18	0.73
26:W:366:MET:O	26:W:370:TYR:N	2.20	0.73
30:F:53:LYS:H	30:F:53:LYS:HD2	1.51	0.73
4:c:299:CYS:O	4:c:303:MET:HG2	1.89	0.73
25:f:325:GLN:O	25:f:329:ASN:ND2	2.21	0.73
27:V:175:MET:HE1	27:V:187:ILE:HB	1.69	0.73
32:U:673:GLU:OE2	32:U:708:GLN:NE2	2.20	0.73
16:R:135:ALA:HB2	16:R:163:ALA:HB2	1.71	0.73
24:d:270:GLU:OE2	27:V:443:ARG:NH1	2.20	0.73
20:Y:290:PRO:HB2	20:Y:291:HIS:ND1	2.04	0.73
21:Z:256:GLN:O	21:Z:260:VAL:HB	1.89	0.73
27:V:190:ASP:O	27:V:194:LYS:NZ	2.21	0.73
2:C:280:LEU:HD21	2:C:291:VAL:HG11	1.71	0.73
25:f:764:LEU:O	25:f:858:LYS:NZ	2.21	0.73
31:E:34:LYS:O	31:E:37:THR:OG1	2.06	0.73
16:R:35:ILE:HD13	16:R:56:GLU:HG3	1.71	0.73
22:a:156:TYR:HB2	22:a:179:PHE:HB2	1.71	0.73
22:a:186:LYS:HB3	22:a:193:GLN:HE22	1.52	0.72
33:g:256:ARG:HB3	33:g:268:ALA:HB3	1.70	0.72
2:C:340:ARG:NH2	20:Y:175:ASP:OD1	2.23	0.72
11:M:75:MET:HE2	11:M:75:MET:HA	1.70	0.72
25:f:672:LEU:HD22	25:f:708:ASP:HB3	1.71	0.72
25:f:826:GLN:HB2	25:f:865:PHE:HE1	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:308:LEU:HG	26:W:315:MET:HE2	1.71	0.72
11:M:71:ARG:HH12	18:T:75:GLU:HB3	1.54	0.72
23:b:11:ASP:O	23:b:29:GLN:NE2	2.22	0.72
30:F:200:GLU:OE1	30:F:350:ARG:NH2	2.21	0.72
1:B:222:VAL:HG22	1:B:349:ARG:HB2	1.71	0.72
5:G:50:ILE:HD12	5:G:79:VAL:HB	1.71	0.72
17:S:88:ILE:O	17:S:92:LEU:HD22	1.90	0.72
25:f:721:VAL:HG11	25:f:754:LYS:HE3	1.69	0.72
30:F:189:GLY:H	37:F:501:ADP:HN62	1.36	0.72
6:H:166:ASN:OD1	6:H:169:ASN:ND2	2.19	0.72
10:L:65:HIS:HB3	10:L:223:ILE:HD11	1.70	0.72
20:Y:369:THR:HG21	21:Z:257:MET:HE1	1.72	0.72
29:A:319:MET:HA	29:A:319:MET:HE2	1.69	0.72
32:U:628:ARG:NH1	32:U:749:GLN:OE1	2.23	0.72
2:C:45:LEU:HB3	3:D:61:ILE:HG21	1.70	0.72
13:O:135:MET:HE2	13:O:135:MET:HA	1.72	0.72
2:C:333:SER:HA	2:C:336:MET:HG3	1.71	0.71
22:a:312:MET:HE1	26:W:369:TYR:CD2	2.25	0.71
19:X:143:TYR:CZ	19:X:144:GLN:HG2	2.26	0.71
21:Z:259:VAL:O	21:Z:260:VAL:C	2.32	0.71
21:Z:260:VAL:CB	27:V:480:ILE:HD11	2.20	0.71
30:F:249:LEU:HB2	30:F:283:ILE:HA	1.70	0.71
1:B:111:THR:OG1	1:B:124:SER:OG	2.08	0.71
10:L:39:LYS:H	10:L:157:ARG:HH12	1.38	0.71
20:Y:194:PHE:HB3	20:Y:229:ILE:HG23	1.70	0.71
21:Z:34:ARG:HG2	21:Z:98:GLY:HA3	1.70	0.71
25:f:665:GLU:OE2	25:f:665:GLU:N	2.19	0.71
31:E:309:ARG:NH2	31:E:332:VAL:O	2.21	0.71
13:O:97:ALA:HB1	13:O:127:MET:HE2	1.70	0.71
25:f:545:LYS:O	25:f:548:THR:OG1	2.08	0.71
1:B:50:PRO:O	1:B:52:VAL:HG23	1.90	0.71
4:c:71:ASP:OD1	4:c:72:VAL:N	2.24	0.71
25:f:685:THR:H	25:f:689:ALA:HB3	1.56	0.71
30:F:232:GLY:HA2	37:F:501:ADP:H5'2	1.69	0.71
32:U:66:LYS:O	32:U:70:HIS:ND1	2.22	0.71
32:U:691:SER:HG	32:U:713:TYR:HH	1.36	0.71
20:Y:237:ARG:HA	20:Y:241:ILE:HB	1.71	0.71
27:V:463:MET:HA	27:V:463:MET:HE2	1.73	0.71
30:F:132:TYR:HE2	31:E:56:ILE:HD13	1.54	0.71
1:B:401:GLU:OE2	2:C:313:ARG:NH1	2.22	0.71
25:f:791:VAL:HG13	25:f:800:LEU:HD21	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:251:TYR:O	26:W:257:GLN:NE2	2.24	0.71
26:W:416:GLN:O	26:W:417:ARG:C	2.34	0.71
30:F:154:ASN:OD1	30:F:157:SER:N	2.24	0.71
19:X:264:PRO:HB3	19:X:291:ALA:HB1	1.73	0.71
20:Y:44:ALA:HA	20:Y:49:ASN:HD21	1.55	0.71
21:Z:109:ASN:OD1	21:Z:119:SER:OG	2.09	0.71
30:F:382:GLU:HB3	30:F:386:ARG:HH21	1.56	0.71
17:S:194:ARG:NH2	17:S:196:CYS:SG	2.63	0.70
20:Y:228:MET:HE1	20:Y:260:LEU:HA	1.73	0.70
10:L:140:MET:SD	10:L:140:MET:N	2.64	0.70
16:R:102:CYS:HB3	16:R:111:LEU:HD23	1.71	0.70
30:F:143:GLU:N	30:F:143:GLU:OE2	2.23	0.70
2:C:351:MET:HE2	2:C:387:VAL:HG22	1.72	0.70
21:Z:260:VAL:HA	27:V:480:ILE:CD1	2.21	0.70
20:Y:111:LEU:O	20:Y:116:ASP:N	2.24	0.70
10:L:16:GLN:HB2	10:L:18:ARG:HH22	1.56	0.70
20:Y:196:GLN:HA	20:Y:199:GLU:HG2	1.73	0.70
25:f:766:GLN:NE2	25:f:769:THR:OG1	2.25	0.70
32:U:265:ILE:HD11	32:U:326:ILE:HG23	1.73	0.70
10:L:88:MET:HA	10:L:88:MET:HE3	1.73	0.70
31:E:71:VAL:HG21	31:E:107:ILE:HD11	1.74	0.70
31:E:147:GLU:HA	31:E:151:LEU:HG	1.72	0.70
32:U:75:GLU:OE2	32:U:75:GLU:N	2.18	0.70
9:K:55:THR:HG21	29:A:430:MET:HE1	1.73	0.70
25:f:340:MET:HE3	25:f:340:MET:H	1.56	0.70
30:F:86:LEU:HG	30:F:87:PRO:HD3	1.74	0.70
20:Y:180:LEU:HD21	20:Y:201:PHE:CE2	2.26	0.70
25:f:460:ASP:OD2	25:f:494:ARG:NH2	2.25	0.70
29:A:99:THR:HG22	29:A:100:LYS:H	1.56	0.70
29:A:115:VAL:HG23	29:A:118:PHE:HB3	1.74	0.70
30:F:251:LEU:HB2	30:F:285:ILE:HG13	1.73	0.70
23:b:9:CYS:HB2	23:b:111:ALA:HA	1.74	0.69
24:d:119:LEU:HD21	24:d:147:ILE:HD12	1.74	0.69
25:f:471:LEU:HG	25:f:504:VAL:HG22	1.72	0.69
26:W:326:MET:HE3	26:W:326:MET:H	1.56	0.69
15:Q:1:MET:SD	15:Q:1:MET:N	2.63	0.69
23:b:3:LEU:HD12	23:b:105:HIS:CD2	2.26	0.69
25:f:228:LYS:HB3	25:f:233:LEU:HD11	1.74	0.69
34:u:218:LEU:HD21	34:u:231:VAL:HG11	1.72	0.69
6:H:122:THR:HG22	6:H:129:PRO:HB3	1.73	0.69
25:f:731:MET:SD	25:f:750:GLN:NE2	2.65	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:381:ASP:OD1	8:J:200:GLN:NE2	2.25	0.69
9:K:38:ILE:HD13	9:K:169:ALA:HB2	1.73	0.69
10:L:196:ARG:HD3	10:L:239:ARG:HD3	1.73	0.69
10:L:225:ASP:H	10:L:228:ASP:HB2	1.57	0.69
11:M:44:GLY:HA2	11:M:140:TYR:HB2	1.75	0.69
12:N:104:ASP:N	12:N:104:ASP:OD1	2.25	0.69
25:f:672:LEU:HD13	25:f:708:ASP:HA	1.75	0.69
25:f:857:GLY:H	25:f:860:LYS:HD2	1.57	0.69
33:g:258:LEU:HB3	33:g:266:CYS:HB3	1.74	0.69
10:L:182:CYS:HB2	10:L:187:LEU:HG	1.74	0.69
29:A:135:GLU:OE2	29:A:255:ARG:NH2	2.26	0.69
32:U:213:PHE:HB3	32:U:248:ILE:HD11	1.75	0.69
32:U:529:ILE:HD11	32:U:566:LEU:HD22	1.75	0.69
4:c:295:ASN:HB2	21:Z:259:VAL:HB	1.75	0.69
10:L:104:PRO:HB3	18:T:81:HIS:HD2	1.57	0.69
11:M:76:ALA:HB3	11:M:136:MET:HB2	1.75	0.69
12:N:119:MET:HA	18:T:61:GLN:HE22	1.58	0.69
20:Y:107:LYS:HZ1	20:Y:120:ALA:H	1.39	0.69
29:A:238:ILE:HB	29:A:272:ILE:HA	1.74	0.69
16:R:57:ARG:NH1	16:R:57:ARG:O	2.26	0.69
30:F:406:ILE:O	30:F:410:ARG:N	2.26	0.69
6:H:46:LEU:HD22	6:H:75:VAL:HG23	1.75	0.69
26:W:247:TYR:HA	26:W:250:ILE:HD12	1.75	0.69
31:E:327:ASP:OD1	31:E:364:GLN:NE2	2.26	0.69
32:U:701:ILE:HD12	32:U:810:THR:HA	1.75	0.69
19:X:130:GLU:HB3	19:X:153:LEU:HD22	1.75	0.68
25:f:606:VAL:HG13	25:f:607:LEU:HD22	1.75	0.68
25:f:650:GLN:N	25:f:650:GLN:OE1	2.25	0.68
26:W:331:GLY:HA2	26:W:337:ALA:HB2	1.74	0.68
29:A:165:GLN:HA	29:A:239:ARG:H	1.58	0.68
1:B:225:TYR:CE1	1:B:352:GLU:HG2	2.27	0.68
20:Y:188:CYS:SG	20:Y:189:VAL:N	2.66	0.68
31:E:250:ASP:O	31:E:254:GLN:HG2	1.92	0.68
1:B:412:MET:HG3	25:f:52:LEU:HD13	1.75	0.68
20:Y:147:ILE:HA	20:Y:150:PHE:CD2	2.29	0.68
25:f:636:ASP:HB3	25:f:637:LYS:HD3	1.76	0.68
4:c:101:GLN:OE1	23:b:101:GLN:NE2	2.27	0.68
5:G:45:LYS:HZ1	5:G:190:THR:HA	1.58	0.68
8:J:96:LEU:HD21	15:Q:59:TYR:HA	1.75	0.68
25:f:369:ARG:HG3	25:f:740:ARG:HD3	1.75	0.68
25:f:712:LYS:O	25:f:716:ASP:HB2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:166:LEU:HD21	26:W:192:LEU:HG	1.73	0.68
30:F:317:LEU:HD11	30:F:347:ARG:HA	1.76	0.68
7:I:49:ARG:NH1	7:I:209:GLU:O	2.25	0.68
8:J:92:GLN:HG3	15:Q:66:LEU:HB2	1.76	0.68
10:L:7:ASP:HB3	10:L:20:HIS:HB2	1.75	0.68
20:Y:214:MET:HE2	20:Y:219:PHE:HA	1.76	0.68
22:a:333:MET:HA	22:a:333:MET:HE3	1.74	0.68
20:Y:50:MET:O	20:Y:50:MET:HE3	1.94	0.68
20:Y:297:ARG:NH2	28:e:45:ASP:OD2	2.26	0.68
31:E:265:ASP:OD1	31:E:291:ARG:NH2	2.25	0.68
25:f:267:ARG:HE	25:f:299:GLY:HA2	1.59	0.68
25:f:834:ASP:H	25:f:839:PRO:HA	1.57	0.68
29:A:255:ARG:O	29:A:258:ARG:HB3	1.94	0.68
14:P:113:ASP:HB3	14:P:118:LYS:H	1.59	0.68
18:T:15:LYS:NZ	18:T:133:GLU:OE2	2.26	0.68
25:f:680:ARG:HB3	25:f:714:SER:HB2	1.74	0.68
26:W:407:ASP:OD1	26:W:408:ARG:N	2.27	0.68
30:F:375:VAL:HB	30:F:415:LEU:HD23	1.76	0.68
12:N:95:MET:HA	12:N:95:MET:HE3	1.76	0.68
20:Y:53:TYR:HA	20:Y:56:ALA:HB3	1.74	0.68
32:U:185:MET:HA	32:U:185:MET:HE3	1.76	0.68
3:D:98:GLN:OE1	3:D:98:GLN:N	2.27	0.67
20:Y:389:MET:N	20:Y:389:MET:SD	2.67	0.67
21:Z:15:VAL:HG12	21:Z:53:SER:HB3	1.74	0.67
22:a:35:HIS:HB2	23:b:17:ARG:HB3	1.77	0.67
22:a:342:ASP:O	22:a:345:GLN:N	2.27	0.67
25:f:209:MET:HE1	25:f:211:ILE:HB	1.74	0.67
26:W:296:LEU:HD23	26:W:303:LYS:HE3	1.75	0.67
3:D:264:ILE:HB	3:D:309:MET:HG2	1.76	0.67
7:I:43:VAL:HG23	7:I:216:LEU:HB3	1.77	0.67
10:L:205:LEU:HA	10:L:209:ASN:HD22	1.59	0.67
15:Q:142:ILE:O	15:Q:146:TYR:HB2	1.93	0.67
29:A:102:ILE:HG21	29:A:110:LYS:HG2	1.76	0.67
1:B:57:GLN:NE2	29:A:42:SER:HA	2.09	0.67
8:J:87:ALA:HB1	8:J:107:ILE:HD11	1.75	0.67
24:d:130:PRO:HG3	32:U:1:MET:HA	1.75	0.67
5:G:80:MET:HE2	5:G:138:MET:HB2	1.76	0.67
6:H:118:MET:SD	6:H:149:SER:OG	2.52	0.67
20:Y:187:TYR:HB2	20:Y:192:ARG:HB2	1.75	0.67
22:a:188:LEU:HB2	22:a:193:GLN:HE21	1.59	0.67
14:P:12:MET:HE3	14:P:146:MET:HG3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:29:GLY:HA2	14:P:35:VAL:HG22	1.77	0.67
25:f:115:PRO:HD2	25:f:118:ASN:HA	1.75	0.67
27:V:311:ASN:OD1	27:V:314:ARG:NH1	2.27	0.67
31:E:135:ILE:HD12	31:E:136:GLY:N	2.09	0.67
22:a:335:TRP:CD1	22:a:337:GLN:H	2.12	0.67
30:F:396:CYS:HA	30:F:399:VAL:HG12	1.76	0.67
2:C:369:TYR:HE2	2:C:385:MET:HB2	1.58	0.67
3:D:391:ARG:HH21	3:D:394:VAL:HA	1.59	0.67
31:E:132:TYR:HE1	31:E:146:ARG:HH11	1.42	0.67
2:C:338:LEU:HD12	2:C:342:ILE:HG13	1.77	0.67
19:X:137:TYR:HB3	19:X:146:ALA:HB2	1.75	0.67
31:E:352:MET:HA	31:E:352:MET:HE3	1.76	0.67
32:U:399:TRP:O	32:U:402:PHE:HB3	1.94	0.67
6:H:95:GLN:NE2	13:O:64:GLU:OE1	2.28	0.67
14:P:45:MET:HE2	14:P:67:LEU:HD23	1.75	0.67
24:d:156:ILE:HG13	24:d:258:PHE:HD1	1.60	0.67
25:f:524:MET:HG3	25:f:776:LEU:HD13	1.77	0.67
25:f:759:LEU:HB2	25:f:809:ILE:HD12	1.77	0.67
26:W:301:LYS:HD2	26:W:327:GLU:HG3	1.77	0.67
5:G:74:GLU:OE2	5:G:75:ASN:ND2	2.28	0.66
20:Y:109:GLU:O	20:Y:113:ARG:HG2	1.94	0.66
25:f:680:ARG:NE	25:f:714:SER:O	2.27	0.66
6:H:93:LEU:HD21	6:H:113:ARG:HD3	1.77	0.66
6:H:185:GLU:HA	6:H:188:ILE:HD12	1.77	0.66
25:f:651:GLY:O	25:f:655:LEU:HD23	1.96	0.66
26:W:220:GLU:H	26:W:223:LYS:HE3	1.59	0.66
1:B:177:GLU:N	1:B:177:GLU:OE2	2.28	0.66
22:a:286:ALA:HA	22:a:289:ARG:HG2	1.78	0.66
25:f:180:GLN:HB3	25:f:181:ARG:HH21	1.61	0.66
31:E:136:GLY:HA3	31:E:312:ILE:HD13	1.77	0.66
2:C:36:ASN:ND2	27:V:89:LYS:O	2.29	0.66
4:c:255:TYR:OH	21:Z:273:HIS:ND1	2.24	0.66
10:L:43:HIS:CD2	10:L:216:GLY:HA3	2.31	0.66
14:P:14:MET:HB3	14:P:21:ALA:HB3	1.75	0.66
17:S:118:LYS:NZ	17:S:119:GLY:O	2.28	0.66
29:A:142:VAL:HG12	29:A:149:ILE:HA	1.76	0.66
33:g:291:PRO:HG2	33:g:294:GLY:HA3	1.77	0.66
24:d:188:MET:HE2	24:d:188:MET:HA	1.76	0.66
27:V:337:LEU:HD21	27:V:364:THR:HG23	1.78	0.66
3:D:352:MET:HE2	3:D:352:MET:HA	1.77	0.66
19:X:282:ARG:HE	19:X:312:GLU:HG2	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Y:51:ALA:N	20:Y:114:ILE:O	2.29	0.66
25:f:706:ILE:HG22	25:f:745:LEU:HD23	1.78	0.66
26:W:407:ASP:OD1	26:W:408:ARG:NH1	2.29	0.66
6:H:203:MET:HG3	6:H:230:LEU:HD11	1.78	0.66
13:O:19:ARG:NH1	13:O:167:LEU:O	2.29	0.66
26:W:367:ALA:HA	26:W:413:ILE:HG23	1.76	0.66
5:G:45:LYS:HD3	5:G:188:ASP:HB2	1.77	0.66
22:a:317:VAL:HG23	22:a:319:LEU:HD13	1.78	0.66
25:f:343:LYS:HA	25:f:387:GLN:HE22	1.61	0.66
25:f:637:LYS:CE	25:f:655:LEU:HD22	2.25	0.66
34:u:184:GLY:HA2	34:u:261:SER:H	1.60	0.66
20:Y:50:MET:HB2	20:Y:74:LYS:HE2	1.78	0.66
29:A:241:ILE:HG22	29:A:244:GLU:H	1.60	0.66
1:B:74:MET:HB3	25:f:613:LEU:HD23	1.78	0.66
4:c:217:LEU:HD22	21:Z:172:VAL:HG22	1.78	0.66
20:Y:101:ARG:CZ	20:Y:136:HIS:HB3	2.26	0.66
32:U:370:VAL:HG11	32:U:404:ALA:HA	1.78	0.66
7:I:69:ASN:HB3	7:I:72:MET:HB2	1.78	0.65
26:W:123:ARG:O	26:W:127:THR:HG23	1.95	0.65
9:K:101:PHE:HA	16:R:57:ARG:HE	1.60	0.65
9:K:121:LEU:HD23	9:K:160:GLY:HA3	1.76	0.65
21:Z:12:HIS:ND1	21:Z:50:VAL:O	2.28	0.65
2:C:92:GLU:OE2	2:C:92:GLU:N	2.28	0.65
14:P:14:MET:HE2	14:P:14:MET:HA	1.77	0.65
4:c:118:PHE:O	4:c:121:TRP:NE1	2.21	0.65
27:V:175:MET:HE3	27:V:184:ALA:CA	2.25	0.65
34:u:146:PHE:HA	34:u:157:LEU:HD13	1.79	0.65
2:C:369:TYR:CE2	2:C:385:MET:HB2	2.32	0.65
14:P:107:PRO:HG2	14:P:124:LEU:HB3	1.79	0.65
14:P:159:ASP:O	14:P:163:LEU:N	2.28	0.65
31:E:246:GLY:O	31:E:251:ARG:NH2	2.29	0.65
32:U:431:THR:HG23	32:U:433:PRO:HD2	1.79	0.65
1:B:225:TYR:HE2	1:B:350:LYS:HE3	1.60	0.65
15:Q:95:ARG:HG3	15:Q:96:THR:HG23	1.78	0.65
24:d:234:GLN:HB3	27:V:400:HIS:CD2	2.32	0.65
25:f:3:GLU:HG3	25:f:6:ARG:HB2	1.77	0.65
8:J:71:MET:HE1	8:J:73:PHE:CD2	2.31	0.65
7:I:33:THR:OG1	7:I:166:ASN:O	2.15	0.65
12:N:149:LYS:O	12:N:149:LYS:NZ	2.25	0.65
21:Z:260:VAL:CG1	21:Z:261:TYR:H	2.08	0.65
29:A:165:GLN:HB3	29:A:238:ILE:HA	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:172:VAL:HB	30:F:274:LEU:HD22	1.79	0.65
20:Y:385:ARG:NH2	27:V:282:ASN:OD1	2.29	0.65
25:f:271:MET:HE1	25:f:275:MET:SD	2.37	0.65
25:f:450:ILE:HG13	25:f:804:LEU:HD11	1.78	0.65
26:W:360:GLU:OE2	26:W:364:ARG:NH2	2.24	0.65
26:W:417:ARG:O	26:W:418:PRO:C	2.40	0.65
31:E:56:ILE:HB	31:E:100:LEU:HB2	1.78	0.65
15:Q:192:ASP:OD1	15:Q:192:ASP:N	2.29	0.65
20:Y:16:ASP:H	20:Y:146:ARG:HH22	1.44	0.65
23:b:21:PHE:CD1	23:b:23:PRO:HD2	2.32	0.65
25:f:623:LYS:HG3	25:f:625:LYS:H	1.61	0.65
28:e:51:ASP:CG	28:e:52:PHE:H	2.05	0.65
29:A:333:ARG:NH2	29:A:334:PRO:O	2.30	0.65
18:T:5:MET:N	18:T:5:MET:SD	2.70	0.64
19:X:62:GLN:N	19:X:65:GLU:OE2	2.30	0.64
25:f:364:GLN:NE2	25:f:366:ASP:OD1	2.30	0.64
26:W:147:LYS:O	26:W:150:ALA:HB3	1.97	0.64
27:V:368:ARG:HG3	27:V:409:MET:HE1	1.78	0.64
25:f:716:ASP:HA	25:f:719:PRO:HG3	1.78	0.64
29:A:240:VAL:O	29:A:275:ASP:N	2.29	0.64
30:F:234:THR:HG23	30:F:284:PHE:CE2	2.27	0.64
2:C:248:MET:HB2	2:C:293:MET:HG2	1.80	0.64
14:P:11:VAL:HG11	14:P:52:GLY:HA3	1.79	0.64
21:Z:73:ASP:OD2	21:Z:74:TYR:N	2.30	0.64
26:W:362:ASN:O	26:W:366:MET:HG3	1.98	0.64
29:A:190:VAL:HG11	29:A:212:VAL:HG21	1.79	0.64
13:O:38:SER:HB3	13:O:41:ILE:HG22	1.80	0.64
25:f:338:ASP:HB3	25:f:340:MET:HE1	1.78	0.64
9:K:42:THR:OG1	9:K:189:MET:O	2.15	0.64
20:Y:134:LEU:HA	20:Y:137:ARG:HD3	1.79	0.64
25:f:213:GLN:O	25:f:217:LEU:HD12	1.97	0.64
26:W:382:LEU:HD13	26:W:384:LEU:HB2	1.79	0.64
30:F:381:TYR:HA	30:F:384:LEU:HD12	1.80	0.64
7:I:140:ASP:HB2	7:I:146:GLN:HE22	1.62	0.64
9:K:4:THR:OG1	9:K:7:GLU:OE2	2.16	0.64
14:P:149:MET:O	14:P:153:LEU:CB	2.45	0.64
18:T:74:GLU:HB2	18:T:83:TYR:CZ	2.33	0.64
30:F:278:LYS:O	30:F:281:SER:OG	2.15	0.64
6:H:159:LYS:HE2	7:I:55:LEU:HA	1.79	0.64
7:I:103:GLU:HG3	7:I:104:PRO:HD2	1.80	0.64
31:E:21:GLU:HG2	31:E:22:ILE:H	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:164:ARG:NH1	10:L:198:THR:O	2.31	0.64
11:M:68:ASN:HB3	11:M:224:HIS:HD2	1.62	0.64
17:S:22:ILE:HG13	17:S:197:ILE:HG23	1.78	0.64
25:f:633:GLU:OE2	25:f:673:ARG:NH2	2.31	0.64
29:A:332:MET:N	29:A:332:MET:SD	2.71	0.64
12:N:173:VAL:HG12	12:N:190:LEU:HD13	1.80	0.64
15:Q:19:ARG:NH2	15:Q:193:ASN:OD1	2.30	0.64
25:f:527:VAL:O	25:f:569:LYS:NZ	2.31	0.64
25:f:829:MET:HA	25:f:829:MET:HE3	1.80	0.64
25:f:829:MET:HE1	25:f:859:PRO:HB2	1.80	0.64
14:P:30:ILE:HG23	14:P:32:ALA:H	1.63	0.64
20:Y:71:ASN:HA	20:Y:74:LYS:HE3	1.78	0.64
22:a:284:ARG:O	22:a:289:ARG:NH1	2.29	0.64
24:d:286:GLU:HG3	24:d:289:ARG:HH12	1.63	0.64
26:W:34:LEU:HG	26:W:39:ARG:HD3	1.80	0.64
32:U:545:LEU:HB3	32:U:577:ILE:HG21	1.80	0.64
2:C:135:VAL:HA	2:C:138:MET:SD	2.37	0.63
15:Q:83:PHE:O	15:Q:87:ASN:ND2	2.31	0.63
25:f:446:LEU:HD11	25:f:801:VAL:HG11	1.79	0.63
25:f:869:THR:HA	25:f:884:THR:HA	1.80	0.63
10:L:152:ASN:OD1	11:M:85:ARG:NH1	2.29	0.63
19:X:309:TYR:O	19:X:312:GLU:N	2.30	0.63
26:W:140:ILE:O	26:W:143:ALA:HB3	1.98	0.63
30:F:236:LEU:HD13	30:F:354:PHE:CZ	2.33	0.63
24:d:343:GLU:HA	24:d:346:LYS:HE2	1.79	0.63
31:E:41:GLU:O	31:E:44:GLU:HB2	1.98	0.63
5:G:125:TYR:CG	5:G:131:MET:HG2	2.33	0.63
27:V:212:TYR:HA	27:V:253:LEU:HD21	1.79	0.63
29:A:272:ILE:HG23	29:A:317:VAL:HA	1.81	0.63
10:L:43:HIS:HD2	10:L:216:GLY:HA3	1.64	0.63
14:P:200:LEU:HD23	14:P:200:LEU:H	1.63	0.63
17:S:27:THR:OG1	17:S:38:ARG:O	2.15	0.63
19:X:130:GLU:HA	19:X:133:LEU:HD23	1.80	0.63
19:X:183:LEU:HD21	19:X:221:GLU:HG2	1.81	0.63
21:Z:113:LYS:NZ	21:Z:117:PRO:O	2.28	0.63
22:a:373:ASP:OD2	24:d:353:ARG:NH1	2.32	0.63
25:f:785:ARG:NE	25:f:785:ARG:O	2.31	0.63
30:F:402:GLU:HA	30:F:405:MET:HE3	1.80	0.63
34:u:184:GLY:H	34:u:225:ILE:HG23	1.63	0.63
2:C:163:GLU:OE1	2:C:313:ARG:NH2	2.32	0.63
4:c:168:MET:HA	4:c:168:MET:HE3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:215:GLN:OE1	8:J:215:GLN:N	2.32	0.63
11:M:229:LYS:NZ	11:M:229:LYS:O	2.32	0.63
25:f:610:GLN:O	25:f:614:HIS:HB2	1.99	0.63
2:C:49:ARG:NE	3:D:64:GLU:OE2	2.29	0.63
4:c:295:ASN:CB	21:Z:259:VAL:HB	2.28	0.63
11:M:71:ARG:HD3	18:T:72:ILE:HG23	1.80	0.63
16:R:41:LEU:HD11	16:R:101:ILE:HG23	1.81	0.63
17:S:146:GLN:HG3	17:S:147:PRO:HD3	1.80	0.63
20:Y:350:VAL:HG12	27:V:416:ARG:HH12	1.64	0.63
26:W:266:ALA:O	26:W:270:VAL:HG23	1.97	0.63
15:Q:14:LEU:HD22	15:Q:182:ILE:HG22	1.80	0.63
26:W:105:VAL:HG21	26:W:138:VAL:HG11	1.80	0.63
28:e:51:ASP:OD1	28:e:52:PHE:N	2.32	0.63
33:g:253:SER:HA	33:g:270:ASN:HD21	1.63	0.63
8:J:31:THR:OG1	8:J:163:ARG:O	2.16	0.63
10:L:157:ARG:NH1	10:L:157:ARG:O	2.32	0.63
10:L:199:LEU:HD12	10:L:200:PRO:HD2	1.80	0.63
13:O:6:VAL:HG23	13:O:124:TYR:HB3	1.80	0.63
21:Z:65:ASP:O	21:Z:104:ASN:ND2	2.31	0.63
22:a:226:ARG:HH21	22:a:230:ARG:HB2	1.64	0.63
24:d:117:GLY:HA2	24:d:120:LYS:HE2	1.80	0.63
30:F:239:ALA:O	30:F:243:GLN:NE2	2.32	0.63
8:J:42:VAL:HG12	8:J:210:VAL:HG12	1.81	0.62
19:X:264:PRO:HG2	19:X:295:LYS:HB3	1.81	0.62
19:X:317:PRO:C	19:X:319:ILE:H	2.06	0.62
23:b:17:ARG:HH21	23:b:80:PRO:HG2	1.64	0.62
26:W:48:LEU:HG	26:W:52:LYS:HD2	1.80	0.62
17:S:108:ASN:HB2	17:S:124:PHE:HB2	1.81	0.62
23:b:7:MET:HE1	23:b:63:THR:HA	1.81	0.62
24:d:197:LEU:HB3	24:d:259:PHE:HE1	1.63	0.62
25:f:825:MET:HA	25:f:825:MET:HE3	1.80	0.62
29:A:112:ILE:HG22	29:A:122:VAL:HB	1.80	0.62
2:C:44:ARG:HH12	24:d:359:VAL:HG21	1.64	0.62
2:C:280:LEU:HB3	2:C:310:ARG:HG2	1.81	0.62
6:H:204:THR:H	6:H:207:ASN:HB2	1.63	0.62
12:N:186:ARG:HH21	12:N:188:VAL:HB	1.64	0.62
14:P:183:MET:HE1	14:P:204:MET:HB2	1.81	0.62
16:R:186:ARG:HH21	16:R:189:SER:HB3	1.64	0.62
18:T:126:ASP:OD1	18:T:130:VAL:N	2.32	0.62
19:X:317:PRO:O	19:X:319:ILE:N	2.30	0.62
20:Y:297:ARG:HG2	20:Y:300:ARG:HH21	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:94:LEU:O	22:a:98:GLU:HG2	2.00	0.62
25:f:683:GLU:HB2	25:f:687:ARG:HD3	1.80	0.62
26:W:93:ARG:O	26:W:96:GLN:NE2	2.32	0.62
30:F:284:PHE:CD1	30:F:329:ILE:HG23	2.34	0.62
30:F:373:MET:HA	30:F:373:MET:HE3	1.79	0.62
6:H:50:LYS:NZ	6:H:62:VAL:O	2.32	0.62
24:d:168:MET:O	24:d:172:LYS:HG2	2.00	0.62
25:f:170:TRP:HB3	25:f:182:GLU:OE2	1.98	0.62
26:W:101:VAL:O	26:W:105:VAL:HG22	1.99	0.62
26:W:285:ASP:HA	26:W:288:HIS:CE1	2.34	0.62
27:V:198:GLN:O	27:V:241:ARG:NH2	2.31	0.62
20:Y:73:MET:H	20:Y:73:MET:HE3	1.63	0.62
20:Y:325:VAL:HG21	28:e:60:LEU:HB2	1.81	0.62
21:Z:260:VAL:HG13	27:V:480:ILE:CD1	2.29	0.62
25:f:605:ASN:HD21	25:f:608:LYS:HB2	1.64	0.62
33:g:170:LYS:HD2	33:g:171:PRO:HD2	1.80	0.62
3:D:59:GLU:OE1	32:U:600:ARG:NH1	2.33	0.62
8:J:57:ARG:O	8:J:60:ARG:NH2	2.33	0.62
12:N:78:THR:O	12:N:82:LEU:HD22	1.99	0.62
24:d:224:VAL:HG22	24:d:252:PRO:HB3	1.82	0.62
25:f:106:LEU:HG	25:f:137:ARG:HG3	1.80	0.62
25:f:169:GLU:O	25:f:173:LEU:N	2.31	0.62
27:V:269:LYS:HD3	32:U:37:GLU:HG3	1.81	0.62
32:U:750:SER:N	32:U:754:HIS:O	2.33	0.62
1:B:383:LEU:O	1:B:423:LYS:NZ	2.33	0.62
4:c:60:GLU:OE1	34:u:240:ASN:ND2	2.33	0.62
10:L:171:TYR:OH	10:L:193:ARG:NH1	2.33	0.62
20:Y:16:ASP:N	20:Y:146:ARG:HH22	1.97	0.62
24:d:264:LEU:O	24:d:268:ARG:HG3	1.99	0.62
32:U:727:LYS:O	32:U:731:ILE:HG12	2.00	0.62
2:C:320:PRO:O	2:C:325:ARG:NH1	2.33	0.62
9:K:203:LYS:HB2	9:K:210:LEU:HD11	1.81	0.62
13:O:41:ILE:HG13	13:O:102:GLY:HA3	1.82	0.62
25:f:182:GLU:H	25:f:182:GLU:CD	2.08	0.62
30:F:236:LEU:HD13	30:F:354:PHE:HZ	1.65	0.62
1:B:53:THR:OG1	1:B:54:PRO:HD3	1.98	0.62
1:B:59:ARG:HB3	25:f:184:LEU:HD21	1.80	0.62
20:Y:23:ARG:HH22	20:Y:55:GLU:C	2.07	0.62
22:a:365:MET:HE2	22:a:365:MET:HA	1.81	0.62
25:f:307:LEU:HG	25:f:309:GLU:H	1.65	0.62
31:E:305:ASN:OD1	31:E:307:GLN:N	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:382:ASP:OD1	1:B:382:ASP:N	2.21	0.62
2:C:52:LEU:HD22	3:D:68:LEU:HB3	1.82	0.62
20:Y:389:MET:HG3	27:V:95:LEU:HD11	1.82	0.62
22:a:129:GLN:HE21	22:a:130:VAL:HG12	1.65	0.62
23:b:125:VAL:HG23	23:b:159:THR:HG21	1.80	0.62
24:d:308:TRP:NE1	24:d:316:TYR:HB3	2.13	0.62
25:f:234:THR:O	25:f:238:ASN:ND2	2.30	0.62
3:D:153:MET:SD	3:D:257:ASN:ND2	2.73	0.61
4:c:146:ASP:OD2	4:c:149:GLN:NE2	2.33	0.61
5:G:80:MET:HB3	5:G:138:MET:HA	1.81	0.61
12:N:28:ASN:HD22	13:O:122:LEU:HD11	1.65	0.61
14:P:58:THR:O	15:Q:85:ARG:NH2	2.32	0.61
9:K:71:ASP:OD1	9:K:72:ALA:N	2.33	0.61
25:f:670:MET:HG2	25:f:673:ARG:HH12	1.65	0.61
25:f:761:MET:HE2	25:f:763:ARG:HB3	1.83	0.61
33:g:217:PHE:HA	33:g:297:MET:HA	1.82	0.61
3:D:315:ASP:OD1	3:D:315:ASP:N	2.32	0.61
8:J:51:ALA:H	8:J:54:GLN:HE22	1.47	0.61
11:M:51:LYS:NZ	11:M:63:ASN:O	2.23	0.61
24:d:108:ASN:HB3	24:d:111:LYS:HB3	1.81	0.61
28:e:50:ASP:O	28:e:54:ASN:ND2	2.33	0.61
30:F:233:LYS:CD	30:F:331:ALA:HB1	2.31	0.61
31:E:250:ASP:OD1	31:E:250:ASP:N	2.26	0.61
11:M:15:SER:OG	11:M:18:GLY:N	2.33	0.61
14:P:14:MET:HB2	14:P:167:ILE:HD13	1.82	0.61
28:e:53:SER:O	28:e:57:ARG:HG2	1.99	0.61
29:A:145:ASN:OD1	29:A:146:LYS:N	2.33	0.61
30:F:362:ARG:NH1	30:F:388:THR:O	2.34	0.61
1:B:95:GLU:HA	1:B:98:LYS:HE2	1.82	0.61
1:B:382:ASP:HA	1:B:385:MET:HE2	1.81	0.61
14:P:41:LYS:HE3	14:P:60:VAL:HG11	1.82	0.61
22:a:49:CYS:SG	22:a:50:PHE:N	2.73	0.61
25:f:757:ASN:HB3	25:f:810:ILE:HG23	1.83	0.61
27:V:485:ASP:O	27:V:489:MET:HG3	2.00	0.61
34:u:118:ASP:O	34:u:119:ILE:HG13	2.01	0.61
1:B:75:GLU:O	1:B:79:ILE:HG13	1.99	0.61
8:J:146:GLN:OE1	8:J:159:ASN:ND2	2.33	0.61
23:b:15:TYR:CD1	23:b:116:PRO:HD2	2.34	0.61
30:F:397:LYS:O	30:F:401:VAL:HG22	2.01	0.61
2:C:78:ARG:HH11	29:A:65:ILE:HD11	1.65	0.61
35:C:501:ATP:O1G	3:D:326:ARG:NH2	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:40:ARG:NH1	12:N:180:ALA:O	2.34	0.61
14:P:62:THR:HG23	15:Q:85:ARG:NH2	2.15	0.61
15:Q:28:MET:HB3	16:R:126:PHE:HE1	1.66	0.61
17:S:123:SER:O	17:S:130:TYR:HA	1.99	0.61
23:b:1:MET:HE1	23:b:43:SER:HB2	1.81	0.61
29:A:115:VAL:C	29:A:116:LYS:HG2	2.25	0.61
29:A:178:GLY:O	37:A:501:ADP:N6	2.34	0.61
30:F:344:ARG:NH1	30:F:345:SER:O	2.33	0.61
1:B:59:ARG:HB2	29:A:41:TYR:CE2	2.36	0.61
3:D:338:ARG:NH1	19:X:234:GLU:OE2	2.34	0.61
4:c:292:MET:HE3	24:d:355:LEU:HD11	1.81	0.61
8:J:52:LYS:HB3	8:J:53:LEU:HD22	1.83	0.61
8:J:88:ARG:NH2	15:Q:69:MET:O	2.33	0.61
13:O:108:PRO:O	13:O:109:HIS:ND1	2.34	0.61
16:R:135:ALA:O	16:R:139:MET:HG3	2.01	0.61
22:a:312:MET:HA	22:a:312:MET:HE3	1.82	0.61
24:d:190:GLN:NE2	24:d:255:SER:OG	2.33	0.61
26:W:200:ILE:HD12	26:W:201:ARG:H	1.64	0.61
2:C:326:LEU:HD22	2:C:345:ARG:HE	1.65	0.61
15:Q:137:PHE:HA	15:Q:140:LEU:HD23	1.83	0.61
16:R:37:ILE:HB	16:R:60:ALA:HB2	1.83	0.61
25:f:122:ALA:HB1	25:f:130:ALA:HB3	1.81	0.61
26:W:83:LEU:O	26:W:87:ILE:HG12	2.00	0.61
26:W:120:ILE:HD12	26:W:121:LYS:N	2.16	0.61
14:P:118:LYS:NZ	14:P:119:PRO:O	2.33	0.61
20:Y:122:THR:HA	20:Y:125:ARG:HE	1.66	0.61
21:Z:130:ASP:OD1	21:Z:130:ASP:N	2.25	0.61
25:f:670:MET:SD	25:f:670:MET:N	2.69	0.61
33:g:170:LYS:HZ1	33:g:173:MET:HB3	1.65	0.61
33:g:187:HIS:CG	33:g:187:HIS:O	2.54	0.61
15:Q:78:THR:O	15:Q:82:ASN:ND2	2.24	0.60
17:S:50:THR:HG22	17:S:110:ILE:HD12	1.81	0.60
26:W:378:MET:HE3	26:W:378:MET:C	2.26	0.60
4:c:80:THR:HG23	33:g:274:MET:HE2	1.83	0.60
5:G:75:ASN:HD21	5:G:108:GLU:HG3	1.66	0.60
8:J:222:PRO:HA	8:J:225:ILE:HD11	1.83	0.60
10:L:200:PRO:O	10:L:239:ARG:NH2	2.34	0.60
15:Q:37:LYS:O	15:Q:61:GLN:NE2	2.32	0.60
25:f:301:HIS:HA	25:f:305:LEU:HD23	1.83	0.60
25:f:395:GLY:O	25:f:398:TRP:HB3	2.01	0.60
3:D:101:ALA:HB2	3:D:115:ILE:HD11	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:186:LEU:HD13	13:O:189:TYR:HD1	1.65	0.60
14:P:91:VAL:HG23	14:P:124:LEU:HD22	1.82	0.60
20:Y:290:PRO:HB3	28:e:39:TRP:HH2	1.65	0.60
22:a:18:GLN:HG3	22:a:19:PRO:HD3	1.83	0.60
22:a:68:GLU:CD	22:a:71:VAL:HB	2.26	0.60
26:W:149:LEU:O	26:W:152:ILE:HG22	2.01	0.60
32:U:33:ASP:HB3	32:U:34:PHE:HD2	1.67	0.60
34:u:226:LYS:HD2	34:u:226:LYS:N	2.16	0.60
19:X:207:GLN:NE2	19:X:211:ASP:OD2	2.33	0.60
20:Y:349:LYS:O	20:Y:351:ASN:N	2.35	0.60
23:b:123:ASP:HA	23:b:126:LYS:HG2	1.83	0.60
29:A:293:ASN:O	30:F:173:LYS:NZ	2.34	0.60
30:F:344:ARG:HH12	31:E:344:ARG:NH1	2.00	0.60
2:C:375:ARG:NH2	2:C:382:ASP:OD2	2.34	0.60
14:P:98:LYS:HZ3	14:P:103:TYR:H	1.50	0.60
19:X:271:VAL:HG21	19:X:288:LYS:HD2	1.84	0.60
9:K:70:ILE:H	9:K:70:ILE:HD12	1.67	0.60
13:O:34:ILE:HD13	13:O:176:CYS:HB2	1.83	0.60
13:O:41:ILE:HD11	13:O:76:VAL:HG13	1.83	0.60
13:O:182:LYS:HD2	13:O:184:ASP:HB2	1.84	0.60
26:W:332:SER:OG	26:W:335:SER:O	2.18	0.60
29:A:110:LYS:HA	29:A:123:VAL:O	2.02	0.60
34:u:147:ASP:HB3	34:u:151:ARG:HH11	1.64	0.60
1:B:209:GLU:HB3	25:f:722:SER:HB3	1.84	0.60
9:K:59:MET:HA	9:K:59:MET:HE3	1.82	0.60
26:W:418:PRO:O	26:W:419:LYS:C	2.44	0.60
30:F:212:PHE:CZ	31:E:352:MET:HE1	2.36	0.60
30:F:281:SER:H	30:F:326:VAL:HG22	1.67	0.60
5:G:53:GLN:NE2	5:G:54:LYS:O	2.35	0.60
5:G:141:ILE:HG22	5:G:151:VAL:HG22	1.84	0.60
7:I:44:LEU:HD22	7:I:190:LEU:HG	1.84	0.60
11:M:45:VAL:HG21	11:M:138:GLY:HA3	1.84	0.60
17:S:211:ARG:NH1	17:S:213:ASP:O	2.35	0.60
18:T:42:ILE:HD13	18:T:199:ILE:HD11	1.82	0.60
30:F:69:MET:HE1	31:E:36:LEU:HB3	1.84	0.60
1:B:244:SER:HB2	25:f:684:PRO:HB2	1.82	0.60
4:c:308:VAL:HG12	22:a:363:MET:HE3	1.83	0.60
21:Z:101:LEU:N	26:W:450:GLU:OE2	2.33	0.60
26:W:38:GLY:C	26:W:39:ARG:HE	2.10	0.60
30:F:200:GLU:HA	30:F:204:LEU:HB3	1.83	0.60
2:C:138:MET:HE2	2:C:214:VAL:HG23	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:c:307:VAL:HG22	22:a:363:MET:HE1	1.83	0.60
8:J:2:SER:OG	8:J:3:TYR:N	2.30	0.60
9:K:54:ILE:HD11	9:K:59:MET:HB3	1.83	0.60
10:L:129:GLY:HA2	10:L:149:PRO:HB3	1.84	0.60
16:R:147:LEU:HD23	16:R:152:ALA:HA	1.83	0.60
19:X:118:LYS:O	19:X:118:LYS:NZ	2.35	0.60
19:X:256:LEU:HD22	19:X:319:ILE:HG13	1.82	0.60
22:a:55:GLY:HA2	22:a:58:LYS:HZ2	1.67	0.60
24:d:172:LYS:HD2	24:d:175:TYR:CD1	2.37	0.60
25:f:753:ALA:HB3	25:f:754:LYS:HZ2	1.66	0.60
14:P:103:TYR:HA	15:Q:93:ARG:HH22	1.66	0.59
17:S:57:PHE:HB3	17:S:60:ASP:HB2	1.83	0.59
17:S:90:ALA:O	17:S:94:THR:HG23	2.01	0.59
24:d:143:LEU:O	24:d:147:ILE:HG12	2.01	0.59
25:f:288:VAL:HA	25:f:291:GLN:HB3	1.84	0.59
25:f:608:LYS:HB3	25:f:639:LYS:HE2	1.83	0.59
33:g:233:PHE:HB2	33:g:244:PHE:HB3	1.84	0.59
1:B:214:MET:N	1:B:214:MET:HE2	2.17	0.59
12:N:19:ARG:HG3	12:N:26:ILE:HD13	1.84	0.59
12:N:104:ASP:OD1	12:N:110:GLN:NE2	2.34	0.59
15:Q:85:ARG:HB2	15:Q:118:MET:HE3	1.83	0.59
21:Z:245:PHE:HA	26:W:424:LEU:HD21	1.83	0.59
26:W:144:ARG:HA	26:W:147:LYS:HD2	1.84	0.59
3:D:89:ILE:HD11	31:E:80:VAL:HG13	1.83	0.59
4:c:192:LEU:HA	4:c:196:LEU:HB3	1.85	0.59
5:G:180:GLU:HA	5:G:183:VAL:HG22	1.84	0.59
10:L:66:VAL:HG21	10:L:88:MET:HB3	1.82	0.59
13:O:91:GLN:HE21	13:O:93:TYR:HE2	1.49	0.59
15:Q:21:ALA:O	15:Q:28:MET:N	2.35	0.59
20:Y:233:ARG:N	20:Y:234:PRO:HD3	2.17	0.59
25:f:347:ASP:OD1	25:f:347:ASP:N	2.36	0.59
25:f:828:ARG:HB3	25:f:843:SER:HB2	1.83	0.59
26:W:75:TYR:HA	26:W:80:TRP:HZ3	1.66	0.59
27:V:343:PRO:O	28:e:43:TRP:NE1	2.30	0.59
5:G:32:ILE:HD13	5:G:137:CYS:HB2	1.84	0.59
15:Q:11:ASP:OD2	15:Q:11:ASP:N	2.35	0.59
20:Y:180:LEU:O	20:Y:183:TYR:N	2.36	0.59
23:b:118:GLU:OE2	23:b:118:GLU:N	2.30	0.59
25:f:282:PHE:HA	25:f:286:LYS:HB3	1.84	0.59
26:W:442:THR:O	26:W:445:LEU:HB3	2.02	0.59
31:E:243:PHE:H	31:E:254:GLN:NE2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:U:127:ASP:OD2	32:U:130:LEU:N	2.30	0.59
32:U:247:GLN:HE21	32:U:904:LYS:HE3	1.67	0.59
1:B:411:ARG:NH2	1:B:418:ASP:OD2	2.35	0.59
11:M:187:ARG:O	11:M:191:LYS:NZ	2.36	0.59
19:X:371:ASP:OD1	20:Y:233:ARG:NH1	2.36	0.59
23:b:133:LYS:HG3	34:u:139:ASN:HD21	1.67	0.59
25:f:27:LYS:HD2	25:f:27:LYS:O	2.01	0.59
25:f:773:LYS:NZ	25:f:805:ASP:HA	2.17	0.59
29:A:213:LEU:HD21	29:A:321:THR:HG22	1.83	0.59
30:F:262:GLY:HA2	30:F:265:ALA:HB3	1.85	0.59
32:U:672:LEU:HA	32:U:675:MET:HE3	1.84	0.59
5:G:220:VAL:HG22	5:G:227:PHE:HA	1.85	0.59
30:F:225:MET:CE	30:F:233:LYS:HB2	2.32	0.59
31:E:122:MET:HE3	31:E:198:VAL:HG22	1.83	0.59
1:B:357:ASP:N	1:B:360:THR:OG1	2.36	0.59
5:G:37:LEU:HD23	5:G:37:LEU:H	1.66	0.59
16:R:178:HIS:HD2	16:R:185:ILE:HD11	1.67	0.59
18:T:145:LEU:HD22	18:T:176:LEU:HG	1.83	0.59
24:d:354:GLN:HA	24:d:357:MET:HE3	1.85	0.59
25:f:814:SER:OG	25:f:881:GLU:OE1	2.18	0.59
29:A:332:MET:HA	29:A:337:LEU:HD13	1.84	0.59
31:E:235:ILE:HG23	31:E:285:LEU:HD11	1.84	0.59
34:u:195:LYS:HB3	34:u:214:PRO:HB3	1.83	0.59
1:B:289:ALA:O	2:C:271:ARG:NH1	2.34	0.59
14:P:109:ILE:HG12	14:P:122:CYS:HB3	1.85	0.59
18:T:122:LEU:HB3	18:T:137:LEU:HD13	1.85	0.59
25:f:747:GLN:O	25:f:751:TYR:HB2	2.03	0.59
27:V:113:LEU:HD22	27:V:174:PHE:HD2	1.68	0.59
29:A:401:ARG:NH2	29:A:408:ASP:OD1	2.36	0.59
1:B:169:PRO:HD3	2:C:77:VAL:HG22	1.85	0.59
5:G:165:ALA:HB3	6:H:56:LEU:HD23	1.84	0.59
11:M:75:MET:HE1	11:M:135:PHE:HD2	1.68	0.59
15:Q:44:LEU:HD11	15:Q:102:LEU:HD11	1.84	0.59
22:a:246:GLU:HG3	22:a:249:GLN:HB3	1.85	0.59
23:b:14:GLU:N	23:b:82:GLY:O	2.35	0.59
26:W:272:LEU:HD12	26:W:338:THR:HG21	1.84	0.59
32:U:757:MET:HE3	32:U:758:PRO:CD	2.33	0.59
11:M:68:ASN:HB3	11:M:224:HIS:CD2	2.38	0.59
15:Q:151:ILE:HA	15:Q:155:ARG:HD3	1.85	0.59
18:T:110:MET:HE1	18:T:112:ILE:HB	1.84	0.59
26:W:178:GLU:O	26:W:182:ARG:NH2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:272:PHE:O	30:F:276:LYS:HG2	2.03	0.59
34:u:166:LEU:HD21	34:u:204:MET:HB3	1.85	0.59
1:B:229:GLY:HA3	2:C:307:ARG:HD2	1.85	0.58
1:B:410:ARG:HB3	25:f:53:GLN:HB2	1.85	0.58
3:D:231:VAL:HG21	31:E:262:ASN:CG	2.28	0.58
14:P:191:GLU:HG2	14:P:193:ASP:H	1.68	0.58
25:f:134:SER:O	25:f:138:GLU:HG3	2.03	0.58
25:f:224:ASN:HD21	25:f:238:ASN:CG	2.11	0.58
10:L:153:TYR:H	11:M:85:ARG:HH12	1.50	0.58
12:N:1:THR:OG1	12:N:2:THR:N	2.34	0.58
24:d:171:LEU:HG	24:d:175:TYR:CE1	2.39	0.58
25:f:236:CYS:O	25:f:240:VAL:HG23	2.03	0.58
27:V:171:VAL:O	27:V:175:MET:HG2	2.03	0.58
30:F:221:LYS:NZ	30:F:318:ASP:HA	2.18	0.58
30:F:302:GLY:O	30:F:304:ARG:NE	2.35	0.58
30:F:396:CYS:O	30:F:399:VAL:N	2.36	0.58
31:E:222:ALA:HB2	31:E:230:ILE:HD11	1.84	0.58
8:J:98:VAL:HG23	8:J:100:ASP:H	1.68	0.58
14:P:67:LEU:HD11	14:P:91:VAL:HG12	1.83	0.58
25:f:675:PHE:HE2	25:f:691:PRO:HB2	1.68	0.58
26:W:378:MET:HE1	26:W:382:LEU:HD21	1.85	0.58
31:E:148:VAL:HG13	31:E:149:ILE:HD13	1.84	0.58
7:I:37:ILE:HG22	7:I:44:LEU:HG	1.85	0.58
9:K:33:LEU:O	9:K:53:ARG:NH2	2.37	0.58
10:L:50:LYS:HB3	10:L:59:HIS:HB3	1.84	0.58
17:S:37:THR:HG22	17:S:39:ASP:H	1.67	0.58
20:Y:292:TYR:OH	20:Y:293:ARG:NH1	2.37	0.58
22:a:84:VAL:HG21	22:a:97:LEU:HD21	1.85	0.58
4:c:35:SER:HB3	21:Z:175:LEU:HD13	1.86	0.58
24:d:94:MET:SD	24:d:118:ARG:NH1	2.77	0.58
26:W:359:VAL:HG13	26:W:382:LEU:HD22	1.84	0.58
27:V:287:ARG:NH1	28:e:21:GLU:OE2	2.36	0.58
29:A:125:LEU:O	29:A:148:GLN:NE2	2.36	0.58
29:A:173:THR:HG23	29:A:175:SER:H	1.69	0.58
32:U:160:LEU:HD11	32:U:196:LYS:HB3	1.85	0.58
2:C:160:GLU:HA	2:C:313:ARG:HH21	1.69	0.58
5:G:158:GLY:O	6:H:84:ARG:NH1	2.30	0.58
11:M:123:THR:HA	11:M:130:PRO:HB3	1.84	0.58
20:Y:308:LEU:HD12	20:Y:356:THR:HG22	1.85	0.58
23:b:9:CYS:N	23:b:110:ILE:O	2.36	0.58
27:V:440:LYS:HE2	27:V:443:ARG:HH12	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:U:613:ASP:OD1	32:U:616:ARG:NH2	2.29	0.58
32:U:793:LYS:NZ	32:U:794:ASP:OD1	2.37	0.58
34:u:162:ASP:OD1	34:u:162:ASP:N	2.34	0.58
7:I:91:ARG:HH11	14:P:76:LEU:HB3	1.69	0.58
10:L:104:PRO:HG2	10:L:107:ARG:HD2	1.85	0.58
13:O:3:ILE:O	13:O:126:THR:OG1	2.16	0.58
23:b:120:ASN:HD21	23:b:122:LYS:HD3	1.68	0.58
24:d:295:THR:HG22	24:d:298:LYS:H	1.69	0.58
25:f:417:ILE:HG22	25:f:418:LEU:HD23	1.85	0.58
25:f:721:VAL:HG21	25:f:754:LYS:HZ1	1.68	0.58
26:W:69:ALA:O	26:W:73:MET:HG2	2.03	0.58
1:B:378:VAL:HA	1:B:416:ASN:HB2	1.86	0.58
2:C:81:ASP:OD1	2:C:82:LYS:N	2.37	0.58
2:C:327:ASP:O	2:C:331:ILE:HD12	2.04	0.58
4:c:226:MET:HG2	26:W:436:MET:HG3	1.84	0.58
6:H:39:LYS:HA	6:H:44:VAL:HG12	1.86	0.58
10:L:112:ILE:O	10:L:116:THR:HG22	2.03	0.58
20:Y:383:LEU:O	20:Y:387:ILE:HG12	2.04	0.58
26:W:81:ASP:OD2	26:W:81:ASP:N	2.33	0.58
29:A:96:ALA:HB2	29:A:115:VAL:HG12	1.85	0.58
2:C:150:MET:HA	2:C:331:ILE:HG21	1.86	0.58
25:f:343:LYS:HB3	25:f:390:LEU:HD21	1.86	0.58
25:f:716:ASP:OD1	25:f:753:ALA:HA	2.03	0.58
3:D:340:GLN:O	3:D:344:ILE:HG12	2.04	0.58
6:H:93:LEU:HD11	6:H:113:ARG:HB3	1.84	0.58
9:K:145:GLY:HA2	9:K:220:VAL:HG11	1.84	0.58
17:S:13:LEU:HG	17:S:137:ALA:HB2	1.86	0.58
19:X:334:ASN:HB3	19:X:354:ILE:HD11	1.86	0.58
20:Y:110:TYR:O	20:Y:113:ARG:N	2.37	0.58
21:Z:255:ASP:O	21:Z:259:VAL:HG12	2.04	0.58
22:a:68:GLU:HG3	22:a:69:HIS:H	1.69	0.58
25:f:831:VAL:HG11	25:f:844:VAL:HB	1.86	0.58
27:V:224:LEU:O	27:V:257:ASN:ND2	2.36	0.58
29:A:215:PHE:CE2	29:A:342:GLU:HG2	2.39	0.58
30:F:72:LYS:HD3	30:F:73:ILE:N	2.19	0.58
31:E:261:LEU:HD21	31:E:289:LEU:HB2	1.86	0.58
31:E:349:GLU:O	31:E:353:PHE:N	2.29	0.58
10:L:76:GLY:O	30:F:439:ALA:N	2.32	0.57
11:M:45:VAL:HG22	11:M:216:VAL:HG12	1.84	0.57
14:P:121:ILE:HD12	14:P:137:VAL:HG22	1.84	0.57
2:C:60:ARG:NH1	3:D:71:GLU:OE1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:182:LYS:HG3	5:G:189:TRP:HZ2	1.69	0.57
6:H:181:ASP:OD1	6:H:181:ASP:N	2.32	0.57
12:N:129:GLY:O	12:N:132:SER:OG	2.22	0.57
14:P:24:ALA:HB2	14:P:42:ILE:HG12	1.86	0.57
21:Z:260:VAL:O	21:Z:261:TYR:C	2.47	0.57
22:a:163:TYR:HA	22:a:168:ASN:HB3	1.85	0.57
25:f:373:ALA:HB2	25:f:744:MET:HG2	1.87	0.57
27:V:225:ASP:OD1	27:V:225:ASP:N	2.25	0.57
30:F:357:PRO:O	30:F:362:ARG:NH2	2.37	0.57
7:I:179:TYR:O	8:J:52:LYS:NZ	2.36	0.57
20:Y:180:LEU:HD12	20:Y:197:ALA:HA	1.86	0.57
21:Z:260:VAL:HG12	21:Z:261:TYR:N	2.16	0.57
29:A:324:PRO:O	29:A:326:THR:N	2.37	0.57
32:U:212:ASP:OD2	32:U:215:ASN:ND2	2.37	0.57
32:U:666:LYS:NZ	32:U:702:THR:O	2.37	0.57
33:g:177:LEU:HB3	33:g:228:CR8:C6	2.35	0.57
10:L:164:ARG:HD3	30:F:425:LEU:HD13	1.84	0.57
20:Y:192:ARG:C	20:Y:194:PHE:H	2.11	0.57
20:Y:346:LYS:NZ	27:V:412:LEU:O	2.36	0.57
23:b:124:LEU:HD12	23:b:156:PHE:HB2	1.86	0.57
25:f:125:ILE:HG13	25:f:129:LEU:HD13	1.87	0.57
27:V:236:ARG:O	27:V:240:LEU:HD22	2.03	0.57
30:F:371:ARG:HB3	30:F:372:LYS:HZ2	1.68	0.57
31:E:216:ARG:O	31:E:220:ASN:ND2	2.37	0.57
33:g:218:ALA:HB2	33:g:299:LYS:HA	1.86	0.57
34:u:208:GLU:O	34:u:212:SER:N	2.31	0.57
2:C:252:ASP:OD2	2:C:297:ARG:NH1	2.37	0.57
5:G:71:LYS:HD2	5:G:227:PHE:HB3	1.87	0.57
8:J:64:ALA:HA	8:J:70:CYS:HA	1.86	0.57
21:Z:11:VAL:HA	21:Z:50:VAL:HG22	1.85	0.57
27:V:62:HIS:O	27:V:66:GLU:HG2	2.04	0.57
30:F:233:LYS:HD3	30:F:331:ALA:HB1	1.85	0.57
30:F:288:LEU:HB2	30:F:333:ASN:H	1.70	0.57
1:B:112:LEU:HD22	1:B:144:LEU:HD12	1.86	0.57
8:J:45:VAL:HG23	8:J:207:GLU:HB2	1.85	0.57
18:T:142:GLY:O	18:T:146:ALA:N	2.37	0.57
21:Z:43:TRP:HZ2	21:Z:118:ASN:HB2	1.69	0.57
22:a:109:GLU:HA	22:a:112:ILE:HD13	1.86	0.57
25:f:335:ARG:NH2	25:f:336:GLU:OE2	2.37	0.57
26:W:306:LEU:O	26:W:310:THR:HG23	2.05	0.57
30:F:359:GLU:HA	30:F:362:ARG:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:u:189:GLN:HE21	34:u:255:GLU:HG2	1.70	0.57
9:K:125:GLU:OE2	10:L:125:ARG:NH2	2.38	0.57
21:Z:204:LYS:HD2	26:W:442:THR:HG21	1.87	0.57
22:a:71:VAL:HA	23:b:17:ARG:HH11	1.69	0.57
32:U:131:GLU:OE1	32:U:135:ASN:ND2	2.36	0.57
11:M:34:SER:OG	11:M:65:ARG:NH1	2.38	0.57
11:M:70:ASP:HB3	11:M:73:VAL:HB	1.87	0.57
18:T:90:SER:O	18:T:94:ARG:HG2	2.05	0.57
20:Y:272:PHE:CE1	20:Y:323:PHE:HE1	2.23	0.57
23:b:55:ALA:HB1	23:b:82:GLY:HA3	1.86	0.57
24:d:358:ILE:HG22	24:d:359:VAL:H	1.70	0.57
25:f:514:VAL:O	25:f:518:THR:HG23	2.04	0.57
29:A:79:ASP:OD2	33:g:372:LYS:NZ	2.34	0.57
30:F:344:ARG:HE	31:E:341:ALA:HB1	1.70	0.57
2:C:69:GLN:HG3	2:C:118:ASN:HD21	1.70	0.57
2:C:263:SER:OG	2:C:264:GLY:N	2.34	0.57
7:I:68:LEU:HD13	7:I:90:LEU:HD13	1.87	0.57
25:f:737:ASN:HA	25:f:746:ARG:HH22	1.70	0.57
31:E:243:PHE:H	31:E:254:GLN:HE22	1.53	0.57
20:Y:49:ASN:HB3	20:Y:113:ARG:HG3	1.87	0.57
20:Y:207:THR:O	20:Y:207:THR:OG1	2.23	0.57
23:b:151:GLU:H	23:b:151:GLU:CD	2.12	0.57
25:f:664:GLU:HG3	25:f:667:GLY:H	1.69	0.57
26:W:294:LYS:H	26:W:294:LYS:HD3	1.70	0.57
27:V:256:ARG:NH2	28:e:21:GLU:O	2.38	0.57
3:D:92:PHE:HZ	3:D:95:ALA:HB2	1.69	0.56
14:P:28:PHE:HB2	14:P:39:PHE:HB2	1.87	0.56
19:X:312:GLU:CB	19:X:313:LEU:HD22	2.35	0.56
19:X:370:LEU:HD21	20:Y:306:GLN:HG2	1.87	0.56
20:Y:42:MET:O	20:Y:46:ARG:HG2	2.04	0.56
25:f:392:THR:HG23	25:f:414:LEU:HD21	1.87	0.56
26:W:326:MET:H	26:W:326:MET:CE	2.17	0.56
30:F:314:LEU:HD12	30:F:315:ASN:N	2.20	0.56
3:D:229:ARG:HD3	31:E:267:PHE:CD1	2.41	0.56
5:G:40:VAL:HG13	5:G:51:VAL:HG13	1.87	0.56
5:G:230:LEU:HG	5:G:234:GLU:HG3	1.87	0.56
8:J:7:ILE:HG23	8:J:8:THR:HG23	1.86	0.56
10:L:215:VAL:HB	10:L:221:PHE:HD1	1.70	0.56
18:T:22:ILE:HD11	18:T:122:LEU:HD21	1.87	0.56
18:T:174:ARG:NH1	18:T:206:GLU:O	2.38	0.56
20:Y:192:ARG:NH1	20:Y:196:GLN:OE1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:b:59:GLU:OE1	23:b:59:GLU:N	2.36	0.56
25:f:102:HIS:CE1	25:f:137:ARG:HD3	2.39	0.56
25:f:351:THR:O	25:f:357:ARG:NH2	2.38	0.56
30:F:396:CYS:O	30:F:397:LYS:C	2.48	0.56
2:C:120:SER:HB3	4:c:193:ILE:HD11	1.86	0.56
3:D:181:VAL:HG11	3:D:308:ILE:HD11	1.87	0.56
4:c:89:PRO:HG3	33:g:250:LYS:HG3	1.86	0.56
9:K:168:ARG:HA	9:K:178:GLN:HE22	1.68	0.56
10:L:66:VAL:O	17:S:77:HIS:NE2	2.38	0.56
17:S:181:SER:HA	17:S:184:GLU:HG2	1.86	0.56
18:T:89:HIS:CE1	18:T:131:ALA:HB1	2.40	0.56
19:X:151:SER:OG	19:X:155:ARG:NH2	2.39	0.56
19:X:170:GLN:OE1	19:X:192:SER:OG	2.17	0.56
20:Y:98:SER:OG	20:Y:130:LYS:NZ	2.36	0.56
20:Y:174:TRP:O	20:Y:177:ARG:NH2	2.38	0.56
23:b:1:MET:SD	23:b:1:MET:N	2.66	0.56
23:b:6:THR:HA	23:b:108:ARG:O	2.06	0.56
24:d:172:LYS:HA	24:d:175:TYR:HD1	1.70	0.56
25:f:43:GLN:O	25:f:47:GLU:HB2	2.05	0.56
25:f:721:VAL:HG22	25:f:725:SER:HB3	1.88	0.56
25:f:779:CYS:SG	25:f:780:PRO:HD3	2.44	0.56
27:V:195:ILE:HG22	27:V:203:LEU:HD11	1.86	0.56
29:A:67:GLU:HA	29:A:68:SER:HB2	1.88	0.56
29:A:102:ILE:HD11	30:F:165:PRO:HD2	1.88	0.56
30:F:428:GLN:OE1	30:F:428:GLN:N	2.29	0.56
31:E:35:GLU:HA	31:E:38:LYS:HZ3	1.70	0.56
32:U:247:GLN:NE2	32:U:904:LYS:HE3	2.21	0.56
33:g:266:CYS:HA	33:g:287:GLY:HA2	1.87	0.56
2:C:189:TYR:CZ	2:C:316:GLU:HB2	2.40	0.56
4:c:46:ARG:HH21	4:c:148:ILE:HG22	1.71	0.56
16:R:139:MET:O	16:R:143:TYR:N	2.39	0.56
21:Z:103:LYS:HE2	26:W:455:LEU:HD11	1.87	0.56
26:W:39:ARG:NH2	26:W:43:VAL:HG11	2.21	0.56
29:A:213:LEU:HB2	29:A:337:LEU:HD23	1.87	0.56
29:A:243:SER:HA	29:A:246:VAL:HG12	1.88	0.56
30:F:187:ASP:N	30:F:187:ASP:OD1	2.36	0.56
32:U:505:ASP:HB3	32:U:508:THR:HG22	1.88	0.56
2:C:141:GLU:OE1	2:C:141:GLU:N	2.31	0.56
3:D:39:ASP:N	3:D:42:SER:HG	2.03	0.56
11:M:69:VAL:HG23	11:M:75:MET:HB2	1.86	0.56
13:O:78:THR:O	13:O:82:MET:HG3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:206:LYS:HZ2	14:P:161:ASP:HB2	1.69	0.56
16:R:8:PHE:HE2	16:R:10:HIS:HB3	1.71	0.56
22:a:255:TRP:O	22:a:258:GLN:NE2	2.37	0.56
25:f:267:ARG:HH12	25:f:272:LEU:HD23	1.70	0.56
26:W:174:TYR:OH	26:W:182:ARG:NH2	2.39	0.56
31:E:159:PHE:O	31:E:163:GLY:N	2.29	0.56
1:B:391:SER:H	1:B:394:ASP:HB2	1.70	0.56
8:J:212:ARG:HB3	8:J:215:GLN:NE2	2.21	0.56
9:K:71:ASP:HB3	9:K:74:ILE:HG22	1.88	0.56
11:M:23:VAL:O	11:M:27:MET:HG2	2.05	0.56
12:N:119:MET:HE2	18:T:57:TYR:HB3	1.88	0.56
15:Q:12:TYR:OH	15:Q:151:ILE:O	2.21	0.56
19:X:97:LEU:HD13	19:X:136:LEU:HD13	1.88	0.56
24:d:91:ALA:HA	24:d:94:MET:HG2	1.88	0.56
27:V:104:THR:HA	27:V:107:ARG:HH21	1.71	0.56
27:V:289:LEU:HD22	27:V:308:THR:HG23	1.88	0.56
12:N:19:ARG:HB2	12:N:171:GLY:N	2.19	0.56
19:X:315:ASP:N	19:X:315:ASP:OD1	2.36	0.56
25:f:76:GLU:HG2	25:f:83:ARG:HD3	1.87	0.56
26:W:349:LYS:HD2	26:W:350:ARG:HH12	1.71	0.56
1:B:141:LYS:HA	1:B:144:LEU:HD23	1.88	0.56
19:X:338:VAL:C	19:X:340:GLU:H	2.12	0.56
30:F:62:VAL:HA	30:F:65:GLU:HG3	1.87	0.56
32:U:490:ARG:HB2	32:U:493:VAL:HG12	1.88	0.56
32:U:764:LEU:O	32:U:767:THR:OG1	2.22	0.56
3:D:309:MET:HE2	3:D:327:LEU:HD21	1.86	0.56
5:G:70:PHE:HD2	5:G:91:VAL:HG11	1.70	0.56
20:Y:268:TYR:HA	20:Y:271:PHE:HB3	1.88	0.56
25:f:124:ASP:OD1	25:f:124:ASP:N	2.29	0.56
25:f:189:LYS:HG3	25:f:190:GLU:HG3	1.86	0.56
25:f:596:ASP:OD1	25:f:600:TYR:OH	2.16	0.56
26:W:135:LYS:HD2	26:W:139:GLU:HB2	1.87	0.56
26:W:179:LYS:HB3	26:W:212:LYS:HD2	1.87	0.56
27:V:211:TYR:OH	27:V:234:ARG:NH2	2.35	0.56
29:A:143:ASP:OD1	29:A:147:TYR:N	2.35	0.56
12:N:19:ARG:HB2	12:N:171:GLY:H	1.70	0.56
14:P:125:ASP:HB2	14:P:129:CYS:HB3	1.87	0.56
18:T:62:TYR:O	18:T:65:GLN:HG2	2.05	0.56
19:X:77:LEU:HD22	19:X:116:TRP:HE1	1.69	0.56
20:Y:23:ARG:O	20:Y:32:ARG:NH1	2.39	0.56
20:Y:363:ASN:HD21	27:V:466:ILE:HG22	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Z:94:TRP:CZ2	21:Z:121:LEU:HD12	2.41	0.56
22:a:321:LYS:NZ	22:a:334:THR:O	2.33	0.56
23:b:3:LEU:HD22	23:b:44:ASN:ND2	2.21	0.56
31:E:270:LEU:HD22	31:E:273:VAL:HG11	1.87	0.56
32:U:167:ILE:O	32:U:170:SER:OG	2.24	0.56
4:c:291:LEU:O	4:c:295:ASN:ND2	2.39	0.55
9:K:124:GLY:O	10:L:125:ARG:NE	2.40	0.55
11:M:72:HIS:ND1	11:M:139:SER:OG	2.35	0.55
12:N:114:VAL:HA	12:N:119:MET:O	2.06	0.55
18:T:96:MET:HB3	18:T:106:LEU:HD12	1.88	0.55
25:f:298:LEU:HD11	25:f:492:SER:HA	1.87	0.55
25:f:664:GLU:HG3	25:f:666:ILE:H	1.70	0.55
25:f:680:ARG:NH1	25:f:680:ARG:O	2.39	0.55
30:F:389:ASP:N	30:F:389:ASP:OD1	2.39	0.55
31:E:65:THR:HG22	31:E:68:LYS:HB2	1.87	0.55
4:c:82:VAL:HG21	4:c:113:HIS:CD2	2.41	0.55
20:Y:111:LEU:HA	20:Y:114:ILE:CB	2.30	0.55
20:Y:147:ILE:HD12	20:Y:150:PHE:HD2	1.70	0.55
21:Z:44:GLN:HB3	21:Z:46:LYS:HZ3	1.70	0.55
22:a:207:GLY:O	22:a:271:LYS:NZ	2.38	0.55
25:f:681:TYR:OH	25:f:761:MET:HE1	2.06	0.55
26:W:436:MET:O	26:W:439:VAL:HG12	2.05	0.55
30:F:229:PRO:HA	37:F:501:ADP:PB	2.46	0.55
33:g:175:ILE:HG13	33:g:279:PHE:HB3	1.88	0.55
3:D:271:ALA:HA	3:D:289:LEU:HD13	1.88	0.55
4:c:164:ASN:OD1	4:c:166:ASN:ND2	2.37	0.55
9:K:6:SER:O	9:K:10:ARG:NH1	2.38	0.55
9:K:93:ARG:NH1	16:R:68:LEU:O	2.40	0.55
19:X:341:PRO:HG2	19:X:342:PHE:HD2	1.71	0.55
20:Y:137:ARG:H	20:Y:137:ARG:HD2	1.70	0.55
25:f:441:LYS:O	25:f:445:LEU:HG	2.06	0.55
32:U:609:ASP:OD1	32:U:610:VAL:N	2.40	0.55
3:D:99:ASN:O	3:D:115:ILE:N	2.34	0.55
8:J:104:VAL:HG21	8:J:143:ARG:HB2	1.88	0.55
11:M:54:LEU:HB2	11:M:58:TYR:HE2	1.70	0.55
14:P:59:ASP:OD2	15:Q:93:ARG:NH2	2.39	0.55
17:S:20:PHE:HB3	17:S:199:THR:HB	1.89	0.55
20:Y:326:GLY:HA3	20:Y:329:PHE:HB3	1.89	0.55
20:Y:363:ASN:ND2	27:V:465:ASP:OD1	2.39	0.55
25:f:617:SER:OG	25:f:632:LYS:HD3	2.06	0.55
27:V:114:TYR:HA	27:V:135:LEU:HD21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:393:GLY:O	30:F:396:CYS:N	2.35	0.55
31:E:136:GLY:HA2	31:E:315:ILE:HD12	1.88	0.55
32:U:21:GLU:OE1	32:U:55:ARG:NE	2.39	0.55
33:g:293:ASN:OD1	33:g:298:GLN:NE2	2.40	0.55
1:B:71:TYR:HH	25:f:640:LYS:HZ3	1.52	0.55
2:C:127:LEU:HD22	3:D:102:ILE:HD11	1.89	0.55
3:D:391:ARG:NE	3:D:393:ILE:O	2.40	0.55
3:D:407:ILE:HG13	3:D:407:ILE:O	2.05	0.55
11:M:10:SER:HG	11:M:126:SER:HG	1.54	0.55
13:O:159:ILE:O	13:O:163:ILE:HG12	2.06	0.55
16:R:18:SER:HB3	16:R:173:ALA:H	1.72	0.55
19:X:338:VAL:HG22	19:X:339:ILE:H	1.70	0.55
20:Y:16:ASP:HB2	20:Y:286:TRP:CE2	2.41	0.55
30:F:132:TYR:CE1	30:F:158:TYR:HE2	2.24	0.55
30:F:139:LEU:HD11	31:E:50:LEU:HD21	1.89	0.55
6:H:51:LYS:HE2	6:H:207:ASN:HD21	1.70	0.55
7:I:174:MET:HE1	7:I:195:LYS:HG3	1.89	0.55
13:O:89:ARG:O	13:O:91:GLN:NE2	2.39	0.55
15:Q:19:ARG:HD2	15:Q:177:THR:HG23	1.88	0.55
21:Z:12:HIS:HE1	21:Z:49:ASP:HB2	1.71	0.55
25:f:99:LEU:HB3	25:f:101:PRO:HD2	1.89	0.55
25:f:131:MET:N	25:f:131:MET:SD	2.80	0.55
25:f:194:TYR:HB2	25:f:198:HIS:NE2	2.22	0.55
25:f:647:GLY:CA	25:f:650:GLN:HE22	2.17	0.55
32:U:161:ASP:OD1	32:U:161:ASP:N	2.31	0.55
5:G:144:ASP:OD2	5:G:147:GLN:NE2	2.40	0.55
7:I:86:LEU:HD23	7:I:134:LEU:HD21	1.89	0.55
11:M:35:THR:HA	11:M:165:ILE:O	2.06	0.55
12:N:45:ARG:HB3	12:N:52:THR:HB	1.88	0.55
23:b:161:ASN:HD21	23:b:168:SER:H	1.54	0.55
34:u:222:GLU:HA	34:u:225:ILE:HD12	1.88	0.55
2:C:62:GLU:OE2	3:D:117:SER:N	2.37	0.55
9:K:118:ASN:HD21	10:L:82:ARG:NH2	2.04	0.55
22:a:257:GLN:NE2	22:a:259:PRO:O	2.40	0.55
25:f:826:GLN:NE2	25:f:863:THR:OG1	2.38	0.55
26:W:265:GLN:NE2	26:W:336:PRO:O	2.39	0.55
2:C:336:MET:HE3	3:D:196:ILE:HD13	1.89	0.55
3:D:238:LYS:HG3	31:E:207:TYR:CD2	2.42	0.55
3:D:389:GLU:OE1	3:D:397:LYS:NZ	2.40	0.55
6:H:97:TYR:CD2	6:H:105:ILE:HG13	2.41	0.55
8:J:24:GLU:HA	8:J:27:LYS:HE3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:40:ILE:HD11	9:K:47:CYS:HB3	1.88	0.55
9:K:234:LEU:HA	9:K:237:VAL:HG12	1.89	0.55
10:L:78:THR:HG22	30:F:439:ALA:HB2	1.89	0.55
11:M:141:SER:OG	11:M:143:ASN:OD1	2.25	0.55
11:M:220:THR:OG1	11:M:223:ARG:O	2.19	0.55
12:N:167:ASP:OD1	12:N:169:SER:OG	2.23	0.55
14:P:49:LEU:HD11	14:P:84:PRO:HB3	1.88	0.55
15:Q:21:ALA:HB2	15:Q:32:HIS:HB2	1.89	0.55
15:Q:164:LEU:HA	15:Q:167:LEU:HD12	1.88	0.55
19:X:177:TYR:CD1	19:X:185:LYS:HB3	2.42	0.55
19:X:177:TYR:CE1	19:X:185:LYS:HB3	2.42	0.55
20:Y:23:ARG:NH1	20:Y:60:SER:HB3	2.22	0.55
20:Y:232:GLU:N	20:Y:234:PRO:HD3	2.22	0.55
20:Y:382:LYS:O	20:Y:386:VAL:HG13	2.07	0.55
23:b:10:VAL:HG21	23:b:75:LEU:HD21	1.88	0.55
25:f:411:ALA:HB3	25:f:443:GLY:HA3	1.89	0.55
31:E:249:ALA:HA	33:g:156:LEU:HD11	1.89	0.55
31:E:363:VAL:HG23	31:E:366:ASP:H	1.72	0.55
2:C:194:THR:N	35:C:501:ATP:O1B	2.27	0.55
13:O:143:ARG:NH2	13:O:150:GLU:OE1	2.36	0.55
16:R:80:SER:OG	16:R:120:ARG:NH2	2.24	0.55
20:Y:34:ASP:H	20:Y:37:VAL:HG23	1.71	0.55
20:Y:183:TYR:O	20:Y:192:ARG:HG3	2.06	0.55
24:d:258:PHE:C	24:d:258:PHE:CD2	2.85	0.55
25:f:670:MET:HG2	25:f:673:ARG:NH1	2.21	0.55
26:W:200:ILE:HD12	26:W:201:ARG:N	2.21	0.55
27:V:168:GLN:HB3	27:V:191:LEU:HD23	1.89	0.55
30:F:280:PRO:HB3	30:F:325:GLN:HE22	1.72	0.55
33:g:367:ASP:OD2	33:g:367:ASP:N	2.37	0.55
34:u:183:GLN:HE21	34:u:262:TYR:HB3	1.72	0.55
7:I:105:ILE:HD12	7:I:106:PRO:HD2	1.90	0.54
9:K:92:ALA:O	9:K:95:GLU:HG2	2.06	0.54
11:M:46:VAL:HG12	11:M:215:TRP:HB3	1.88	0.54
14:P:186:ILE:HD12	14:P:199:THR:HB	1.89	0.54
15:Q:43:LEU:HD11	15:Q:183:ILE:HD11	1.87	0.54
17:S:14:ALA:HA	17:S:22:ILE:O	2.07	0.54
19:X:125:LEU:O	19:X:129:LEU:HG	2.07	0.54
20:Y:110:TYR:O	20:Y:112:CYS:N	2.39	0.54
21:Z:199:LYS:NZ	22:a:364:GLU:OE2	2.38	0.54
25:f:340:MET:H	25:f:340:MET:CE	2.19	0.54
26:W:140:ILE:HB	26:W:144:ARG:HH21	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:151:ILE:HD12	29:A:152:PRO:HD2	1.90	0.54
30:F:225:MET:HE2	30:F:233:LYS:HB2	1.89	0.54
30:F:420:TYR:O	30:F:424:ILE:HG23	2.07	0.54
6:H:56:LEU:H	6:H:56:LEU:HD12	1.71	0.54
9:K:118:ASN:HD21	10:L:82:ARG:HH21	1.54	0.54
13:O:113:ILE:HD12	13:O:119:THR:HB	1.87	0.54
15:Q:50:ALA:HB3	16:R:117:GLU:HG3	1.87	0.54
19:X:339:ILE:HD12	19:X:385:LEU:HD21	1.90	0.54
20:Y:190:ALA:HB3	28:e:40:GLU:OE1	2.07	0.54
21:Z:259:VAL:HG13	21:Z:260:VAL:CG2	2.38	0.54
23:b:86:PHE:O	23:b:90:ILE:HG22	2.07	0.54
25:f:278:VAL:HG23	25:f:279:GLU:H	1.71	0.54
25:f:664:GLU:O	25:f:669:GLU:N	2.40	0.54
25:f:703:ARG:HD3	25:f:785:ARG:HH22	1.71	0.54
27:V:403:ILE:O	27:V:407:VAL:HG23	2.06	0.54
30:F:356:MET:HA	30:F:356:MET:HE3	1.88	0.54
7:I:45:LEU:HD13	7:I:75:SER:HB3	1.90	0.54
16:R:8:PHE:CE2	16:R:10:HIS:HB3	2.42	0.54
19:X:88:LEU:O	19:X:92:LEU:HG	2.07	0.54
20:Y:69:LEU:O	20:Y:73:MET:HE1	2.07	0.54
20:Y:89:GLU:HA	20:Y:99:GLU:OE1	2.07	0.54
21:Z:19:VAL:HG21	21:Z:124:ILE:HD12	1.89	0.54
21:Z:54:PHE:CG	21:Z:78:MET:HG2	2.42	0.54
23:b:48:ASN:HB3	23:b:64:LEU:HD12	1.89	0.54
25:f:510:SER:HB2	25:f:514:VAL:HB	1.89	0.54
26:W:297:GLU:OE1	26:W:297:GLU:N	2.40	0.54
27:V:172:VAL:HA	27:V:175:MET:HE2	1.88	0.54
32:U:7:GLY:O	32:U:10:SER:OG	2.21	0.54
1:B:293:LYS:HD2	1:B:339:PRO:HD3	1.88	0.54
3:D:200:ARG:N	3:D:328:ASP:OD2	2.37	0.54
5:G:240:VAL:O	5:G:244:GLU:HG2	2.07	0.54
8:J:34:GLY:O	8:J:158:ALA:HA	2.07	0.54
12:N:12:VAL:HG11	12:N:101:ALA:HB1	1.88	0.54
21:Z:69:PHE:HD1	21:Z:70:LEU:N	2.05	0.54
24:d:191:LEU:HA	24:d:194:LEU:HB2	1.88	0.54
25:f:402:ASN:HB2	25:f:406:GLY:HA3	1.88	0.54
25:f:487:LEU:HD12	25:f:524:MET:HE1	1.89	0.54
25:f:665:GLU:HA	25:f:669:GLU:HB2	1.89	0.54
30:F:391:PHE:CE2	30:F:427:VAL:HG11	2.43	0.54
32:U:38:ILE:HD12	32:U:38:ILE:H	1.72	0.54
32:U:184:CYS:HA	32:U:188:MET:HG3	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:u:188:GLY:O	34:u:253:GLY:N	2.29	0.54
4:c:140:ALA:H	4:c:161:ARG:HE	1.54	0.54
4:c:164:ASN:OD1	4:c:167:MET:N	2.41	0.54
5:G:86:ASP:HA	11:M:120:HIS:HE1	1.73	0.54
6:H:19:LEU:HD22	6:H:19:LEU:H	1.73	0.54
9:K:35:SER:HB3	9:K:66:LYS:HE3	1.89	0.54
17:S:78:SER:OG	17:S:79:ASN:OD1	2.24	0.54
20:Y:111:LEU:O	20:Y:115:GLY:N	2.41	0.54
25:f:105:LYS:O	25:f:109:ILE:HB	2.07	0.54
25:f:606:VAL:O	25:f:610:GLN:N	2.40	0.54
26:W:84:ASN:O	26:W:88:MET:HG2	2.07	0.54
26:W:407:ASP:HB3	26:W:410:ALA:HB3	1.90	0.54
30:F:284:PHE:CZ	30:F:286:ASP:HB3	2.42	0.54
32:U:68:PHE:HD2	32:U:76:GLU:HB3	1.73	0.54
32:U:88:PHE:CE1	32:U:97:VAL:HG23	2.43	0.54
1:B:297:SER:HB3	1:B:302:GLU:HG3	1.90	0.54
8:J:153:TYR:O	8:J:154:HIS:ND1	2.41	0.54
13:O:18:THR:O	13:O:31:CYS:N	2.31	0.54
22:a:180:LEU:HD13	22:a:221:VAL:HG11	1.88	0.54
22:a:313:LYS:O	22:a:317:VAL:HG22	2.07	0.54
29:A:97:ARG:HE	29:A:139:ARG:HG3	1.72	0.54
6:H:68:ILE:HG21	6:H:110:LEU:HD21	1.89	0.54
8:J:166:LYS:O	8:J:170:GLU:HG2	2.06	0.54
16:R:37:ILE:HD11	16:R:41:LEU:HD12	1.88	0.54
19:X:163:LYS:CB	19:X:200:ILE:HG13	2.38	0.54
19:X:255:LEU:HB2	19:X:287:LEU:HD13	1.90	0.54
20:Y:349:LYS:O	20:Y:352:GLU:N	2.28	0.54
22:a:335:TRP:NE1	22:a:337:GLN:O	2.38	0.54
26:W:80:TRP:O	26:W:83:LEU:HG	2.08	0.54
27:V:470:ARG:NH1	27:V:473:GLN:OE1	2.40	0.54
29:A:356:LYS:O	29:A:360:ARG:HG3	2.08	0.54
31:E:270:LEU:HD22	31:E:273:VAL:CG1	2.38	0.54
1:B:220:LYS:NZ	1:B:345:GLY:O	2.41	0.54
1:B:340:ALA:HA	1:B:343:ARG:HG3	1.89	0.54
2:C:161:ILE:HD11	2:C:188:LEU:HD21	1.89	0.54
9:K:165:CYS:HA	10:L:57:ALA:HA	1.89	0.54
12:N:56:ALA:O	12:N:60:THR:OG1	2.21	0.54
13:O:53:ASP:O	13:O:57:GLN:HG2	2.08	0.54
18:T:126:ASP:OD1	18:T:129:GLY:N	2.40	0.54
20:Y:117:LYS:HB3	20:Y:147:ILE:HG12	1.89	0.54
22:a:113:LEU:CD1	22:a:154:ARG:HG3	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:196:ARG:HG2	22:a:196:ARG:HH11	1.73	0.54
30:F:261:ILE:HG12	31:E:206:LYS:HG2	1.88	0.54
1:B:436:GLU:HG2	1:B:437:GLY:H	1.72	0.54
4:c:100:LYS:HG3	4:c:105:PRO:HB3	1.89	0.54
4:c:251:LEU:HB3	4:c:284:LEU:HD13	1.88	0.54
9:K:12:VAL:HG12	9:K:23:GLN:HG2	1.90	0.54
9:K:38:ILE:HD11	9:K:181:LEU:HD11	1.90	0.54
25:f:146:GLY:HA2	25:f:150:GLU:HA	1.88	0.54
25:f:180:GLN:HB3	25:f:181:ARG:NH2	2.23	0.54
26:W:48:LEU:HD11	26:W:93:ARG:HH22	1.73	0.54
26:W:231:ILE:HD11	26:W:246:HIS:HB3	1.90	0.54
30:F:192:ASP:OD1	30:F:192:ASP:N	2.40	0.54
31:E:353:PHE:HB3	31:E:366:ASP:OD1	2.08	0.54
1:B:59:ARG:HA	1:B:62:LEU:HB2	1.90	0.54
1:B:439:TYR:CD2	8:J:28:LYS:HB3	2.43	0.54
2:C:113:ARG:HG3	2:C:130:LYS:HB2	1.89	0.54
27:V:189:ASP:HA	27:V:192:MET:SD	2.48	0.54
27:V:227:VAL:O	27:V:231:LEU:HD23	2.07	0.54
29:A:257:VAL:HA	29:A:260:LEU:HB3	1.89	0.54
31:E:291:ARG:NH1	31:E:292:PRO:O	2.40	0.54
32:U:439:GLU:HB3	32:U:473:VAL:HG22	1.90	0.54
2:C:306:LEU:O	2:C:314:LYS:NZ	2.40	0.53
5:G:72:ILE:HG22	5:G:73:THR:HG23	1.91	0.53
8:J:71:MET:SD	8:J:84:ILE:HD11	2.48	0.53
18:T:97:TYR:O	18:T:101:SER:OG	2.26	0.53
20:Y:108:ALA:O	20:Y:112:CYS:HB2	2.08	0.53
21:Z:106:ILE:HG12	21:Z:153:LYS:HG3	1.89	0.53
21:Z:164:ALA:HB3	21:Z:169:GLU:HG2	1.88	0.53
22:a:150:SER:O	22:a:154:ARG:HG2	2.07	0.53
22:a:156:TYR:OH	22:a:196:ARG:NH2	2.41	0.53
25:f:93:PRO:O	25:f:97:LYS:HB3	2.08	0.53
26:W:178:GLU:HG3	26:W:180:LYS:HG3	1.89	0.53
29:A:174:TYR:OH	29:A:192:GLU:OE2	2.24	0.53
30:F:365:ILE:HD11	37:F:501:ADP:N1	2.23	0.53
31:E:205:ASP:OD1	31:E:206:LYS:N	2.41	0.53
32:U:374:SER:HB2	32:U:407:SER:HB2	1.90	0.53
9:K:115:ALA:HA	9:K:118:ASN:OD1	2.07	0.53
10:L:132:LEU:HB2	10:L:147:THR:OG1	2.08	0.53
12:N:116:MET:HA	12:N:116:MET:HE2	1.89	0.53
20:Y:134:LEU:HD13	20:Y:137:ARG:NH1	2.23	0.53
20:Y:232:GLU:CD	20:Y:302:HIS:HB3	2.32	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Z:261:TYR:O	21:Z:262:LEU:C	2.52	0.53
23:b:100:ARG:NH1	23:b:105:HIS:O	2.42	0.53
25:f:655:LEU:HD11	25:f:675:PHE:CE1	2.44	0.53
25:f:753:ALA:HB3	25:f:754:LYS:NZ	2.23	0.53
25:f:826:GLN:HB2	25:f:865:PHE:CE1	2.40	0.53
27:V:168:GLN:O	27:V:172:VAL:HG23	2.07	0.53
27:V:238:ALA:HB1	27:V:243:ASP:HB3	1.90	0.53
1:B:369:THR:HA	1:B:372:MET:HG3	1.91	0.53
1:B:405:MET:SD	1:B:408:ARG:NH2	2.82	0.53
5:G:107:TYR:CD1	13:O:75:ARG:HD2	2.43	0.53
5:G:113:MET:HE2	13:O:70:THR:HA	1.89	0.53
7:I:41:ASP:OD1	7:I:41:ASP:N	2.39	0.53
9:K:157:ASP:OD2	30:F:436:GLN:NE2	2.39	0.53
10:L:182:CYS:HB3	10:L:186:GLU:HB2	1.90	0.53
19:X:309:TYR:CD2	19:X:313:LEU:HB2	2.43	0.53
20:Y:104:MET:HA	20:Y:107:LYS:HB3	1.90	0.53
21:Z:259:VAL:HG13	21:Z:260:VAL:HB	1.90	0.53
22:a:322:GLY:HA3	22:a:332:HIS:O	2.07	0.53
23:b:98:LYS:HG2	34:u:203:SER:HB2	1.90	0.53
26:W:44:ILE:HG13	26:W:82:LEU:HD11	1.90	0.53
26:W:200:ILE:O	26:W:204:ILE:HG12	2.09	0.53
27:V:172:VAL:HA	27:V:175:MET:SD	2.49	0.53
27:V:292:THR:O	27:V:296:LYS:HG3	2.09	0.53
30:F:193:LYS:NZ	30:F:197:GLU:OE1	2.36	0.53
1:B:254:GLU:HA	2:C:232:ARG:HH21	1.73	0.53
4:c:163:ILE:N	4:c:199:HIS:O	2.37	0.53
7:I:235:GLN:O	7:I:238:LYS:HG2	2.08	0.53
9:K:40:ILE:HD12	9:K:40:ILE:O	2.08	0.53
11:M:8:ASP:HB3	11:M:21:PHE:HB2	1.90	0.53
11:M:77:VAL:HG11	11:M:84:ALA:HB1	1.90	0.53
13:O:34:ILE:HG12	13:O:44:CYS:SG	2.49	0.53
14:P:203:ARG:NH1	14:P:205:ASP:OD2	2.41	0.53
18:T:143:ALA:HA	18:T:147:GLN:HB2	1.90	0.53
19:X:292:GLN:HA	19:X:295:LYS:HG2	1.89	0.53
20:Y:66:ASP:HA	20:Y:69:LEU:HB3	1.90	0.53
20:Y:386:VAL:HG23	20:Y:387:ILE:HD13	1.90	0.53
21:Z:260:VAL:HG13	27:V:480:ILE:CG1	2.39	0.53
22:a:326:GLU:O	22:a:329:LYS:NZ	2.33	0.53
25:f:600:TYR:HB2	25:f:639:LYS:HB3	1.91	0.53
27:V:185:GLN:NE2	27:V:218:TYR:OH	2.42	0.53
30:F:181:PRO:HG2	30:F:242:ALA:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:421:MET:O	30:F:425:LEU:HG	2.09	0.53
31:E:206:LYS:HA	33:g:156:LEU:HD23	1.90	0.53
4:c:94:LYS:HB3	21:Z:81:MET:HE1	1.90	0.53
5:G:125:TYR:CD1	5:G:131:MET:HG2	2.43	0.53
9:K:85:ALA:HB2	9:K:139:VAL:HG11	1.91	0.53
10:L:40:SER:O	10:L:142:PRO:HG2	2.08	0.53
12:N:130:SER:OG	12:N:169:SER:OG	2.26	0.53
13:O:17:ASP:HB3	13:O:159:ILE:HD11	1.90	0.53
14:P:99:ARG:HD2	14:P:127:ILE:HD11	1.91	0.53
17:S:44:TYR:HD2	17:S:52:ILE:HG23	1.73	0.53
21:Z:43:TRP:CD1	21:Z:48:LEU:HD12	2.43	0.53
22:a:238:TYR:O	22:a:242:SER:HB3	2.07	0.53
25:f:19:ALA:HB3	25:f:34:ARG:HH12	1.72	0.53
2:C:255:GLY:HA2	2:C:273:MET:HG3	1.90	0.53
6:H:103:GLU:HG2	6:H:104:PRO:HD2	1.89	0.53
8:J:160:ALA:O	8:J:169:ARG:NH2	2.39	0.53
19:X:69:LEU:HA	19:X:72:TYR:HB3	1.90	0.53
23:b:9:CYS:HB3	23:b:54:LEU:HD11	1.91	0.53
23:b:161:ASN:HA	23:b:165:GLY:HA3	1.91	0.53
24:d:189:HIS:HB3	24:d:223:ASN:ND2	2.24	0.53
24:d:257:THR:HA	24:d:260:ILE:HB	1.90	0.53
24:d:258:PHE:C	24:d:258:PHE:HD2	2.17	0.53
25:f:675:PHE:CE2	25:f:691:PRO:HB2	2.43	0.53
27:V:192:MET:HA	27:V:195:ILE:HG12	1.91	0.53
32:U:376:MET:HE2	32:U:738:ASP:HB2	1.90	0.53
2:C:340:ARG:HH12	20:Y:174:TRP:CB	2.19	0.53
13:O:76:VAL:HG21	13:O:109:HIS:HB2	1.90	0.53
13:O:207:GLY:N	14:P:165:GLU:OE2	2.41	0.53
17:S:166:LEU:HD13	17:S:170:ARG:HD3	1.89	0.53
20:Y:22:LEU:O	20:Y:24:PHE:N	2.42	0.53
22:a:138:VAL:O	22:a:142:LEU:HB2	2.09	0.53
23:b:100:ARG:NH2	23:b:103:LYS:O	2.38	0.53
24:d:218:LYS:HG3	24:d:219:ASP:OD1	2.08	0.53
26:W:395:ASN:O	26:W:399:ASN:ND2	2.42	0.53
27:V:236:ARG:HH22	32:U:32:ASN:HA	1.74	0.53
29:A:145:ASN:ND2	33:g:170:LYS:HE3	2.13	0.53
33:g:183:VAL:HG23	33:g:287:GLY:HA3	1.89	0.53
13:O:22:GLU:HG2	13:O:27:ALA:HB2	1.91	0.53
17:S:85:THR:HA	17:S:88:ILE:HD12	1.90	0.53
21:Z:188:SER:OG	22:a:374:ILE:O	2.27	0.53
25:f:482:ILE:HD11	25:f:517:VAL:HG13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:259:LEU:HD21	27:V:295:ILE:HD11	1.90	0.53
29:A:186:LYS:O	29:A:190:VAL:HG23	2.09	0.53
29:A:229:VAL:HG22	29:A:233:THR:HG23	1.90	0.53
1:B:288:ASP:OD1	1:B:288:ASP:N	2.37	0.53
2:C:21:ARG:HD3	32:U:149:GLN:HE22	1.74	0.53
6:H:34:PRO:HD2	6:H:49:GLU:HG2	1.91	0.53
6:H:221:LEU:HB3	6:H:225:GLU:HG3	1.91	0.53
11:M:150:MET:HE2	11:M:150:MET:HA	1.91	0.53
13:O:37:ILE:HA	13:O:60:SER:HB3	1.91	0.53
16:R:14:VAL:HG22	16:R:177:TYR:HB2	1.90	0.53
20:Y:186:LEU:O	28:e:38:VAL:HG13	2.09	0.53
24:d:137:THR:HG22	24:d:140:GLN:H	1.73	0.53
25:f:66:LYS:NZ	25:f:67:ASP:OD1	2.28	0.53
25:f:99:LEU:HG	25:f:100:ARG:H	1.74	0.53
25:f:483:PHE:CZ	25:f:802:SER:HB3	2.44	0.53
25:f:646:MET:C	25:f:646:MET:HE3	2.33	0.53
26:W:136:ILE:HD11	26:W:142:ARG:HH22	1.73	0.53
31:E:18:GLU:OE2	31:E:20:LYS:NZ	2.32	0.53
32:U:337:LEU:HB3	32:U:789:ILE:HD13	1.90	0.53
32:U:568:GLU:OE1	32:U:601:ARG:NH2	2.42	0.53
3:D:171:ASP:OD1	3:D:171:ASP:N	2.42	0.53
6:H:76:TYR:HB3	6:H:83:TYR:CD1	2.44	0.53
13:O:18:THR:HB	13:O:30:ASN:HA	1.91	0.53
20:Y:68:ASP:HA	20:Y:71:ASN:HB2	1.91	0.53
20:Y:122:THR:HG22	20:Y:125:ARG:HH21	1.74	0.53
25:f:12:GLN:HB2	25:f:13:PRO:HD3	1.90	0.53
25:f:327:ASN:HD22	25:f:420:TRP:HD1	1.56	0.53
27:V:175:MET:CE	27:V:184:ALA:HA	2.34	0.53
29:A:159:PRO:HB3	29:A:166:VAL:HG12	1.91	0.53
30:F:65:GLU:OE2	31:E:34:LYS:NZ	2.29	0.53
3:D:161:ASP:OD1	3:D:161:ASP:N	2.32	0.52
8:J:94:HIS:HB2	8:J:106:TYR:HE2	1.73	0.52
9:K:91:LYS:HG2	9:K:119:LEU:HD22	1.91	0.52
9:K:96:THR:HA	9:K:107:MET:SD	2.49	0.52
10:L:231:PRO:HA	10:L:234:GLU:HG2	1.90	0.52
14:P:104:TYR:HA	14:P:126:LEU:HG	1.91	0.52
17:S:57:PHE:HD1	17:S:60:ASP:H	1.56	0.52
19:X:375:HIS:ND1	19:X:390:GLU:OE1	2.35	0.52
21:Z:72:HIS:NE2	23:b:61:LEU:O	2.36	0.52
22:a:7:PHE:O	22:a:11:SER:OG	2.27	0.52
25:f:438:ASP:O	25:f:477:MET:HE1	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:626:GLU:H	25:f:626:GLU:CD	2.18	0.52
31:E:178:THR:HG22	31:E:301:ILE:HG22	1.91	0.52
31:E:179:GLY:N	37:E:501:ADP:O2B	2.38	0.52
34:u:264:THR:OG1	34:u:265:PHE:N	2.41	0.52
4:c:122:LEU:HG	4:c:126:ASP:HB3	1.92	0.52
11:M:50:GLU:HB2	11:M:197:ILE:HD11	1.91	0.52
11:M:92:ARG:HD3	18:T:76:LEU:HD13	1.90	0.52
13:O:1:THR:O	13:O:129:SER:N	2.40	0.52
16:R:17:ASP:O	16:R:33:LYS:HG3	2.10	0.52
23:b:12:ASN:HB2	23:b:80:PRO:HA	1.91	0.52
25:f:122:ALA:HA	25:f:129:LEU:HD22	1.90	0.52
25:f:634:LYS:HG3	25:f:635:LYS:HD3	1.90	0.52
25:f:689:ALA:O	25:f:693:ALA:CB	2.53	0.52
26:W:139:GLU:HA	26:W:142:ARG:HH11	1.74	0.52
26:W:191:ARG:HA	26:W:229:LEU:HD11	1.92	0.52
30:F:288:LEU:HD22	30:F:334:ARG:HB2	1.92	0.52
31:E:182:LEU:HD22	37:E:501:ADP:C8	2.44	0.52
32:U:137:MET:HA	32:U:137:MET:HE3	1.90	0.52
14:P:12:MET:HE3	14:P:146:MET:CG	2.38	0.52
15:Q:157:VAL:HA	15:Q:160:LEU:HG	1.90	0.52
20:Y:148:GLY:HA3	20:Y:153:ASP:HB3	1.90	0.52
24:d:104:ARG:HH11	24:d:106:SER:H	1.58	0.52
25:f:267:ARG:O	25:f:271:MET:HB3	2.09	0.52
7:I:122:THR:HB	7:I:129:PRO:HB3	1.92	0.52
15:Q:174:ASN:OD1	15:Q:174:ASN:N	2.42	0.52
16:R:100:MET:HB3	16:R:111:LEU:HD21	1.90	0.52
17:S:58:HIS:CE1	18:T:131:ALA:H	2.27	0.52
18:T:26:MET:CE	18:T:188:GLN:HG2	2.39	0.52
19:X:166:LEU:HD23	19:X:196:THR:HG21	1.91	0.52
19:X:342:PHE:CD1	19:X:345:VAL:HB	2.45	0.52
20:Y:108:ALA:HA	20:Y:112:CYS:SG	2.50	0.52
20:Y:381:GLN:HB2	27:V:482:PHE:HZ	1.74	0.52
25:f:182:GLU:OE1	25:f:182:GLU:N	2.26	0.52
30:F:181:PRO:HB2	30:F:238:ARG:HB3	1.91	0.52
31:E:86:GLN:OE1	31:E:86:GLN:N	2.42	0.52
31:E:181:THR:OG1	37:E:501:ADP:O3A	2.27	0.52
31:E:216:ARG:NH1	31:E:259:GLU:OE2	2.37	0.52
31:E:338:PHE:HA	31:E:378:LYS:NZ	2.24	0.52
2:C:144:PRO:O	2:C:205:HIS:ND1	2.43	0.52
5:G:10:ASP:HB2	5:G:27:TYR:HE2	1.74	0.52
21:Z:57:PRO:HG2	21:Z:71:ASP:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:94:LYS:HB3	25:f:102:HIS:NE2	2.25	0.52
26:W:35:ALA:HA	26:W:39:ARG:NH2	2.24	0.52
26:W:268:LYS:HE3	26:W:302:TYR:OH	2.09	0.52
31:E:329:GLU:OE1	31:E:329:GLU:N	2.41	0.52
5:G:52:THR:HG21	5:G:68:HIS:HB2	1.92	0.52
8:J:76:LEU:HD23	8:J:76:LEU:H	1.74	0.52
11:M:67:PHE:HB2	11:M:75:MET:HB3	1.91	0.52
12:N:161:ALA:O	12:N:165:GLU:HG2	2.10	0.52
14:P:26:ARG:NH1	14:P:199:THR:OG1	2.42	0.52
15:Q:21:ALA:HB3	15:Q:29:LYS:HB3	1.91	0.52
20:Y:111:LEU:C	20:Y:114:ILE:H	2.17	0.52
25:f:158:TYR:HA	25:f:161:HIS:ND1	2.25	0.52
25:f:322:SER:O	25:f:323:ASN:ND2	2.43	0.52
25:f:327:ASN:HD22	25:f:420:TRP:CD1	2.27	0.52
32:U:516:LEU:HB3	32:U:532:MET:SD	2.49	0.52
1:B:59:ARG:HB2	29:A:41:TYR:HE2	1.73	0.52
1:B:181:GLN:OE1	1:B:181:GLN:N	2.29	0.52
3:D:159:LYS:HD2	3:D:221:HIS:HD2	1.75	0.52
5:G:54:LYS:NZ	5:G:213:SER:O	2.33	0.52
9:K:31:ILE:HD13	9:K:140:ALA:HB2	1.92	0.52
20:Y:100:ILE:O	20:Y:104:MET:HG2	2.10	0.52
22:a:236:THR:OG1	22:a:253:THR:HG21	2.10	0.52
25:f:494:ARG:NE	25:f:496:ASP:OD2	2.42	0.52
32:U:202:VAL:O	32:U:206:MET:HG2	2.10	0.52
33:g:220:ASP:O	33:g:223:THR:HG22	2.10	0.52
1:B:116:ILE:HG22	1:B:117:ASP:H	1.75	0.52
1:B:439:TYR:HD2	8:J:28:LYS:HB3	1.75	0.52
9:K:4:THR:OG1	9:K:4:THR:O	2.26	0.52
11:M:114:ARG:O	11:M:117:MET:HG3	2.10	0.52
16:R:37:ILE:HD12	16:R:38:ASN:N	2.25	0.52
17:S:145:LEU:HD21	17:S:182:ALA:HB2	1.92	0.52
17:S:205:GLU:OE1	17:S:205:GLU:N	2.43	0.52
20:Y:301:ILE:HD13	20:Y:342:ARG:HD3	1.92	0.52
22:a:97:LEU:HD12	22:a:118:ILE:HG13	1.90	0.52
24:d:189:HIS:NE2	24:d:219:ASP:OD2	2.39	0.52
25:f:447:ALA:O	25:f:450:ILE:HG22	2.10	0.52
29:A:163:MET:O	29:A:164:MET:HE2	2.10	0.52
31:E:354:ALA:HA	31:E:359:HIS:HD2	1.74	0.52
34:u:226:LYS:HD2	34:u:226:LYS:H	1.74	0.52
1:B:203:LEU:HA	1:B:206:THR:HG22	1.92	0.52
10:L:84:LEU:O	10:L:88:MET:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:2:THR:N	12:N:17:ASP:OD2	2.41	0.52
14:P:178:ASP:OD2	14:P:181:SER:OG	2.25	0.52
16:R:148:GLU:OE2	16:R:151:GLN:N	2.40	0.52
20:Y:73:MET:H	20:Y:73:MET:CE	2.23	0.52
21:Z:127:LYS:HB2	21:Z:128:PRO:HD3	1.92	0.52
21:Z:246:VAL:HG22	24:d:339:ILE:HG13	1.92	0.52
21:Z:259:VAL:HG13	21:Z:260:VAL:HG23	1.92	0.52
26:W:138:VAL:HG22	26:W:141:GLU:HB2	1.92	0.52
26:W:227:TYR:HB3	26:W:250:ILE:HD11	1.91	0.52
31:E:309:ARG:O	31:E:313:LEU:HD22	2.10	0.52
32:U:95:GLU:N	32:U:95:GLU:OE2	2.43	0.52
32:U:432:SER:OG	32:U:433:PRO:HD3	2.10	0.52
5:G:71:LYS:HE3	5:G:74:GLU:HA	1.92	0.52
5:G:212:PRO:HG3	5:G:239:LEU:HD11	1.92	0.52
7:I:49:ARG:NH1	7:I:211:VAL:O	2.43	0.52
9:K:41:GLN:HA	9:K:46:VAL:HG12	1.92	0.52
11:M:67:PHE:N	11:M:75:MET:O	2.40	0.52
20:Y:289:ALA:N	20:Y:290:PRO:HD2	2.25	0.52
22:a:72:ASN:OD1	22:a:75:SER:OG	2.23	0.52
24:d:200:LEU:HD11	24:d:233:GLU:HB2	1.91	0.52
25:f:512:MET:CE	25:f:548:THR:HB	2.40	0.52
25:f:749:ALA:HA	25:f:752:HIS:CE1	2.45	0.52
26:W:30:GLU:HA	26:W:33:LYS:HD3	1.92	0.52
26:W:104:MET:SD	26:W:105:VAL:HG13	2.49	0.52
31:E:44:GLU:O	31:E:47:LEU:HG	2.09	0.52
31:E:261:LEU:HA	31:E:264:MET:HE2	1.92	0.52
31:E:340:GLY:HA3	37:E:501:ADP:C2	2.45	0.52
2:C:256:SER:O	2:C:302:ASP:N	2.43	0.51
3:D:78:GLU:OE1	3:D:81:ARG:NH2	2.38	0.51
7:I:182:GLY:N	7:I:184:MET:HE1	2.25	0.51
9:K:44:GLU:HB2	9:K:191:LEU:HG	1.92	0.51
21:Z:16:LEU:HD23	21:Z:124:ILE:HD13	1.92	0.51
25:f:289:VAL:HA	25:f:292:LYS:HG2	1.91	0.51
25:f:562:LEU:HD21	25:f:577:LEU:HD22	1.91	0.51
27:V:303:SER:HA	27:V:339:LEU:HD11	1.92	0.51
30:F:132:TYR:CE1	30:F:158:TYR:CE2	2.99	0.51
30:F:344:ARG:NE	31:E:341:ALA:HB1	2.25	0.51
32:U:521:LEU:HD21	32:U:757:MET:SD	2.50	0.51
1:B:211:TYR:HE1	1:B:219:PRO:HD3	1.75	0.51
1:B:279:PRO:HB3	1:B:324:ASP:HB2	1.92	0.51
11:M:119:VAL:HG23	11:M:131:PHE:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Y:144:LEU:HA	20:Y:147:ILE:HG22	1.91	0.51
25:f:243:PRO:O	25:f:246:SER:OG	2.26	0.51
25:f:327:ASN:O	25:f:331:LEU:HG	2.10	0.51
25:f:545:LYS:HE3	25:f:548:THR:HG23	1.92	0.51
25:f:690:VAL:O	25:f:694:LEU:HG	2.10	0.51
25:f:720:GLU:O	25:f:722:SER:N	2.43	0.51
26:W:395:ASN:OD1	26:W:399:ASN:ND2	2.36	0.51
27:V:309:MET:HB3	27:V:332:LEU:HD13	1.93	0.51
30:F:233:LYS:CE	30:F:331:ALA:HB1	2.40	0.51
6:H:145:TYR:HB3	6:H:147:PHE:HE1	1.75	0.51
8:J:116:GLN:HG3	9:K:83:ALA:HB1	1.93	0.51
11:M:71:ARG:NH1	18:T:75:GLU:OE1	2.43	0.51
11:M:143:ASN:OD1	11:M:143:ASN:N	2.43	0.51
16:R:136:TYR:HA	16:R:139:MET:SD	2.51	0.51
24:d:117:GLY:O	24:d:120:LYS:HG2	2.09	0.51
25:f:107:LYS:HA	25:f:111:GLU:HB2	1.93	0.51
25:f:808:ASN:OD1	25:f:808:ASN:N	2.44	0.51
29:A:20:LYS:HD2	29:A:21:PRO:HD2	1.92	0.51
30:F:364:ARG:HA	30:F:367:GLN:CD	2.36	0.51
30:F:427:VAL:O	30:F:430:LYS:NZ	2.27	0.51
31:E:159:PHE:CD1	31:E:164:ILE:HD11	2.45	0.51
9:K:44:GLU:OE1	9:K:191:LEU:N	2.44	0.51
10:L:61:LYS:HE2	10:L:64:LEU:HD22	1.92	0.51
11:M:68:ASN:O	11:M:92:ARG:NE	2.35	0.51
14:P:49:LEU:HD22	14:P:111:GLY:HA3	1.92	0.51
20:Y:37:VAL:HB	20:Y:38:ARG:HH21	1.75	0.51
25:f:169:GLU:C	25:f:173:LEU:HD23	2.35	0.51
25:f:545:LYS:NZ	25:f:547:GLU:HB3	2.25	0.51
26:W:50:LEU:O	26:W:53:GLN:HG3	2.10	0.51
27:V:355:ARG:O	27:V:358:MET:HB3	2.09	0.51
29:A:135:GLU:O	29:A:138:MET:HG2	2.11	0.51
29:A:224:LEU:HA	29:A:227:ARG:HB2	1.93	0.51
31:E:108:MET:HA	31:E:108:MET:HE3	1.92	0.51
32:U:510:GLU:HG3	32:U:543:LYS:HB3	1.93	0.51
33:g:241:GLN:HE21	33:g:350:LYS:HG2	1.75	0.51
1:B:268:ARG:NH1	1:B:311:GLU:OE2	2.43	0.51
4:c:61:PHE:HD1	4:c:67:VAL:HG22	1.74	0.51
17:S:179:PHE:CE2	17:S:193:LEU:HB2	2.46	0.51
17:S:199:THR:HG1	17:S:200:LYS:HZ3	1.57	0.51
23:b:109:ILE:HG12	23:b:138:VAL:HG23	1.92	0.51
25:f:66:LYS:HG3	25:f:67:ASP:N	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:731:MET:O	25:f:746:ARG:NH1	2.43	0.51
25:f:774:GLY:HA2	25:f:805:ASP:HB3	1.92	0.51
26:W:36:LYS:HA	26:W:36:LYS:HE2	1.91	0.51
29:A:251:GLY:HA2	29:A:294:GLU:HG2	1.93	0.51
30:F:368:ILE:HG23	30:F:371:ARG:HH12	1.76	0.51
31:E:70:ILE:HG12	31:E:80:VAL:HG12	1.93	0.51
1:B:225:TYR:HE1	1:B:352:GLU:HG2	1.75	0.51
2:C:62:GLU:O	2:C:66:LEU:HB2	2.11	0.51
2:C:168:PRO:HB2	2:C:290:LYS:HE3	1.91	0.51
4:c:163:ILE:HG12	4:c:174:PRO:HB3	1.91	0.51
6:H:64:LYS:N	6:H:209:GLU:OE1	2.44	0.51
7:I:161:ALA:HB1	7:I:175:LEU:HD21	1.93	0.51
8:J:43:LEU:HD11	8:J:134:VAL:HG21	1.92	0.51
8:J:70:CYS:SG	8:J:217:LEU:HD21	2.50	0.51
11:M:70:ASP:OD2	11:M:99:ARG:NH2	2.43	0.51
11:M:219:LEU:HG	11:M:220:THR:HG23	1.92	0.51
12:N:14:LEU:HD11	12:N:42:PHE:HB3	1.92	0.51
16:R:8:PHE:CE1	16:R:13:ILE:HG12	2.46	0.51
23:b:22:LEU:HD22	23:b:22:LEU:H	1.76	0.51
25:f:419:LEU:HD12	25:f:420:TRP:N	2.25	0.51
26:W:366:MET:HE1	26:W:378:MET:HG2	1.93	0.51
29:A:350:GLY:O	29:A:354:ILE:HG12	2.11	0.51
1:B:199:GLU:O	1:B:211:TYR:OH	2.27	0.51
5:G:143:ILE:HG12	5:G:220:VAL:HG12	1.93	0.51
9:K:121:LEU:HD22	10:L:79:ALA:HA	1.91	0.51
14:P:56:LEU:H	14:P:56:LEU:HD12	1.74	0.51
15:Q:80:ALA:O	15:Q:84:THR:HG23	2.10	0.51
16:R:83:LEU:HA	16:R:86:MET:SD	2.51	0.51
18:T:86:ARG:NH2	18:T:119:GLU:OE1	2.44	0.51
19:X:341:PRO:HG3	26:W:394:SER:HB3	1.92	0.51
19:X:348:GLU:OE1	19:X:348:GLU:N	2.41	0.51
20:Y:385:ARG:HH22	27:V:282:ASN:HA	1.75	0.51
25:f:141:LYS:HD2	25:f:141:LYS:C	2.36	0.51
25:f:866:GLN:O	25:f:866:GLN:HG2	2.11	0.51
27:V:92:ARG:NH1	27:V:95:LEU:HD13	2.25	0.51
27:V:124:ASN:CG	27:V:128:ARG:HH21	2.19	0.51
27:V:195:ILE:CG2	27:V:203:LEU:HD11	2.41	0.51
27:V:203:LEU:O	27:V:203:LEU:HD13	2.10	0.51
29:A:102:ILE:HG23	29:A:102:ILE:O	2.10	0.51
29:A:330:ALA:O	29:A:336:ARG:NH1	2.43	0.51
31:E:23:ASP:O	31:E:25:ARG:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:44:ARG:HH22	24:d:359:VAL:HG21	1.76	0.51
2:C:214:VAL:HG13	2:C:248:MET:HE3	1.92	0.51
5:G:103:TYR:O	13:O:81:ARG:NH1	2.39	0.51
6:H:159:LYS:NZ	7:I:56:LEU:O	2.43	0.51
7:I:122:THR:O	8:J:125:ARG:NH1	2.43	0.51
10:L:49:LEU:HD12	10:L:195:LEU:HD11	1.91	0.51
12:N:13:VAL:HG21	12:N:152:CYS:HB3	1.93	0.51
12:N:30:VAL:O	12:N:175:ARG:NH2	2.44	0.51
12:N:42:PHE:HB2	12:N:179:ILE:HD11	1.92	0.51
13:O:50:ALA:HB3	14:P:127:ILE:HG23	1.93	0.51
14:P:188:HIS:HD2	14:P:197:THR:HB	1.76	0.51
20:Y:25:LEU:O	20:Y:31:HIS:N	2.43	0.51
21:Z:176:LEU:O	21:Z:177:ARG:HB2	2.11	0.51
22:a:217:LEU:H	22:a:217:LEU:HD12	1.75	0.51
24:d:300:THR:O	24:d:304:LYS:HG2	2.10	0.51
25:f:350:LYS:HA	25:f:751:TYR:CE2	2.46	0.51
25:f:461:PRO:O	25:f:465:LEU:HB2	2.10	0.51
26:W:117:ASP:OD1	26:W:119:PRO:HD2	2.11	0.51
29:A:187:LEU:O	29:A:191:VAL:HG12	2.11	0.51
30:F:177:VAL:HG21	30:F:274:LEU:HD21	1.93	0.51
30:F:308:ARG:NH1	31:E:201:SER:O	2.44	0.51
31:E:347:CYS:O	31:E:350:ALA:HB3	2.10	0.51
1:B:71:TYR:HA	1:B:74:MET:HE3	1.93	0.51
3:D:143:LEU:HD22	31:E:64:LEU:HD11	1.93	0.51
3:D:386:ALA:HB2	3:D:394:VAL:HG12	1.93	0.51
4:c:98:MET:O	21:Z:74:TYR:OH	2.29	0.51
9:K:95:GLU:OE2	9:K:115:ALA:HB3	2.11	0.51
15:Q:35:MET:HG2	15:Q:45:LEU:HG	1.93	0.51
16:R:115:ASP:OD1	16:R:119:ASN:N	2.44	0.51
25:f:136:GLU:HA	25:f:139:CYS:SG	2.50	0.51
27:V:209:LYS:O	27:V:213:TYR:HD2	1.94	0.51
27:V:399:ARG:HD2	27:V:400:HIS:CE1	2.45	0.51
30:F:141:ASP:HB2	30:F:143:GLU:OE2	2.11	0.51
33:g:228:CR8:CA3	33:g:254:TRP:HE1	2.24	0.51
1:B:171:VAL:HA	1:B:174:MET:HG3	1.93	0.51
3:D:61:ILE:HD11	32:U:639:LEU:HD12	1.92	0.51
10:L:104:PRO:HB3	18:T:81:HIS:CD2	2.42	0.51
17:S:135:PHE:O	17:S:136:LYS:HD2	2.11	0.51
17:S:194:ARG:HH21	17:S:205:GLU:HB2	1.76	0.51
20:Y:283:LYS:C	20:Y:288:PHE:HB2	2.37	0.51
24:d:151:GLY:O	24:d:155:SER:OG	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:d:268:ARG:HD2	24:d:291:LEU:O	2.11	0.51
30:F:170:SER:OG	30:F:171:ARG:N	2.42	0.51
31:E:83:CYS:SG	31:E:89:LYS:NZ	2.67	0.51
32:U:538:GLU:OE1	34:u:234:ARG:NH2	2.44	0.51
32:U:797:MET:HE1	32:U:881:PRO:HG3	1.93	0.51
1:B:117:ASP:O	1:B:119:ASN:N	2.38	0.50
1:B:235:LEU:HD22	1:B:353:PHE:HZ	1.75	0.50
4:c:29:GLU:OE2	4:c:161:ARG:NH1	2.30	0.50
7:I:206:LEU:HG	7:I:237:ILE:HD11	1.93	0.50
11:M:216:VAL:HG23	11:M:223:ARG:C	2.37	0.50
21:Z:250:TYR:O	21:Z:253:THR:OG1	2.26	0.50
24:d:224:VAL:HA	24:d:227:LYS:HB2	1.92	0.50
26:W:268:LYS:HG3	26:W:302:TYR:CZ	2.47	0.50
27:V:236:ARG:CZ	32:U:70:HIS:CD2	2.94	0.50
29:A:213:LEU:HD22	29:A:214:LEU:H	1.76	0.50
33:g:369:ASP:OD1	33:g:369:ASP:N	2.33	0.50
3:D:167:ILE:HB	3:D:174:LYS:HE2	1.94	0.50
5:G:50:ILE:HG23	5:G:141:ILE:HD13	1.93	0.50
10:L:36:VAL:HA	10:L:159:MET:O	2.11	0.50
16:R:19:ARG:HE	16:R:21:THR:HG21	1.76	0.50
17:S:92:LEU:HA	17:S:95:ILE:HG22	1.93	0.50
18:T:96:MET:C	18:T:96:MET:HE2	2.36	0.50
18:T:146:ALA:O	18:T:150:LEU:HG	2.11	0.50
19:X:281:GLY:H	19:X:284:THR:HG22	1.75	0.50
20:Y:23:ARG:CZ	20:Y:60:SER:HB3	2.40	0.50
20:Y:133:ALA:O	20:Y:136:HIS:ND1	2.38	0.50
20:Y:147:ILE:HD12	20:Y:150:PHE:CD2	2.46	0.50
21:Z:58:PHE:CE2	21:Z:60:GLU:HB2	2.47	0.50
21:Z:223:ASN:HB3	21:Z:226:ILE:HB	1.93	0.50
22:a:291:LEU:HD12	22:a:291:LEU:O	2.10	0.50
26:W:126:ASP:O	26:W:130:MET:HG2	2.10	0.50
26:W:408:ARG:NH2	26:W:409:LEU:HD13	2.27	0.50
33:g:289:ASN:ND2	33:g:289:ASN:O	2.45	0.50
1:B:334:ILE:HD12	1:B:337:LEU:HD12	1.93	0.50
5:G:112:ASP:HB3	5:G:152:TYR:CZ	2.46	0.50
7:I:218:ARG:NH2	7:I:223:THR:OG1	2.44	0.50
8:J:158:ALA:HB1	8:J:172:LEU:HD13	1.92	0.50
9:K:88:LEU:HD23	9:K:119:LEU:HD23	1.93	0.50
10:L:67:ASP:OD1	10:L:69:HIS:ND1	2.44	0.50
12:N:66:HIS:CE1	12:N:70:LEU:HD11	2.46	0.50
14:P:155:GLU:HG3	14:P:158:MET:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:S:15:ILE:HD13	17:S:135:PHE:HB3	1.93	0.50
17:S:102:PHE:CZ	18:T:103:MET:HE1	2.46	0.50
18:T:63:LEU:HD21	18:T:106:LEU:HD13	1.93	0.50
18:T:111:VAL:HG22	18:T:124:TYR:HB2	1.94	0.50
19:X:286:ALA:HB1	19:X:309:TYR:CE1	2.47	0.50
21:Z:71:ASP:HB3	21:Z:74:TYR:HB3	1.93	0.50
24:d:140:GLN:O	24:d:143:LEU:HG	2.10	0.50
25:f:794:ALA:HA	25:f:797:LEU:HD21	1.93	0.50
25:f:811:LEU:N	25:f:854:GLY:O	2.37	0.50
26:W:110:THR:HG23	26:W:111:TYR:HD1	1.76	0.50
27:V:449:ALA:HA	27:V:460:SER:HA	1.92	0.50
30:F:427:VAL:HB	30:F:428:GLN:OE1	2.11	0.50
32:U:20:LYS:HB3	32:U:48:LEU:HD21	1.93	0.50
1:B:271:PHE:O	1:B:275:GLU:HG2	2.11	0.50
1:B:349:ARG:NH1	29:A:391:GLU:OE1	2.44	0.50
3:D:237:GLN:HE21	3:D:246:MET:HE2	1.76	0.50
7:I:6:ASP:O	7:I:20:GLN:NE2	2.44	0.50
8:J:117:ARG:HA	8:J:120:GLN:CD	2.36	0.50
9:K:185:TYR:HA	9:K:189:MET:HE1	1.92	0.50
12:N:42:PHE:HD1	12:N:43:CYS:H	1.59	0.50
14:P:56:LEU:HD11	14:P:104:TYR:HB2	1.93	0.50
14:P:83:LYS:O	14:P:86:THR:OG1	2.19	0.50
21:Z:226:ILE:HG22	21:Z:227:ILE:HD13	1.92	0.50
22:a:176:ALA:HB1	22:a:200:LEU:HD21	1.94	0.50
22:a:289:ARG:HD2	22:a:333:MET:HB2	1.91	0.50
23:b:103:LYS:HB2	34:u:134:GLY:HA2	1.93	0.50
26:W:401:THR:OG1	26:W:402:ILE:N	2.45	0.50
29:A:167:GLU:OE2	29:A:168:GLU:N	2.44	0.50
29:A:223:THR:HG23	29:A:273:PHE:HE2	1.75	0.50
30:F:340:PRO:O	30:F:344:ARG:HB3	2.11	0.50
32:U:707:ASN:O	32:U:711:GLN:HG2	2.12	0.50
1:B:392:GLY:HA3	35:B:501:ATP:C8	2.46	0.50
8:J:210:VAL:O	8:J:217:LEU:HB2	2.11	0.50
12:N:34:LEU:HB3	12:N:42:PHE:CE1	2.46	0.50
16:R:8:PHE:HE1	16:R:13:ILE:HG12	1.76	0.50
21:Z:33:LYS:C	21:Z:34:ARG:HG3	2.37	0.50
22:a:87:MET:HE1	22:a:92:VAL:HG23	1.93	0.50
25:f:165:GLU:HA	25:f:168:LYS:HE2	1.92	0.50
25:f:616:CYS:HB3	25:f:632:LYS:HG3	1.94	0.50
26:W:59:ASP:OD1	26:W:60:MET:N	2.45	0.50
30:F:356:MET:HE3	30:F:357:PRO:HD2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E:335:SER:O	31:E:335:SER:OG	2.29	0.50
32:U:896:GLU:CD	32:U:896:GLU:H	2.19	0.50
33:g:365:SER:HB3	33:g:374:LYS:HB3	1.92	0.50
3:D:121:ARG:N	3:D:121:ARG:HD2	2.26	0.50
4:c:242:GLU:OE2	4:c:246:LYS:NZ	2.45	0.50
7:I:231:LYS:O	7:I:234:GLU:HG2	2.12	0.50
11:M:65:ARG:HH22	11:M:78:ALA:HA	1.77	0.50
19:X:338:VAL:O	19:X:339:ILE:HG12	2.11	0.50
20:Y:13:LYS:O	20:Y:146:ARG:NH2	2.45	0.50
20:Y:18:ARG:O	20:Y:22:LEU:HB2	2.12	0.50
20:Y:103:ALA:HB3	20:Y:104:MET:HE3	1.94	0.50
20:Y:351:ASN:H	27:V:416:ARG:NH2	2.09	0.50
22:a:101:ARG:HB3	22:a:114:CYS:SG	2.52	0.50
22:a:214:GLY:C	22:a:216:LEU:H	2.20	0.50
25:f:263:PRO:O	25:f:264:GLU:HG2	2.11	0.50
25:f:274:ASP:OD1	25:f:275:MET:N	2.45	0.50
25:f:566:HIS:CE1	25:f:573:ILE:HG12	2.46	0.50
25:f:568:GLY:N	25:f:599:ALA:O	2.45	0.50
32:U:685:GLN:NE2	32:U:725:MET:HB3	2.27	0.50
32:U:700:GLU:HG2	32:U:707:ASN:OD1	2.11	0.50
33:g:230:ASN:OD1	33:g:231:ARG:N	2.36	0.50
4:c:58:LEU:HD21	4:c:73:PHE:HE1	1.76	0.50
4:c:130:GLN:OE1	4:c:142:ALA:HB2	2.11	0.50
13:O:19:ARG:HG3	13:O:170:GLY:O	2.12	0.50
13:O:163:ILE:HD12	13:O:170:GLY:HA2	1.93	0.50
14:P:13:ALA:HB3	14:P:137:VAL:CG2	2.40	0.50
19:X:163:LYS:HB3	19:X:200:ILE:HG13	1.93	0.50
19:X:377:ILE:HG22	19:X:386:ILE:HB	1.93	0.50
22:a:334:THR:O	22:a:334:THR:OG1	2.28	0.50
23:b:10:VAL:HG22	23:b:29:GLN:NE2	2.26	0.50
24:d:212:LEU:HD22	24:d:220:ILE:HD13	1.93	0.50
24:d:234:GLN:HB3	27:V:400:HIS:HD2	1.76	0.50
25:f:114:ALA:HB1	25:f:118:ASN:HB3	1.93	0.50
26:W:150:ALA:O	26:W:153:LYS:HG2	2.12	0.50
26:W:403:PHE:CE2	26:W:416:GLN:HA	2.47	0.50
27:V:444:ASP:OD1	27:V:444:ASP:N	2.45	0.50
30:F:341:ALA:O	30:F:347:ARG:NH1	2.43	0.50
32:U:521:LEU:HD21	32:U:761:VAL:HG21	1.94	0.50
32:U:571:CYS:SG	32:U:601:ARG:NH1	2.85	0.50
33:g:322:ILE:HG12	33:g:338:PHE:HB2	1.93	0.50
3:D:255:LYS:NZ	3:D:302:ASN:OD1	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:390:ASN:HA	26:W:208:LYS:HE2	1.94	0.50
7:I:57:ASP:HB2	7:I:59:VAL:HG12	1.93	0.50
7:I:112:THR:HG23	8:J:81:ARG:HD2	1.93	0.50
9:K:36:THR:HA	9:K:171:GLY:HA3	1.92	0.50
9:K:98:ASN:HA	16:R:61:ARG:NH2	2.27	0.50
14:P:83:LYS:HG3	14:P:86:THR:H	1.76	0.50
20:Y:107:LYS:HD2	20:Y:111:LEU:HB2	1.94	0.50
24:d:212:LEU:HD23	24:d:215:LEU:HD11	1.94	0.50
25:f:257:ARG:HE	25:f:261:ARG:HB2	1.77	0.50
25:f:391:LEU:HD13	25:f:398:TRP:CE2	2.47	0.50
25:f:474:SER:HB3	25:f:477:MET:HG2	1.94	0.50
25:f:584:SER:HB2	25:f:588:ARG:HB3	1.92	0.50
30:F:57:SER:O	30:F:60:LEU:HG	2.12	0.50
31:E:138:LEU:HD11	31:E:301:ILE:HG23	1.93	0.50
1:B:52:VAL:HG13	1:B:55:HIS:NE2	2.27	0.50
2:C:174:LEU:H	2:C:174:LEU:HD12	1.77	0.50
7:I:194:ILE:HG13	7:I:236:LEU:HD11	1.94	0.50
13:O:80:ASN:OD1	13:O:81:ARG:N	2.45	0.50
20:Y:68:ASP:O	20:Y:72:LYS:HE3	2.12	0.50
21:Z:142:GLU:HG3	22:a:146:PRO:HG3	1.93	0.50
25:f:190:GLU:OE1	25:f:197:ALA:N	2.45	0.50
25:f:771:LEU:HG	25:f:774:GLY:N	2.16	0.50
26:W:222:LEU:HD23	26:W:222:LEU:H	1.77	0.50
28:e:61:GLU:OE1	28:e:61:GLU:N	2.45	0.50
30:F:362:ARG:NH1	30:F:391:PHE:O	2.45	0.50
32:U:384:GLN:NE2	32:U:388:ASP:OD1	2.43	0.50
32:U:462:LEU:HD12	32:U:481:LEU:HD21	1.94	0.50
2:C:373:GLU:OE1	2:C:375:ARG:NH1	2.45	0.49
4:c:180:ASN:ND2	32:U:685:GLN:OE1	2.42	0.49
5:G:70:PHE:CD2	5:G:91:VAL:HG11	2.47	0.49
6:H:69:THR:OG1	6:H:70:LYS:N	2.41	0.49
8:J:149:PRO:C	8:J:151:GLY:H	2.19	0.49
9:K:192:LYS:O	9:K:195:ILE:HG22	2.12	0.49
14:P:88:MET:HA	14:P:91:VAL:HG22	1.93	0.49
18:T:73:ASP:HA	18:T:76:LEU:HB2	1.93	0.49
19:X:341:PRO:HG2	19:X:342:PHE:CD2	2.46	0.49
20:Y:294:TYR:CZ	20:Y:298:GLU:HG3	2.47	0.49
21:Z:144:VAL:O	21:Z:152:SER:N	2.45	0.49
24:d:129:LEU:N	24:d:174:TYR:OH	2.36	0.49
25:f:52:LEU:HD22	29:A:33:LEU:HD13	1.94	0.49
25:f:231:LEU:HG	25:f:234:THR:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:236:CYS:SG	25:f:237:VAL:N	2.85	0.49
25:f:382:ASN:HB2	25:f:417:ILE:HD12	1.94	0.49
26:W:450:GLU:HA	26:W:453:HIS:ND1	2.27	0.49
31:E:29:LEU:HD12	31:E:33:LEU:HD21	1.94	0.49
31:E:65:THR:HG23	31:E:67:GLU:H	1.77	0.49
31:E:178:THR:HG21	31:E:301:ILE:O	2.12	0.49
32:U:527:GLN:O	32:U:530:GLU:HG3	2.12	0.49
32:U:654:MET:HE2	32:U:767:THR:HG22	1.93	0.49
5:G:54:LYS:HG3	5:G:68:HIS:HE1	1.77	0.49
11:M:163:CYS:HB2	11:M:173:LYS:HZ1	1.77	0.49
13:O:126:THR:HG21	13:O:134:ALA:HB3	1.94	0.49
17:S:45:LYS:HG3	17:S:203:ILE:HD13	1.94	0.49
17:S:92:LEU:HD23	17:S:124:PHE:CZ	2.47	0.49
17:S:199:THR:OG1	17:S:200:LYS:NZ	2.34	0.49
22:a:173:TYR:HE1	22:a:216:LEU:HD22	1.76	0.49
29:A:331:LEU:HG	29:A:337:LEU:HD11	1.93	0.49
30:F:55:MET:HE1	31:E:23:ASP:OD2	2.11	0.49
31:E:206:LYS:O	33:g:156:LEU:HA	2.12	0.49
1:B:209:GLU:OE1	1:B:209:GLU:N	2.45	0.49
1:B:301:GLY:HA3	33:g:160:CYS:HB2	1.93	0.49
4:c:304:LEU:HD13	21:Z:198:LEU:HD11	1.94	0.49
6:H:38:ILE:HD12	6:H:191:ALA:HB2	1.94	0.49
12:N:59:VAL:HG21	12:N:83:PHE:CE2	2.48	0.49
17:S:58:HIS:CE1	17:S:62:LEU:HD23	2.46	0.49
20:Y:133:ALA:HB3	20:Y:136:HIS:CE1	2.33	0.49
20:Y:188:CYS:HA	20:Y:193:ASP:N	2.27	0.49
22:a:137:ASP:O	22:a:140:GLU:HG3	2.12	0.49
23:b:52:ILE:HD13	23:b:60:VAL:HA	1.94	0.49
25:f:119:LYS:HB3	25:f:123:ALA:H	1.76	0.49
25:f:206:ASP:HB2	25:f:248:LEU:HB3	1.94	0.49
25:f:609:VAL:HB	25:f:639:LYS:NZ	2.27	0.49
25:f:773:LYS:HZ1	25:f:805:ASP:HA	1.77	0.49
29:A:189:GLU:O	29:A:193:THR:OG1	2.31	0.49
30:F:376:SER:N	30:F:414:GLU:OE2	2.45	0.49
32:U:587:ALA:HB2	32:U:621:SER:HB3	1.94	0.49
3:D:78:GLU:OE1	3:D:78:GLU:HA	2.12	0.49
5:G:183:VAL:HA	5:G:189:TRP:CH2	2.34	0.49
6:H:157:ALA:HB1	7:I:57:ASP:HB2	1.93	0.49
7:I:119:GLN:O	7:I:123:GLN:N	2.45	0.49
11:M:134:SER:HB3	11:M:150:MET:SD	2.52	0.49
15:Q:67:TYR:O	15:Q:71:ASN:ND2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:S:108:ASN:C	17:S:109:ILE:HD13	2.37	0.49
22:a:129:GLN:NE2	22:a:130:VAL:HG12	2.27	0.49
23:b:16:MET:HA	23:b:16:MET:HE2	1.93	0.49
25:f:102:HIS:HE1	25:f:133:MET:HG2	1.74	0.49
25:f:136:GLU:OE2	29:A:40:THR:OG1	2.30	0.49
25:f:540:GLN:HA	25:f:543:MET:HG3	1.94	0.49
25:f:610:GLN:HG2	25:f:614:HIS:ND1	2.28	0.49
25:f:634:LYS:HD3	25:f:673:ARG:HG2	1.94	0.49
25:f:710:LEU:HB2	25:f:745:LEU:HD21	1.93	0.49
32:U:492:ASP:OD1	32:U:493:VAL:N	2.46	0.49
32:U:583:MET:N	32:U:583:MET:HE2	2.27	0.49
32:U:672:LEU:HD21	32:U:690:ALA:HB3	1.95	0.49
2:C:195:GLY:O	2:C:199:LEU:N	2.30	0.49
4:c:41:MET:HG2	4:c:112:TYR:CD2	2.46	0.49
4:c:124:GLY:H	33:g:172:ASP:HB2	1.77	0.49
5:G:181:LYS:HA	5:G:184:LYS:HE3	1.95	0.49
8:J:210:VAL:HG22	8:J:220:LEU:HD21	1.94	0.49
11:M:215:TRP:CZ2	11:M:228:PRO:HD2	2.48	0.49
12:N:135:ILE:HD13	12:N:163:ALA:HB2	1.94	0.49
15:Q:85:ARG:HG3	15:Q:124:LEU:HG	1.94	0.49
19:X:347:ILE:HA	19:X:350:ILE:HG22	1.93	0.49
20:Y:65:ILE:HD13	20:Y:65:ILE:H	1.77	0.49
22:a:60:TYR:O	22:a:64:ILE:HG12	2.13	0.49
23:b:101:GLN:OE1	23:b:101:GLN:HA	2.13	0.49
25:f:287:ASP:OD1	25:f:288:VAL:N	2.45	0.49
30:F:305:GLU:O	30:F:308:ARG:HG2	2.13	0.49
32:U:361:ARG:HD3	32:U:720:LYS:HE3	1.95	0.49
1:B:164:MET:SD	1:B:164:MET:N	2.70	0.49
2:C:377:HIS:HB3	20:Y:174:TRP:CH2	2.48	0.49
4:c:235:SER:HA	26:W:422:ASN:HD21	1.77	0.49
7:I:149:GLN:NE2	7:I:150:SER:O	2.45	0.49
9:K:211:ASN:ND2	9:K:214:ASN:OD1	2.46	0.49
11:M:87:LEU:HD11	11:M:135:PHE:CE1	2.47	0.49
15:Q:153:ARG:O	15:Q:157:VAL:HG13	2.12	0.49
18:T:173:MET:HE2	18:T:187:PHE:CE2	2.48	0.49
19:X:126:ARG:NH2	19:X:156:GLU:OE2	2.45	0.49
20:Y:236:LEU:HD12	20:Y:237:ARG:N	2.28	0.49
22:a:251:LEU:HD12	22:a:254:ALA:HB3	1.95	0.49
22:a:341:LEU:HB3	22:a:346:ILE:HG12	1.95	0.49
29:A:194:PRO:HB3	29:A:208:PRO:HB3	1.94	0.49
2:C:145:ASP:OD1	2:C:145:ASP:N	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:254:ILE:HG13	2:C:255:GLY:N	2.28	0.49
3:D:231:VAL:HG21	31:E:262:ASN:ND2	2.28	0.49
6:H:112:GLN:HG2	6:H:155:TYR:CZ	2.48	0.49
7:I:160:LYS:HG3	8:J:53:LEU:HD12	1.94	0.49
12:N:43:CYS:HB2	12:N:98:ILE:HD11	1.94	0.49
12:N:63:LEU:HD21	12:N:82:LEU:HD23	1.94	0.49
21:Z:23:PHE:HD2	21:Z:126:VAL:HG11	1.76	0.49
21:Z:101:LEU:HB3	21:Z:105:ASP:OD2	2.12	0.49
23:b:187:PRO:O	23:b:191:GLY:N	2.45	0.49
25:f:493:ASN:OD1	25:f:493:ASN:N	2.45	0.49
25:f:681:TYR:CE1	25:f:858:LYS:HB2	2.47	0.49
26:W:35:ALA:HA	26:W:39:ARG:CZ	2.42	0.49
27:V:392:TYR:O	27:V:396:ILE:HG12	2.13	0.49
28:e:19:PHE:HB3	28:e:22:PHE:HD2	1.78	0.49
31:E:242:ARG:NH1	31:E:258:MET:SD	2.85	0.49
31:E:265:ASP:HB3	31:E:294:ARG:HG2	1.95	0.49
32:U:249:CYS:SG	32:U:325:MET:HB3	2.52	0.49
34:u:127:MET:HE2	34:u:127:MET:HA	1.93	0.49
1:B:333:ARG:NH1	2:C:258:ARG:O	2.33	0.49
11:M:7:TYR:O	11:M:13:THR:OG1	2.30	0.49
19:X:344:ARG:HG3	19:X:384:VAL:HG11	1.95	0.49
20:Y:188:CYS:SG	28:e:39:TRP:NE1	2.84	0.49
22:a:162:TYR:C	22:a:168:ASN:HD22	2.21	0.49
25:f:308:SER:O	25:f:308:SER:OG	2.29	0.49
25:f:613:LEU:HA	25:f:617:SER:OG	2.13	0.49
25:f:678:LEU:HD13	25:f:679:LEU:HB2	1.95	0.49
25:f:731:MET:HG3	25:f:746:ARG:HD2	1.94	0.49
26:W:154:GLU:HA	26:W:154:GLU:OE2	2.12	0.49
27:V:243:ASP:OD1	27:V:244:ALA:N	2.46	0.49
29:A:206:ILE:HB	30:F:373:MET:HE1	1.94	0.49
32:U:653:ALA:HB2	32:U:675:MET:SD	2.53	0.49
2:C:210:THR:O	2:C:210:THR:OG1	2.31	0.49
4:c:198:ARG:CZ	4:c:198:ARG:HB3	2.43	0.49
4:c:255:TYR:CE1	4:c:281:LYS:HB2	2.48	0.49
5:G:10:ASP:OD1	5:G:11:ARG:NH1	2.39	0.49
7:I:93:ILE:HD11	7:I:117:ILE:HD11	1.95	0.49
7:I:197:LEU:O	7:I:201:MET:HG3	2.13	0.49
7:I:238:LYS:O	7:I:241:GLU:HG2	2.13	0.49
12:N:174:ILE:HB	12:N:189:LEU:HB2	1.95	0.49
14:P:30:ILE:HG22	14:P:33:GLN:HG3	1.94	0.49
14:P:83:LYS:NZ	14:P:113:ASP:OD2	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Q:19:ARG:HH21	15:Q:179:SER:HA	1.78	0.49
16:R:115:ASP:OD1	16:R:118:GLY:N	2.46	0.49
17:S:61:CYS:O	17:S:65:THR:HG22	2.13	0.49
18:T:43:MET:HE1	18:T:64:LYS:HB2	1.94	0.49
19:X:141:LYS:HD2	19:X:141:LYS:HA	1.54	0.49
20:Y:325:VAL:HG22	20:Y:326:GLY:N	2.28	0.49
21:Z:190:ARG:O	21:Z:194:GLN:HG2	2.13	0.49
23:b:63:THR:OG1	23:b:64:LEU:N	2.43	0.49
25:f:323:ASN:OD1	25:f:455:VAL:HA	2.12	0.49
25:f:496:ASP:OD1	25:f:497:VAL:N	2.46	0.49
25:f:840:LEU:HG	25:f:841:PRO:HD2	1.95	0.49
32:U:354:LYS:NZ	32:U:358:ASP:OD1	2.46	0.49
32:U:538:GLU:HB3	34:u:236:VAL:HG11	1.94	0.49
1:B:211:TYR:CE1	29:A:394:MET:HE1	2.48	0.49
1:B:230:THR:N	35:B:501:ATP:O2B	2.46	0.49
3:D:204:MET:HG2	3:D:333:PHE:CE1	2.48	0.49
3:D:268:ASP:OD1	3:D:268:ASP:N	2.36	0.49
5:G:112:ASP:OD1	5:G:113:MET:N	2.45	0.49
9:K:53:ARG:NH1	29:A:432:TYR:O	2.43	0.49
9:K:72:ALA:O	9:K:226:PHE:N	2.30	0.49
10:L:33:SER:HB2	10:L:51:ARG:HE	1.77	0.49
11:M:181:MET:O	11:M:183:GLU:N	2.46	0.49
15:Q:19:ARG:HA	15:Q:34:LYS:HZ1	1.77	0.49
15:Q:28:MET:HB3	16:R:126:PHE:CE1	2.47	0.49
19:X:143:TYR:CG	19:X:144:GLN:N	2.81	0.49
20:Y:23:ARG:HH12	20:Y:56:ALA:HA	1.76	0.49
20:Y:137:ARG:O	20:Y:141:VAL:HG23	2.13	0.49
22:a:211:PHE:CD2	22:a:319:LEU:HD21	2.48	0.49
25:f:545:LYS:CE	25:f:548:THR:HG23	2.42	0.49
25:f:774:GLY:O	25:f:777:THR:HG22	2.13	0.49
25:f:828:ARG:HH21	25:f:847:GLY:HA2	1.78	0.49
30:F:218:GLN:OE1	30:F:219:PRO:HD2	2.12	0.49
30:F:393:GLY:HA3	37:F:501:ADP:C8	2.47	0.49
31:E:282:PRO:HA	31:E:285:LEU:HD23	1.93	0.49
32:U:695:MET:HE1	32:U:706:VAL:HA	1.95	0.49
2:C:46:GLN:O	2:C:50:ASN:ND2	2.32	0.48
4:c:113:HIS:NE2	4:c:115:HIS:CD2	2.78	0.48
5:G:55:LYS:HD2	5:G:55:LYS:C	2.38	0.48
6:H:44:VAL:HG23	6:H:213:CYS:HB3	1.95	0.48
6:H:139:TRP:CD1	6:H:215:GLU:HA	2.48	0.48
7:I:21:VAL:O	7:I:25:MET:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:158:ALA:HB3	9:K:58:LEU:HD11	1.94	0.48
21:Z:259:VAL:HG22	21:Z:260:VAL:N	2.19	0.48
22:a:152:HIS:HB2	22:a:182:CYS:SG	2.53	0.48
23:b:135:LYS:HE3	34:u:140:GLU:HG2	1.95	0.48
25:f:550:LEU:HD23	25:f:551:LYS:HE2	1.95	0.48
27:V:236:ARG:NH2	32:U:32:ASN:HA	2.28	0.48
30:F:222:GLY:HA3	30:F:347:ARG:O	2.13	0.48
31:E:357:ALA:HB3	31:E:359:HIS:NE2	2.27	0.48
32:U:649:ARG:NE	32:U:678:ASP:OD2	2.43	0.48
32:U:681:ASN:ND2	32:U:723:ASP:OD2	2.46	0.48
2:C:299:ASP:OD1	2:C:299:ASP:N	2.42	0.48
10:L:7:ASP:N	10:L:7:ASP:OD1	2.45	0.48
11:M:39:ILE:HA	11:M:162:GLY:HA2	1.95	0.48
12:N:114:VAL:HG22	12:N:120:MET:HA	1.96	0.48
15:Q:8:GLN:HG2	15:Q:128:PRO:HA	1.94	0.48
17:S:63:THR:HG21	18:T:97:TYR:CE2	2.48	0.48
17:S:199:THR:HG23	17:S:201:GLU:HG3	1.95	0.48
18:T:6:VAL:O	18:T:56:ASP:HA	2.13	0.48
24:d:172:LYS:HD2	24:d:175:TYR:HD1	1.75	0.48
25:f:105:LYS:HD3	25:f:105:LYS:HA	1.66	0.48
25:f:323:ASN:OD1	25:f:455:VAL:HG22	2.12	0.48
27:V:72:LEU:O	27:V:76:LYS:HG2	2.13	0.48
27:V:228:ARG:HD3	27:V:258:TYR:CE1	2.48	0.48
27:V:403:ILE:HG21	27:V:437:ILE:HD13	1.94	0.48
32:U:82:LEU:C	32:U:129:ARG:HE	2.21	0.48
32:U:111:GLN:HG2	32:U:126:ILE:HG22	1.95	0.48
34:u:225:ILE:HD11	34:u:252:GLN:NE2	2.28	0.48
2:C:90:HIS:CE1	2:C:91:PRO:HB3	2.48	0.48
2:C:281:ASP:HB3	2:C:310:ARG:HG3	1.94	0.48
9:K:240:ASP:OD1	9:K:240:ASP:N	2.41	0.48
12:N:51:ASP:OD1	12:N:51:ASP:N	2.45	0.48
14:P:85:TYR:HA	14:P:88:MET:HG3	1.94	0.48
14:P:88:MET:HE2	14:P:88:MET:C	2.38	0.48
15:Q:45:LEU:HD13	15:Q:103:LEU:HB2	1.96	0.48
17:S:108:ASN:O	17:S:109:ILE:HD13	2.13	0.48
20:Y:346:LYS:HG2	27:V:415:SER:HB2	1.95	0.48
22:a:139:GLU:HB3	22:a:155:PHE:CZ	2.48	0.48
22:a:249:GLN:O	22:a:253:THR:HG22	2.13	0.48
24:d:148:LEU:HD12	24:d:174:TYR:HD2	1.79	0.48
24:d:266:THR:HA	24:d:269:ASP:OD2	2.13	0.48
24:d:286:GLU:OE1	24:d:286:GLU:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:227:TYR:O	26:W:231:ILE:HD13	2.13	0.48
33:g:288:THR:HG22	33:g:289:ASN:N	2.29	0.48
5:G:212:PRO:HB3	5:G:239:LEU:HD21	1.95	0.48
11:M:72:HIS:NE2	11:M:105:ASN:HB2	2.28	0.48
17:S:66:LYS:O	17:S:69:GLU:HG3	2.13	0.48
18:T:58:ALA:HA	18:T:61:GLN:HE21	1.77	0.48
18:T:193:THR:OG1	18:T:195:LYS:HG3	2.14	0.48
19:X:116:TRP:CD1	19:X:116:TRP:C	2.91	0.48
20:Y:20:ALA:O	20:Y:25:LEU:HD23	2.13	0.48
20:Y:221:THR:HG22	20:Y:256:VAL:HG21	1.96	0.48
20:Y:299:MET:HA	20:Y:299:MET:HE3	1.95	0.48
21:Z:63:LYS:C	21:Z:65:ASP:H	2.21	0.48
22:a:70:ARG:HH12	23:b:18:ASN:H	1.60	0.48
23:b:179:LEU:O	23:b:183:LEU:HG	2.14	0.48
24:d:194:LEU:HD13	24:d:259:PHE:HZ	1.79	0.48
25:f:869:THR:HB	25:f:882:LEU:HB3	1.96	0.48
26:W:22:ALA:HA	26:W:25:ASP:OD2	2.14	0.48
26:W:104:MET:C	26:W:104:MET:HE2	2.39	0.48
30:F:83:ASN:HD22	31:E:50:LEU:HD12	1.78	0.48
8:J:89:VAL:HG22	15:Q:66:LEU:HD21	1.95	0.48
10:L:138:ASP:OD1	10:L:138:ASP:N	2.46	0.48
10:L:202:GLU:OE2	10:L:202:GLU:N	2.47	0.48
20:Y:188:CYS:HB2	20:Y:193:ASP:HB2	1.95	0.48
25:f:513:GLU:O	25:f:517:VAL:HG12	2.13	0.48
25:f:696:LEU:HD21	25:f:731:MET:SD	2.53	0.48
25:f:698:SER:O	25:f:698:SER:OG	2.22	0.48
29:A:221:GLY:O	29:A:224:LEU:HG	2.13	0.48
29:A:223:THR:HG23	29:A:273:PHE:CE2	2.49	0.48
29:A:273:PHE:HE1	29:A:320:ALA:HB3	1.79	0.48
30:F:391:PHE:HE2	30:F:427:VAL:HG11	1.78	0.48
31:E:100:LEU:HD21	31:E:107:ILE:HD13	1.96	0.48
32:U:212:ASP:O	32:U:216:VAL:HG23	2.13	0.48
1:B:193:GLN:NE2	1:B:352:GLU:O	2.38	0.48
2:C:38:LYS:HE2	3:D:55:GLU:HG2	1.94	0.48
2:C:209:CYS:HB3	2:C:243:PRO:O	2.13	0.48
3:D:67:ASN:ND2	32:U:607:VAL:O	2.37	0.48
5:G:114:LEU:O	5:G:118:ILE:HG12	2.14	0.48
9:K:96:THR:O	9:K:107:MET:HE1	2.13	0.48
9:K:98:ASN:HA	16:R:61:ARG:HH21	1.77	0.48
10:L:122:ARG:NH2	11:M:122:TYR:OH	2.46	0.48
10:L:192:LEU:HD12	10:L:236:LEU:HD22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Y:124:PHE:HA	20:Y:127:THR:HG22	1.95	0.48
22:a:50:PHE:HD2	22:a:52:GLN:HG2	1.79	0.48
22:a:116:THR:HA	22:a:158:LEU:HD22	1.94	0.48
23:b:150:THR:HG23	23:b:153:LEU:HD23	1.95	0.48
25:f:512:MET:HE1	25:f:548:THR:HB	1.95	0.48
25:f:564:LEU:HD22	25:f:776:LEU:HD23	1.95	0.48
25:f:589:SER:O	25:f:593:THR:HG23	2.12	0.48
25:f:821:LEU:HD22	25:f:882:LEU:HB2	1.96	0.48
31:E:135:ILE:HD13	31:E:138:LEU:HB2	1.94	0.48
32:U:188:MET:HE3	32:U:188:MET:HB3	1.66	0.48
1:B:92:GLN:O	1:B:94:GLU:N	2.47	0.48
2:C:135:VAL:HG21	2:C:234:LEU:HA	1.95	0.48
3:D:351:LYS:O	31:E:163:GLY:HA3	2.12	0.48
4:c:104:ARG:HH22	21:Z:21:ASP:CG	2.22	0.48
4:c:116:PRO:HA	4:c:147:PRO:HD2	1.95	0.48
7:I:182:GLY:H	7:I:184:MET:HE1	1.78	0.48
15:Q:38:MET:HE2	15:Q:38:MET:HA	1.96	0.48
18:T:11:VAL:HG13	18:T:24:ALA:HB2	1.96	0.48
19:X:338:VAL:HG21	19:X:353:LEU:HD22	1.95	0.48
20:Y:33:GLY:HA2	20:Y:37:VAL:HG21	1.94	0.48
23:b:31:ASP:OD2	23:b:31:ASP:N	2.45	0.48
23:b:113:VAL:HG13	23:b:142:ASN:HA	1.96	0.48
23:b:161:ASN:HD21	23:b:168:SER:N	2.10	0.48
29:A:111:TYR:HE2	29:A:125:LEU:HD11	1.78	0.48
32:U:485:ALA:HB3	32:U:519:VAL:HG22	1.96	0.48
1:B:181:GLN:H	1:B:181:GLN:CD	2.19	0.48
2:C:258:ARG:HD3	2:C:274:LEU:HD21	1.95	0.48
3:D:377:SER:OG	3:D:378:ILE:N	2.46	0.48
4:c:26:ASP:OD1	4:c:178:THR:OG1	2.31	0.48
4:c:83:SER:OG	4:c:84:VAL:N	2.44	0.48
4:c:115:HIS:HB3	4:c:118:PHE:HB2	1.96	0.48
8:J:155:ALA:N	9:K:63:SER:OG	2.40	0.48
12:N:2:THR:HG23	12:N:127:ILE:HD11	1.95	0.48
12:N:77:HIS:CE1	12:N:120:MET:HE1	2.49	0.48
13:O:3:ILE:HD12	13:O:99:VAL:HG12	1.95	0.48
22:a:342:ASP:O	22:a:344:GLN:N	2.46	0.48
24:d:283:LEU:HB3	24:d:286:GLU:OE1	2.14	0.48
25:f:119:LYS:HB3	25:f:123:ALA:N	2.29	0.48
25:f:833:PHE:CD2	25:f:842:VAL:HA	2.49	0.48
26:W:315:MET:HG2	26:W:358:VAL:HG23	1.95	0.48
26:W:396:LEU:O	26:W:401:THR:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E:68:LYS:C	31:E:69:PHE:HD1	2.21	0.48
1:B:136:LEU:HD23	1:B:160:ILE:HG22	1.95	0.48
1:B:142:ASP:OD1	1:B:142:ASP:N	2.44	0.48
3:D:342:ARG:NH2	19:X:234:GLU:OE2	2.42	0.48
7:I:166:ASN:N	7:I:166:ASN:OD1	2.44	0.48
9:K:121:LEU:HA	9:K:123:PHE:CE2	2.48	0.48
10:L:99:PHE:HB3	10:L:101:ARG:HG2	1.96	0.48
12:N:37:ILE:HG12	12:N:43:CYS:HB3	1.94	0.48
12:N:110:GLN:HB3	12:N:112:TYR:HE1	1.79	0.48
18:T:151:ARG:HA	18:T:154:LEU:HG	1.95	0.48
22:a:25:LEU:HD22	22:a:60:TYR:HE2	1.78	0.48
25:f:297:MET:HG3	25:f:301:HIS:NE2	2.29	0.48
25:f:305:LEU:HA	25:f:314:TYR:HE2	1.79	0.48
25:f:478:ARG:HH22	25:f:509:LYS:HE3	1.79	0.48
30:F:244:THR:O	30:F:245:LYS:HG2	2.14	0.48
30:F:264:GLY:HA2	30:F:268:VAL:H	1.78	0.48
31:E:311:ASP:HA	31:E:314:LYS:HG2	1.96	0.48
31:E:342:ASP:O	31:E:345:ASN:HB3	2.14	0.48
32:U:221:ILE:HD11	32:U:252:LEU:HD13	1.96	0.48
32:U:899:ARG:HH21	32:U:922:GLU:HA	1.79	0.48
1:B:220:LYS:HB3	1:B:220:LYS:HE3	1.64	0.48
3:D:202:VAL:HG12	3:D:329:ARG:HB2	1.96	0.48
4:c:39:LEU:HD12	21:Z:17:LEU:HD22	1.96	0.48
11:M:49:VAL:HG21	11:M:65:ARG:HD3	1.95	0.48
13:O:93:TYR:O	14:P:99:ARG:NH2	2.45	0.48
18:T:6:VAL:O	18:T:6:VAL:HG23	2.14	0.48
22:a:65:SER:HA	22:a:68:GLU:CD	2.39	0.48
23:b:26:LEU:HD12	23:b:29:GLN:HE21	1.78	0.48
24:d:161:ILE:HD12	24:d:161:ILE:H	1.79	0.48
24:d:283:LEU:HD23	24:d:284:PHE:N	2.29	0.48
25:f:160:ARG:O	25:f:160:ARG:NH1	2.38	0.48
25:f:407:MET:HB2	25:f:439:TYR:HB3	1.95	0.48
25:f:603:SER:OG	25:f:639:LYS:HB2	2.13	0.48
30:F:72:LYS:HD3	30:F:73:ILE:HG12	1.95	0.48
32:U:714:SER:O	32:U:718:ASN:ND2	2.47	0.48
32:U:723:ASP:OD1	32:U:724:VAL:N	2.46	0.48
2:C:66:LEU:HD23	3:D:82:ILE:HD13	1.96	0.47
2:C:357:ALA:HB2	35:C:501:ATP:H5'2	1.96	0.47
5:G:27:TYR:CE1	11:M:16:PRO:HA	2.49	0.47
11:M:40:ARG:NH1	11:M:146:ALA:O	2.40	0.47
11:M:230:ASP:O	11:M:233:GLU:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:18:SER:O	12:N:18:SER:OG	2.31	0.47
14:P:24:ALA:HB1	14:P:41:LYS:HB2	1.95	0.47
20:Y:121:LEU:O	20:Y:125:ARG:HG3	2.14	0.47
21:Z:7:GLN:OE1	21:Z:7:GLN:N	2.38	0.47
25:f:14:GLN:HG2	25:f:63:LEU:HD22	1.96	0.47
25:f:65:GLU:O	25:f:69:SER:OG	2.27	0.47
25:f:106:LEU:HB3	25:f:111:GLU:OE2	2.13	0.47
25:f:466:LEU:O	25:f:470:VAL:HG13	2.14	0.47
25:f:553:THR:HA	25:f:556:ARG:CZ	2.44	0.47
25:f:756:PRO:HB2	25:f:757:ASN:OD1	2.13	0.47
25:f:828:ARG:HD2	25:f:845:ARG:H	1.79	0.47
25:f:858:LYS:HA	25:f:858:LYS:HD2	1.60	0.47
25:f:878:GLU:O	25:f:879:ARG:HD2	2.14	0.47
26:W:183:VAL:HG23	26:W:183:VAL:O	2.14	0.47
30:F:269:ARG:HA	30:F:316:GLN:OE1	2.14	0.47
31:E:285:LEU:HD12	31:E:289:LEU:HD22	1.95	0.47
32:U:4:SER:OG	32:U:5:ALA:N	2.47	0.47
3:D:396:ALA:O	3:D:400:GLU:HB3	2.14	0.47
4:c:143:VAL:HA	4:c:159:ALA:HA	1.97	0.47
12:N:28:ASN:ND2	13:O:122:LEU:HD21	2.29	0.47
17:S:201:GLU:OE2	17:S:204:ARG:NH1	2.47	0.47
18:T:11:VAL:N	18:T:139:THR:OG1	2.40	0.47
19:X:317:PRO:C	19:X:319:ILE:N	2.72	0.47
20:Y:22:LEU:C	20:Y:24:PHE:H	2.21	0.47
21:Z:260:VAL:CG1	21:Z:261:TYR:N	2.76	0.47
22:a:304:VAL:O	22:a:307:VAL:HG12	2.13	0.47
24:d:177:ASP:HB2	32:U:3:THR:HB	1.96	0.47
25:f:398:TRP:HA	25:f:401:LYS:HG2	1.96	0.47
27:V:264:TYR:CE1	27:V:298:ILE:HD12	2.49	0.47
30:F:133:PHE:HE2	31:E:109:ARG:HH11	1.61	0.47
30:F:406:ILE:HA	30:F:409:ARG:HB2	1.96	0.47
31:E:29:LEU:HA	31:E:33:LEU:HD21	1.96	0.47
31:E:55:GLN:OE1	31:E:108:MET:HG3	2.14	0.47
31:E:60:VAL:HG21	31:E:92:LEU:HD12	1.95	0.47
32:U:446:LEU:HD12	32:U:446:LEU:HA	1.78	0.47
1:B:82:GLN:HG2	1:B:86:LYS:HD2	1.97	0.47
2:C:139:MET:HE1	2:C:210:THR:HB	1.96	0.47
3:D:277:ALA:HB1	3:D:282:ASP:HB2	1.95	0.47
6:H:96:GLN:O	6:H:100:VAL:HG23	2.14	0.47
8:J:103:THR:OG1	8:J:137:ASP:OD2	2.30	0.47
10:L:16:GLN:HB2	10:L:18:ARG:HH12	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:153:LEU:HD11	14:P:166:THR:HB	1.96	0.47
15:Q:22:ALA:HA	15:Q:28:MET:H	1.79	0.47
19:X:266:ASP:OD2	19:X:266:ASP:N	2.47	0.47
20:Y:320:ALA:HA	20:Y:330:ILE:HD12	1.95	0.47
21:Z:166:GLU:HA	21:Z:166:GLU:OE2	2.13	0.47
23:b:97:LEU:O	23:b:100:ARG:HD3	2.14	0.47
24:d:228:HIS:HB3	24:d:229:PRO:HD3	1.96	0.47
25:f:133:MET:O	25:f:137:ARG:HG2	2.14	0.47
25:f:267:ARG:HH11	25:f:271:MET:HB3	1.79	0.47
25:f:556:ARG:H	25:f:556:ARG:HD2	1.80	0.47
28:e:37:HIS:CG	28:e:39:TRP:HB2	2.50	0.47
29:A:193:THR:OG1	29:A:194:PRO:HD3	2.13	0.47
29:A:427:PRO:HD2	29:A:428:ARG:NH2	2.29	0.47
30:F:366:MET:HG3	30:F:396:CYS:SG	2.53	0.47
31:E:171:LEU:HD21	31:E:279:THR:HG22	1.96	0.47
32:U:137:MET:HE1	32:U:140:ARG:HE	1.78	0.47
32:U:434:GLY:C	32:U:436:ALA:H	2.22	0.47
1:B:358:GLU:H	1:B:358:GLU:CD	2.23	0.47
2:C:364:THR:HA	3:D:196:ILE:HG12	1.96	0.47
3:D:214:MET:HE1	37:D:501:ADP:H2'	1.95	0.47
3:D:352:MET:HE1	31:E:164:ILE:HG22	1.96	0.47
5:G:88:ARG:HA	5:G:91:VAL:HG22	1.96	0.47
8:J:4:ASP:OD2	8:J:21:TYR:OH	2.33	0.47
8:J:98:VAL:HG12	16:R:82:LEU:HD21	1.96	0.47
10:L:146:GLN:HB2	10:L:159:MET:HG2	1.95	0.47
15:Q:38:MET:HE3	15:Q:44:LEU:HB2	1.96	0.47
18:T:187:PHE:CZ	18:T:203:LEU:HB3	2.49	0.47
19:X:171:LEU:HD23	19:X:171:LEU:HA	1.67	0.47
20:Y:50:MET:HB2	20:Y:74:LYS:CE	2.43	0.47
20:Y:194:PHE:HB2	20:Y:230:ALA:CA	2.45	0.47
22:a:68:GLU:HG3	22:a:69:HIS:N	2.27	0.47
25:f:242:GLU:OE1	25:f:242:GLU:N	2.47	0.47
25:f:314:TYR:CZ	25:f:315:GLU:HB3	2.50	0.47
25:f:703:ARG:HA	25:f:706:ILE:HD12	1.96	0.47
26:W:439:VAL:HA	26:W:442:THR:HG22	1.96	0.47
27:V:476:PHE:O	27:V:480:ILE:HG12	2.14	0.47
28:e:38:VAL:HG22	28:e:38:VAL:O	2.14	0.47
30:F:54:ILE:HD12	30:F:55:MET:N	2.29	0.47
32:U:655:ALA:O	32:U:659:CYS:HB2	2.14	0.47
33:g:228:CR8:C5	33:g:283:VAL:HG21	2.44	0.47
34:u:130:ILE:HD13	34:u:169:VAL:HG11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:PHE:O	1:B:369:THR:OG1	2.20	0.47
1:B:401:GLU:HB3	1:B:422:SER:OG	2.14	0.47
6:H:143:ARG:HB3	6:H:145:TYR:HE1	1.80	0.47
7:I:11:ILE:HD11	8:J:5:ARG:HA	1.97	0.47
11:M:131:PHE:O	11:M:153:PRO:HB3	2.14	0.47
19:X:57:LEU:O	19:X:61:GLY:N	2.44	0.47
22:a:70:ARG:CZ	23:b:17:ARG:HA	2.44	0.47
23:b:68:THR:O	23:b:71:ILE:HG23	2.15	0.47
25:f:171:GLN:CD	25:f:182:GLU:HG2	2.40	0.47
25:f:288:VAL:HG21	25:f:879:ARG:O	2.15	0.47
26:W:162:ALA:O	26:W:166:LEU:HG	2.14	0.47
28:e:60:LEU:HD23	28:e:65:TYR:CE2	2.49	0.47
30:F:274:LEU:HA	30:F:277:GLU:OE1	2.14	0.47
1:B:438:LEU:HA	7:I:155:ASN:ND2	2.29	0.47
4:c:26:ASP:OD2	4:c:27:THR:N	2.47	0.47
8:J:65:LEU:HD11	8:J:87:ALA:HB3	1.97	0.47
8:J:228:TYR:O	8:J:232:ILE:HG12	2.15	0.47
15:Q:139:THR:O	15:Q:143:LEU:HG	2.15	0.47
15:Q:154:GLU:O	15:Q:157:VAL:HG22	2.14	0.47
19:X:253:TYR:CZ	19:X:318:ILE:HD11	2.49	0.47
20:Y:127:THR:O	20:Y:131:THR:OG1	2.21	0.47
20:Y:279:GLU:HB2	20:Y:296:VAL:HG11	1.95	0.47
20:Y:381:GLN:HB2	27:V:482:PHE:CZ	2.50	0.47
21:Z:211:TYR:HB2	26:W:445:LEU:HD21	1.96	0.47
22:a:198:PHE:HD1	22:a:226:ARG:HH22	1.61	0.47
23:b:3:LEU:HD12	23:b:105:HIS:NE2	2.30	0.47
23:b:187:PRO:HA	23:b:191:GLY:C	2.40	0.47
27:V:130:PHE:O	27:V:133:PRO:HD2	2.14	0.47
29:A:214:LEU:N	29:A:319:MET:O	2.48	0.47
30:F:250:LYS:HA	30:F:284:PHE:HB3	1.96	0.47
32:U:417:LYS:HA	32:U:417:LYS:HD3	1.75	0.47
1:B:58:CYS:SG	25:f:219:LYS:HE2	2.55	0.47
1:B:174:MET:HE3	1:B:270:LEU:HD13	1.96	0.47
2:C:337:ASN:HB3	20:Y:174:TRP:CZ2	2.50	0.47
4:c:82:VAL:HG23	4:c:82:VAL:O	2.14	0.47
5:G:228:ARG:NH1	5:G:234:GLU:OE2	2.47	0.47
6:H:213:CYS:HB2	6:H:218:PHE:HB2	1.95	0.47
8:J:172:LEU:O	8:J:176:TYR:N	2.38	0.47
10:L:70:ILE:HD11	10:L:105:VAL:HG22	1.96	0.47
12:N:91:ARG:NH1	18:T:1:THR:OG1	2.47	0.47
13:O:1:THR:N	13:O:168:GLY:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:48:THR:OG1	13:O:95:GLY:O	2.30	0.47
14:P:22:ILE:HG22	14:P:188:HIS:HB2	1.97	0.47
16:R:134:TYR:HB2	16:R:163:ALA:HA	1.97	0.47
17:S:57:PHE:HB2	17:S:105:TYR:HD2	1.80	0.47
17:S:150:ASP:HB3	17:S:156:LYS:HB2	1.97	0.47
18:T:124:TYR:HB3	18:T:137:LEU:HD23	1.97	0.47
20:Y:192:ARG:C	20:Y:194:PHE:N	2.73	0.47
22:a:27:GLU:HA	22:a:30:THR:HG22	1.97	0.47
22:a:317:VAL:CG2	22:a:319:LEU:HD13	2.44	0.47
23:b:26:LEU:HD11	23:b:78:VAL:HG11	1.97	0.47
23:b:140:ILE:HG23	23:b:170:LEU:HD23	1.96	0.47
24:d:217:ALA:HA	24:d:220:ILE:HG13	1.95	0.47
24:d:275:ILE:HD11	24:d:290:ILE:HD11	1.97	0.47
25:f:39:LYS:HZ3	25:f:120:ARG:HH22	1.62	0.47
25:f:66:LYS:O	25:f:70:LEU:HB2	2.15	0.47
25:f:73:PRO:C	25:f:75:LEU:H	2.22	0.47
25:f:125:ILE:HB	25:f:131:MET:HE1	1.96	0.47
25:f:129:LEU:O	25:f:133:MET:HE3	2.15	0.47
25:f:567:LEU:HA	25:f:599:ALA:HA	1.96	0.47
26:W:210:ASN:OD1	26:W:211:THR:N	2.48	0.47
26:W:248:ARG:HE	26:W:286:LEU:HD21	1.80	0.47
26:W:393:LEU:O	26:W:397:VAL:HG12	2.13	0.47
27:V:294:ARG:NH2	27:V:390:GLY:O	2.40	0.47
29:A:162:THR:HG22	29:A:249:TYR:CD2	2.49	0.47
30:F:391:PHE:HA	30:F:395:GLN:HG3	1.96	0.47
31:E:159:PHE:HB3	31:E:164:ILE:HG13	1.97	0.47
32:U:5:ALA:HB2	32:U:34:PHE:CE1	2.50	0.47
32:U:25:HIS:HA	32:U:59:PHE:HE2	1.80	0.47
32:U:693:LEU:HD21	32:U:779:LEU:HD11	1.97	0.47
32:U:772:TRP:CD1	32:U:774:PRO:HG2	2.50	0.47
2:C:337:ASN:HB3	20:Y:174:TRP:HZ2	1.80	0.47
2:C:395:SER:OG	2:C:396:GLU:N	2.48	0.47
6:H:58:ASP:OD2	6:H:61:SER:N	2.48	0.47
6:H:212:ILE:HG12	6:H:221:LEU:HD21	1.97	0.47
8:J:87:ALA:HA	8:J:110:TYR:HE2	1.80	0.47
9:K:102:THR:HA	17:S:94:THR:HG21	1.96	0.47
9:K:133:MET:HE2	9:K:133:MET:HA	1.96	0.47
10:L:73:SER:OG	10:L:133:LEU:HB2	2.14	0.47
10:L:157:ARG:HE	10:L:179:PHE:HB3	1.78	0.47
18:T:66:VAL:HG12	18:T:91:TRP:HH2	1.79	0.47
20:Y:72:LYS:HG3	20:Y:73:MET:CE	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Y:220:VAL:HG21	20:Y:249:VAL:HG21	1.96	0.47
20:Y:349:LYS:HB2	27:V:417:ILE:HA	1.97	0.47
21:Z:187:LEU:O	21:Z:191:ILE:HG12	2.14	0.47
21:Z:202:ASN:HD21	22:a:361:LYS:HB2	1.80	0.47
22:a:80:ILE:HG13	22:a:100:THR:HG21	1.97	0.47
22:a:320:VAL:HG12	22:a:335:TRP:HB2	1.95	0.47
23:b:161:ASN:ND2	23:b:168:SER:H	2.13	0.47
24:d:187:TYR:HB3	24:d:191:LEU:HD13	1.96	0.47
27:V:139:MET:SD	27:V:139:MET:N	2.87	0.47
27:V:266:GLN:OE1	27:V:266:GLN:N	2.48	0.47
30:F:147:PRO:HG2	31:E:120:TYR:CE2	2.50	0.47
31:E:122:MET:HE2	31:E:122:MET:HB2	1.78	0.47
32:U:421:GLN:O	32:U:424:ALA:HB3	2.15	0.47
34:u:167:ILE:HG23	34:u:246:ILE:HB	1.96	0.47
1:B:129:SER:HA	29:A:116:LYS:HD2	1.96	0.47
1:B:224:LEU:HB3	1:B:353:PHE:CE1	2.50	0.47
2:C:193:GLY:O	2:C:355:SER:HB2	2.15	0.47
7:I:61:PHE:CD2	7:I:61:PHE:N	2.83	0.47
13:O:215:LYS:HB3	14:P:197:THR:OG1	2.15	0.47
20:Y:127:THR:O	20:Y:131:THR:N	2.48	0.47
20:Y:232:GLU:HB2	20:Y:302:HIS:ND1	2.30	0.47
20:Y:265:GLU:OE1	20:Y:267:ARG:NH1	2.48	0.47
20:Y:287:LEU:HD23	20:Y:287:LEU:O	2.15	0.47
20:Y:288:PHE:CG	20:Y:289:ALA:N	2.82	0.47
24:d:178:TYR:HB3	32:U:1:MET:HB3	1.96	0.47
25:f:198:HIS:NE2	25:f:236:CYS:SG	2.87	0.47
25:f:198:HIS:HB3	25:f:240:VAL:HG22	1.96	0.47
26:W:68:VAL:HG23	26:W:107:GLN:HG3	1.96	0.47
26:W:119:PRO:O	26:W:122:LEU:HG	2.15	0.47
29:A:369:ARG:HE	29:A:372:LEU:HD12	1.80	0.47
32:U:22:PHE:CZ	32:U:26:LYS:HE3	2.49	0.47
34:u:121:LYS:HD2	34:u:122:GLY:N	2.29	0.47
12:N:189:LEU:HD22	12:N:193:GLN:HB3	1.97	0.47
18:T:174:ARG:HH12	18:T:206:GLU:H	1.63	0.47
21:Z:150:PRO:HB3	22:a:184:ASP:HB3	1.97	0.47
22:a:125:ILE:HD12	22:a:125:ILE:O	2.15	0.47
22:a:138:VAL:HA	22:a:141:MET:CE	2.44	0.47
23:b:51:LEU:HB3	23:b:62:THR:HB	1.97	0.47
24:d:223:ASN:HD21	24:d:225:TYR:HB2	1.80	0.47
25:f:119:LYS:HA	25:f:122:ALA:HB3	1.97	0.47
25:f:186:THR:HA	25:f:189:LYS:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:529:SER:O	25:f:565:ASN:ND2	2.43	0.47
25:f:640:LYS:HA	25:f:640:LYS:HE3	1.96	0.47
25:f:755:ASP:N	25:f:755:ASP:OD1	2.48	0.47
25:f:807:ARG:NH2	25:f:878:GLU:OE1	2.48	0.47
26:W:370:TYR:HB2	26:W:413:ILE:HG21	1.97	0.47
29:A:155:PRO:HG2	29:A:252:GLU:HB2	1.96	0.47
30:F:94:ILE:H	30:F:124:ILE:HA	1.80	0.47
31:E:176:PRO:HD3	31:E:280:ASN:HD22	1.80	0.47
32:U:247:GLN:HE21	32:U:904:LYS:HB2	1.80	0.47
32:U:550:VAL:HG21	32:U:768:GLN:HG3	1.97	0.47
32:U:567:ILE:HD13	32:U:586:VAL:HG22	1.97	0.47
3:D:354:LEU:HB2	3:D:393:ILE:HD12	1.96	0.46
3:D:397:LYS:HG3	3:D:398:ASP:H	1.80	0.46
8:J:57:ARG:NH1	8:J:58:THR:OG1	2.48	0.46
9:K:60:GLU:HG3	9:K:61:PRO:HD2	1.97	0.46
9:K:78:MET:N	9:K:78:MET:HE3	2.30	0.46
10:L:38:LEU:C	10:L:144:ILE:HD11	2.40	0.46
11:M:68:ASN:O	18:T:76:LEU:HD22	2.15	0.46
11:M:223:ARG:NH2	18:T:75:GLU:OE2	2.48	0.46
12:N:119:MET:HE3	18:T:6:VAL:HG21	1.96	0.46
13:O:8:TYR:HB2	13:O:146:MET:O	2.16	0.46
13:O:12:ILE:HB	13:O:178:ILE:HB	1.96	0.46
17:S:57:PHE:HZ	18:T:128:LEU:HB3	1.80	0.46
19:X:51:LEU:HD12	19:X:76:PHE:HZ	1.80	0.46
19:X:166:LEU:HG	19:X:170:GLN:HE21	1.80	0.46
20:Y:107:LYS:HD2	20:Y:107:LYS:O	2.15	0.46
20:Y:235:ASP:OD1	20:Y:235:ASP:N	2.48	0.46
21:Z:22:HIS:CE1	21:Z:55:ALA:HB1	2.51	0.46
21:Z:74:TYR:CE1	21:Z:78:MET:HE3	2.50	0.46
24:d:126:LEU:O	24:d:126:LEU:HD13	2.15	0.46
25:f:157:GLU:O	25:f:161:HIS:ND1	2.48	0.46
25:f:365:VAL:HG12	25:f:367:SER:H	1.81	0.46
25:f:741:LEU:HD23	25:f:742:ALA:H	1.79	0.46
25:f:763:ARG:HE	25:f:767:GLY:CA	2.28	0.46
26:W:84:ASN:ND2	26:W:123:ARG:HH22	2.13	0.46
29:A:222:LYS:N	37:A:501:ADP:O1B	2.48	0.46
29:A:296:GLN:HG2	30:F:174:ALA:HA	1.96	0.46
30:F:388:THR:HB	30:F:391:PHE:HB2	1.97	0.46
33:g:175:ILE:HG13	33:g:279:PHE:O	2.15	0.46
34:u:194:VAL:HG13	34:u:246:ILE:HG23	1.97	0.46
2:C:69:GLN:HG3	2:C:118:ASN:ND2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:50:VAL:HG11	8:J:56:GLU:HG3	1.97	0.46
9:K:70:ILE:HD13	9:K:74:ILE:HG12	1.97	0.46
9:K:221:GLN:OE1	9:K:221:GLN:N	2.48	0.46
14:P:172:LEU:HA	14:P:175:VAL:HG12	1.97	0.46
18:T:63:LEU:O	18:T:67:LEU:HD22	2.14	0.46
19:X:96:PHE:HZ	19:X:105:GLN:HG3	1.80	0.46
20:Y:134:LEU:HD13	20:Y:137:ARG:HH11	1.80	0.46
20:Y:377:LEU:HA	20:Y:380:VAL:HG12	1.97	0.46
24:d:104:ARG:HD3	24:d:106:SER:H	1.80	0.46
25:f:91:SER:HB3	25:f:121:PHE:HZ	1.79	0.46
25:f:317:LEU:O	25:f:321:MET:HG3	2.15	0.46
26:W:452:ILE:O	26:W:456:GLN:N	2.48	0.46
27:V:172:VAL:HG13	27:V:175:MET:HE2	1.97	0.46
27:V:371:ASN:HB3	27:V:374:LYS:HB2	1.98	0.46
30:F:168:TYR:CG	30:F:173:LYS:HB2	2.50	0.46
30:F:195:ILE:HD12	30:F:198:LEU:HD23	1.97	0.46
33:g:283:VAL:O	33:g:283:VAL:HG12	2.15	0.46
1:B:74:MET:HA	1:B:77:GLU:HG3	1.96	0.46
1:B:276:GLU:HG2	1:B:277:HIS:ND1	2.29	0.46
9:K:74:ILE:HD12	9:K:109:VAL:HG12	1.97	0.46
16:R:138:VAL:HG21	16:R:159:ALA:HA	1.96	0.46
17:S:7:PHE:HD1	17:S:9:GLY:H	1.63	0.46
17:S:45:LYS:HA	17:S:51:VAL:HG22	1.96	0.46
17:S:175:VAL:HA	17:S:178:VAL:HG22	1.98	0.46
20:Y:184:GLN:HE21	20:Y:291:HIS:HE1	1.63	0.46
21:Z:166:GLU:C	21:Z:168:GLU:H	2.23	0.46
23:b:16:MET:HE1	23:b:114:GLY:HA3	1.97	0.46
24:d:281:LYS:HA	24:d:281:LYS:HD3	1.60	0.46
26:W:121:LYS:O	26:W:125:ILE:HG12	2.16	0.46
26:W:451:MET:O	26:W:455:LEU:HD13	2.15	0.46
33:g:180:GLU:HG2	33:g:189:VAL:HG12	1.96	0.46
1:B:92:GLN:NE2	1:B:95:GLU:OE1	2.48	0.46
4:c:303:MET:O	4:c:307:VAL:HG12	2.15	0.46
6:H:83:TYR:O	6:H:87:VAL:HG23	2.16	0.46
15:Q:12:TYR:HB3	15:Q:184:ASP:OD1	2.15	0.46
15:Q:37:LYS:HE3	15:Q:188:ILE:HG21	1.98	0.46
15:Q:185:LYS:HB3	15:Q:185:LYS:HE3	1.62	0.46
19:X:335:LEU:HA	19:X:338:VAL:HG12	1.96	0.46
25:f:140:LEU:HD22	25:f:143:ARG:HH21	1.81	0.46
25:f:407:MET:N	25:f:407:MET:HE2	2.30	0.46
25:f:763:ARG:HG2	25:f:767:GLY:HA2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:778:LEU:HB3	25:f:782:HIS:HE1	1.79	0.46
27:V:121:PHE:HE2	27:V:125:ASN:H	1.63	0.46
31:E:239:GLY:HA2	31:E:257:LEU:HD13	1.98	0.46
4:c:303:MET:HB3	4:c:303:MET:HE2	1.77	0.46
6:H:134:LEU:HB2	6:H:149:SER:HB3	1.96	0.46
7:I:90:LEU:HG	7:I:114:LEU:HD11	1.97	0.46
11:M:72:HIS:CE1	11:M:73:VAL:HG23	2.50	0.46
15:Q:24:ASN:OD1	15:Q:25:ILE:HG12	2.15	0.46
24:d:232:LEU:HD12	24:d:244:VAL:HG13	1.98	0.46
25:f:230:CYS:HB3	25:f:232:TYR:CD1	2.50	0.46
25:f:642:ALA:HB3	25:f:770:HIS:NE2	2.31	0.46
25:f:716:ASP:OD2	25:f:752:HIS:CE1	2.68	0.46
25:f:857:GLY:N	25:f:860:LYS:HD2	2.27	0.46
26:W:357:ARG:HD3	26:W:357:ARG:HA	1.64	0.46
30:F:126:THR:HG22	30:F:130:GLN:O	2.15	0.46
30:F:185:TYR:CZ	30:F:195:ILE:HG21	2.51	0.46
30:F:194:GLN:NE2	30:F:353:GLU:O	2.47	0.46
31:E:47:LEU:HD12	31:E:48:LYS:N	2.31	0.46
32:U:899:ARG:NH2	32:U:923:GLU:OE1	2.41	0.46
33:g:173:MET:HE1	33:g:274:MET:SD	2.55	0.46
33:g:182:ASN:HB2	33:g:284:ARG:HH22	1.80	0.46
33:g:321:ASP:OD1	33:g:339:ARG:HD2	2.15	0.46
3:D:281:ALA:HB2	33:g:156:LEU:O	2.16	0.46
4:c:32:TYR:HA	4:c:206:ASN:O	2.15	0.46
8:J:131:ALA:HB3	8:J:147:THR:HG22	1.97	0.46
9:K:202:LEU:HD23	9:K:202:LEU:HA	1.77	0.46
10:L:14:SER:N	10:L:18:ARG:O	2.41	0.46
10:L:89:ARG:HD3	17:S:77:HIS:HB3	1.97	0.46
10:L:203:GLN:O	10:L:239:ARG:NH2	2.48	0.46
14:P:63:VAL:O	14:P:67:LEU:HB2	2.16	0.46
20:Y:377:LEU:HD11	27:V:483:CYS:SG	2.56	0.46
21:Z:65:ASP:C	21:Z:104:ASN:HD21	2.24	0.46
22:a:113:LEU:HD13	22:a:154:ARG:HG3	1.96	0.46
22:a:131:THR:O	22:a:134:THR:OG1	2.27	0.46
24:d:126:LEU:HD11	24:d:143:LEU:HD11	1.98	0.46
25:f:9:ALA:O	25:f:13:PRO:HD2	2.15	0.46
25:f:323:ASN:HA	25:f:326:LEU:HG	1.98	0.46
25:f:404:ASP:HB2	25:f:439:TYR:CE1	2.50	0.46
31:E:103:THR:OG1	31:E:104:THR:N	2.49	0.46
32:U:1:MET:CE	32:U:2:ILE:HG22	2.41	0.46
32:U:268:LEU:HD21	32:U:325:MET:HE3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:U:330:SER:O	32:U:453:HIS:NE2	2.49	0.46
1:B:78:PHE:CD2	25:f:658:ALA:HB1	2.51	0.46
2:C:223:PHE:HE1	33:g:163:ILE:HG23	1.81	0.46
2:C:245:ILE:HA	2:C:290:LYS:O	2.15	0.46
7:I:184:MET:HE3	7:I:184:MET:N	2.30	0.46
9:K:71:ASP:OD2	9:K:73:HIS:ND1	2.39	0.46
10:L:159:MET:HE3	10:L:160:SER:N	2.24	0.46
12:N:96:ALA:C	12:N:116:MET:HE1	2.41	0.46
12:N:98:ILE:HG23	12:N:114:VAL:HB	1.98	0.46
14:P:146:MET:HE2	14:P:146:MET:HA	1.97	0.46
18:T:50:MET:O	18:T:112:ILE:HD12	2.16	0.46
20:Y:385:ARG:NH2	27:V:282:ASN:HA	2.31	0.46
21:Z:61:ASP:HB3	21:Z:67:VAL:HG13	1.98	0.46
25:f:731:MET:HG3	25:f:746:ARG:CD	2.46	0.46
26:W:101:VAL:HA	26:W:104:MET:HG3	1.96	0.46
28:e:33:ASP:OD1	28:e:36:ALA:N	2.49	0.46
29:A:215:PHE:HB2	29:A:324:PRO:HG3	1.97	0.46
31:E:329:GLU:O	31:E:333:LYS:HG2	2.15	0.46
1:B:130:GLU:OE1	29:A:116:LYS:HE2	2.15	0.46
2:C:284:GLU:HA	2:C:284:GLU:OE2	2.16	0.46
3:D:184:PRO:HG3	3:D:191:TYR:CZ	2.51	0.46
4:c:98:MET:HE3	21:Z:78:MET:HE2	1.97	0.46
4:c:249:LEU:HD11	19:X:402:GLU:HG2	1.98	0.46
4:c:292:MET:HA	21:Z:259:VAL:CG2	2.37	0.46
11:M:71:ARG:NH1	18:T:72:ILE:O	2.49	0.46
13:O:59:ILE:HD11	13:O:82:MET:HB2	1.98	0.46
15:Q:4:LEU:HB3	15:Q:45:LEU:HD22	1.97	0.46
19:X:258:LYS:HB3	19:X:267:VAL:HG23	1.97	0.46
21:Z:19:VAL:HG22	21:Z:95:TYR:CE1	2.51	0.46
24:d:123:LEU:HA	24:d:126:LEU:HB3	1.97	0.46
24:d:187:TYR:O	24:d:191:LEU:HD13	2.15	0.46
24:d:197:LEU:HD21	24:d:260:ILE:HG12	1.97	0.46
24:d:297:LYS:HA	24:d:297:LYS:HD2	1.76	0.46
25:f:273:ASN:OD1	25:f:273:ASN:N	2.47	0.46
25:f:637:LYS:HD3	25:f:637:LYS:N	2.31	0.46
25:f:673:ARG:H	25:f:673:ARG:HD3	1.81	0.46
29:A:55:LEU:O	29:A:59:ILE:HG12	2.16	0.46
29:A:164:MET:HG3	29:A:165:GLN:HG3	1.98	0.46
31:E:130:VAL:HG23	31:E:186:ALA:HA	1.98	0.46
32:U:756:HIS:CE1	32:U:758:PRO:HG2	2.51	0.46
2:C:358:GLU:HA	3:D:324:PRO:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:130:VAL:HG12	3:D:142:VAL:HG12	1.98	0.46
5:G:63:SER:HA	5:G:66:VAL:HG22	1.97	0.46
8:J:37:GLY:HA2	8:J:181:ILE:HB	1.98	0.46
10:L:40:SER:OG	10:L:43:HIS:N	2.42	0.46
14:P:189:ILE:HB	14:P:196:THR:OG1	2.16	0.46
15:Q:168:GLN:HE21	15:Q:178:PHE:HZ	1.64	0.46
16:R:81:LYS:HG2	16:R:120:ARG:CZ	2.46	0.46
16:R:177:TYR:CE1	16:R:186:ARG:HD3	2.51	0.46
16:R:177:TYR:OH	16:R:186:ARG:NH1	2.49	0.46
20:Y:217:LYS:H	20:Y:217:LYS:HG2	1.56	0.46
22:a:201:GLY:HA3	22:a:233:LEU:HD21	1.98	0.46
23:b:21:PHE:HB2	23:b:25:ARG:HH11	1.80	0.46
24:d:95:TYR:HA	24:d:98:LEU:HB3	1.96	0.46
25:f:131:MET:HB3	25:f:170:TRP:HE1	1.80	0.46
25:f:452:ASN:O	25:f:488:ALA:HA	2.16	0.46
25:f:809:ILE:HG23	25:f:855:GLN:HG2	1.98	0.46
29:A:244:GLU:HA	29:A:247:GLN:OE1	2.15	0.46
30:F:77:SER:O	30:F:80:ILE:HG22	2.16	0.46
32:U:419:ALA:O	32:U:422:LEU:HG	2.15	0.46
1:B:57:GLN:HE22	29:A:42:SER:HA	1.79	0.46
3:D:176:GLU:HG2	3:D:329:ARG:HD3	1.98	0.46
3:D:380:GLN:HE22	31:E:167:PRO:HA	1.81	0.46
4:c:46:ARG:O	4:c:46:ARG:HD3	2.14	0.46
5:G:32:ILE:O	5:G:82:GLY:HA2	2.16	0.46
7:I:175:LEU:HD13	7:I:196:VAL:HG21	1.98	0.46
10:L:187:LEU:HD23	10:L:187:LEU:HA	1.76	0.46
14:P:75:GLU:O	14:P:79:GLY:N	2.40	0.46
15:Q:68:LYS:HA	15:Q:73:TYR:O	2.16	0.46
19:X:252:LYS:HD2	19:X:313:LEU:HD11	1.97	0.46
21:Z:147:ASP:OD1	21:Z:148:GLY:N	2.48	0.46
23:b:15:TYR:HB2	23:b:115:SER:HB2	1.98	0.46
24:d:92:THR:HA	24:d:95:TYR:CD1	2.52	0.46
25:f:35:ASP:HB3	25:f:85:SER:HB3	1.97	0.46
25:f:126:ILE:HG13	25:f:127:SER:OG	2.16	0.46
25:f:600:TYR:HB3	25:f:603:SER:HB3	1.98	0.46
26:W:40:LEU:O	26:W:44:ILE:HG12	2.16	0.46
26:W:257:GLN:HA	26:W:263:TRP:NE1	2.31	0.46
31:E:369:LYS:O	31:E:373:LYS:HG2	2.16	0.46
32:U:926:GLU:H	32:U:926:GLU:CD	2.24	0.46
1:B:225:TYR:CE2	1:B:350:LYS:HE3	2.47	0.45
2:C:161:ILE:HD13	2:C:161:ILE:HA	1.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:155:THR:OG1	3:D:157:ASP:OD1	2.27	0.45
9:K:101:PHE:CE2	16:R:57:ARG:HG3	2.51	0.45
15:Q:183:ILE:HD13	15:Q:188:ILE:HA	1.99	0.45
16:R:10:HIS:CD2	16:R:149:VAL:HG22	2.51	0.45
16:R:133:VAL:HA	16:R:136:TYR:HB3	1.98	0.45
17:S:90:ALA:O	17:S:93:SER:OG	2.28	0.45
20:Y:28:LEU:HB3	20:Y:29:PRO:HD3	1.97	0.45
20:Y:55:GLU:H	20:Y:55:GLU:CD	2.24	0.45
22:a:189:PRO:HG2	22:a:192:GLU:HB2	1.97	0.45
25:f:51:GLN:OE1	25:f:53:GLN:HB3	2.16	0.45
25:f:352:HIS:HB3	25:f:729:MET:HE3	1.98	0.45
25:f:679:LEU:HD13	25:f:687:ARG:NH2	2.32	0.45
27:V:480:ILE:O	27:V:481:SER:C	2.56	0.45
30:F:362:ARG:O	30:F:365:ILE:N	2.49	0.45
31:E:316:HIS:HE1	37:E:501:ADP:C8	2.34	0.45
5:G:203:SER:O	5:G:207:SER:N	2.46	0.45
6:H:86:LEU:HD21	6:H:130:PHE:CD2	2.51	0.45
7:I:115:CYS:HB3	8:J:81:ARG:NH2	2.31	0.45
7:I:141:LYS:HE2	7:I:142:HIS:NE2	2.31	0.45
13:O:171:SER:O	13:O:172:ASN:ND2	2.49	0.45
14:P:164:PHE:CE1	14:P:198:ARG:HD3	2.51	0.45
18:T:62:TYR:O	18:T:66:VAL:HG23	2.16	0.45
20:Y:290:PRO:HB2	20:Y:291:HIS:CE1	2.51	0.45
25:f:421:ASP:HB3	25:f:425:GLY:H	1.80	0.45
25:f:778:LEU:O	25:f:782:HIS:ND1	2.48	0.45
27:V:292:THR:HG23	27:V:308:THR:HG21	1.97	0.45
29:A:211:GLY:HA3	29:A:336:ARG:O	2.17	0.45
31:E:340:GLY:HA3	37:E:501:ADP:N3	2.31	0.45
32:U:247:GLN:HE22	32:U:912:ILE:HA	1.81	0.45
32:U:321:GLN:OE1	32:U:322:THR:N	2.45	0.45
32:U:813:TYR:CZ	32:U:883:ARG:HD3	2.51	0.45
2:C:115:ALA:HB2	2:C:127:LEU:HD11	1.98	0.45
4:c:44:HIS:ND1	4:c:112:TYR:OH	2.35	0.45
4:c:121:TRP:HZ3	4:c:123:SER:HB3	1.82	0.45
8:J:71:MET:C	8:J:71:MET:HE2	2.41	0.45
15:Q:4:LEU:O	15:Q:131:ALA:HA	2.17	0.45
17:S:5:TYR:HA	17:S:57:PHE:CD2	2.51	0.45
17:S:17:GLY:N	17:S:20:PHE:O	2.49	0.45
17:S:141:ALA:HB1	17:S:145:LEU:HD23	1.98	0.45
20:Y:272:PHE:CZ	20:Y:323:PHE:HE1	2.34	0.45
20:Y:370:ILE:HD13	20:Y:370:ILE:HA	1.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Z:48:LEU:HD11	21:Z:92:VAL:HG13	1.99	0.45
21:Z:178:ASP:HB2	21:Z:180:LYS:HG2	1.98	0.45
22:a:21:VAL:HG23	22:a:22:TRP:CD1	2.51	0.45
22:a:132:LYS:O	22:a:136:GLU:HG2	2.16	0.45
24:d:118:ARG:O	24:d:122:VAL:HG13	2.16	0.45
25:f:195:ASN:HA	25:f:198:HIS:CD2	2.52	0.45
25:f:218:GLU:OE1	25:f:835:GLU:HB3	2.16	0.45
25:f:297:MET:HE1	25:f:321:MET:HE1	1.97	0.45
27:V:132:LEU:HD23	27:V:135:LEU:HD23	1.98	0.45
29:A:226:ALA:O	29:A:229:VAL:HG12	2.16	0.45
30:F:55:MET:HE3	30:F:55:MET:C	2.41	0.45
30:F:235:LEU:HD22	37:F:501:ADP:N3	2.31	0.45
1:B:298:ASN:N	1:B:298:ASN:OD1	2.49	0.45
1:B:403:GLY:HA3	2:C:180:ILE:HG21	1.97	0.45
3:D:349:THR:HG21	3:D:360:LEU:HD21	1.98	0.45
4:c:307:VAL:HG13	22:a:363:MET:CE	2.46	0.45
8:J:136:PHE:H	8:J:211:MET:HE1	1.81	0.45
9:K:66:LYS:HE2	29:A:433:ASN:C	2.42	0.45
9:K:236:GLU:O	9:K:239:LYS:HG2	2.16	0.45
15:Q:43:LEU:HD21	15:Q:188:ILE:HD12	1.97	0.45
15:Q:118:MET:SD	15:Q:124:LEU:HA	2.57	0.45
17:S:194:ARG:NH2	17:S:196:CYS:HG	2.13	0.45
20:Y:22:LEU:C	20:Y:23:ARG:HG2	2.41	0.45
25:f:228:LYS:CB	25:f:233:LEU:HD11	2.45	0.45
25:f:258:LYS:HA	25:f:769:THR:HG21	1.99	0.45
25:f:502:LEU:HA	25:f:505:MET:HB3	1.98	0.45
25:f:557:TRP:HH2	25:f:796:LEU:HD23	1.80	0.45
26:W:317:TRP:CE3	26:W:358:VAL:HG11	2.50	0.45
27:V:163:VAL:O	27:V:167:LEU:HG	2.16	0.45
27:V:475:ALA:O	27:V:479:ARG:HD2	2.16	0.45
30:F:225:MET:CB	30:F:352:ILE:HB	2.47	0.45
31:E:150:GLU:OE1	31:E:191:LEU:HD11	2.17	0.45
32:U:360:VAL:HG23	32:U:365:CYS:HB2	1.98	0.45
33:g:323:GLU:OE1	33:g:323:GLU:N	2.38	0.45
1:B:295:TYR:CE1	2:C:262:GLY:HA3	2.51	0.45
1:B:417:GLU:HA	1:B:420:LYS:HE2	1.98	0.45
3:D:164:TYR:CD1	3:D:218:ALA:HB1	2.51	0.45
5:G:55:LYS:NZ	5:G:57:PRO:HA	2.32	0.45
9:K:211:ASN:OD1	9:K:212:ALA:N	2.49	0.45
9:K:238:ILE:HG13	9:K:241:ILE:HD11	1.99	0.45
16:R:21:THR:HA	16:R:27:ALA:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:211:ILE:O	18:T:215:ILE:HG12	2.17	0.45
20:Y:72:LYS:HG3	20:Y:73:MET:HE1	1.99	0.45
20:Y:142:PHE:CB	20:Y:179:ARG:HE	2.29	0.45
20:Y:149:LEU:HD12	20:Y:149:LEU:HA	1.82	0.45
20:Y:194:PHE:HB2	20:Y:230:ALA:HB2	1.97	0.45
22:a:55:GLY:O	22:a:59:LEU:HG	2.15	0.45
22:a:144:ASN:O	22:a:144:ASN:ND2	2.49	0.45
22:a:252:LYS:O	22:a:256:GLY:N	2.49	0.45
24:d:171:LEU:HG	24:d:175:TYR:CZ	2.52	0.45
24:d:306:ARG:HD3	24:d:308:TRP:HE3	1.81	0.45
25:f:436:SER:H	25:f:441:LYS:HZ1	1.65	0.45
26:W:294:LYS:H	26:W:294:LYS:CD	2.30	0.45
28:e:60:LEU:HD23	28:e:65:TYR:CD2	2.52	0.45
29:A:180:CYS:HB3	29:A:183:GLN:HB2	1.99	0.45
30:F:212:PHE:HZ	31:E:352:MET:HE1	1.80	0.45
30:F:383:GLU:O	30:F:386:ARG:HG2	2.16	0.45
31:E:307:GLN:O	31:E:310:LEU:HG	2.16	0.45
32:U:456:ASP:OD1	32:U:457:ILE:N	2.50	0.45
1:B:49:LEU:HD21	25:f:650:GLN:HB3	1.98	0.45
2:C:79:ALA:O	29:A:65:ILE:HG21	2.16	0.45
4:c:39:LEU:HD23	4:c:39:LEU:HA	1.71	0.45
5:G:60:LEU:HD11	11:M:160:TYR:HB3	1.98	0.45
8:J:69:VAL:HG12	8:J:104:VAL:HG12	1.99	0.45
15:Q:56:PHE:CZ	15:Q:88:LEU:HG	2.52	0.45
17:S:110:ILE:HB	17:S:122:TYR:HB2	1.98	0.45
18:T:145:LEU:HD21	18:T:175:VAL:HG13	1.97	0.45
19:X:317:PRO:O	19:X:318:ILE:HG13	2.17	0.45
21:Z:288:LYS:C	21:Z:290:GLY:N	2.74	0.45
22:a:133:GLU:H	22:a:133:GLU:CD	2.22	0.45
23:b:24:THR:HG22	23:b:27:GLN:H	1.81	0.45
25:f:42:GLU:OE1	25:f:56:LEU:HD22	2.15	0.45
25:f:179:VAL:O	25:f:216:MET:HE1	2.17	0.45
25:f:266:LEU:HD13	25:f:269:ALA:HB3	1.99	0.45
25:f:266:LEU:HD23	25:f:266:LEU:HA	1.79	0.45
25:f:718:ASP:OD2	25:f:809:ILE:HD13	2.16	0.45
27:V:494:MET:HE3	27:V:494:MET:HB3	1.77	0.45
30:F:96:LEU:C	30:F:97:LEU:HD23	2.41	0.45
30:F:129:ARG:HH21	33:g:166:MET:HG2	1.80	0.45
32:U:368:ALA:HB2	32:U:728:PHE:CD2	2.51	0.45
32:U:465:LEU:HB3	32:U:496:LEU:HD21	1.99	0.45
33:g:293:ASN:C	33:g:298:GLN:HE22	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:LYS:HA	1:B:387:LYS:HD3	1.73	0.45
2:C:143:VAL:HG22	2:C:205:HIS:HA	1.98	0.45
2:C:248:MET:HB2	2:C:293:MET:CG	2.45	0.45
2:C:323:GLU:CD	2:C:323:GLU:H	2.24	0.45
3:D:179:GLU:O	3:D:191:TYR:OH	2.32	0.45
11:M:65:ARG:HH12	11:M:78:ALA:HA	1.82	0.45
13:O:212:LEU:HB2	14:P:199:THR:HG23	1.97	0.45
14:P:62:THR:HG23	15:Q:85:ARG:HH22	1.79	0.45
14:P:83:LYS:HE2	14:P:83:LYS:HB2	1.81	0.45
14:P:99:ARG:HG3	14:P:100:PHE:HD1	1.82	0.45
18:T:49:THR:HG21	18:T:88:ILE:HD13	1.99	0.45
19:X:369:ILE:HB	20:Y:310:SER:HB2	1.99	0.45
22:a:119:GLY:O	22:a:123:LEU:HD23	2.17	0.45
23:b:55:ALA:C	23:b:57:ASP:H	2.22	0.45
25:f:672:LEU:O	25:f:675:PHE:HB2	2.17	0.45
25:f:674:THR:O	25:f:678:LEU:N	2.41	0.45
25:f:828:ARG:CD	25:f:845:ARG:H	2.29	0.45
26:W:55:ARG:HH22	26:W:90:LEU:HB2	1.81	0.45
26:W:450:GLU:HA	26:W:453:HIS:CG	2.51	0.45
28:e:49:GLU:OE2	28:e:51:ASP:N	2.43	0.45
30:F:221:LYS:HZ3	30:F:318:ASP:HA	1.81	0.45
31:E:309:ARG:NH1	31:E:336:ASP:HA	2.31	0.45
1:B:78:PHE:CD2	1:B:78:PHE:C	2.95	0.45
1:B:92:GLN:CD	1:B:95:GLU:HB3	2.42	0.45
1:B:408:ARG:HD2	29:A:22:ILE:HD13	1.99	0.45
3:D:296:MET:SD	3:D:307:VAL:HG21	2.57	0.45
7:I:39:ALA:HA	7:I:184:MET:SD	2.57	0.45
8:J:115:LYS:NZ	8:J:147:THR:HG23	2.32	0.45
9:K:21:LEU:HD11	10:L:126:ARG:NH1	2.31	0.45
10:L:64:LEU:HB2	10:L:72:ILE:HD11	1.99	0.45
14:P:191:GLU:HG2	14:P:194:LYS:H	1.81	0.45
18:T:4:PRO:HG3	18:T:107:TRP:CE2	2.52	0.45
18:T:36:PHE:CE2	18:T:39:ILE:HG23	2.52	0.45
18:T:58:ALA:HA	18:T:61:GLN:NE2	2.31	0.45
21:Z:129:LYS:HB2	21:Z:129:LYS:HE2	1.75	0.45
21:Z:288:LYS:O	21:Z:289:GLU:C	2.59	0.45
23:b:21:PHE:N	23:b:25:ARG:HH11	2.15	0.45
25:f:441:LYS:HE2	25:f:441:LYS:HB2	1.79	0.45
25:f:782:HIS:HD1	25:f:782:HIS:H	1.64	0.45
25:f:785:ARG:HG3	25:f:786:GLN:OE1	2.16	0.45
27:V:83:GLU:O	27:V:86:VAL:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:166:TYR:CE2	27:V:170:LEU:HD11	2.51	0.45
27:V:182:LYS:HA	27:V:182:LYS:HD3	1.73	0.45
30:F:388:THR:O	30:F:391:PHE:HB2	2.17	0.45
32:U:20:LYS:O	32:U:24:LEU:HG	2.17	0.45
32:U:552:ILE:HG21	32:U:570:LEU:HD11	1.99	0.45
1:B:291:GLY:HA2	1:B:309:MET:CE	2.46	0.45
2:C:293:MET:HE2	2:C:293:MET:HB2	1.78	0.45
3:D:98:GLN:O	3:D:121:ARG:NH1	2.40	0.45
6:H:139:TRP:CZ2	6:H:142:GLY:HA2	2.52	0.45
6:H:158:TRP:N	7:I:57:ASP:OD2	2.48	0.45
6:H:180:GLU:OE1	6:H:180:GLU:N	2.48	0.45
18:T:167:ASP:HA	18:T:170:GLU:HB2	1.98	0.45
19:X:97:LEU:HD12	19:X:132:ARG:HH21	1.82	0.45
23:b:3:LEU:HD11	23:b:46:GLU:HG2	1.99	0.45
23:b:104:ASN:OD1	23:b:104:ASN:N	2.41	0.45
25:f:609:VAL:HB	25:f:639:LYS:HZ1	1.82	0.45
26:W:202:THR:HA	26:W:205:ILE:HD12	1.97	0.45
28:e:60:LEU:HB3	28:e:65:TYR:HB2	1.99	0.45
30:F:307:GLN:O	30:F:311:LEU:HG	2.17	0.45
30:F:345:SER:HB3	31:E:345:ASN:CG	2.41	0.45
31:E:152:PRO:HG3	31:E:167:PRO:HD2	1.99	0.45
32:U:192:GLN:HG2	32:U:193:PHE:N	2.32	0.45
32:U:337:LEU:HD13	32:U:789:ILE:HG21	1.99	0.45
3:D:154:LEU:HD21	3:D:229:ARG:HE	1.79	0.45
4:c:189:ILE:O	4:c:193:ILE:HD13	2.17	0.45
5:G:20:GLY:HA3	6:H:28:ALA:HB2	1.98	0.45
6:H:114:VAL:O	6:H:117:VAL:HG12	2.17	0.45
7:I:4:ARG:HH11	7:I:6:ASP:HB2	1.82	0.45
7:I:6:ASP:OD2	7:I:23:TYR:OH	2.22	0.45
16:R:86:MET:O	16:R:89:GLN:NE2	2.49	0.45
17:S:19:ASP:O	17:S:200:LYS:NZ	2.50	0.45
20:Y:184:GLN:HE21	20:Y:291:HIS:CE1	2.35	0.45
21:Z:101:LEU:HD11	21:Z:138:TYR:HE2	1.81	0.45
22:a:173:TYR:HB2	22:a:203:ALA:HB1	1.98	0.45
22:a:292:THR:HG23	22:a:295:GLU:HG3	1.99	0.45
22:a:320:VAL:HB	22:a:333:MET:HE1	1.99	0.45
23:b:26:LEU:HD22	23:b:80:PRO:HG3	1.99	0.45
24:d:353:ARG:O	24:d:357:MET:HG3	2.17	0.45
25:f:100:ARG:C	25:f:102:HIS:H	2.25	0.45
25:f:426:LEU:HA	25:f:429:ILE:HG22	1.99	0.45
25:f:757:ASN:HA	25:f:809:ILE:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:125:ILE:HD12	26:W:149:LEU:HD12	1.99	0.45
26:W:203:GLN:O	26:W:203:GLN:NE2	2.40	0.45
30:F:233:LYS:HD3	30:F:331:ALA:CB	2.47	0.45
30:F:391:PHE:CZ	30:F:427:VAL:HG21	2.52	0.45
30:F:426:GLU:O	30:F:430:LYS:N	2.50	0.45
31:E:200:SER:HB3	31:E:238:ILE:HG12	1.99	0.45
31:E:353:PHE:HA	31:E:356:ARG:HE	1.82	0.45
33:g:180:GLU:O	33:g:285:PHE:N	2.39	0.45
33:g:218:ALA:O	33:g:221:ILE:HG22	2.17	0.45
1:B:109:VAL:CG2	2:C:94:LYS:HB2	2.46	0.44
2:C:321:ASN:OD1	2:C:321:ASN:N	2.48	0.44
4:c:118:PHE:N	4:c:118:PHE:CD1	2.85	0.44
6:H:119:GLN:HB3	6:H:153:GLY:HA3	1.98	0.44
8:J:168:VAL:O	8:J:172:LEU:HG	2.18	0.44
8:J:188:ILE:HD13	8:J:188:ILE:HA	1.82	0.44
9:K:38:ILE:HD11	9:K:181:LEU:CD1	2.47	0.44
12:N:85:GLU:HB3	12:N:89:ARG:NH2	2.32	0.44
14:P:34:MET:N	14:P:34:MET:SD	2.91	0.44
14:P:53:LEU:HD12	14:P:107:PRO:HB3	1.98	0.44
14:P:99:ARG:HA	14:P:127:ILE:HD11	1.98	0.44
16:R:62:GLN:O	16:R:65:ILE:HG22	2.17	0.44
16:R:163:ALA:O	16:R:167:ASP:HB2	2.17	0.44
18:T:70:MET:HG2	18:T:83:TYR:CE2	2.52	0.44
20:Y:94:ASN:HB3	20:Y:98:SER:HB2	1.99	0.44
20:Y:137:ARG:HB3	20:Y:163:LYS:NZ	2.32	0.44
22:a:109:GLU:HA	22:a:112:ILE:CD1	2.47	0.44
25:f:886:GLU:H	25:f:886:GLU:CD	2.25	0.44
26:W:250:ILE:O	26:W:253:THR:HG22	2.17	0.44
27:V:230:PHE:O	27:V:234:ARG:HG2	2.17	0.44
27:V:251:LEU:HD12	27:V:251:LEU:HA	1.82	0.44
29:A:381:THR:O	29:A:385:ILE:HG13	2.17	0.44
31:E:88:ASP:OD1	31:E:90:SER:OG	2.26	0.44
1:B:81:ASN:HB2	25:f:618:GLU:HG3	1.99	0.44
2:C:96:VAL:HG23	2:C:96:VAL:O	2.18	0.44
2:C:205:HIS:CD2	2:C:206:HIS:CD2	3.05	0.44
3:D:160:PRO:HG3	3:D:217:LYS:HG2	1.99	0.44
3:D:355:SER:HA	3:D:394:VAL:O	2.18	0.44
5:G:49:VAL:HG21	5:G:195:VAL:HG22	1.99	0.44
7:I:186:LEU:HD23	7:I:186:LEU:HA	1.84	0.44
8:J:51:ALA:H	8:J:54:GLN:NE2	2.14	0.44
10:L:185:ASN:O	10:L:189:LYS:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:M:50:GLU:HG3	11:M:209:PHE:CD2	2.53	0.44
13:O:108:PRO:C	13:O:109:HIS:HD1	2.25	0.44
14:P:96:TYR:C	14:P:98:LYS:H	2.24	0.44
17:S:11:THR:O	17:S:25:SER:HA	2.16	0.44
19:X:100:GLU:OE1	19:X:100:GLU:N	2.49	0.44
19:X:143:TYR:HB2	19:X:180:LEU:HD21	1.99	0.44
19:X:171:LEU:HD11	19:X:210:LEU:HA	1.98	0.44
21:Z:70:LEU:HD13	21:Z:111:LEU:HD22	1.99	0.44
25:f:103:TYR:HD2	25:f:137:ARG:HH21	1.65	0.44
25:f:317:LEU:HA	25:f:320:ILE:HG12	1.98	0.44
25:f:529:SER:HA	25:f:566:HIS:CE1	2.52	0.44
25:f:534:VAL:O	25:f:537:THR:OG1	2.33	0.44
26:W:377:ARG:HD2	26:W:380:GLN:HE21	1.83	0.44
27:V:181:TYR:HB3	27:V:221:LEU:HD13	1.99	0.44
27:V:294:ARG:O	27:V:298:ILE:HG13	2.18	0.44
29:A:122:VAL:HG13	30:F:88:TYR:HB2	2.00	0.44
1:B:211:TYR:CE1	1:B:218:PRO:HA	2.53	0.44
2:C:307:ARG:HH21	2:C:310:ARG:NH2	2.15	0.44
7:I:199:LYS:HD3	7:I:199:LYS:HA	1.77	0.44
7:I:226:ARG:HH12	7:I:228:LEU:HA	1.82	0.44
9:K:50:VAL:HG23	9:K:216:GLU:HB2	1.99	0.44
13:O:73:LEU:HD23	13:O:74:PRO:HD2	1.99	0.44
13:O:206:LYS:HA	14:P:165:GLU:HG3	1.98	0.44
14:P:158:MET:SD	14:P:163:LEU:HA	2.57	0.44
14:P:164:PHE:O	14:P:168:SER:OG	2.29	0.44
17:S:122:TYR:HA	17:S:131:GLN:O	2.17	0.44
17:S:135:PHE:CD1	17:S:135:PHE:C	2.94	0.44
19:X:132:ARG:O	19:X:135:SER:OG	2.28	0.44
20:Y:144:LEU:HD22	20:Y:147:ILE:HG21	1.98	0.44
20:Y:263:LEU:HB2	20:Y:271:PHE:CE1	2.52	0.44
21:Z:11:VAL:HG13	21:Z:15:VAL:HG23	1.99	0.44
21:Z:70:LEU:HD11	21:Z:112:MET:HE1	1.98	0.44
21:Z:98:GLY:O	21:Z:100:LYS:N	2.50	0.44
22:a:112:ILE:O	22:a:116:THR:HG22	2.17	0.44
25:f:113:MET:HE1	25:f:115:PRO:HG3	1.99	0.44
25:f:819:TYR:C	25:f:819:TYR:CD2	2.95	0.44
29:A:254:ALA:O	29:A:257:VAL:HG22	2.16	0.44
30:F:396:CYS:C	30:F:400:CYS:SG	3.00	0.44
31:E:270:LEU:HD23	31:E:270:LEU:HA	1.79	0.44
1:B:411:ARG:HG2	25:f:51:GLN:HA	1.99	0.44
2:C:76:VAL:HG12	2:C:112:CYS:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:223:PHE:CE1	33:g:163:ILE:HG23	2.52	0.44
3:D:374:ASP:O	3:D:377:SER:OG	2.23	0.44
4:c:167:MET:SD	4:c:172:HIS:HB2	2.58	0.44
5:G:160:TYR:HE1	6:H:84:ARG:HD2	1.82	0.44
10:L:16:GLN:HB2	10:L:18:ARG:NH2	2.29	0.44
10:L:31:GLN:HB2	30:F:438:TYR:CE2	2.51	0.44
10:L:50:LYS:HE2	10:L:59:HIS:HB2	1.99	0.44
11:M:169:ARG:O	11:M:173:LYS:HG2	2.17	0.44
11:M:173:LYS:HA	11:M:176:ILE:HG22	1.99	0.44
12:N:57:ASP:OD2	13:O:84:LYS:NZ	2.45	0.44
14:P:30:ILE:HD12	14:P:30:ILE:HA	1.84	0.44
16:R:63:CYS:SG	16:R:74:ILE:HD13	2.58	0.44
16:R:153:TYR:HB3	16:R:157:ARG:NH1	2.33	0.44
21:Z:178:ASP:C	21:Z:180:LYS:H	2.23	0.44
21:Z:248:ALA:HB2	26:W:425:LEU:HD21	1.99	0.44
24:d:241:TYR:CG	24:d:271:ILE:HD11	2.52	0.44
25:f:335:ARG:HG2	25:f:341:GLU:OE1	2.17	0.44
26:W:72:LYS:O	26:W:76:GLU:HG2	2.17	0.44
26:W:276:LEU:HD22	26:W:350:ARG:HB3	1.99	0.44
27:V:185:GLN:HB3	27:V:186:LYS:NZ	2.32	0.44
30:F:275:ALA:HB1	30:F:326:VAL:HG11	1.99	0.44
30:F:366:MET:HB3	30:F:420:TYR:OH	2.18	0.44
31:E:87:LEU:HD12	31:E:87:LEU:HA	1.75	0.44
37:E:501:ADP:H8	37:E:501:ADP:H2'	1.72	0.44
32:U:94:SER:HB3	32:U:97:VAL:HG12	1.99	0.44
32:U:144:ASP:HB3	32:U:146:LYS:HE3	2.00	0.44
34:u:121:LYS:HD2	34:u:122:GLY:H	1.83	0.44
3:D:83:GLN:HG2	3:D:140:VAL:HG13	1.99	0.44
3:D:196:ILE:HD12	3:D:196:ILE:HA	1.78	0.44
4:c:104:ARG:HD3	4:c:106:GLU:OE1	2.17	0.44
4:c:170:LEU:HB3	4:c:172:HIS:ND1	2.33	0.44
8:J:119:THR:HG22	8:J:126:PRO:HB3	2.00	0.44
8:J:234:LYS:O	8:J:237:GLU:HG3	2.17	0.44
9:K:69:GLU:OE2	16:R:71:LYS:NZ	2.46	0.44
13:O:7:VAL:HG22	13:O:123:PRO:O	2.18	0.44
13:O:89:ARG:HD2	13:O:89:ARG:HA	1.71	0.44
15:Q:100:VAL:O	15:Q:120:TYR:HA	2.18	0.44
20:Y:111:LEU:HD13	20:Y:115:GLY:H	1.82	0.44
21:Z:259:VAL:HG13	21:Z:260:VAL:CB	2.46	0.44
22:a:260:ASP:O	22:a:264:ASN:ND2	2.50	0.44
24:d:211:GLU:OE1	24:d:211:GLU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:162:LEU:O	25:f:165:GLU:HG2	2.18	0.44
26:W:287:VAL:O	26:W:290:ILE:HG13	2.18	0.44
27:V:394:LEU:HA	27:V:397:ARG:HD3	2.00	0.44
29:A:79:ASP:O	29:A:82:ALA:N	2.50	0.44
30:F:63:THR:HB	31:E:29:LEU:HD21	1.98	0.44
31:E:20:LYS:H	31:E:20:LYS:HD3	1.83	0.44
31:E:188:ALA:O	31:E:192:ASP:N	2.47	0.44
32:U:517:GLY:HA3	32:U:551:GLY:HA2	1.99	0.44
34:u:181:LYS:HG2	34:u:230:ILE:HG12	1.99	0.44
1:B:103:ARG:HB3	1:B:107:MET:HE3	1.99	0.44
1:B:184:TYR:HE1	1:B:242:GLN:HB3	1.82	0.44
2:C:79:ALA:HA	2:C:85:VAL:HG22	1.99	0.44
4:c:48:GLY:HA3	4:c:53:VAL:CG1	2.48	0.44
4:c:82:VAL:HG21	4:c:113:HIS:HD2	1.81	0.44
4:c:122:LEU:HD13	4:c:160:PHE:CD1	2.52	0.44
4:c:295:ASN:HB2	21:Z:259:VAL:CB	2.44	0.44
5:G:58:ASP:OD1	5:G:59:LYS:N	2.50	0.44
8:J:88:ARG:HH21	15:Q:69:MET:HE2	1.81	0.44
9:K:50:VAL:HG21	9:K:66:LYS:HB3	1.98	0.44
10:L:26:MET:HE2	10:L:150:SER:HB3	2.00	0.44
11:M:87:LEU:O	11:M:90:ILE:HG22	2.18	0.44
11:M:104:TYR:CE1	12:N:78:THR:HG22	2.53	0.44
12:N:149:LYS:NZ	12:N:153:LEU:HB2	2.32	0.44
14:P:27:ARG:HB2	14:P:182:GLY:O	2.17	0.44
18:T:61:GLN:HA	18:T:64:LYS:HB3	2.00	0.44
20:Y:50:MET:O	20:Y:53:TYR:HB2	2.18	0.44
20:Y:214:MET:HE3	20:Y:218:THR:HG22	2.00	0.44
22:a:164:GLN:OE1	22:a:164:GLN:N	2.36	0.44
24:d:138:LYS:O	24:d:142:ILE:HG13	2.18	0.44
25:f:256:PHE:O	25:f:260:SER:N	2.51	0.44
25:f:507:ASP:OD1	25:f:508:SER:N	2.51	0.44
25:f:748:LEU:O	25:f:752:HIS:ND1	2.38	0.44
26:W:84:ASN:HD21	26:W:123:ARG:HH22	1.65	0.44
26:W:201:ARG:NH2	26:W:205:ILE:HG13	2.33	0.44
26:W:201:ARG:HH21	26:W:205:ILE:N	2.15	0.44
30:F:233:LYS:HE2	30:F:331:ALA:HB1	1.99	0.44
31:E:145:LEU:HD23	31:E:183:LEU:HD11	2.00	0.44
1:B:268:ARG:HB2	1:B:311:GLU:OE2	2.17	0.44
1:B:411:ARG:HH22	1:B:414:VAL:HA	1.82	0.44
3:D:87:LEU:HB2	31:E:80:VAL:HG22	1.99	0.44
3:D:148:ASP:OD1	3:D:148:ASP:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:c:146:ASP:O	4:c:150:SER:OG	2.27	0.44
4:c:149:GLN:HB3	4:c:156:VAL:HG21	2.00	0.44
10:L:26:MET:HA	10:L:149:PRO:HG2	2.00	0.44
11:M:71:ARG:CZ	18:T:72:ILE:HA	2.48	0.44
13:O:218:PRO:HA	14:P:194:LYS:HA	2.00	0.44
17:S:18:GLU:O	17:S:118:LYS:HA	2.18	0.44
18:T:50:MET:C	18:T:50:MET:HE2	2.43	0.44
20:Y:282:MET:HE3	20:Y:287:LEU:CD2	2.47	0.44
21:Z:243:GLN:HA	21:Z:246:VAL:HB	1.99	0.44
22:a:8:LEU:HD22	22:a:26:GLU:HG3	1.98	0.44
22:a:22:TRP:HA	22:a:25:LEU:HD12	1.98	0.44
22:a:109:GLU:H	22:a:109:GLU:CD	2.26	0.44
24:d:85:GLY:O	24:d:88:LEU:HG	2.18	0.44
25:f:135:GLY:HA2	25:f:138:GLU:OE2	2.17	0.44
25:f:222:ASP:OD1	25:f:222:ASP:N	2.51	0.44
25:f:799:VAL:HG23	25:f:800:LEU:HD12	2.00	0.44
26:W:356:ASN:HB2	26:W:357:ARG:NH1	2.33	0.44
27:V:192:MET:HA	27:V:195:ILE:CG1	2.47	0.44
29:A:143:ASP:OD2	29:A:148:GLN:N	2.50	0.44
30:F:55:MET:HE3	30:F:56:LYS:N	2.32	0.44
32:U:49:TYR:CD1	32:U:61:ALA:HB2	2.53	0.44
32:U:164:GLU:HG3	32:U:204:ILE:HD11	2.00	0.44
32:U:206:MET:SD	32:U:216:VAL:HG11	2.57	0.44
33:g:190:ILE:HG13	33:g:209:VAL:HA	1.99	0.44
6:H:97:TYR:OH	14:P:78:GLU:OE2	2.31	0.44
10:L:229:VAL:HA	10:L:232:PHE:HD2	1.82	0.44
16:R:82:LEU:HB3	16:R:86:MET:HE1	2.00	0.44
17:S:52:ILE:HG13	17:S:53:GLY:N	2.33	0.44
18:T:184:TYR:HE2	18:T:186:ARG:HD3	1.82	0.44
19:X:93:LEU:O	19:X:97:LEU:HG	2.18	0.44
20:Y:285:ASP:OD1	20:Y:286:TRP:N	2.50	0.44
21:Z:204:LYS:O	21:Z:208:ILE:HG13	2.17	0.44
22:a:279:GLU:O	22:a:283:THR:N	2.50	0.44
22:a:308:GLU:O	22:a:312:MET:HG2	2.17	0.44
25:f:286:LYS:HB2	25:f:286:LYS:HE3	1.76	0.44
25:f:351:THR:HG23	25:f:356:ASN:HB3	1.99	0.44
25:f:470:VAL:HG21	25:f:500:LEU:HD11	1.99	0.44
25:f:701:ASN:OD1	25:f:703:ARG:HG2	2.18	0.44
25:f:705:ASN:O	25:f:709:THR:OG1	2.24	0.44
25:f:775:THR:O	25:f:778:LEU:HD23	2.18	0.44
26:W:108:CYS:SG	26:W:128:LEU:HD21	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:144:LYS:HG2	30:F:145:LEU:H	1.83	0.44
30:F:390:ASP:O	30:F:390:ASP:OD2	2.36	0.44
31:E:61:LEU:HD13	31:E:72:LYS:HB3	2.00	0.44
31:E:174:GLY:O	31:E:180:LYS:NZ	2.50	0.44
31:E:322:LYS:HD3	31:E:326:ILE:HB	2.00	0.44
32:U:43:ASP:OD1	32:U:43:ASP:N	2.50	0.44
5:G:72:ILE:HG21	5:G:114:LEU:HD21	2.00	0.44
8:J:35:VAL:HG13	8:J:158:ALA:HB2	2.00	0.44
8:J:195:LEU:HD23	8:J:206:ILE:HG22	2.00	0.44
14:P:123:SER:OG	14:P:131:MET:HB3	2.18	0.44
19:X:312:GLU:O	19:X:313:LEU:HD13	2.18	0.44
20:Y:144:LEU:O	20:Y:147:ILE:HG22	2.17	0.44
20:Y:156:LEU:HA	20:Y:159:ARG:HH11	1.83	0.44
22:a:98:GLU:HA	22:a:101:ARG:HG2	2.00	0.44
22:a:109:GLU:OE1	22:a:109:GLU:N	2.46	0.44
25:f:72:ARG:HH12	25:f:83:ARG:HG3	1.82	0.44
25:f:616:CYS:SG	25:f:632:LYS:HB2	2.58	0.44
26:W:276:LEU:HD23	26:W:341:PHE:HE1	1.83	0.44
29:A:87:LEU:HD23	29:A:87:LEU:HA	1.91	0.44
30:F:364:ARG:O	30:F:367:GLN:HG2	2.18	0.44
31:E:122:MET:HE3	31:E:198:VAL:CG2	2.48	0.44
32:U:136:LYS:HE2	32:U:136:LYS:HB2	1.75	0.44
32:U:636:VAL:HG13	32:U:637:VAL:HG23	1.99	0.44
32:U:811:PHE:CD2	32:U:888:GLN:HB2	2.53	0.44
1:B:225:TYR:C	1:B:225:TYR:CD1	2.96	0.43
1:B:275:GLU:OE2	1:B:319:PHE:HB3	2.18	0.43
5:G:46:ASP:HA	5:G:149:PRO:HD3	2.00	0.43
7:I:125:GLY:HA3	7:I:127:LYS:HE2	2.00	0.43
9:K:166:ASP:OD2	9:K:166:ASP:N	2.50	0.43
10:L:137:TYR:CZ	10:L:217:LYS:HG2	2.53	0.43
14:P:65:GLN:OE1	15:Q:85:ARG:NH1	2.51	0.43
16:R:138:VAL:HG11	16:R:162:GLN:HG2	1.99	0.43
17:S:138:GLY:HA2	17:S:142:SER:HB3	2.00	0.43
18:T:45:VAL:HG23	18:T:46:ASN:OD1	2.18	0.43
20:Y:282:MET:HE3	20:Y:287:LEU:HD22	2.00	0.43
21:Z:127:LYS:HB2	21:Z:127:LYS:HE2	1.87	0.43
21:Z:252:LYS:HZ3	24:d:339:ILE:HD13	1.83	0.43
21:Z:262:LEU:HD23	21:Z:262:LEU:HA	1.66	0.43
21:Z:272:LEU:O	21:Z:276:ILE:HG12	2.18	0.43
22:a:4:VAL:HA	22:a:7:PHE:CE2	2.53	0.43
25:f:419:LEU:HD12	25:f:420:TRP:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:360:GLU:CD	26:W:364:ARG:HH12	2.25	0.43
32:U:68:PHE:CD2	32:U:76:GLU:HB3	2.53	0.43
2:C:49:ARG:HD2	32:U:639:LEU:HD13	2.01	0.43
5:G:15:ILE:HD13	5:G:15:ILE:HA	1.84	0.43
5:G:202:LEU:HD23	5:G:202:LEU:HA	1.79	0.43
5:G:244:GLU:OE1	26:W:52:LYS:HE3	2.18	0.43
8:J:36:ARG:NH2	8:J:157:LYS:HG2	2.33	0.43
9:K:110:GLU:O	9:K:113:THR:HG22	2.18	0.43
10:L:194:ALA:O	10:L:198:THR:HG23	2.17	0.43
11:M:42:LYS:O	11:M:42:LYS:NZ	2.33	0.43
12:N:179:ILE:HG12	12:N:184:VAL:HG22	2.00	0.43
14:P:58:THR:HG21	15:Q:121:LEU:O	2.18	0.43
17:S:16:ALA:HB2	17:S:121:VAL:HG23	1.99	0.43
18:T:17:GLU:OE1	18:T:159:VAL:HB	2.18	0.43
18:T:107:TRP:CE2	18:T:127:MET:HE2	2.53	0.43
20:Y:22:LEU:HD11	20:Y:37:VAL:HG22	2.00	0.43
20:Y:192:ARG:HA	20:Y:192:ARG:HE	1.82	0.43
20:Y:231:LEU:O	20:Y:236:LEU:HD23	2.17	0.43
20:Y:369:THR:HG21	21:Z:257:MET:CE	2.45	0.43
20:Y:386:VAL:HG12	27:V:282:ASN:HD22	1.83	0.43
22:a:35:HIS:HD1	23:b:15:TYR:HD2	1.66	0.43
23:b:12:ASN:OD1	23:b:12:ASN:N	2.49	0.43
26:W:169:LEU:HD13	26:W:169:LEU:HA	1.84	0.43
29:A:185:GLU:O	29:A:189:GLU:HG3	2.18	0.43
29:A:222:LYS:HG2	29:A:343:PHE:CD2	2.52	0.43
30:F:361:ALA:O	30:F:364:ARG:HG2	2.18	0.43
34:u:177:LEU:HD12	34:u:238:PHE:CD2	2.53	0.43
3:D:370:ILE:HG21	3:D:407:ILE:HG21	2.00	0.43
4:c:305:ASP:HB3	26:W:432:LEU:CD1	2.49	0.43
8:J:115:LYS:O	8:J:119:THR:HG23	2.19	0.43
11:M:228:PRO:HG2	11:M:231:ILE:HG13	2.00	0.43
18:T:63:LEU:C	18:T:67:LEU:HD22	2.44	0.43
18:T:109:THR:HB	18:T:124:TYR:HE1	1.83	0.43
19:X:255:LEU:O	19:X:259:ILE:HG13	2.18	0.43
20:Y:22:LEU:HD11	20:Y:37:VAL:HG13	2.01	0.43
20:Y:278:VAL:O	20:Y:282:MET:HB2	2.18	0.43
20:Y:313:SER:HA	20:Y:354:VAL:O	2.18	0.43
21:Z:62:ASP:OD1	21:Z:62:ASP:N	2.32	0.43
22:a:24:ARG:HA	22:a:27:GLU:HG2	2.00	0.43
25:f:215:ASP:HA	25:f:218:GLU:HG3	2.00	0.43
25:f:478:ARG:HE	25:f:510:SER:HB3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:535:THR:O	25:f:538:ILE:HG12	2.18	0.43
25:f:721:VAL:O	25:f:725:SER:N	2.32	0.43
25:f:728:ALA:HB2	25:f:750:GLN:HB3	2.00	0.43
26:W:272:LEU:HD23	26:W:272:LEU:HA	1.82	0.43
27:V:117:VAL:HG12	27:V:128:ARG:HH11	1.83	0.43
27:V:224:LEU:HD22	27:V:224:LEU:HA	1.82	0.43
29:A:101:ILE:O	29:A:102:ILE:HG22	2.18	0.43
30:F:247:THR:O	30:F:282:ILE:N	2.47	0.43
31:E:157:GLU:HA	31:E:160:GLN:HG2	2.00	0.43
31:E:235:ILE:HD12	31:E:235:ILE:HA	1.84	0.43
33:g:224:THR:OG1	33:g:256:ARG:NH1	2.51	0.43
2:C:328:ILE:HA	2:C:331:ILE:HD12	2.00	0.43
3:D:116:LEU:HD23	3:D:117:SER:N	2.33	0.43
4:c:98:MET:HE1	21:Z:77:ASN:HB3	2.00	0.43
4:c:234:TYR:CD2	21:Z:251:LEU:HD23	2.53	0.43
9:K:51:GLU:HB3	9:K:206:MET:HE3	2.00	0.43
9:K:202:LEU:O	9:K:206:MET:N	2.42	0.43
10:L:196:ARG:NH1	10:L:239:ARG:HA	2.33	0.43
16:R:147:LEU:HA	16:R:151:GLN:OE1	2.19	0.43
18:T:162:GLN:HG2	18:T:163:THR:N	2.32	0.43
19:X:297:ARG:HH21	19:X:333:GLN:HG2	1.82	0.43
21:Z:52:ASN:OD1	21:Z:53:SER:N	2.50	0.43
22:a:96:PHE:HA	22:a:99:LYS:HE2	2.01	0.43
22:a:114:CYS:SG	22:a:115:LYS:N	2.91	0.43
25:f:113:MET:HE2	25:f:114:ALA:N	2.33	0.43
25:f:183:PRO:O	25:f:187:LEU:HG	2.18	0.43
25:f:855:GLN:HE22	25:f:860:LYS:HE2	1.83	0.43
26:W:262:LYS:HD2	26:W:262:LYS:HA	1.61	0.43
30:F:223:VAL:HG23	30:F:350:ARG:HB3	2.01	0.43
31:E:264:MET:CE	31:E:294:ARG:HB3	2.48	0.43
32:U:148:LYS:HE3	32:U:176:MET:HE1	2.00	0.43
32:U:341:PHE:CE2	32:U:787:CYS:HB3	2.53	0.43
32:U:617:ALA:HA	32:U:620:GLU:HG3	2.00	0.43
33:g:230:ASN:C	33:g:231:ARG:HG2	2.44	0.43
2:C:256:SER:OG	2:C:257:SER:N	2.50	0.43
3:D:153:MET:HB3	3:D:153:MET:HE2	1.72	0.43
4:c:158:ASP:HB3	4:c:160:PHE:CZ	2.54	0.43
5:G:122:SER:OG	5:G:156:PRO:O	2.36	0.43
8:J:58:THR:HG23	8:J:60:ARG:HH12	1.84	0.43
9:K:103:TYR:HB2	9:K:105:GLU:HG2	2.01	0.43
12:N:91:ARG:HH22	18:T:1:THR:HG23	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:S:19:ASP:C	17:S:113:LEU:HD21	2.43	0.43
18:T:42:ILE:HD12	18:T:42:ILE:O	2.19	0.43
20:Y:42:MET:HA	20:Y:45:VAL:HG22	2.00	0.43
20:Y:152:MET:O	20:Y:152:MET:HG2	2.18	0.43
22:a:36:GLN:H	22:a:36:GLN:CD	2.24	0.43
22:a:276:CYS:O	22:a:280:MET:HG2	2.19	0.43
23:b:147:GLU:OE2	23:b:150:THR:HB	2.19	0.43
24:d:228:HIS:O	24:d:232:LEU:HD22	2.18	0.43
25:f:257:ARG:HH21	25:f:261:ARG:HG2	1.83	0.43
25:f:611:GLN:HA	25:f:615:ILE:HD12	1.99	0.43
25:f:814:SER:O	25:f:881:GLU:HA	2.18	0.43
27:V:309:MET:HG3	27:V:328:VAL:HG13	1.99	0.43
29:A:260:LEU:HA	29:A:263:MET:HG3	2.00	0.43
30:F:228:PRO:O	30:F:231:THR:HG22	2.18	0.43
32:U:554:LEU:HD22	32:U:761:VAL:HG22	1.99	0.43
33:g:170:LYS:NZ	33:g:171:PRO:O	2.27	0.43
2:C:132:ASP:OD1	2:C:135:VAL:HG12	2.19	0.43
3:D:351:LYS:HB2	3:D:351:LYS:HE3	1.59	0.43
8:J:146:GLN:O	8:J:153:TYR:HA	2.19	0.43
11:M:102:PHE:CE1	12:N:82:LEU:HD11	2.53	0.43
11:M:109:LYS:NZ	12:N:71:ASN:OD1	2.52	0.43
17:S:57:PHE:CZ	18:T:128:LEU:HD12	2.54	0.43
17:S:84:THR:OG1	17:S:85:THR:N	2.52	0.43
18:T:110:MET:HE1	18:T:112:ILE:CB	2.49	0.43
18:T:184:TYR:HD2	18:T:186:ARG:HB2	1.84	0.43
19:X:62:GLN:HB2	19:X:65:GLU:HG3	2.01	0.43
19:X:297:ARG:NH2	19:X:334:ASN:OD1	2.51	0.43
20:Y:107:LYS:CD	20:Y:111:LEU:HB2	2.49	0.43
20:Y:122:THR:HA	20:Y:125:ARG:NE	2.32	0.43
22:a:54:ASP:OD1	22:a:58:LYS:NZ	2.47	0.43
22:a:74:LEU:HD13	22:a:74:LEU:HA	1.74	0.43
24:d:283:LEU:HD12	24:d:315:TYR:CZ	2.54	0.43
25:f:98:PHE:CD2	25:f:105:LYS:HG2	2.54	0.43
25:f:130:ALA:O	25:f:134:SER:HB2	2.19	0.43
25:f:314:TYR:O	25:f:318:THR:OG1	2.37	0.43
25:f:350:LYS:HA	25:f:751:TYR:HE2	1.83	0.43
26:W:345:GLU:CD	26:W:346:GLU:H	2.27	0.43
29:A:369:ARG:N	29:A:406:GLU:OE2	2.49	0.43
30:F:198:LEU:HD22	30:F:236:LEU:HD21	2.00	0.43
30:F:217:ILE:HD12	30:F:217:ILE:HA	1.92	0.43
30:F:225:MET:HG3	30:F:331:ALA:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E:113:ARG:HH11	31:E:220:ASN:HB3	1.84	0.43
32:U:236:LEU:HD12	32:U:241:ASN:HB3	1.99	0.43
32:U:803:LYS:HG3	32:U:875:PHE:HD2	1.82	0.43
34:u:191:PRO:O	34:u:252:GLN:NE2	2.48	0.43
1:B:181:GLN:N	1:B:181:GLN:CD	2.77	0.43
1:B:320:ASP:OD2	1:B:322:ARG:HB2	2.18	0.43
3:D:352:MET:HE1	31:E:164:ILE:CG2	2.48	0.43
14:P:61:GLN:HB2	15:Q:85:ARG:NH2	2.33	0.43
15:Q:101:ASN:ND2	15:Q:120:TYR:HB3	2.33	0.43
16:R:41:LEU:HD21	16:R:76:VAL:HG12	2.00	0.43
17:S:72:LEU:HD23	17:S:83:MET:HE1	2.00	0.43
18:T:39:ILE:HD12	18:T:39:ILE:O	2.18	0.43
19:X:253:TYR:CE1	19:X:318:ILE:HD11	2.53	0.43
19:X:391:PRO:HA	19:X:392:PRO:HD3	1.86	0.43
20:Y:111:LEU:HD13	20:Y:115:GLY:N	2.33	0.43
20:Y:142:PHE:HB3	20:Y:179:ARG:HE	1.84	0.43
20:Y:192:ARG:HA	20:Y:192:ARG:NE	2.33	0.43
20:Y:217:LYS:O	20:Y:221:THR:HG23	2.19	0.43
21:Z:257:MET:HE2	21:Z:257:MET:HB2	1.34	0.43
21:Z:261:TYR:HD1	21:Z:261:TYR:HA	1.58	0.43
23:b:17:ARG:HH11	23:b:17:ARG:HG2	1.84	0.43
23:b:24:THR:HG22	23:b:26:LEU:N	2.33	0.43
23:b:131:LEU:HD12	23:b:136:VAL:HB	2.00	0.43
25:f:682:GLY:HA2	25:f:688:ARG:NH1	2.15	0.43
26:W:212:LYS:O	26:W:213:PHE:HB2	2.17	0.43
27:V:254:LEU:HD12	27:V:254:LEU:HA	1.76	0.43
27:V:284:GLU:OE2	27:V:287:ARG:NH2	2.50	0.43
29:A:67:GLU:HA	29:A:68:SER:CB	2.48	0.43
30:F:232:GLY:HA2	37:F:501:ADP:C5'	2.44	0.43
31:E:98:VAL:HG12	31:E:110:TYR:HA	2.00	0.43
32:U:681:ASN:OD1	32:U:681:ASN:N	2.50	0.43
32:U:792:ASN:OD1	32:U:796:LYS:N	2.51	0.43
1:B:78:PHE:CE2	25:f:658:ALA:HB1	2.54	0.43
1:B:117:ASP:OD1	1:B:117:ASP:N	2.49	0.43
2:C:30:GLU:O	2:C:33:LEU:HG	2.18	0.43
3:D:238:LYS:HG3	31:E:207:TYR:HD2	1.82	0.43
5:G:95:ARG:HD3	12:N:68:ILE:HD12	2.00	0.43
19:X:417:LYS:HE3	19:X:417:LYS:HB3	1.79	0.43
21:Z:131:LEU:HD12	21:Z:200:GLY:HA2	2.01	0.43
22:a:156:TYR:CG	22:a:179:PHE:CG	3.06	0.43
22:a:247:ARG:NH2	22:a:250:THR:HB	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:f:152:ALA:HB3	25:f:156:HIS:HB2	2.01	0.43
25:f:489:TYR:HB2	25:f:525:ILE:HD12	2.01	0.43
25:f:545:LYS:HZ2	25:f:547:GLU:HB3	1.84	0.43
25:f:637:LYS:N	25:f:637:LYS:CD	2.81	0.43
26:W:440:ASN:HA	26:W:443:THR:HG22	2.00	0.43
29:A:82:ALA:O	29:A:86:THR:HG23	2.19	0.43
31:E:326:ILE:HA	31:E:364:GLN:OE1	2.19	0.43
32:U:88:PHE:HE1	32:U:97:VAL:HG23	1.81	0.43
32:U:803:LYS:HG3	32:U:875:PHE:CD2	2.54	0.43
32:U:899:ARG:NH2	32:U:922:GLU:HA	2.34	0.43
1:B:96:ARG:O	1:B:99:VAL:HG12	2.19	0.43
1:B:332:ASN:HD22	2:C:258:ARG:HH12	1.66	0.43
1:B:411:ARG:HB2	1:B:411:ARG:CZ	2.49	0.43
2:C:139:MET:HE3	2:C:139:MET:HB3	1.81	0.43
2:C:139:MET:SD	2:C:237:MET:HE2	2.59	0.43
2:C:296:ASN:ND2	35:C:501:ATP:O3G	2.50	0.43
4:c:32:TYR:HE1	4:c:206:ASN:HD22	1.65	0.43
5:G:12:HIS:HB2	5:G:15:ILE:HG12	1.99	0.43
6:H:108:ALA:O	6:H:112:GLN:HG3	2.19	0.43
6:H:189:HIS:HB3	6:H:233:ILE:HD11	2.01	0.43
7:I:90:LEU:HA	7:I:90:LEU:HD23	1.81	0.43
8:J:16:LEU:HD23	8:J:16:LEU:HA	1.77	0.43
13:O:31:CYS:HA	14:P:131:MET:HE1	2.00	0.43
13:O:197:THR:OG1	13:O:198:ARG:N	2.51	0.43
15:Q:108:ASP:HB3	15:Q:111:GLU:HG2	2.00	0.43
16:R:113:TYR:O	16:R:120:ARG:HA	2.19	0.43
19:X:346:GLN:CD	26:W:408:ARG:HD2	2.43	0.43
19:X:380:GLN:OE1	20:Y:315:THR:OG1	2.35	0.43
19:X:394:ASP:HB2	20:Y:365:GLN:OE1	2.19	0.43
19:X:394:ASP:N	19:X:394:ASP:OD1	2.50	0.43
24:d:277:LYS:HA	24:d:277:LYS:HD3	1.77	0.43
24:d:287:ALA:O	24:d:291:LEU:HB2	2.19	0.43
25:f:211:ILE:O	25:f:214:VAL:HG22	2.19	0.43
25:f:281:ILE:HG13	25:f:284:SER:HB3	2.01	0.43
25:f:315:GLU:O	25:f:319:GLU:HG3	2.19	0.43
27:V:172:VAL:HA	27:V:175:MET:CE	2.49	0.43
27:V:191:LEU:HD11	27:V:210:CYS:SG	2.59	0.43
29:A:230:ALA:HB1	29:A:237:PHE:HB2	2.01	0.43
29:A:305:GLN:O	29:A:309:PHE:HB3	2.18	0.43
30:F:421:MET:SD	30:F:422:GLU:N	2.92	0.43
31:E:34:LYS:HD3	31:E:34:LYS:HA	1.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:U:516:LEU:HD23	32:U:532:MET:HG2	2.01	0.43
1:B:82:GLN:O	1:B:86:LYS:HB2	2.19	0.43
3:D:259:PRO:HB3	3:D:304:ASN:HB3	2.00	0.43
5:G:45:LYS:HZ3	5:G:45:LYS:H	1.66	0.43
5:G:55:LYS:HZ1	5:G:57:PRO:HA	1.84	0.43
5:G:69:LEU:HB3	5:G:79:VAL:HG23	2.00	0.43
9:K:24:VAL:O	9:K:28:ILE:HG12	2.19	0.43
9:K:81:LEU:HD23	9:K:84:ASP:HB2	2.01	0.43
9:K:230:THR:HG22	9:K:231:LYS:H	1.84	0.43
10:L:62:LYS:NZ	30:F:439:ALA:O	2.45	0.43
11:M:28:LYS:HA	11:M:31:GLU:OE2	2.19	0.43
11:M:227:VAL:HG22	11:M:228:PRO:O	2.19	0.43
13:O:61:SER:O	13:O:65:LEU:HD13	2.19	0.43
15:Q:60:ILE:HD13	15:Q:60:ILE:HA	1.81	0.43
17:S:113:LEU:HD23	17:S:113:LEU:HA	1.82	0.43
18:T:15:LYS:HE3	18:T:122:LEU:HB2	2.01	0.43
20:Y:113:ARG:HG3	20:Y:113:ARG:O	2.19	0.43
21:Z:264:SER:O	21:Z:265:LEU:C	2.62	0.43
22:a:68:GLU:C	22:a:70:ARG:H	2.27	0.43
22:a:293:PHE:HE1	22:a:331:VAL:HG23	1.83	0.43
24:d:210:THR:O	24:d:214:ARG:HG2	2.19	0.43
25:f:230:CYS:HB3	25:f:232:TYR:CE1	2.54	0.43
25:f:456:ARG:HD3	25:f:492:SER:OG	2.19	0.43
25:f:817:VAL:HG23	25:f:818:LEU:H	1.83	0.43
26:W:208:LYS:HA	26:W:208:LYS:HD2	1.76	0.43
26:W:217:GLU:O	26:W:223:LYS:HE2	2.18	0.43
27:V:443:ARG:NH2	27:V:444:ASP:OD1	2.51	0.43
29:A:363:SER:OG	29:A:402:LYS:O	2.31	0.43
30:F:227:GLY:HA3	30:F:354:PHE:HB2	2.01	0.43
30:F:251:LEU:N	30:F:284:PHE:O	2.41	0.43
33:g:242:ASP:O	33:g:246:GLN:HG3	2.19	0.43
34:u:178:TYR:C	34:u:178:TYR:CD2	2.97	0.43
2:C:195:GLY:HA2	2:C:198:LEU:HB3	2.00	0.42
3:D:79:VAL:O	3:D:82:ILE:HG22	2.19	0.42
4:c:141:VAL:HG12	4:c:203:ILE:HD12	2.01	0.42
6:H:168:VAL:O	6:H:172:THR:HG23	2.19	0.42
9:K:171:GLY:O	9:K:174:SER:OG	2.36	0.42
9:K:239:LYS:HE2	9:K:239:LYS:HB3	1.77	0.42
10:L:79:ALA:O	10:L:83:LEU:HD23	2.19	0.42
12:N:149:LYS:HZ3	12:N:153:LEU:HB2	1.82	0.42
16:R:86:MET:HA	16:R:89:GLN:HE22	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:S:17:GLY:HA3	17:S:20:PHE:CD1	2.54	0.42
18:T:108:ASN:OD1	18:T:110:MET:HB2	2.19	0.42
18:T:138:ALA:N	18:T:147:GLN:OE1	2.52	0.42
20:Y:25:LEU:HB3	20:Y:31:HIS:HD2	1.84	0.42
20:Y:167:LEU:O	20:Y:170:GLU:HG2	2.19	0.42
20:Y:205:VAL:HA	20:Y:219:PHE:HE1	1.84	0.42
21:Z:144:VAL:HB	21:Z:151:THR:HA	2.01	0.42
21:Z:211:TYR:CE1	26:W:449:GLU:HG3	2.54	0.42
25:f:255:VAL:HA	25:f:258:LYS:HD3	2.00	0.42
27:V:435:GLU:OE2	27:V:453:HIS:ND1	2.45	0.42
29:A:306:LEU:HD13	29:A:306:LEU:HA	1.83	0.42
32:U:583:MET:SD	32:U:605:VAL:HG11	2.59	0.42
33:g:311:MET:HG2	33:g:318:LEU:HD21	2.00	0.42
5:G:115:CYS:SG	5:G:154:CYS:HB2	2.59	0.42
10:L:147:THR:HG22	10:L:153:TYR:HB3	2.01	0.42
12:N:143:TYR:HA	12:N:155:PHE:CE2	2.54	0.42
13:O:138:PHE:O	13:O:142:PHE:HB3	2.18	0.42
19:X:57:LEU:HD21	19:X:65:GLU:C	2.44	0.42
20:Y:117:LYS:HD3	20:Y:147:ILE:HG21	2.01	0.42
20:Y:288:PHE:C	20:Y:290:PRO:HD2	2.44	0.42
21:Z:118:ASN:OD1	21:Z:118:ASN:N	2.51	0.42
21:Z:202:ASN:HD21	22:a:361:LYS:HE2	1.84	0.42
23:b:29:GLN:O	23:b:33:VAL:HG13	2.19	0.42
24:d:120:LYS:O	24:d:124:LEU:HG	2.19	0.42
25:f:331:LEU:O	25:f:335:ARG:HG3	2.19	0.42
26:W:301:LYS:HG2	26:W:324:TYR:CE2	2.54	0.42
29:A:145:ASN:N	33:g:277:ASP:OD2	2.46	0.42
30:F:144:LYS:HB3	30:F:144:LYS:HE3	1.74	0.42
30:F:370:SER:O	30:F:373:MET:HB2	2.19	0.42
32:U:206:MET:HE3	32:U:206:MET:HB3	1.89	0.42
32:U:709:PHE:O	32:U:712:LEU:HB3	2.18	0.42
32:U:737:LEU:HD12	32:U:737:LEU:HA	1.81	0.42
32:U:904:LYS:HG3	32:U:905:PRO:HD2	2.01	0.42
33:g:213:GLY:O	33:g:214:PRO:C	2.62	0.42
3:D:383:GLY:HA3	31:E:164:ILE:HG21	2.01	0.42
4:c:120:CYS:SG	4:c:156:VAL:HG12	2.59	0.42
6:H:75:VAL:HG12	6:H:76:TYR:H	1.84	0.42
7:I:160:LYS:H	7:I:160:LYS:HG2	1.64	0.42
11:M:56:LYS:H	11:M:56:LYS:HD2	1.84	0.42
14:P:57:ALA:O	14:P:61:GLN:HG2	2.19	0.42
14:P:84:PRO:HB2	14:P:120:PHE:CD2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:R:41:LEU:HD13	16:R:42:LEU:N	2.35	0.42
16:R:51:ASP:OD2	17:S:100:ARG:NH2	2.52	0.42
19:X:177:TYR:HB3	19:X:186:ALA:HB2	2.01	0.42
19:X:355:LYS:HE2	19:X:355:LYS:HB2	1.92	0.42
20:Y:26:LEU:O	20:Y:29:PRO:HD2	2.19	0.42
20:Y:96:GLY:O	20:Y:130:LYS:NZ	2.50	0.42
22:a:4:VAL:HB	22:a:5:PRO:HD3	2.01	0.42
22:a:184:ASP:OD1	22:a:184:ASP:N	2.52	0.42
25:f:521:ALA:O	25:f:525:ILE:HG12	2.19	0.42
25:f:703:ARG:HD3	25:f:785:ARG:NH2	2.35	0.42
25:f:803:PHE:C	25:f:805:ASP:H	2.27	0.42
26:W:359:VAL:HG22	26:W:382:LEU:HB2	2.00	0.42
27:V:182:LYS:O	27:V:186:LYS:HG2	2.19	0.42
29:A:170:PRO:O	29:A:231:ASN:ND2	2.50	0.42
30:F:205:PRO:HB3	30:F:212:PHE:CE2	2.54	0.42
31:E:119:VAL:HA	31:E:122:MET:HE2	1.99	0.42
32:U:411:ILE:HG22	32:U:412:HIS:ND1	2.34	0.42
2:C:313:ARG:O	2:C:315:ILE:HG13	2.19	0.42
3:D:124:LEU:HD12	3:D:124:LEU:HA	1.80	0.42
3:D:228:ILE:HD11	3:D:253:LEU:HD22	2.01	0.42
4:c:27:THR:HG21	4:c:183:HIS:HE1	1.84	0.42
4:c:97:ASP:OD2	4:c:97:ASP:C	2.62	0.42
8:J:8:THR:HB	9:K:135:ARG:HB3	2.02	0.42
8:J:224:GLU:OE1	8:J:224:GLU:N	2.45	0.42
10:L:38:LEU:HD13	10:L:158:ALA:HB2	2.01	0.42
11:M:184:MET:HE3	11:M:184:MET:HB3	1.74	0.42
11:M:193:VAL:O	11:M:196:ILE:HG22	2.20	0.42
12:N:103:TRP:CZ2	12:N:181:GLU:HG2	2.55	0.42
13:O:24:MET:HE3	13:O:24:MET:HA	2.01	0.42
15:Q:155:ARG:O	15:Q:159:LEU:HG	2.19	0.42
16:R:104:TRP:HA	16:R:109:PRO:HA	2.01	0.42
17:S:144:MET:HG3	17:S:186:ASP:OD1	2.19	0.42
19:X:380:GLN:HB2	20:Y:311:TYR:CE1	2.54	0.42
20:Y:134:LEU:HA	20:Y:137:ARG:HH11	1.83	0.42
22:a:65:SER:HA	22:a:68:GLU:HG2	2.00	0.42
22:a:109:GLU:HB2	22:a:151:VAL:HG21	2.02	0.42
22:a:153:SER:O	22:a:156:TYR:HD2	2.03	0.42
25:f:493:ASN:HA	25:f:525:ILE:HG22	2.01	0.42
25:f:530:CYS:HB3	25:f:533:ASP:OD1	2.19	0.42
27:V:134:PHE:CD1	27:V:187:ILE:HD11	2.54	0.42
29:A:119:ALA:HB1	30:F:127:SER:OG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:165:GLN:HG3	29:A:165:GLN:H	1.66	0.42
30:F:206:MET:O	30:F:209:LYS:NZ	2.52	0.42
30:F:250:LYS:NZ	30:F:286:ASP:OD2	2.36	0.42
30:F:406:ILE:HA	30:F:406:ILE:HD13	1.86	0.42
32:U:90:VAL:HG13	32:U:101:ILE:HD11	2.00	0.42
32:U:641:SER:OG	32:U:675:MET:HE2	2.19	0.42
32:U:701:ILE:H	32:U:701:ILE:HG13	1.57	0.42
32:U:757:MET:N	32:U:758:PRO:HD2	2.34	0.42
34:u:131:ASN:HD21	34:u:133:ALA:HB3	1.83	0.42
1:B:404:LEU:HD23	1:B:404:LEU:HA	1.79	0.42
2:C:214:VAL:HG21	2:C:234:LEU:HD22	2.00	0.42
5:G:17:SER:HB3	5:G:21:ARG:O	2.20	0.42
5:G:153:LYS:O	5:G:160:TYR:HA	2.19	0.42
5:G:191:PHE:O	5:G:194:THR:OG1	2.35	0.42
8:J:47:LYS:HE2	8:J:207:GLU:HG2	2.01	0.42
12:N:90:TYR:O	12:N:94:LEU:N	2.52	0.42
13:O:210:ALA:HB3	14:P:201:LYS:HB3	2.01	0.42
14:P:52:GLY:O	14:P:53:LEU:HD13	2.19	0.42
15:Q:60:ILE:HG21	15:Q:84:THR:HG22	2.01	0.42
17:S:11:THR:N	17:S:26:ASP:OD1	2.51	0.42
17:S:36:HIS:CD2	18:T:132:TYR:HE2	2.38	0.42
19:X:338:VAL:HG11	19:X:350:ILE:HD11	2.01	0.42
19:X:397:TYR:HA	19:X:400:ALA:HB3	2.02	0.42
19:X:421:LEU:C	21:Z:283:ARG:HH22	2.27	0.42
20:Y:13:LYS:O	20:Y:146:ARG:NE	2.52	0.42
21:Z:37:GLY:HA3	21:Z:95:TYR:CZ	2.54	0.42
21:Z:248:ALA:O	21:Z:252:LYS:HG3	2.19	0.42
22:a:252:LYS:HA	22:a:255:TRP:CE2	2.55	0.42
22:a:305:ASN:OD1	22:a:305:ASN:N	2.52	0.42
25:f:15:GLN:HA	25:f:18:ALA:HB3	2.01	0.42
25:f:108:GLU:O	25:f:112:ASN:ND2	2.52	0.42
25:f:384:ALA:HB2	25:f:419:LEU:HB3	2.01	0.42
26:W:84:ASN:HD21	26:W:123:ARG:NH2	2.18	0.42
26:W:294:LYS:HA	26:W:297:GLU:OE2	2.20	0.42
27:V:345:ARG:HG3	28:e:43:TRP:CD2	2.54	0.42
29:A:142:VAL:HG23	29:A:143:ASP:O	2.20	0.42
29:A:363:SER:OG	29:A:363:SER:O	2.37	0.42
30:F:229:PRO:HA	37:F:501:ADP:O3B	2.19	0.42
31:E:281:ARG:HA	31:E:281:ARG:HE	1.84	0.42
32:U:78:LEU:O	32:U:82:LEU:HG	2.20	0.42
32:U:183:LEU:HD23	32:U:183:LEU:HA	1.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:26:SER:O	2:C:29:GLU:HG3	2.19	0.42
3:D:294:ASN:O	3:D:298:GLY:HA3	2.19	0.42
3:D:392:TYR:HE2	26:W:208:LYS:HD3	1.83	0.42
7:I:50:ARG:HH22	7:I:166:ASN:ND2	2.18	0.42
11:M:43:ASP:OD1	11:M:43:ASP:N	2.52	0.42
11:M:67:PHE:HB3	11:M:92:ARG:NH2	2.35	0.42
13:O:21:THR:HG22	13:O:26:VAL:HG23	2.01	0.42
14:P:103:TYR:HA	15:Q:93:ARG:NH2	2.34	0.42
16:R:7:LYS:NZ	16:R:111:LEU:HB3	2.35	0.42
17:S:57:PHE:HB2	17:S:105:TYR:CD2	2.54	0.42
19:X:154:LEU:HD11	19:X:170:GLN:HG2	2.01	0.42
19:X:338:VAL:C	19:X:340:GLU:N	2.78	0.42
21:Z:26:ILE:HD13	21:Z:26:ILE:HA	1.88	0.42
22:a:73:PRO:HB2	22:a:110:ALA:HB2	2.01	0.42
22:a:135:ILE:HG12	22:a:158:LEU:HG	2.01	0.42
22:a:355:PHE:O	22:a:358:THR:HG22	2.19	0.42
23:b:109:ILE:CG1	23:b:138:VAL:HG23	2.50	0.42
24:d:337:THR:HG22	24:d:338:THR:HG23	2.02	0.42
24:d:340:PRO:HG2	24:d:344:LEU:HD21	2.01	0.42
25:f:119:LYS:HE3	25:f:123:ALA:HB2	2.02	0.42
25:f:351:THR:HG23	25:f:356:ASN:HD22	1.84	0.42
25:f:353:LEU:HD21	25:f:355:ASN:HB3	2.02	0.42
25:f:637:LYS:HB3	25:f:678:LEU:HB2	2.00	0.42
28:e:19:PHE:HD2	28:e:22:PHE:HE2	1.68	0.42
29:A:327:LEU:HD22	29:A:327:LEU:H	1.85	0.42
30:F:96:LEU:HD11	30:F:145:LEU:HB3	2.01	0.42
30:F:185:TYR:OH	30:F:195:ILE:HG21	2.20	0.42
30:F:235:LEU:HD13	37:F:501:ADP:H2'	2.01	0.42
31:E:178:THR:HG22	31:E:178:THR:O	2.19	0.42
32:U:615:ARG:O	32:U:619:VAL:HG23	2.20	0.42
2:C:31:LEU:HD11	3:D:48:GLN:HG3	2.01	0.42
3:D:349:THR:HA	3:D:352:MET:HG2	2.02	0.42
4:c:302:ALA:O	4:c:306:THR:HG23	2.20	0.42
5:G:119:ALA:HB1	5:G:158:GLY:O	2.19	0.42
6:H:98:TYR:O	6:H:102:GLN:N	2.41	0.42
8:J:212:ARG:O	8:J:214:ASP:N	2.51	0.42
9:K:97:GLN:HB3	16:R:61:ARG:NE	2.35	0.42
9:K:236:GLU:HA	9:K:239:LYS:HE3	2.00	0.42
10:L:41:LYS:HE2	10:L:41:LYS:HB2	1.74	0.42
10:L:189:LYS:HA	10:L:189:LYS:HD3	1.73	0.42
11:M:215:TRP:CH2	11:M:227:VAL:HG23	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:R:161:TYR:CE2	16:R:195:LEU:HB3	2.53	0.42
16:R:177:TYR:HE1	16:R:186:ARG:HB2	1.85	0.42
19:X:46:LYS:HE2	19:X:46:LYS:HB2	1.80	0.42
19:X:286:ALA:HB1	19:X:309:TYR:HE1	1.83	0.42
20:Y:26:LEU:HD13	20:Y:32:ARG:NH1	2.35	0.42
20:Y:178:ASN:OD1	20:Y:204:THR:HG21	2.20	0.42
25:f:288:VAL:O	25:f:292:LYS:N	2.38	0.42
25:f:515:ALA:O	25:f:518:THR:OG1	2.28	0.42
25:f:754:LYS:HD3	25:f:754:LYS:HA	1.71	0.42
26:W:363:ILE:HG23	26:W:413:ILE:HD11	2.02	0.42
29:A:144:ARG:NH1	33:g:169:ILE:O	2.50	0.42
29:A:262:GLU:O	29:A:266:THR:HG23	2.19	0.42
30:F:189:GLY:O	37:F:501:ADP:N6	2.53	0.42
31:E:351:GLY:O	31:E:354:ALA:HB3	2.20	0.42
32:U:108:TYR:CD2	32:U:134:VAL:HG11	2.55	0.42
32:U:461:LEU:HD23	32:U:461:LEU:HA	1.85	0.42
32:U:658:ILE:HD11	32:U:767:THR:HG21	2.01	0.42
32:U:923:GLU:H	32:U:923:GLU:CD	2.27	0.42
33:g:188:PHE:CE2	33:g:222:LEU:HD22	2.54	0.42
34:u:204:MET:CE	34:u:208:GLU:HB2	2.49	0.42
1:B:213:GLU:HB3	1:B:214:MET:HE2	2.02	0.42
2:C:297:ARG:NH1	3:D:274:ARG:HD2	2.34	0.42
5:G:131:MET:HE1	11:M:124:LEU:HD13	2.02	0.42
6:H:4:ARG:HE	6:H:4:ARG:HB3	1.70	0.42
6:H:58:ASP:OD2	6:H:58:ASP:C	2.62	0.42
17:S:6:VAL:HG22	17:S:57:PHE:CE2	2.55	0.42
17:S:22:ILE:CG2	17:S:195:ILE:HD11	2.50	0.42
20:Y:38:ARG:HE	20:Y:38:ARG:N	2.17	0.42
20:Y:131:THR:HG22	20:Y:132:VAL:H	1.83	0.42
22:a:76:LEU:O	22:a:80:ILE:HG12	2.19	0.42
25:f:585:GLU:HG2	25:f:587:PHE:HB3	2.01	0.42
25:f:591:ALA:O	25:f:595:VAL:HG12	2.20	0.42
25:f:676:GLY:HA2	25:f:714:SER:CB	2.39	0.42
25:f:741:LEU:HD12	25:f:792:ALA:HB1	2.00	0.42
26:W:273:TYR:CE1	26:W:340:VAL:HG11	2.54	0.42
26:W:414:ASN:HB3	26:W:415:PHE:H	1.59	0.42
28:e:37:HIS:CD2	28:e:39:TRP:H	2.38	0.42
32:U:588:MET:SD	32:U:764:LEU:HD22	2.59	0.42
32:U:654:MET:HE3	32:U:654:MET:HB3	1.84	0.42
34:u:137:CYS:SG	34:u:140:GLU:HB3	2.59	0.42
3:D:349:THR:HG22	3:D:352:MET:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:c:170:LEU:HB3	4:c:172:HIS:CE1	2.55	0.42
5:G:45:LYS:HG3	5:G:188:ASP:O	2.20	0.42
7:I:176:LYS:HE2	8:J:52:LYS:HB2	2.01	0.42
7:I:245:ALA:O	7:I:248:GLU:HG3	2.19	0.42
9:K:69:GLU:HB3	9:K:226:PHE:CD1	2.55	0.42
12:N:35:THR:OG1	12:N:43:CYS:SG	2.56	0.42
19:X:226:LYS:HE3	19:X:226:LYS:HB3	1.83	0.42
20:Y:73:MET:HE3	20:Y:73:MET:N	2.32	0.42
20:Y:178:ASN:HD21	20:Y:208:PHE:HE1	1.68	0.42
21:Z:211:TYR:HE1	26:W:449:GLU:HG3	1.84	0.42
24:d:179:LYS:HB3	24:d:182:LEU:HD22	2.00	0.42
24:d:223:ASN:HD22	24:d:226:ILE:HG12	1.85	0.42
29:A:213:LEU:HD22	29:A:214:LEU:N	2.34	0.42
32:U:416:GLU:OE2	32:U:453:HIS:ND1	2.44	0.42
34:u:200:LEU:HD23	34:u:200:LEU:HA	1.88	0.42
1:B:106:PRO:HG3	2:C:121:TYR:CD2	2.55	0.42
2:C:146:SER:O	2:C:202:ALA:HA	2.20	0.42
3:D:50:GLU:O	3:D:54:LEU:HD23	2.20	0.42
4:c:48:GLY:HA3	4:c:53:VAL:HG11	2.02	0.42
4:c:102:THR:HG21	21:Z:55:ALA:HB3	2.02	0.42
5:G:101:TRP:HE1	5:G:108:GLU:C	2.28	0.42
5:G:148:GLY:O	5:G:150:GLN:NE2	2.52	0.42
6:H:52:GLN:N	6:H:52:GLN:OE1	2.53	0.42
10:L:230:SER:O	10:L:233:LEU:HG	2.20	0.42
11:M:53:VAL:HG13	11:M:208:ALA:HB1	2.02	0.42
13:O:195:LYS:HA	13:O:195:LYS:HD2	1.86	0.42
14:P:22:ILE:HD12	14:P:22:ILE:HA	1.85	0.42
14:P:98:LYS:NZ	14:P:103:TYR:H	2.16	0.42
17:S:166:LEU:HD12	17:S:171:ALA:HB2	2.00	0.42
19:X:59:LYS:HD3	19:X:59:LYS:HA	1.75	0.42
21:Z:257:MET:HE1	27:V:476:PHE:CZ	2.55	0.42
22:a:112:ILE:CG1	22:a:141:MET:HE1	2.50	0.42
22:a:160:SER:O	22:a:163:TYR:HB3	2.20	0.42
25:f:72:ARG:HA	25:f:72:ARG:HD2	1.87	0.42
25:f:438:ASP:OD1	25:f:476:THR:OG1	2.32	0.42
25:f:582:VAL:HA	25:f:588:ARG:HD3	2.02	0.42
27:V:121:PHE:HD2	27:V:128:ARG:CZ	2.32	0.42
30:F:391:PHE:HZ	30:F:427:VAL:HG21	1.85	0.42
31:E:57:VAL:O	31:E:74:THR:HG23	2.20	0.42
31:E:64:LEU:HD23	31:E:64:LEU:HA	1.81	0.42
31:E:84:ARG:HH21	31:E:87:LEU:HD13	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:U:587:ALA:HB2	32:U:621:SER:CB	2.50	0.42
32:U:725:MET:H	32:U:725:MET:HG2	1.67	0.42
32:U:763:VAL:O	32:U:767:THR:HG23	2.20	0.42
1:B:59:ARG:HD3	25:f:184:LEU:HD21	2.02	0.41
1:B:374:LEU:HB3	1:B:378:VAL:HG11	2.00	0.41
2:C:28:ILE:HG21	3:D:43:ARG:HH21	1.85	0.41
2:C:242:ALA:HB1	2:C:243:PRO:HD2	2.02	0.41
3:D:392:TYR:HE1	31:E:161:ARG:HG2	1.85	0.41
5:G:43:ARG:NH1	5:G:164:LYS:HA	2.35	0.41
5:G:234:GLU:O	5:G:238:HIS:ND1	2.44	0.41
8:J:68:ASN:ND2	8:J:102:VAL:O	2.39	0.41
10:L:98:VAL:HA	18:T:94:ARG:HG3	2.01	0.41
11:M:27:MET:CE	11:M:153:PRO:HG2	2.50	0.41
11:M:27:MET:HE1	11:M:152:ASP:OD1	2.20	0.41
11:M:220:THR:O	11:M:221:ASN:ND2	2.53	0.41
12:N:79:ALA:O	12:N:83:PHE:HD1	2.02	0.41
16:R:19:ARG:HD3	16:R:170:SER:C	2.45	0.41
18:T:125:VAL:HG22	18:T:131:ALA:HB2	2.02	0.41
19:X:212:MET:HE2	19:X:212:MET:HB3	1.81	0.41
19:X:245:PRO:O	19:X:248:ILE:HG22	2.20	0.41
20:Y:49:ASN:HB3	20:Y:113:ARG:O	2.20	0.41
20:Y:97:GLU:H	20:Y:97:GLU:HG2	1.69	0.41
20:Y:137:ARG:HB3	20:Y:163:LYS:HZ3	1.85	0.41
23:b:25:ARG:HD2	23:b:25:ARG:HA	1.79	0.41
23:b:100:ARG:NH1	23:b:102:GLY:O	2.53	0.41
26:W:144:ARG:HH12	26:W:183:VAL:HG12	1.84	0.41
27:V:280:ALA:HB3	27:V:285:TRP:CD1	2.55	0.41
29:A:192:GLU:HG2	29:A:233:THR:HG22	2.02	0.41
29:A:255:ARG:HD3	29:A:259:GLU:HG3	2.02	0.41
30:F:153:VAL:HG23	30:F:159:LEU:C	2.44	0.41
30:F:155:LYS:C	30:F:158:TYR:HE1	2.28	0.41
30:F:223:VAL:HG13	30:F:223:VAL:O	2.20	0.41
31:E:46:ASP:HA	31:E:49:ALA:HB3	2.00	0.41
32:U:42:VAL:O	32:U:46:GLU:HG2	2.20	0.41
32:U:184:CYS:SG	32:U:185:MET:N	2.93	0.41
32:U:193:PHE:HD1	32:U:196:LYS:HE3	1.85	0.41
33:g:178:ARG:NE	33:g:280:TYR:OH	2.52	0.41
33:g:268:ALA:HB2	33:g:285:PHE:CE1	2.55	0.41
2:C:63:LEU:O	2:C:67:GLN:HG2	2.21	0.41
3:D:152:MET:HE2	3:D:152:MET:HB2	1.90	0.41
4:c:291:LEU:HD23	4:c:291:LEU:HA	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:81:THR:OG1	5:G:82:GLY:N	2.52	0.41
9:K:54:ILE:HD12	9:K:54:ILE:HA	1.76	0.41
9:K:67:ILE:HD11	9:K:216:GLU:HB3	2.01	0.41
9:K:110:GLU:O	9:K:114:GLN:HG2	2.19	0.41
9:K:125:GLU:HA	10:L:125:ARG:HE	1.84	0.41
15:Q:74:GLU:OE1	15:Q:75:LEU:HD12	2.20	0.41
21:Z:204:LYS:HD3	21:Z:204:LYS:HA	1.77	0.41
22:a:227:ASN:HA	22:a:231:GLN:OE1	2.19	0.41
25:f:290:VAL:HG12	25:f:321:MET:HG2	2.02	0.41
26:W:305:LEU:HD12	26:W:324:TYR:CD2	2.55	0.41
29:A:145:ASN:OD1	29:A:146:LYS:HG2	2.20	0.41
29:A:187:LEU:HD23	29:A:187:LEU:HA	1.78	0.41
32:U:703:CYS:O	32:U:706:VAL:HG12	2.20	0.41
1:B:386:ALA:HB3	1:B:423:LYS:HZ3	1.85	0.41
2:C:53:ASN:ND2	32:U:642:GLU:O	2.49	0.41
2:C:381:GLU:O	2:C:385:MET:HG3	2.19	0.41
4:c:279:ASP:OD1	4:c:279:ASP:N	2.52	0.41
5:G:71:LYS:HB2	5:G:227:PHE:HD2	1.86	0.41
9:K:15:PHE:HB3	10:L:24:TYR:HB3	2.01	0.41
9:K:100:TRP:O	9:K:104:ASN:HA	2.21	0.41
10:L:41:LYS:H	10:L:41:LYS:HD3	1.85	0.41
12:N:83:PHE:CD2	12:N:98:ILE:HG12	2.55	0.41
13:O:94:ILE:HA	14:P:99:ARG:NH1	2.30	0.41
15:Q:6:GLY:O	15:Q:129:PHE:HA	2.20	0.41
16:R:18:SER:OG	16:R:31:VAL:N	2.53	0.41
18:T:173:MET:HA	18:T:176:LEU:HD12	2.01	0.41
20:Y:81:LEU:HG	20:Y:110:TYR:OH	2.20	0.41
22:a:179:PHE:HE2	22:a:196:ARG:HH12	1.68	0.41
24:d:137:THR:HB	24:d:140:GLN:HB2	2.02	0.41
24:d:189:HIS:HA	24:d:192:LEU:HB2	2.02	0.41
25:f:257:ARG:O	25:f:261:ARG:N	2.52	0.41
25:f:729:MET:HA	25:f:732:VAL:HG12	2.03	0.41
27:V:69:THR:O	27:V:73:GLU:HG2	2.20	0.41
27:V:469:THR:C	27:V:471:GLU:H	2.28	0.41
28:e:18:GLU:HB2	28:e:20:GLU:CD	2.45	0.41
29:A:382:GLY:HA3	37:A:501:ADP:C8	2.54	0.41
30:F:133:PHE:CD1	31:E:111:LEU:HD11	2.55	0.41
30:F:387:CYS:HB3	30:F:424:ILE:HD12	2.02	0.41
31:E:148:VAL:HG13	31:E:149:ILE:CD1	2.50	0.41
32:U:429:LYS:HE2	32:U:429:LYS:HB2	1.88	0.41
33:g:254:TRP:HA	33:g:341:THR:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:109:ILE:HG12	5:G:114:LEU:HB2	2.01	0.41
5:G:189:TRP:HB3	5:G:194:THR:HG23	2.01	0.41
7:I:112:THR:O	7:I:116:ASP:OD2	2.38	0.41
7:I:214:ALA:HB2	7:I:227:VAL:HG12	2.03	0.41
8:J:47:LYS:HB2	8:J:207:GLU:HG3	2.03	0.41
8:J:103:THR:HG23	8:J:106:TYR:H	1.84	0.41
11:M:11:ALA:HB1	11:M:123:THR:O	2.20	0.41
11:M:194:ALA:HB2	11:M:235:ALA:HB1	2.01	0.41
12:N:34:LEU:HA	12:N:43:CYS:O	2.19	0.41
18:T:29:SER:HA	18:T:35:ARG:H	1.85	0.41
20:Y:48:ASN:HB3	20:Y:74:LYS:HG3	2.01	0.41
20:Y:292:TYR:O	20:Y:296:VAL:HG13	2.20	0.41
23:b:65:THR:HG21	23:b:70:ARG:HD3	2.03	0.41
25:f:42:GLU:HG2	25:f:92:VAL:HG21	2.02	0.41
25:f:651:GLY:O	25:f:654:VAL:HB	2.21	0.41
25:f:826:GLN:O	25:f:862:ILE:HA	2.21	0.41
26:W:74:CYS:SG	26:W:82:LEU:HD22	2.61	0.41
27:V:355:ARG:HE	28:e:27:TRP:HA	1.86	0.41
28:e:62:LYS:H	28:e:62:LYS:HG2	1.68	0.41
30:F:233:LYS:HD2	37:F:501:ADP:O1B	2.21	0.41
31:E:168:LYS:HD3	31:E:168:LYS:HA	1.94	0.41
31:E:195:PHE:CE2	31:E:197:LYS:HB2	2.55	0.41
31:E:280:ASN:OD1	31:E:280:ASN:N	2.54	0.41
31:E:326:ILE:HD13	31:E:364:GLN:OE1	2.20	0.41
32:U:59:PHE:HD1	32:U:87:LEU:HD13	1.85	0.41
33:g:250:LYS:HD2	33:g:345:LYS:HG3	2.01	0.41
1:B:363:ARG:HD2	1:B:363:ARG:HA	1.98	0.41
1:B:369:THR:HB	1:B:374:LEU:HD11	2.02	0.41
3:D:170:MET:H	3:D:340:GLN:HE22	1.68	0.41
4:c:75:MET:SD	4:c:87:VAL:HG12	2.60	0.41
6:H:130:PHE:O	6:H:151:PRO:HB3	2.21	0.41
8:J:155:ALA:H	9:K:63:SER:CB	2.34	0.41
9:K:141:LEU:HD23	9:K:141:LEU:HA	1.85	0.41
9:K:206:MET:O	29:A:369:ARG:NH2	2.51	0.41
10:L:50:LYS:HG3	10:L:211:SER:HB2	2.02	0.41
11:M:135:PHE:CZ	11:M:151:ILE:HB	2.56	0.41
13:O:37:ILE:HG23	13:O:60:SER:HA	2.01	0.41
19:X:121:LYS:HE2	19:X:121:LYS:HB2	1.78	0.41
19:X:338:VAL:O	19:X:340:GLU:N	2.48	0.41
22:a:21:VAL:HG12	22:a:24:ARG:HH22	1.85	0.41
22:a:229:ASP:OD1	22:a:230:ARG:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:b:157:VAL:HG21	23:b:170:LEU:HG	2.03	0.41
25:f:77:GLU:CD	25:f:82:ILE:HD13	2.45	0.41
25:f:534:VAL:O	25:f:538:ILE:HG23	2.21	0.41
25:f:759:LEU:HD22	25:f:761:MET:H	1.85	0.41
26:W:425:LEU:HD23	26:W:425:LEU:HA	1.65	0.41
28:e:51:ASP:HB3	28:e:54:ASN:HD21	1.85	0.41
29:A:203:ASN:O	30:F:374:ASN:ND2	2.54	0.41
29:A:264:ALA:HA	29:A:270:CYS:SG	2.60	0.41
31:E:305:ASN:N	31:E:308:ALA:HB3	2.34	0.41
32:U:122:GLU:OE1	32:U:122:GLU:N	2.53	0.41
32:U:696:ILE:HA	32:U:737:LEU:HD12	2.03	0.41
33:g:311:MET:HG2	33:g:318:LEU:CD2	2.51	0.41
2:C:399:MET:HE1	7:I:51:ASN:HB3	2.01	0.41
3:D:313:ARG:HH12	31:E:242:ARG:HD2	1.85	0.41
5:G:132:ARG:O	5:G:134:LEU:N	2.51	0.41
8:J:50:VAL:HA	8:J:54:GLN:NE2	2.36	0.41
8:J:147:THR:HA	8:J:152:THR:O	2.21	0.41
10:L:193:ARG:HG2	10:L:196:ARG:NH2	2.35	0.41
11:M:70:ASP:CG	11:M:99:ARG:HH21	2.27	0.41
15:Q:66:LEU:HA	15:Q:69:MET:SD	2.61	0.41
16:R:153:TYR:CZ	16:R:187:VAL:HG21	2.55	0.41
18:T:90:SER:O	18:T:93:THR:OG1	2.32	0.41
18:T:100:ARG:HB2	18:T:105:PRO:HB3	2.01	0.41
19:X:172:LEU:O	19:X:176:THR:HG23	2.19	0.41
19:X:213:GLN:NE2	19:X:217:ILE:HG12	2.35	0.41
19:X:347:ILE:HG12	19:X:383:GLY:O	2.21	0.41
20:Y:22:LEU:HD22	20:Y:22:LEU:HA	1.78	0.41
20:Y:65:ILE:HG12	20:Y:66:ASP:N	2.36	0.41
20:Y:72:LYS:H	20:Y:72:LYS:HG2	1.66	0.41
20:Y:137:ARG:HD2	20:Y:137:ARG:N	2.34	0.41
21:Z:144:VAL:HG23	21:Z:145:HIS:N	2.27	0.41
22:a:35:HIS:CE1	23:b:14:GLU:HB3	2.56	0.41
22:a:179:PHE:HE2	22:a:196:ARG:NH1	2.19	0.41
23:b:75:LEU:HD22	23:b:75:LEU:HA	1.90	0.41
23:b:91:ARG:HD2	23:b:130:ARG:HH22	1.85	0.41
25:f:631:LYS:N	25:f:631:LYS:HE2	2.35	0.41
25:f:817:VAL:HG23	25:f:818:LEU:N	2.35	0.41
26:W:143:ALA:HB1	26:W:147:LYS:HZ1	1.86	0.41
31:E:171:LEU:HD23	31:E:172:LEU:N	2.36	0.41
31:E:305:ASN:OD1	31:E:306:GLU:N	2.53	0.41
32:U:713:TYR:O	32:U:717:ILE:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:179:MET:HE3	33:g:179:MET:HB2	1.81	0.41
1:B:383:LEU:HD11	1:B:419:PHE:HB3	2.02	0.41
3:D:92:PHE:CE2	3:D:124:LEU:HG	2.55	0.41
3:D:267:ILE:HG22	3:D:311:THR:HB	2.02	0.41
4:c:112:TYR:HA	4:c:143:VAL:O	2.20	0.41
8:J:88:ARG:CZ	15:Q:70:ARG:HA	2.50	0.41
8:J:156:TRP:CD1	9:K:59:MET:HE1	2.55	0.41
8:J:159:ASN:OD1	8:J:160:ALA:N	2.52	0.41
8:J:204:LYS:HD3	8:J:204:LYS:HA	1.72	0.41
14:P:107:PRO:HD2	14:P:124:LEU:HB3	2.02	0.41
15:Q:88:LEU:HD23	15:Q:88:LEU:HA	1.95	0.41
15:Q:151:ILE:HG23	15:Q:155:ARG:HG3	2.02	0.41
15:Q:172:ILE:HG22	15:Q:173:LEU:HD22	2.02	0.41
17:S:57:PHE:CZ	18:T:128:LEU:HB3	2.55	0.41
18:T:107:TRP:HA	18:T:127:MET:HG2	2.02	0.41
22:a:156:TYR:O	22:a:160:SER:OG	2.26	0.41
22:a:284:ARG:CZ	22:a:285:PRO:HD2	2.51	0.41
23:b:26:LEU:HD22	23:b:80:PRO:HD3	2.02	0.41
23:b:56:ASN:N	23:b:83:LYS:O	2.42	0.41
25:f:382:ASN:HD22	25:f:388:ASP:HB2	1.86	0.41
26:W:38:GLY:O	26:W:39:ARG:NE	2.40	0.41
27:V:92:ARG:C	27:V:94:VAL:H	2.28	0.41
29:A:178:GLY:H	37:A:501:ADP:HN62	1.68	0.41
29:A:348:LEU:HD12	29:A:348:LEU:HA	1.87	0.41
30:F:66:LEU:CD2	31:E:33:LEU:HD13	2.38	0.41
30:F:283:ILE:HG22	30:F:328:VAL:HG23	2.03	0.41
31:E:84:ARG:HD3	31:E:108:MET:HE1	2.02	0.41
32:U:357:LYS:HE3	32:U:357:LYS:HB3	1.87	0.41
32:U:756:HIS:ND1	32:U:759:SER:OG	2.46	0.41
1:B:98:LYS:HG3	29:A:80:LEU:HD22	2.02	0.41
1:B:197:ILE:HG21	1:B:235:LEU:HD11	2.03	0.41
2:C:65:LEU:HD13	2:C:65:LEU:HA	1.87	0.41
4:c:304:LEU:O	4:c:308:VAL:HG13	2.21	0.41
5:G:41:ALA:HB2	5:G:50:ILE:HG22	2.02	0.41
5:G:80:MET:SD	5:G:87:SER:HB3	2.60	0.41
6:H:50:LYS:NZ	6:H:59:GLU:O	2.44	0.41
6:H:74:LEU:HD21	6:H:87:VAL:HG22	2.01	0.41
7:I:68:LEU:HG	7:I:72:MET:HB3	2.02	0.41
7:I:82:ASP:N	7:I:82:ASP:OD1	2.53	0.41
7:I:194:ILE:HG13	7:I:236:LEU:CD1	2.50	0.41
8:J:56:GLU:H	8:J:56:GLU:CD	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:142:LEU:HD12	9:K:142:LEU:HA	1.95	0.41
10:L:112:ILE:HD13	10:L:112:ILE:HA	1.64	0.41
13:O:147:GLU:HB3	13:O:150:GLU:HG2	2.03	0.41
13:O:179:SER:HB3	13:O:182:LYS:HB3	2.03	0.41
13:O:208:THR:OG1	14:P:165:GLU:OE1	2.36	0.41
14:P:88:MET:SD	14:P:89:SER:N	2.94	0.41
15:Q:56:PHE:HB2	15:Q:98:TYR:CD2	2.56	0.41
18:T:21:VAL:O	18:T:22:ILE:HD13	2.20	0.41
19:X:57:LEU:HD22	19:X:69:LEU:HD22	2.02	0.41
19:X:323:LEU:HD23	19:X:323:LEU:HA	1.78	0.41
19:X:346:GLN:OE1	26:W:408:ARG:HD2	2.20	0.41
19:X:405:GLN:O	19:X:408:SER:HB3	2.21	0.41
20:Y:44:ALA:HA	20:Y:49:ASN:ND2	2.29	0.41
20:Y:69:LEU:HA	20:Y:72:LYS:HE3	2.03	0.41
20:Y:124:PHE:CD2	20:Y:140:ILE:HD13	2.55	0.41
20:Y:188:CYS:HG	20:Y:291:HIS:CG	2.37	0.41
20:Y:231:LEU:HB2	20:Y:236:LEU:HB3	2.02	0.41
21:Z:208:ILE:HD13	26:W:441:LYS:NZ	2.36	0.41
22:a:126:GLY:HA3	22:a:129:GLN:HE22	1.84	0.41
22:a:280:MET:HA	22:a:283:THR:HG22	2.02	0.41
23:b:100:ARG:NE	23:b:107:MET:SD	2.93	0.41
24:d:269:ASP:HB3	24:d:302:TYR:OH	2.21	0.41
25:f:182:GLU:CD	25:f:182:GLU:N	2.77	0.41
25:f:631:LYS:O	25:f:635:LYS:HG2	2.21	0.41
26:W:55:ARG:HG2	26:W:95:SER:O	2.20	0.41
27:V:259:LEU:HD22	27:V:264:TYR:CE1	2.56	0.41
27:V:446:VAL:HG12	27:V:447:ILE:HG13	2.03	0.41
28:e:54:ASN:HA	28:e:57:ARG:NE	2.36	0.41
29:A:101:ILE:HG23	29:A:111:TYR:CE1	2.55	0.41
30:F:79:LYS:HA	30:F:82:VAL:HB	2.03	0.41
32:U:766:PHE:HB2	32:U:779:LEU:HB2	2.03	0.41
32:U:797:MET:HE1	32:U:881:PRO:CG	2.51	0.41
33:g:180:GLU:OE2	33:g:282:LYS:NZ	2.53	0.41
2:C:167:LEU:HB3	2:C:168:PRO:HD3	2.03	0.41
2:C:214:VAL:CG1	2:C:248:MET:HG2	2.51	0.41
2:C:338:LEU:HD13	2:C:338:LEU:HA	1.91	0.41
4:c:128:ASN:C	33:g:231:ARG:HH22	2.29	0.41
4:c:166:ASN:HA	4:c:169:VAL:HG22	2.03	0.41
4:c:233:ASP:OD2	26:W:426:ASN:ND2	2.39	0.41
4:c:234:TYR:CE2	26:W:425:LEU:HD13	2.56	0.41
4:c:257:LYS:HD2	4:c:257:LYS:HA	1.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:13:ILE:HG13	5:G:24:GLN:HG3	2.02	0.41
6:H:172:THR:O	6:H:176:LYS:HG3	2.20	0.41
8:J:16:LEU:HB3	8:J:19:VAL:HG23	2.03	0.41
8:J:43:LEU:HD22	8:J:62:ILE:HD11	2.03	0.41
8:J:96:LEU:HD23	15:Q:62:LYS:HD2	2.03	0.41
8:J:189:LYS:HA	8:J:232:ILE:HD11	2.03	0.41
9:K:21:LEU:HD21	10:L:126:ARG:CZ	2.51	0.41
10:L:92:CYS:SG	10:L:103:LEU:HD12	2.60	0.41
10:L:164:ARG:NH1	10:L:200:PRO:HD3	2.35	0.41
11:M:150:MET:HB3	11:M:160:TYR:CE1	2.56	0.41
11:M:182:LYS:HB2	11:M:182:LYS:HE2	1.80	0.41
11:M:201:HIS:ND1	11:M:203:GLU:OE2	2.43	0.41
14:P:87:LEU:O	14:P:91:VAL:HG13	2.20	0.41
14:P:162:HIS:O	14:P:166:THR:OG1	2.38	0.41
15:Q:65:GLN:O	15:Q:69:MET:HG3	2.21	0.41
16:R:26:ILE:HG21	16:R:29:GLN:NE2	2.36	0.41
16:R:122:SER:OG	16:R:123:GLY:N	2.54	0.41
18:T:72:ILE:O	18:T:76:LEU:HB2	2.21	0.41
18:T:141:TYR:HD1	18:T:141:TYR:HA	1.76	0.41
18:T:150:LEU:O	18:T:153:VAL:HG12	2.21	0.41
18:T:173:MET:SD	18:T:174:ARG:N	2.94	0.41
19:X:55:SER:O	19:X:59:LYS:HG2	2.20	0.41
20:Y:15:PRO:C	20:Y:17:LEU:N	2.77	0.41
20:Y:82:LYS:HD2	20:Y:82:LYS:HA	1.75	0.41
20:Y:145:LEU:HA	20:Y:157:ILE:HG12	2.02	0.41
20:Y:237:ARG:HG3	20:Y:238:GLU:OE1	2.21	0.41
20:Y:319:MET:HE3	20:Y:319:MET:HB2	1.98	0.41
22:a:34:TRP:O	22:a:38:THR:HG23	2.21	0.41
22:a:192:GLU:OE2	22:a:196:ARG:NH2	2.54	0.41
22:a:214:GLY:O	22:a:215:GLU:HB3	2.21	0.41
23:b:38:HIS:HB3	23:b:42:ARG:NH2	2.35	0.41
24:d:262:ILE:O	24:d:266:THR:OG1	2.31	0.41
24:d:262:ILE:HD12	24:d:262:ILE:HA	1.89	0.41
25:f:228:LYS:HG3	25:f:229:VAL:H	1.85	0.41
25:f:330:PHE:HE1	25:f:757:ASN:HB2	1.86	0.41
25:f:545:LYS:HD2	25:f:548:THR:H	1.86	0.41
25:f:655:LEU:HA	25:f:659:LEU:HB2	2.02	0.41
25:f:681:TYR:HE1	25:f:858:LYS:HB2	1.84	0.41
25:f:714:SER:C	25:f:716:ASP:H	2.27	0.41
25:f:862:ILE:HD11	25:f:876:HIS:HB3	2.03	0.41
26:W:51:GLU:OE2	26:W:63:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:247:TYR:HD2	26:W:270:VAL:HG22	1.85	0.41
29:A:97:ARG:HH12	29:A:251:GLY:HA3	1.86	0.41
29:A:328:ASP:O	29:A:332:MET:HE1	2.21	0.41
30:F:144:LYS:HD2	30:F:144:LYS:H	1.86	0.41
30:F:150:LEU:HB3	30:F:164:LEU:HD11	2.03	0.41
30:F:177:VAL:HG13	30:F:249:LEU:HD13	2.03	0.41
30:F:232:GLY:N	37:F:501:ADP:O1A	2.54	0.41
30:F:345:SER:HA	30:F:349:ASP:OD1	2.21	0.41
30:F:347:ARG:O	30:F:348:LEU:HD22	2.21	0.41
30:F:362:ARG:O	30:F:363:ALA:C	2.64	0.41
30:F:421:MET:O	30:F:424:ILE:HG12	2.20	0.41
32:U:240:ASP:O	32:U:242:LEU:N	2.53	0.41
32:U:368:ALA:HB1	32:U:731:ILE:HB	2.03	0.41
32:U:673:GLU:O	32:U:676:THR:OG1	2.37	0.41
1:B:48:LYS:NZ	29:A:56:LEU:HD22	2.35	0.41
2:C:111:ASN:OD1	2:C:111:ASN:N	2.54	0.41
3:D:390:ASN:ND2	26:W:172:GLU:OE1	2.54	0.41
3:D:417:TYR:OH	5:G:21:ARG:HG3	2.20	0.41
4:c:303:MET:HG2	4:c:303:MET:H	1.53	0.41
5:G:96:TYR:C	5:G:96:TYR:CD2	2.98	0.41
5:G:191:PHE:HE1	5:G:219:VAL:HG21	1.86	0.41
9:K:21:LEU:HD11	10:L:126:ARG:HH12	1.86	0.41
12:N:3:ILE:HG22	12:N:16:ALA:HB2	2.04	0.41
14:P:196:THR:HB	14:P:198:ARG:HE	1.85	0.41
15:Q:91:CYS:O	15:Q:94:SER:OG	2.38	0.41
16:R:46:ALA:HB3	16:R:98:GLY:O	2.21	0.41
17:S:27:THR:HB	17:S:40:SER:H	1.86	0.41
19:X:85:ALA:O	19:X:88:LEU:HG	2.21	0.41
19:X:124:PHE:N	19:X:124:PHE:CD2	2.89	0.41
19:X:240:ASP:O	19:X:242:ILE:HG12	2.20	0.41
20:Y:75:LYS:HA	20:Y:78:GLU:HG3	2.03	0.41
20:Y:220:VAL:HG11	20:Y:249:VAL:HB	2.01	0.41
21:Z:242:LEU:O	21:Z:244:GLU:N	2.41	0.41
21:Z:249:PHE:CE1	27:V:470:ARG:HB2	2.55	0.41
22:a:183:VAL:HG22	22:a:185:ILE:O	2.21	0.41
24:d:179:LYS:C	24:d:181:GLN:H	2.29	0.41
25:f:813:LYS:HD3	25:f:853:VAL:HG12	2.02	0.41
26:W:287:VAL:CG1	26:W:310:THR:HG22	2.51	0.41
29:A:111:TYR:CZ	29:A:125:LEU:HD21	2.55	0.41
31:E:144:GLU:OE1	31:E:297:ARG:NH2	2.53	0.41
32:U:381:THR:HA	32:U:412:HIS:ND1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:U:906:LEU:HD23	32:U:912:ILE:HD13	2.03	0.41
33:g:248:PHE:HB3	33:g:249:PRO:HA	2.02	0.41
1:B:207:HIS:HB2	1:B:209:GLU:OE1	2.22	0.40
1:B:435:PRO:HG2	1:B:438:LEU:HB2	2.03	0.40
2:C:97:VAL:HB	2:C:121:TYR:O	2.20	0.40
3:D:45:LYS:HD3	3:D:45:LYS:HA	1.87	0.40
3:D:300:ASP:N	3:D:300:ASP:OD1	2.45	0.40
4:c:132:SER:HB2	33:g:231:ARG:NH1	2.36	0.40
4:c:162:LEU:HD23	4:c:162:LEU:HA	1.88	0.40
5:G:132:ARG:HH21	11:M:124:LEU:HB3	1.86	0.40
8:J:227:LYS:HE2	8:J:227:LYS:HB2	1.89	0.40
8:J:227:LYS:O	8:J:231:GLU:HG3	2.21	0.40
13:O:39:PRO:O	13:O:183:LEU:HD12	2.21	0.40
17:S:38:ARG:HH12	18:T:155:GLU:HG2	1.86	0.40
17:S:74:MET:SD	17:S:75:TYR:N	2.94	0.40
19:X:407:MET:HE2	21:Z:266:ILE:HG23	2.02	0.40
20:Y:71:ASN:HA	20:Y:74:LYS:CE	2.49	0.40
20:Y:298:GLU:OE2	20:Y:342:ARG:NH1	2.23	0.40
21:Z:121:LEU:HD23	21:Z:122:VAL:N	2.36	0.40
21:Z:222:ILE:HD11	22:a:343:LEU:HD21	2.02	0.40
21:Z:225:GLN:HG2	21:Z:226:ILE:N	2.36	0.40
22:a:132:LYS:HB3	22:a:132:LYS:HE3	1.72	0.40
25:f:169:GLU:HB3	25:f:173:LEU:HD23	2.03	0.40
25:f:179:VAL:HG11	25:f:212:GLU:HG3	2.03	0.40
25:f:340:MET:HE3	25:f:340:MET:N	2.28	0.40
25:f:353:LEU:HG	25:f:355:ASN:H	1.86	0.40
25:f:672:LEU:HD13	25:f:708:ASP:CA	2.47	0.40
26:W:376:LYS:H	26:W:376:LYS:HG2	1.68	0.40
27:V:161:PRO:HA	27:V:164:GLU:CD	2.47	0.40
27:V:235:LEU:HA	27:V:250:LEU:HD13	2.02	0.40
27:V:435:GLU:OE1	27:V:451:ILE:HD13	2.21	0.40
28:e:60:LEU:HD12	28:e:60:LEU:HA	1.87	0.40
29:A:140:VAL:HB	29:A:149:ILE:HG23	2.03	0.40
30:F:245:LYS:HG2	30:F:245:LYS:HZ2	1.73	0.40
30:F:414:GLU:O	30:F:416:THR:HG23	2.21	0.40
1:B:80:ARG:HD2	1:B:81:ASN:OD1	2.20	0.40
1:B:129:SER:N	29:A:117:GLN:HE22	2.19	0.40
3:D:185:LEU:CD2	3:D:225:ALA:HB2	2.51	0.40
4:c:103:GLY:O	4:c:105:PRO:HD3	2.21	0.40
4:c:251:LEU:HD21	4:c:283:HIS:HB3	2.03	0.40
5:G:189:TRP:HB3	5:G:194:THR:CG2	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:13:PHE:HD1	6:H:13:PHE:HA	1.75	0.40
15:Q:42:ILE:HD12	15:Q:105:ALA:C	2.46	0.40
15:Q:86:ARG:HA	15:Q:86:ARG:HD2	1.72	0.40
16:R:34:VAL:HB	16:R:177:TYR:CE2	2.56	0.40
16:R:195:LEU:HA	16:R:195:LEU:HD23	1.81	0.40
18:T:84:SER:O	18:T:88:ILE:HD12	2.21	0.40
20:Y:336:ARG:NH1	28:e:44:ASP:OD1	2.53	0.40
21:Z:48:LEU:HD21	21:Z:92:VAL:HG11	2.02	0.40
22:a:80:ILE:O	22:a:83:VAL:HG12	2.21	0.40
24:d:339:ILE:HG22	24:d:341:SER:OG	2.21	0.40
25:f:131:MET:HB3	25:f:170:TRP:NE1	2.37	0.40
25:f:320:ILE:HB	25:f:325:GLN:HG2	2.02	0.40
25:f:632:LYS:HD2	25:f:633:GLU:N	2.36	0.40
27:V:72:LEU:HA	27:V:75:ILE:HD12	2.03	0.40
27:V:471:GLU:N	27:V:472:PRO:HD2	2.36	0.40
29:A:181:LYS:HA	29:A:184:ILE:HG22	2.04	0.40
30:F:92:ASN:OD1	30:F:92:ASN:N	2.54	0.40
30:F:95:GLU:HG2	30:F:123:VAL:CG1	2.51	0.40
30:F:250:LYS:O	30:F:251:LEU:HD13	2.21	0.40
31:E:372:ARG:NE	31:E:372:ARG:HA	2.36	0.40
32:U:268:LEU:HD12	32:U:268:LEU:HA	1.84	0.40
32:U:408:LEU:HD21	32:U:426:TYR:CE1	2.56	0.40
32:U:457:ILE:HD13	32:U:457:ILE:HA	1.82	0.40
1:B:102:LEU:HD12	1:B:102:LEU:HA	1.76	0.40
1:B:227:PRO:HD2	1:B:353:PHE:O	2.21	0.40
2:C:286:THR:HB	2:C:289:ILE:HG13	2.03	0.40
3:D:261:ILE:HA	3:D:306:LYS:O	2.21	0.40
3:D:351:LYS:HG2	31:E:163:GLY:HA2	2.03	0.40
4:c:44:HIS:CE1	4:c:74:ALA:HB1	2.56	0.40
6:H:89:ARG:HH11	6:H:89:ARG:HA	1.86	0.40
6:H:116:SER:O	6:H:119:GLN:HG3	2.20	0.40
6:H:222:THR:O	6:H:225:GLU:HG2	2.22	0.40
8:J:30:SER:HB3	8:J:61:LYS:NZ	2.35	0.40
8:J:134:VAL:HG12	8:J:144:LEU:HD12	2.04	0.40
9:K:155:HIS:HB3	9:K:165:CYS:SG	2.61	0.40
9:K:191:LEU:HA	9:K:191:LEU:HD23	1.84	0.40
13:O:212:LEU:HB2	14:P:199:THR:CG2	2.52	0.40
13:O:215:LYS:HD3	13:O:215:LYS:HA	1.95	0.40
14:P:12:MET:HE2	14:P:12:MET:HA	2.04	0.40
14:P:145:GLN:O	14:P:149:MET:HG2	2.22	0.40
16:R:7:LYS:HE3	16:R:124:ALA:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:R:50:ALA:HB2	17:S:127:VAL:HG13	2.04	0.40
18:T:51:LEU:HD21	18:T:67:LEU:HG	2.03	0.40
19:X:407:MET:HE3	21:Z:266:ILE:HA	2.03	0.40
21:Z:251:LEU:HD12	21:Z:251:LEU:HA	1.88	0.40
22:a:106:SER:C	22:a:108:ASP:H	2.29	0.40
25:f:66:LYS:HE2	25:f:66:LYS:HB2	1.96	0.40
25:f:233:LEU:HD12	25:f:234:THR:N	2.36	0.40
25:f:361:SER:O	25:f:361:SER:OG	2.36	0.40
25:f:369:ARG:HG3	25:f:740:ARG:HH11	1.86	0.40
25:f:632:LYS:HE3	25:f:632:LYS:HB3	1.98	0.40
25:f:670:MET:H	25:f:670:MET:CE	2.34	0.40
26:W:222:LEU:HA	26:W:225:LYS:HE2	2.02	0.40
26:W:436:MET:N	26:W:436:MET:SD	2.94	0.40
29:A:158:ASP:OD2	29:A:160:THR:OG1	2.39	0.40
29:A:163:MET:HE2	29:A:163:MET:C	2.45	0.40
29:A:168:GLU:O	29:A:236:CYS:HA	2.21	0.40
29:A:200:ARG:HB2	30:F:412:ALA:HB2	2.04	0.40
30:F:144:LYS:HB2	30:F:146:LYS:NZ	2.36	0.40
30:F:305:GLU:H	30:F:305:GLU:CD	2.27	0.40
32:U:234:GLU:O	32:U:238:LYS:HD3	2.21	0.40
33:g:207:LEU:HD23	33:g:219:PHE:CZ	2.56	0.40
34:u:221:THR:OG1	34:u:222:GLU:N	2.55	0.40
1:B:163:LEU:HD23	1:B:163:LEU:HA	1.90	0.40
2:C:364:THR:HA	3:D:196:ILE:CG1	2.52	0.40
4:c:65:TYR:CD1	4:c:65:TYR:N	2.89	0.40
4:c:234:TYR:HB2	26:W:426:ASN:OD1	2.22	0.40
5:G:54:LYS:HA	5:G:68:HIS:CE1	2.56	0.40
6:H:50:LYS:HE2	6:H:50:LYS:HB3	1.93	0.40
6:H:65:VAL:O	6:H:220:ARG:NH1	2.54	0.40
8:J:144:LEU:HB3	8:J:156:TRP:O	2.20	0.40
8:J:211:MET:HB2	8:J:217:LEU:HD22	2.02	0.40
9:K:123:PHE:HA	9:K:133:MET:O	2.21	0.40
10:L:61:LYS:NZ	10:L:64:LEU:HD13	2.37	0.40
11:M:124:LEU:HD12	11:M:125:TYR:N	2.37	0.40
12:N:28:ASN:HD21	13:O:122:LEU:HD21	1.87	0.40
12:N:191:GLY:O	12:N:194:ILE:HG12	2.21	0.40
14:P:45:MET:HB3	14:P:71:LEU:HD13	2.03	0.40
14:P:95:LEU:HA	14:P:98:LYS:HE3	2.03	0.40
15:Q:49:GLU:HB3	15:Q:99:HIS:O	2.21	0.40
16:R:95:LEU:HD12	16:R:95:LEU:HA	1.84	0.40
18:T:7:THR:HG22	18:T:8:GLY:H	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:99:ARG:HB3	18:T:104:ASN:O	2.20	0.40
19:X:111:LEU:HD13	19:X:111:LEU:HA	1.93	0.40
19:X:158:LYS:HD2	19:X:158:LYS:HA	1.88	0.40
19:X:318:ILE:HD12	19:X:318:ILE:C	2.46	0.40
20:Y:351:ASN:HB2	27:V:416:ARG:NH2	2.36	0.40
24:d:148:LEU:HA	24:d:148:LEU:HD23	1.83	0.40
24:d:184:GLU:OE1	24:d:184:GLU:HA	2.21	0.40
25:f:157:GLU:OE1	25:f:157:GLU:N	2.55	0.40
25:f:293:GLN:HE22	25:f:296:PHE:HB3	1.85	0.40
25:f:395:GLY:O	25:f:399:LEU:HD23	2.22	0.40
25:f:664:GLU:H	25:f:668:ALA:HB3	1.86	0.40
25:f:682:GLY:C	25:f:688:ARG:HH22	2.30	0.40
25:f:824:ALA:HA	25:f:851:ASP:HA	2.03	0.40
25:f:858:LYS:C	25:f:860:LYS:H	2.28	0.40
26:W:86:ASN:O	26:W:89:LEU:HG	2.22	0.40
26:W:97:LEU:HD23	26:W:97:LEU:HA	1.84	0.40
26:W:312:MET:HG3	26:W:369:TYR:OH	2.22	0.40
28:e:51:ASP:HB3	28:e:54:ASN:OD1	2.22	0.40
29:A:243:SER:O	29:A:247:GLN:N	2.49	0.40
31:E:145:LEU:HA	31:E:148:VAL:HG12	2.02	0.40
31:E:334:LEU:O	31:E:372:ARG:NH2	2.55	0.40
32:U:9:ILE:O	32:U:12:LEU:HB2	2.21	0.40
32:U:418:GLU:HA	32:U:421:GLN:NE2	2.36	0.40
32:U:471:ASP:OD2	32:U:507:VAL:HB	2.21	0.40
33:g:155:LEU:HG	33:g:157:PHE:HD1	1.85	0.40
34:u:262:TYR:HD1	34:u:263:PHE:N	2.18	0.40
1:B:51:LEU:HD11	1:B:61:LYS:HG3	2.02	0.40
4:c:249:LEU:CD1	19:X:402:GLU:HG2	2.51	0.40
6:H:109:GLN:NE2	14:P:78:GLU:HA	2.37	0.40
7:I:140:ASP:HB2	7:I:146:GLN:NE2	2.35	0.40
8:J:132:LEU:HD22	8:J:144:LEU:HD21	2.03	0.40
8:J:183:THR:OG1	8:J:186:LEU:HG	2.22	0.40
9:K:92:ALA:HA	9:K:95:GLU:CD	2.46	0.40
10:L:125:ARG:NH1	10:L:125:ARG:HB3	2.37	0.40
11:M:67:PHE:O	11:M:75:MET:N	2.54	0.40
12:N:64:GLY:O	12:N:68:ILE:HG12	2.22	0.40
13:O:146:MET:HE1	13:O:150:GLU:C	2.47	0.40
17:S:118:LYS:HE2	17:S:118:LYS:HB2	1.93	0.40
18:T:176:LEU:O	18:T:180:ASP:N	2.55	0.40
19:X:102:ALA:HB3	19:X:105:GLN:CD	2.46	0.40
19:X:132:ARG:HD2	19:X:132:ARG:HA	1.97	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:X:143:TYR:HD2	19:X:180:LEU:HD11	1.87	0.40
21:Z:133:LEU:H	21:Z:133:LEU:HD23	1.86	0.40
22:a:196:ARG:HG2	22:a:196:ARG:NH1	2.37	0.40
23:b:147:GLU:O	23:b:150:THR:HG22	2.21	0.40
25:f:109:ILE:HD13	25:f:109:ILE:HA	1.86	0.40
25:f:273:ASN:HA	25:f:277:LEU:HB2	2.03	0.40
25:f:487:LEU:HA	25:f:524:MET:HE1	2.04	0.40
25:f:556:ARG:HE	25:f:786:GLN:HG3	1.86	0.40
25:f:566:HIS:CD2	25:f:577:LEU:HD11	2.57	0.40
25:f:757:ASN:HB3	25:f:810:ILE:CG2	2.51	0.40
26:W:61:VAL:O	26:W:65:ARG:HG2	2.21	0.40
26:W:218:ASN:OD1	26:W:218:ASN:N	2.55	0.40
27:V:92:ARG:HH11	27:V:95:LEU:HD13	1.85	0.40
28:e:52:PHE:O	28:e:56:LEU:HG	2.20	0.40
31:E:221:TYR:HE1	31:E:225:HIS:CD2	2.39	0.40
31:E:373:LYS:HA	31:E:373:LYS:HD3	1.84	0.40
32:U:427:LEU:HD12	32:U:428:PRO:O	2.20	0.40
32:U:554:LEU:HD23	32:U:554:LEU:HA	1.95	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	393/440 (89%)	354 (90%)	36 (9%)	3 (1%)	16	47
2	C	384/406 (95%)	354 (92%)	30 (8%)	0	100	100
3	D	373/418 (89%)	354 (95%)	18 (5%)	1 (0%)	36	67
4	c	276/424 (65%)	258 (94%)	18 (6%)	0	100	100
5	G	239/246 (97%)	228 (95%)	11 (5%)	0	100	100
6	H	230/234 (98%)	216 (94%)	14 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	I	246/261 (94%)	236 (96%)	10 (4%)	0	100	100
8	J	237/248 (96%)	219 (92%)	18 (8%)	0	100	100
9	K	236/241 (98%)	231 (98%)	5 (2%)	0	100	100
10	L	238/263 (90%)	227 (95%)	11 (5%)	0	100	100
11	M	240/255 (94%)	232 (97%)	8 (3%)	0	100	100
12	N	193/239 (81%)	185 (96%)	8 (4%)	0	100	100
13	O	218/277 (79%)	208 (95%)	10 (5%)	0	100	100
14	P	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
15	Q	197/201 (98%)	187 (95%)	10 (5%)	0	100	100
16	R	199/263 (76%)	195 (98%)	4 (2%)	0	100	100
17	S	211/241 (88%)	204 (97%)	7 (3%)	0	100	100
18	T	214/264 (81%)	204 (95%)	10 (5%)	0	100	100
19	X	377/422 (89%)	358 (95%)	17 (4%)	2 (0%)	24	57
20	Y	376/389 (97%)	325 (86%)	49 (13%)	2 (0%)	24	57
21	Z	284/324 (88%)	241 (85%)	40 (14%)	3 (1%)	11	39
22	a	371/376 (99%)	340 (92%)	30 (8%)	1 (0%)	36	67
23	b	189/377 (50%)	168 (89%)	21 (11%)	0	100	100
24	d	244/350 (70%)	222 (91%)	21 (9%)	1 (0%)	30	61
25	f	880/908 (97%)	743 (84%)	136 (16%)	1 (0%)	48	78
26	W	435/456 (95%)	401 (92%)	30 (7%)	4 (1%)	14	44
27	V	426/534 (80%)	398 (93%)	28 (7%)	0	100	100
28	e	48/70 (69%)	38 (79%)	10 (21%)	0	100	100
29	A	390/433 (90%)	351 (90%)	37 (10%)	2 (0%)	24	57
30	F	353/439 (80%)	308 (87%)	42 (12%)	3 (1%)	16	47
31	E	362/389 (93%)	338 (93%)	24 (7%)	0	100	100
32	U	823/953 (86%)	797 (97%)	26 (3%)	0	100	100
33	g	189/390 (48%)	165 (87%)	24 (13%)	0	100	100
34	u	153/300 (51%)	148 (97%)	4 (3%)	1 (1%)	18	49
All	All	10426/12236 (85%)	9629 (92%)	773 (7%)	24 (0%)	44	73

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	X	318	ILE
19	X	339	ILE
20	Y	111	LEU
21	Z	261	TYR
24	d	358	ILE
26	W	414	ASN
26	W	418	PRO
30	F	86	LEU
1	B	93	GLU
1	B	156	VAL
30	F	427	VAL
21	Z	260	VAL
26	W	419	LYS
3	D	338	ARG
25	f	834	ASP
26	W	417	ARG
1	B	414	VAL
20	Y	350	VAL
21	Z	259	VAL
22	a	343	LEU
34	u	119	ILE
29	A	36	TYR
29	A	102	ILE
30	F	177	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	B	351/385 (91%)	330 (94%)	21 (6%)	17	47
2	C	338/352 (96%)	321 (95%)	17 (5%)	22	53
3	D	330/366 (90%)	321 (97%)	9 (3%)	39	67
4	c	246/359 (68%)	239 (97%)	7 (3%)	38	66
5	G	203/210 (97%)	196 (97%)	7 (3%)	32	63
6	H	188/191 (98%)	177 (94%)	11 (6%)	18	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	I	202/221 (91%)	195 (96%)	7 (4%)	32	62
8	J	197/211 (93%)	195 (99%)	2 (1%)	68	79
9	K	197/203 (97%)	182 (92%)	15 (8%)	12	39
10	L	202/224 (90%)	198 (98%)	4 (2%)	48	72
11	M	198/212 (93%)	187 (94%)	11 (6%)	19	49
12	N	152/181 (84%)	144 (95%)	8 (5%)	20	51
13	O	178/228 (78%)	172 (97%)	6 (3%)	32	63
14	P	172/174 (99%)	163 (95%)	9 (5%)	21	51
15	Q	168/171 (98%)	160 (95%)	8 (5%)	23	54
16	R	156/202 (77%)	149 (96%)	7 (4%)	24	56
17	S	175/199 (88%)	164 (94%)	11 (6%)	16	45
18	T	178/215 (83%)	172 (97%)	6 (3%)	32	63
19	X	326/362 (90%)	309 (95%)	17 (5%)	21	51
20	Y	334/344 (97%)	313 (94%)	21 (6%)	16	45
21	Z	256/295 (87%)	237 (93%)	19 (7%)	13	40
22	a	333/336 (99%)	318 (96%)	15 (4%)	24	56
23	b	167/312 (54%)	157 (94%)	10 (6%)	17	47
24	d	221/294 (75%)	214 (97%)	7 (3%)	34	64
25	f	742/763 (97%)	709 (96%)	33 (4%)	25	56
26	W	402/416 (97%)	372 (92%)	30 (8%)	12	39
27	V	383/460 (83%)	373 (97%)	10 (3%)	40	68
28	e	44/63 (70%)	41 (93%)	3 (7%)	14	42
29	A	346/372 (93%)	335 (97%)	11 (3%)	34	64
30	F	306/379 (81%)	286 (94%)	20 (6%)	15	44
31	E	318/341 (93%)	306 (96%)	12 (4%)	29	60
32	U	705/816 (86%)	691 (98%)	14 (2%)	48	72
33	g	171/338 (51%)	156 (91%)	15 (9%)	9	33
34	u	141/263 (54%)	135 (96%)	6 (4%)	26	57
All	All	9026/10458 (86%)	8617 (96%)	409 (4%)	26	56

All (409) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	51	LEU
1	B	56	THR
1	B	75	GLU
1	B	102	LEU
1	B	142	ASP
1	B	150	VAL
1	B	152	LEU
1	B	203	LEU
1	B	205	LEU
1	B	213	GLU
1	B	217	LYS
1	B	250	VAL
1	B	251	VAL
1	B	298	ASN
1	B	305	ILE
1	B	325	VAL
1	B	327	VAL
1	B	379	THR
1	B	382	ASP
1	B	391	SER
1	B	426	VAL
2	C	35	VAL
2	C	51	GLU
2	C	63	LEU
2	C	65	LEU
2	C	73	VAL
2	C	76	VAL
2	C	89	VAL
2	C	105	ILE
2	C	161	ILE
2	C	194	THR
2	C	208	ASP
2	C	237	MET
2	C	300	ILE
2	C	312	ASP
2	C	358	GLU
2	C	362	VAL
2	C	375	ARG
3	D	139	LEU
3	D	153	MET
3	D	214	MET
3	D	240	LEU
3	D	279	THR

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Mol	Chain	Res	Type
3	D	307	VAL
3	D	343	LEU
3	D	392	TYR
3	D	394	VAL
4	c	107	MET
4	c	132	SER
4	c	143	VAL
4	c	145	VAL
4	c	160	PHE
4	c	164	ASN
4	c	166	ASN
5	G	17	SER
5	G	40	VAL
5	G	45	LYS
5	G	51	VAL
5	G	80	MET
5	G	111	VAL
5	G	190	THR
6	H	9	SER
6	H	20	VAL
6	H	46	LEU
6	H	74	LEU
6	H	84	ARG
6	H	107	THR
6	H	124	SER
6	H	127	VAL
6	H	168	VAL
6	H	174	LEU
6	H	225	GLU
7	I	43	VAL
7	I	52	ILE
7	I	72	MET
7	I	121	TYR
7	I	124	PHE
7	I	151	ASP
7	I	217	THR
8	J	76	LEU
8	J	102	VAL
9	K	7	GLU
9	K	9	ASP
9	K	21	LEU
9	K	24	VAL

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Mol	Chain	Res	Type
9	K	41	GLN
9	K	63	SER
9	K	68	VAL
9	K	107	MET
9	K	108	THR
9	K	113	THR
9	K	134	SER
9	K	156	MET
9	K	198	SER
9	K	213	THR
9	K	230	THR
10	L	7	ASP
10	L	112	ILE
10	L	148	CYS
10	L	223	ILE
11	M	31	GLU
11	M	53	VAL
11	M	63	ASN
11	M	123	THR
11	M	150	MET
11	M	152	ASP
11	M	177	GLU
11	M	179	LEU
11	M	186	CYS
11	M	189	ILE
11	M	200	VAL
12	N	1	THR
12	N	24	SER
12	N	28	ASN
12	N	43	CYS
12	N	51	ASP
12	N	104	ASP
12	N	119	MET
12	N	188	VAL
13	O	87	LEU
13	O	94	ILE
13	O	103	VAL
13	O	110	LEU
13	O	118	SER
13	O	120	ASP
14	P	7	ASN
14	P	25	ASP

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Mol	Chain	Res	Type
14	P	33	GLN
14	P	53	LEU
14	P	56	LEU
14	P	108	VAL
14	P	151	GLU
14	P	162	HIS
14	P	168	SER
15	Q	20	VAL
15	Q	30	ASP
15	Q	53	THR
15	Q	54	VAL
15	Q	61	GLN
15	Q	150	THR
15	Q	192	ASP
15	Q	193	ASN
16	R	21	THR
16	R	45	MET
16	R	111	LEU
16	R	132	SER
16	R	176	LEU
16	R	190	ASP
16	R	196	HIS
17	S	11	THR
17	S	27	THR
17	S	36	HIS
17	S	44	TYR
17	S	50	THR
17	S	72	LEU
17	S	106	VAL
17	S	110	ILE
17	S	114	ASP
17	S	133	ASP
17	S	172	MET
18	T	17	GLU
18	T	21	VAL
18	T	42	ILE
18	T	43	MET
18	T	107	TRP
18	T	192	VAL
19	X	45	VAL
19	X	78	ASN
19	X	116	TRP

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Mol	Chain	Res	Type
19	X	133	LEU
19	X	134	VAL
19	X	154	LEU
19	X	168	GLU
19	X	244	SER
19	X	306	LEU
19	X	312	GLU
19	X	337	ARG
19	X	345	VAL
19	X	352	SER
19	X	374	PHE
19	X	378	LEU
19	X	384	VAL
19	X	385	LEU
20	Y	16	ASP
20	Y	22	LEU
20	Y	37	VAL
20	Y	47	ASP
20	Y	65	ILE
20	Y	81	LEU
20	Y	95	LEU
20	Y	104	MET
20	Y	131	THR
20	Y	134	LEU
20	Y	168	ILE
20	Y	207	THR
20	Y	231	LEU
20	Y	239	LYS
20	Y	250	LEU
20	Y	281	GLU
20	Y	306	GLN
20	Y	331	ASP
20	Y	346	LYS
20	Y	347	ILE
20	Y	370	ILE
21	Z	6	VAL
21	Z	29	VAL
21	Z	42	SER
21	Z	48	LEU
21	Z	50	VAL
21	Z	62	ASP
21	Z	67	VAL

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Mol	Chain	Res	Type
21	Z	118	ASN
21	Z	123	ILE
21	Z	130	ASP
21	Z	135	THR
21	Z	149	THR
21	Z	158	VAL
21	Z	235	ASN
21	Z	258	VAL
21	Z	261	TYR
21	Z	262	LEU
21	Z	265	LEU
21	Z	266	ILE
22	a	74	LEU
22	a	75	SER
22	a	84	VAL
22	a	92	VAL
22	a	123	LEU
22	a	125	ILE
22	a	151	VAL
22	a	156	TYR
22	a	169	HIS
22	a	234	ILE
22	a	246	GLU
22	a	253	THR
22	a	269	LEU
22	a	335	TRP
22	a	341	LEU
23	b	2	VAL
23	b	6	THR
23	b	8	VAL
23	b	22	LEU
23	b	71	ILE
23	b	90	ILE
23	b	109	ILE
23	b	143	PHE
23	b	150	THR
23	b	186	SER
24	d	155	SER
24	d	161	ILE
24	d	176	PHE
24	d	257	THR
24	d	258	PHE

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Mol	Chain	Res	Type
24	d	341	SER
24	d	344	LEU
25	f	105	LYS
25	f	108	GLU
25	f	111	GLU
25	f	124	ASP
25	f	170	TRP
25	f	186	THR
25	f	192	VAL
25	f	202	HIS
25	f	226	TYR
25	f	260	SER
25	f	273	ASN
25	f	325	GLN
25	f	333	LEU
25	f	344	VAL
25	f	376	PHE
25	f	402	ASN
25	f	423	ASP
25	f	448	CYS
25	f	514	VAL
25	f	567	LEU
25	f	587	PHE
25	f	600	TYR
25	f	674	THR
25	f	680	ARG
25	f	715	HIS
25	f	745	LEU
25	f	759	LEU
25	f	785	ARG
25	f	799	VAL
25	f	806	VAL
25	f	833	PHE
25	f	835	GLU
25	f	866	GLN
26	W	39	ARG
26	W	60	MET
26	W	67	LEU
26	W	81	ASP
26	W	118	LEU
26	W	140	ILE
26	W	169	LEU

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Mol	Chain	Res	Type
26	W	192	LEU
26	W	200	ILE
26	W	203	GLN
26	W	231	ILE
26	W	243	ILE
26	W	246	HIS
26	W	267	LEU
26	W	288	HIS
26	W	340	VAL
26	W	344	THR
26	W	365	ILE
26	W	401	THR
26	W	406	VAL
26	W	408	ARG
26	W	412	ILE
26	W	413	ILE
26	W	414	ASN
26	W	415	PHE
26	W	416	GLN
26	W	418	PRO
26	W	419	LYS
26	W	440	ASN
26	W	444	HIS
27	V	94	VAL
27	V	224	LEU
27	V	225	ASP
27	V	283	ASN
27	V	300	LEU
27	V	332	LEU
27	V	410	ILE
27	V	444	ASP
27	V	467	TYR
27	V	469	THR
28	e	39	TRP
28	e	41	ASP
28	e	54	ASN
29	A	40	THR
29	A	55	LEU
29	A	62	LEU
29	A	122	VAL
29	A	185	GLU
29	A	246	VAL

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Mol	Chain	Res	Type
29	A	249	TYR
29	A	272	ILE
29	A	306	LEU
29	A	309	PHE
29	A	384	GLU
30	F	59	VAL
30	F	80	ILE
30	F	82	VAL
30	F	90	VAL
30	F	144	LYS
30	F	159	LEU
30	F	162	GLU
30	F	169	ASP
30	F	187	ASP
30	F	192	ASP
30	F	233	LYS
30	F	257	VAL
30	F	277	GLU
30	F	335	VAL
30	F	337	ILE
30	F	358	ASN
30	F	365	ILE
30	F	402	GLU
30	F	408	LEU
30	F	426	GLU
31	E	57	VAL
31	E	103	THR
31	E	104	THR
31	E	121	ASN
31	E	122	MET
31	E	250	ASP
31	E	251	ARG
31	E	269	THR
31	E	273	VAL
31	E	275	MET
31	E	339	ASN
31	E	378	LYS
32	U	31	VAL
32	U	42	VAL
32	U	184	CYS
32	U	200	VAL
32	U	208	LEU

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Mol	Chain	Res	Type
32	U	218	GLN
32	U	321	GLN
32	U	356	THR
32	U	360	VAL
32	U	373	ASN
32	U	452	ASN
32	U	457	ILE
32	U	578	LEU
32	U	608	SER
33	g	154	ASN
33	g	186	HIS
33	g	187	HIS
33	g	191	ASP
33	g	209	VAL
33	g	280	TYR
33	g	302	LEU
33	g	313	VAL
33	g	322	ILE
33	g	326	LEU
33	g	351	LEU
33	g	361	ILE
33	g	369	ASP
33	g	380	VAL
33	g	382	HIS
34	u	162	ASP
34	u	167	ILE
34	u	186	ASP
34	u	203	SER
34	u	244	VAL
34	u	270	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (82) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	92	GLN
1	B	425	ASN
2	C	118	ASN
2	C	205	HIS
3	D	57	GLN
3	D	193	GLN
3	D	222	HIS
3	D	237	GLN

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Mol	Chain	Res	Type
4	c	131	GLN
4	c	197	ASN
4	c	221	HIS
4	c	237	HIS
5	G	75	ASN
6	H	112	GLN
7	I	155	ASN
9	K	98	ASN
9	K	224	GLN
10	L	16	GLN
10	L	53	GLN
10	L	65	HIS
10	L	209	ASN
11	M	120	HIS
11	M	221	ASN
11	M	224	HIS
12	N	110	GLN
13	O	57	GLN
13	O	62	ASN
13	O	66	HIS
14	P	93	ASN
14	P	162	HIS
15	Q	63	ASN
16	R	89	GLN
16	R	178	HIS
17	S	58	HIS
17	S	151	ASN
18	T	61	GLN
19	X	144	GLN
19	X	152	GLN
20	Y	64	GLN
20	Y	363	ASN
21	Z	104	ASN
21	Z	202	ASN
22	a	86	GLN
22	a	129	GLN
22	a	193	GLN
22	a	212	ASN
24	d	223	ASN
24	d	228	HIS
24	d	354	GLN
25	f	12	GLN

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Mol	Chain	Res	Type
25	f	102	HIS
25	f	180	GLN
25	f	405	HIS
25	f	566	HIS
25	f	815	HIS
25	f	826	GLN
26	W	106	GLN
26	W	156	ASN
26	W	235	GLN
26	W	414	ASN
26	W	416	GLN
26	W	422	ASN
26	W	456	GLN
27	V	78	HIS
27	V	168	GLN
27	V	400	HIS
28	e	37	HIS
29	A	47	GLN
29	A	128	GLN
29	A	231	ASN
29	A	296	GLN
30	F	67	GLN
30	F	76	ASN
30	F	130	GLN
30	F	243	GLN
31	E	55	GLN
31	E	121	ASN
31	E	339	ASN
31	E	359	HIS
32	U	149	GLN
32	U	218	GLN
32	U	347	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
33	CR8	g	228	33	25,27,28	6.12	11 (44%)	24,37,39	3.63	12 (50%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	CR8	g	228	33	-	6/12/25/26	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	g	228	CR8	C4-C11	-17.93	1.01	1.46
33	g	228	CR8	C12-C11	-17.69	1.02	1.46
33	g	228	CR8	C5-C7	9.95	1.69	1.41
33	g	228	CR8	C6-C7	8.85	1.66	1.41
33	g	228	CR8	C8-CA2	6.16	1.54	1.40
33	g	228	CR8	C1-N2	4.31	1.38	1.32
33	g	228	CR8	C21-N22	-3.70	1.31	1.37
33	g	228	CR8	C20-C21	3.58	1.55	1.49
33	g	228	CR8	O2-C2	3.14	1.40	1.31
33	g	228	CR8	CA2-N2	-3.08	1.32	1.38
33	g	228	CR8	C8-C7	-2.17	1.33	1.39

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	g	228	CR8	C6-C7-C5	-9.94	94.17	115.81
33	g	228	CR8	C4-C11-C12	7.51	130.62	116.67
33	g	228	CR8	C6-C12-C11	5.53	128.76	121.25
33	g	228	CR8	N3-C1-N2	-4.71	107.78	111.48
33	g	228	CR8	O13-C11-C12	-4.45	114.40	121.56
33	g	228	CR8	C5-C4-C11	4.38	127.19	121.25
33	g	228	CR8	O13-C11-C4	-4.08	114.98	121.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	g	228	CR8	CA1-C1-N3	3.50	129.40	124.84
33	g	228	CR8	C12-C6-C7	-3.09	119.18	122.10
33	g	228	CR8	CA1-C20-C21	-2.87	108.47	113.23
33	g	228	CR8	C8-CA2-C2	-2.61	123.95	129.19
33	g	228	CR8	C4-C5-C7	-2.13	120.08	122.10

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
33	g	228	CR8	C7-C8-CA2-N2
33	g	228	CR8	C3-CA3-N3-C2
33	g	228	CR8	CA1-C20-C21-N22
33	g	228	CR8	C3-CA3-N3-C1
33	g	228	CR8	CA1-C20-C21-C23
33	g	228	CR8	C7-C8-CA2-C2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	g	228	CR8	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	ATP	B	501	36	32,33,33	0.75	2 (6%)	48,52,52	0.37	0
37	ADP	A	501	-	28,29,29	1.42	4 (14%)	43,45,45	1.88	8 (18%)
37	ADP	E	501	-	28,29,29	1.42	5 (17%)	43,45,45	1.77	9 (20%)
37	ADP	D	501	36	28,29,29	1.37	3 (10%)	43,45,45	1.89	8 (18%)
35	ATP	C	501	36	32,33,33	0.74	2 (6%)	48,52,52	0.36	0
37	ADP	F	501	-	28,29,29	1.59	6 (21%)	43,45,45	2.00	9 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	ATP	B	501	36	-	1/22/38/38	0/3/3/3
37	ADP	A	501	-	-	2/16/32/32	0/3/3/3
37	ADP	E	501	-	-	7/16/32/32	0/3/3/3
37	ADP	D	501	36	-	5/16/32/32	0/3/3/3
35	ATP	C	501	36	-	2/22/38/38	0/3/3/3
37	ADP	F	501	-	-	4/16/32/32	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	F	501	ADP	C5-C4	4.80	1.47	1.39
37	A	501	ADP	C5-C4	4.72	1.47	1.39
37	E	501	ADP	C5-C4	4.57	1.47	1.39
37	D	501	ADP	C5-C4	4.47	1.47	1.39
37	F	501	ADP	PA-O3A	3.31	1.63	1.59
35	C	501	ATP	PA-O3A	-2.90	1.56	1.59
37	D	501	ADP	C5-N7	-2.81	1.34	1.39
35	B	501	ATP	PA-O3A	-2.80	1.56	1.59
37	A	501	ADP	C5-C6	2.69	1.48	1.41
37	F	501	ADP	C5-C6	2.64	1.48	1.41
37	E	501	ADP	C5-C6	2.64	1.48	1.41
37	A	501	ADP	C5-N7	-2.48	1.34	1.39
37	F	501	ADP	C5-N7	-2.48	1.34	1.39
37	E	501	ADP	C5-N7	-2.47	1.34	1.39
35	B	501	ATP	PB-O3B	-2.41	1.56	1.59
37	F	501	ADP	PB-O1B	2.37	1.57	1.50
37	E	501	ADP	C8-N7	2.35	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	A	501	ADP	C8-N7	2.25	1.36	1.31
35	C	501	ATP	PB-O3B	-2.22	1.57	1.59
37	D	501	ADP	C5-C6	2.18	1.47	1.41
37	E	501	ADP	C4-N9	-2.18	1.33	1.37
37	F	501	ADP	C8-N7	2.17	1.35	1.31

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	F	501	ADP	C5-C4-N3	-6.63	117.59	126.72
37	A	501	ADP	C5-C4-N3	-6.29	118.05	126.72
37	D	501	ADP	C5-C4-N3	-6.17	118.22	126.72
37	E	501	ADP	C5-C4-N3	-5.76	118.78	126.72
37	F	501	ADP	N3-C4-N9	5.16	135.95	127.17
37	D	501	ADP	N3-C4-N9	5.10	135.84	127.17
37	A	501	ADP	N3-C4-N9	4.90	135.51	127.17
37	E	501	ADP	N3-C4-N9	4.27	134.42	127.17
37	F	501	ADP	C2-N3-C4	4.06	121.75	111.83
37	A	501	ADP	C2-N3-C4	3.85	121.23	111.83
37	E	501	ADP	C4-C5-N7	-3.63	106.43	110.58
37	D	501	ADP	C2-N3-C4	3.57	120.55	111.83
37	A	501	ADP	C4-C5-N7	-3.51	106.57	110.58
37	E	501	ADP	C2-N3-C4	3.50	120.38	111.83
37	F	501	ADP	N3-C2-N1	-3.40	123.44	128.58
37	F	501	ADP	C4-C5-N7	-3.28	106.83	110.58
37	A	501	ADP	N3-C2-N1	-3.13	123.85	128.58
37	F	501	ADP	O3A-PA-O1A	-2.96	101.80	110.70
37	D	501	ADP	N3-C2-N1	-2.92	124.17	128.58
37	D	501	ADP	C4-C5-N7	-2.91	107.26	110.58
37	D	501	ADP	C3'-C2'-C1'	2.83	106.81	101.46
37	A	501	ADP	C3'-C2'-C1'	2.83	106.81	101.46
37	E	501	ADP	N3-C2-N1	-2.71	124.48	128.58
37	F	501	ADP	O3B-PB-O2B	-2.59	98.08	107.80
37	A	501	ADP	C5-N7-C8	2.54	107.44	103.45
37	E	501	ADP	C5-N7-C8	2.38	107.19	103.45
37	E	501	ADP	C4-N9-C8	2.26	108.11	105.74
37	F	501	ADP	C5-N7-C8	2.24	106.97	103.45
37	F	501	ADP	O2B-PB-O1B	2.21	119.44	110.83
37	D	501	ADP	C4-N9-C8	2.21	108.05	105.74
37	A	501	ADP	C4-N9-C8	2.18	108.02	105.74
37	E	501	ADP	C3'-C2'-C1'	2.16	105.55	101.46
37	E	501	ADP	C6-C5-N7	2.15	136.23	132.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	D	501	ADP	C5-N7-C8	2.13	106.80	103.45

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
37	D	501	ADP	C5'-O5'-PA-O1A
37	D	501	ADP	C5'-O5'-PA-O2A
37	D	501	ADP	C5'-O5'-PA-O3A
37	A	501	ADP	C5'-O5'-PA-O2A
37	F	501	ADP	C5'-O5'-PA-O3A
37	E	501	ADP	PA-O3A-PB-O2B
37	E	501	ADP	PA-O3A-PB-O3B
37	E	501	ADP	C5'-O5'-PA-O2A
37	E	501	ADP	C5'-O5'-PA-O3A
37	E	501	ADP	C2'-C1'-N9-C8
37	E	501	ADP	C2'-C1'-N9-C4
37	F	501	ADP	C2'-C1'-N9-C4
37	F	501	ADP	C2'-C1'-N9-C8
35	B	501	ATP	C5'-O5'-PA-O3A
35	C	501	ATP	C5'-O5'-PA-O1A
37	A	501	ADP	C5'-O5'-PA-O3A
37	F	501	ADP	C5'-O5'-PA-O1A
37	E	501	ADP	C4'-C5'-O5'-PA
37	D	501	ADP	O4'-C4'-C5'-O5'
35	C	501	ATP	PB-O3B-PG-O1G
37	D	501	ADP	C3'-C4'-C5'-O5'

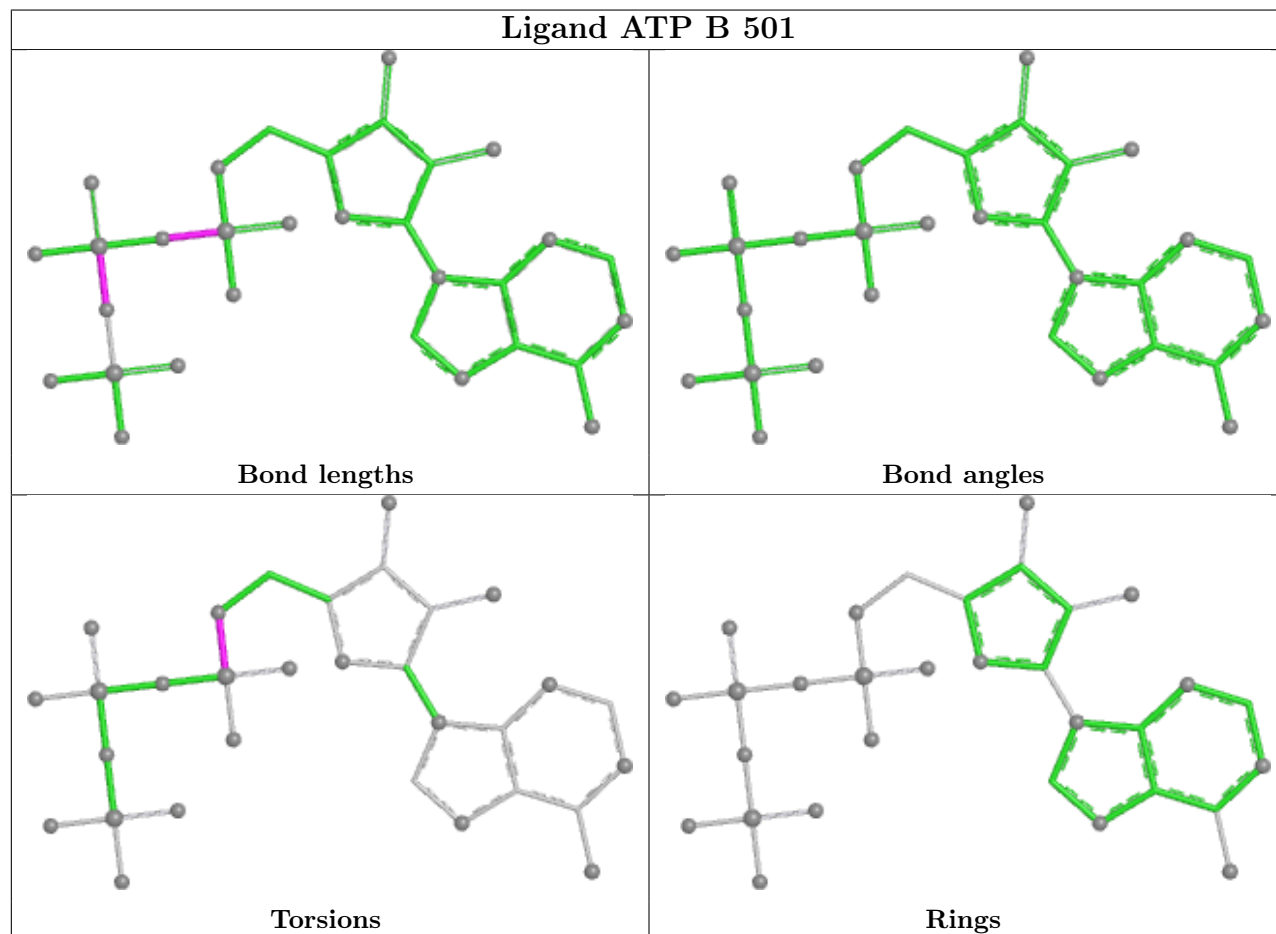
There are no ring outliers.

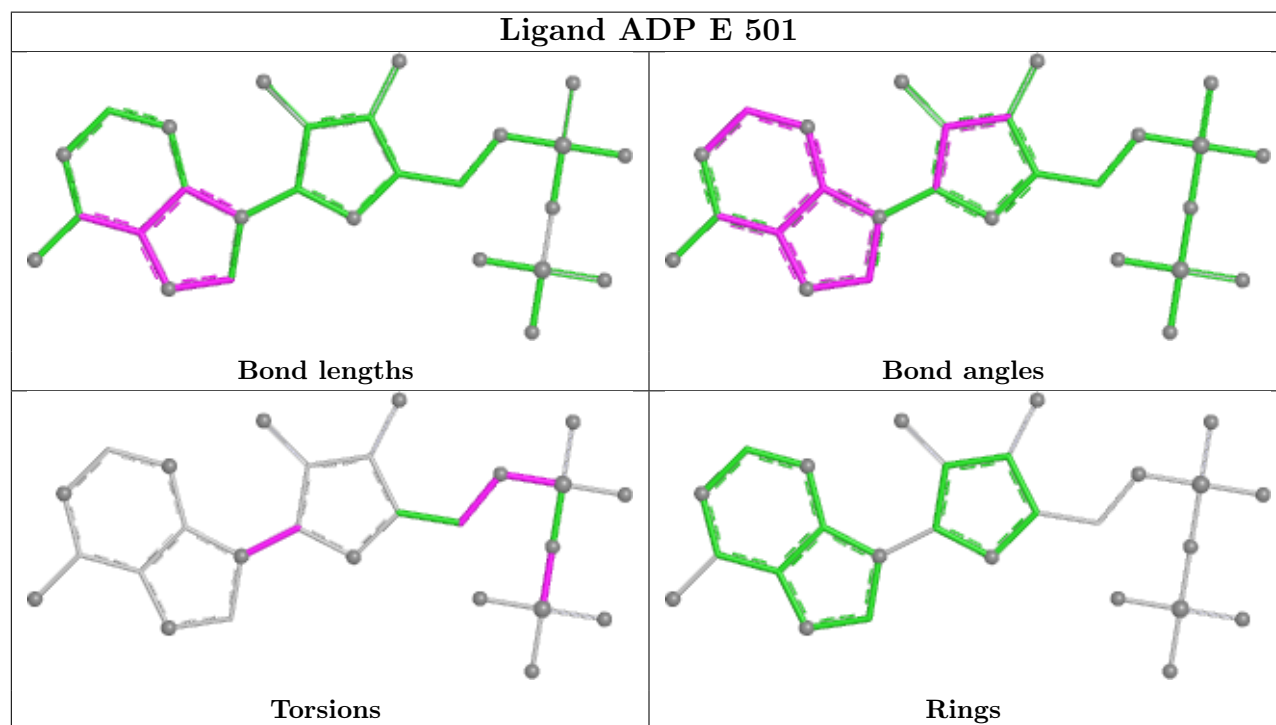
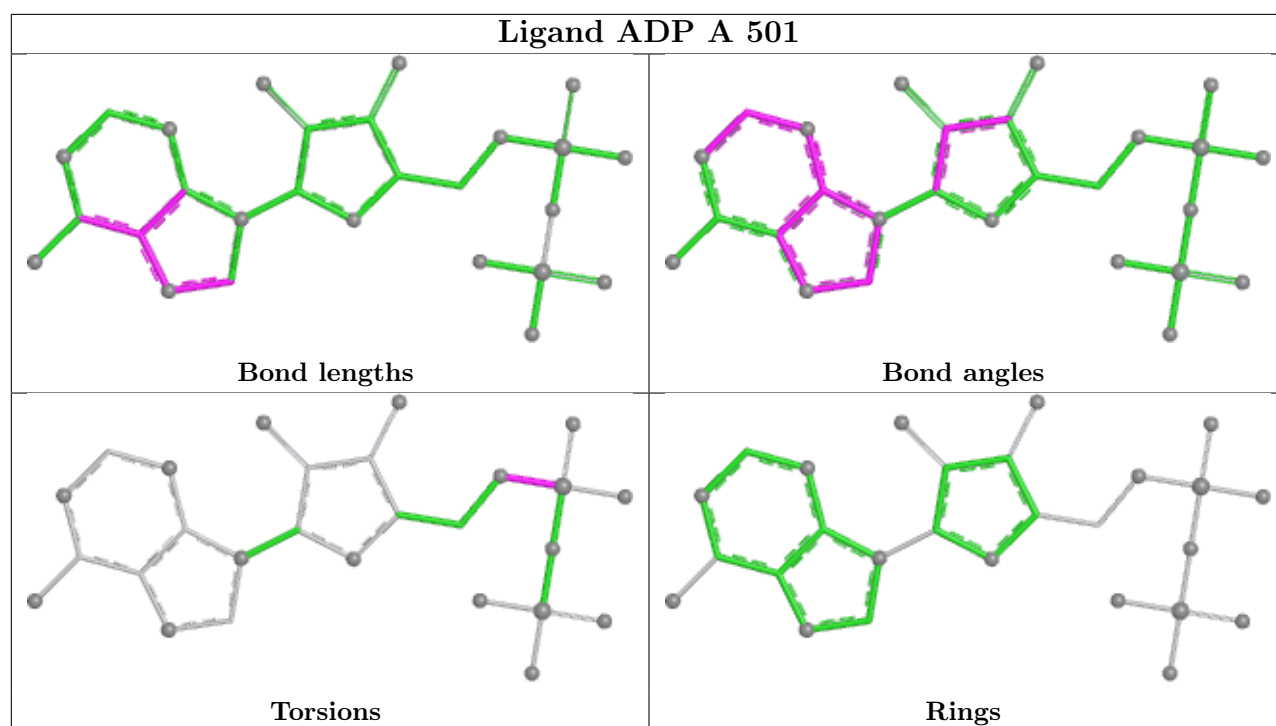
6 monomers are involved in 32 short contacts:

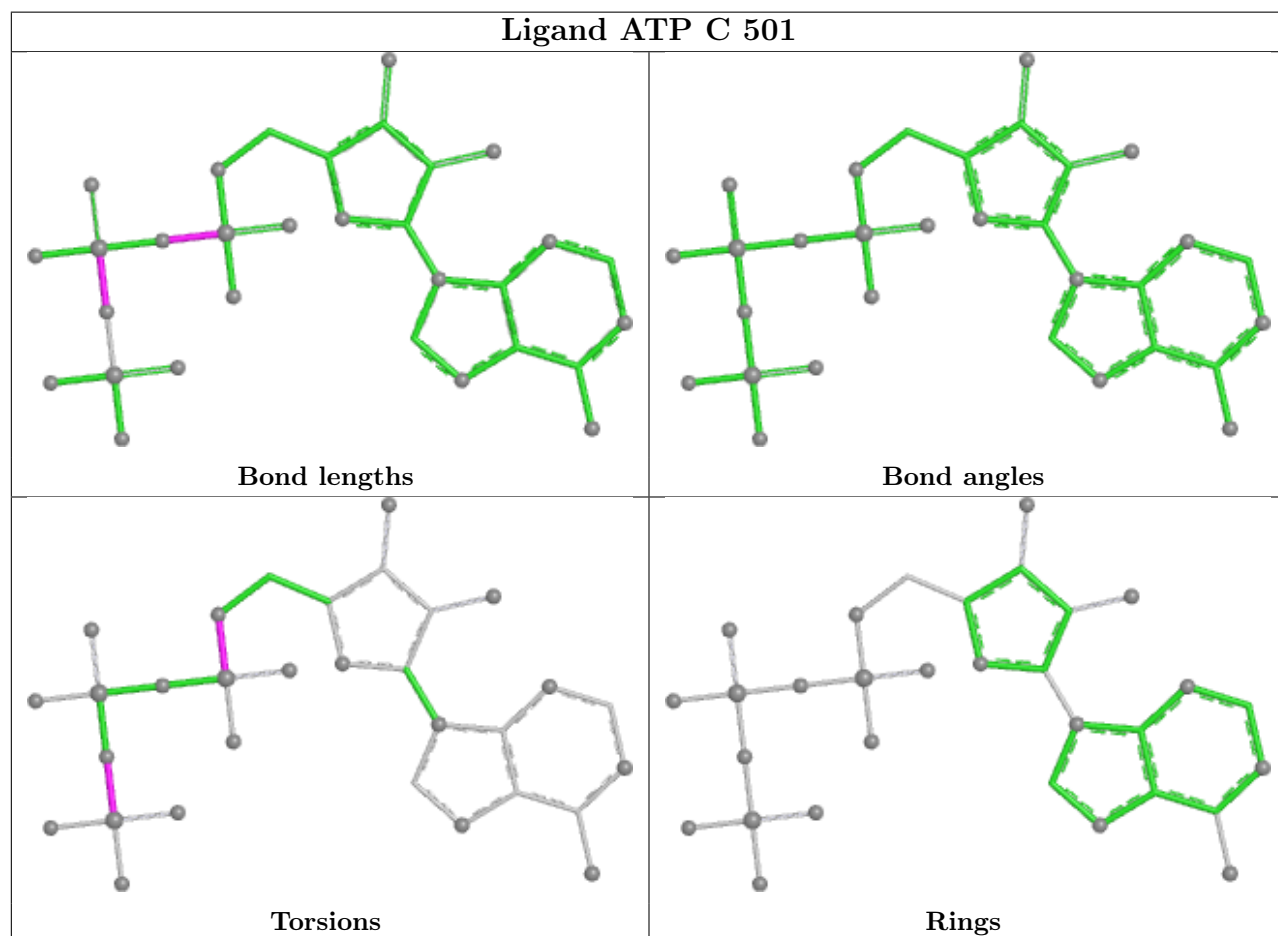
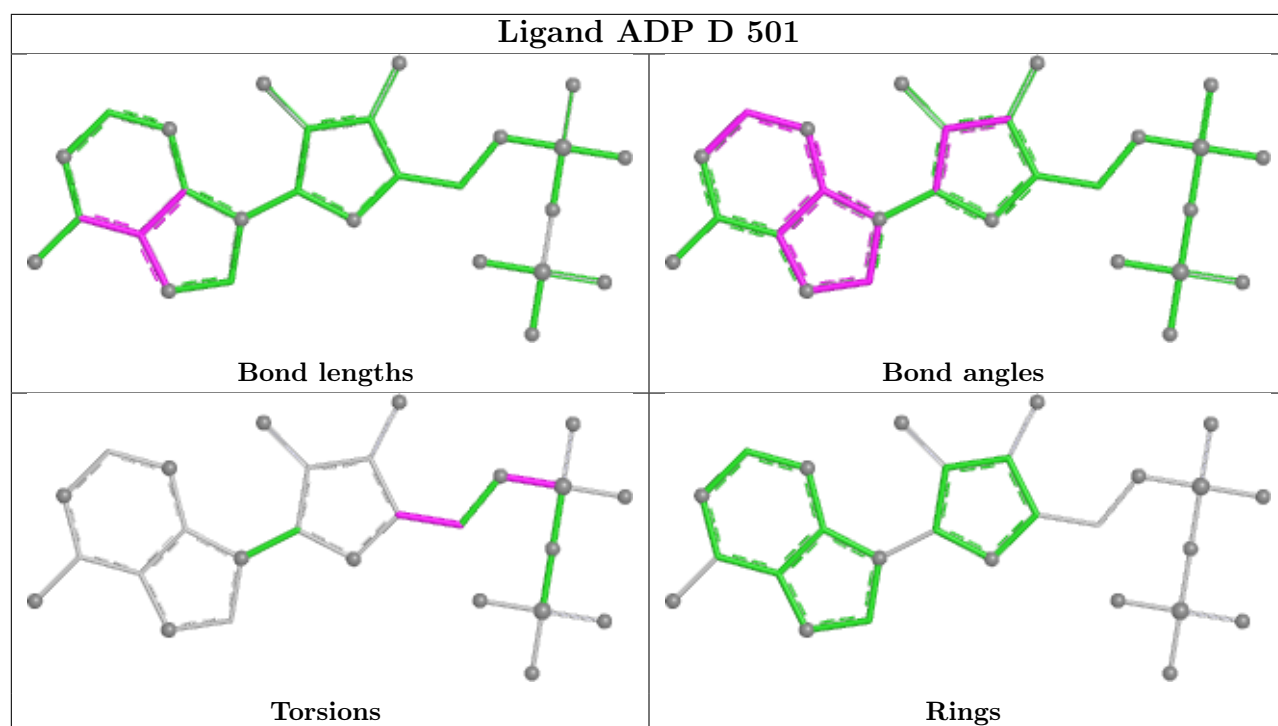
Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	B	501	ATP	3	0
37	A	501	ADP	4	0
37	E	501	ADP	8	0
37	D	501	ADP	1	0
35	C	501	ATP	4	0
37	F	501	ADP	12	0

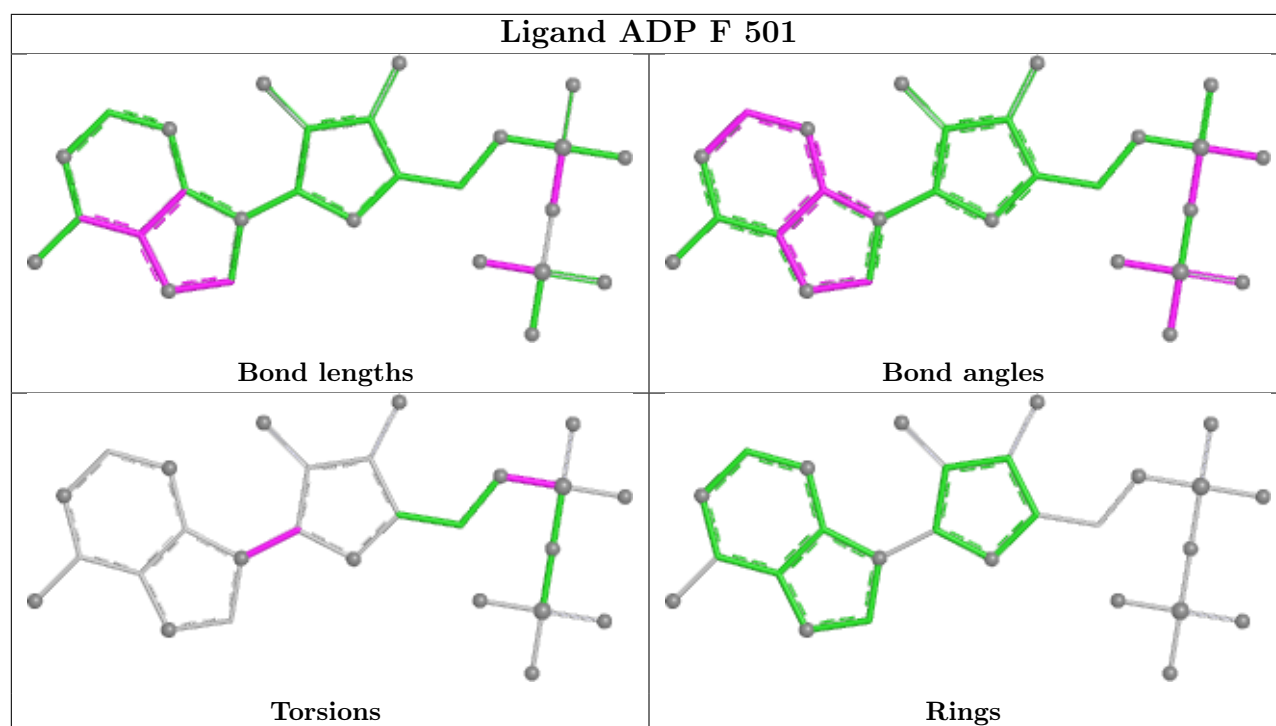
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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.

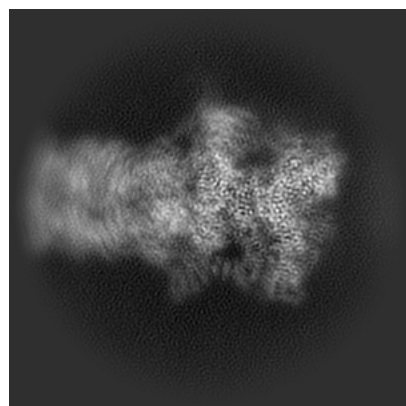
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47726. These allow visual inspection of the internal detail of the map and identification of artifacts.

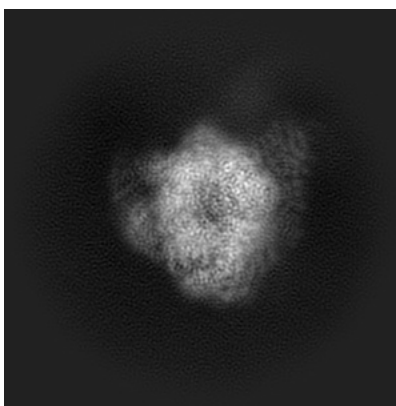
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

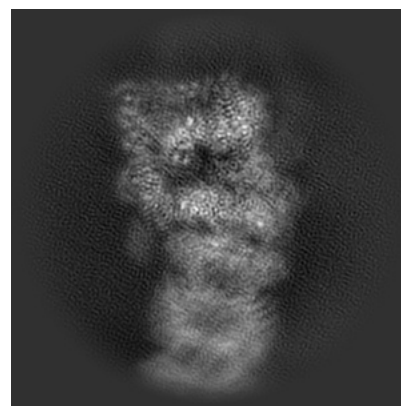
6.1.1 Primary map



X

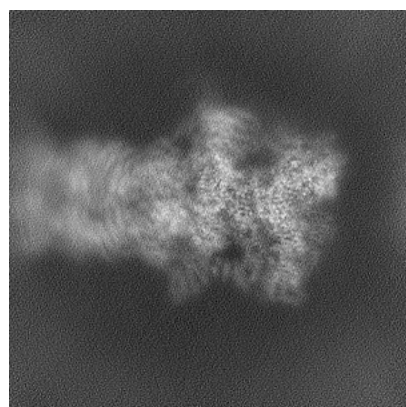


Y

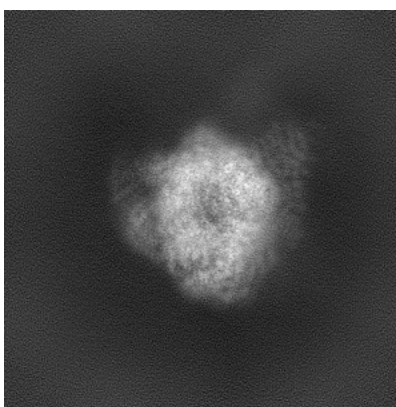


Z

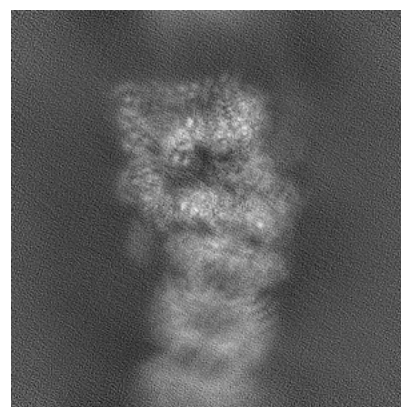
6.1.2 Raw map



X



Y

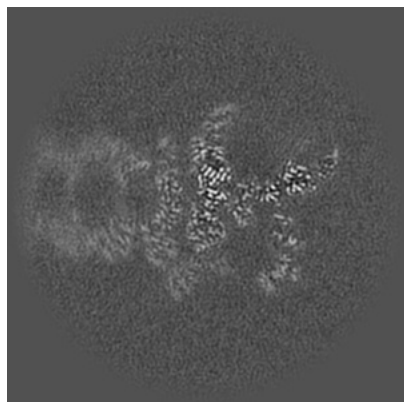


Z

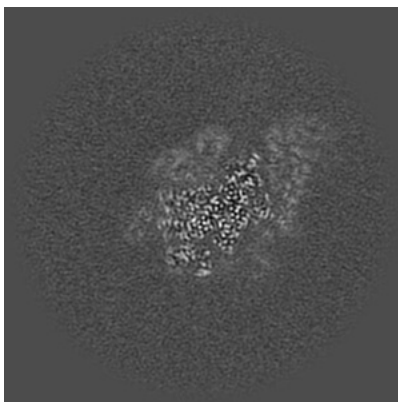
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

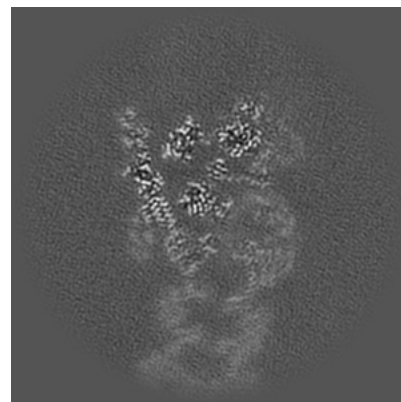
6.2.1 Primary map



X Index: 170

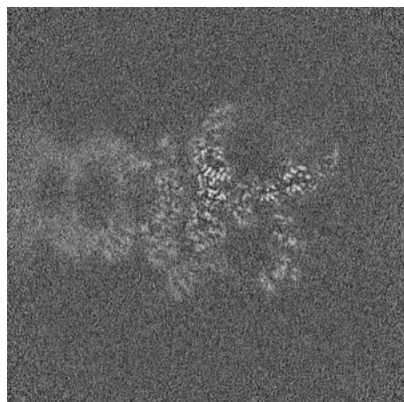


Y Index: 170

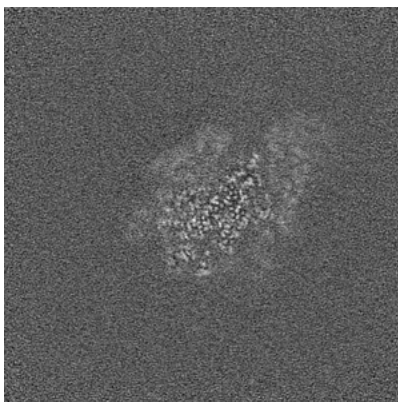


Z Index: 170

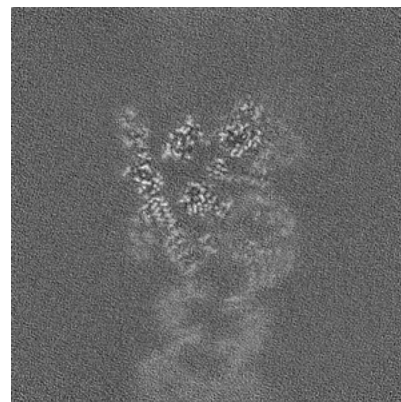
6.2.2 Raw map



X Index: 170



Y Index: 170

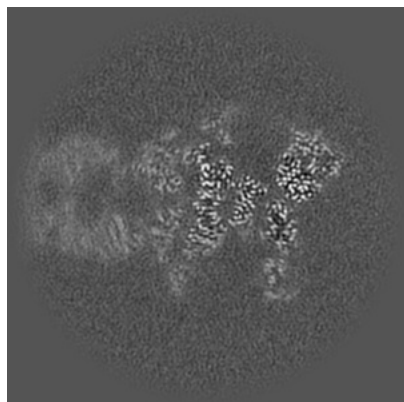


Z Index: 170

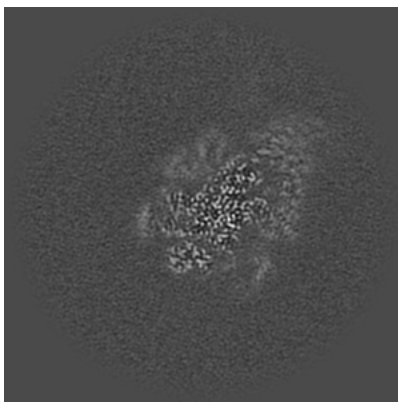
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

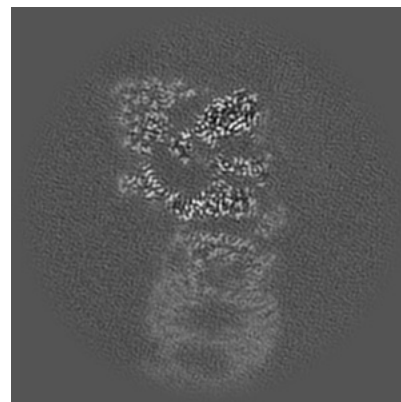
6.3.1 Primary map



X Index: 178

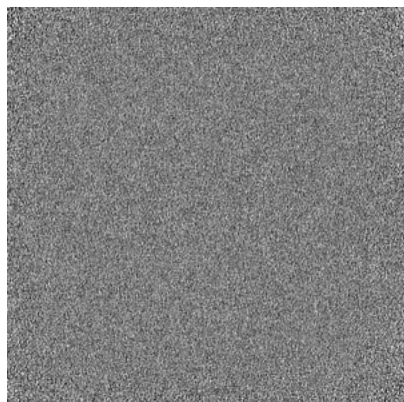


Y Index: 173

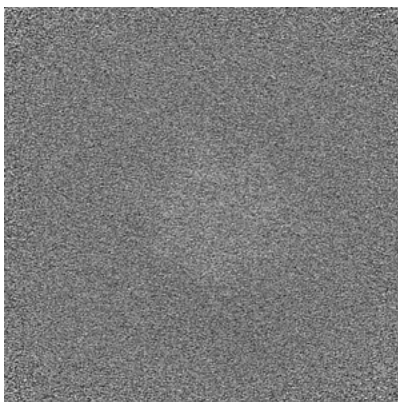


Z Index: 190

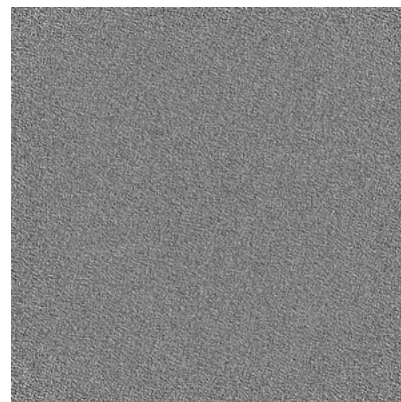
6.3.2 Raw map



X Index: 0



Y Index: 0

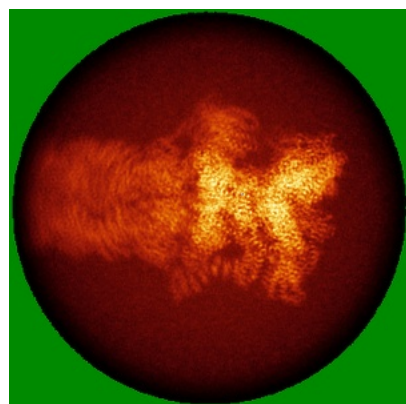


Z Index: 0

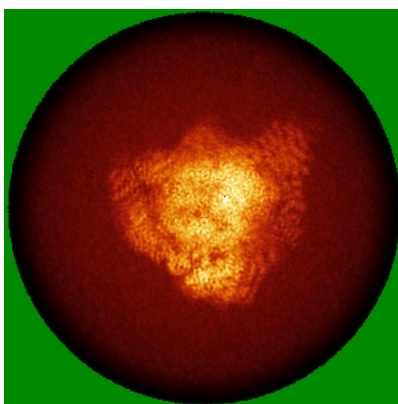
The images above show the largest variance slices of the map in three orthogonal directions.

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

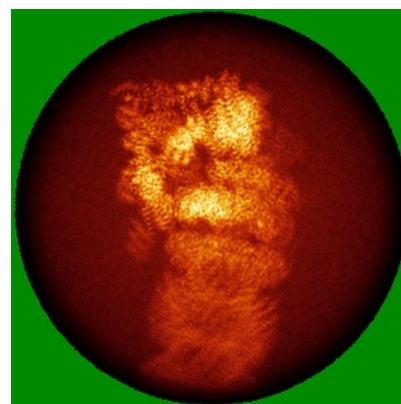
6.4.1 Primary map



X

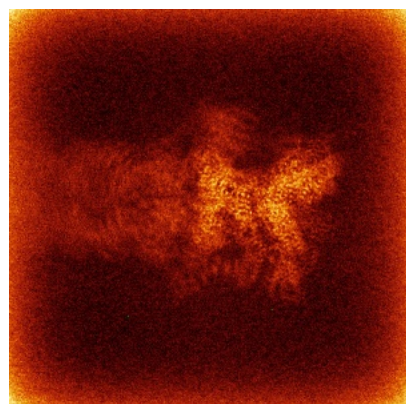


Y

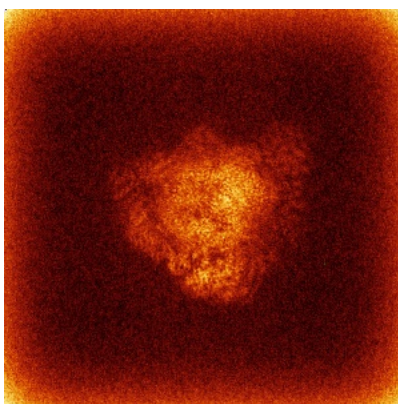


Z

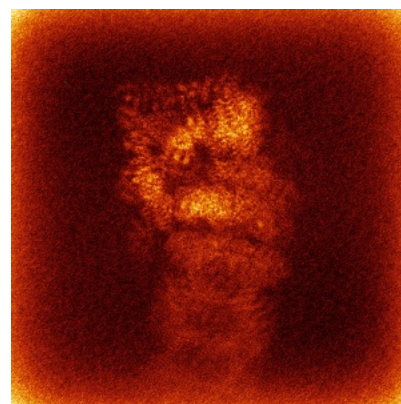
6.4.2 Raw map



X



Y

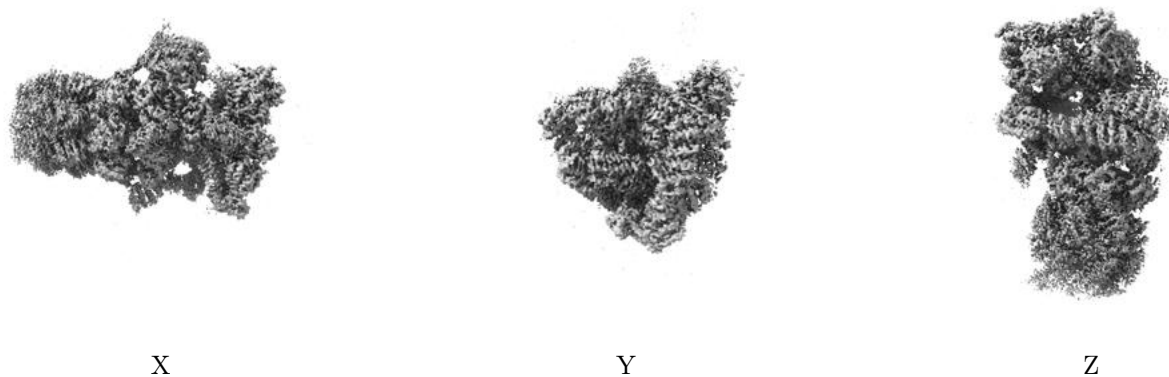


Z

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.

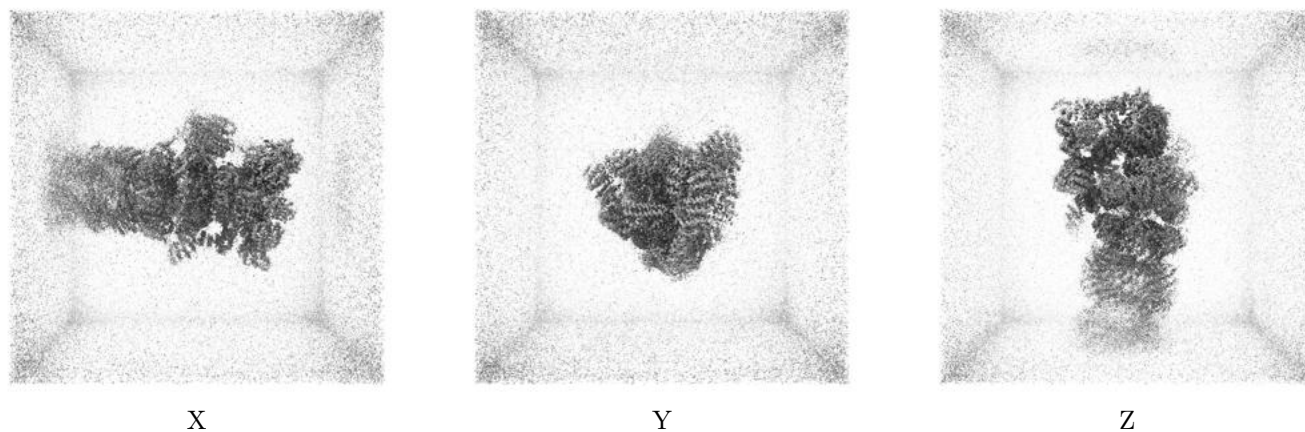
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.17. 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.

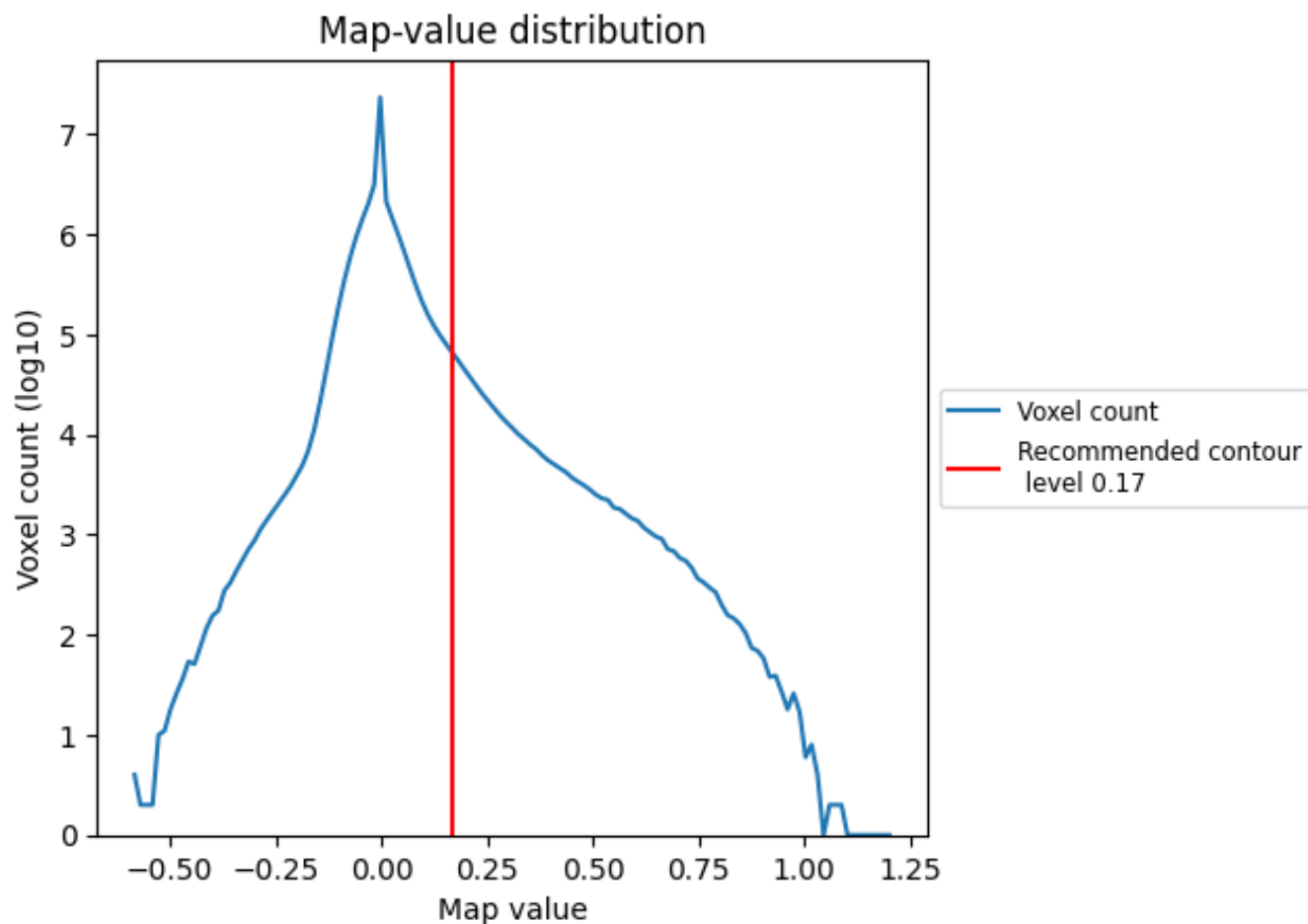
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

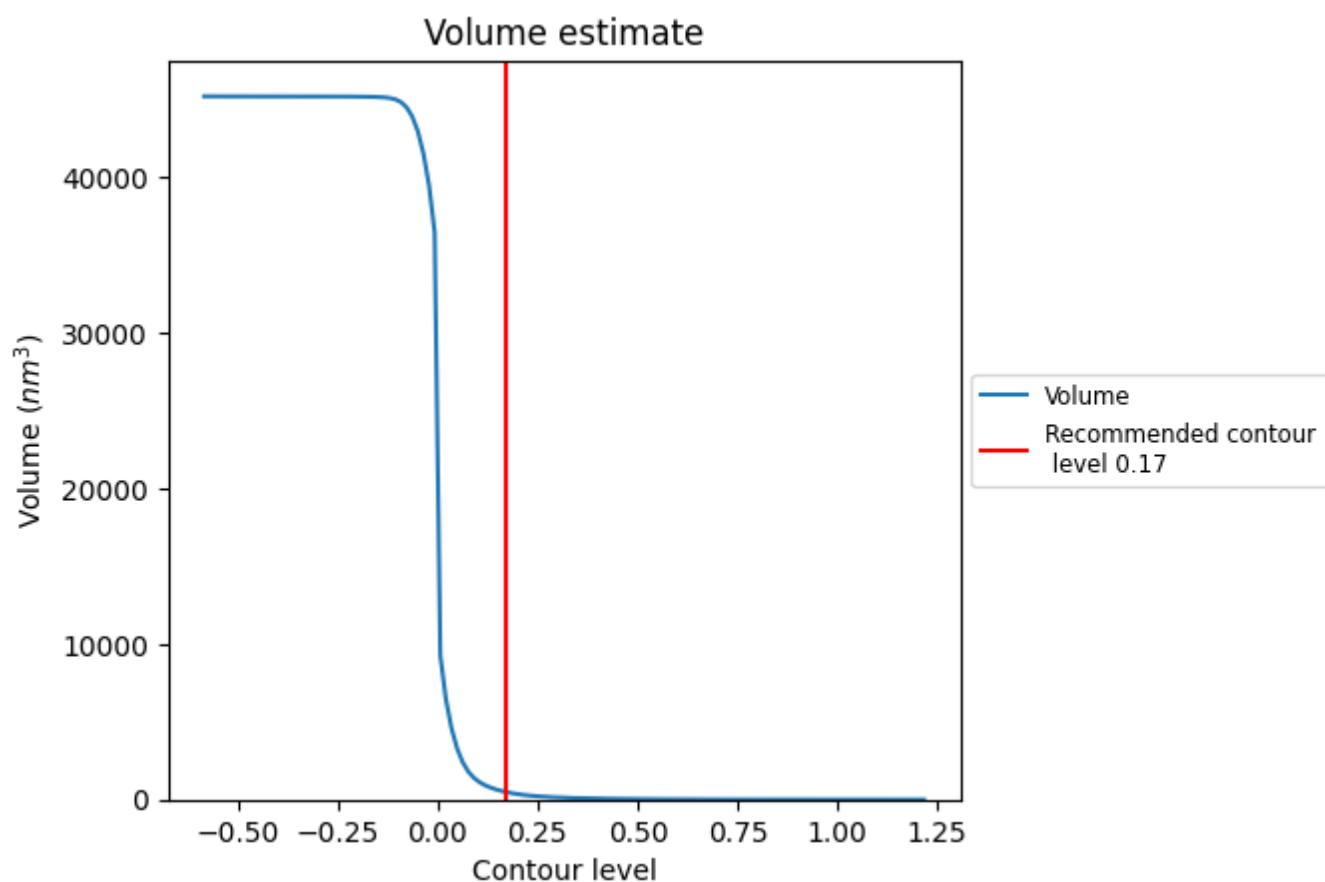
This section contains the results of statistical analysis of the map.

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.

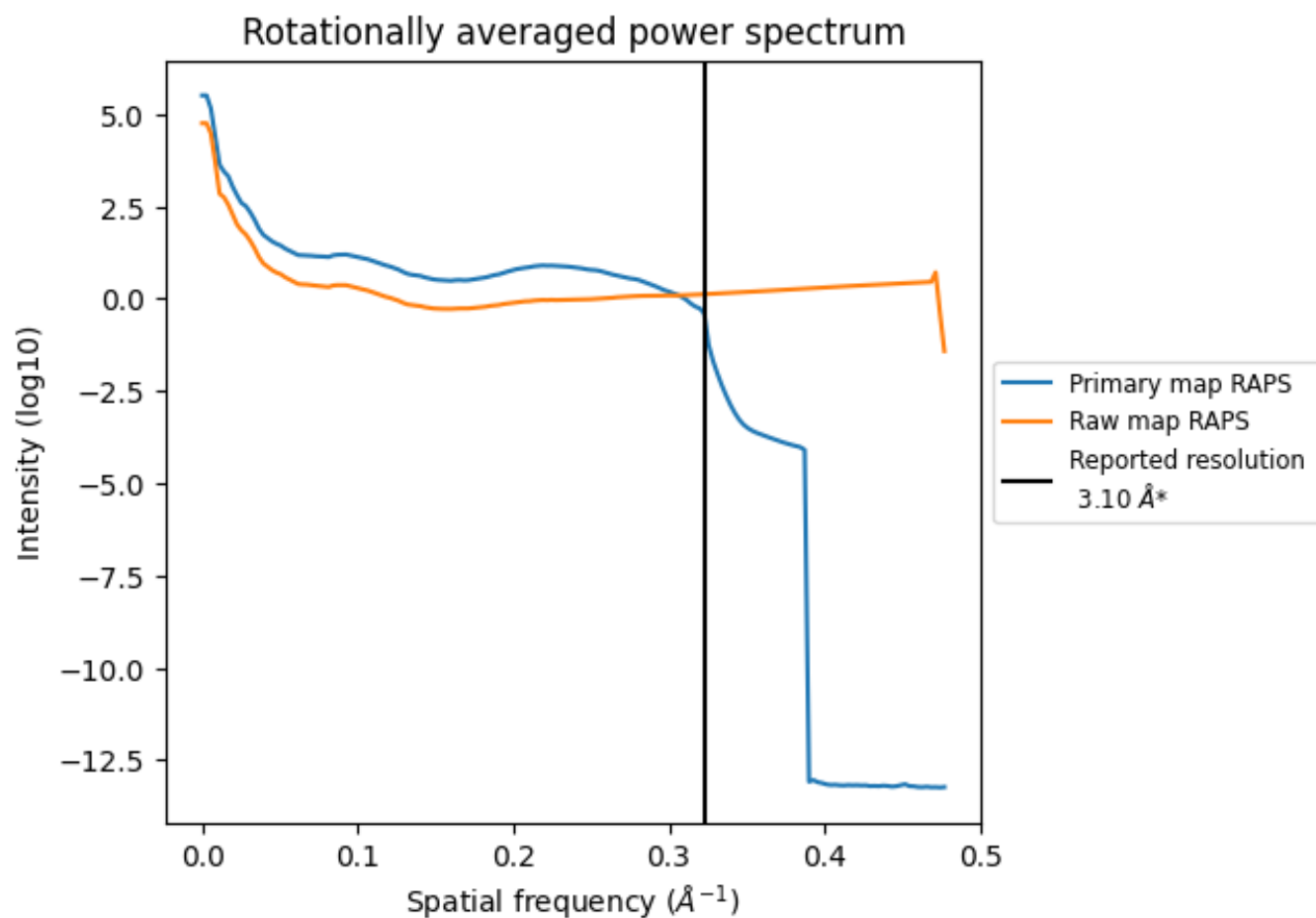
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 493 nm³; this corresponds to an approximate mass of 445 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 ⓘ

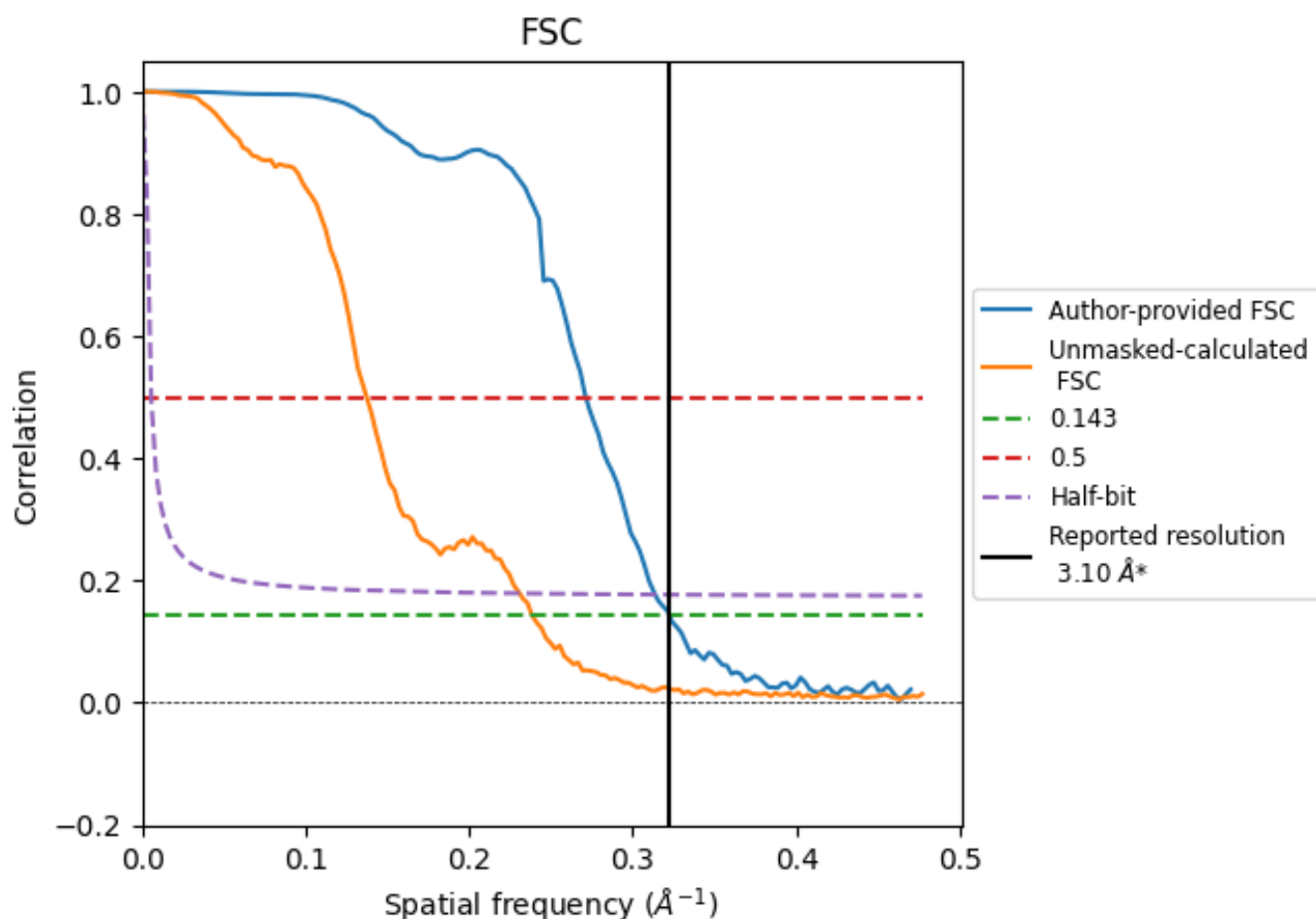


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

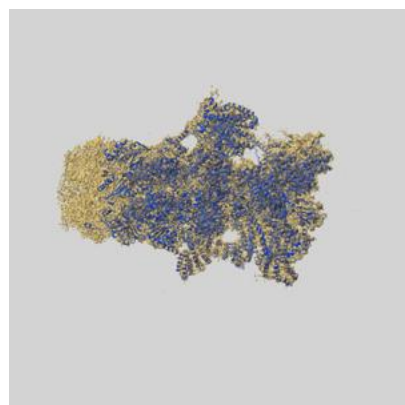
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.10	3.68	3.19
Unmasked-calculated*	4.19	7.28	4.33

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.19 differs from the reported value 3.1 by more than 10 %

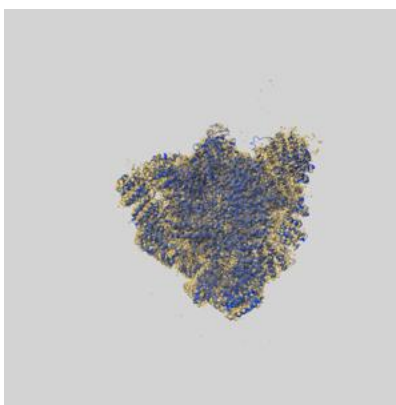
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47726 and PDB model 9E8O. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

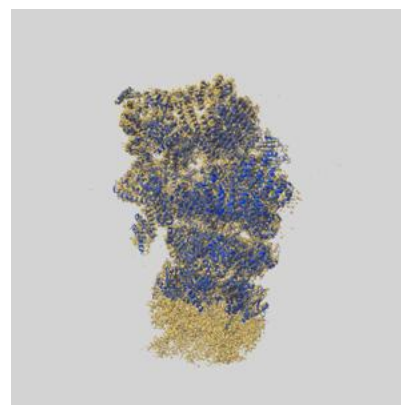
9.1 Map-model overlay [i](#)



X



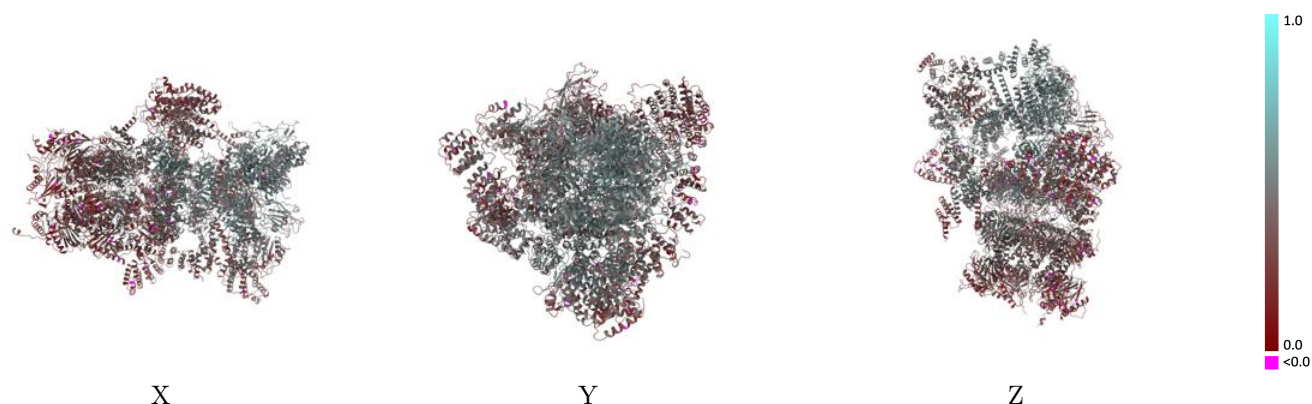
Y



Z

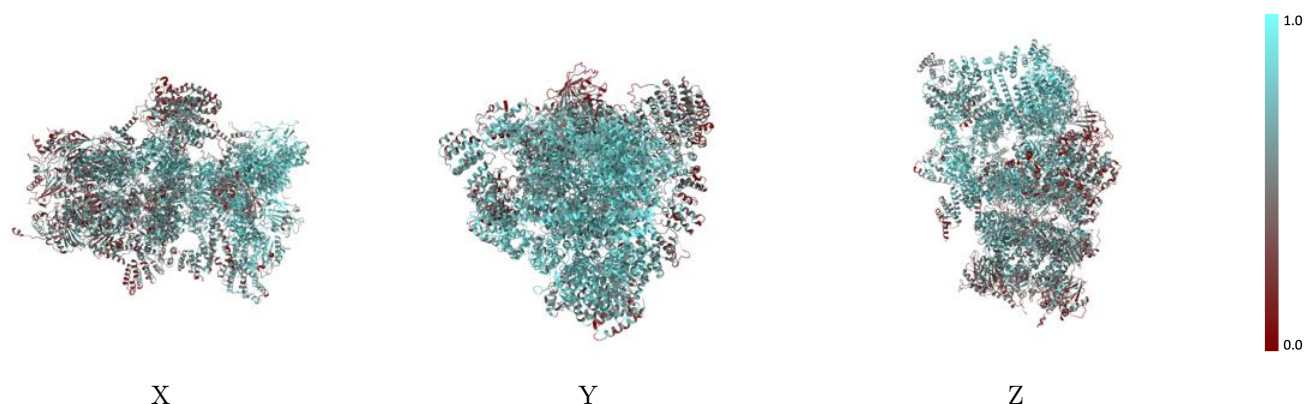
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



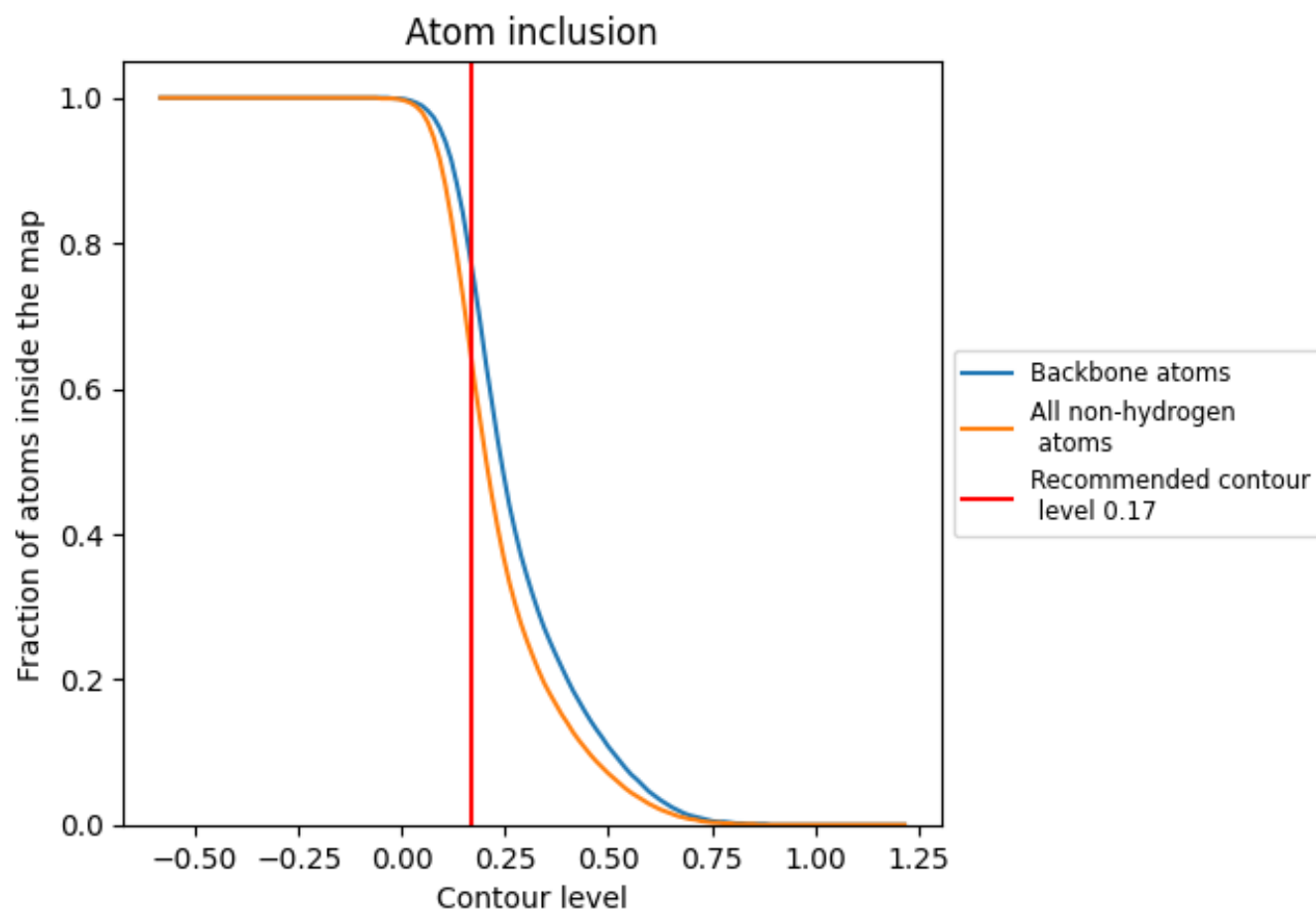
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 63% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6340	 0.4020
A	 0.5660	 0.3860
B	 0.7390	 0.4870
C	 0.8450	 0.5370
D	 0.8370	 0.5270
E	 0.6780	 0.4310
F	 0.4860	 0.3300
G	 0.6120	 0.3840
H	 0.7420	 0.4590
I	 0.6810	 0.4310
J	 0.6080	 0.3920
K	 0.5890	 0.3820
L	 0.5240	 0.3370
M	 0.5210	 0.3330
N	 0.5240	 0.3090
O	 0.5020	 0.3280
P	 0.4950	 0.3130
Q	 0.4660	 0.2970
R	 0.4530	 0.2820
S	 0.4280	 0.2680
T	 0.4660	 0.2580
U	 0.8230	 0.5130
V	 0.7110	 0.4450
W	 0.5260	 0.3260
X	 0.7220	 0.4230
Y	 0.7580	 0.4130
Z	 0.8000	 0.4870
a	 0.6880	 0.4020
b	 0.6830	 0.4180
c	 0.8390	 0.5360
d	 0.6220	 0.3810
e	 0.5700	 0.3110
f	 0.4350	 0.2970
g	 0.3210	 0.4050
u	 0.6840	 0.4830

