



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 05:05 PM UTC

PDB ID : 7PUA / pdb_00007pua
EMDB ID : EMD-13660
Title : Middle assembly intermediate of the Trypanosoma brucei mitoribosomal small subunit
Authors : Lenarcic, T.; Leibundgut, M.; Saurer, M.; Ramrath, D.J.F.; Fluegel, T.; Boehringer, D.; Ban, N.
Deposited on : 2021-09-29
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

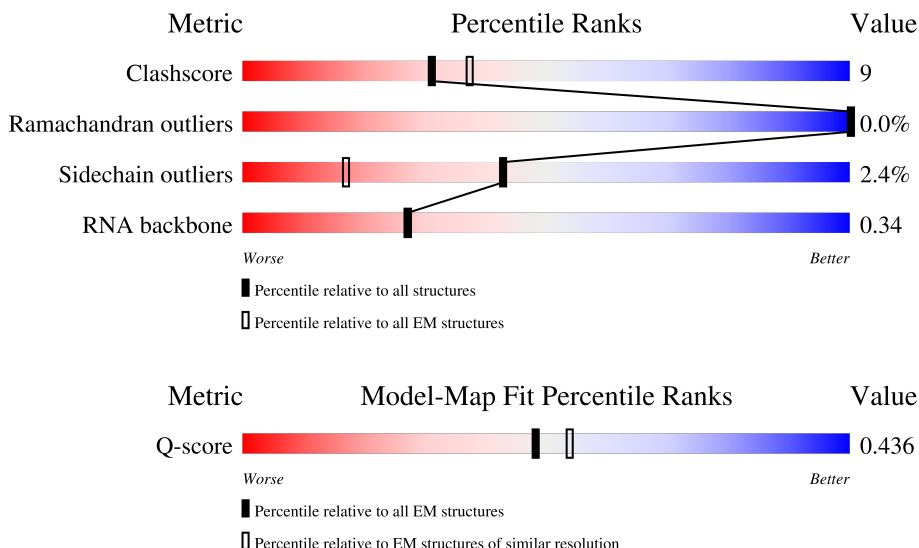
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	CA	621	22% 35% 35% 10% 19%
2	CB	3	33% 33% 33%
3	CC	74	22% 70% 24% 5%

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Mol	Chain	Length	Quality of chain
4	CE	435	
5	CF	160	
6	CH	282	
7	CI	443	
8	CJ	817	
9	CK	326	
10	CL	87	
11	CN	166	
12	CO	429	
13	CP	188	
14	CQ	307	
15	CR	320	
16	CS	244	
17	CU	193	
18	Ca	602	
19	Cb	325	
20	Cd	440	
21	Cg	498	
22	Ci	181	
23	Cj	257	
24	Ck	874	
25	Cm	215	
26	Cn	250	
27	Cp	187	
28	DB	1181	

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Mol	Chain	Length	Quality of chain
29	DC	1165	
30	DD	812	
31	DE	747	
32	DF	666	
33	DG	631	
34	DH	581	
35	DI	407	
36	DJ	396	
37	DK	324	
38	DL	307	
39	DO	282	
40	DP	274	
41	DR	270	
42	DT	247	
43	DU	228	
44	DV	183	
45	DW	179	
46	DX	169	
47	DY	163	
48	DZ	94	
49	Da	64	
50	F2	1024	
51	F3	966	
52	F5	754	
53	F6	676	

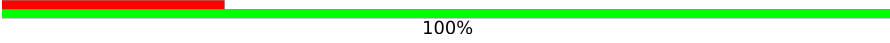
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Mol	Chain	Length	Quality of chain
54	F7	679	
55	F9	607	
56	FM	370	
56	FN	370	
57	FO	334	
58	FP	349	
59	FW	263	
60	FX	239	
61	FZ	178	
62	Fb	151	
63	Fc	148	
64	Fd	143	
65	Ff	848	
66	Fg	550	
67	Fh	318	
68	Fi	629	
69	IA	787	
70	IB	803	
71	U8	30	
72	UC	9	
73	UD	13	
74	UF	36	
75	UG	15	
76	UI	6	
77	UK	24	

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Mol	Chain	Length	Quality of chain
78	UM	8	 100%
78	UN	8	 25% 88% 12%
78	UQ	8	 25% 100%
79	UP	32	 41% 100%
80	Ua	10	 10% 100%
81	Ug	271	 35% 87% 12%

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 205280 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 RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	501	Total	C	N	O	P	0	0
			9866	4403	1529	3433	501		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	614	U	-	expression tag	GB 13740
CA	615	U	-	expression tag	GB 13740
CA	616	U	-	expression tag	GB 13740
CA	617	U	-	expression tag	GB 13740
CA	618	U	-	expression tag	GB 13740
CA	619	U	-	expression tag	GB 13740
CA	620	U	-	expression tag	GB 13740
CA	621	U	-	expression tag	GB 13740

- Molecule 2 is a RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CB	3	Total	C	N	O	P	0	0
			64	29	12	20	3		

- Molecule 3 is a protein called uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CC	74	Total	C	N	O	S	0	0
			646	451	96	98	1		

- Molecule 4 is a protein called Ribosomal_S5_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CE	373	Total	C	N	O	S	0	0
			3024	1915	556	538	15		

- Molecule 5 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CF	155	Total	C	N	O	S	0	0
			1279	810	226	237	6		

- Molecule 6 is a protein called 30S ribosomal protein S8, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CH	219	Total	C	N	O	S	0	0
			1799	1130	343	317	9		

- Molecule 7 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CI	421	Total	C	N	O	S	0	0
			3352	2111	598	627	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CI	370	ALA	VAL	conflict	UNP Q57W62

- Molecule 8 is a protein called LysM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CJ	782	Total	C	N	O	S	0	0
			6376	4034	1122	1191	29		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CJ	488	SER	ASN	conflict	UNP C9ZPU0

- Molecule 9 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CK	177	Total	C	N	O	S	0	0
			1440	895	273	264	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CK	3	ARG	GLN	conflict	UNP Q389T7
CK	138	UNK	ILE	conflict	UNP Q389T7

- Molecule 10 is a protein called uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CL	83	Total	C	N	O	S	0	0
			701	480	109	102	10		

- Molecule 11 is a protein called uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CN	157	Total	C	N	O	S	0	0
			1322	843	251	220	8		

- Molecule 12 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CO	360	Total	C	N	O	S	0	0
			2989	1899	557	517	16		

- Molecule 13 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CP	180	Total	C	N	O	S	0	0
			1489	956	274	250	9		

- Molecule 14 is a protein called 30S Ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CQ	247	Total	C	N	O	S	0	0
			2015	1279	379	348	9		

- Molecule 15 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CR	124	Total	C	N	O	S	0	0
			1051	680	196	173	2		

- Molecule 16 is a protein called uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CS	99	Total	C	N	O	S	0	0
			822	534	144	140	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CS	-11	ILE	ASN	conflict	UNP A0A3L6L621
CS	-10	VAL	CYS	conflict	UNP A0A3L6L621
CS	-9	TYR	LEU	conflict	UNP A0A3L6L621
CS	-8	PHE	LEU	conflict	UNP A0A3L6L621
CS	-7	HIS	PRO	conflict	UNP A0A3L6L621
CS	-6	CYS	LEU	conflict	UNP A0A3L6L621
CS	-5	CYS	LEU	conflict	UNP A0A3L6L621
CS	-4	THR	TYR	conflict	UNP A0A3L6L621
CS	-3	ARG	GLU	conflict	UNP A0A3L6L621
CS	-2	LYS	GLU	conflict	UNP A0A3L6L621
CS	?	-	VAL	deletion	UNP A0A3L6L621
CS	?	-	ARG	deletion	UNP A0A3L6L621

- Molecule 17 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CU	35	Total	C	N	O	S	0	0
			288	182	57	47	2		

- Molecule 18 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ca	501	Total	C	N	O	S	0	0
			4247	2720	753	753	21		

- Molecule 19 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Cb	149	Total	C	N	O	S	0	0
			1242	801	226	209	6		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cb	302	GLY	ARG	conflict	UNP C9ZNU0
Cb	312	UNK	-	expression tag	UNP C9ZNU0

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Chain	Residue	Modelled	Actual	Comment	Reference
Cb	313	CYS	-	expression tag	UNP C9ZNU0
Cb	314	SER	-	expression tag	UNP C9ZNU0
Cb	315	ARG	-	expression tag	UNP C9ZNU0
Cb	316	ASP	-	expression tag	UNP C9ZNU0
Cb	317	GLY	-	expression tag	UNP C9ZNU0
Cb	318	PHE	-	expression tag	UNP C9ZNU0
Cb	319	ALA	-	expression tag	UNP C9ZNU0
Cb	320	LEU	-	expression tag	UNP C9ZNU0
Cb	321	MET	-	expression tag	UNP C9ZNU0
Cb	322	LYS	-	expression tag	UNP C9ZNU0
Cb	323	ALA	-	expression tag	UNP C9ZNU0
Cb	324	ASN	-	expression tag	UNP C9ZNU0
Cb	325	LYS	-	expression tag	UNP C9ZNU0

- Molecule 20 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cd	205	Total	C	N	O	S	0	0
			1768	1124	323	312	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cd	299	UNK	GLY	conflict	UNP Q38DK6
Cd	364	UNK	GLY	conflict	UNP Q38DK6

- Molecule 21 is a protein called mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Cg	487	Total	C	N	O	S	0	0
			3943	2524	691	708	20		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cg	181	VAL	ALA	conflict	UNP Q585C2
Cg	498	ARG	-	expression tag	UNP Q585C2

- Molecule 22 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ci	165	Total	C	N	O	S	0	0
			1348	848	247	244	9		

- Molecule 23 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Cj	226	Total	C	N	O	S	0	0
			1792	1138	310	340	4		

- Molecule 24 is a protein called mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ck	673	Total	C	N	O	S	0	0
			5371	3371	974	1002	24		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ck	107	SER	LEU	conflict	UNP Q387C7
Ck	144	PHE	LEU	conflict	UNP Q387C7
Ck	253	TYR	PHE	conflict	UNP Q387C7
Ck	339	GLU	VAL	conflict	UNP Q387C7
Ck	815	GLY	ARG	conflict	UNP Q387C7
Ck	871	GLY	GLU	conflict	UNP Q387C7

- Molecule 25 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cm	31	Total	C	N	O	S	0	0
			232	136	43	47	6		

- Molecule 26 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Cn	49	Total	C	N	O	S	0	0
			425	278	88	56	3		

- Molecule 27 is a protein called Protein FYV4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Cp	168	Total	C	N	O	S	0	0
			1428	904	259	260	5		

- Molecule 28 is a protein called mS49.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	DB	1106	Total	C	N	O	S	0	0
			9112	5669	1712	1703	28		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DB	359	ILE	THR	conflict	UNP C9ZJE4

- Molecule 29 is a protein called mS50.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	DC	1099	Total	C	N	O	S	0	0
			8766	5528	1548	1659	31		

- Molecule 30 is a protein called mS51.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DD	764	Total	C	N	O	S	0	0
			6308	3998	1131	1143	36		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	1	UNK	-	expression tag	UNP D0A752
DD	2	UNK	-	expression tag	UNP D0A752
DD	3	UNK	-	expression tag	UNP D0A752
DD	4	UNK	-	expression tag	UNP D0A752
DD	5	UNK	-	expression tag	UNP D0A752
DD	6	UNK	-	expression tag	UNP D0A752
DD	7	UNK	-	expression tag	UNP D0A752
DD	8	UNK	-	expression tag	UNP D0A752
DD	9	UNK	-	expression tag	UNP D0A752
DD	10	UNK	-	expression tag	UNP D0A752
DD	11	UNK	-	expression tag	UNP D0A752
DD	12	UNK	-	expression tag	UNP D0A752
DD	13	UNK	-	expression tag	UNP D0A752
DD	14	UNK	-	expression tag	UNP D0A752
DD	15	UNK	-	expression tag	UNP D0A752
DD	16	UNK	-	expression tag	UNP D0A752
DD	17	UNK	-	expression tag	UNP D0A752
DD	26	UNK	ARG	conflict	UNP D0A752

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Chain	Residue	Modelled	Actual	Comment	Reference
DD	27	UNK	MET	conflict	UNP D0A752
DD	28	UNK	MET	conflict	UNP D0A752
DD	29	UNK	ARG	conflict	UNP D0A752
DD	30	UNK	ALA	conflict	UNP D0A752
DD	31	UNK	GLY	conflict	UNP D0A752
DD	32	UNK	SER	conflict	UNP D0A752
DD	33	UNK	GLY	conflict	UNP D0A752
DD	34	UNK	TYR	conflict	UNP D0A752
DD	35	UNK	GLN	conflict	UNP D0A752
DD	36	UNK	GLN	conflict	UNP D0A752
DD	37	UNK	LEU	conflict	UNP D0A752
DD	38	UNK	ARG	conflict	UNP D0A752
DD	39	UNK	ARG	conflict	UNP D0A752
DD	40	UNK	MET	conflict	UNP D0A752
DD	41	UNK	GLY	conflict	UNP D0A752
DD	42	UNK	MET	conflict	UNP D0A752
DD	43	UNK	PRO	conflict	UNP D0A752
DD	44	UNK	MET	conflict	UNP D0A752
DD	45	UNK	GLN	conflict	UNP D0A752
DD	46	UNK	VAL	conflict	UNP D0A752
DD	47	UNK	GLY	conflict	UNP D0A752
DD	48	UNK	MET	conflict	UNP D0A752
DD	49	UNK	GLY	conflict	UNP D0A752
DD	50	UNK	TRP	conflict	UNP D0A752
DD	51	UNK	ARG	conflict	UNP D0A752
DD	52	UNK	LYS	conflict	UNP D0A752
DD	53	UNK	VAL	conflict	UNP D0A752
DD	54	UNK	ASP	conflict	UNP D0A752
DD	55	UNK	SER	conflict	UNP D0A752
DD	56	UNK	PHE	conflict	UNP D0A752

- Molecule 31 is a protein called mS52.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	DE	628	Total	C	N	O	S	0	0
			5114	3243	926	924	21		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DE	378	UNK	LYS	conflict	UNP Q386Q7
DE	384	UNK	THR	conflict	UNP Q386Q7

- Molecule 32 is a protein called mS53.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	DF	594	Total	C	N	O	S	0	0
			4785	3001	904	855	25		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DF	18	THR	ALA	conflict	UNP C9ZXX4
DF	372	ASN	ASP	conflict	UNP C9ZXX4
DF	406	ASN	SER	conflict	UNP C9ZXX4
DF	636	UNK	GLY	conflict	UNP C9ZXX4
DF	638	LYS	ARG	conflict	UNP C9ZXX4

- Molecule 33 is a protein called mS54.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	DG	557	Total	C	N	O	S	0	0
			4511	2835	826	819	31		

- Molecule 34 is a protein called mS55.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	DH	568	Total	C	N	O	S	0	0
			4608	2888	858	840	22		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DH	75	GLN	LYS	conflict	UNP A0A3L6LGC8

- Molecule 35 is a protein called mS56.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	DI	390	Total	C	N	O	S	0	0
			3182	2020	554	594	14		

- Molecule 36 is a protein called mS57.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	DJ	356	Total	C	N	O	S	0	0
			2908	1855	511	528	14		

- Molecule 37 is a protein called mS58.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	DK	264	Total	C	N	O	S	0	0
			2092	1317	375	395	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DK	97	ASP	SER	conflict	UNP A0A3L6L3U6

- Molecule 38 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	DL	234	Total	C	N	O	S	0	0
			1904	1216	342	335	11		

- Molecule 39 is a protein called mS62.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	DO	194	Total	C	N	O	S	0	0
			1567	981	286	291	9		

- Molecule 40 is a protein called mS63.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	DP	210	Total	C	N	O	S	0	0
			1784	1145	318	312	9		

- Molecule 41 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	DR	252	Total	C	N	O	S	0	0
			2034	1309	371	344	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DR	128	PRO	SER	conflict	UNP C9ZPP1

- Molecule 42 is a protein called Rhodanese domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	DT	239	Total	C	N	O	S	0	0
			2058	1321	364	362	11		

- Molecule 43 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	DU	217	Total	C	N	O	S	0	0
			1730	1091	305	329	5		

- Molecule 44 is a protein called mS69.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	DV	160	Total	C	N	O	S	0	0
			1346	855	252	235	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DV	163	ALA	THR	conflict	UNP Q57UZ6

- Molecule 45 is a protein called mS70.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	DW	136	Total	C	N	O	S	0	0
			1160	741	220	194	5		

- Molecule 46 is a protein called mS71.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	DX	129	Total	C	N	O	S	0	0
			1097	697	206	187	7		

- Molecule 47 is a protein called mS72.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	DY	154	Total	C	N	O	S	0	0
			1295	829	247	214	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DY	34	HIS	ASP	conflict	UNP Q57YD4

- Molecule 48 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	DZ	28	Total	C	N	O	S	0	0
			237	156	39	41	1		

- Molecule 49 is a protein called mS74.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Da	36	Total	C	N	O	S	0	0
			320	202	70	46	2		

- Molecule 50 is a protein called PPR_long domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F2	890	Total	C	N	O	S	0	0
			7125	4483	1254	1349	39		

- Molecule 51 is a protein called mt-SAF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	F3	911	Total	C	N	O	S	0	0
			7039	4391	1250	1346	52		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	44	THR	ALA	conflict	UNP Q38E61
F3	190	VAL	ILE	conflict	UNP Q38E61
F3	303	ALA	SER	conflict	UNP Q38E61
F3	418	ASP	ASN	conflict	UNP Q38E61

- Molecule 52 is a protein called mt-SAF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F5	620	Total	C	N	O	S	0	0
			5056	3154	938	933	31		

- Molecule 53 is a protein called DUF4460 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	F6	522	Total	C	N	O	S	0	0
			4195	2655	729	794	17		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F6	285	ARG	HIS	conflict	UNP Q38FQ8
F6	291	ILE	THR	conflict	UNP Q38FQ8
F6	602	ALA	VAL	conflict	UNP Q38FQ8
F6	676	CYS	-	expression tag	UNP Q38FQ8

- Molecule 54 is a protein called mt-SAF7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	F7	652	Total	C	N	O	S	0	0
			5166	3284	908	938	36		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F7	36	ILE	THR	conflict	UNP Q57UW6
F7	470	GLU	LYS	conflict	UNP Q57UW6
F7	474	VAL	ALA	conflict	UNP Q57UW6

- Molecule 55 is a protein called mt-SAF9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	F9	540	Total	C	N	O	S	0	0
			4422	2732	830	845	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F9	?	-	GLU	deletion	UNP C9ZSL5

- Molecule 56 is a protein called mt-SAF21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	FM	327	Total	C	N	O	S	0	0
			2457	1521	450	466	20		
56	FN	320	Total	C	N	O	S	0	0
			2403	1484	440	459	20		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FM	326	HIS	ARG	conflict	UNP C9ZJW2
FM	330	UNK	GLY	conflict	UNP C9ZJW2
FN	326	HIS	ARG	conflict	UNP C9ZJW2
FN	330	UNK	GLY	conflict	UNP C9ZJW2

- Molecule 57 is a protein called mt-SAF22.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	FO	328	Total	C	N	O	S	0	0
			2700	1692	513	481	14		

- Molecule 58 is a protein called mt-SAF23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	FP	348	Total	C	N	O	S	0	0
			2643	1682	464	487	10		

- Molecule 59 is a protein called LMWPc domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	FW	238	Total	C	N	O	S	0	0
			1960	1227	375	352	6		

- Molecule 60 is a protein called mt-SAF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	FX	220	Total	C	N	O	S	0	0
			1741	1093	318	316	14		

- Molecule 61 is a protein called mt-SAF29.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	FZ	160	Total	C	N	O	S	0	0
			1262	786	212	257	7		

- Molecule 62 is a protein called mt-SAF31.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Fb	125	Total	C	N	O	S	0	0
			1061	682	194	178	7		

- Molecule 63 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Fc	83	Total	C	N	O	S	0	0
			660	421	104	134	1		

- Molecule 64 is a protein called DUF4379 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Fd	93	Total	C	N	O	S	0	0
			738	469	143	118	8		

- Molecule 65 is a protein called DNA photolyase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ff	623	Total	C	N	O	S	0	0
			5006	3176	896	911	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ff	109	ALA	VAL	conflict	UNP D0A9A9
Ff	127	UNK	TYR	conflict	UNP D0A9A9
Ff	138	GLN	ARG	conflict	UNP D0A9A9

- Molecule 66 is a protein called Acyl transferase-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Fg	520	Total	C	N	O	S	0	0
			4048	2545	710	763	30		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Fg	159	ILE	VAL	conflict	UNP C9ZYZ4
Fg	271	ILE	VAL	conflict	UNP C9ZYZ4
Fg	363	MET	ARG	conflict	UNP C9ZYZ4
Fg	399	UNK	GLU	conflict	UNP C9ZYZ4
Fg	436	ASP	GLU	conflict	UNP C9ZYZ4

- Molecule 67 is a protein called mt-SAF37.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Fh	239	Total	C	N	O	S	0	0
			1867	1159	346	348	14		

- Molecule 68 is a protein called mt-SAF38.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Fi	475	Total	C	N	O	S	0	0
			3797	2410	693	670	24		

- Molecule 69 is a protein called Translation initiation factor IF-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	IA	704	Total	C	N	O	S	0	0
			5478	3433	986	1032	27		

- Molecule 70 is a protein called mt-SAF39.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	IB	491	Total	C	N	O	S	0	0
			3867	2415	723	712	17		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IB	98	LYS	GLU	conflict	UNP D0A0V4
IB	206	ILE	MET	conflict	UNP D0A0V4
IB	572	HIS	ARG	conflict	UNP D0A0V4
IB	798	PRO	ALA	conflict	UNP D0A0V4

- Molecule 71 is a protein called Unk8.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	U8	30	Total	C	N	O	0	0
			150	90	30	30		

- Molecule 72 is a protein called UnkC.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	UC	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 73 is a protein called UnkD.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	UD	13	Total	C	N	O	0	0
			65	39	13	13		

- Molecule 74 is a protein called UnkF.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	UF	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 75 is a protein called UnkG.

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

- Molecule 76 is a protein called UnkI.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	UI	6	Total	C	N	O	0	0
			30	18	6	6		

- Molecule 77 is a protein called UnkK.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	UK	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 78 is a protein called Unk.

Mol	Chain	Residues	Atoms				AltConf	Trace
78	UM	8	Total	C	N	O	0	0
			40	24	8	8		
78	UN	8	Total	C	N	O	0	0
			40	24	8	8		
78	UQ	8	Total	C	N	O	0	0
			40	24	8	8		

- Molecule 79 is a protein called UnkP.

Mol	Chain	Residues	Atoms				AltConf	Trace
79	UP	32	Total	C	N	O	0	0
			160	96	32	32		

- Molecule 80 is a protein called Unka.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	Ua	10	Total	C	N	O	0	0
			50	30	10	10		

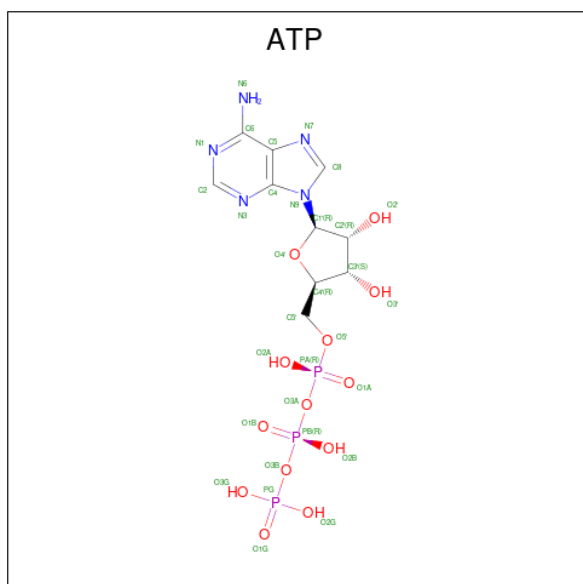
- Molecule 81 is a protein called Unkg.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	Ug	238	Total	C	N	O	0	0
			1190	714	238	238		

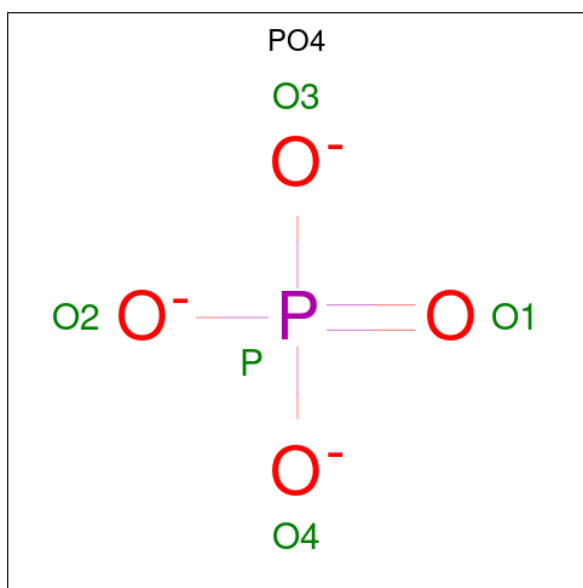
- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	CA	4	Total	Mg	0
			4	4	
82	CQ	1	Total	Mg	0
			1	1	
82	Cg	1	Total	Mg	0
			1	1	
82	IA	1	Total	Mg	0
			1	1	

- Molecule 83 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

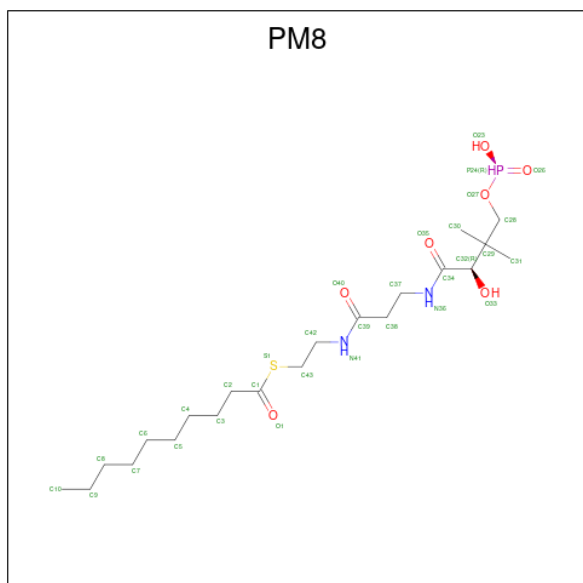


- Molecule 84 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			AltConf
84	FW	1	Total	O	P	0
			5	4	1	
84	IA	1	Total	O	P	0
			5	4	1	

- Molecule 85 is S-(2-([N-(2-HYDROXY-4-([HYDROXY(OXIDO)PHOSPHINO]OXY)-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (CCD ID: PM8) (formula: $C_{21}H_{41}N_2O_7PS$).

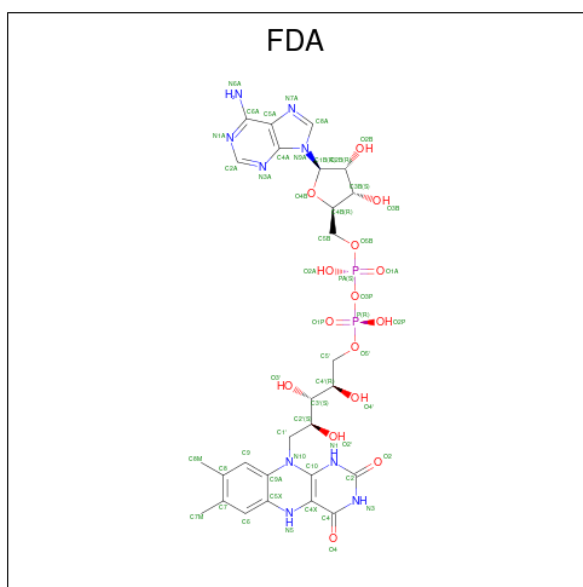


Mol	Chain	Residues	Atoms						AltConf
85	Fc	1	Total	C	N	O	P	S	0
			32	21	2	7	1	1	

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

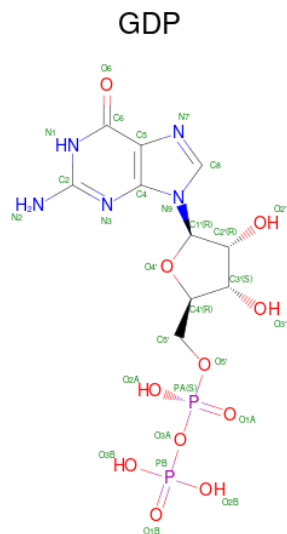
Mol	Chain	Residues	Atoms	AltConf
86	Fd	1	Total Zn 1 1	0

- Molecule 87 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					AltConf
87	Ff	1	Total 53	C 27	N 9	O 15	P 2	0

- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
88	IA	1	Total 28	C 10	N 5	O 11	P 2	0

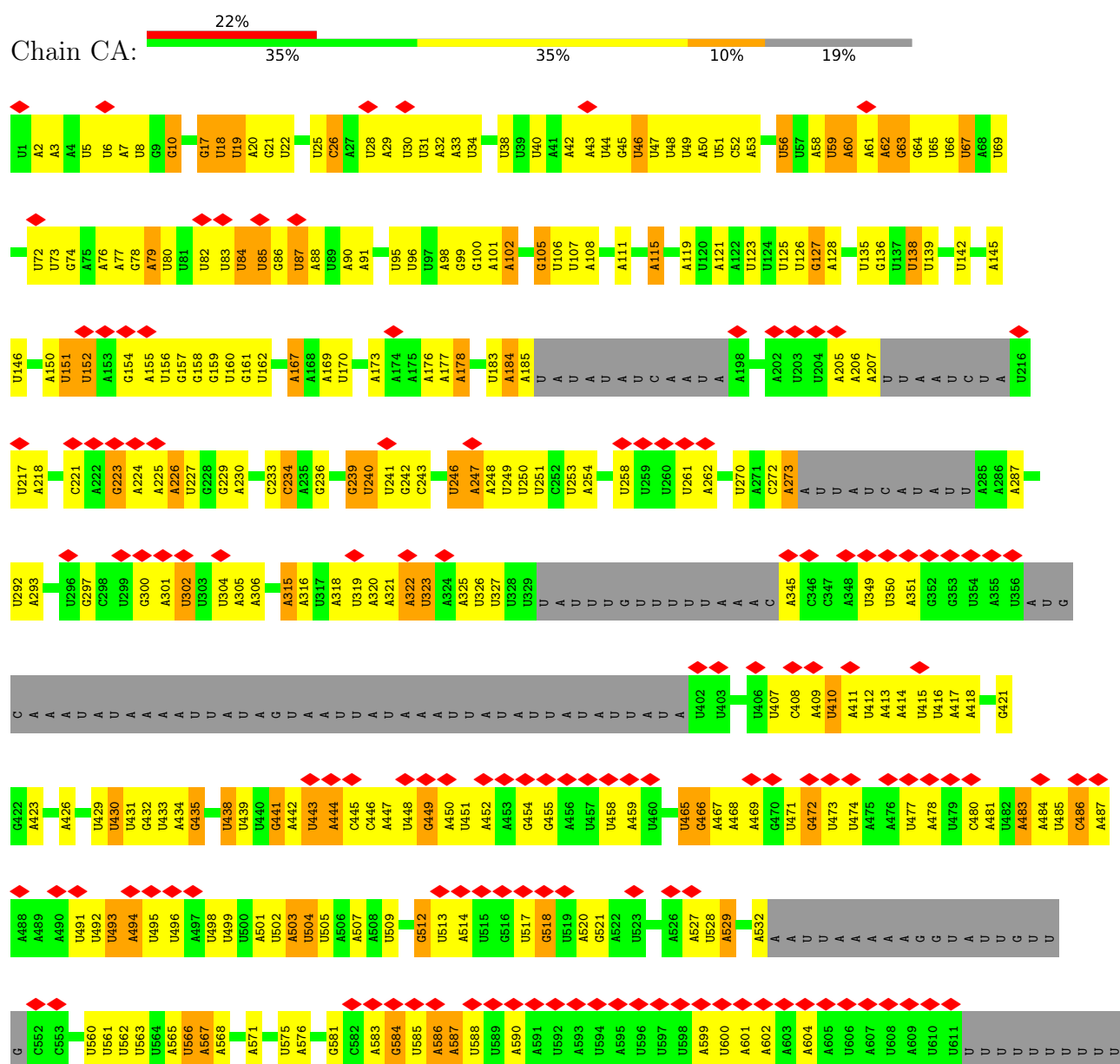
- Molecule 89 is water.

Mol	Chain	Residues	Atoms	AltConf
89	Cg	3	Total O 3 3	0
89	IA	2	Total O 2 2	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.

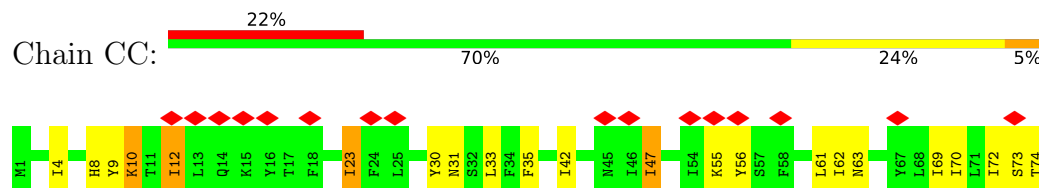
• Molecule 1: 9S rRNA



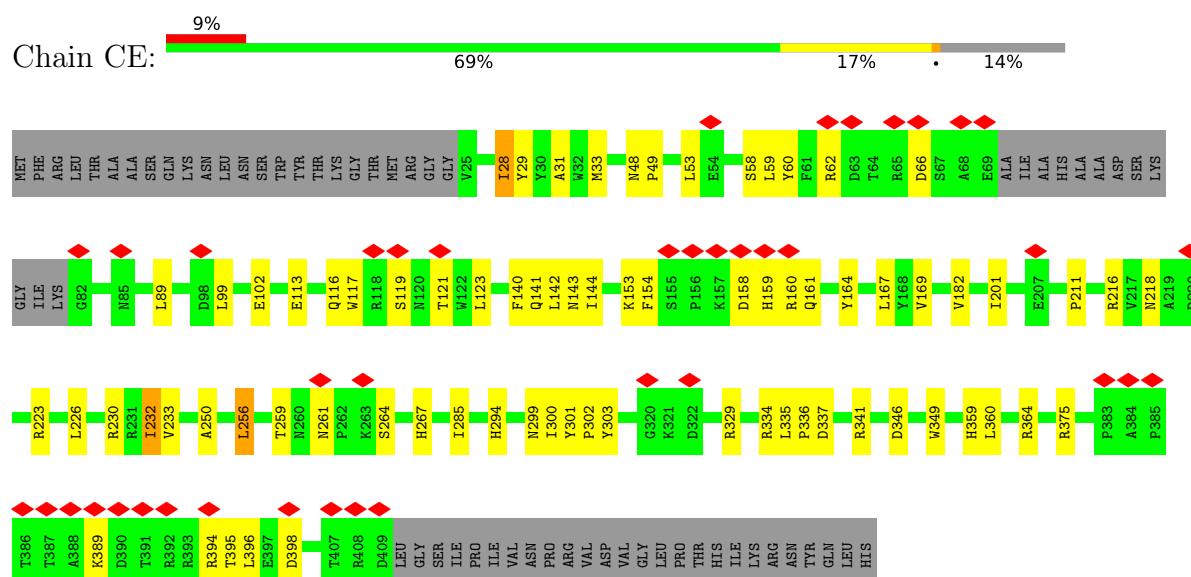
• Molecule 2: 9S rRNA



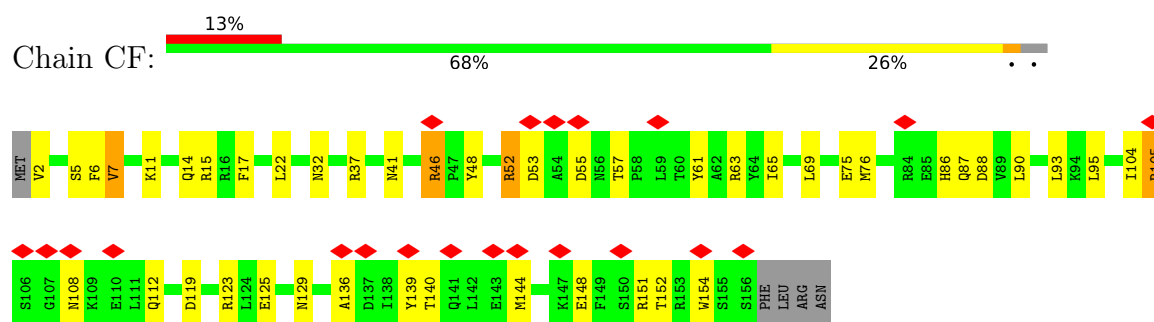
- Molecule 3: uS3m



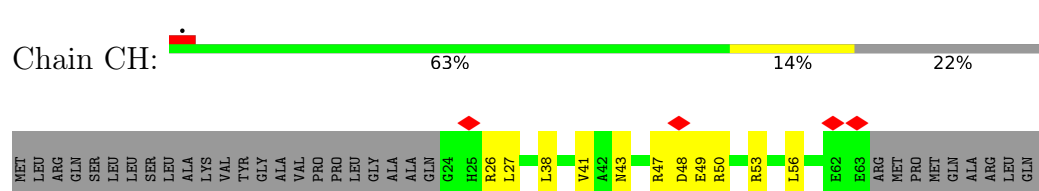
- Molecule 4: Ribosomal_S5_C domain-containing protein

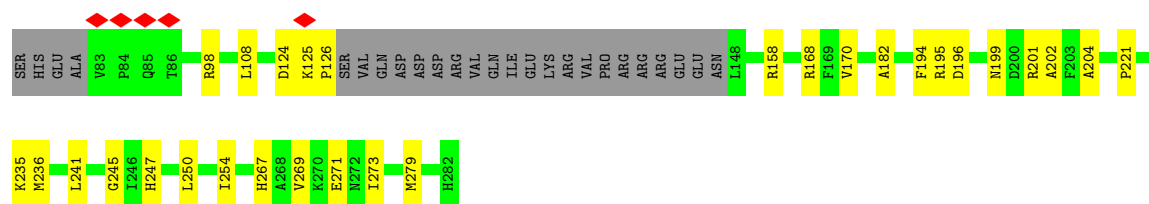


- Molecule 5: bS6m

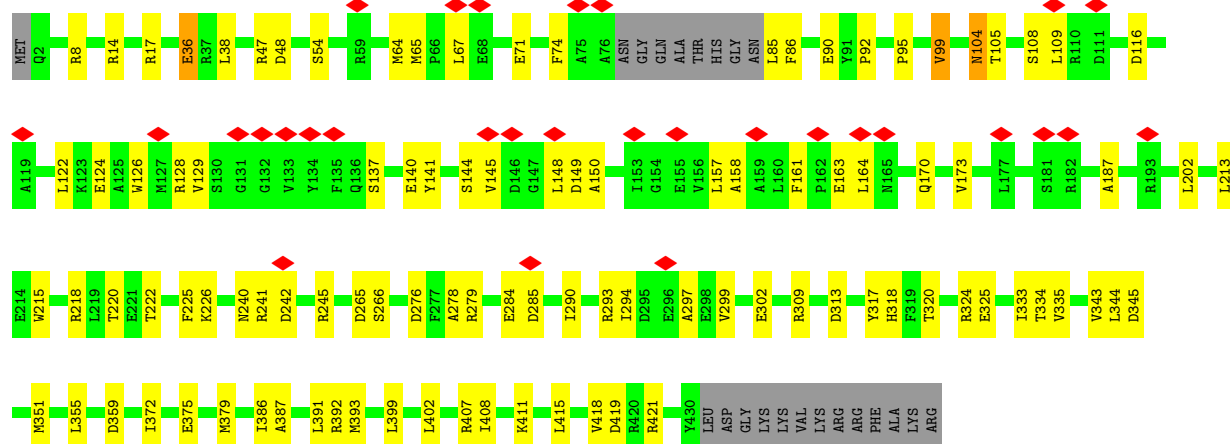


- Molecule 6: 30S ribosomal protein S8, putative

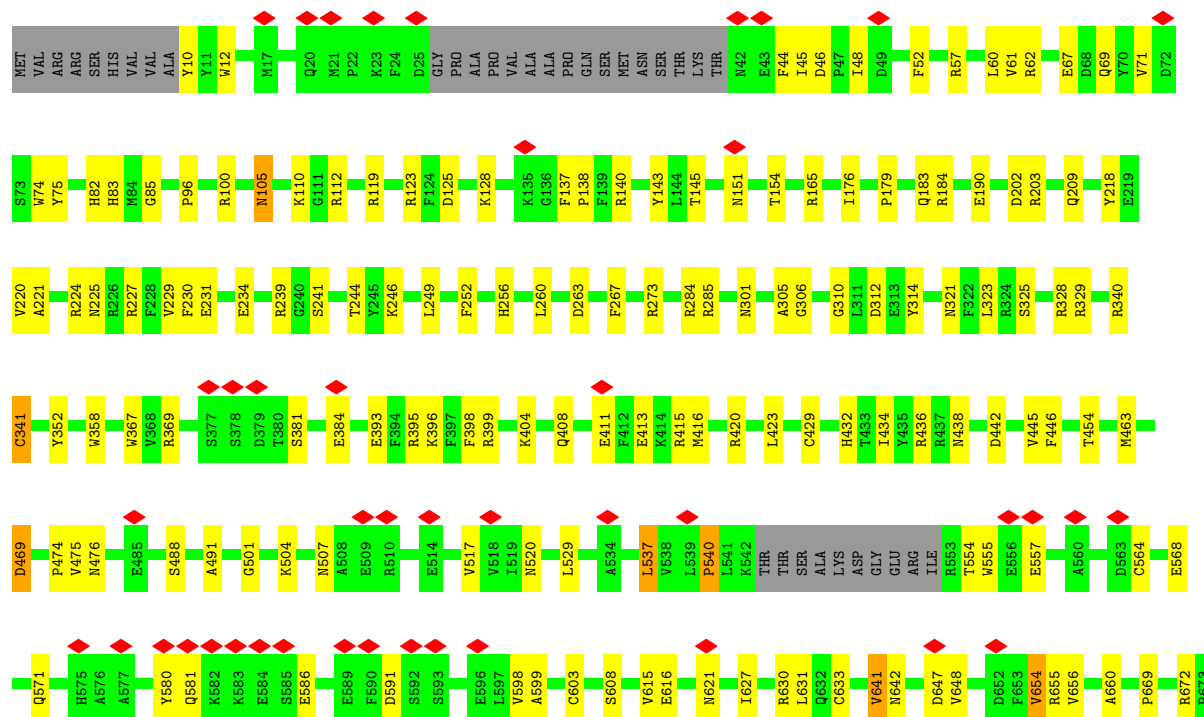
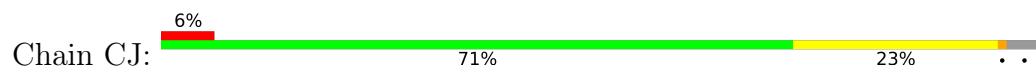




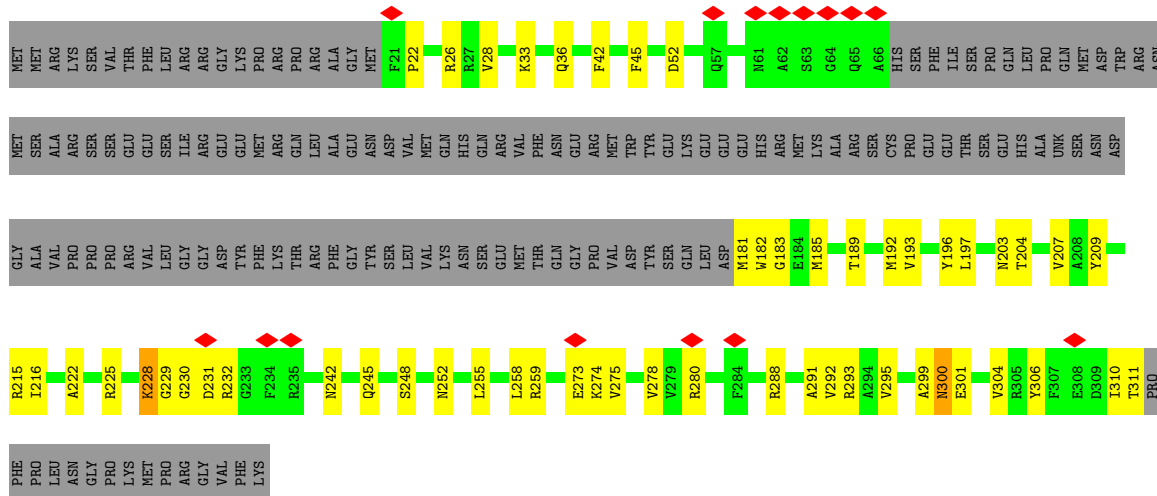
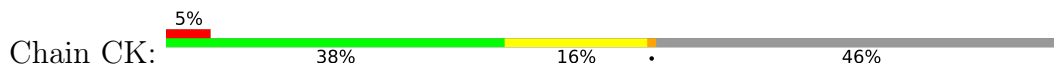
• Molecule 7: uS9m



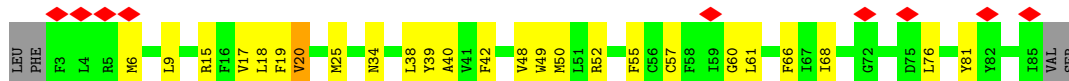
• Molecule 8: LysM domain-containing protein



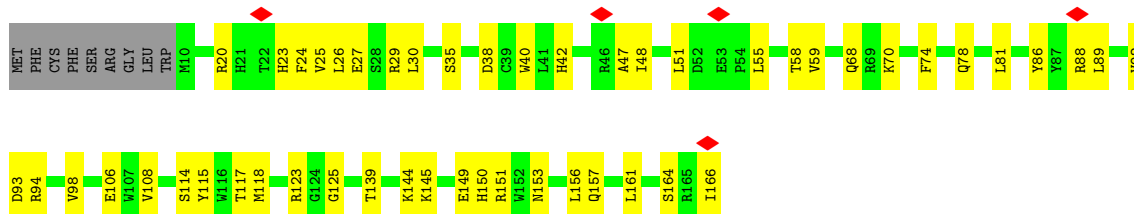
- Molecule 9: uS11m



- Molecule 10: uS12m

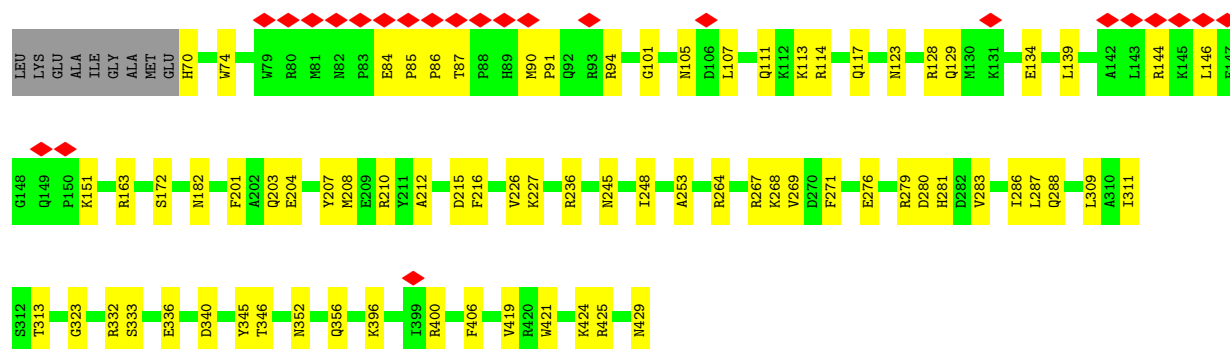


- Molecule 11: uS14m

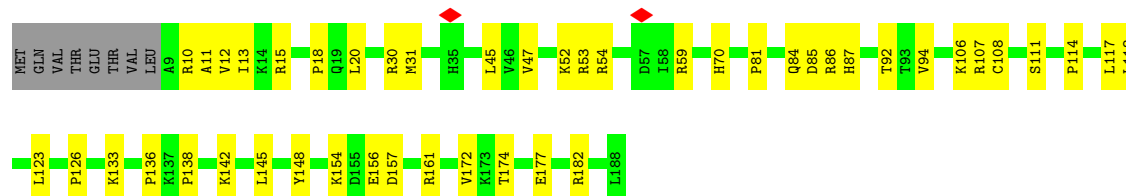


- Molecule 12: uS15m

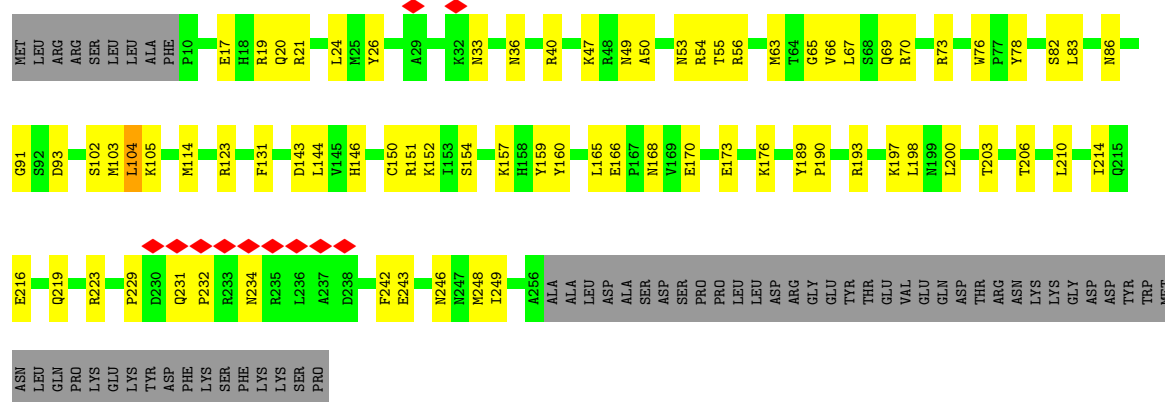




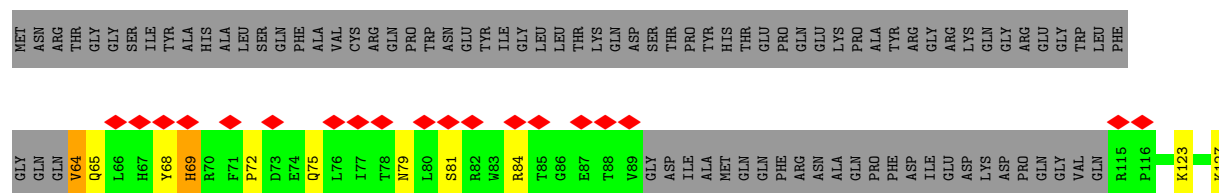
• Molecule 13: bS16m

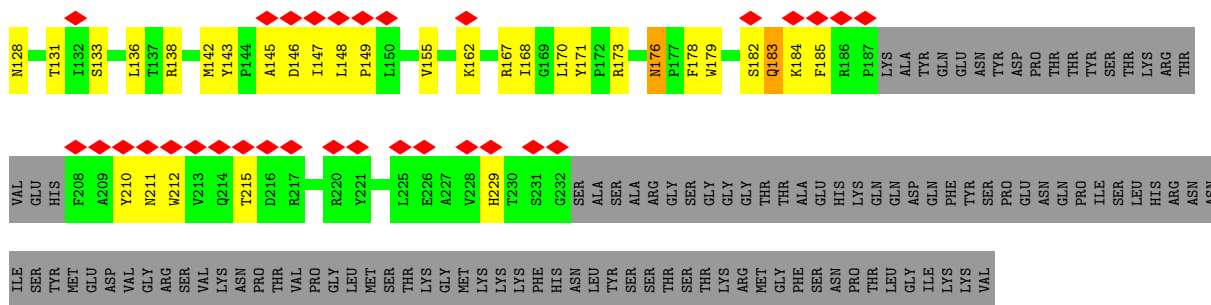


• Molecule 14: 30S Ribosomal protein S17, putative

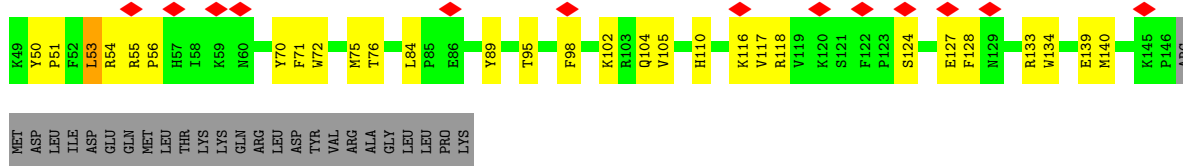
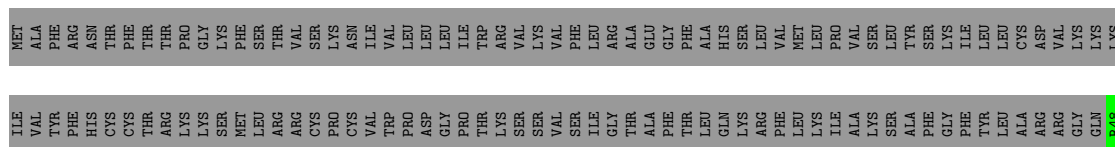


• Molecule 15: bS18m

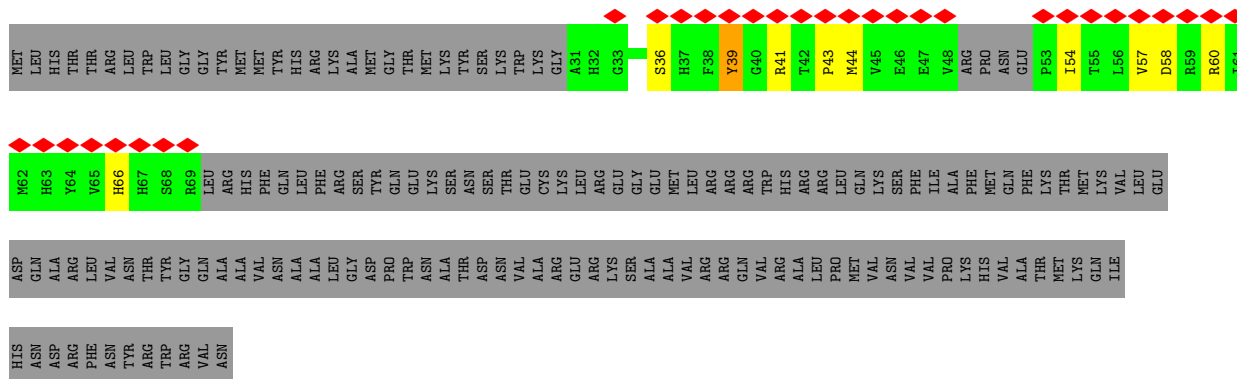




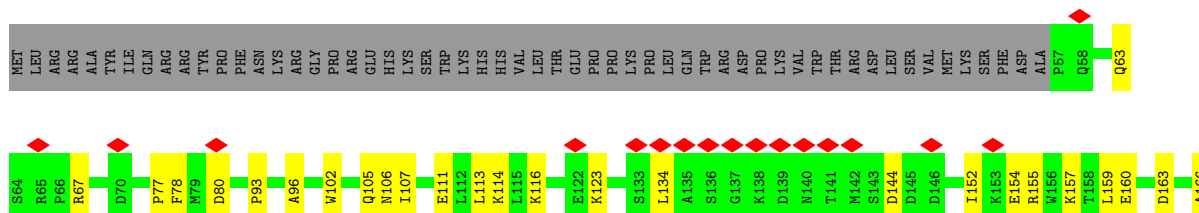
• Molecule 16: uS19m



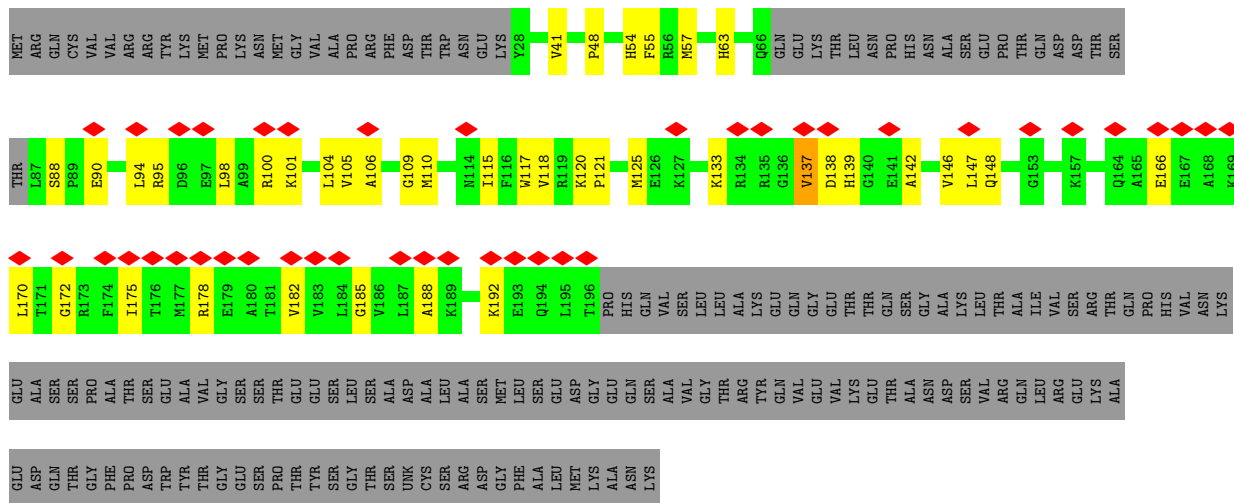
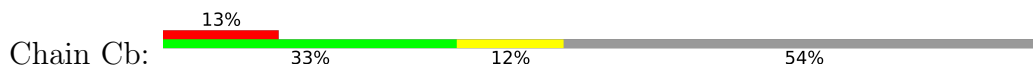
• Molecule 17: bS21m



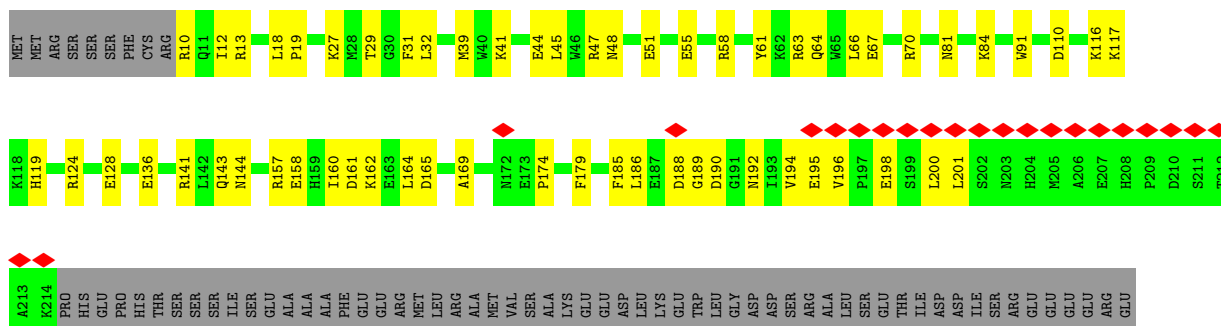
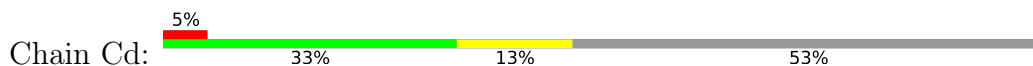
• Molecule 18: mS22

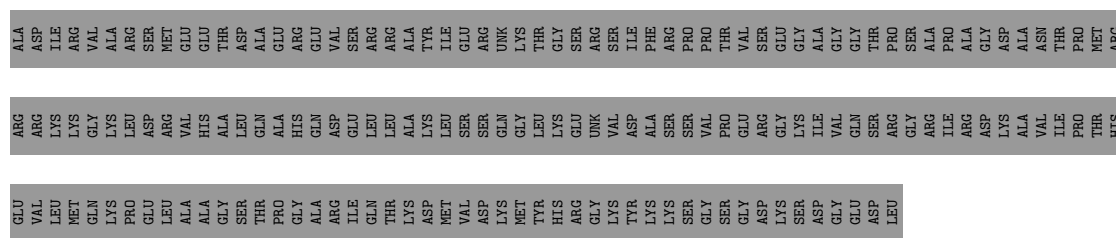


- Molecule 19: mS23



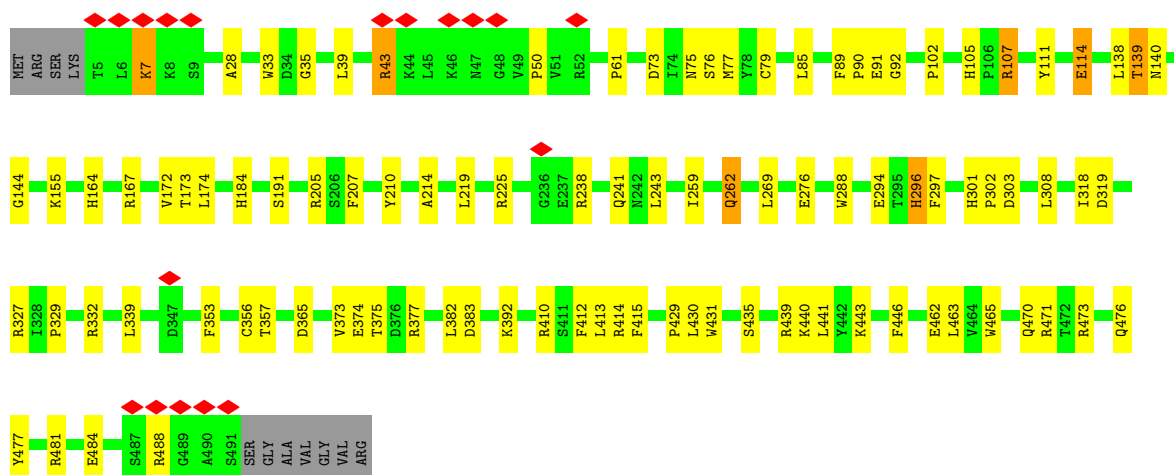
- Molecule 20: mS26





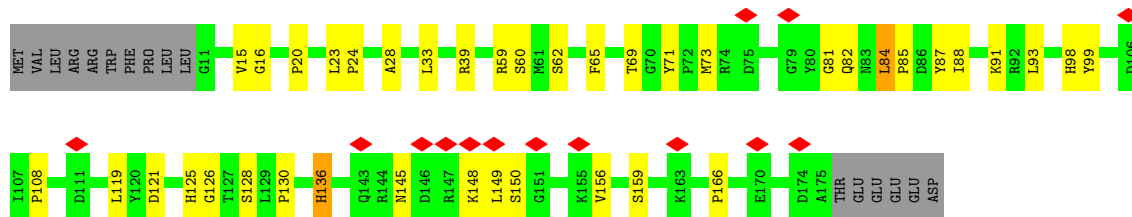
• Molecule 21: mS29

Chain Cg: 78% 18% ..



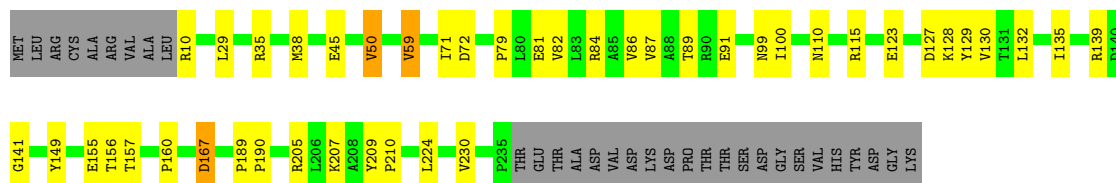
• Molecule 22: mS33

Chain Ci: 8% 69% 21% 9%



• Molecule 23: mS34

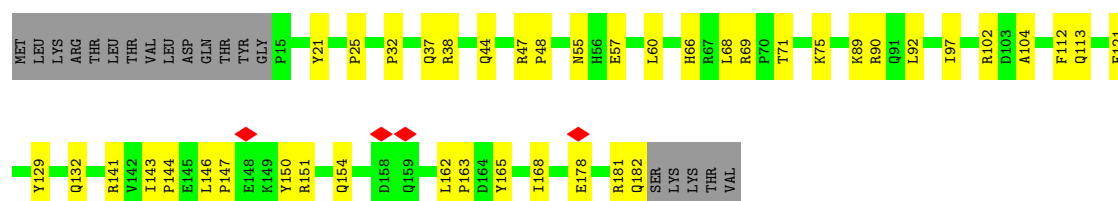
Chain Cj: 71% 16% 12%



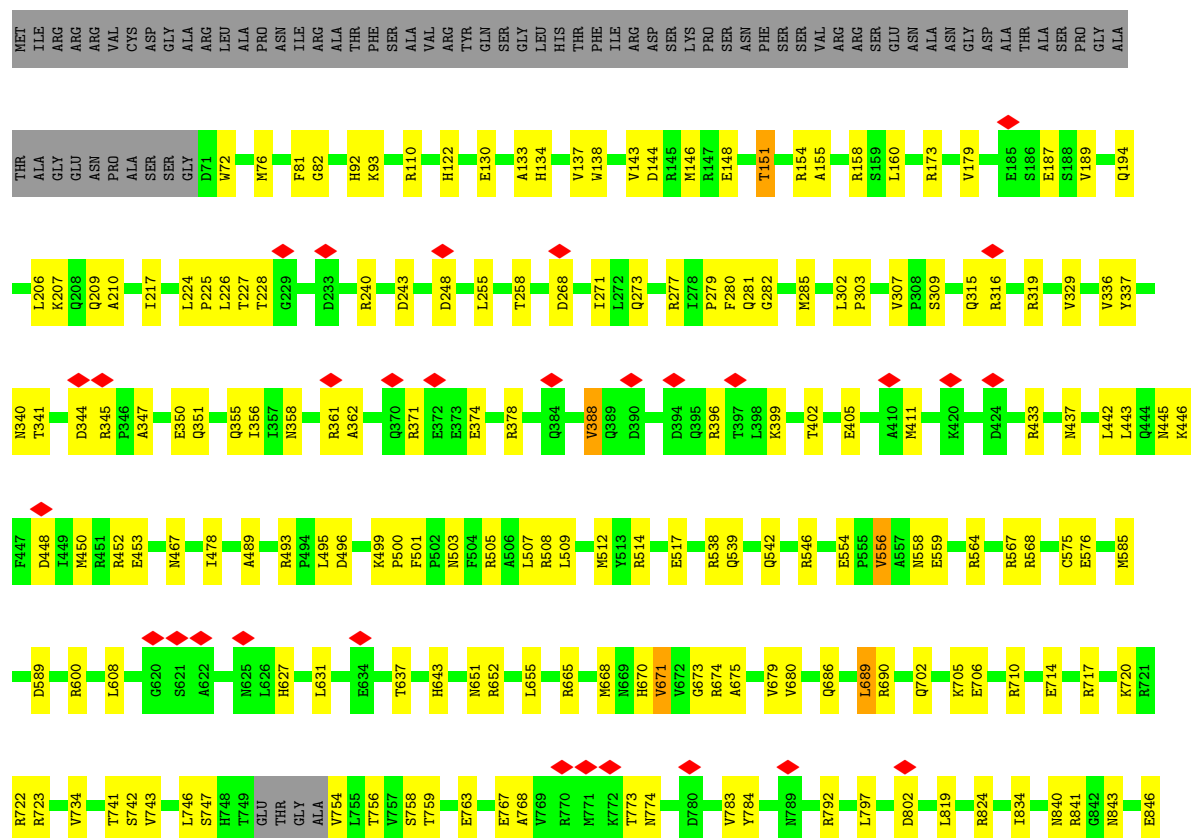
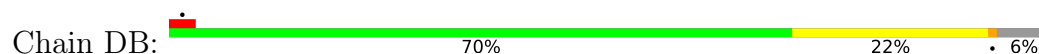
• Molecule 24: mS35

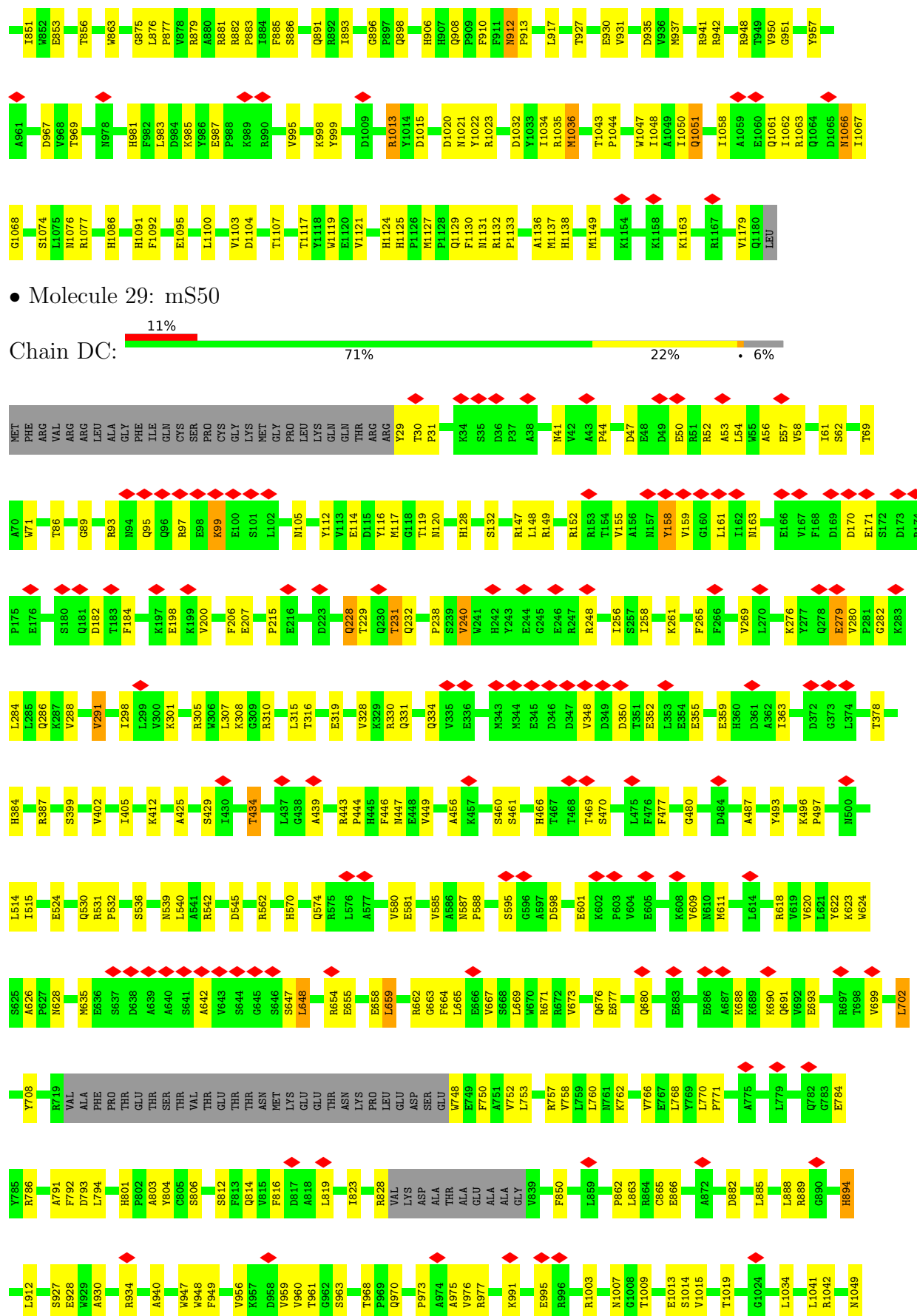
Chain Ck: 6% 59% 18% 23%

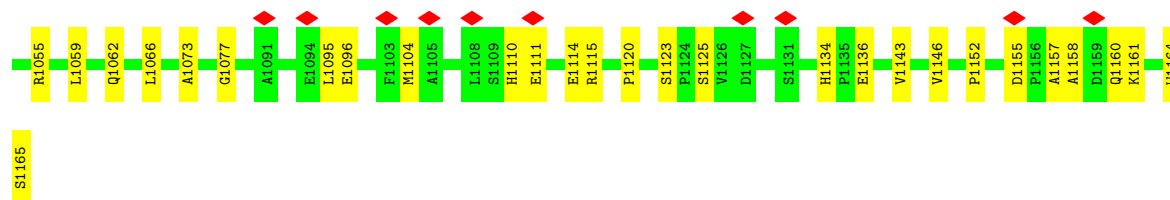
- Molecule 27: Protein FYV4, mitochondrial



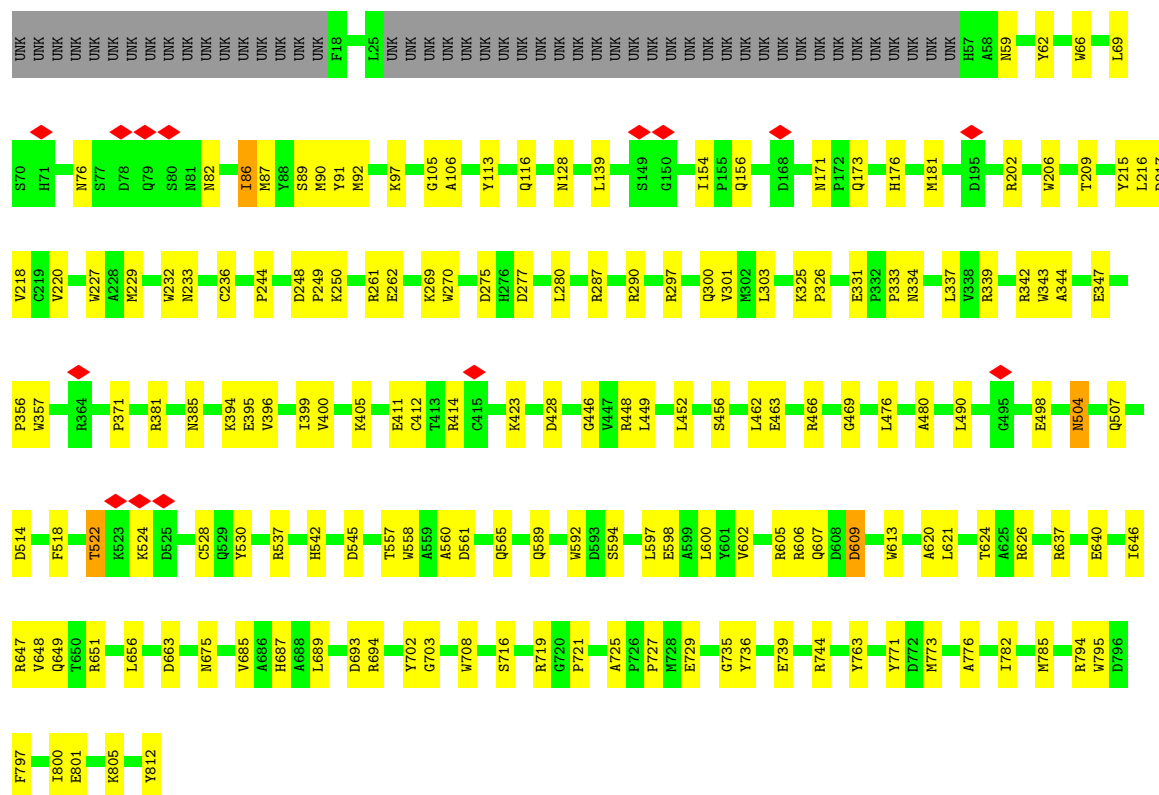
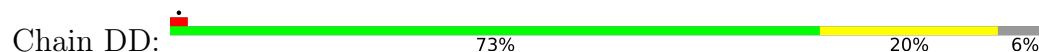
- Molecule 28: mS49



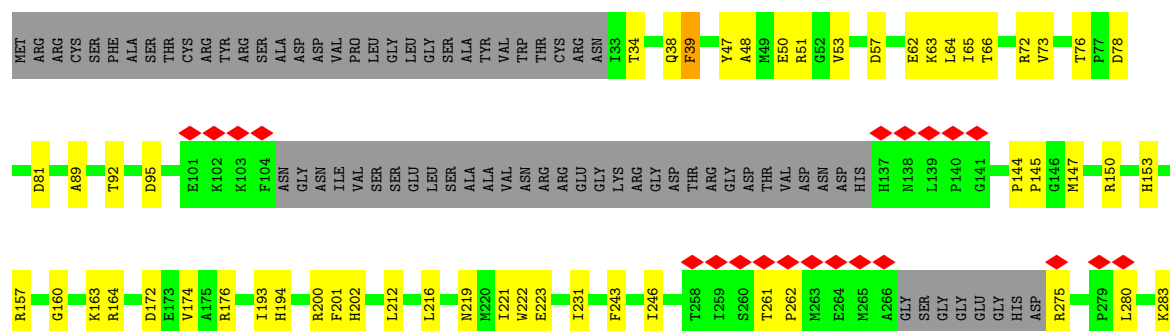


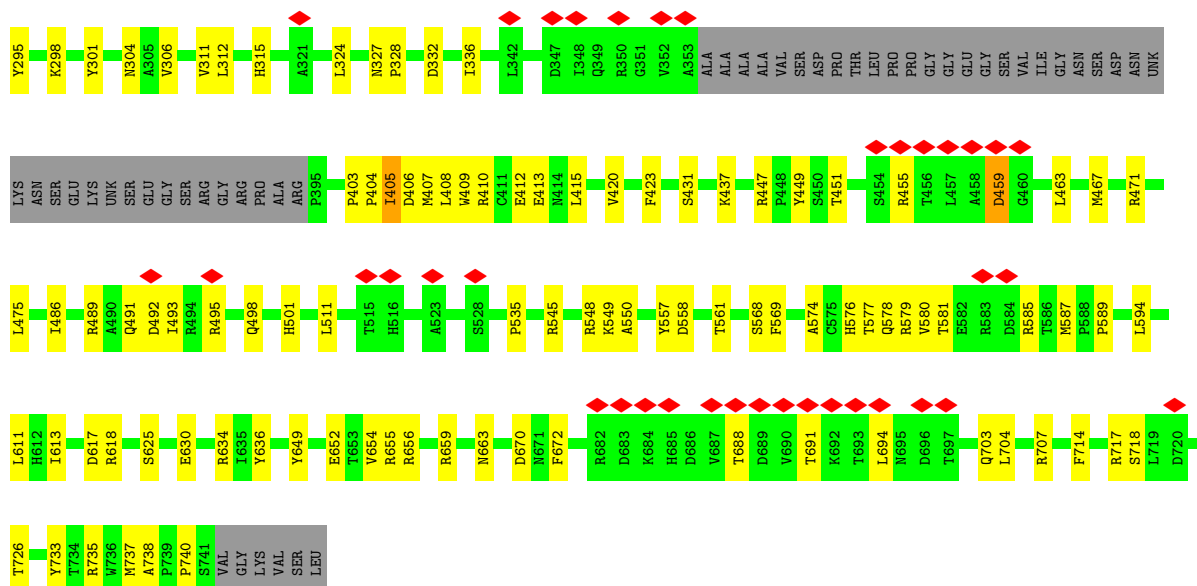


• Molecule 30: mS51



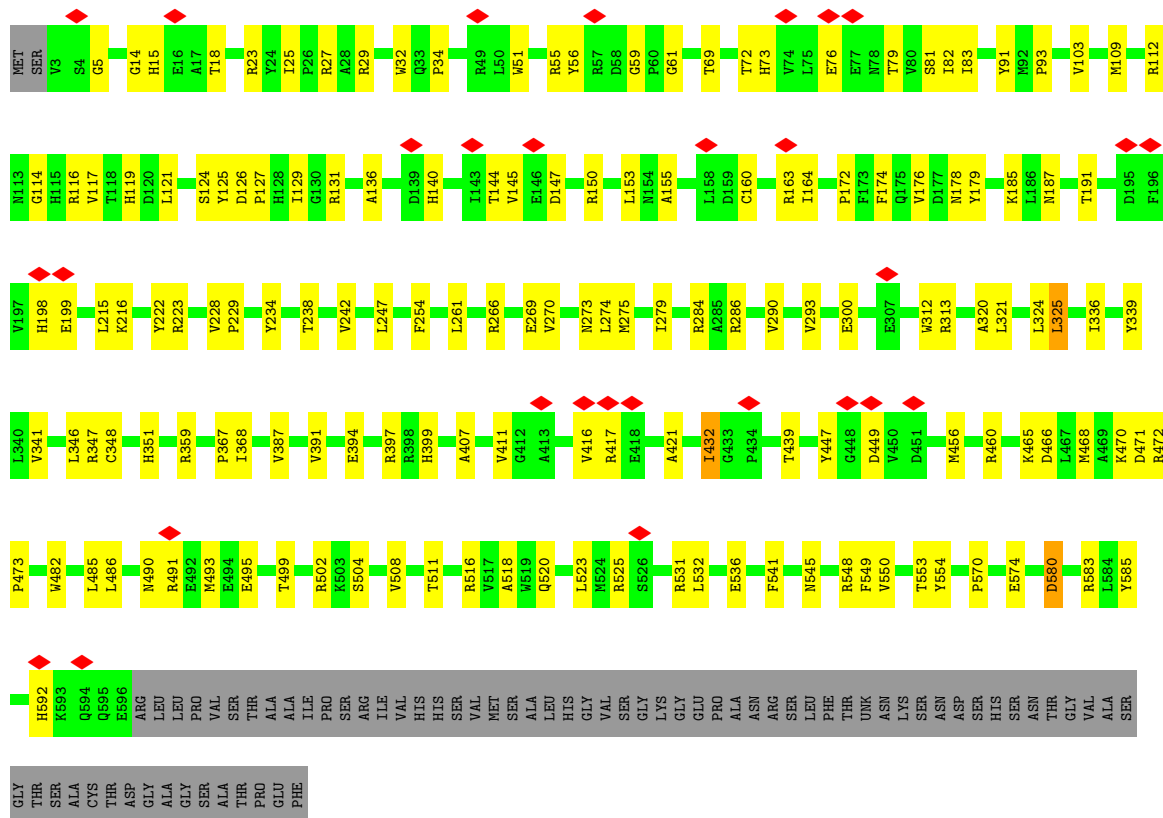
• Molecule 31: mS52





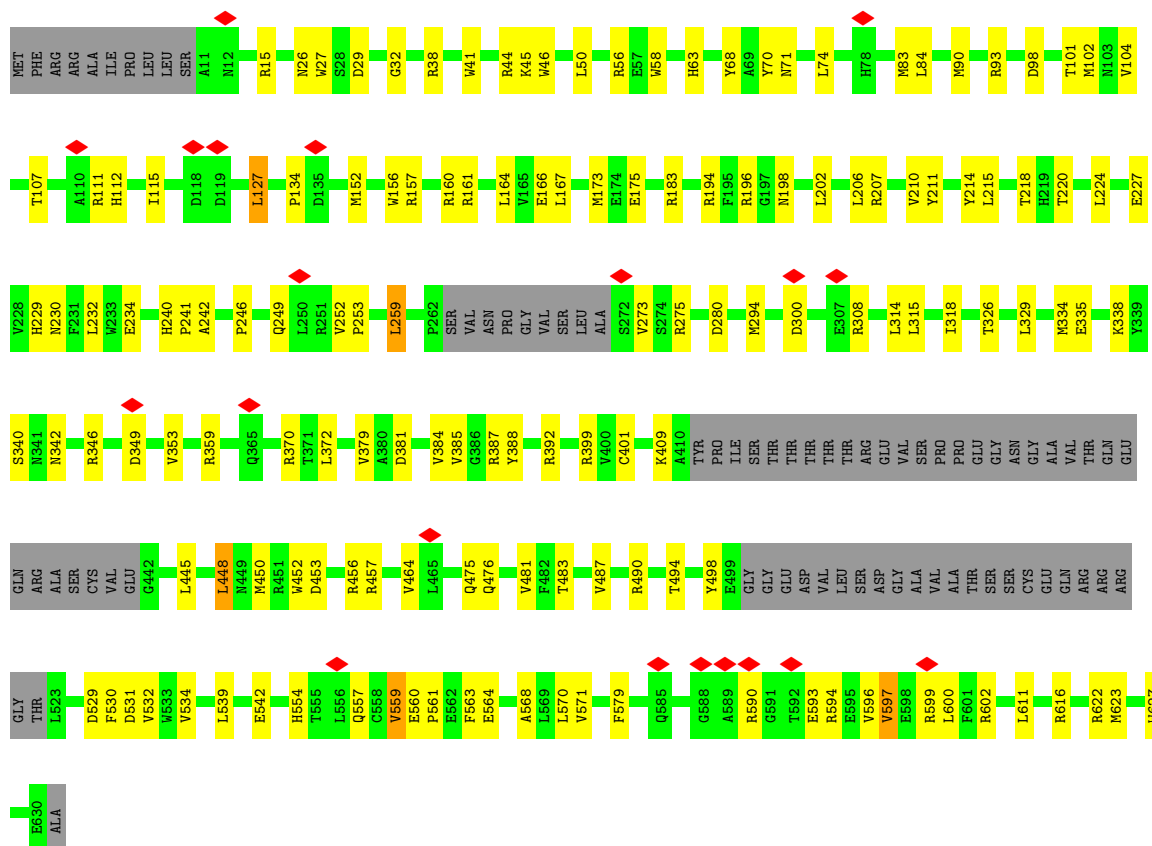
• Molecule 32: mS53

Chain DF: 66% 23% 11%

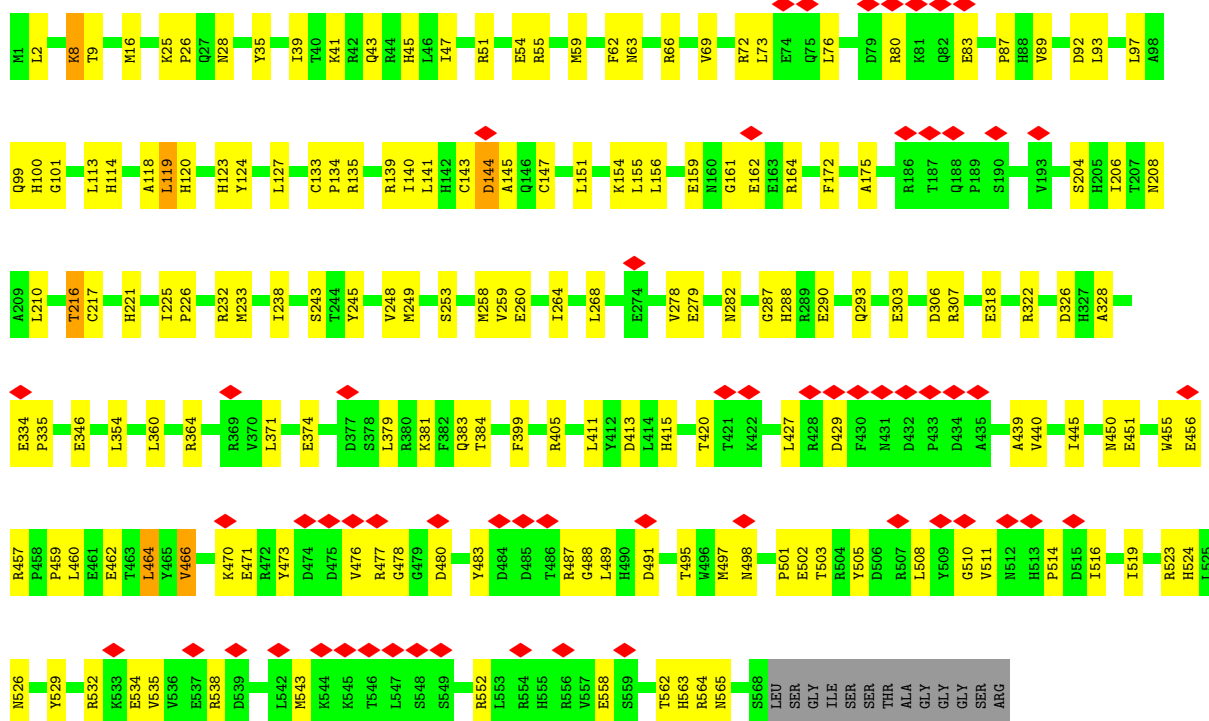


• Molecule 33: mS54

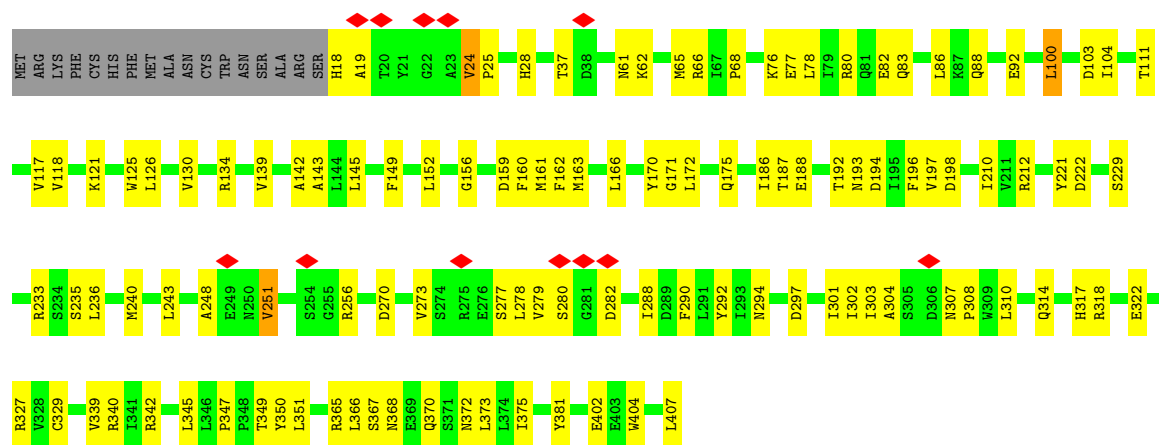
Chain DG: 65% 23% 12%



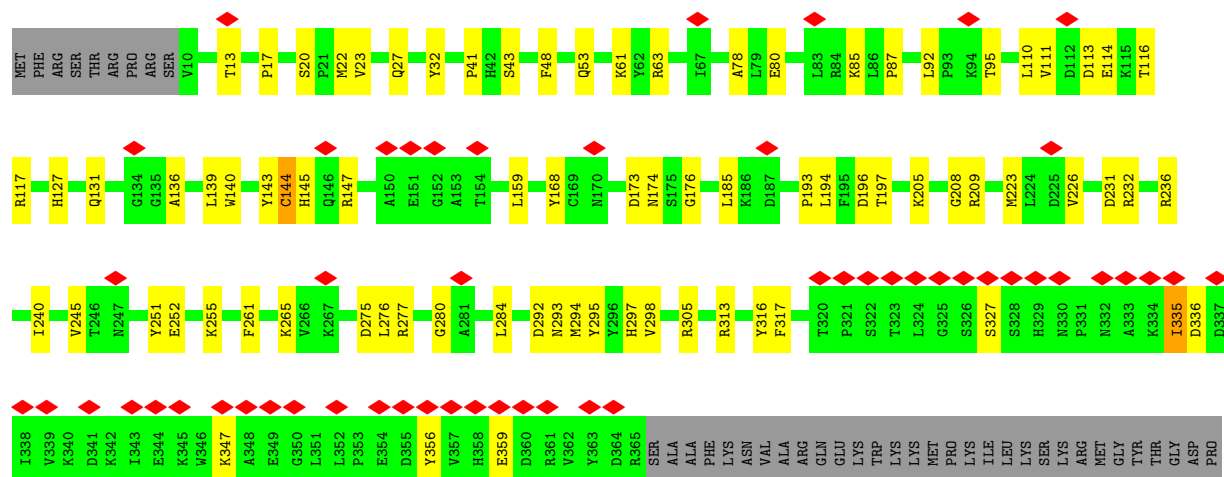
• Molecule 34: mS55



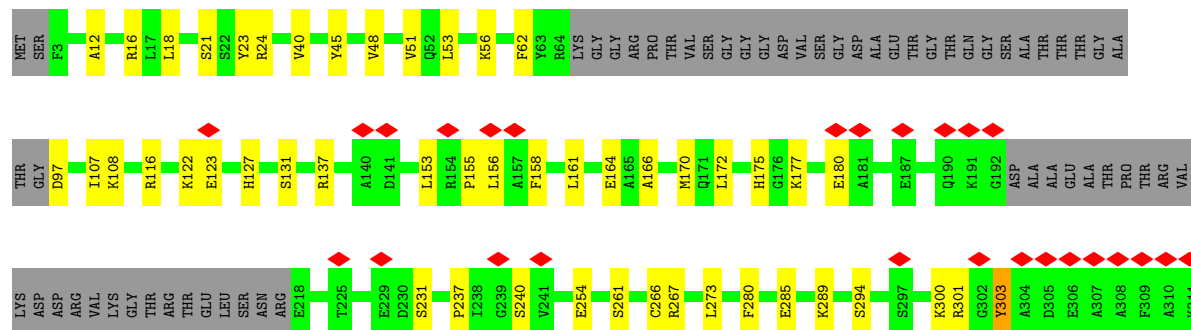
Chain DI: 68% 28% ..

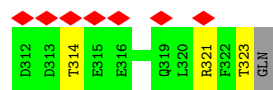


Chain DJ:

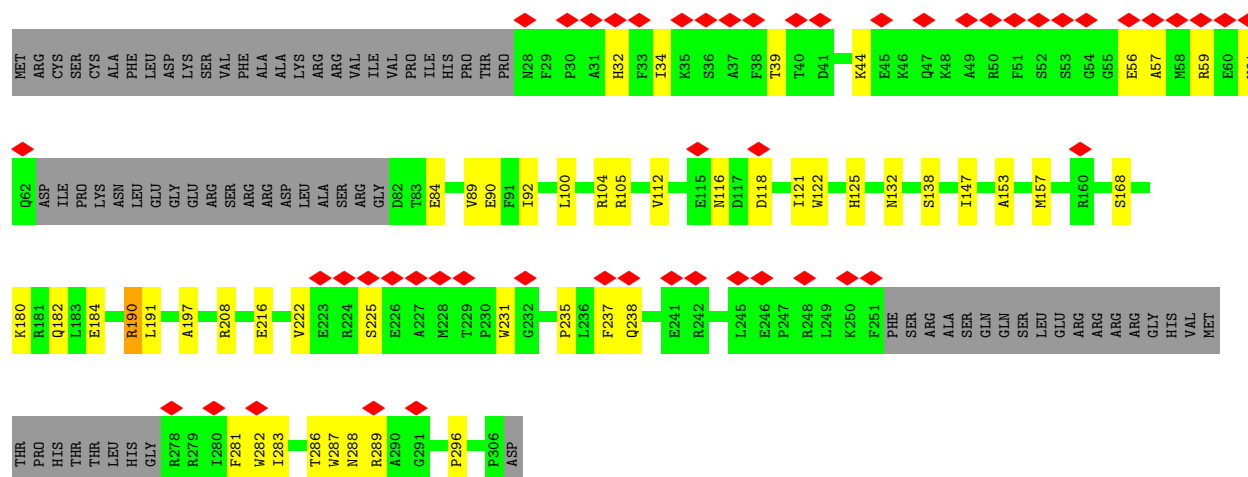


Chain DK:

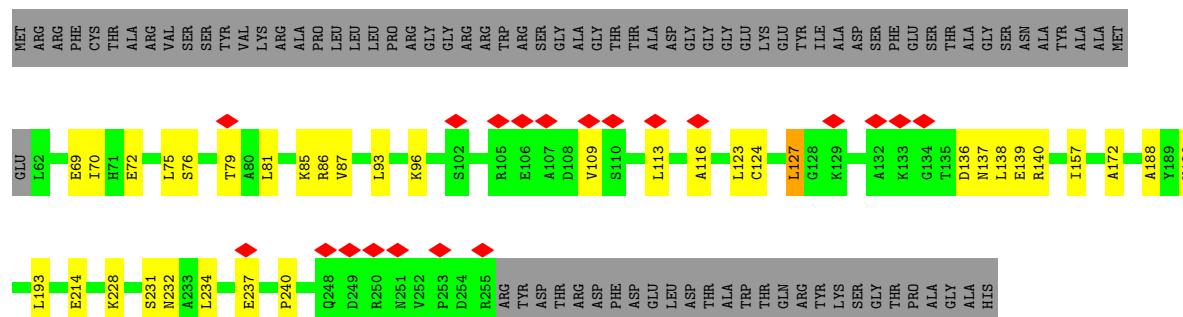




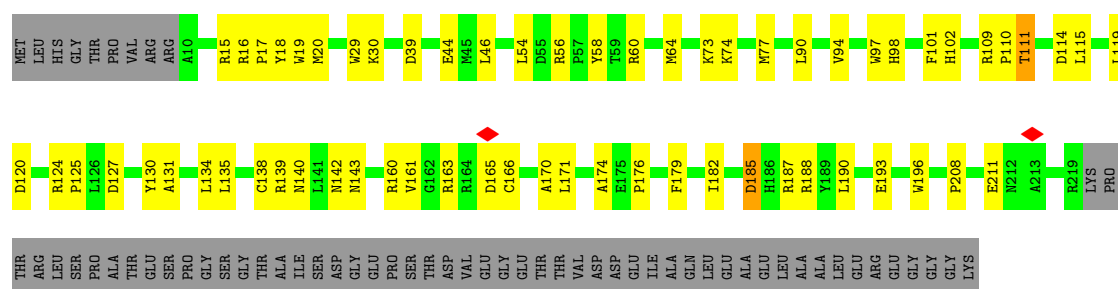
• Molecule 38: mS59



• Molecule 39: mS62



• Molecule 40: mS63



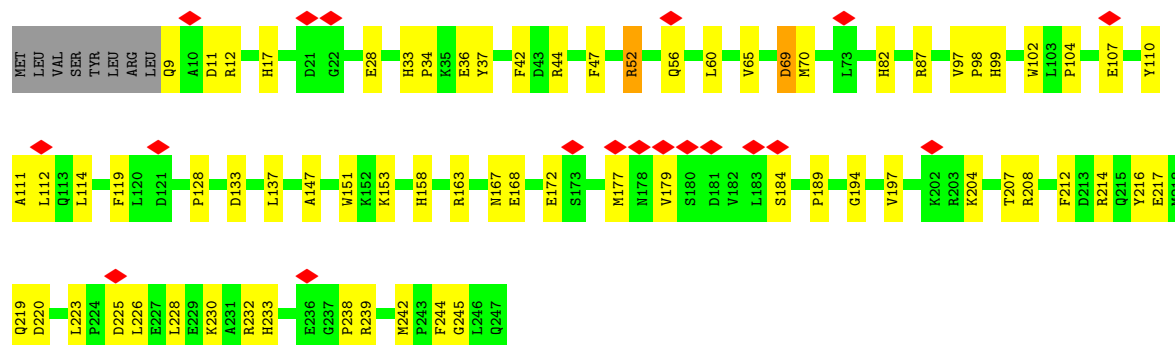
• Molecule 41: mS65

Chain DR: 



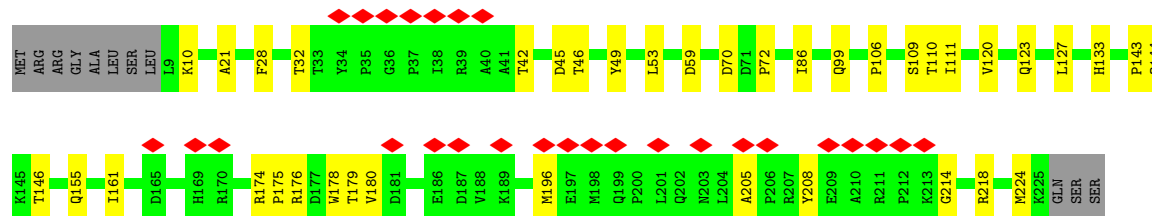
• Molecule 42: Rhodanese domain-containing protein

Chain DT: 



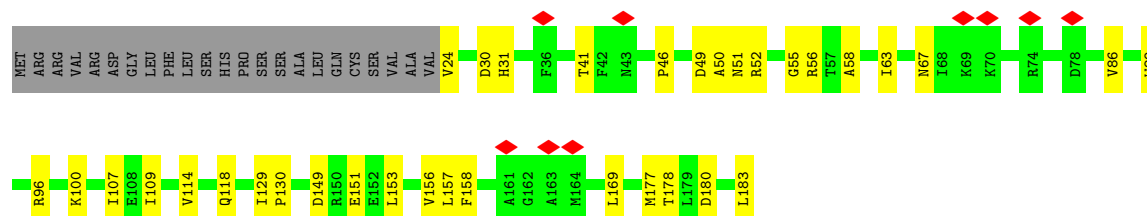
• Molecule 43: Ubiquitin-like domain-containing protein

Chain DU: 



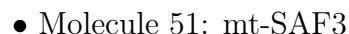
• Molecule 44: mS69

Chain DV: 



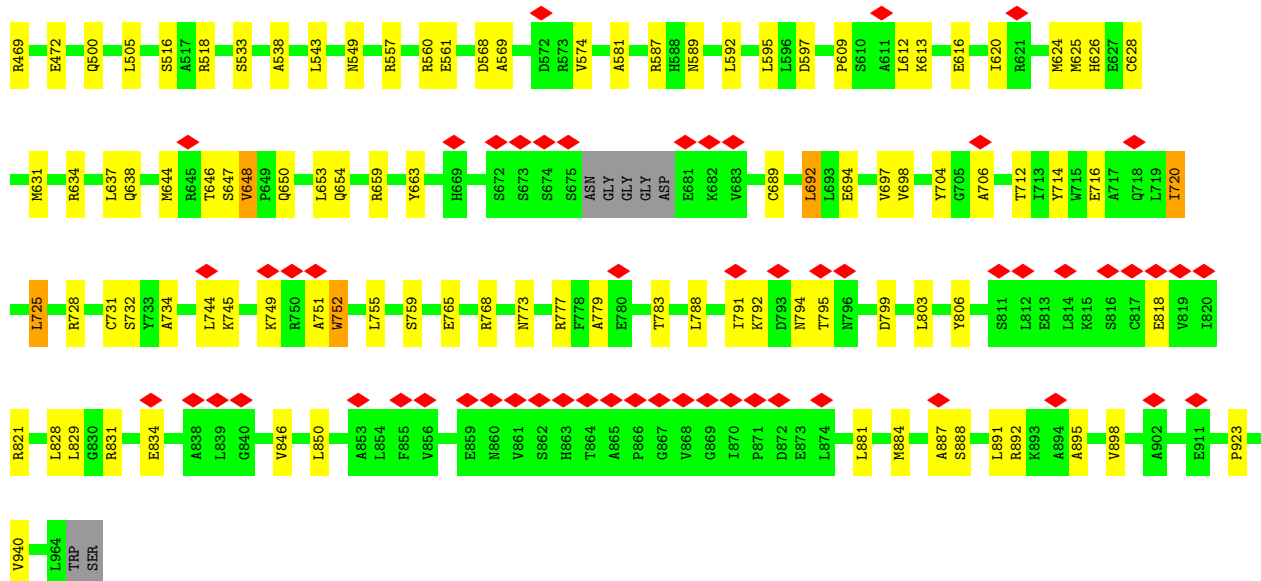
• Molecule 45: mS70

Frequency	Percentage
Daily	71%
Weekly	16%
Monthly	13%

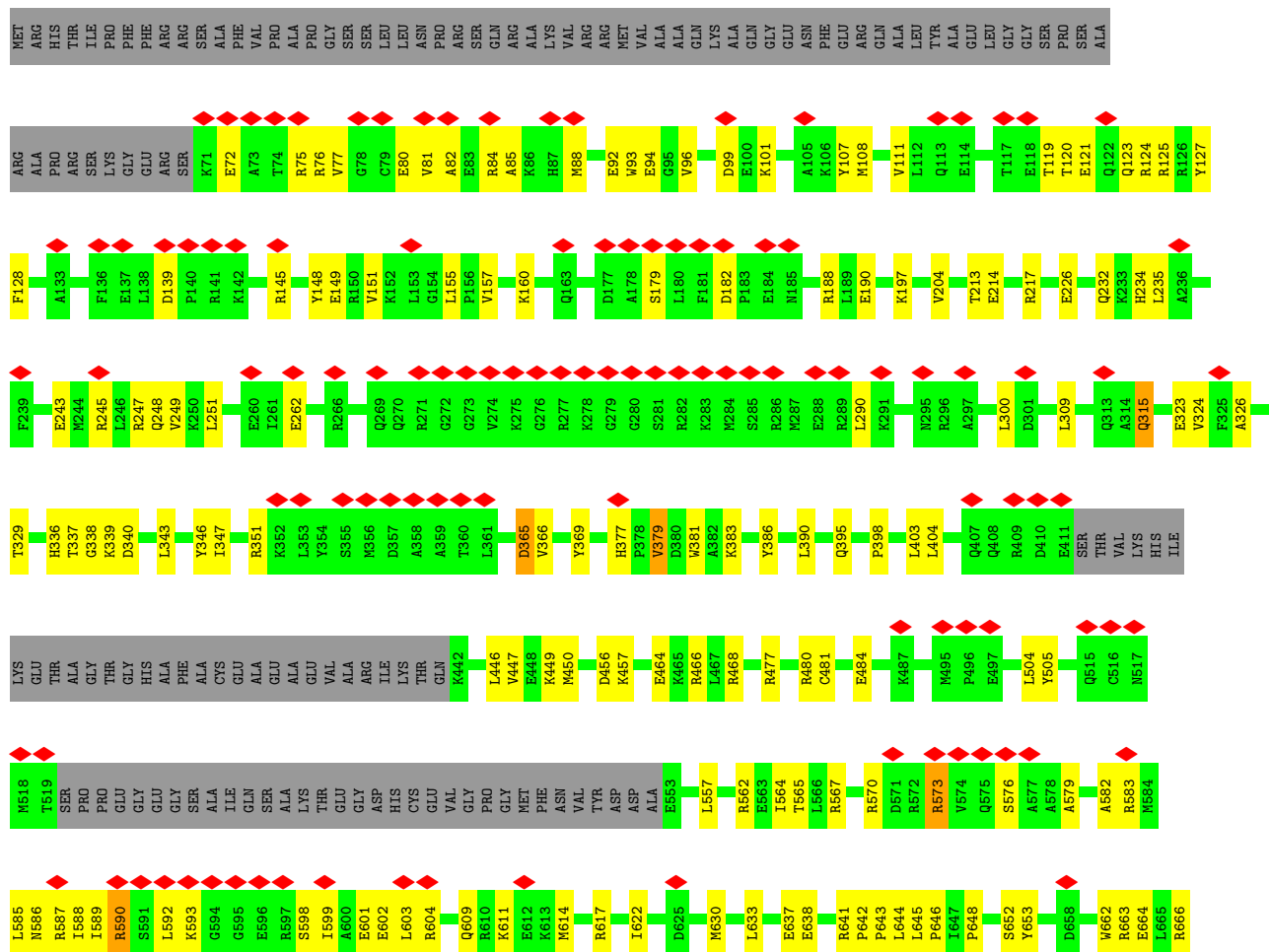


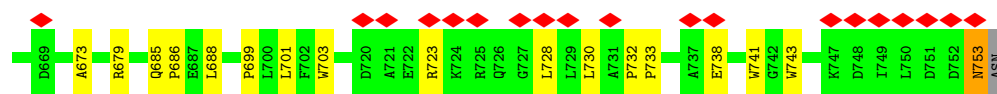
Frequency	Percentage
10%	10%
75%	75%
18%	18%
6%	6%



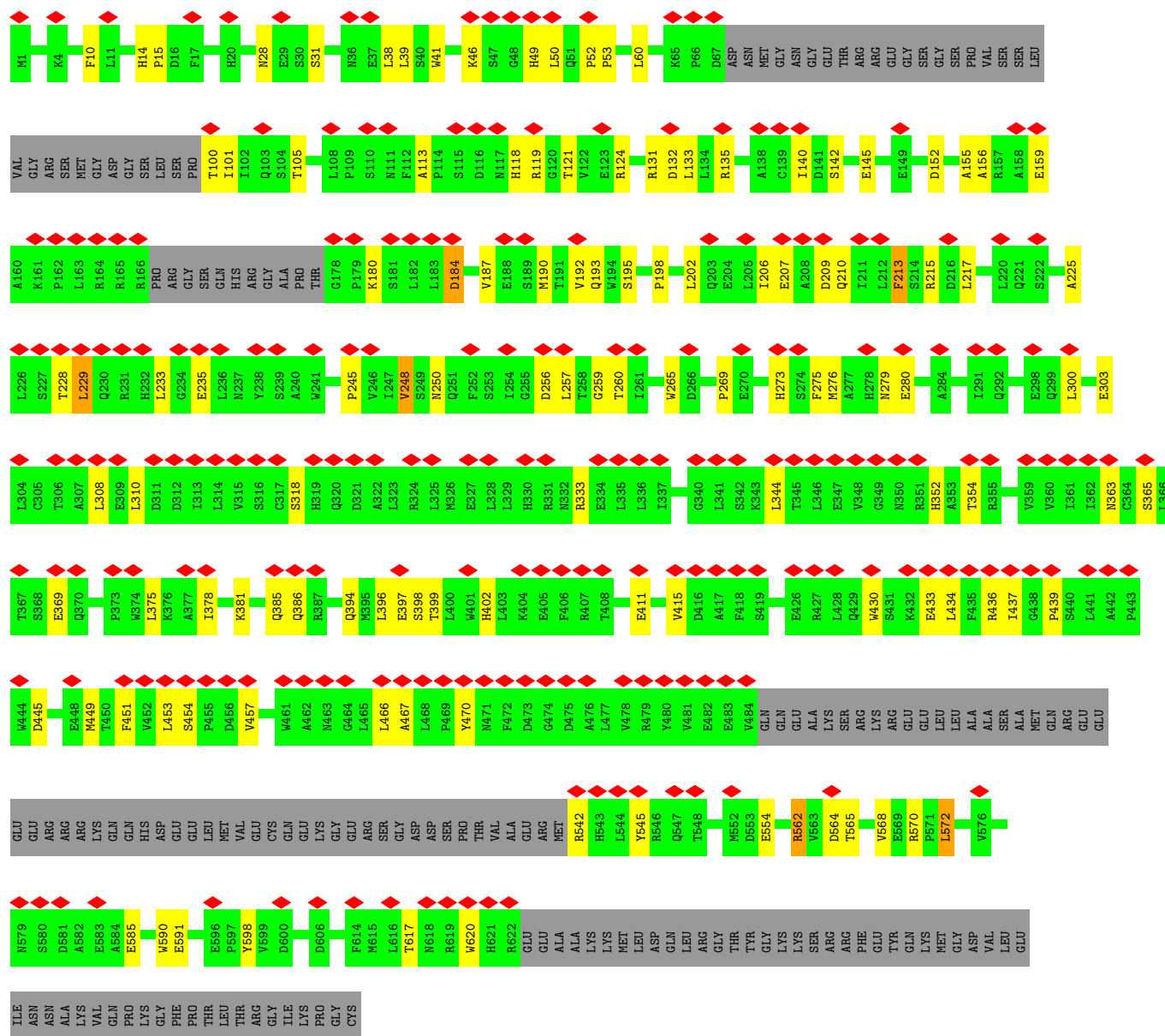


• Molecule 52: mt-SAF5

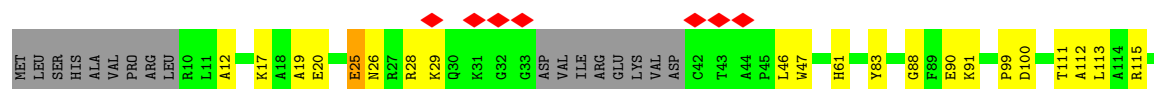
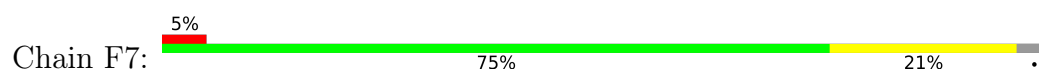


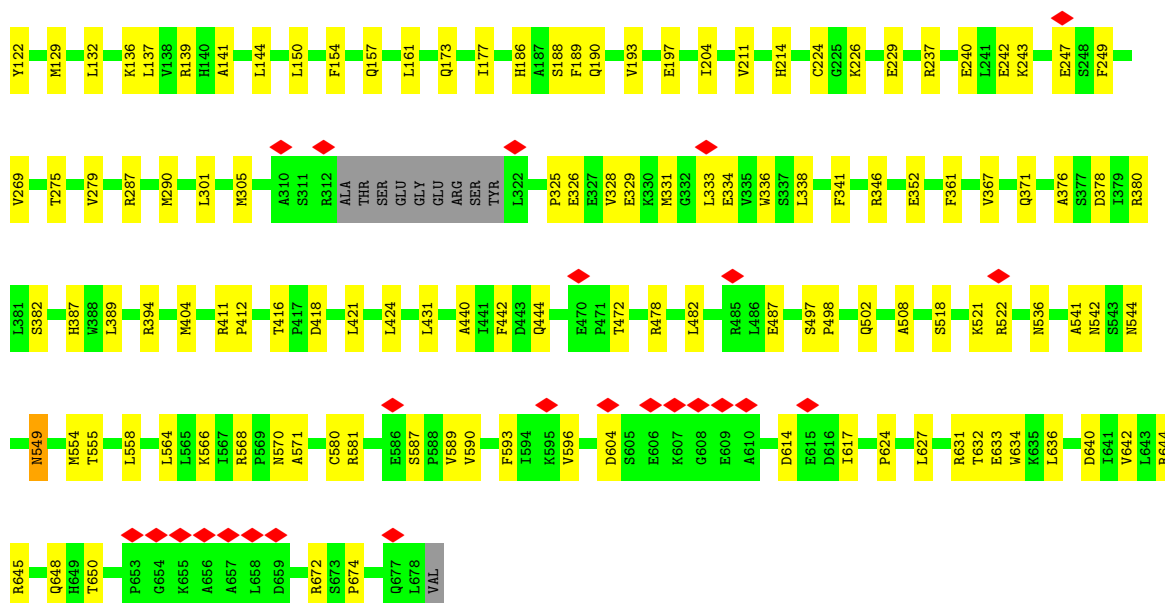


• Molecule 53: DUF4460 domain-containing protein

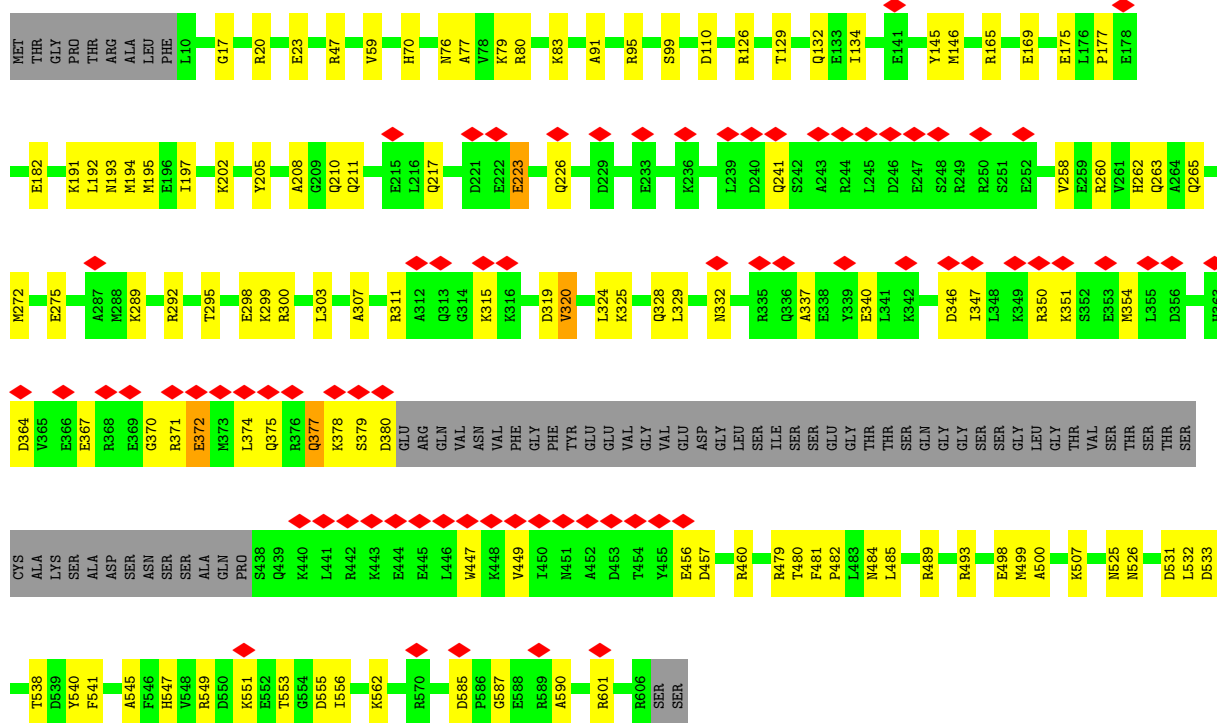


• Molecule 54: mt-SAF7



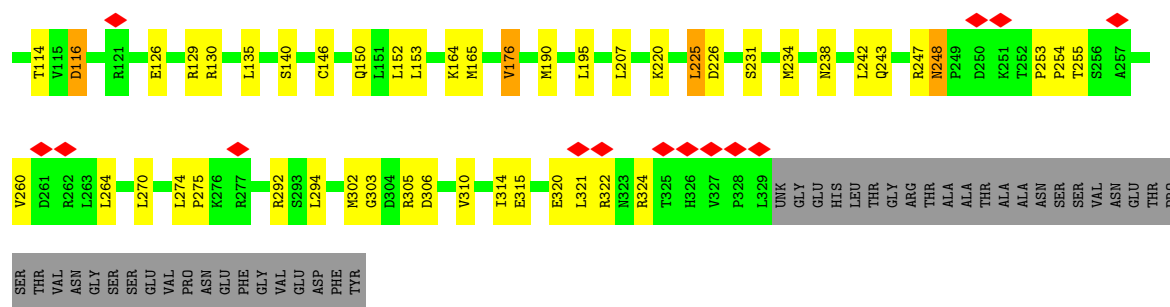


• Molecule 55: mt-SAF9

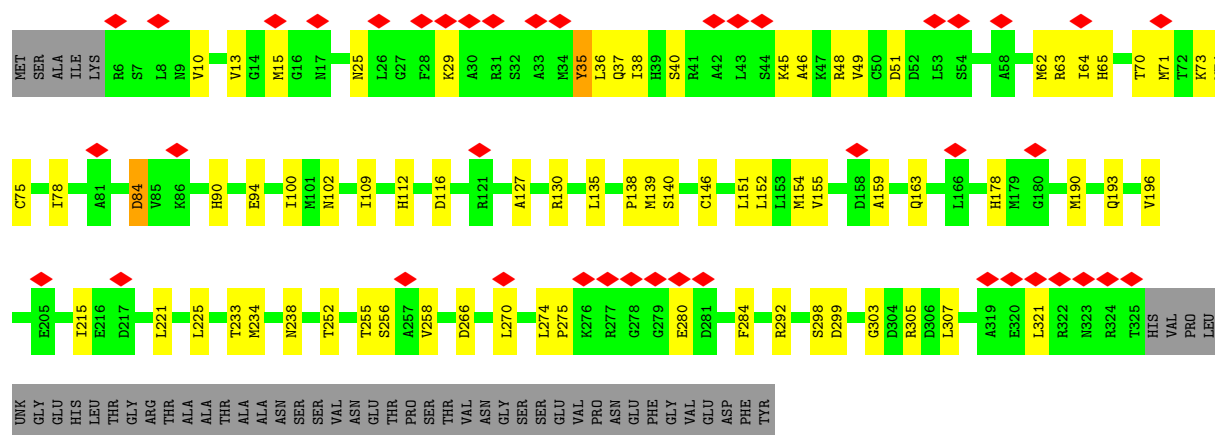


• Molecule 56: mt-SAF21

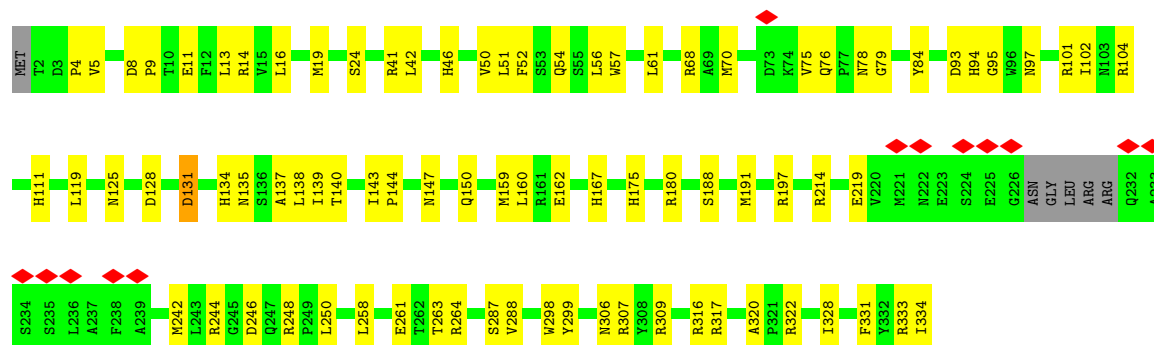
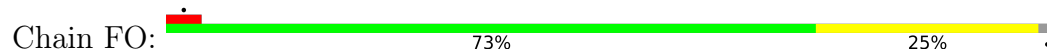




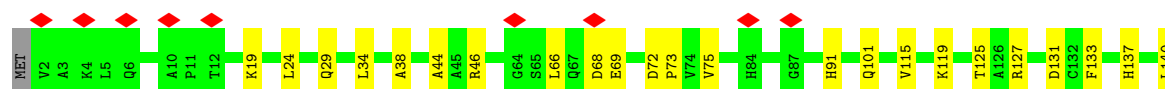
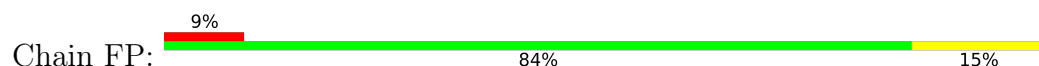
• Molecule 56: mt-SAF21



• Molecule 57: mt-SAF22

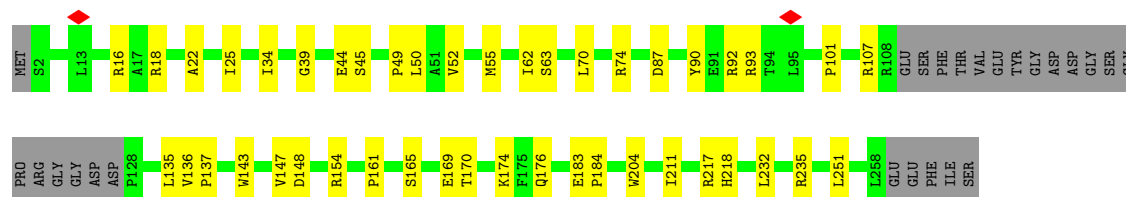
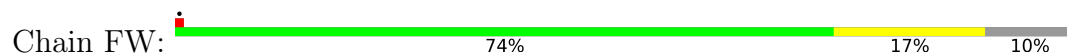


• Molecule 58: mt-SAF23

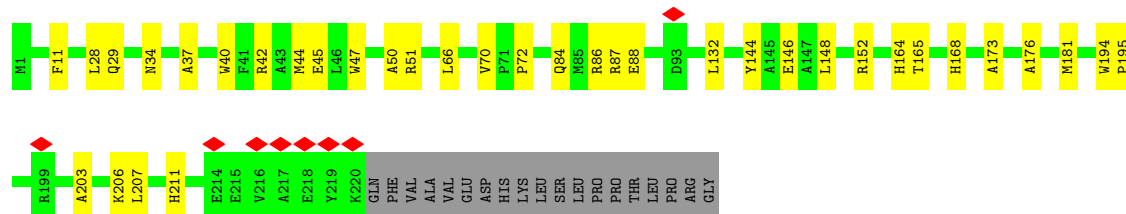
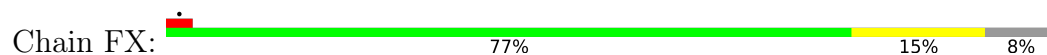




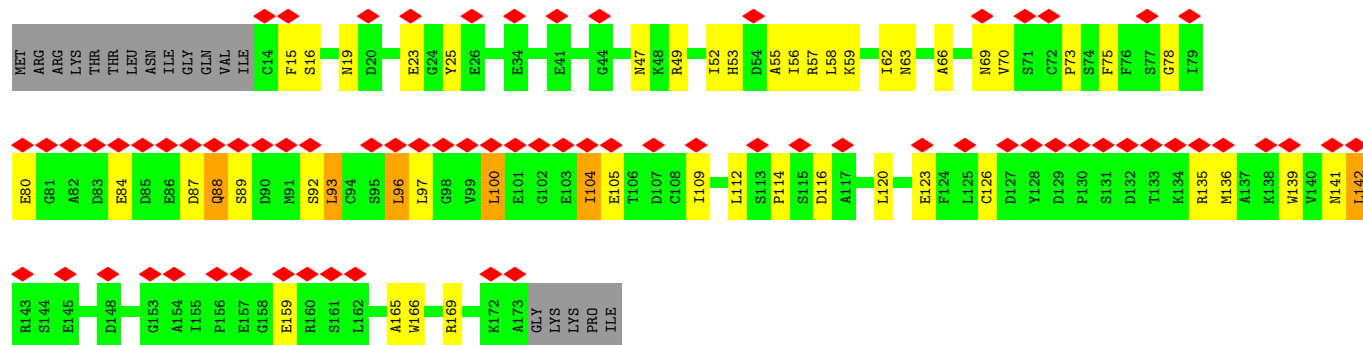
- Molecule 59: LMWPc domain-containing protein



- Molecule 60: mt-SAF27

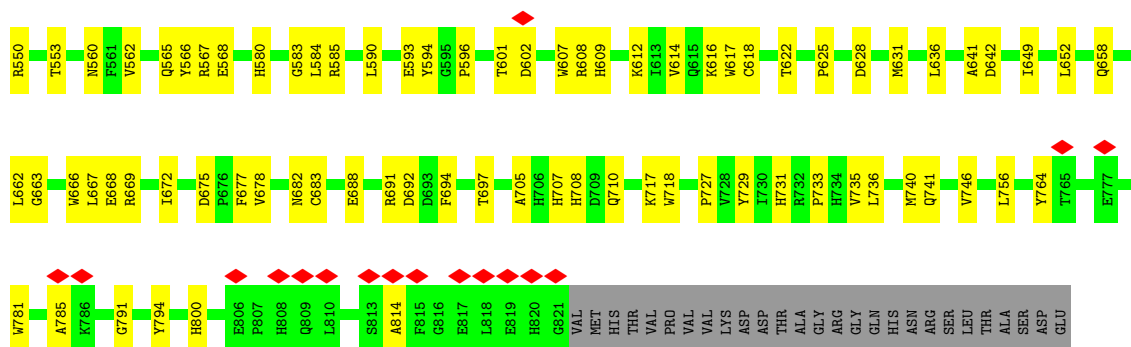


- Molecule 61: mt-SAF29

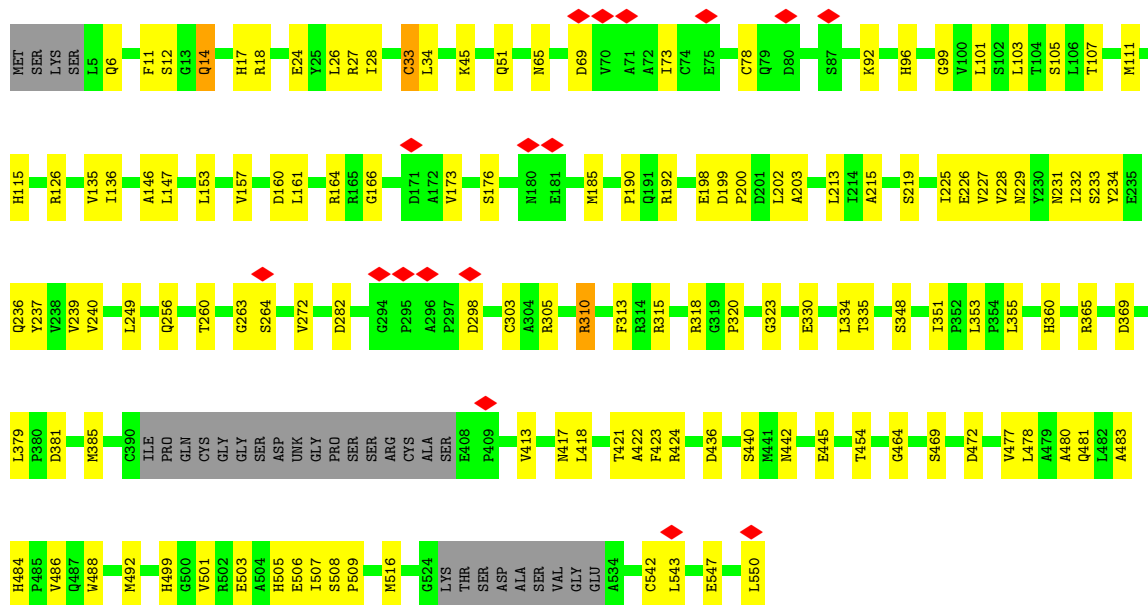


- Molecule 62: mt-SAF31

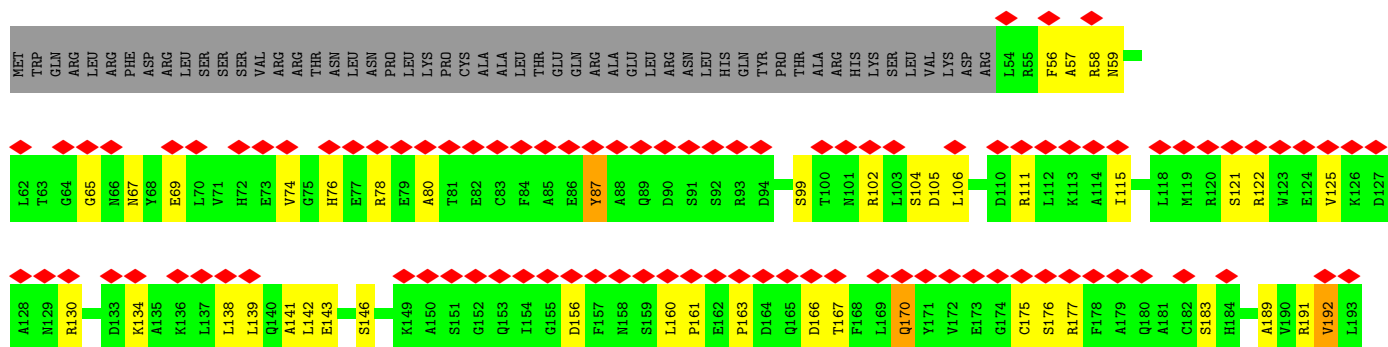


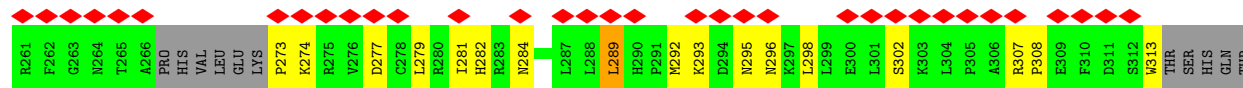


- Molecule 66: Acyl transferase-like protein, putative

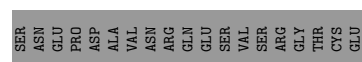
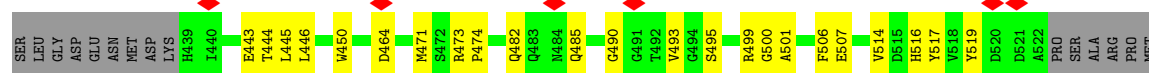
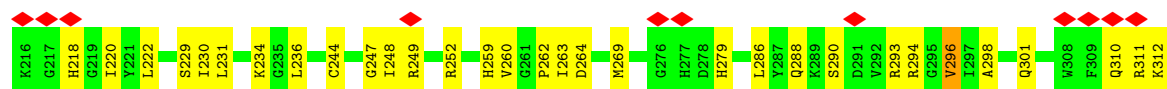
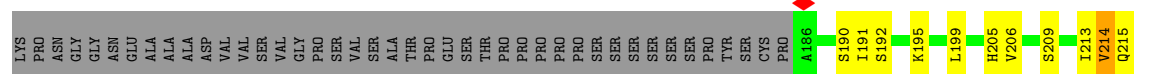


- Molecule 67: mt-SAF37



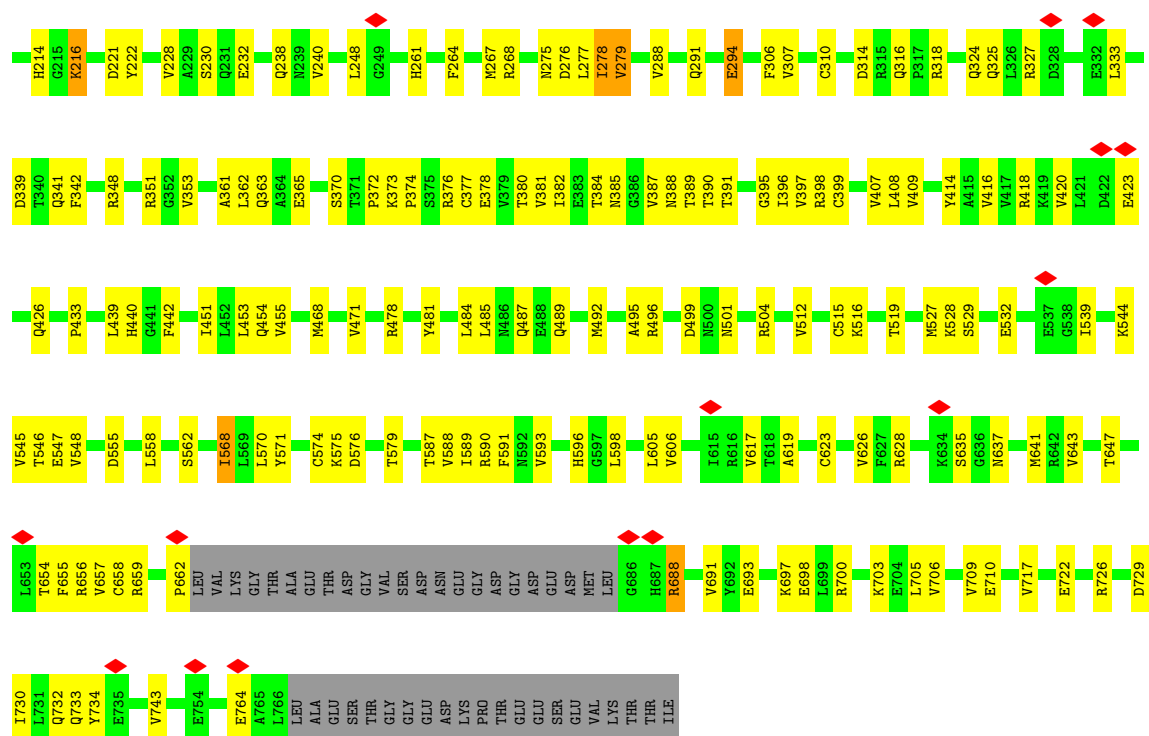


Chain Fi:

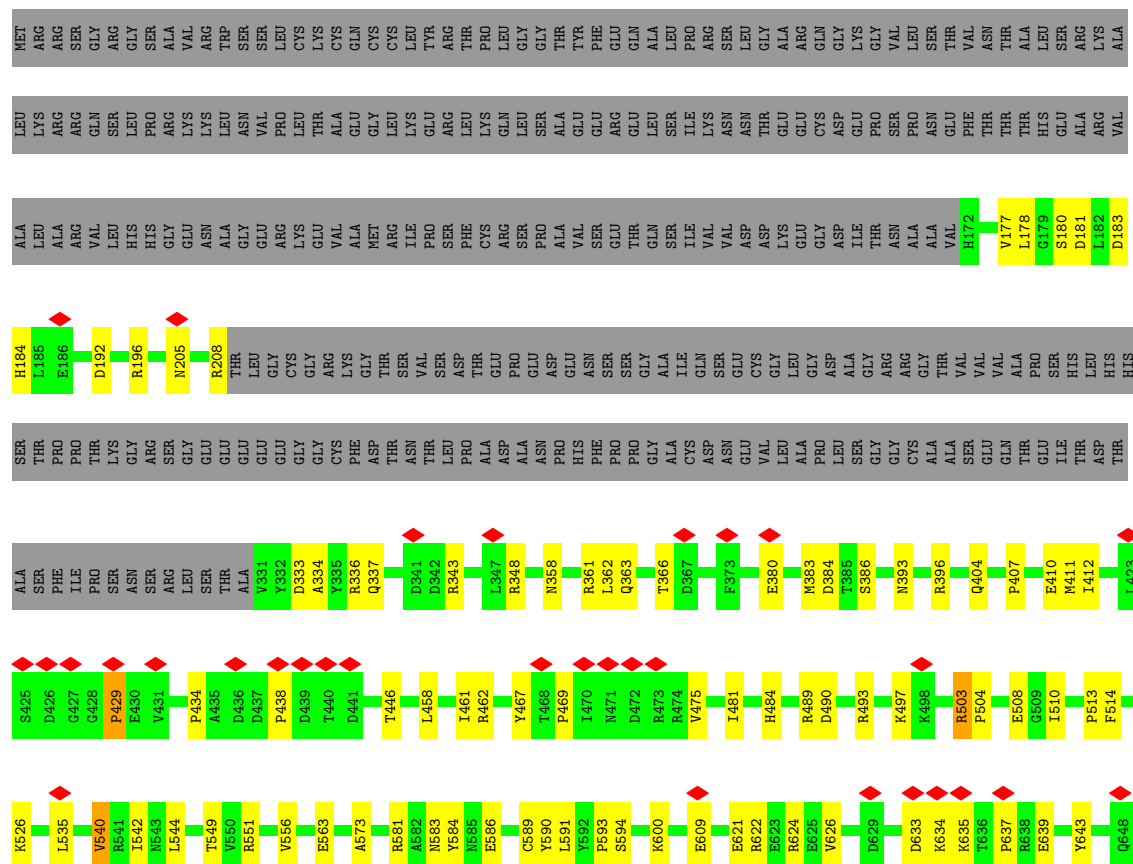


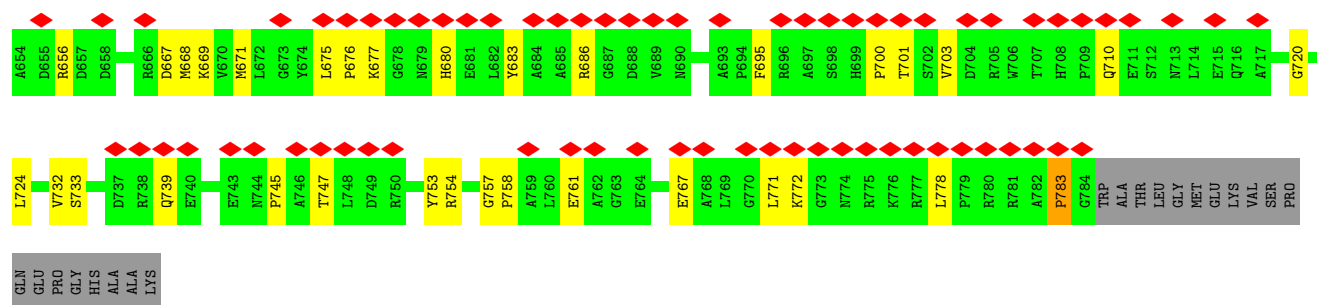
Chain IA: 63% 25% 11%



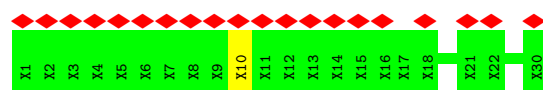


• Molecule 70: mt-SAF39





• Molecule 71: Unk8



• Molecule 72: UnkC

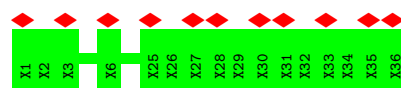


There are no outlier residues recorded for this chain.

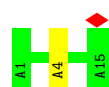
• Molecule 73: UnkD



• Molecule 74: UnkF



• Molecule 75: UnkG

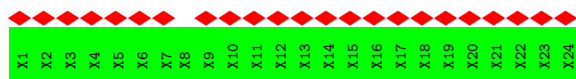


• Molecule 76: UnkI





- Molecule 77: UnkK

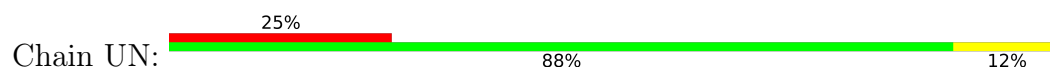


- Molecule 78: Unk



There are no outlier residues recorded for this chain.

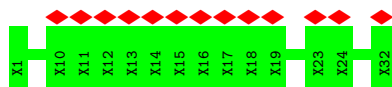
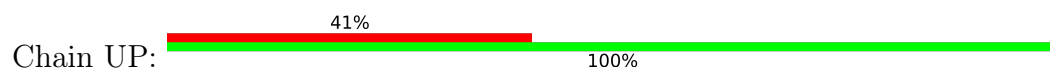
- Molecule 78: Unk



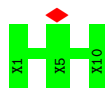
- Molecule 78: Unk



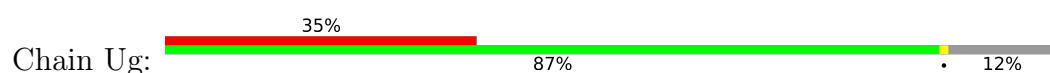
- Molecule 79: UnkP

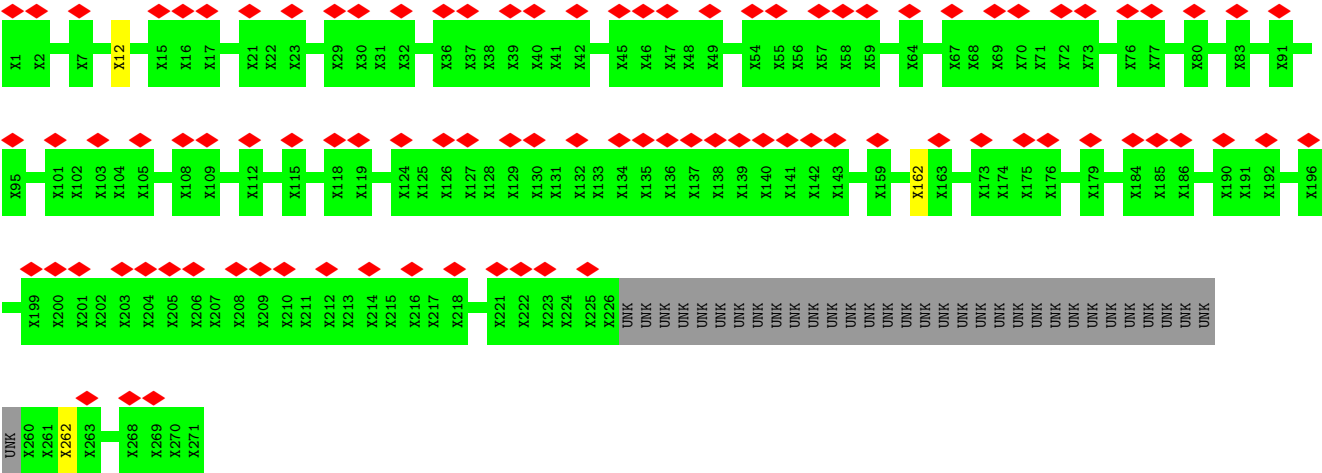


- Molecule 80: Unka



- Molecule 81: Unkg





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38531	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.264	Depositor
Minimum map value	-0.127	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	500.4, 500.4, 500.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, MG, ZN, PM8, GDP, FDA, PO4

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	CA	0.11	1/11001 (0.0%)	0.19	0/17084
2	CB	0.07	0/71	0.14	0/108
3	CC	0.09	0/666	0.23	0/900
4	CE	0.10	0/3100	0.26	0/4193
5	CF	0.09	0/1305	0.23	0/1761
6	CH	0.10	0/1839	0.23	0/2479
7	CI	0.09	0/3420	0.24	0/4619
8	CJ	0.10	0/6561	0.26	1/8927 (0.0%)
9	CK	0.10	0/1468	0.24	0/1971
10	CL	0.21	0/726	0.31	0/981
11	CN	0.09	0/1361	0.27	0/1840
12	CO	0.11	0/3070	0.24	0/4145
13	CP	0.11	0/1533	0.27	0/2074
14	CQ	0.11	0/2072	0.24	0/2808
15	CR	0.09	0/1083	0.23	0/1467
16	CS	0.09	0/851	0.26	0/1150
17	CU	0.07	0/296	0.18	0/397
18	Ca	0.11	0/4378	0.25	0/5921
19	Cb	0.09	0/1273	0.23	0/1711
20	Cd	0.12	0/1818	0.22	0/2447
21	Cg	0.08	0/4064	0.21	0/5518
22	Ci	0.09	0/1388	0.22	0/1878
23	Cj	0.09	0/1842	0.23	0/2511
24	Ck	0.09	0/5469	0.24	0/7396
25	Cm	0.09	0/231	0.22	0/305
26	Cn	0.09	0/434	0.21	0/573
27	Cp	0.08	0/1472	0.22	0/1996
28	DB	0.09	0/9332	0.24	0/12641
29	DC	0.09	0/8971	0.25	0/12172
30	DD	0.14	0/6494	0.27	0/8808
31	DE	0.10	0/5246	0.24	0/7111
32	DF	0.09	0/4895	0.24	0/6635

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	DG	0.10	0/4608	0.25	0/6242
34	DH	0.10	0/4716	0.24	0/6392
35	DI	0.10	0/3248	0.23	0/4401
36	DJ	0.12	0/2993	0.26	0/4063
37	DK	0.09	0/2132	0.23	0/2877
38	DL	0.10	0/1952	0.23	0/2629
39	DO	0.10	0/1597	0.25	0/2153
40	DP	0.10	0/1837	0.25	0/2488
41	DR	0.14	0/2099	0.29	0/2861
42	DT	0.09	0/2133	0.22	0/2889
43	DU	0.09	0/1772	0.23	0/2404
44	DV	0.10	0/1382	0.26	0/1871
45	DW	0.11	0/1202	0.24	0/1639
46	DX	0.10	0/1128	0.26	0/1516
47	DY	0.11	0/1337	0.30	0/1814
48	DZ	0.09	0/246	0.20	0/332
49	Da	0.11	0/332	0.28	0/441
50	F2	0.10	0/7281	0.22	0/9837
51	F3	0.10	0/7158	0.25	0/9686
52	F5	0.11	0/5144	0.24	0/6918
53	F6	0.09	0/4297	0.25	0/5841
54	F7	0.10	0/5281	0.24	0/7149
55	F9	0.15	0/4497	0.27	0/6031
56	FM	0.09	0/2497	0.21	0/3376
56	FN	0.09	0/2441	0.23	0/3299
57	FO	0.10	0/2763	0.24	0/3735
58	FP	0.11	0/2710	0.26	0/3709
59	FW	0.10	0/2002	0.23	0/2704
60	FX	0.11	0/1783	0.25	0/2410
61	FZ	0.09	0/1287	0.24	0/1737
62	Fb	0.10	0/1092	0.24	0/1471
63	Fc	0.09	0/670	0.27	0/912
64	Fd	0.08	0/759	0.23	0/1028
65	Ff	0.09	0/5149	0.25	0/7008
66	Fg	0.10	0/4129	0.26	0/5595
67	Fh	0.10	0/1902	0.23	0/2566
68	Fi	0.10	0/3899	0.26	0/5296
69	IA	0.15	0/5577	0.29	1/7550 (0.0%)
70	IB	0.11	0/3944	0.38	6/5333 (0.1%)
73	UD	0.07	0/64	0.24	0/88
75	UG	0.08	0/74	0.26	0/102
All	All	0.10	1/208844 (0.0%)	0.25	8/284920 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	302	U	Cl'-N1	6.26	1.57	1.48

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	IB	429	PRO	N-CA-CB	7.92	111.57	103.25
70	IB	424	PRO	N-CA-CB	7.45	111.08	103.25
8	CJ	540	PRO	N-CA-CB	7.37	110.99	103.25
70	IB	434	PRO	N-CA-CB	6.78	110.37	103.25
69	IA	662	PRO	N-CA-CB	6.77	110.45	103.00
70	IB	469	PRO	N-CA-CB	6.16	110.11	103.33
70	IB	438	PRO	N-CA-CB	5.96	110.11	103.44
70	IB	783	PRO	N-CA-CB	5.44	108.97	103.25

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CA	9866	0	4936	153	0
2	CB	64	0	33	1	0
3	CC	646	0	682	21	0
4	CE	3024	0	2960	56	0
5	CF	1279	0	1270	36	0
6	CH	1799	0	1773	31	0
7	CI	3352	0	3304	72	0
8	CJ	6376	0	6087	142	0
9	CK	1440	0	1401	40	0
10	CL	701	0	704	22	0
11	CN	1322	0	1304	44	0
12	CO	2989	0	2984	54	0
13	CP	1489	0	1510	40	0
14	CQ	2015	0	2008	68	0
15	CR	1051	0	1046	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	CS	822	0	809	29	0
17	CU	288	0	279	8	0
18	Ca	4247	0	4045	98	0
19	Cb	1242	0	1257	31	0
20	Cd	1768	0	1709	47	0
21	Cg	3943	0	3834	73	0
22	Ci	1348	0	1306	37	0
23	Cj	1792	0	1744	36	0
24	Ck	5371	0	5388	112	0
25	Cm	232	0	232	4	0
26	Cn	425	0	474	11	0
27	Cp	1428	0	1390	33	0
28	DB	9112	0	8794	202	0
29	DC	8766	0	8550	179	0
30	DD	6308	0	6064	131	0
31	DE	5114	0	5060	122	0
32	DF	4785	0	4759	118	0
33	DG	4511	0	4432	97	0
34	DH	4608	0	4548	123	0
35	DI	3182	0	3153	72	0
36	DJ	2908	0	2815	63	0
37	DK	2092	0	2074	45	0
38	DL	1904	0	1882	38	0
39	DO	1567	0	1543	26	0
40	DP	1784	0	1745	47	0
41	DR	2034	0	2037	45	0
42	DT	2058	0	1928	51	0
43	DU	1730	0	1638	32	0
44	DV	1346	0	1335	30	0
45	DW	1160	0	1133	34	0
46	DX	1097	0	1079	26	0
47	DY	1295	0	1290	35	0
48	DZ	237	0	213	5	0
49	Da	320	0	304	9	0
50	F2	7125	0	6991	114	0
51	F3	7039	0	7008	115	0
52	F5	5056	0	5050	115	0
53	F6	4195	0	4089	84	0
54	F7	5166	0	5148	100	0
55	F9	4422	0	4325	93	0
56	FM	2457	0	2451	56	0
56	FN	2403	0	2388	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	FO	2700	0	2663	58	0
58	FP	2643	0	2554	37	0
59	FW	1960	0	1972	31	0
60	FX	1741	0	1693	29	0
61	FZ	1262	0	1203	49	0
62	Fb	1061	0	1059	21	0
63	Fc	660	0	650	11	0
64	Fd	738	0	741	22	0
65	Ff	5006	0	4844	108	0
66	Fg	4048	0	4012	90	0
67	Fh	1867	0	1765	59	0
68	Fi	3797	0	3773	81	0
69	IA	5478	0	5498	132	0
70	IB	3867	0	3749	81	0
71	U8	150	0	33	1	0
72	UC	45	0	13	0	0
73	UD	65	0	52	0	0
74	UF	180	0	38	0	0
75	UG	75	0	56	2	0
76	UI	30	0	11	0	0
77	UK	120	0	26	0	0
78	UM	40	0	13	0	0
78	UN	40	0	11	1	0
78	UQ	40	0	10	0	0
79	UP	160	0	35	0	0
80	Ua	50	0	15	0	0
81	Ug	1190	0	252	2	0
82	CA	4	0	0	0	0
82	CQ	1	0	0	0	0
82	Cg	1	0	0	0	0
82	IA	1	0	0	0	0
83	Cg	31	0	12	0	0
84	FW	5	0	0	1	0
84	IA	5	0	0	1	0
85	Fc	32	0	39	1	0
86	Fd	1	0	0	0	0
87	Ff	53	0	33	2	0
88	IA	28	0	12	1	0
89	Cg	3	0	0	0	0
89	IA	2	0	0	0	0
All	All	205280	0	195132	3529	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 9.

All (3529) 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)
50:F2:280:HIS:HE2	50:F2:314:THR:HG1	1.15	0.93
23:Cj:110:ASN:HB3	23:Cj:135:ILE:HD11	1.63	0.80
22:Ci:125:HIS:HE2	34:DH:9:THR:HG1	1.28	0.80
22:Ci:159:SER:HB3	32:DF:5:GLY:HA3	1.64	0.79
69:IA:619:ALA:HB3	69:IA:733:GLN:HE21	1.46	0.79
68:Fi:130:PRO:HG2	68:Fi:192:SER:HB3	1.65	0.79
37:DK:254:GLU:HB3	37:DK:261:SER:HB3	1.64	0.78
18:Ca:443:MET:HE2	18:Ca:491:TRP:HE1	1.49	0.78
7:CI:104:ASN:H	33:DG:194:ARG:HH12	1.29	0.78
7:CI:421:ARG:HD2	9:CK:28:VAL:HG22	1.66	0.78
36:DJ:174:ASN:HD22	36:DJ:176:GLY:H	1.31	0.78
6:CH:196:ASP:H	50:F2:307:ASN:HD21	1.28	0.78
24:Ck:662:GLY:H	24:Ck:669:ASN:HD21	1.32	0.77
14:CQ:19:ARG:NH1	30:DD:800:ILE:O	2.17	0.77
40:DP:174:ALA:HB1	40:DP:179:PHE:HB2	1.67	0.77
6:CH:241:LEU:HD22	6:CH:269:VAL:HG21	1.68	0.76
65:Ff:590:LEU:HA	65:Ff:596:PRO:HG3	1.67	0.76
50:F2:352:ARG:NH2	50:F2:387:VAL:O	2.18	0.76
7:CI:392:ARG:HD3	7:CI:415:LEU:HG	1.68	0.76
65:Ff:406:GLY:HA3	65:Ff:409:TRP:HD1	1.51	0.76
52:F5:88:MET:HG2	52:F5:123:GLN:HE21	1.50	0.75
28:DB:110:ARG:NH2	28:DB:309:SER:O	2.19	0.75
19:Cb:178:ARG:HD3	53:F6:207:GLU:HA	1.68	0.75
28:DB:668:MET:HA	28:DB:671:VAL:HG12	1.69	0.75
34:DH:379:LEU:O	34:DH:383:GLN:HB3	1.85	0.75
20:Cd:70:ARG:HH11	30:DD:156:GLN:HE21	1.33	0.74
32:DF:518:ALA:HB2	32:DF:549:PHE:HB3	1.69	0.74
10:CL:25:MET:SD	69:IA:47:GLN:NE2	2.61	0.74
28:DB:340:ASN:HD21	28:DB:347:ALA:H	1.34	0.74
51:F3:386:VAL:HG13	51:F3:390:GLU:HB2	1.69	0.74
65:Ff:186:SER:O	65:Ff:302:ARG:NH2	2.21	0.73
8:CJ:442:ASP:HB3	24:Ck:667:GLN:HG2	1.70	0.73
65:Ff:506:GLY:HA2	65:Ff:527:ARG:HG2	1.70	0.73
32:DF:23:ARG:HH11	42:DT:238:PRO:HD3	1.54	0.73
34:DH:466:VAL:HG13	34:DH:487:ARG:HG3	1.71	0.73
68:Fi:378:VAL:HG11	68:Fi:386:LEU:HB2	1.71	0.72
4:CE:300:ILE:HG22	4:CE:302:PRO:HD2	1.71	0.72
6:CH:48:ASP:OD1	6:CH:201:ARG:NH1	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CI:140:GLU:O	7:CI:144:SER:HB3	1.89	0.72
34:DH:175:ALA:HB1	34:DH:206:ILE:HD13	1.72	0.72
27:Cp:69:ARG:HD2	27:Cp:104:ALA:HB2	1.72	0.72
3:CC:10:LYS:HD2	3:CC:12:ILE:HG23	1.72	0.71
8:CJ:301:ASN:HD21	8:CJ:314:TYR:H	1.38	0.71
33:DG:112:HIS:HB3	33:DG:115:ILE:HB	1.72	0.71
69:IA:40:GLN:NE2	69:IA:123:ARG:O	2.23	0.71
12:CO:253:ALA:HB2	54:F7:648:GLN:HB3	1.70	0.71
55:F9:553:THR:HG23	55:F9:555:ASP:H	1.54	0.71
33:DG:74:LEU:HD22	33:DG:83:MET:HG3	1.72	0.71
57:FO:160:LEU:HD22	57:FO:197:ARG:HH21	1.55	0.71
51:F3:85:GLU:H	66:Fg:260:THR:HB	1.56	0.71
1:CA:509:U:O4	11:CN:88:ARG:NH2	2.22	0.71
12:CO:208:MET:O	12:CO:212:ALA:HB2	1.91	0.70
28:DB:942:ARG:NH1	28:DB:950:VAL:O	2.25	0.70
34:DH:76:LEU:HD23	34:DH:93:LEU:HD22	1.73	0.70
36:DJ:114:GLU:OE2	36:DJ:147:ARG:NH1	2.25	0.70
53:F6:38:LEU:HD12	53:F6:41:TRP:HE1	1.55	0.70
65:Ff:221:ASN:HB3	65:Ff:224:LEU:HB2	1.73	0.70
66:Fg:126:ARG:HD2	66:Fg:547:GLU:HG3	1.73	0.70
22:CI:84:LEU:HD12	22:CI:87:TYR:H	1.56	0.70
27:Cp:151:ARG:H	27:Cp:154:GLN:HE21	1.40	0.70
53:F6:50:LEU:HD21	53:F6:119:ARG:HB2	1.72	0.70
7:CI:145:VAL:HG22	50:F2:58:ARG:HH12	1.56	0.70
11:CN:166:ILE:HD13	24:Ck:748:LEU:HD22	1.73	0.70
32:DF:103:VAL:HG22	32:DF:117:VAL:HG12	1.73	0.70
7:CI:279:ARG:HG3	7:CI:284:GLU:HB2	1.74	0.69
13:CP:31:MET:HG3	13:CP:114:PRO:HG3	1.74	0.69
32:DF:520:GLN:O	32:DF:531:ARG:NH2	2.24	0.69
1:CA:566:U:O2	51:F3:66:ARG:NH2	2.24	0.69
51:F3:829:LEU:HD13	51:F3:850:LEU:HD11	1.74	0.69
65:Ff:482:ALA:HB1	65:Ff:717:LYS:HG2	1.72	0.69
4:CE:62:ARG:HH11	70:IB:700:PRO:HG3	1.56	0.69
15:CR:138:ARG:O	15:CR:176:ASN:ND2	2.25	0.69
24:Ck:660:PRO:HG3	28:DB:1068:GLY:HA2	1.75	0.69
30:DD:303:LEU:HD21	30:DD:400:VAL:HG23	1.73	0.69
51:F3:818:GLU:HB2	51:F3:821:ARG:HG2	1.74	0.69
18:Ca:420:GLN:HA	18:Ca:481:ARG:HA	1.75	0.69
29:DC:469:THR:OG1	37:DK:285:GLU:OE1	2.11	0.69
14:CQ:242:PHE:O	14:CQ:246:ASN:ND2	2.25	0.69
42:DT:177:MET:HB3	42:DT:179:VAL:HG23	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:FO:135:ASN:HD22	57:FO:167:HIS:HB2	1.58	0.69
1:CA:493:U:O2'	1:CA:494:A:O5'	2.10	0.68
29:DC:784:GLU:HA	29:DC:814:GLN:HA	1.75	0.68
31:DE:495:ARG:NH1	61:FZ:84:GLU:OE2	2.26	0.68
37:DK:131:SER:O	37:DK:137:ARG:NH2	2.26	0.68
41:DR:252:ALA:HA	41:DR:262:ARG:HG3	1.74	0.68
8:CJ:45:ILE:HG22	38:DL:281:PHE:HB3	1.76	0.68
66:Fg:51:GLN:NE2	69:IA:232:GLU:O	2.27	0.68
68:Fi:129:LEU:HD21	68:Fi:195:LYS:HG2	1.74	0.68
28:DB:768:ALA:HB1	28:DB:774:ASN:HB2	1.75	0.68
65:Ff:292:ARG:NH2	65:Ff:457:TYR:O	2.27	0.68
9:CK:181:MET:N	9:CK:185:MET:SD	2.67	0.68
50:F2:758:GLY:HA2	50:F2:769:SER:HB2	1.75	0.68
68:Fi:348:CYS:SG	68:Fi:380:GLN:NE2	2.67	0.68
1:CA:465:U:OP1	7:CI:293:ARG:NH2	2.27	0.68
7:CI:71:GLU:O	45:DW:99:HIS:NE2	2.26	0.68
28:DB:303:PRO:O	31:DE:489:ARG:NH2	2.27	0.68
50:F2:838:TYR:HB2	50:F2:851:LEU:HD23	1.75	0.68
51:F3:887:ALA:HB3	51:F3:892:ARG:HE	1.57	0.68
12:CO:117:GLN:HE21	12:CO:201:PHE:HB2	1.58	0.67
14:CQ:206:THR:HG21	54:F7:61:HIS:HE1	1.58	0.67
28:DB:1032:ASP:HB3	28:DB:1036:MET:HB2	1.76	0.67
47:DY:10:ASN:N	47:DY:120:TYR:O	2.27	0.67
52:F5:592:LEU:HD12	52:F5:602:GLU:HB2	1.76	0.67
66:Fg:78:CYS:SG	66:Fg:164:ARG:NH1	2.67	0.67
51:F3:637:LEU:HD23	51:F3:698:VAL:HG13	1.77	0.67
55:F9:456:GLU:HG3	67:Fh:130:ARG:HG3	1.76	0.67
28:DB:824:ARG:HD3	32:DF:508:VAL:HG13	1.76	0.67
53:F6:131:ARG:NH1	53:F6:152:ASP:OD2	2.28	0.67
1:CA:509:U:O2'	16:CS:75:MET:SD	2.53	0.67
30:DD:414:ARG:NH1	30:DD:514:ASP:OD1	2.27	0.67
48:DZ:75:PHE:O	48:DZ:80:TRP:NE1	2.27	0.67
66:Fg:442:ASN:HB2	66:Fg:445:GLU:HB2	1.77	0.67
68:Fi:215:GLN:NE2	68:Fi:218:HIS:O	2.28	0.67
12:CO:419:VAL:HG22	57:FO:97:ASN:HD22	1.60	0.66
24:Ck:272:ASP:OD2	28:DB:898:GLN:NE2	2.28	0.66
5:CF:119:ASP:OD2	20:Cd:141:ARG:NE	2.28	0.66
51:F3:783:THR:HG23	51:F3:831:ARG:HH12	1.60	0.66
54:F7:404:MET:SD	54:F7:444:GLN:NE2	2.67	0.66
8:CJ:369:ARG:NH2	8:CJ:804:ASN:O	2.27	0.66
1:CA:272:C:O2'	54:F7:672:ARG:NH2	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CS:133:ARG:NH1	28:DB:1124:HIS:O	2.29	0.66
30:DD:597:LEU:HD13	30:DD:620:ALA:HB1	1.76	0.66
32:DF:394:GLU:OE1	32:DF:397:ARG:NH2	2.29	0.66
33:DG:388:TYR:OH	33:DG:392:ARG:NH1	2.28	0.66
41:DR:51:LEU:HD22	41:DR:84:LEU:HD21	1.76	0.66
70:IB:635:LYS:HG2	70:IB:637:PRO:HD2	1.77	0.66
69:IA:182:ALA:HB2	69:IA:376:ARG:HD3	1.77	0.66
28:DB:194:GLN:HE22	31:DE:471:ARG:HD2	1.59	0.66
28:DB:1015:ASP:OD1	33:DG:38:ARG:NH2	2.28	0.66
43:DU:106:PRO:HG2	43:DU:109:SER:HB3	1.77	0.66
32:DF:554:TYR:HA	32:DF:570:PRO:HA	1.77	0.66
53:F6:229:LEU:HA	53:F6:233:LEU:HD12	1.78	0.66
54:F7:371:GLN:HG3	54:F7:389:LEU:HD11	1.77	0.66
68:Fi:450:TRP:HB3	68:Fi:543:MET:HG3	1.77	0.66
28:DB:746:LEU:HB3	28:DB:784:TYR:HB3	1.78	0.66
34:DH:204:SER:O	34:DH:208:ASN:ND2	2.22	0.66
56:FM:302:MET:HE3	56:FM:305:ARG:HG3	1.77	0.66
66:Fg:233:SER:O	66:Fg:237:TYR:OH	2.13	0.66
69:IA:333:LEU:HD11	69:IA:342:PHE:HB2	1.78	0.66
16:CS:118:ARG:HB3	16:CS:127:GLU:HG3	1.78	0.66
24:Ck:135:ASN:ND2	24:Ck:137:THR:O	2.29	0.66
24:Ck:362:TYR:HB2	24:Ck:365:ILE:HG12	1.76	0.66
51:F3:162:PRO:HG2	51:F3:171:LEU:HB2	1.76	0.66
61:FZ:59:LYS:O	61:FZ:63:ASN:ND2	2.29	0.66
70:IB:334:ALA:O	70:IB:337:GLN:NE2	2.29	0.66
16:CS:72:TRP:O	16:CS:76:THR:OG1	2.12	0.66
24:Ck:644:HIS:HD2	24:Ck:669:ASN:H	1.44	0.66
34:DH:489:LEU:O	42:DT:153:LYS:NZ	2.29	0.66
34:DH:523:ARG:HH21	34:DH:524:HIS:HE1	1.44	0.66
8:CJ:145:THR:OG1	8:CJ:151:ASN:ND2	2.29	0.65
32:DF:116:ARG:NH1	32:DF:179:TYR:OH	2.29	0.65
65:Ff:697:THR:HG22	70:IB:497:LYS:HE2	1.76	0.65
56:FM:140:SER:HB3	56:FM:152:LEU:HB3	1.77	0.65
65:Ff:266:ARG:NH1	65:Ff:668:GLU:O	2.30	0.65
27:Cp:162:LEU:HD12	27:Cp:163:PRO:HD2	1.79	0.65
55:F9:70:HIS:HE1	55:F9:146:MET:HE3	1.61	0.65
65:Ff:501:TRP:CE2	65:Ff:529:SER:HB3	2.31	0.65
8:CJ:241:SER:OG	8:CJ:404:LYS:NZ	2.29	0.65
12:CO:332:ARG:NH1	12:CO:340:ASP:OD2	2.29	0.65
13:CP:133:LYS:HG2	27:Cp:113:GLN:HB3	1.79	0.65
29:DC:348:VAL:HG13	29:DC:350:ASP:H	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:F6:192:VAL:HG23	53:F6:193:GLN:HG3	1.77	0.65
7:CI:92:PRO:HG3	7:CI:99:VAL:HB	1.79	0.65
14:CQ:123:ARG:HH12	30:DD:727:PRO:HG2	1.60	0.65
14:CQ:151:ARG:NH2	41:DR:13:PHE:O	2.29	0.65
11:CN:93:ASP:OD1	11:CN:98:VAL:N	2.27	0.65
12:CO:313:THR:OG1	14:CQ:166:GLU:OE2	2.15	0.65
29:DC:977:ARG:HG3	31:DE:589:PRO:HB3	1.78	0.65
53:F6:572:LEU:HG	65:Ff:735:VAL:HG12	1.79	0.65
23:Cj:205:ARG:NH2	41:DR:232:THR:O	2.29	0.65
24:Ck:48:ALA:HB3	28:DB:273:GLN:HE22	1.60	0.65
58:FP:237:LEU:HG	58:FP:239:GLY:H	1.61	0.65
67:Fh:57:ALA:HB3	70:IB:686:ARG:HH12	1.60	0.65
18:Ca:363:ARG:O	18:Ca:367:ASN:ND2	2.29	0.65
56:FM:247:ARG:NH2	69:IA:189:ASP:OD1	2.30	0.65
11:CN:149:GLU:O	11:CN:153:ASN:ND2	2.30	0.65
52:F5:592:LEU:HD22	52:F5:598:SER:HB2	1.78	0.65
55:F9:562:LYS:HA	55:F9:590:ALA:HA	1.79	0.65
28:DB:743:VAL:HG12	28:DB:758:SER:HA	1.79	0.65
34:DH:526:ASN:HD21	34:DH:529:TYR:HD1	1.44	0.65
39:DO:81:LEU:H	39:DO:86:ARG:HH21	1.45	0.65
8:CJ:301:ASN:ND2	8:CJ:312:ASP:O	2.30	0.64
43:DU:86:ILE:HD13	43:DU:99:GLN:HB2	1.78	0.64
51:F3:624:MET:HB3	54:F7:376:ALA:HB2	1.79	0.64
57:FO:101:ARG:HE	57:FO:104:ARG:HA	1.62	0.64
14:CQ:20:GLN:HE21	43:DU:218:ARG:HH11	1.44	0.64
14:CQ:229:PRO:O	26:Cn:183:ARG:NH2	2.31	0.64
15:CR:176:ASN:H	15:CR:176:ASN:HD22	1.43	0.64
34:DH:144:ASP:N	34:DH:144:ASP:OD1	2.27	0.64
51:F3:77:LEU:O	57:FO:41:ARG:NH1	2.30	0.64
52:F5:125:ARG:NH1	52:F5:149:GLU:OE2	2.30	0.64
32:DF:198:HIS:HD2	32:DF:199:GLU:HG2	1.62	0.64
36:DJ:261:PHE:O	36:DJ:305:ARG:NH1	2.30	0.64
55:F9:447:TRP:NE1	67:Fh:143:GLU:OE2	2.26	0.64
65:Ff:263:SER:HB3	65:Ff:669:ARG:HG2	1.80	0.64
1:CA:121:A:H5"	14:CQ:102:SER:HB2	1.80	0.64
5:CF:5:SER:HB3	5:CF:95:LEU:HB2	1.80	0.64
8:CJ:475:VAL:HG11	8:CJ:669:PRO:HB2	1.80	0.64
20:Cd:198:GLU:HB3	53:F6:436:ARG:HD3	1.80	0.64
30:DD:232:TRP:HA	30:DD:236:CYS:HB2	1.80	0.64
32:DF:485:LEU:O	32:DF:491:ARG:NH2	2.31	0.64
33:DG:338:LYS:O	33:DG:346:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:F5:232:GLN:HG2	52:F5:611:LYS:HD3	1.79	0.64
8:CJ:792:HIS:HB3	8:CJ:795:LYS:HB2	1.78	0.64
28:DB:433:ARG:HA	28:DB:442:LEU:HD21	1.80	0.64
29:DC:53:ALA:HB1	37:DK:267:ARG:HG3	1.80	0.64
34:DH:502:GLU:O	37:DK:300:LYS:NZ	2.31	0.64
36:DJ:17:PRO:HA	36:DJ:23:VAL:HG21	1.80	0.64
65:Ff:593:GLU:O	68:Fi:590:TYR:OH	2.11	0.64
8:CJ:123:ARG:NH2	28:DB:913:PRO:O	2.31	0.64
8:CJ:165:ARG:HG2	8:CJ:176:ILE:HG21	1.79	0.64
8:CJ:642:ASN:HD21	8:CJ:654:VAL:HG23	1.62	0.64
31:DE:694:LEU:HD13	37:DK:62:PHE:HB2	1.79	0.64
7:CI:54:SER:OG	21:Cg:414:ARG:NH2	2.31	0.63
28:DB:546:ARG:NH1	28:DB:875:GLY:O	2.31	0.63
45:DW:63:THR:H	45:DW:66:HIS:HD2	1.45	0.63
56:FM:153:LEU:HB2	56:FM:176:VAL:HG12	1.80	0.63
58:FP:133:PHE:O	58:FP:137:HIS:HB2	1.97	0.63
68:Fi:365:ASN:HA	68:Fi:473:ARG:HD3	1.80	0.63
31:DE:718:SER:HB3	31:DE:726:THR:HG22	1.79	0.63
68:Fi:259:HIS:HB2	68:Fi:298:ALA:HB3	1.80	0.63
1:CA:99:G:N1	14:CQ:49:ASN:O	2.30	0.63
67:Fh:292:MET:SD	67:Fh:296:ASN:ND2	2.67	0.63
8:CJ:724:THR:HG21	21:Cg:302:PRO:HG3	1.80	0.63
18:Ca:404:ARG:NH2	18:Ca:499:ASP:O	2.31	0.63
20:Cd:67:GLU:HG2	30:DD:156:GLN:HE22	1.64	0.63
30:DD:333:PRO:HB3	43:DU:196:MET:HE1	1.80	0.63
44:DV:178:THR:OG1	44:DV:180:ASP:OD1	2.17	0.63
45:DW:157:ASN:ND2	45:DW:159:THR:OG1	2.31	0.63
46:DX:80:TRP:O	46:DX:138:LYS:NZ	2.31	0.63
1:CA:56:U:O2'	13:CP:20:LEU:O	2.15	0.63
8:CJ:52:PHE:HD2	8:CJ:57:ARG:HB2	1.64	0.63
29:DC:316:THR:HG22	29:DC:319:GLU:HG2	1.81	0.63
58:FP:144:LEU:HD21	58:FP:195:VAL:HG11	1.79	0.63
70:IB:343:ARG:O	70:IB:551:ARG:NH2	2.32	0.63
1:CA:322:A:OP1	43:DU:10:LYS:NZ	2.31	0.63
21:Cg:484:GLU:OE1	21:Cg:488:ARG:NH2	2.32	0.63
28:DB:1058:ILE:HB	28:DB:1061:GLN:HB2	1.79	0.63
29:DC:665:LEU:HB2	29:DC:758:VAL:HB	1.80	0.63
51:F3:103:ASP:O	51:F3:175:ARG:NH1	2.32	0.63
53:F6:10:PHE:O	53:F6:14:HIS:HB2	1.99	0.63
14:CQ:55:THR:HG22	14:CQ:56:ARG:HG2	1.80	0.63
8:CJ:469:ASP:OD1	8:CJ:469:ASP:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Ca:326:PHE:HB3	18:Ca:329:GLU:HB2	1.81	0.63
35:DI:188:GLU:OE2	35:DI:193:ASN:ND2	2.32	0.63
35:DI:367:SER:H	35:DI:370:GLN:HE21	1.47	0.63
38:DL:56:GLU:OE1	38:DL:59:ARG:NH1	2.32	0.63
29:DC:461:SER:HA	29:DC:477:PHE:HB3	1.81	0.62
36:DJ:140:TRP:O	36:DJ:144:CYS:HB3	1.99	0.62
54:F7:90:GLU:OE2	54:F7:91:LYS:NZ	2.32	0.62
1:CA:472:G:OP1	38:DL:289:ARG:NH1	2.33	0.62
12:CO:215:ASP:OD2	20:CD:124:ARG:NH1	2.32	0.62
26:Cn:191:ALA:HB2	57:FO:4:PRO:HG3	1.81	0.62
28:DB:1074:SER:O	28:DB:1077:ARG:NH1	2.32	0.62
10:CL:34:ASN:ND2	69:IA:501:ASN:OD1	2.32	0.62
18:Ca:192:GLN:NE2	50:F2:759:SER:OG	2.32	0.62
18:Ca:405:ARG:HE	30:DD:776:ALA:HB1	1.64	0.62
29:DC:940:ALA:HB1	29:DC:948:TRP:CD1	2.34	0.62
35:DI:159:ASP:HB2	35:DI:162:PHE:HB2	1.81	0.62
14:CQ:65:GLY:O	14:CQ:69:GLN:NE2	2.32	0.62
31:DE:222:TRP:NE1	31:DE:403:PRO:O	2.31	0.62
33:DG:196:ARG:NH2	33:DG:211:TYR:OH	2.27	0.62
1:CA:86:G:N2	43:DU:205:ALA:O	2.32	0.62
50:F2:245:ARG:HG3	50:F2:281:GLU:HG3	1.82	0.62
69:IA:174:SER:O	69:IA:178:ASN:ND2	2.32	0.62
70:IB:540:VAL:HG22	70:IB:591:LEU:HB2	1.80	0.62
1:CA:571:A:OP1	26:Cn:179:ARG:NH2	2.32	0.62
9:CK:248:SER:O	9:CK:252:ASN:ND2	2.32	0.62
43:DU:111:ILE:HB	43:DU:143:PRO:HA	1.82	0.62
46:DX:83:ARG:NH1	47:DY:135:TYR:OH	2.29	0.62
7:CI:302:GLU:OE1	8:CJ:119:ARG:NH2	2.33	0.62
11:CN:93:ASP:HB3	11:CN:114:SER:H	1.64	0.62
29:DC:609:VAL:HB	29:DC:618:ARG:HH21	1.64	0.62
31:DE:630:GLU:HG3	31:DE:634:ARG:HE	1.64	0.62
11:CN:42:HIS:HB2	11:CN:81:LEU:HD21	1.82	0.62
14:CQ:54:ARG:NH1	54:F7:83:TYR:O	2.33	0.62
28:DB:302:LEU:HD21	31:DE:486:ILE:HD13	1.82	0.62
35:DI:318:ARG:NH1	35:DI:322:GLU:OE2	2.31	0.62
12:CO:288:GLN:HE21	54:F7:642:VAL:HG21	1.65	0.62
28:DB:160:LEU:HD23	29:DC:648:LEU:HB2	1.82	0.62
35:DI:303:ILE:O	35:DI:314:GLN:NE2	2.33	0.62
50:F2:244:TYR:OH	50:F2:270:ASN:ND2	2.32	0.62
53:F6:190:MET:O	53:F6:195:SER:OG	2.13	0.62
56:FN:90:HIS:HA	56:FN:94:GLU:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:FP:156:TRP:O	60:FX:42:ARG:NH2	2.33	0.62
69:IA:656:ARG:NH2	69:IA:732:GLN:OE1	2.32	0.62
1:CA:326:U:O2'	54:F7:115:ARG:NH1	2.32	0.62
8:CJ:798:GLN:HA	8:CJ:805:HIS:HB2	1.82	0.62
55:F9:457:ASP:HB3	55:F9:460:ARG:HG2	1.81	0.62
56:FN:196:VAL:HG13	56:FN:234:MET:HE3	1.81	0.62
7:CI:335:VAL:HB	7:CI:343:VAL:HG21	1.81	0.61
24:Ck:735:ILE:O	24:Ck:738:GLN:NE2	2.33	0.61
28:DB:717:ARG:HA	28:DB:720:LYS:HD3	1.81	0.61
40:DP:90:LEU:HD13	40:DP:127:ASP:HB3	1.81	0.61
65:Ff:616:LYS:HD2	65:Ff:756:LEU:HD21	1.82	0.61
68:Fi:213:ILE:HG13	68:Fi:214:VAL:HG13	1.81	0.61
35:DI:368:ASN:OD1	35:DI:372:ASN:ND2	2.32	0.61
40:DP:109:ARG:NH2	40:DP:142:ASN:O	2.32	0.61
56:FM:226:ASP:HA	56:FM:231:SER:HB3	1.81	0.61
69:IA:697:LYS:HG2	69:IA:698:GLU:HG3	1.82	0.61
30:DD:605:ARG:O	41:DR:227:ARG:NH2	2.33	0.61
57:FO:128:ASP:OD1	66:Fg:348:SER:OG	2.18	0.61
57:FO:214:ARG:HD2	57:FO:242:MET:HG2	1.82	0.61
65:Ff:512:ARG:NH1	65:Ff:519:THR:OG1	2.34	0.61
28:DB:134:HIS:NE2	28:DB:227:THR:OG1	2.33	0.61
29:DC:41:ASN:ND2	42:DT:168:GLU:O	2.33	0.61
51:F3:280:LEU:HD11	51:F3:334:ILE:HD11	1.81	0.61
51:F3:728:ARG:HG2	51:F3:777:ARG:HH11	1.65	0.61
66:Fg:12:SER:HB2	66:Fg:508:SER:HB2	1.82	0.61
1:CA:465:U:OP2	7:CI:411:LYS:NZ	2.30	0.61
1:CA:562:U:OP2	66:Fg:305:ARG:NH2	2.33	0.61
16:CS:84:LEU:HD22	16:CS:105:VAL:HG11	1.82	0.61
38:DL:118:ASP:OD2	38:DL:208:ARG:NH1	2.33	0.61
57:FO:162:GLU:O	66:Fg:192:ARG:NH2	2.33	0.61
58:FP:284:PHE:HA	58:FP:309:LEU:HD13	1.83	0.61
65:Ff:316:THR:HG22	65:Ff:384:SER:HB3	1.83	0.61
13:CP:11:ALA:O	40:DP:15:ARG:NH1	2.33	0.61
16:CS:118:ARG:NH2	32:DF:81:SER:O	2.33	0.61
23:Cj:139:ARG:NH1	40:DP:101:PHE:O	2.33	0.61
32:DF:109:MET:HG2	32:DF:114:GLY:HA2	1.82	0.61
34:DH:26:PRO:HG3	36:DJ:17:PRO:HB2	1.83	0.61
18:Ca:444:PHE:HB2	18:Ca:472:VAL:HG12	1.83	0.61
21:Cg:184:HIS:HD2	21:Cg:382:LEU:HD22	1.65	0.61
24:Ck:834:MET:N	24:Ck:834:MET:SD	2.73	0.61
52:F5:570:ARG:HA	52:F5:573:ARG:HH21	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:FO:125:ASN:O	66:Fg:256:GLN:NE2	2.34	0.61
65:Ff:302:ARG:NH1	65:Ff:339:VAL:O	2.33	0.61
65:Ff:529:SER:OG	87:Ff:901:FDA:O1A	2.18	0.61
69:IA:199:TYR:HB3	69:IA:370:SER:HB2	1.82	0.61
6:CH:41:VAL:HG21	6:CH:47:ARG:HG2	1.82	0.61
8:CJ:352:TYR:OH	8:CJ:399:ARG:NH1	2.34	0.61
9:CK:52:ASP:OD2	21:Cg:481:ARG:NH2	2.34	0.61
40:DP:185:ASP:OD1	40:DP:185:ASP:N	2.34	0.61
46:DX:119:ARG:O	46:DX:123:ASN:ND2	2.32	0.61
68:Fi:443:GLU:OE2	68:Fi:547:ARG:NH1	2.33	0.61
1:CA:493:U:O2'	1:CA:494:A:O4'	2.18	0.61
8:CJ:674:GLN:NE2	11:CN:58:THR:O	2.33	0.61
21:Cg:33:TRP:HZ3	21:Cg:39:LEU:HD21	1.66	0.61
30:DD:609:ASP:N	30:DD:609:ASP:OD1	2.34	0.61
38:DL:125:HIS:HB3	38:DL:197:ALA:HB1	1.82	0.61
1:CA:218:A:H61	1:CA:258:U:H3	1.48	0.61
9:CK:242:ASN:HA	9:CK:245:GLN:HE21	1.66	0.61
18:Ca:419:GLN:HB2	58:FP:334:THR:HG23	1.81	0.61
24:Ck:75:ARG:NH1	28:DB:437:ASN:O	2.31	0.61
24:Ck:184:LYS:HE3	24:Ck:228:LEU:HG	1.83	0.61
24:Ck:704:ASN:HD21	24:Ck:749:ASP:HB3	1.66	0.61
53:F6:118:HIS:HA	53:F6:121:THR:HG22	1.83	0.61
53:F6:617:THR:HA	53:F6:620:TRP:CD1	2.35	0.61
1:CA:77:A:OP2	23:Cj:10:ARG:NH2	2.27	0.60
8:CJ:677:THR:HG21	11:CN:58:THR:HB	1.82	0.60
14:CQ:21:ARG:NH2	43:DU:214:GLY:O	2.34	0.60
18:Ca:67:ARG:NH2	18:Ca:181:GLU:OE1	2.34	0.60
20:Cd:44:GLU:OE1	20:Cd:47:ARG:NH2	2.33	0.60
21:Cg:356:CYS:SG	21:Cg:357:THR:N	2.74	0.60
24:Ck:687:ARG:NH2	34:DH:28:ASN:O	2.34	0.60
31:DE:659:ARG:O	31:DE:663:ASN:ND2	2.32	0.60
35:DI:368:ASN:O	35:DI:372:ASN:ND2	2.30	0.60
55:F9:217:GLN:HE22	70:IB:732:VAL:H	1.48	0.60
56:FM:90:HIS:HA	56:FM:94:GLU:HB2	1.82	0.60
65:Ff:512:ARG:HB2	65:Ff:515:ARG:HG3	1.82	0.60
24:Ck:375:PHE:HA	24:Ck:378:LYS:HE2	1.83	0.60
29:DC:753:LEU:HD22	29:DC:930:ALA:HB1	1.81	0.60
34:DH:80:ARG:HB3	34:DH:83:GLU:HB2	1.81	0.60
42:DT:36:GLU:OE1	42:DT:214:ARG:NH2	2.34	0.60
58:FP:115:VAL:HG13	58:FP:119:LYS:HE3	1.83	0.60
60:FX:148:LEU:HB3	60:FX:181:MET:HE3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:IA:96:TYR:OH	70:IB:208:ARG:NH2	2.34	0.60
30:DD:89:SER:HB2	30:DD:812:TYR:HB2	1.82	0.60
36:DJ:95:THR:O	36:DJ:131:GLN:NE2	2.34	0.60
40:DP:16:ARG:HD2	40:DP:20:MET:HE2	1.82	0.60
51:F3:96:THR:O	57:FO:68:ARG:NH2	2.34	0.60
1:CA:454:G:N2	1:CA:471:U:O2'	2.34	0.60
13:CP:118:LEU:HD22	13:CP:123:LEU:HD12	1.82	0.60
31:DE:48:ALA:HB1	31:DE:53:VAL:HB	1.82	0.60
33:DG:214:TYR:HE2	33:DG:227:GLU:HG3	1.66	0.60
42:DT:208:ARG:NH2	42:DT:217:GLU:OE1	2.33	0.60
53:F6:303:GLU:OE1	53:F6:333:ARG:NH1	2.33	0.60
56:FM:231:SER:OG	56:FN:233:THR:OG1	2.18	0.60
69:IA:205:VAL:HG13	69:IA:276:ASP:H	1.67	0.60
1:CA:59:U:OP2	13:CP:53:ARG:NH2	2.35	0.60
1:CA:431:U:O2	32:DF:185:LYS:NZ	2.34	0.60
8:CJ:125:ASP:HB3	8:CJ:128:LYS:HG2	1.83	0.60
18:Ca:134:LEU:HA	61:FZ:58:LEU:HD21	1.83	0.60
21:Cg:329:PRO:HG2	21:Cg:332:ARG:HG2	1.82	0.60
32:DF:359:ARG:HG3	36:DJ:78:ALA:HA	1.83	0.60
33:DG:448:LEU:HD12	33:DG:532:VAL:HG13	1.82	0.60
42:DT:104:PRO:HG2	42:DT:107:GLU:HB2	1.83	0.60
50:F2:857:ALA:O	55:F9:165:ARG:NH2	2.34	0.60
16:CS:95:THR:HG21	32:DF:69:THR:H	1.67	0.60
18:Ca:363:ARG:NH2	18:Ca:512:GLU:OE2	2.31	0.60
23:Cj:59:VAL:HG21	23:Cj:91:GLU:HB3	1.84	0.60
30:DD:181:MET:HE1	30:DD:215:TYR:HD1	1.65	0.60
35:DI:104:ILE:HG23	35:DI:118:VAL:HG21	1.82	0.60
56:FM:220:LYS:NZ	56:FN:178:HIS:O	2.34	0.60
29:DC:114:GLU:HG2	29:DC:120:ASN:HB2	1.84	0.60
32:DF:55:ARG:NH2	32:DF:145:VAL:O	2.33	0.60
34:DH:501:PRO:HA	37:DK:301:ARG:HB3	1.84	0.60
39:DO:81:LEU:HB2	39:DO:86:ARG:HE	1.66	0.60
45:DW:93:HIS:O	45:DW:97:SER:HB3	2.02	0.60
54:F7:568:ARG:NH2	54:F7:604:ASP:OD2	2.34	0.60
64:Fd:97:LYS:HB2	64:Fd:101:ARG:HH21	1.66	0.60
1:CA:435:G:O2'	32:DF:27:ARG:NH1	2.34	0.60
1:CA:66:U:OP1	12:CO:424:LYS:NZ	2.25	0.60
21:Cg:219:LEU:HD22	21:Cg:243:LEU:HD23	1.83	0.60
24:Ck:80:GLU:O	24:Ck:92:ARG:NH1	2.35	0.60
27:Cp:141:ARG:HH11	40:DP:15:ARG:HD2	1.64	0.60
31:DE:223:GLU:HB3	31:DE:312:LEU:HD11	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DH:216:THR:O	34:DH:216:THR:OG1	2.19	0.60
70:IB:407:PRO:HD2	70:IB:462:ARG:HB3	1.84	0.60
1:CA:51:U:H2'	23:Cj:50:VAL:HG22	1.84	0.60
10:CL:20:VAL:HG13	10:CL:39:TYR:HB3	1.83	0.60
24:Ck:138:PHE:O	24:Ck:140:ARG:NH1	2.35	0.60
55:F9:194:MET:HG2	70:IB:733:SER:HA	1.83	0.60
5:CF:52:ARG:HG3	5:CF:90:LEU:HD21	1.84	0.59
6:CH:53:ARG:HE	20:Cd:119:HIS:HD2	1.49	0.59
43:DU:175:PRO:HG2	43:DU:178:TRP:HB2	1.83	0.59
59:FW:18:ARG:N	84:FW:301:PO4:O3	2.35	0.59
1:CA:123:U:O2'	12:CO:425:ARG:NH1	2.36	0.59
18:Ca:387:GLN:OE1	58:FP:316:ARG:NH1	2.35	0.59
29:DC:258:ILE:HD13	29:DC:387:ARG:HH22	1.66	0.59
34:DH:489:LEU:HD11	42:DT:60:LEU:HD21	1.84	0.59
34:DH:508:LEU:HD22	34:DH:514:PRO:HB3	1.83	0.59
35:DI:277:SER:HB3	51:F3:923:PRO:HG3	1.84	0.59
62:Fb:26:TRP:N	63:Fc:129:GLU:OE1	2.35	0.59
69:IA:40:GLN:HE22	69:IA:124:CYS:HA	1.66	0.59
4:CE:142:LEU:HD11	4:CE:167:LEU:HD13	1.84	0.59
9:CK:229:GLY:HA3	65:Ff:707:HIS:CD2	2.37	0.59
12:CO:163:ARG:NE	12:CO:172:SER:OG	2.33	0.59
29:DC:62:SER:O	29:DC:539:ASN:ND2	2.35	0.59
29:DC:117:MET:HE3	31:DE:569:PHE:HB2	1.84	0.59
29:DC:128:HIS:ND1	31:DE:153:HIS:O	2.35	0.59
69:IA:141:LYS:O	69:IA:495:ALA:N	2.32	0.59
3:CC:55:LYS:HE3	38:DL:282:TRP:HA	1.83	0.59
5:CF:112:GLN:O	12:CO:113:LYS:NZ	2.35	0.59
8:CJ:507:ASN:ND2	8:CJ:520:ASN:O	2.31	0.59
14:CQ:200:LEU:HD22	54:F7:136:LYS:HB3	1.83	0.59
24:Ck:825:LYS:NZ	24:Ck:829:LEU:O	2.33	0.59
28:DB:879:ARG:HB3	28:DB:937:MET:HB2	1.85	0.59
51:F3:533:SER:HB3	51:F3:574:VAL:HG22	1.84	0.59
56:FN:112:HIS:HB3	56:FN:139:MET:HG3	1.84	0.59
65:Ff:282:GLU:OE2	65:Ff:458:ARG:NH2	2.35	0.59
69:IA:206:VAL:HA	69:IA:277:LEU:O	2.03	0.59
5:CF:69:LEU:HD12	5:CF:76:MET:HE1	1.84	0.59
23:Cj:210:PRO:HA	41:DR:266:TRP:CG	2.37	0.59
24:Ck:415:ASN:OD1	24:Ck:541:ARG:NH1	2.36	0.59
28:DB:358:ASN:HB3	34:DH:543:MET:HE1	1.85	0.59
28:DB:1133:PRO:HA	28:DB:1137:MET:HB2	1.84	0.59
37:DK:177:LYS:HB3	37:DK:180:GLU:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:DO:157:ILE:HG13	39:DO:188:ALA:HB1	1.85	0.59
60:FX:203:ALA:HA	60:FX:206:LYS:HE2	1.84	0.59
6:CH:194:PHE:HB2	50:F2:304:MET:HG2	1.83	0.59
21:Cg:92:GLY:HA2	45:DW:79:LEU:HD11	1.85	0.59
27:Cp:178:GLU:OE2	27:Cp:181:ARG:NH2	2.35	0.59
34:DH:113:LEU:HB3	34:DH:119:LEU:HD23	1.84	0.59
70:IB:669:LYS:HD2	71:U8:10:UNK:HA	1.85	0.59
7:CI:309:ARG:HD3	8:CJ:110:LYS:HG3	1.84	0.59
8:CJ:580:TYR:OH	8:CJ:591:ASP:OD1	2.18	0.59
18:Ca:531:ASP:OD1	30:DD:202:ARG:NH2	2.35	0.59
28:DB:1117:THR:HG1	28:DB:1119:TRP:CD1	2.20	0.59
34:DH:558:GLU:O	34:DH:565:ASN:ND2	2.35	0.59
52:F5:638:GLU:OE2	61:FZ:63:ASN:ND2	2.36	0.59
53:F6:457:VAL:HA	53:F6:467:ALA:HB3	1.84	0.59
54:F7:542:ASN:ND2	54:F7:580:CYS:SG	2.76	0.59
10:CL:17:VAL:HB	10:CL:40:ALA:HB1	1.84	0.59
11:CN:38:ASP:OD1	32:DF:112:ARG:NH2	2.31	0.59
18:Ca:77:PRO:HB2	52:F5:743:TRP:HZ2	1.66	0.59
21:Cg:477:TYR:OH	21:Cg:481:ARG:NH2	2.36	0.59
29:DC:116:TYR:O	31:DE:150:ARG:NH1	2.36	0.59
54:F7:242:GLU:HA	54:F7:249:PHE:HB3	1.85	0.59
58:FP:262:ARG:NH1	58:FP:267:ASP:OD1	2.36	0.59
21:Cg:105:HIS:O	21:Cg:107:ARG:NH2	2.32	0.59
40:DP:139:ARG:NH1	40:DP:176:PRO:O	2.35	0.59
58:FP:174:THR:O	58:FP:185:ARG:NH1	2.36	0.59
66:Fg:126:ARG:NH2	66:Fg:550:LEU:O	2.35	0.59
14:CQ:17:GLU:HG2	43:DU:224:MET:HE3	1.83	0.59
27:Cp:32:PRO:HB3	56:FM:31:ARG:HH21	1.67	0.59
65:Ff:794:TYR:HE2	65:Ff:814:ALA:HB1	1.68	0.59
68:Fi:27:MET:HB2	68:Fi:30:ALA:HB3	1.85	0.59
1:CA:441:G:O6	22:CI:136:HIS:NE2	2.33	0.58
8:CJ:621:ASN:ND2	22:CI:24:PRO:O	2.36	0.58
12:CO:203:GLN:HG2	54:F7:632:THR:HG21	1.85	0.58
19:Cb:166:GLU:HB3	53:F6:318:SER:HA	1.85	0.58
35:DI:68:PRO:O	35:DI:76:LYS:NZ	2.36	0.58
36:DJ:327:SER:HB2	36:DJ:335:ILE:HG23	1.85	0.58
40:DP:196:TRP:HA	40:DP:208:PRO:HD2	1.85	0.58
46:DX:56:ASP:OD1	46:DX:59:ARG:NH2	2.35	0.58
52:F5:447:VAL:HA	52:F5:450:MET:HE2	1.85	0.58
52:F5:645:LEU:HD12	52:F5:646:PRO:HD2	1.85	0.58
55:F9:202:LYS:HE2	55:F9:210:GLN:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:F9:601:ARG:NH2	69:IA:492:MET:SD	2.75	0.58
62:Fb:26:TRP:N	62:Fb:30:GLN:OE1	2.36	0.58
4:CE:395:THR:HG23	4:CE:398:ASP:H	1.68	0.58
7:CI:105:THR:HG23	7:CI:108:SER:H	1.68	0.58
8:CJ:641:VAL:O	8:CJ:655:ARG:NH1	2.34	0.58
30:DD:528:CYS:O	41:DR:223:GLN:NE2	2.36	0.58
33:DG:194:ARG:O	33:DG:198:ASN:ND2	2.32	0.58
34:DH:8:LYS:H	34:DH:8:LYS:HD2	1.67	0.58
53:F6:46:LYS:O	53:F6:119:ARG:NH2	2.36	0.58
66:Fg:422:ALA:HB3	66:Fg:424:ARG:HE	1.68	0.58
68:Fi:321:ARG:NE	68:Fi:536:ASN:OD1	2.36	0.58
69:IA:178:ASN:OD1	69:IA:376:ARG:NH2	2.35	0.58
1:CA:452:A:H61	1:CA:474:U:H3	1.51	0.58
8:CJ:627:ILE:HD13	8:CJ:654:VAL:HG11	1.84	0.58
28:DB:277:ARG:NH1	28:DB:957:TYR:OH	2.36	0.58
29:DC:562:ARG:NH1	29:DC:928:GLU:OE1	2.36	0.58
40:DP:120:ASP:HA	40:DP:160:ARG:HH12	1.68	0.58
42:DT:33:HIS:CD2	42:DT:34:PRO:HD2	2.38	0.58
64:Fd:59:HIS:HD2	64:Fd:61:GLU:H	1.50	0.58
68:Fi:199:LEU:HD22	68:Fi:230:ILE:HD11	1.85	0.58
20:Cd:189:GLY:O	20:Cd:192:ASN:ND2	2.36	0.58
24:Ck:793:LYS:HE3	24:Ck:794:PRO:HD2	1.86	0.58
28:DB:388:VAL:HG23	34:DH:510:GLY:H	1.67	0.58
29:DC:574:GLN:HE22	29:DC:806:SER:HA	1.67	0.58
34:DH:516:ILE:HA	34:DH:519:ILE:HG12	1.85	0.58
34:DH:534:GLU:OE1	62:Fb:131:TRP:NE1	2.36	0.58
50:F2:61:ASP:OD1	55:F9:47:ARG:NH2	2.34	0.58
51:F3:881:LEU:HA	51:F3:884:MET:HE3	1.86	0.58
59:FW:52:VAL:HG21	59:FW:63:SER:HB2	1.85	0.58
66:Fg:18:ARG:NH1	66:Fg:509:PRO:O	2.36	0.58
5:CF:148:GLU:OE2	19:Cb:148:GLN:NE2	2.36	0.58
29:DC:50:GLU:OE2	29:DC:460:SER:OG	2.22	0.58
31:DE:200:ARG:HD2	31:DE:415:LEU:HD22	1.84	0.58
32:DF:222:TYR:HE1	32:DF:229:PRO:HG3	1.68	0.58
33:DG:456:ARG:NH2	33:DG:542:GLU:OE2	2.36	0.58
33:DG:590:ARG:HB2	33:DG:593:GLU:HB2	1.85	0.58
51:F3:352:PHE:H	51:F3:405:ASN:HD21	1.52	0.58
1:CA:10:G:O6	50:F2:485:ASN:ND2	2.23	0.58
8:CJ:179:PRO:O	8:CJ:184:ARG:NH1	2.35	0.58
8:CJ:501:GLY:HA2	8:CJ:504:LYS:HE2	1.85	0.58
21:Cg:43:ARG:HB3	21:Cg:50:PRO:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DB:559:GLU:OE1	28:DB:567:ARG:NH1	2.37	0.58
32:DF:359:ARG:NH2	36:DJ:80:GLU:OE1	2.35	0.58
39:DO:87:VAL:HG23	39:DO:127:LEU:HB2	1.85	0.58
51:F3:745:LYS:HA	51:F3:749:LYS:HG3	1.86	0.58
56:FN:35:TYR:OH	56:FN:63:ARG:NH2	2.37	0.58
56:FN:100:ILE:HD12	56:FN:127:ALA:HB2	1.86	0.58
68:Fi:247:GLY:N	68:Fi:252:ARG:O	2.34	0.58
1:CA:586:A:H5'	1:CA:587:A:H2'	1.85	0.58
9:CK:274:LYS:NZ	9:CK:299:ALA:O	2.35	0.58
21:Cg:167:ARG:HE	21:Cg:173:THR:HB	1.68	0.58
24:Ck:704:ASN:ND2	24:Ck:751:ASP:OD1	2.29	0.58
28:DB:76:MET:HE2	28:DB:179:VAL:HG22	1.86	0.58
54:F7:90:GLU:HG2	54:F7:91:LYS:HG3	1.85	0.58
69:IA:387:VAL:HG13	69:IA:574:CYS:HA	1.85	0.58
19:Cb:54:HIS:HB3	38:DL:147:ILE:HD13	1.84	0.58
30:DD:640:GLU:OE2	30:DD:651:ARG:NE	2.35	0.58
32:DF:313:ARG:NH1	32:DF:339:TYR:OH	2.36	0.58
47:DY:144:HIS:HB2	47:DY:151:LEU:HD21	1.84	0.58
68:Fi:260:VAL:HG12	68:Fi:296:VAL:HA	1.84	0.58
21:Cg:259:ILE:O	21:Cg:262:GLN:NE2	2.37	0.58
29:DC:56:ALA:N	29:DC:480:GLY:O	2.35	0.58
38:DL:84:GLU:HG3	38:DL:112:VAL:HG12	1.86	0.58
50:F2:499:MET:HE1	50:F2:546:GLN:HG2	1.85	0.58
51:F3:181:ARG:NH2	51:F3:249:GLU:O	2.36	0.58
52:F5:365:ASP:OD1	52:F5:365:ASP:N	2.36	0.58
56:FN:140:SER:HB3	56:FN:152:LEU:HB3	1.86	0.58
4:CE:218:ASN:HD22	4:CE:223:ARG:HG2	1.68	0.58
11:CN:23:HIS:HE1	32:DF:155:ALA:HB1	1.67	0.58
15:CR:184:LYS:HG3	53:F6:411:GLU:HG3	1.86	0.58
21:Cg:301:HIS:HD2	21:Cg:303:ASP:H	1.51	0.58
33:DG:102:MET:HE1	33:DG:134:PRO:HA	1.85	0.58
62:Fb:88:ILE:HG23	62:Fb:92:MET:HE3	1.85	0.58
66:Fg:369:ASP:OD2	66:Fg:454:THR:OG1	2.20	0.58
68:Fi:288:GLN:H	68:Fi:294:ARG:HH22	1.49	0.58
9:CK:300:ASN:OD1	9:CK:300:ASN:N	2.33	0.57
14:CQ:82:SER:O	30:DD:269:LYS:NZ	2.32	0.57
21:Cg:205:ARG:HH21	21:Cg:259:ILE:HG12	1.69	0.57
23:Cj:72:ASP:OD1	23:Cj:72:ASP:N	2.37	0.57
24:Ck:389:SER:HA	24:Ck:416:ARG:HH21	1.69	0.57
29:DC:819:LEU:HD23	29:DC:885:LEU:HD22	1.85	0.57
30:DD:530:TYR:OH	30:DD:606:ARG:NH2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DK:53:LEU:HD23	37:DK:56:LYS:HG2	1.86	0.57
41:DR:78:ARG:NH1	51:F3:435:GLN:OE1	2.36	0.57
41:DR:249:GLU:O	41:DR:262:ARG:NH1	2.31	0.57
53:F6:228:THR:HG23	53:F6:229:LEU:HD13	1.86	0.57
15:CR:123:LYS:HB3	15:CR:131:THR:HG21	1.86	0.57
29:DC:1114:GLU:HG3	29:DC:1115:ARG:HG2	1.86	0.57
31:DE:301:TYR:O	31:DE:437:LYS:NZ	2.37	0.57
36:DJ:20:SER:HB3	36:DJ:23:VAL:HG22	1.86	0.57
53:F6:39:LEU:HB3	53:F6:187:VAL:HG12	1.86	0.57
1:CA:243:C:OP2	70:IB:677:LYS:NZ	2.30	0.57
15:CR:64:VAL:HB	19:Cb:182:VAL:HG21	1.86	0.57
15:CR:136:LEU:HD21	15:CR:162:LYS:HD2	1.86	0.57
29:DC:588:PRO:HD3	29:DC:618:ARG:HA	1.86	0.57
30:DD:290:ARG:NH2	30:DD:331:GLU:OE1	2.36	0.57
55:F9:311:ARG:HH22	55:F9:319:ASP:HB2	1.69	0.57
61:FZ:100:LEU:HD12	61:FZ:104:ILE:HD13	1.87	0.57
64:Fd:38:ALA:HA	64:Fd:42:HIS:HB2	1.85	0.57
69:IA:407:VAL:HG22	69:IA:416:VAL:HG22	1.86	0.57
70:IB:333:ASP:H	70:IB:336:ARG:HG3	1.70	0.57
4:CE:28:ILE:HG12	4:CE:31:ALA:HB3	1.87	0.57
7:CI:222:THR:HG23	7:CI:225:PHE:H	1.68	0.57
24:Ck:700:VAL:O	24:Ck:703:ARG:HD2	2.05	0.57
28:DB:723:ARG:HA	28:DB:819:LEU:HA	1.86	0.57
30:DD:647:ARG:NH2	41:DR:231:ALA:O	2.36	0.57
31:DE:200:ARG:NH2	31:DE:410:ARG:O	2.38	0.57
38:DL:116:ASN:HD22	38:DL:118:ASP:H	1.52	0.57
65:Ff:248:ARG:HH11	65:Ff:248:ARG:H	1.52	0.57
65:Ff:342:ASP:HB2	65:Ff:343:PRO:HD3	1.85	0.57
24:Ck:98:ARG:O	33:DG:15:ARG:NH2	2.37	0.57
24:Ck:361:GLN:O	24:Ck:583:ARG:NH2	2.37	0.57
65:Ff:460:ARG:NH1	65:Ff:461:ALA:O	2.37	0.57
69:IA:388:ASN:HA	69:IA:575:LYS:HD3	1.86	0.57
70:IB:393:ASN:HA	70:IB:396:ARG:HH11	1.68	0.57
23:Cj:155:GLU:OE1	30:DD:626:ARG:NH1	2.36	0.57
28:DB:722:ARG:HH22	28:DB:802:ASP:HB3	1.69	0.57
35:DI:256:ARG:HB2	35:DI:270:ASP:HB3	1.86	0.57
43:DU:110:THR:HA	43:DU:146:THR:HA	1.86	0.57
52:F5:643:PRO:O	62:Fb:118:ARG:NH1	2.31	0.57
55:F9:370:GLY:O	55:F9:374:LEU:HG	2.04	0.57
65:Ff:622:THR:OG1	65:Ff:628:ASP:OD1	2.18	0.57
68:Fi:400:VAL:HG13	68:Fi:471:MET:HE1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Cp:147:PRO:HG2	27:Cp:150:TYR:HB3	1.87	0.57
47:DY:58:THR:HG21	47:DY:102:GLU:HG2	1.86	0.57
52:F5:366:VAL:HA	52:F5:369:TYR:CZ	2.40	0.57
55:F9:484:ASN:ND2	69:IA:547:GLU:OE2	2.37	0.57
64:Fd:91:TYR:OH	64:Fd:98:ARG:NH1	2.38	0.57
7:CI:116:ASP:OD2	33:DG:111:ARG:NH1	2.38	0.57
10:CL:15:ARG:NH2	55:F9:500:ALA:O	2.34	0.57
14:CQ:47:LYS:HB2	14:CQ:50:ALA:HB3	1.87	0.57
24:Ck:167:PHE:HA	24:Ck:171:VAL:HB	1.87	0.57
29:DC:1077:GLY:O	31:DE:579:ARG:NH1	2.38	0.57
32:DF:124:SER:OG	32:DF:126:ASP:OD2	2.23	0.57
56:FN:252:THR:OG1	56:FN:305:ARG:NH1	2.38	0.57
57:FO:261:GLU:OE1	57:FO:264:ARG:NH2	2.37	0.57
67:Fh:139:LEU:HD22	67:Fh:192:VAL:HB	1.86	0.57
67:Fh:176:SER:OG	67:Fh:212:MET:SD	2.59	0.57
68:Fi:229:SER:OG	68:Fi:493:VAL:O	2.19	0.57
3:CC:23:ILE:HG12	29:DC:1146:VAL:HG13	1.87	0.57
18:Ca:232:GLN:NE2	61:FZ:47:ASN:OD1	2.38	0.57
52:F5:213:THR:OG1	52:F5:217:ARG:NH1	2.38	0.57
67:Fh:122:ARG:HH21	67:Fh:125:VAL:HG21	1.69	0.57
69:IA:78:TYR:HB2	70:IB:517:GLY:HA2	1.87	0.57
1:CA:125:U:OP2	14:CQ:189:TYR:OH	2.15	0.57
1:CA:229:G:H5''	1:CA:247:A:H62	1.70	0.57
1:CA:316:A:N1	1:CA:323:U:O2'	2.35	0.57
8:CJ:753:ASN:ND2	22:CI:16:GLY:O	2.38	0.57
9:CK:258:LEU:HD21	9:CK:275:VAL:HG21	1.87	0.57
24:Ck:384:LEU:HD23	24:Ck:545:ILE:HG23	1.86	0.57
29:DC:991:LYS:HE2	29:DC:1003:ARG:HD3	1.87	0.57
33:DG:498:TYR:OH	33:DG:564:GLU:OE2	2.23	0.57
55:F9:372:GLU:HA	55:F9:375:GLN:CD	2.30	0.57
69:IA:378:GLU:O	69:IA:398:ARG:N	2.32	0.57
8:CJ:367:TRP:NE1	8:CJ:806:GLU:OE1	2.32	0.56
54:F7:554:MET:HE3	54:F7:558:LEU:HD11	1.87	0.56
54:F7:644:ARG:HH22	54:F7:650:THR:HG23	1.69	0.56
68:Fi:482:GLN:HE22	68:Fi:500:GLY:H	1.52	0.56
68:Fi:501:ALA:HB1	68:Fi:550:LEU:HD13	1.87	0.56
4:CE:230:ARG:NH1	6:CH:245:GLY:O	2.37	0.56
24:Ck:364:LEU:HD13	24:Ck:562:CYS:HB3	1.86	0.56
28:DB:399:LYS:HE2	28:DB:402:THR:HG21	1.86	0.56
28:DB:1058:ILE:HD13	34:DH:384:THR:HG23	1.86	0.56
29:DC:676:GLN:O	29:DC:680:GLN:NE2	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DH:39:ILE:HG23	34:DH:43:GLN:HB3	1.87	0.56
36:DJ:143:TYR:O	36:DJ:147:ARG:NH2	2.35	0.56
36:DJ:293:ASN:HD22	42:DT:226:LEU:HB3	1.69	0.56
41:DR:96:PHE:HB3	41:DR:126:LEU:HB3	1.88	0.56
53:F6:554:GLU:HG2	65:Ff:612:LYS:HD3	1.86	0.56
62:Fb:147:PRO:HB2	62:Fb:149:PRO:HD2	1.86	0.56
65:Ff:335:GLN:O	65:Ff:337:ARG:NH1	2.38	0.56
70:IB:758:PRO:HG2	70:IB:761:GLU:HB2	1.87	0.56
1:CA:91:A:OP1	14:CQ:152:LYS:NZ	2.30	0.56
5:CF:7:VAL:HG13	5:CF:93:LEU:HB3	1.87	0.56
5:CF:151:ARG:HG3	5:CF:152:THR:HG23	1.87	0.56
12:CO:279:ARG:NH2	54:F7:416:THR:OG1	2.37	0.56
18:Ca:262:LYS:HE3	50:F2:738:PRO:HG3	1.87	0.56
18:Ca:508:GLU:OE2	50:F2:588:THR:OG1	2.23	0.56
19:Cb:178:ARG:NH2	53:F6:209:ASP:OD1	2.35	0.56
21:Cg:413:LEU:HD23	21:Cg:441:LEU:HD12	1.88	0.56
28:DB:556:VAL:HG12	28:DB:559:GLU:HB3	1.87	0.56
28:DB:967:ASP:OD2	52:F5:160:LYS:NZ	2.33	0.56
35:DI:288:ILE:HG22	35:DI:302:ILE:HD11	1.87	0.56
57:FO:16:LEU:HA	57:FO:19:MET:HE2	1.87	0.56
68:Fi:191:ILE:HD11	68:Fi:269:MET:HE2	1.88	0.56
69:IA:149:ASP:N	69:IA:149:ASP:OD1	2.37	0.56
70:IB:362:LEU:HD23	70:IB:624:ARG:HD3	1.87	0.56
1:CA:465:U:H4'	1:CA:466:G:OP1	2.04	0.56
6:CH:168:ARG:HE	50:F2:345:VAL:HG12	1.69	0.56
9:CK:189:THR:H	9:CK:192:MET:HE2	1.71	0.56
14:CQ:176:LYS:O	54:F7:380:ARG:NH2	2.39	0.56
21:Cg:308:LEU:HG	46:DX:106:LYS:HE2	1.87	0.56
50:F2:463:GLU:OE2	50:F2:876:LYS:NZ	2.38	0.56
52:F5:351:ARG:NH2	52:F5:464:GLU:OE1	2.39	0.56
53:F6:38:LEU:HA	53:F6:41:TRP:CD1	2.41	0.56
54:F7:570:ASN:OD1	54:F7:571:ALA:N	2.38	0.56
69:IA:570:LEU:HD12	69:IA:590:ARG:HG2	1.86	0.56
18:Ca:107:ILE:HD12	18:Ca:152:ILE:HG23	1.87	0.56
18:Ca:378:GLU:OE1	18:Ca:392:TYR:OH	2.23	0.56
24:Ck:276:GLN:HE22	28:DB:885:PHE:H	1.52	0.56
36:DJ:335:ILE:HD12	36:DJ:336:ASP:H	1.69	0.56
36:DJ:347:LYS:HZ1	36:DJ:356:TYR:H	1.53	0.56
45:DW:155:ARG:H	45:DW:155:ARG:HD2	1.71	0.56
50:F2:672:ILE:O	56:FM:164:LYS:NZ	2.38	0.56
66:Fg:173:VAL:O	66:Fg:176:SER:OG	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:IB:626:VAL:HG21	70:IB:653:TRP:HA	1.87	0.56
3:CC:42:ILE:HG12	3:CC:69:ILE:HG22	1.88	0.56
5:CF:140:THR:HG21	19:Cb:100:ARG:HE	1.69	0.56
18:Ca:113:LEU:HD21	18:Ca:123:LYS:HD3	1.87	0.56
20:Cd:161:ASP:OD1	20:Cd:162:LYS:N	2.38	0.56
29:DC:52:ARG:NH1	37:DK:266:CYS:SG	2.79	0.56
30:DD:250:LYS:HB2	30:DD:287:ARG:HB2	1.86	0.56
33:DG:70:TYR:HB3	33:DG:90:MET:HE2	1.87	0.56
44:DV:41:THR:HA	45:DW:59:PRO:HG3	1.86	0.56
68:Fi:220:ILE:HD13	68:Fi:310:GLN:HG2	1.88	0.56
16:CS:134:TRP:O	28:DB:1125:HIS:NE2	2.37	0.56
35:DI:233:ARG:HD3	35:DI:273:VAL:HG12	1.87	0.56
40:DP:182:ILE:HB	40:DP:187:ARG:HE	1.69	0.56
41:DR:41:HIS:HA	41:DR:44:VAL:HG22	1.87	0.56
50:F2:951:VAL:HG13	52:F5:446:LEU:HD22	1.87	0.56
54:F7:555:THR:OG1	54:F7:580:CYS:SG	2.59	0.56
69:IA:373:LYS:HB3	69:IA:374:PRO:HD3	1.87	0.56
8:CJ:263:ASP:OD1	28:DB:1023:ARG:NH2	2.39	0.56
11:CN:93:ASP:OD2	11:CN:117:THR:OG1	2.18	0.56
14:CQ:231:GLN:HG3	14:CQ:232:PRO:HD3	1.87	0.56
24:Ck:74:SER:O	31:DE:735:ARG:NH2	2.38	0.56
29:DC:119:THR:O	29:DC:530:GLN:NE2	2.35	0.56
32:DF:407:ALA:HB1	32:DF:421:ALA:HB3	1.86	0.56
34:DH:379:LEU:O	34:DH:383:GLN:CB	2.53	0.56
53:F6:398:SER:O	53:F6:402:HIS:ND1	2.28	0.56
65:Ff:189:THR:O	65:Ff:194:ARG:NE	2.31	0.56
66:Fg:418:LEU:HD23	66:Fg:418:LEU:H	1.70	0.56
68:Fi:96:LEU:HD12	68:Fi:98:VAL:HB	1.88	0.56
18:Ca:204:PRO:HG3	18:Ca:257:ILE:HD12	1.87	0.56
28:DB:92:HIS:NE2	31:DE:447:ARG:O	2.38	0.56
29:DC:585:VAL:HG12	29:DC:620:VAL:HG22	1.88	0.56
32:DF:160:CYS:O	32:DF:164:ILE:HG12	2.05	0.56
35:DI:37:THR:OG1	35:DI:212:ARG:NH1	2.39	0.56
56:FN:298:SER:HA	56:FN:303:GLY:HA2	1.88	0.56
68:Fi:248:ILE:HG22	68:Fi:249:ARG:HG3	1.88	0.56
1:CA:46:U:OP1	13:CP:15:ARG:NH1	2.38	0.56
5:CF:46:ARG:HB2	9:CK:181:MET:HG2	1.88	0.56
12:CO:267:ARG:NE	14:CQ:170:GLU:OE1	2.38	0.56
19:Cb:178:ARG:NH1	53:F6:206:ILE:O	2.30	0.56
24:Ck:46:ILE:HD11	28:DB:478:ILE:HG22	1.86	0.56
56:FN:36:LEU:HB2	56:FN:62:MET:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:FN:215:ILE:HG21	56:FN:221:LEU:HD22	1.88	0.56
69:IA:139:GLN:HA	69:IA:496:ARG:HA	1.88	0.56
6:CH:98:ARG:HH22	35:DI:308:PRO:HG3	1.72	0.55
10:CL:6:MET:HB3	10:CL:9:LEU:HD12	1.88	0.55
16:CS:102:LYS:HA	16:CS:140:MET:HB2	1.87	0.55
29:DC:531:ARG:HG3	29:DC:532:PRO:HD3	1.88	0.55
50:F2:352:ARG:HH21	50:F2:386:ILE:HG22	1.71	0.55
51:F3:773:ASN:ND2	51:F3:806:TYR:OH	2.39	0.55
55:F9:191:LYS:NZ	70:IB:739:GLN:OE1	2.35	0.55
4:CE:341:ARG:HH22	35:DI:143:ALA:HB2	1.70	0.55
9:CK:288:ARG:NE	17:CU:58:ASP:OD1	2.39	0.55
18:Ca:116:LYS:O	52:F5:662:TRP:NE1	2.35	0.55
20:Cd:66:LEU:HD12	30:DD:154:ILE:HD11	1.87	0.55
21:Cg:75:ASN:N	21:Cg:111:TYR:O	2.34	0.55
28:DB:651:ASN:OD1	28:DB:843:ASN:ND2	2.30	0.55
29:DC:995:GLU:O	29:DC:995:GLU:HG2	2.05	0.55
43:DU:144:GLN:NE2	51:F3:516:SER:O	2.40	0.55
50:F2:17:GLN:NE2	50:F2:418:GLU:OE2	2.38	0.55
50:F2:673:LEU:HD23	56:FM:164:LYS:HE3	1.88	0.55
51:F3:368:LEU:O	51:F3:372:MET:HG2	2.06	0.55
68:Fi:329:LEU:O	68:Fi:334:TYR:OH	2.20	0.55
5:CF:11:LYS:NZ	5:CF:55:ASP:OD2	2.37	0.55
13:CP:182:ARG:HG2	30:DD:227:TRP:HE1	1.71	0.55
28:DB:433:ARG:NH2	29:DC:1165:SER:OG	2.40	0.55
29:DC:963:SER:HB2	29:DC:1066:LEU:HB2	1.88	0.55
30:DD:342:ARG:NH2	43:DU:59:ASP:O	2.40	0.55
31:DE:471:ARG:HB3	31:DE:475:LEU:HD12	1.87	0.55
34:DH:226:PRO:HB3	34:DH:248:VAL:HG13	1.88	0.55
35:DI:288:ILE:HA	35:DI:302:ILE:HG12	1.86	0.55
51:F3:141:TYR:HB2	51:F3:176:HIS:CE1	2.41	0.55
56:FN:84:ASP:OD1	56:FN:84:ASP:N	2.39	0.55
65:Ff:254:SER:OG	65:Ff:259:PHE:N	2.39	0.55
70:IB:205:ASN:O	70:IB:348:ARG:NH2	2.39	0.55
5:CF:41:ASN:HD22	20:Cd:164:LEU:HA	1.72	0.55
5:CF:105:ARG:HA	5:CF:112:GLN:HG2	1.89	0.55
8:CJ:100:ARG:HG2	33:DG:58:TRP:HB3	1.88	0.55
29:DC:200:VAL:HG11	29:DC:206:PHE:HB2	1.88	0.55
35:DI:24:VAL:HG22	35:DI:25:PRO:HD2	1.87	0.55
36:DJ:275:ASP:O	36:DJ:280:GLY:N	2.37	0.55
55:F9:328:GLN:O	55:F9:332:ASN:ND2	2.39	0.55
5:CF:144:MET:HE1	19:Cb:104:LEU:HD12	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CF:144:MET:HE2	19:Cb:101:LYS:HD3	1.89	0.55
8:CJ:529:LEU:HD21	8:CJ:608:SER:HA	1.86	0.55
18:Ca:304:TRP:HA	50:F2:763:MET:HE1	1.88	0.55
28:DB:710:ARG:NH2	28:DB:714:GLU:OE2	2.39	0.55
29:DC:1007:ASN:ND2	29:DC:1009:THR:OG1	2.39	0.55
30:DD:466:ARG:HH21	30:DD:507:GLN:HE22	1.54	0.55
31:DE:150:ARG:O	31:DE:157:ARG:NH1	2.39	0.55
34:DH:141:LEU:HA	34:DH:145:ALA:HB3	1.87	0.55
35:DI:18:HIS:HD2	35:DI:65:MET:HB2	1.72	0.55
68:Fi:490:GLY:O	68:Fi:495:SER:OG	2.17	0.55
8:CJ:413:GLU:OE2	28:DB:1063:ARG:NH2	2.40	0.55
18:Ca:78:PHE:HE2	18:Ca:176:ILE:HG22	1.72	0.55
37:DK:314:THR:HG21	42:DT:189:PRO:HD2	1.88	0.55
51:F3:121:SER:HA	51:F3:126:LEU:HD22	1.89	0.55
51:F3:697:VAL:HG21	51:F3:732:SER:HB3	1.87	0.55
53:F6:363:ASN:ND2	53:F6:365:SER:OG	2.40	0.55
55:F9:146:MET:HE1	55:F9:177:PRO:HG3	1.88	0.55
69:IA:248:LEU:HD13	69:IA:361:ALA:HB2	1.88	0.55
69:IA:382:ILE:HG12	69:IA:395:GLY:HA2	1.89	0.55
70:IB:489:ARG:HH21	70:IB:493:ARG:HB3	1.71	0.55
27:Cp:21:TYR:HB3	27:Cp:25:PRO:HD2	1.88	0.55
29:DC:95:GLN:HG3	29:DC:105:ASN:HD21	1.71	0.55
52:F5:84:ARG:NH2	52:F5:107:TYR:OH	2.40	0.55
52:F5:456:ASP:OD1	52:F5:457:LYS:N	2.39	0.55
61:FZ:59:LYS:HD2	61:FZ:62:ILE:HD11	1.88	0.55
66:Fg:101:LEU:O	66:Fg:107:THR:OG1	2.15	0.55
69:IA:208:ILE:HA	69:IA:279:VAL:HG13	1.89	0.55
1:CA:87:U:OP2	30:DD:339:ARG:NH1	2.40	0.55
4:CE:66:ASP:HB3	4:CE:89:LEU:HB3	1.88	0.55
7:CI:294:ILE:HD11	7:CI:408:ILE:HD11	1.89	0.55
9:CK:209:TYR:OH	9:CK:215:ARG:NH1	2.39	0.55
11:CN:94:ARG:HB2	22:CI:108:PRO:HA	1.88	0.55
28:DB:1066:ASN:N	28:DB:1066:ASN:OD1	2.40	0.55
32:DF:129:ILE:O	32:DF:163:ARG:NH1	2.37	0.55
32:DF:284:ARG:NH2	34:DH:360:LEU:O	2.39	0.55
35:DI:82:GLU:OE2	35:DI:221:TYR:OH	2.24	0.55
39:DO:137:ASN:OD1	39:DO:138:LEU:N	2.39	0.55
41:DR:52:LEU:HD12	41:DR:113:LEU:HD11	1.89	0.55
42:DT:167:ASN:ND2	42:DT:172:GLU:O	2.40	0.55
50:F2:226:ARG:NH2	50:F2:266:GLU:OE2	2.40	0.55
52:F5:315:GLN:NE2	52:F5:377:HIS:O	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:FM:274:LEU:HD12	56:FM:275:PRO:HD2	1.89	0.55
59:FW:92:ARG:HB3	59:FW:101:PRO:HB2	1.87	0.55
69:IA:117:VAL:HG13	69:IA:121:ASP:HB3	1.89	0.55
4:CE:58:SER:HB2	4:CE:141:GLN:HE22	1.72	0.55
8:CJ:616:GLU:HG3	8:CJ:631:LEU:HD21	1.88	0.55
16:CS:117:VAL:HG23	16:CS:128:PHE:HB2	1.89	0.55
25:Cm:104:ARG:NH1	53:F6:585:GLU:OE1	2.35	0.55
29:DC:429:SER:HB2	29:DC:444:PRO:HB2	1.89	0.55
31:DE:57:ASP:OD1	31:DE:57:ASP:N	2.40	0.55
31:DE:618:ARG:HD3	31:DE:618:ARG:H	1.72	0.55
33:DG:275:ARG:NH2	33:DG:326:THR:OG1	2.40	0.55
51:F3:725:LEU:HD23	51:F3:725:LEU:H	1.72	0.55
54:F7:177:ILE:HG12	54:F7:188:SER:HB3	1.89	0.55
65:Ff:580:HIS:NE2	65:Ff:675:ASP:OD2	2.40	0.55
3:CC:56:TYR:HB3	3:CC:72:ILE:HG23	1.87	0.55
4:CE:359:HIS:O	4:CE:364:ARG:NH2	2.40	0.55
7:CI:140:GLU:O	7:CI:144:SER:CB	2.54	0.55
11:CN:123:ARG:NH2	38:DL:288:ASN:O	2.37	0.55
21:Cg:294:GLU:HG2	21:Cg:327:ARG:HH21	1.72	0.55
24:Ck:132:TYR:CZ	24:Ck:140:ARG:HG3	2.42	0.55
30:DD:229:MET:HG2	35:DI:186:ILE:HG21	1.89	0.55
41:DR:237:TYR:OH	41:DR:269:TRP:O	2.24	0.55
50:F2:375:GLU:OE2	55:F9:95:ARG:NE	2.39	0.55
51:F3:101:LEU:HD22	57:FO:61:LEU:HG	1.88	0.55
51:F3:628:CYS:O	51:F3:663:TYR:OH	2.25	0.55
52:F5:243:GLU:HB3	61:FZ:135:ARG:HD2	1.88	0.55
66:Fg:26:LEU:HD13	69:IA:230:SER:HB3	1.87	0.55
70:IB:407:PRO:HB2	70:IB:412:ILE:HG12	1.88	0.55
21:Cg:294:GLU:HA	21:Cg:329:PRO:HA	1.90	0.54
28:DB:702:GLN:NE2	28:DB:706:GLU:OE2	2.37	0.54
29:DC:355:GLU:O	29:DC:359:GLU:HG2	2.07	0.54
43:DU:123:GLN:HG2	43:DU:176:ARG:HH22	1.72	0.54
55:F9:299:LYS:HE2	55:F9:328:GLN:HE22	1.73	0.54
56:FM:67:ARG:NH2	56:FM:97:GLU:OE2	2.33	0.54
62:Fb:33:TYR:OH	63:Fc:110:GLU:OE2	2.22	0.54
12:CO:311:ILE:HG22	30:DD:261:ARG:HD2	1.90	0.54
16:CS:84:LEU:HD11	28:DB:1121:VAL:HG21	1.89	0.54
34:DH:488:GLY:N	34:DH:491:ASP:OD2	2.40	0.54
40:DP:171:LEU:HD22	40:DP:190:LEU:HB2	1.88	0.54
50:F2:826:ARG:NH1	50:F2:838:TYR:OH	2.38	0.54
52:F5:96:VAL:HB	52:F5:101:LYS:HZ3	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:F7:508:ALA:HA	54:F7:541:ALA:HB2	1.88	0.54
55:F9:17:GLY:HA2	55:F9:20:ARG:HE	1.72	0.54
1:CA:64:G:N2	1:CA:65:U:O4	2.39	0.54
7:CI:129:VAL:HG21	81:Ug:12:UNK:HA	1.89	0.54
8:CJ:681:LEU:HD21	11:CN:59:VAL:HG11	1.89	0.54
8:CJ:729:ASP:N	8:CJ:729:ASP:OD1	2.39	0.54
13:CP:108:CYS:O	20:Cd:58:ARG:NH2	2.41	0.54
20:Cd:27:LYS:HB2	27:Cp:121:PHE:HZ	1.73	0.54
22:CI:59:ARG:NH1	44:DV:30:ASP:OD1	2.35	0.54
28:DB:92:HIS:ND1	28:DB:93:LYS:O	2.36	0.54
29:DC:1155:ASP:N	29:DC:1155:ASP:OD1	2.40	0.54
30:DD:735:GLY:HA2	30:DD:739:GLU:HB2	1.90	0.54
32:DF:266:ARG:HH21	32:DF:300:GLU:HG2	1.72	0.54
51:F3:51:ARG:NH2	66:Fg:282:ASP:OD1	2.34	0.54
68:Fi:31:GLN:HB2	68:Fi:34:ALA:HB2	1.90	0.54
11:CN:25:VAL:HG22	11:CN:92:VAL:HG23	1.89	0.54
28:DB:969:THR:O	33:DG:45:LYS:NZ	2.39	0.54
31:DE:431:SER:OG	34:DH:564:ARG:NH2	2.41	0.54
35:DI:342:ARG:NH2	35:DI:402:GLU:O	2.40	0.54
36:DJ:335:ILE:HG22	55:F9:258:VAL:HG23	1.90	0.54
52:F5:247:ARG:HG3	61:FZ:135:ARG:HH22	1.73	0.54
61:FZ:89:SER:HB3	61:FZ:92:SER:HB3	1.89	0.54
66:Fg:464:GLY:HA2	66:Fg:469:SER:OG	2.08	0.54
12:CO:333:SER:OG	12:CO:336:GLU:OE1	2.25	0.54
22:CI:60:SER:OG	22:CI:69:THR:OG1	2.26	0.54
29:DC:93:ARG:NH2	29:DC:112:TYR:OH	2.40	0.54
40:DP:188:ARG:HB3	40:DP:193:GLU:HB2	1.90	0.54
42:DT:70:MET:HE2	42:DT:137:LEU:HD21	1.90	0.54
54:F7:338:LEU:HA	54:F7:341:PHE:HB3	1.88	0.54
55:F9:77:ALA:HB1	55:F9:182:GLU:HB2	1.88	0.54
55:F9:194:MET:HE1	61:FZ:165:ALA:H	1.72	0.54
56:FN:10:VAL:O	56:FN:36:LEU:HA	2.07	0.54
57:FO:93:ASP:OD1	57:FO:93:ASP:N	2.41	0.54
57:FO:307:ARG:NH2	69:IA:579:THR:O	2.41	0.54
8:CJ:420:ARG:HA	8:CJ:423:LEU:HG	1.89	0.54
24:Ck:540:SER:HA	24:Ck:543:GLN:HG2	1.89	0.54
31:DE:406:ASP:HA	31:DE:409:TRP:CD1	2.43	0.54
32:DF:502:ARG:HD3	32:DF:518:ALA:HB1	1.90	0.54
43:DU:174:ARG:HH21	43:DU:178:TRP:HD1	1.56	0.54
44:DV:46:PRO:O	44:DV:52:ARG:NH1	2.40	0.54
46:DX:107:LEU:HB3	46:DX:112:TYR:HE1	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Da:18:LYS:HZ2	49:Da:20:ARG:HE	1.56	0.54
51:F3:77:LEU:HD13	57:FO:9:PRO:HB2	1.89	0.54
51:F3:650:GLN:HE22	51:F3:653:LEU:HD23	1.72	0.54
52:F5:204:VAL:HG11	52:F5:630:MET:HE1	1.90	0.54
60:FX:34:ASN:HD21	60:FX:37:ALA:HB2	1.72	0.54
65:Ff:397:PRO:HD3	65:Ff:417:ALA:HB2	1.89	0.54
69:IA:221:ASP:OD2	69:IA:228:VAL:N	2.40	0.54
7:Cl:359:ASP:OD2	21:Cg:439:ARG:NH2	2.40	0.54
34:DH:278:VAL:O	34:DH:282:ASN:ND2	2.40	0.54
37:DK:280:PHE:CE2	42:DT:102:TRP:HB2	2.43	0.54
40:DP:56:ARG:HH12	57:FO:263:THR:HG22	1.72	0.54
51:F3:395:LEU:HD12	51:F3:505:LEU:HD22	1.89	0.54
53:F6:308:LEU:HB2	53:F6:310:LEU:HG	1.90	0.54
69:IA:468:MET:HA	69:IA:471:VAL:HG22	1.89	0.54
15:CR:142:MET:HE2	15:CR:147:ILE:HD11	1.90	0.54
17:CU:57:VAL:HG22	17:CU:60:ARG:HH21	1.73	0.54
20:Cd:39:MET:HG3	23:Cj:224:LEU:HD13	1.89	0.54
30:DD:59:ASN:HD21	30:DD:62:TYR:HB2	1.73	0.54
33:DG:401:CYS:SG	33:DG:457:ARG:NE	2.74	0.54
34:DH:73:LEU:HD13	34:DH:97:LEU:HD11	1.90	0.54
52:F5:315:GLN:HG2	52:F5:377:HIS:CG	2.42	0.54
55:F9:260:ARG:HG3	69:IA:145:LYS:HE2	1.89	0.54
68:Fi:101:LEU:HD11	68:Fi:206:VAL:HG23	1.89	0.54
8:CJ:62:ARG:NH2	8:CJ:67:GLU:OE1	2.41	0.54
9:CK:45:PHE:HE2	21:Cg:473:ARG:HB3	1.73	0.54
9:CK:197:LEU:HD13	9:CK:291:ALA:HB1	1.90	0.54
14:CQ:223:ARG:HH21	54:F7:88:GLY:H	1.56	0.54
21:Cg:85:LEU:HD22	21:Cg:107:ARG:HG2	1.89	0.54
24:Ck:732:ARG:NH1	24:Ck:783:TYR:O	2.41	0.54
31:DE:451:THR:OG1	31:DE:501:HIS:ND1	2.39	0.54
50:F2:475:ARG:NH2	50:F2:880:TYR:O	2.40	0.54
52:F5:336:HIS:ND1	52:F5:340:ASP:OD2	2.33	0.54
67:Fh:146:SER:HB3	67:Fh:199:ILE:HG23	1.90	0.54
1:CA:145:A:O2'	1:CA:272:C:N4	2.41	0.54
4:CE:346:ASP:OD1	35:DI:134:ARG:NH2	2.39	0.54
9:CK:259:ARG:HH21	9:CK:273:GLU:HG2	1.73	0.54
28:DB:906:HIS:O	28:DB:912:ASN:ND2	2.40	0.54
34:DH:59:MET:HE3	34:DH:63:ASN:HD21	1.74	0.54
46:DX:64:SER:HA	46:DX:162:VAL:HG13	1.90	0.54
52:F5:82:ALA:HB1	61:FZ:114:PRO:HD2	1.89	0.54
56:FM:13:VAL:HB	56:FM:80:LEU:HG	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:IB:180:SER:O	70:IB:184:HIS:ND1	2.36	0.54
3:CC:31:ASN:ND2	34:DH:450:ASN:OD1	2.42	0.53
7:CI:318:HIS:HB3	7:CI:375:GLU:HG3	1.89	0.53
7:CI:345:ASP:OD1	21:Cg:377:ARG:NH1	2.41	0.53
12:CO:151:LYS:HG2	20:Cd:143:GLN:HE21	1.72	0.53
29:DC:30:THR:OG1	42:DT:44:ARG:NH1	2.42	0.53
32:DF:56:TYR:HA	32:DF:61:GLY:HA3	1.90	0.53
32:DF:72:THR:OG1	32:DF:79:THR:OG1	2.24	0.53
32:DF:269:GLU:OE1	32:DF:273:ASN:ND2	2.41	0.53
34:DH:495:THR:OG1	34:DH:498:ASN:OD1	2.26	0.53
50:F2:729:SER:O	50:F2:732:GLN:NE2	2.41	0.53
59:FW:107:ARG:HH21	59:FW:136:VAL:HG12	1.71	0.53
8:CJ:83:HIS:ND1	8:CJ:85:GLY:O	2.40	0.53
18:Ca:105:GLN:HE22	52:F5:652:SER:H	1.56	0.53
31:DE:280:LEU:HA	31:DE:283:LYS:HD2	1.91	0.53
33:DG:464:VAL:HG21	33:DG:481:VAL:HG11	1.89	0.53
34:DH:35:TYR:OH	34:DH:381:LYS:O	2.22	0.53
50:F2:823:ASP:OD2	50:F2:839:ARG:NH2	2.38	0.53
50:F2:891:ASP:OD1	52:F5:449:LYS:NZ	2.34	0.53
51:F3:55:THR:HG22	51:F3:73:PRO:HB3	1.90	0.53
56:FN:274:LEU:HD12	56:FN:275:PRO:HD2	1.90	0.53
66:Fg:27:ARG:HG3	66:Fg:28:ILE:HD12	1.89	0.53
1:CA:493:U:H4'	1:CA:494:A:OP1	2.07	0.53
14:CQ:86:ASN:O	30:DD:128:ASN:ND2	2.38	0.53
16:CS:50:TYR:HD2	16:CS:55:ARG:HH11	1.56	0.53
18:Ca:268:GLY:HA3	18:Ca:305:HIS:CE1	2.43	0.53
26:Cn:188:ALA:HB1	68:Fi:315:LEU:HG	1.91	0.53
27:Cp:182:GLN:NE2	40:DP:161:VAL:O	2.42	0.53
29:DC:669:LEU:HB2	29:DC:752:VAL:HG12	1.90	0.53
29:DC:801:HIS:HB3	29:DC:804:TYR:HD2	1.73	0.53
30:DD:90:MET:SD	30:DD:90:MET:N	2.69	0.53
33:DG:599:ARG:HH11	33:DG:602:ARG:HH22	1.55	0.53
42:DT:184:SER:O	42:DT:216:TYR:OH	2.23	0.53
51:F3:689:CYS:HB3	51:F3:720:ILE:HG22	1.89	0.53
52:F5:247:ARG:HB2	61:FZ:135:ARG:HH12	1.72	0.53
70:IB:583:ASN:OD1	70:IB:584:TYR:N	2.38	0.53
1:CA:107:U:O2'	14:CQ:103:MET:SD	2.66	0.53
8:CJ:227:ARG:NH2	8:CJ:817:PRO:O	2.42	0.53
24:Ck:566:ARG:HD3	24:Ck:572:MET:HG2	1.91	0.53
28:DB:1127:MET:HE2	28:DB:1130:PHE:HB3	1.90	0.53
30:DD:248:ASP:HB3	30:DD:249:PRO:HD3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DD:303:LEU:HD22	30:DD:396:VAL:HG13	1.91	0.53
31:DE:618:ARG:O	31:DE:625:SER:OG	2.27	0.53
45:DW:98:GLN:O	47:DY:101:GLN:NE2	2.42	0.53
51:F3:568:ASP:OD1	51:F3:569:ALA:N	2.41	0.53
52:F5:504:LEU:HD22	52:F5:557:LEU:HD22	1.89	0.53
68:Fi:124:TRP:HB3	68:Fi:127:LEU:HD13	1.90	0.53
1:CA:206:A:O2'	59:FW:165:SER:O	2.27	0.53
8:CJ:183:GLN:NE2	8:CJ:190:GLU:O	2.42	0.53
13:CP:10:ARG:NH2	13:CP:12:VAL:O	2.37	0.53
21:Cg:102:PRO:O	21:Cg:107:ARG:NH2	2.42	0.53
28:DB:143:VAL:HA	28:DB:146:MET:HE2	1.91	0.53
28:DB:345:ARG:HH12	31:DE:89:ALA:HB2	1.72	0.53
28:DB:576:GLU:O	28:DB:643:HIS:ND1	2.41	0.53
29:DC:580:VAL:HG12	29:DC:624:TRP:HA	1.91	0.53
50:F2:20:ARG:NH1	55:F9:110:ASP:OD2	2.37	0.53
50:F2:823:ASP:HA	50:F2:826:ARG:HG2	1.89	0.53
53:F6:275:PHE:O	53:F6:279:ASN:ND2	2.41	0.53
53:F6:454:SER:HB3	53:F6:467:ALA:HB1	1.89	0.53
54:F7:25:GLU:HG3	54:F7:28:ARG:HH21	1.74	0.53
54:F7:214:HIS:HE1	54:F7:237:ARG:HD3	1.74	0.53
69:IA:84:GLN:HG2	70:IB:549:THR:HG22	1.90	0.53
69:IA:623:CYS:HA	69:IA:641:MET:HB3	1.89	0.53
1:CA:239:G:H4'	1:CA:240:U:OP1	2.08	0.53
8:CJ:537:LEU:HB3	8:CJ:599:ALA:HB3	1.91	0.53
11:CN:51:LEU:HD23	11:CN:55:LEU:HD23	1.90	0.53
18:Ca:154:GLU:OE2	61:FZ:57:ARG:NH2	2.42	0.53
29:DC:750:PHE:HB2	29:DC:927:SER:HB3	1.90	0.53
30:DD:537:ARG:NH1	41:DR:218:TRP:O	2.40	0.53
33:DG:246:PRO:O	33:DG:249:GLN:NE2	2.42	0.53
41:DR:126:LEU:HB2	41:DR:135:CYS:HB3	1.90	0.53
41:DR:128:PRO:HG3	41:DR:133:LEU:H	1.73	0.53
50:F2:634:MET:HE1	60:FX:88:GLU:HG2	1.91	0.53
55:F9:482:PRO:HA	55:F9:485:LEU:HG	1.90	0.53
57:FO:11:GLU:OE2	57:FO:14:ARG:NH2	2.33	0.53
8:CJ:61:VAL:HG11	38:DL:296:PRO:HB2	1.91	0.53
11:CN:40:TRP:HD1	22:CI:93:LEU:HD11	1.73	0.53
24:Ck:287:GLU:OE2	24:Ck:288:ASN:ND2	2.41	0.53
30:DD:325:LYS:O	30:DD:385:ASN:ND2	2.41	0.53
33:DG:242:ALA:HA	33:DG:253:PRO:HA	1.89	0.53
66:Fg:303:CYS:SG	69:IA:53:GLN:NE2	2.82	0.53
67:Fh:208:LYS:HD2	67:Fh:212:MET:HE3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CI:74:PHE:HE2	47:DY:94:TRP:HE1	1.55	0.53
12:CO:236:ARG:HH21	54:F7:636:LEU:HD23	1.74	0.53
18:Ca:372:SER:HB3	18:Ca:501:ARG:HB3	1.90	0.53
18:Ca:485:MET:HE3	18:Ca:489:ARG:HD2	1.89	0.53
28:DB:158:ARG:NH1	31:DE:212:LEU:O	2.42	0.53
31:DE:164:ARG:HH21	31:DE:561:THR:HA	1.74	0.53
55:F9:532:LEU:HD21	69:IA:484:LEU:HD23	1.91	0.53
56:FM:24:ARG:HA	56:FM:53:LEU:HD21	1.91	0.53
58:FP:66:LEU:HG	58:FP:68:ASP:H	1.74	0.53
1:CA:26:C:H42	1:CA:273:A:H2'	1.74	0.53
29:DC:1049:ASN:ND2	37:DK:161:LEU:H	2.07	0.53
29:DC:1158:ALA:HB2	34:DH:41:LYS:HA	1.91	0.53
43:DU:120:VAL:O	43:DU:176:ARG:NH2	2.40	0.53
50:F2:894:PHE:O	50:F2:939:LYS:NZ	2.26	0.53
51:F3:625:MET:O	51:F3:659:ARG:NH2	2.42	0.53
68:Fi:97:CYS:H	68:Fi:205:HIS:CD2	2.27	0.53
70:IB:667:ASP:O	70:IB:671:MET:HG2	2.09	0.53
1:CA:176:A:C4	13:CP:18:PRO:HG2	2.44	0.53
32:DF:411:VAL:O	32:DF:583:ARG:NH1	2.42	0.53
33:DG:475:GLN:HB2	33:DG:557:GLN:HG2	1.91	0.53
41:DR:143:PRO:HB3	41:DR:162:GLN:HB2	1.90	0.53
62:Fb:37:MET:HE1	62:Fb:55:ARG:HA	1.90	0.53
64:Fd:105:CYS:HB3	64:Fd:108:CYS:HB2	1.91	0.53
67:Fh:277:ASP:HB2	67:Fh:289:LEU:HD11	1.91	0.53
68:Fi:88:ARG:HG3	68:Fi:91:ARG:HG2	1.91	0.53
4:CE:48:ASN:HB2	4:CE:89:LEU:HD11	1.91	0.52
14:CQ:53:ASN:ND2	14:CQ:56:ARG:H	2.07	0.52
23:Cj:89:THR:OG1	40:DP:140:ASN:ND2	2.42	0.52
29:DC:93:ARG:HE	29:DC:99:LYS:NZ	2.06	0.52
29:DC:147:ARG:NH1	29:DC:232:GLN:O	2.42	0.52
31:DE:413:GLU:OE1	31:DE:413:GLU:N	2.41	0.52
33:DG:152:MET:O	33:DG:157:ARG:NH2	2.41	0.52
35:DI:327:ARG:NH2	39:DO:237:GLU:OE1	2.42	0.52
46:DX:89:ARG:HD3	46:DX:94:GLY:HA3	1.90	0.52
54:F7:122:TYR:HB2	54:F7:144:LEU:HD23	1.91	0.52
14:CQ:104:LEU:HD13	14:CQ:105:LYS:HG3	1.91	0.52
23:Cj:84:ARG:HA	23:Cj:87:VAL:HG12	1.91	0.52
28:DB:341:THR:HG22	31:DE:39:PHE:HB2	1.89	0.52
51:F3:198:GLU:HB3	51:F3:202:GLY:HA3	1.92	0.52
66:Fg:96:HIS:HD2	66:Fg:99:GLY:H	1.55	0.52
68:Fi:99:ALA:H	68:Fi:117:TYR:HA	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CE:341:ARG:HE	35:DI:139:VAL:HB	1.74	0.52
8:CJ:642:ASN:HA	8:CJ:655:ARG:HH12	1.75	0.52
15:CR:147:ILE:HG23	15:CR:155:VAL:HG21	1.91	0.52
18:Ca:280:GLU:HB3	18:Ca:379:MET:HG3	1.91	0.52
20:Cd:169:ALA:HA	20:Cd:186:LEU:HD21	1.91	0.52
21:Cg:429:PRO:HD2	47:DY:53:LEU:HD11	1.90	0.52
23:Cj:29:LEU:O	41:DR:262:ARG:NH2	2.41	0.52
28:DB:1131:ASN:HB3	28:DB:1136:ALA:O	2.09	0.52
32:DF:187:ASN:HD22	32:DF:191:THR:HG23	1.73	0.52
36:DJ:359:GLU:OE2	67:Fh:102:ARG:NH1	2.42	0.52
39:DO:232:ASN:O	54:F7:521:LYS:NZ	2.30	0.52
50:F2:544:ALA:HB1	50:F2:578:MET:HB2	1.91	0.52
52:F5:214:GLU:OE1	52:F5:217:ARG:NH2	2.42	0.52
54:F7:26:ASN:HA	54:F7:29:LYS:HE2	1.90	0.52
62:Fb:29:GLN:HG2	85:Fc:201:PM8:H32	1.91	0.52
1:CA:517:U:OP2	47:DY:148:ARG:NH2	2.42	0.52
6:CH:53:ARG:HE	20:Cd:119:HIS:CD2	2.26	0.52
12:CO:84:GLU:N	12:CO:85:PRO:HD3	2.25	0.52
32:DF:495:GLU:OE2	34:DH:243:SER:OG	2.22	0.52
33:DG:616:ARG:HD3	33:DG:627:TRP:CD1	2.44	0.52
34:DH:473:TYR:HE2	42:DT:207:THR:HG21	1.74	0.52
42:DT:220:ASP:HA	42:DT:232:ARG:HH22	1.74	0.52
51:F3:270:LEU:HD23	51:F3:270:LEU:H	1.74	0.52
52:F5:76:ARG:O	52:F5:80:GLU:HG2	2.09	0.52
59:FW:16:ARG:HD2	59:FW:45:SER:HB2	1.91	0.52
1:CA:18:U:O4	18:Ca:369:ARG:NH2	2.43	0.52
7:CI:226:LYS:HB3	7:CI:278:ALA:HB1	1.91	0.52
11:CN:125:GLY:HA3	36:DJ:22:MET:HB2	1.91	0.52
13:CP:172:VAL:O	18:Ca:541:ARG:NH2	2.31	0.52
18:Ca:443:MET:HE1	18:Ca:487:GLU:HB3	1.91	0.52
22:CI:148:LYS:HE2	22:CI:150:SER:HB2	1.92	0.52
24:Ck:145:LEU:HD13	24:Ck:148:LEU:HD12	1.90	0.52
29:DC:1152:PRO:HG2	29:DC:1160:GLN:HE22	1.74	0.52
30:DD:702:TYR:OH	30:DD:736:TYR:O	2.26	0.52
31:DE:222:TRP:CZ2	31:DE:408:LEU:HB2	2.44	0.52
34:DH:480:ASP:HB2	38:DL:44:LYS:HB2	1.91	0.52
35:DI:192:THR:OG1	35:DI:194:ASP:OD1	2.27	0.52
47:DY:50:VAL:HG21	47:DY:109:PHE:HE2	1.75	0.52
51:F3:298:SER:HA	51:F3:301:PHE:HD2	1.74	0.52
52:F5:379:VAL:HG21	52:F5:403:LEU:HD13	1.90	0.52
55:F9:377:GLN:O	55:F9:380:ASP:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:IA:391:THR:OG1	69:IA:442:PHE:O	2.26	0.52
1:CA:79:A:OP2	23:Cj:10:ARG:N	2.42	0.52
1:CA:84:U:H3'	1:CA:85:U:H4'	1.92	0.52
6:CH:125:LYS:HE2	6:CH:201:ARG:HG3	1.90	0.52
8:CJ:616:GLU:OE2	8:CJ:630:ARG:NH1	2.41	0.52
16:CS:116:LYS:HD2	16:CS:127:GLU:HB3	1.92	0.52
30:DD:76:ASN:HD21	30:DD:86:ILE:HG22	1.74	0.52
33:DG:529:ASP:OD1	33:DG:530:PHE:N	2.42	0.52
34:DH:511:VAL:HG23	34:DH:514:PRO:HG3	1.91	0.52
53:F6:15:PRO:HB3	53:F6:28:ASN:HB2	1.91	0.52
55:F9:262:HIS:HD2	67:Fh:99:SER:H	1.56	0.52
55:F9:307:ALA:HB2	55:F9:324:LEU:HD11	1.90	0.52
62:Fb:61:GLU:OE1	62:Fb:143:ARG:NH1	2.41	0.52
69:IA:84:GLN:HG2	70:IB:549:THR:H	1.75	0.52
8:CJ:754:VAL:HG22	44:DV:107:ILE:HG12	1.91	0.52
23:Cj:99:ASN:OD1	23:Cj:100:ILE:N	2.43	0.52
29:DC:198:GLU:OE1	29:DC:198:GLU:N	2.43	0.52
29:DC:261:LYS:HG2	29:DC:384:HIS:HE1	1.74	0.52
29:DC:328:VAL:O	29:DC:331:GLN:HG3	2.10	0.52
32:DF:23:ARG:O	42:DT:239:ARG:NH2	2.39	0.52
33:DG:161:ARG:HG3	33:DG:202:LEU:HD22	1.92	0.52
33:DG:531:ASP:OD1	33:DG:532:VAL:N	2.43	0.52
41:DR:63:ILE:HG23	41:DR:64:ILE:HG13	1.92	0.52
59:FW:34:ILE:HD11	59:FW:251:LEU:HD22	1.91	0.52
1:CA:305:A:H2'	1:CA:306:A:C8	2.45	0.52
4:CE:211:PRO:HG3	4:CE:226:LEU:HG	1.91	0.52
7:CI:313:ASP:HB2	7:CI:386:ILE:HG21	1.92	0.52
29:DC:315:LEU:HD12	29:DC:319:GLU:HG3	1.91	0.52
32:DF:290:VAL:HA	32:DF:293:VAL:HG22	1.91	0.52
33:DG:294:MET:HE1	33:DG:314:LEU:HB2	1.91	0.52
54:F7:624:PRO:HA	54:F7:627:LEU:HD12	1.92	0.52
58:FP:158:ASP:OD1	58:FP:158:ASP:N	2.41	0.52
64:Fd:59:HIS:CD2	64:Fd:62:LEU:H	2.28	0.52
65:Ff:560:ASN:ND2	70:IB:508:GLU:OE2	2.43	0.52
65:Ff:601:THR:O	68:Fi:586:ARG:NH1	2.42	0.52
1:CA:223:G:OP1	70:IB:701:THR:OG1	2.23	0.52
8:CJ:306:GLY:N	8:CJ:310:GLY:O	2.37	0.52
16:CS:133:ARG:HH21	28:DB:1149:MET:HE1	1.74	0.52
18:Ca:267:LEU:HD23	18:Ca:293:LEU:HD11	1.92	0.52
24:Ck:115:PRO:O	32:DF:548:ARG:NH2	2.43	0.52
31:DE:78:ASP:OD1	31:DE:78:ASP:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DJ:61:LYS:HG3	36:DJ:63:ARG:HG2	1.91	0.52
40:DP:64:MET:HA	51:F3:472:GLU:HG2	1.91	0.52
52:F5:648:PRO:HD2	62:Fb:96:VAL:HG13	1.91	0.52
56:FN:25:ASN:O	56:FN:29:LYS:HG2	2.09	0.52
59:FW:70:LEU:O	59:FW:74:ARG:HG2	2.10	0.52
70:IB:524:ARG:NE	70:IB:563:GLU:OE2	2.26	0.52
1:CA:435:G:N2	32:DF:25:ILE:O	2.35	0.52
8:CJ:647:ASP:OD1	8:CJ:647:ASP:N	2.40	0.52
29:DC:770:LEU:HD12	29:DC:771:PRO:HD2	1.91	0.52
31:DE:467:MET:HE1	31:DE:486:ILE:HD12	1.91	0.52
36:DJ:173:ASP:OD2	36:DJ:209:ARG:NH1	2.43	0.52
46:DX:156:TYR:OH	47:DY:140:SER:O	2.24	0.52
51:F3:720:ILE:HD13	51:F3:720:ILE:H	1.75	0.52
56:FM:126:GLU:OE1	56:FM:130:ARG:NH1	2.43	0.52
58:FP:158:ASP:HB3	60:FX:42:ARG:HD3	1.92	0.52
64:Fd:76:HIS:CE1	64:Fd:78:GLN:HB2	2.45	0.52
65:Ff:550:ARG:NH2	70:IB:380:GLU:O	2.43	0.52
67:Fh:102:ARG:NH2	67:Fh:105:ASP:OD1	2.43	0.52
68:Fi:301:GLN:NE2	70:IB:410:GLU:O	2.43	0.52
1:CA:229:G:H5''	1:CA:247:A:N6	2.25	0.51
1:CA:301:A:H3'	1:CA:302:U:C6	2.45	0.51
1:CA:465:U:OP2	7:CI:407:ARG:NH2	2.42	0.51
4:CE:159:HIS:CE1	67:Fh:67:ASN:HD21	2.28	0.51
6:CH:195:ARG:HB2	6:CH:204:ALA:HB3	1.91	0.51
11:CN:51:LEU:O	11:CN:68:GLN:NE2	2.43	0.51
12:CO:210:ARG:NH2	12:CO:276:GLU:OE2	2.39	0.51
14:CQ:93:ASP:HB3	14:CQ:146:HIS:HE1	1.74	0.51
15:CR:81:SER:HA	15:CR:84:ARG:HE	1.75	0.51
24:Ck:261:VAL:HG23	24:Ck:262:VAL:HG13	1.91	0.51
30:DD:171:ASN:ND2	30:DD:275:ASP:OD2	2.40	0.51
52:F5:290:LEU:HD13	61:FZ:105:GLU:HB2	1.92	0.51
66:Fg:355:LEU:H	66:Fg:355:LEU:HD12	1.75	0.51
68:Fi:445:LEU:HB3	68:Fi:545:PHE:HB3	1.91	0.51
70:IB:609:GLU:OE1	70:IB:609:GLU:N	2.36	0.51
8:CJ:469:ASP:HA	8:CJ:672:ARG:HB2	1.92	0.51
23:Cj:35:ARG:HB2	23:Cj:38:MET:HG2	1.92	0.51
23:Cj:99:ASN:ND2	23:Cj:167:ASP:O	2.43	0.51
28:DB:388:VAL:HG21	34:DH:508:LEU:HB2	1.93	0.51
40:DP:170:ALA:O	40:DP:174:ALA:HB2	2.08	0.51
45:DW:55:TRP:NE1	45:DW:132:HIS:O	2.35	0.51
51:F3:318:ILE:O	51:F3:322:ALA:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:FN:70:THR:HA	56:FN:73:LYS:HE3	1.92	0.51
58:FP:101:GLN:NE2	58:FP:125:THR:OG1	2.42	0.51
68:Fi:247:GLY:O	70:IB:404:GLN:NE2	2.43	0.51
70:IB:362:LEU:HD21	70:IB:621:GLU:HA	1.91	0.51
3:CC:9:TYR:OH	28:DB:243:ASP:OD2	2.20	0.51
26:Cn:204:LEU:HD12	26:Cn:205:PRO:HD2	1.91	0.51
29:DC:89:GLY:HA2	31:DE:163:LYS:HG2	1.92	0.51
30:DD:371:PRO:HA	30:DD:560:ALA:HB3	1.92	0.51
34:DH:114:HIS:ND1	34:DH:124:TYR:OH	2.36	0.51
35:DI:86:LEU:HD13	35:DI:172:LEU:HD12	1.91	0.51
54:F7:19:ALA:HB1	54:F7:46:LEU:HD13	1.92	0.51
65:Ff:523:MET:HE3	65:Ff:641:ALA:HB3	1.92	0.51
4:CE:140:PHE:HB3	4:CE:169:VAL:HG22	1.91	0.51
8:CJ:777:THR:O	8:CJ:781:HIS:HB2	2.09	0.51
12:CO:268:LYS:HG2	12:CO:309:LEU:HB3	1.92	0.51
15:CR:133:SER:HB3	15:CR:171:TYR:HE2	1.76	0.51
28:DB:351:GLN:O	28:DB:355:GLN:HG2	2.10	0.51
30:DD:621:LEU:O	30:DD:624:THR:OG1	2.26	0.51
35:DI:292:TYR:HE1	35:DI:294:ASN:HB2	1.76	0.51
60:FX:152:ARG:HE	60:FX:181:MET:HE1	1.75	0.51
66:Fg:69:ASP:OD1	66:Fg:69:ASP:N	2.42	0.51
69:IA:206:VAL:HG22	69:IA:277:LEU:HB3	1.93	0.51
4:CE:113:GLU:OE2	55:F9:80:ARG:NH1	2.42	0.51
4:CE:285:ILE:HD13	6:CH:250:LEU:HD21	1.93	0.51
5:CF:125:GLU:OE2	5:CF:129:ASN:ND2	2.43	0.51
7:CI:265:ASP:OD1	7:CI:266:SER:N	2.44	0.51
18:Ca:208:VAL:HG11	18:Ca:250:SER:HB3	1.92	0.51
24:Ck:644:HIS:CD2	24:Ck:669:ASN:H	2.27	0.51
29:DC:152:ARG:HH22	29:DC:182:ASP:HB2	1.75	0.51
29:DC:493:TYR:HD1	29:DC:496:LYS:HD2	1.75	0.51
29:DC:793:ASP:OD1	29:DC:794:LEU:N	2.44	0.51
29:DC:1143:VAL:HG11	34:DH:462:GLU:HB2	1.92	0.51
30:DD:97:LYS:HG2	30:DD:805:LYS:HG2	1.92	0.51
36:DJ:276:LEU:HA	36:DJ:280:GLY:HA3	1.93	0.51
40:DP:44:GLU:OE2	40:DP:60:ARG:NH2	2.34	0.51
52:F5:139:ASP:OD1	52:F5:139:ASP:N	2.44	0.51
53:F6:449:MET:HE2	53:F6:466:LEU:HB2	1.92	0.51
55:F9:541:PHE:HD2	55:F9:549:ARG:HB2	1.75	0.51
57:FO:41:ARG:HD2	68:Fi:27:MET:HE2	1.91	0.51
66:Fg:11:PHE:CD2	66:Fg:507:ILE:HD11	2.46	0.51
66:Fg:111:MET:SD	66:Fg:115:HIS:NE2	2.83	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Fg:199:ASP:OD2	66:Fg:202:LEU:N	2.41	0.51
3:CC:61:LEU:HD21	36:DJ:27:GLN:HA	1.92	0.51
18:Ca:349:ALA:HB3	30:DD:773:MET:HE3	1.93	0.51
30:DD:589:GLN:HB2	41:DR:198:HIS:CE1	2.46	0.51
33:DG:215:LEU:HD22	33:DG:224:LEU:HD12	1.93	0.51
38:DL:89:VAL:HA	38:DL:92:ILE:HG12	1.92	0.51
52:F5:366:VAL:HA	52:F5:369:TYR:CE2	2.45	0.51
57:FO:328:ILE:HG22	57:FO:331:PHE:H	1.76	0.51
61:FZ:23:GLU:OE1	61:FZ:23:GLU:N	2.44	0.51
65:Ff:566:TYR:CE2	70:IB:383:MET:HB3	2.45	0.51
3:CC:47:ILE:HG22	70:IB:757:GLY:HA3	1.93	0.51
8:CJ:469:ASP:HB3	11:CN:58:THR:HG23	1.92	0.51
9:CK:42:PHE:HZ	21:Cg:473:ARG:HH21	1.59	0.51
18:Ca:144:ASP:OD1	18:Ca:144:ASP:N	2.44	0.51
27:Cp:47:ARG:NH1	27:Cp:112:PHE:O	2.44	0.51
27:Cp:66:HIS:HB3	27:Cp:69:ARG:HG3	1.92	0.51
31:DE:649:TYR:HE1	31:DE:737:MET:HE1	1.74	0.51
34:DH:87:PRO:HB3	34:DH:118:ALA:HB1	1.91	0.51
51:F3:280:LEU:HD13	51:F3:323:PRO:HG2	1.93	0.51
65:Ff:614:VAL:HG21	65:Ff:662:LEU:HD13	1.93	0.51
12:CO:201:PHE:HA	12:CO:204:GLU:HG2	1.92	0.51
13:CP:45:LEU:HD21	13:CP:117:LEU:HD23	1.92	0.51
14:CQ:203:THR:O	14:CQ:206:THR:OG1	2.29	0.51
21:Cg:225:ARG:NH2	21:Cg:276:GLU:OE1	2.44	0.51
33:DG:183:ARG:NH2	33:DG:300:ASP:OD2	2.44	0.51
33:DG:215:LEU:O	33:DG:218:THR:OG1	2.23	0.51
50:F2:425:ILE:O	50:F2:429:THR:HG23	2.10	0.51
50:F2:866:GLU:OE2	52:F5:466:ARG:NH2	2.44	0.51
52:F5:583:ARG:HG2	61:FZ:88:GLN:H	1.74	0.51
53:F6:415:VAL:HG22	53:F6:451:PHE:HB2	1.92	0.51
54:F7:508:ALA:O	54:F7:544:ASN:ND2	2.38	0.51
62:Fb:86:ALA:O	62:Fb:90:HIS:ND1	2.43	0.51
66:Fg:227:VAL:HA	66:Fg:239:VAL:HG12	1.93	0.51
67:Fh:76:HIS:HD2	67:Fh:78:ARG:HH21	1.58	0.51
5:CF:136:ALA:HA	5:CF:139:TYR:HD2	1.75	0.51
12:CO:210:ARG:NH2	12:CO:280:ASP:OD2	2.40	0.51
32:DF:127:PRO:HA	32:DF:136:ALA:HB3	1.93	0.51
33:DG:534:VAL:HG12	33:DG:600:LEU:HD22	1.93	0.51
50:F2:877:LEU:HB3	50:F2:881:LYS:HE3	1.93	0.51
53:F6:100:THR:OG1	53:F6:101:ILE:N	2.42	0.51
60:FX:84:GLN:NE2	60:FX:88:GLU:OE2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Fh:122:ARG:HB3	67:Fh:134:LYS:HE3	1.93	0.51
68:Fi:485:GLN:HE21	68:Fi:499:ARG:HH12	1.57	0.51
70:IB:626:VAL:O	70:IB:643:TYR:OH	2.19	0.51
32:DF:550:VAL:HG12	32:DF:574:GLU:HA	1.92	0.51
35:DI:62:LYS:O	35:DI:66:ARG:NH1	2.43	0.51
52:F5:108:MET:HG2	52:F5:127:TYR:HB2	1.93	0.51
54:F7:129:MET:HE3	54:F7:157:GLN:HG3	1.91	0.51
56:FN:73:LYS:HZ2	56:FN:74:TRP:CD1	2.29	0.51
56:FN:234:MET:SD	56:FN:238:ASN:ND2	2.83	0.51
60:FX:86:ARG:NH2	78:UN:1:UNK:O	2.43	0.51
65:Ff:741:GLN:HB2	65:Ff:746:VAL:O	2.11	0.51
66:Fg:200:PRO:HB2	66:Fg:234:TYR:CD1	2.46	0.51
70:IB:594:SER:HA	70:IB:600:LYS:HE3	1.93	0.51
29:DC:284:LEU:HD23	29:DC:284:LEU:H	1.76	0.50
29:DC:748:TRP:HB3	29:DC:786:ARG:HH22	1.77	0.50
30:DD:607:GLN:O	41:DR:227:ARG:NH2	2.44	0.50
36:DJ:144:CYS:SG	36:DJ:145:HIS:N	2.84	0.50
44:DV:151:GLU:HG3	44:DV:169:LEU:HB2	1.93	0.50
52:F5:234:HIS:HD2	61:FZ:139:TRP:HH2	1.59	0.50
52:F5:326:ALA:HA	52:F5:390:LEU:HD21	1.93	0.50
53:F6:433:GLU:OE2	53:F6:436:ARG:NH2	2.44	0.50
53:F6:591:GLU:HG2	65:Ff:740:MET:HE2	1.94	0.50
63:Fc:67:LEU:HD13	63:Fc:67:LEU:H	1.77	0.50
69:IA:593:VAL:HG12	69:IA:596:HIS:H	1.75	0.50
70:IB:584:TYR:HD1	70:IB:622:ARG:HD2	1.76	0.50
5:CF:86:HIS:HD2	5:CF:88:ASP:H	1.59	0.50
10:CL:61:LEU:HD23	10:CL:61:LEU:H	1.75	0.50
12:CO:129:GLN:HE21	12:CO:134:GLU:HA	1.76	0.50
21:Cg:155:LYS:HB3	21:Cg:356:CYS:SG	2.51	0.50
34:DH:470:LYS:NZ	34:DH:483:TYR:OH	2.36	0.50
43:DU:70:ASP:HB3	43:DU:72:PRO:HD2	1.93	0.50
57:FO:137:ALA:O	57:FO:140:THR:OG1	2.29	0.50
65:Ff:678:VAL:O	65:Ff:682:ASN:ND2	2.35	0.50
69:IA:377:CYS:SG	69:IA:454:GLN:HB2	2.51	0.50
4:CE:119:SER:HB2	4:CE:123:LEU:HD11	1.93	0.50
6:CH:43:ASN:ND2	12:CO:227:LYS:HE3	2.27	0.50
8:CJ:321:ASN:HD21	24:Ck:316:ASP:HB2	1.76	0.50
9:CK:28:VAL:HB	9:CK:33:LYS:HD3	1.92	0.50
11:CN:26:LEU:HG	32:DF:164:ILE:HG21	1.93	0.50
18:Ca:350:GLU:HG2	30:DD:773:MET:HE1	1.93	0.50
28:DB:1051:GLN:HE22	36:DJ:41:PRO:HA	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DC:1164:TRP:NE1	34:DH:326:ASP:OD1	2.32	0.50
33:DG:399:ARG:HH21	33:DG:409:LYS:HG2	1.76	0.50
34:DH:354:LEU:HD13	34:DH:364:ARG:HH21	1.76	0.50
39:DO:93:LEU:HA	39:DO:96:LYS:HG2	1.92	0.50
56:FN:100:ILE:HD13	56:FN:109:ILE:HD12	1.93	0.50
58:FP:309:LEU:O	58:FP:313:MET:HG2	2.11	0.50
69:IA:647:THR:O	69:IA:733:GLN:NE2	2.43	0.50
1:CA:518:G:OP2	47:DY:145:ARG:NH1	2.45	0.50
4:CE:164:TYR:HD1	4:CE:182:VAL:HG13	1.76	0.50
31:DE:714:PHE:HA	31:DE:717:ARG:HD2	1.94	0.50
38:DL:100:LEU:O	38:DL:105:ARG:NH2	2.39	0.50
46:DX:164:THR:HG23	46:DX:167:HIS:H	1.76	0.50
50:F2:755:GLU:HG3	50:F2:758:GLY:H	1.76	0.50
55:F9:347:ILE:HG21	67:Fh:227:TYR:HB3	1.93	0.50
57:FO:299:TYR:HE1	67:Fh:302:SER:HA	1.77	0.50
65:Ff:196:PRO:O	65:Ff:438:ARG:NH2	2.44	0.50
68:Fi:90:LEU:HD11	68:Fi:388:GLU:HA	1.92	0.50
70:IB:334:ALA:N	70:IB:563:GLU:OE1	2.36	0.50
1:CA:451:U:H2'	1:CA:452:A:H8	1.76	0.50
4:CE:301:TYR:CG	4:CE:302:PRO:HD3	2.46	0.50
24:Ck:711:ILE:HG22	24:Ck:715:GLN:HE21	1.77	0.50
28:DB:503:ASN:O	28:DB:507:LEU:HB2	2.11	0.50
28:DB:564:ARG:NH1	32:DF:511:THR:OG1	2.45	0.50
28:DB:876:LEU:HD12	28:DB:877:PRO:HD2	1.94	0.50
30:DD:605:ARG:HG2	30:DD:613:TRP:CZ2	2.47	0.50
41:DR:114:SER:HA	41:DR:118:VAL:O	2.12	0.50
46:DX:86:PRO:HG3	46:DX:135:ALA:HA	1.93	0.50
52:F5:641:ARG:HD3	52:F5:642:PRO:HD2	1.94	0.50
55:F9:374:LEU:O	55:F9:378:LYS:HG3	2.12	0.50
55:F9:531:ASP:O	69:IA:139:GLN:NE2	2.44	0.50
65:Ff:507:MET:HG3	65:Ff:565:GLN:HB3	1.92	0.50
70:IB:680:HIS:HA	70:IB:695:PHE:HE2	1.76	0.50
70:IB:710:GLN:HB3	70:IB:778:LEU:HD13	1.94	0.50
1:CA:566:U:H4'	1:CA:567:A:O5'	2.10	0.50
4:CE:144:ILE:HB	70:IB:703:VAL:HG11	1.92	0.50
9:CK:183:GLY:HA2	53:F6:439:PRO:HB2	1.94	0.50
30:DD:721:PRO:HG2	30:DD:725:ALA:HB2	1.94	0.50
52:F5:81:VAL:HG22	52:F5:107:TYR:CE1	2.47	0.50
52:F5:590:ARG:HE	61:FZ:96:LEU:HD13	1.76	0.50
52:F5:644:LEU:HG	61:FZ:55:ALA:HB2	1.93	0.50
56:FM:255:THR:HA	56:FM:305:ARG:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:FZ:141:ASN:OD1	61:FZ:142:LEU:N	2.44	0.50
61:FZ:159:GLU:HB3	61:FZ:166:TRP:HB2	1.93	0.50
66:Fg:190:PRO:HB2	66:Fg:203:ALA:HB1	1.94	0.50
69:IA:277:LEU:HD13	69:IA:363:GLN:HG2	1.93	0.50
7:CI:64:MET:HB3	21:Cg:7:LYS:HG2	1.94	0.50
9:CK:22:PRO:HB2	9:CK:26:ARG:HH12	1.77	0.50
10:CL:60:GLY:HA2	55:F9:525:ASN:HD21	1.77	0.50
11:CN:24:PHE:HA	11:CN:27:GLU:HG2	1.94	0.50
29:DC:791:ALA:HB3	29:DC:806:SER:HB2	1.94	0.50
30:DD:411:GLU:OE1	30:DD:411:GLU:N	2.45	0.50
32:DF:18:THR:OG1	36:DJ:295:TYR:OH	2.26	0.50
50:F2:416:MET:HG3	50:F2:421:ILE:HB	1.93	0.50
50:F2:437:GLN:O	50:F2:441:ARG:HG2	2.12	0.50
50:F2:640:TYR:HA	50:F2:643:ARG:HE	1.76	0.50
56:FN:256:SER:N	56:FN:305:ARG:O	2.45	0.50
59:FW:90:TYR:OH	59:FW:148:ASP:OD1	2.28	0.50
65:Ff:191:GLU:HA	65:Ff:194:ARG:HD2	1.94	0.50
66:Fg:225:ILE:HD11	66:Fg:249:LEU:HD22	1.93	0.50
4:CE:264:SER:HB3	4:CE:267:HIS:HB2	1.94	0.50
8:CJ:799:ASP:OD1	22:CI:99:TYR:OH	2.27	0.50
10:CL:19:PHE:HB2	10:CL:66:PHE:HE2	1.77	0.50
12:CO:210:ARG:HH12	54:F7:631:ARG:HD3	1.77	0.50
24:Ck:380:VAL:HA	24:Ck:383:ILE:HG22	1.94	0.50
32:DF:15:HIS:HB3	32:DF:18:THR:HG22	1.93	0.50
32:DF:391:VAL:HG21	32:DF:456:MET:HE1	1.94	0.50
34:DH:119:LEU:HD13	34:DH:123:HIS:HB2	1.92	0.50
34:DH:233:MET:HG3	34:DH:238:ILE:HB	1.94	0.50
36:DJ:245:VAL:HG21	36:DJ:294:MET:SD	2.52	0.50
51:F3:52:ILE:HG12	51:F3:82:VAL:HG21	1.94	0.50
61:FZ:136:MET:HA	61:FZ:139:TRP:HD1	1.77	0.50
69:IA:380:THR:HG22	69:IA:451:ILE:HG12	1.94	0.50
3:CC:63:ASN:HB2	3:CC:69:ILE:HG13	1.94	0.50
11:CN:30:LEU:HD21	32:DF:164:ILE:HD12	1.93	0.50
23:Cj:156:THR:HG21	23:Cj:190:PRO:HG2	1.94	0.50
29:DC:152:ARG:HH21	29:DC:184:PHE:H	1.59	0.50
30:DD:217:ASP:OD1	30:DD:297:ARG:NE	2.43	0.50
32:DF:144:THR:HG23	32:DF:147:ASP:H	1.77	0.50
32:DF:347:ARG:O	32:DF:351:HIS:ND1	2.44	0.50
37:DK:23:TYR:HD1	37:DK:155:PRO:HG3	1.76	0.50
47:DY:160:GLU:OE1	47:DY:162:ARG:N	2.44	0.50
51:F3:631:MET:HA	51:F3:634:ARG:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:F7:329:GLU:HG2	54:F7:361:PHE:HB3	1.93	0.50
54:F7:367:VAL:HG12	54:F7:389:LEU:HD23	1.94	0.50
54:F7:536:ASN:ND2	54:F7:614:ASP:OD2	2.45	0.50
56:FM:234:MET:SD	56:FM:238:ASN:ND2	2.85	0.50
56:FN:255:THR:HA	56:FN:305:ARG:HA	1.94	0.50
1:CA:67:U:O2'	12:CO:429:ASN:O	2.30	0.49
8:CJ:438:ASN:HD21	24:Ck:669:ASN:HB3	1.76	0.49
10:CL:39:TYR:HE1	10:CL:50:MET:HB3	1.77	0.49
28:DB:1044:PRO:O	28:DB:1048:ILE:HG12	2.12	0.49
29:DC:888:LEU:O	29:DC:894:HIS:NE2	2.42	0.49
32:DF:119:HIS:HD2	32:DF:121:LEU:H	1.60	0.49
55:F9:364:ASP:O	55:F9:367:GLU:HG3	2.11	0.49
55:F9:532:LEU:HD22	69:IA:487:GLN:HG3	1.93	0.49
56:FN:40:SER:HB3	56:FN:45:LYS:HB2	1.94	0.49
58:FP:38:ALA:HB2	58:FP:307:ALA:HB2	1.94	0.49
1:CA:521:G:OP2	45:DW:126:ARG:NH2	2.38	0.49
3:CC:35:PHE:HE1	28:DB:1013:ARG:HH22	1.60	0.49
5:CF:53:ASP:OD2	64:Fd:30:ARG:NH1	2.45	0.49
13:CP:70:HIS:O	30:DD:795:TRP:NE1	2.31	0.49
24:Ck:693:TRP:HA	32:DF:172:PRO:HG3	1.94	0.49
29:DC:54:LEU:HD13	29:DC:412:LYS:HB2	1.94	0.49
29:DC:570:HIS:CE1	29:DC:574:GLN:HE21	2.30	0.49
29:DC:1042:ARG:NH2	37:DK:48:VAL:O	2.41	0.49
31:DE:280:LEU:HD23	31:DE:280:LEU:H	1.77	0.49
31:DE:652:GLU:O	31:DE:656:ARG:HG2	2.12	0.49
36:DJ:294:MET:HE2	36:DJ:298:VAL:HG23	1.93	0.49
44:DV:41:THR:O	45:DW:61:ARG:NH2	2.44	0.49
45:DW:115:ASN:HD22	45:DW:120:ASN:HD22	1.60	0.49
50:F2:94:ALA:O	50:F2:97:GLU:HG3	2.11	0.49
50:F2:970:MET:O	50:F2:974:VAL:HG23	2.11	0.49
51:F3:75:SER:O	51:F3:79:HIS:ND1	2.45	0.49
52:F5:343:LEU:HD23	52:F5:468:ARG:HH21	1.77	0.49
53:F6:180:LYS:HB3	53:F6:184:ASP:HB3	1.94	0.49
53:F6:445:ASP:OD1	53:F6:445:ASP:N	2.43	0.49
58:FP:131:ASP:OD1	58:FP:131:ASP:N	2.42	0.49
59:FW:169:GLU:HG3	59:FW:170:THR:HG23	1.93	0.49
11:CN:157:GLN:HB2	22:Ci:73:MET:HE1	1.93	0.49
12:CO:245:ASN:HB3	12:CO:248:ILE:HB	1.94	0.49
18:Ca:230:GLN:O	18:Ca:234:LYS:NZ	2.45	0.49
18:Ca:253:LEU:HD13	50:F2:745:LEU:HD22	1.93	0.49
22:Ci:33:LEU:HD13	24:Ck:735:ILE:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Cp:48:PRO:HD3	59:FW:143:TRP:HA	1.94	0.49
29:DC:1115:ARG:HD3	36:DJ:193:PRO:HG3	1.94	0.49
49:Da:22:ARG:NH1	49:Da:26:ASP:OD1	2.45	0.49
52:F5:323:GLU:OE1	52:F5:386:TYR:OH	2.29	0.49
55:F9:223:GLU:O	55:F9:226:GLN:HG3	2.12	0.49
66:Fg:543:LEU:HD22	66:Fg:550:LEU:HD22	1.94	0.49
67:Fh:56:PHE:HB3	70:IB:683:TYR:CZ	2.47	0.49
69:IA:278:ILE:O	69:IA:306:PHE:HA	2.12	0.49
1:CA:10:G:N1	50:F2:532:ASP:OD2	2.44	0.49
1:CA:571:A:H5''	26:Cn:179:ARG:HH22	1.78	0.49
7:CI:65:MET:HE1	21:Cg:471:ARG:HD2	1.93	0.49
8:CJ:476:ASN:ND2	32:DF:216:LYS:H	2.10	0.49
10:CL:20:VAL:HG23	69:IA:562:SER:HB2	1.93	0.49
16:CS:98:PHE:CE2	32:DF:73:HIS:HB2	2.47	0.49
24:Ck:737:ALA:HB1	24:Ck:740:ARG:HB2	1.94	0.49
27:Cp:143:ILE:HD11	40:DP:15:ARG:HD3	1.95	0.49
30:DD:139:LEU:HD23	30:DD:339:ARG:HB2	1.94	0.49
34:DH:279:GLU:HA	34:DH:282:ASN:HD21	1.77	0.49
41:DR:80:LEU:HD12	41:DR:133:LEU:HD21	1.94	0.49
45:DW:94:ARG:NH2	45:DW:155:ARG:O	2.44	0.49
51:F3:518:ARG:NH2	51:F3:561:GLU:O	2.46	0.49
53:F6:352:HIS:CD2	53:F6:363:ASN:H	2.30	0.49
55:F9:197:ILE:HD12	61:FZ:169:ARG:HA	1.94	0.49
55:F9:205:TYR:HB3	55:F9:208:ALA:HB3	1.94	0.49
58:FP:73:PRO:HA	59:FW:217:ARG:HH21	1.77	0.49
60:FX:132:LEU:HD22	60:FX:164:HIS:CD2	2.46	0.49
66:Fg:360:HIS:ND1	66:Fg:481:GLN:O	2.42	0.49
1:CA:575:U:H2'	69:IA:111:ARG:HG2	1.93	0.49
8:CJ:75:TYR:HA	38:DL:287:TRP:CD2	2.48	0.49
8:CJ:151:ASN:ND2	8:CJ:209:GLN:O	2.44	0.49
11:CN:139:THR:O	11:CN:144:LYS:NZ	2.45	0.49
19:Cb:142:ALA:O	19:Cb:146:VAL:HG23	2.13	0.49
28:DB:81:PHE:O	28:DB:154:ARG:NH2	2.34	0.49
28:DB:445:ASN:ND2	28:DB:448:ASP:OD2	2.43	0.49
29:DC:149:ARG:HG2	29:DC:170:ASP:HB2	1.94	0.49
30:DD:613:TRP:CZ2	30:DD:646:ILE:HD11	2.47	0.49
56:FM:310:VAL:O	56:FM:314:ILE:HG13	2.12	0.49
62:Fb:32:CYS:HB3	62:Fb:78:VAL:HG23	1.95	0.49
69:IA:628:ARG:HH11	69:IA:637:ASN:HD21	1.59	0.49
69:IA:657:VAL:HB	69:IA:691:VAL:O	2.13	0.49
1:CA:138:U:O4	30:DD:716:SER:OG	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:315:A:H2'	1:CA:316:A:C8	2.48	0.49
4:CE:335:LEU:HD12	4:CE:336:PRO:HD2	1.95	0.49
10:CL:68:ILE:HG23	10:CL:81:TYR:HB3	1.95	0.49
20:Cd:18:LEU:HD12	20:Cd:19:PRO:HD2	1.94	0.49
24:Ck:385:HIS:CE1	24:Ck:545:ILE:HG21	2.48	0.49
24:Ck:752:LYS:HD2	28:DB:1091:HIS:CG	2.48	0.49
28:DB:226:LEU:HA	31:DE:594:LEU:HD23	1.93	0.49
28:DB:500:PRO:HA	33:DG:41:TRP:NE1	2.28	0.49
31:DE:172:ASP:HB3	31:DE:176:ARG:HH21	1.78	0.49
32:DF:325:LEU:HB3	32:DF:482:TRP:CD1	2.48	0.49
39:DO:139:GLU:OE1	54:F7:566:LYS:NZ	2.46	0.49
51:F3:466:GLU:OE2	51:F3:469:ARG:NH2	2.43	0.49
56:FM:195:LEU:HD12	56:FN:225:LEU:HD22	1.95	0.49
56:FN:135:LEU:HD13	56:FN:155:VAL:HG13	1.94	0.49
69:IA:291:GLN:O	69:IA:294:GLU:HG3	2.12	0.49
1:CA:47:U:H2'	1:CA:48:U:C6	2.48	0.49
6:CH:199:ASN:ND2	6:CH:202:ALA:O	2.44	0.49
8:CJ:46:ASP:OD1	8:CJ:46:ASP:N	2.44	0.49
11:CN:145:LYS:O	11:CN:150:HIS:ND1	2.46	0.49
12:CO:346:THR:HB	51:F3:587:ARG:HG3	1.94	0.49
14:CQ:248:MET:HG3	26:Cn:198:MET:HE1	1.95	0.49
15:CR:75:GLN:O	15:CR:79:ASN:ND2	2.46	0.49
15:CR:127:LYS:HE2	20:Cd:179:PHE:HD2	1.77	0.49
18:Ca:366:VAL:HG21	50:F2:592:LEU:HD21	1.95	0.49
24:Ck:204:LEU:O	24:Ck:250:ARG:NH2	2.45	0.49
28:DB:279:PRO:HG2	28:DB:281:GLN:HE22	1.78	0.49
28:DB:941:ARG:N	28:DB:948:ARG:O	2.43	0.49
28:DB:1103:VAL:O	28:DB:1107:THR:HG22	2.12	0.49
29:DC:671:ARG:NH2	29:DC:677:GLU:OE2	2.45	0.49
31:DE:164:ARG:HD2	31:DE:557:TYR:CZ	2.48	0.49
31:DE:262:PRO:HG3	31:DE:275:ARG:HD2	1.94	0.49
34:DH:258:MET:HA	34:DH:258:MET:HE2	1.95	0.49
40:DP:111:THR:OG1	40:DP:114:ASP:OD2	2.26	0.49
42:DT:47:PHE:HB2	42:DT:163:ARG:HH22	1.77	0.49
47:DY:10:ASN:N	47:DY:10:ASN:OD1	2.46	0.49
47:DY:25:ILE:HD12	47:DY:99:GLN:HB3	1.93	0.49
51:F3:62:ASN:HB2	51:F3:68:PHE:HE1	1.78	0.49
55:F9:289:LYS:HG3	55:F9:292:ARG:HH21	1.77	0.49
66:Fg:228:VAL:HG13	66:Fg:360:HIS:HB2	1.94	0.49
67:Fh:80:ALA:HB2	70:IB:720:GLY:HA3	1.94	0.49
1:CA:62:A:O2'	1:CA:63:G:O5'	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:297:G:H5'	1:CA:345:A:H5'	1.94	0.49
1:CA:518:G:OP1	45:DW:44:ASN:ND2	2.45	0.49
7:CI:137:SER:HB3	7:CI:140:GLU:HG3	1.95	0.49
8:CJ:581:GLN:NE2	8:CJ:586:GLU:OE2	2.46	0.49
23:Cj:141:GLY:HA3	40:DP:143:ASN:HB3	1.94	0.49
28:DB:983:LEU:HD13	33:DG:84:LEU:HD11	1.95	0.49
29:DC:947:TRP:HD1	29:DC:1055:ARG:HB2	1.77	0.49
30:DD:371:PRO:HA	30:DD:560:ALA:CB	2.43	0.49
33:DG:308:ARG:NH1	33:DG:349:ASP:OD2	2.45	0.49
40:DP:138:CYS:HA	40:DP:142:ASN:HD22	1.77	0.49
51:F3:788:LEU:HD23	51:F3:791:ILE:HD11	1.94	0.49
55:F9:480:THR:HG23	55:F9:485:LEU:HD23	1.95	0.49
58:FP:24:LEU:HB2	58:FP:29:GLN:HG3	1.93	0.49
7:CI:141:TYR:OH	50:F2:60:ASP:OD2	2.25	0.49
10:CL:25:MET:HE3	10:CL:76:LEU:HD22	1.94	0.49
15:CR:133:SER:OG	15:CR:178:PHE:HB2	2.13	0.49
23:Cj:71:ILE:O	40:DP:130:TYR:OH	2.30	0.49
28:DB:137:VAL:HG12	29:DC:949:PHE:HZ	1.78	0.49
28:DB:896:GLY:O	28:DB:898:GLN:NE2	2.46	0.49
32:DF:449:ASP:OD1	32:DF:449:ASP:N	2.46	0.49
35:DI:248:ALA:HB3	35:DI:251:VAL:HG23	1.95	0.49
52:F5:346:TYR:CE1	52:F5:381:TRP:HB2	2.48	0.49
57:FO:13:LEU:HD13	57:FO:46:HIS:CD2	2.47	0.49
61:FZ:59:LYS:HE3	61:FZ:63:ASN:HD21	1.77	0.49
7:CI:122:LEU:HD21	7:CI:157:LEU:HD21	1.94	0.49
7:CI:355:LEU:HB2	21:Cg:446:PHE:CE2	2.48	0.49
8:CJ:305:ALA:HB3	24:Ck:721:GLY:HA3	1.94	0.49
8:CJ:685:ILE:O	8:CJ:688:GLU:HG3	2.13	0.49
13:CP:157:ASP:O	13:CP:161:ARG:HG2	2.13	0.49
29:DC:305:ARG:O	29:DC:308:LYS:HG2	2.13	0.49
30:DD:449:LEU:HD12	30:DD:452:LEU:HD12	1.94	0.49
34:DH:451:GLU:OE2	34:DH:457:ARG:NH1	2.46	0.49
37:DK:122:LYS:HB3	37:DK:153:LEU:HD12	1.94	0.49
48:DZ:80:TRP:HB3	48:DZ:87:ILE:HD11	1.95	0.49
68:Fi:288:GLN:O	68:Fi:294:ARG:NH2	2.46	0.49
69:IA:576:ASP:OD2	69:IA:590:ARG:NH1	2.40	0.49
1:CA:102:A:O2'	1:CA:128:A:N1	2.42	0.48
1:CA:438:U:N3	42:DT:9:GLN:O	2.46	0.48
9:CK:278:VAL:HG13	9:CK:306:TYR:HB2	1.94	0.48
28:DB:362:ALA:HB2	34:DH:543:MET:HE3	1.94	0.48
29:DC:228:GLN:HG2	29:DC:466:HIS:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DC:611:MET:HG3	29:DC:816:PHE:HZ	1.78	0.48
31:DE:613:ILE:HG22	37:DK:108:LYS:HE3	1.95	0.48
32:DF:127:PRO:O	32:DF:131:ARG:NH1	2.43	0.48
33:DG:273:VAL:HG21	33:DG:372:LEU:HD21	1.95	0.48
33:DG:340:SER:OG	33:DG:342:ASN:OD1	2.31	0.48
35:DI:100:LEU:HD12	35:DI:152:LEU:HD11	1.94	0.48
38:DL:90:GLU:HG2	38:DL:105:ARG:HD2	1.95	0.48
40:DP:171:LEU:HD11	40:DP:187:ARG:HG2	1.95	0.48
46:DX:75:LYS:HA	46:DX:111:ASN:HB3	1.95	0.48
50:F2:178:ALA:HB2	50:F2:235:MET:HB3	1.94	0.48
51:F3:293:HIS:O	51:F3:294:ARG:HG2	2.13	0.48
52:F5:92:GLU:HG3	52:F5:94:GLU:HG2	1.94	0.48
52:F5:151:VAL:HG22	52:F5:157:VAL:HG21	1.95	0.48
52:F5:337:THR:HG23	52:F5:339:LYS:HG2	1.93	0.48
59:FW:22:ALA:HB2	59:FW:232:LEU:HD22	1.93	0.48
65:Ff:224:LEU:HB3	65:Ff:429:ILE:HD11	1.94	0.48
65:Ff:729:TYR:HB3	65:Ff:736:LEU:HD11	1.94	0.48
69:IA:216:LYS:NZ	84:IA:1001:PO4:O4	2.34	0.48
14:CQ:219:GLN:OE1	68:Fi:517:TYR:OH	2.31	0.48
19:Cb:178:ARG:HH12	53:F6:209:ASP:HA	1.78	0.48
21:Cg:91:GLU:HG3	21:Cg:210:TYR:HB3	1.94	0.48
21:Cg:383:ASP:O	44:DV:100:LYS:NZ	2.30	0.48
22:Ci:128:SER:O	32:DF:32:TRP:NE1	2.41	0.48
23:Cj:45:GLU:OE2	23:Cj:128:LYS:NZ	2.43	0.48
28:DB:307:VAL:HG21	61:FZ:73:PRO:HB2	1.95	0.48
28:DB:742:SER:OG	28:DB:759:THR:OG1	2.28	0.48
29:DC:595:SER:N	31:DE:412:GLU:OE2	2.46	0.48
31:DE:298:LYS:HB3	31:DE:336:ILE:HD12	1.95	0.48
31:DE:558:ASP:O	31:DE:561:THR:HG22	2.12	0.48
32:DF:348:CYS:HA	32:DF:351:HIS:HB2	1.93	0.48
32:DF:399:HIS:HE1	32:DF:493:MET:HB3	1.79	0.48
33:DG:335:GLU:HB2	33:DG:387:ARG:HD3	1.94	0.48
50:F2:485:ASN:HB3	50:F2:534:TYR:HD2	1.78	0.48
52:F5:587:ARG:HA	52:F5:590:ARG:HD3	1.95	0.48
54:F7:424:LEU:HD11	54:F7:624:PRO:HB3	1.95	0.48
54:F7:633:GLU:O	54:F7:634:TRP:HD1	1.96	0.48
56:FN:37:GLN:HA	56:FN:63:ARG:O	2.12	0.48
2:CB:2:A:H5'	49:Da:43:PHE:CZ	2.48	0.48
5:CF:152:THR:OG1	19:Cb:109:GLY:O	2.30	0.48
5:CF:154:TRP:CZ3	53:F6:396:LEU:HB3	2.48	0.48
8:CJ:221:ALA:O	8:CJ:225:ASN:ND2	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CJ:463:MET:SD	22:Ci:85:PRO:HB2	2.53	0.48
24:Ck:184:LYS:HG2	24:Ck:228:LEU:HD21	1.93	0.48
29:DC:882:ASP:OD2	31:DE:47:TYR:OH	2.27	0.48
30:DD:462:LEU:HD11	30:DD:480:ALA:HB2	1.95	0.48
30:DD:794:ARG:NH2	59:FW:174:LYS:O	2.38	0.48
35:DI:166:LEU:HD22	35:DI:210:ILE:HD11	1.95	0.48
35:DI:297:ASP:OD2	35:DI:365:ARG:NH2	2.38	0.48
50:F2:30:PHE:HE2	50:F2:951:VAL:HG21	1.78	0.48
51:F3:714:TYR:HE1	51:F3:720:ILE:HD12	1.78	0.48
65:Ff:528:LEU:HB2	65:Ff:530:ARG:HE	1.78	0.48
68:Fi:561:PRO:HB2	68:Fi:570:ARG:HH22	1.78	0.48
69:IA:147:GLY:O	69:IA:481:TYR:OH	2.27	0.48
69:IA:261:HIS:HB3	69:IA:264:PHE:CD2	2.48	0.48
81:Ug:162:UNK:N	81:Ug:262:UNK:O	2.46	0.48
1:CA:33:A:H5'	14:CQ:33:ASN:HD21	1.78	0.48
1:CA:301:A:H3'	1:CA:302:U:H6	1.79	0.48
1:CA:430:U:OP2	1:CA:432:G:O2'	2.27	0.48
1:CA:438:U:OP1	42:DT:245:GLY:N	2.44	0.48
1:CA:512:G:O6	46:DX:165:HIS:N	2.45	0.48
6:CH:108:LEU:HD11	50:F2:261:MET:HG2	1.94	0.48
8:CJ:267:PHE:HB2	28:DB:1023:ARG:HH22	1.77	0.48
11:CN:38:ASP:HB3	11:CN:81:LEU:HG	1.95	0.48
13:CP:136:PRO:HD2	59:FW:137:PRO:HB2	1.95	0.48
28:DB:133:ALA:O	28:DB:137:VAL:HG23	2.14	0.48
28:DB:189:VAL:HG13	31:DE:471:ARG:HG2	1.95	0.48
29:DC:215:PRO:HB3	29:DC:256:ILE:HG21	1.96	0.48
32:DF:432:ILE:HD11	32:DF:439:THR:HA	1.95	0.48
32:DF:520:GLN:HB2	32:DF:525:ARG:HE	1.78	0.48
40:DP:73:LYS:HG2	40:DP:77:MET:HE2	1.96	0.48
51:F3:712:THR:O	51:F3:716:GLU:HG2	2.13	0.48
52:F5:77:VAL:O	52:F5:81:VAL:HG23	2.13	0.48
53:F6:210:GLN:NE2	53:F6:245:PRO:HG3	2.29	0.48
53:F6:235:GLU:OE1	53:F6:235:GLU:N	2.43	0.48
54:F7:593:PHE:HA	54:F7:596:VAL:HG12	1.96	0.48
59:FW:92:ARG:HH21	59:FW:101:PRO:HG2	1.78	0.48
1:CA:585:U:OP2	1:CA:587:A:O2'	2.32	0.48
8:CJ:797:LEU:HB3	22:Ci:98:HIS:HE1	1.79	0.48
9:CK:203:ASN:OD1	9:CK:204:THR:N	2.44	0.48
12:CO:271:PHE:CE2	14:CQ:173:GLU:HG3	2.49	0.48
12:CO:281:HIS:HB3	54:F7:634:TRP:HB2	1.94	0.48
18:Ca:163:ASP:HB3	18:Ca:166:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Cg:184:HIS:HA	21:Cg:296:HIS:CE1	2.48	0.48
24:Ck:108:GLN:OE1	32:DF:545:ASN:ND2	2.46	0.48
29:DC:1041:LEU:HD23	37:DK:48:VAL:HG21	1.95	0.48
31:DE:221:ILE:HD12	31:DE:405:ILE:HG21	1.95	0.48
33:DG:401:CYS:HB3	33:DG:457:ARG:HH21	1.79	0.48
39:DO:69:GLU:O	39:DO:72:GLU:HG2	2.13	0.48
52:F5:673:ALA:HA	52:F5:679:ARG:HG3	1.96	0.48
65:Ff:215:ASP:OD1	65:Ff:215:ASP:N	2.45	0.48
66:Fg:263:GLY:O	66:Fg:264:SER:OG	2.31	0.48
68:Fi:384:LEU:HG	68:Fi:395:THR:HG22	1.96	0.48
8:CJ:340:ARG:HH12	8:CJ:358:TRP:HD1	1.62	0.48
13:CP:174:THR:OG1	13:CP:177:GLU:OE1	2.21	0.48
18:Ca:259:GLU:HG3	50:F2:738:PRO:HB3	1.95	0.48
23:Cj:81:GLU:HA	23:Cj:84:ARG:HG2	1.96	0.48
28:DB:538:ARG:O	28:DB:542:GLN:HG2	2.14	0.48
29:DC:956:VAL:HG11	29:DC:1062:GLN:HG3	1.95	0.48
36:DJ:85:LYS:HD3	36:DJ:95:THR:HG21	1.95	0.48
40:DP:74:LYS:HG3	57:FO:258:LEU:HD21	1.94	0.48
55:F9:241:GLN:HG3	67:Fh:87:TYR:HD1	1.79	0.48
69:IA:635:SER:HB2	69:IA:722:GLU:HG2	1.94	0.48
9:CK:292:VAL:HA	9:CK:295:VAL:HG12	1.95	0.48
22:Ci:28:ALA:HB3	24:Ck:785:PRO:HA	1.95	0.48
29:DC:425:ALA:HB1	29:DC:447:ASN:HD22	1.79	0.48
29:DC:823:ILE:HG22	29:DC:850:PHE:HZ	1.78	0.48
29:DC:1013:GLU:N	29:DC:1013:GLU:OE1	2.47	0.48
30:DD:594:SER:O	30:DD:598:GLU:HG3	2.12	0.48
31:DE:73:VAL:HG13	31:DE:193:ILE:HG22	1.96	0.48
31:DE:243:PHE:HD2	31:DE:423:PHE:HZ	1.60	0.48
35:DI:83:GLN:HE21	35:DI:175:GLN:NE2	2.11	0.48
42:DT:147:ALA:O	42:DT:151:TRP:HD1	1.97	0.48
46:DX:71:PHE:HB2	46:DX:168:ASN:HB3	1.96	0.48
1:CA:151:U:O2'	1:CA:152:U:OP1	2.30	0.48
1:CA:177:A:OP1	20:Cd:10:ARG:N	2.46	0.48
7:CI:47:ARG:NH2	7:CI:48:ASP:OD1	2.46	0.48
11:CN:74:PHE:O	11:CN:78:GLN:HG2	2.13	0.48
23:Cj:79:PRO:HD2	40:DP:163:ARG:HH12	1.78	0.48
29:DC:970:GLN:HB3	31:DE:587:MET:HG2	1.95	0.48
36:DJ:231:ASP:HA	36:DJ:265:LYS:HE3	1.96	0.48
41:DR:187:PRO:O	41:DR:191:GLN:HG2	2.14	0.48
41:DR:210:SER:HA	41:DR:215:ARG:HD3	1.95	0.48
52:F5:99:ASP:OD1	52:F5:99:ASP:N	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:F7:100:ASP:OD2	54:F7:139:ARG:NH2	2.41	0.48
70:IB:675:LEU:HD12	70:IB:676:PRO:HD2	1.95	0.48
5:CF:2:VAL:HG13	5:CF:37:ARG:HD2	1.95	0.48
18:Ca:209:MET:HE1	48:DZ:80:TRP:HZ3	1.79	0.48
29:DC:276:LYS:HG3	29:DC:284:LEU:HB3	1.95	0.48
31:DE:332:ASP:O	31:DE:336:ILE:HG12	2.14	0.48
35:DI:19:ALA:N	35:DI:65:MET:O	2.47	0.48
42:DT:216:TYR:HA	42:DT:219:GLN:HG2	1.96	0.48
47:DY:153:PHE:HB3	47:DY:154:PRO:HD3	1.96	0.48
51:F3:256:GLN:HG3	51:F3:295:VAL:HG22	1.96	0.48
54:F7:214:HIS:CE1	54:F7:237:ARG:HH11	2.31	0.48
57:FO:306:ASN:OD1	57:FO:309:ARG:NH2	2.47	0.48
66:Fg:105:SER:HA	66:Fg:166:GLY:HA3	1.95	0.48
66:Fg:480:ALA:HB1	66:Fg:484:HIS:HD2	1.77	0.48
69:IA:310:CYS:HB2	69:IA:342:PHE:CZ	2.48	0.48
70:IB:767:GLU:HG2	70:IB:772:LYS:HD3	1.96	0.48
1:CA:19:U:H2'	18:Ca:354:THR:HB	1.96	0.48
1:CA:50:A:H5'	20:Cd:31:PHE:HE1	1.79	0.48
9:CK:196:TYR:HB2	9:CK:207:VAL:HG12	1.95	0.48
12:CO:216:PHE:CE1	20:Cd:124:ARG:HG2	2.49	0.48
14:CQ:91:GLY:O	14:CQ:159:TYR:OH	2.29	0.48
14:CQ:243:GLU:OE1	14:CQ:243:GLU:N	2.47	0.48
18:Ca:541:ARG:NH1	18:Ca:545:TRP:HE1	2.12	0.48
27:Cp:92:LEU:HD13	27:Cp:102:ARG:HB2	1.96	0.48
28:DB:505:ARG:NH2	28:DB:951:GLY:O	2.42	0.48
30:DD:448:ARG:HA	43:DU:155:GLN:HE22	1.78	0.48
30:DD:466:ARG:HB2	30:DD:476:LEU:HD11	1.96	0.48
31:DE:492:ASP:HA	31:DE:495:ARG:HD2	1.94	0.48
32:DF:153:LEU:HD11	32:DF:164:ILE:HD13	1.95	0.48
35:DI:117:VAL:O	35:DI:121:LYS:HG2	2.14	0.48
35:DI:329:CYS:SG	35:DI:339:VAL:HG21	2.53	0.48
47:DY:37:ARG:O	47:DY:41:GLN:HG2	2.14	0.48
55:F9:262:HIS:CD2	67:Fh:99:SER:H	2.31	0.48
56:FM:260:VAL:HB	56:FM:303:GLY:HA2	1.95	0.48
62:Fb:110:PRO:O	62:Fb:114:ALA:N	2.41	0.48
65:Ff:479:GLU:HB2	65:Ff:636:LEU:HD11	1.96	0.48
1:CA:444:A:OP1	1:CA:486:C:O2'	2.32	0.47
1:CA:520:A:N7	45:DW:122:ARG:NH1	2.62	0.47
30:DD:206:TRP:HE3	35:DI:61:ASN:HB3	1.78	0.47
30:DD:504:ASN:N	30:DD:504:ASN:OD1	2.46	0.47
35:DI:130:VAL:HG13	35:DI:142:ALA:HB1	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DI:366:LEU:HA	35:DI:370:GLN:HE21	1.80	0.47
51:F3:888:SER:O	51:F3:892:ARG:HG2	2.14	0.47
53:F6:132:ASP:OD1	53:F6:135:ARG:NH2	2.47	0.47
55:F9:489:ARG:O	55:F9:493:ARG:NE	2.47	0.47
56:FN:138:PRO:HB2	56:FN:154:MET:HE2	1.94	0.47
4:CE:60:TYR:CE2	4:CE:143:ASN:HB2	2.49	0.47
9:CK:189:THR:HB	9:CK:192:MET:HG3	1.96	0.47
18:Ca:347:ARG:HD2	30:DD:87:MET:HE3	1.96	0.47
18:Ca:410:MET:HE3	18:Ca:500:PHE:HA	1.96	0.47
18:Ca:460:GLU:OE1	18:Ca:492:TYR:OH	2.31	0.47
22:CI:126:GLY:HA3	42:DT:37:TYR:O	2.14	0.47
28:DB:179:VAL:HG23	28:DB:217:ILE:HD11	1.96	0.47
28:DB:371:ARG:O	28:DB:374:GLU:HG3	2.14	0.47
31:DE:160:GLY:O	31:DE:164:ARG:HG2	2.14	0.47
34:DH:455:TRP:CD1	34:DH:456:GLU:HG3	2.49	0.47
36:DJ:159:LEU:HD22	36:DJ:194:LEU:HD13	1.96	0.47
36:DJ:277:ARG:HH12	36:DJ:292:ASP:HA	1.79	0.47
37:DK:273:LEU:HD21	42:DT:99:HIS:CE1	2.49	0.47
38:DL:222:VAL:O	38:DL:225:SER:OG	2.26	0.47
50:F2:764:ASP:OD2	56:FM:63:ARG:NH2	2.43	0.47
52:F5:603:LEU:HD21	61:FZ:112:LEU:HD22	1.96	0.47
53:F6:213:PHE:HB2	53:F6:248:VAL:HG13	1.95	0.47
53:F6:381:LYS:O	53:F6:385:GLN:HG2	2.14	0.47
55:F9:347:ILE:HA	55:F9:350:ARG:HG2	1.96	0.47
59:FW:25:ILE:HG13	59:FW:55:MET:HE1	1.96	0.47
66:Fg:6:GLN:N	66:Fg:6:GLN:OE1	2.47	0.47
14:CQ:21:ARG:NE	43:DU:224:MET:SD	2.81	0.47
18:Ca:377:TRP:N	18:Ca:380:ASP:OD2	2.39	0.47
21:Cg:303:ASP:O	46:DX:106:LYS:NZ	2.47	0.47
24:Ck:43:GLY:N	24:Ck:93:THR:OG1	2.45	0.47
29:DC:330:ARG:O	29:DC:334:GLN:HG3	2.14	0.47
35:DI:77:GLU:OE2	35:DI:80:ARG:NH2	2.42	0.47
46:DX:97:VAL:HA	46:DX:100:ARG:HG2	1.95	0.47
53:F6:38:LEU:HD12	53:F6:41:TRP:NE1	2.28	0.47
55:F9:129:THR:O	55:F9:132:GLN:HG3	2.14	0.47
56:FM:260:VAL:HG13	56:FM:294:LEU:HD12	1.96	0.47
58:FP:44:ALA:HB1	58:FP:75:VAL:HG13	1.96	0.47
65:Ff:189:THR:OG1	65:Ff:302:ARG:NH2	2.39	0.47
67:Fh:104:SER:HA	67:Fh:111:ARG:HH21	1.78	0.47
68:Fi:111:ASN:ND2	68:Fi:244:CYS:O	2.47	0.47
1:CA:234:C:O5'	69:IA:130:ARG:NH1	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CR:179:TRP:O	15:CR:183:GLN:NE2	2.48	0.47
18:Ca:494:LYS:HE2	30:DD:105:GLY:HA2	1.96	0.47
19:Cb:55:PHE:HE2	38:DL:157:MET:HE1	1.80	0.47
21:Cg:90:PRO:HG3	21:Cg:214:ALA:HB2	1.96	0.47
28:DB:248:ASP:HB3	28:DB:378:ARG:HH22	1.80	0.47
30:DD:244:PRO:HG3	30:DD:326:PRO:HD3	1.96	0.47
31:DE:574:ALA:O	31:DE:577:THR:OG1	2.32	0.47
32:DF:325:LEU:HD11	32:DF:486:LEU:HG	1.97	0.47
32:DF:387:VAL:HG12	32:DF:472:ARG:HH22	1.79	0.47
33:DG:71:ASN:OD1	33:DG:101:THR:HB	2.15	0.47
33:DG:308:ARG:HD3	33:DG:342:ASN:HD21	1.79	0.47
47:DY:21:PRO:O	47:DY:25:ILE:HG12	2.14	0.47
50:F2:631:ARG:HA	50:F2:634:MET:HE2	1.96	0.47
54:F7:12:ALA:HB2	54:F7:334:GLU:HB2	1.95	0.47
58:FP:142:HIS:O	58:FP:146:ILE:HG12	2.14	0.47
64:Fd:34:GLU:HB3	64:Fd:37:VAL:HG12	1.96	0.47
65:Ff:567:ARG:HG3	70:IB:503:ARG:HB3	1.96	0.47
68:Fi:482:GLN:NE2	68:Fi:500:GLY:H	2.13	0.47
1:CA:184:A:H5'	27:Cp:89:LYS:HB2	1.95	0.47
6:CH:49:GLU:O	6:CH:53:ARG:HG2	2.14	0.47
8:CJ:325:SER:HA	8:CJ:328:ARG:HE	1.80	0.47
9:CK:304:VAL:HG21	17:CU:54:ILE:HD13	1.97	0.47
28:DB:316:ARG:HH21	31:DE:511:LEU:HD11	1.80	0.47
28:DB:396:ARG:HH22	28:DB:405:GLU:HB3	1.78	0.47
34:DH:99:GLN:HA	34:DH:134:PRO:HD2	1.96	0.47
34:DH:460:LEU:O	34:DH:464:LEU:HB2	2.15	0.47
35:DI:349:THR:HG23	35:DI:350:TYR:HD2	1.79	0.47
37:DK:16:ARG:HA	37:DK:16:ARG:HH11	1.80	0.47
50:F2:722:LEU:HD23	50:F2:725:MET:HE3	1.97	0.47
51:F3:163:ASP:OD1	51:F3:164:TYR:N	2.47	0.47
53:F6:590:TRP:O	65:Ff:729:TYR:OH	2.27	0.47
65:Ff:406:GLY:HA3	65:Ff:409:TRP:CD1	2.41	0.47
65:Ff:736:LEU:HG	65:Ff:740:MET:SD	2.54	0.47
68:Fi:87:PRO:HB3	68:Fi:382:ARG:HD2	1.96	0.47
68:Fi:262:PRO:HA	68:Fi:294:ARG:HG2	1.97	0.47
69:IA:238:GLN:OE1	69:IA:571:TYR:OH	2.30	0.47
70:IB:535:LEU:HG	70:IB:573:ALA:HB2	1.95	0.47
1:CA:293:A:H5'	15:CR:167:ARG:HH11	1.79	0.47
6:CH:267:HIS:O	6:CH:271:GLU:HG2	2.14	0.47
8:CJ:143:TYR:HE2	44:DV:130:PRO:HG2	1.78	0.47
9:CK:280:ARG:HE	9:CK:310:ILE:HD11	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CQ:131:PHE:HB3	14:CQ:157:LYS:HG2	1.95	0.47
16:CS:55:ARG:HD3	16:CS:56:PRO:HD2	1.97	0.47
18:Ca:350:GLU:HB3	30:DD:106:ALA:O	2.15	0.47
29:DC:155:VAL:HA	29:DC:158:TYR:HD1	1.80	0.47
30:DD:116:GLN:HG3	30:DD:694:ARG:HG2	1.95	0.47
30:DD:646:ILE:HB	30:DD:648:VAL:HG12	1.97	0.47
35:DI:111:THR:HG21	35:DI:125:TRP:CH2	2.49	0.47
41:DR:91:THR:O	41:DR:178:TYR:OH	2.25	0.47
45:DW:54:GLU:OE1	45:DW:54:GLU:N	2.42	0.47
50:F2:424:SER:H	50:F2:427:HIS:CD2	2.33	0.47
55:F9:499:MET:HG3	67:Fh:279:LEU:HD21	1.96	0.47
57:FO:78:ASN:ND2	66:Fg:335:THR:HG22	2.29	0.47
58:FP:145:CYS:HB3	58:FP:303:LEU:HD23	1.97	0.47
64:Fd:59:HIS:O	64:Fd:63:ASN:ND2	2.48	0.47
6:CH:27:LEU:HD23	12:CO:269:VAL:HG12	1.97	0.47
8:CJ:227:ARG:NH1	24:Ck:749:ASP:OD2	2.46	0.47
9:CK:216:ILE:HD13	9:CK:258:LEU:HD13	1.96	0.47
14:CQ:231:GLN:HG2	26:Cn:186:LYS:HD3	1.97	0.47
18:Ca:283:PRO:HD2	18:Ca:286:ARG:HB3	1.97	0.47
24:Ck:258:LEU:HD21	24:Ck:597:LEU:HD11	1.96	0.47
28:DB:248:ASP:HB3	28:DB:378:ARG:NH2	2.30	0.47
28:DB:554:GLU:OE2	28:DB:879:ARG:NH2	2.47	0.47
29:DC:61:ILE:HB	29:DC:536:SER:HB2	1.96	0.47
29:DC:148:LEU:HD21	29:DC:514:LEU:HD23	1.96	0.47
29:DC:642:ALA:HA	29:DC:647:SER:HB2	1.97	0.47
29:DC:970:GLN:OE1	29:DC:970:GLN:N	2.46	0.47
31:DE:201:PHE:HD2	31:DE:202:HIS:HD2	1.62	0.47
31:DE:545:ARG:O	31:DE:549:LYS:HG2	2.15	0.47
32:DF:325:LEU:HD12	32:DF:482:TRP:HA	1.97	0.47
32:DF:341:VAL:HG22	32:DF:346:LEU:HD11	1.96	0.47
33:DG:214:TYR:CE2	33:DG:227:GLU:HG3	2.49	0.47
33:DG:561:PRO:O	33:DG:622:ARG:NH2	2.48	0.47
42:DT:87:ARG:O	42:DT:102:TRP:NE1	2.38	0.47
53:F6:142:SER:O	53:F6:145:GLU:HG3	2.14	0.47
55:F9:551:LYS:H	55:F9:551:LYS:HD2	1.79	0.47
56:FN:146:CYS:HB3	56:FN:151:LEU:HD21	1.95	0.47
66:Fg:232:ILE:HG12	66:Fg:516:MET:HB3	1.95	0.47
67:Fh:281:ILE:HG13	67:Fh:282:HIS:H	1.80	0.47
69:IA:134:MET:SD	69:IA:140:GLN:NE2	2.87	0.47
69:IA:154:LEU:HD13	69:IA:471:VAL:HG12	1.96	0.47
69:IA:376:ARG:NH1	69:IA:453:LEU:HB3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CK:228:LYS:HB2	9:CK:228:LYS:HZ2	1.79	0.47
18:Ca:270:GLU:OE2	18:Ca:291:TYR:OH	2.25	0.47
28:DB:450:MET:HA	28:DB:453:GLU:HG2	1.97	0.47
30:DD:216:LEU:HB3	30:DD:297:ARG:HB3	1.97	0.47
30:DD:300:GLN:HB3	30:DD:399:ILE:HG13	1.96	0.47
30:DD:522:THR:HB	30:DD:524:LYS:HE2	1.96	0.47
31:DE:92:THR:HA	31:DE:95:ASP:OD2	2.14	0.47
34:DH:100:HIS:CE1	34:DH:135:ARG:HG2	2.50	0.47
36:DJ:251:TYR:CE2	36:DJ:255:LYS:HD2	2.50	0.47
42:DT:111:ALA:HB1	42:DT:119:PHE:HE2	1.80	0.47
53:F6:256:ASP:OD1	53:F6:256:ASP:N	2.46	0.47
55:F9:374:LEU:HB3	55:F9:378:LYS:HE3	1.96	0.47
57:FO:102:ILE:HG13	57:FO:288:VAL:HG13	1.96	0.47
67:Fh:65:GLY:H	70:IB:754:ARG:HD2	1.80	0.47
1:CA:246:U:H4'	1:CA:247:A:H4'	1.97	0.47
1:CA:292:U:H2'	1:CA:293:A:H8	1.80	0.47
5:CF:15:ARG:HH12	20:Cd:165:ASP:HB3	1.80	0.47
8:CJ:273:ARG:HB2	8:CJ:341:CYS:SG	2.55	0.47
10:CL:55:PHE:HE1	10:CL:57:CYS:HB3	1.80	0.47
14:CQ:76:TRP:HB3	14:CQ:114:MET:HB3	1.96	0.47
14:CQ:83:LEU:HD11	30:DD:729:GLU:HB2	1.96	0.47
18:Ca:157:LYS:HE3	61:FZ:53:HIS:HB3	1.96	0.47
23:Cj:132:LEU:HD11	23:Cj:135:ILE:HG23	1.97	0.47
31:DE:63:LYS:O	31:DE:66:THR:OG1	2.33	0.47
42:DT:223:LEU:HD22	42:DT:228:LEU:HB3	1.97	0.47
44:DV:31:HIS:HB2	44:DV:86:VAL:HG21	1.97	0.47
45:DW:40:LYS:HD2	45:DW:41:PRO:HD2	1.96	0.47
45:DW:70:LEU:HA	47:DY:117:LEU:HD21	1.96	0.47
54:F7:640:ASP:HA	54:F7:645:ARG:HG3	1.97	0.47
66:Fg:153:LEU:HD21	66:Fg:379:LEU:HD23	1.97	0.47
12:CO:283:VAL:HB	12:CO:286:ILE:HB	1.97	0.47
16:CS:110:HIS:HD2	32:DF:91:TYR:HB2	1.80	0.47
28:DB:689:LEU:HD13	28:DB:689:LEU:HA	1.79	0.47
29:DC:1073:ALA:HB2	31:DE:576:HIS:CE1	2.50	0.47
33:DG:570:LEU:HD12	33:DG:611:LEU:HD23	1.97	0.47
35:DI:88:GLN:NE2	35:DI:92:GLU:OE2	2.38	0.47
36:DJ:136:ALA:HB3	36:DJ:168:TYR:CZ	2.50	0.47
39:DO:70:ILE:HG13	39:DO:116:ALA:HB1	1.97	0.47
40:DP:39:ASP:N	40:DP:39:ASP:OD1	2.46	0.47
45:DW:44:ASN:HD21	47:DY:17:VAL:HA	1.80	0.47
45:DW:137:PRO:HA	45:DW:140:TRP:CD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DX:99:MET:HA	46:DX:103:MET:HG2	1.97	0.47
52:F5:179:SER:O	52:F5:182:ASP:OD1	2.33	0.47
52:F5:347:ILE:HD11	52:F5:468:ARG:HA	1.97	0.47
52:F5:583:ARG:HG2	61:FZ:87:ASP:HA	1.96	0.47
52:F5:598:SER:O	52:F5:601:GLU:HG2	2.14	0.47
54:F7:502:GLN:HE21	54:F7:617:ILE:HD12	1.80	0.47
56:FN:159:ALA:O	56:FN:163:GLN:HG2	2.14	0.47
64:Fd:66:HIS:CD2	64:Fd:67:MET:HG3	2.50	0.47
67:Fh:102:ARG:NE	67:Fh:104:SER:OG	2.44	0.47
67:Fh:293:LYS:HE2	67:Fh:295:ASN:HD21	1.80	0.47
69:IA:211:HIS:HB3	69:IA:214:HIS:CD2	2.49	0.47
69:IA:499:ASP:N	69:IA:499:ASP:OD1	2.48	0.47
1:CA:584:G:O2'	26:Cn:167:ARG:NH1	2.28	0.46
3:CC:62:ILE:HG12	3:CC:70:ILE:HG12	1.96	0.46
7:CI:218:ARG:NH1	50:F2:55:VAL:O	2.47	0.46
8:CJ:83:HIS:ND1	8:CJ:83:HIS:O	2.48	0.46
8:CJ:246:LYS:HB2	8:CJ:432:HIS:HB2	1.96	0.46
18:Ca:368:ARG:O	18:Ca:372:SER:OG	2.28	0.46
28:DB:981:HIS:HD2	28:DB:983:LEU:HB2	1.80	0.46
29:DC:446:PHE:HZ	29:DC:493:TYR:HD2	1.63	0.46
29:DC:786:ARG:HG2	29:DC:812:SER:HA	1.97	0.46
31:DE:306:VAL:HG12	31:DE:535:PRO:HD3	1.97	0.46
32:DF:541:PHE:HB2	34:DH:260:GLU:HB3	1.98	0.46
35:DI:340:ARG:HB3	35:DI:404:TRP:HB3	1.97	0.46
45:DW:111:LYS:HD2	53:F6:598:TYR:HE1	1.79	0.46
51:F3:704:TYR:CE2	51:F3:706:ALA:HB3	2.50	0.46
56:FN:258:VAL:HG22	56:FN:307:LEU:HD11	1.96	0.46
57:FO:70:MET:HG3	57:FO:75:VAL:HB	1.96	0.46
64:Fd:47:LEU:HG	64:Fd:55:ALA:HB2	1.97	0.46
65:Ff:733:PRO:HA	65:Ff:736:LEU:HD13	1.97	0.46
66:Fg:381:ASP:N	66:Fg:381:ASP:OD1	2.45	0.46
69:IA:376:ARG:HH12	69:IA:453:LEU:HD22	1.80	0.46
70:IB:458:LEU:HD12	70:IB:481:ILE:HG22	1.97	0.46
7:CI:187:ALA:HB3	7:CI:220:THR:HG21	1.98	0.46
7:CI:320:THR:OG1	8:CJ:110:LYS:NZ	2.48	0.46
8:CJ:788:LEU:HD22	16:CS:53:LEU:HD11	1.96	0.46
11:CN:108:VAL:HG21	11:CN:118:MET:HG2	1.96	0.46
18:Ca:197:HIS:CD2	18:Ca:201:ARG:HD2	2.51	0.46
21:Cg:28:ALA:HB3	21:Cg:33:TRP:HD1	1.80	0.46
23:Cj:167:ASP:N	23:Cj:167:ASP:OD1	2.48	0.46
28:DB:144:ASP:OD1	31:DE:545:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DB:187:GLU:HG3	28:DB:705:LYS:HB2	1.97	0.46
28:DB:881:ARG:HB2	28:DB:935:ASP:HB3	1.97	0.46
29:DC:152:ARG:NH2	29:DC:184:PHE:H	2.13	0.46
30:DD:229:MET:O	30:DD:233:ASN:ND2	2.32	0.46
32:DF:238:THR:HG21	32:DF:270:VAL:HG13	1.97	0.46
33:DG:385:VAL:HG11	33:DG:464:VAL:HG11	1.96	0.46
55:F9:20:ARG:HA	55:F9:23:GLU:HG3	1.96	0.46
56:FN:38:ILE:HG21	56:FN:49:VAL:HG21	1.97	0.46
69:IA:372:PRO:HD2	69:IA:399:CYS:HB2	1.96	0.46
69:IA:606:VAL:HG21	69:IA:743:VAL:HA	1.96	0.46
1:CA:2:A:N6	50:F2:207:ASP:OD1	2.43	0.46
3:CC:55:LYS:HE2	3:CC:55:LYS:HB3	1.61	0.46
4:CE:360:LEU:HD13	60:FX:195:PRO:HB3	1.97	0.46
4:CE:389:LYS:O	4:CE:394:ARG:NH2	2.48	0.46
10:CL:60:GLY:O	55:F9:526:ASN:ND2	2.47	0.46
12:CO:86:PRO:HG2	12:CO:90:MET:HB2	1.98	0.46
16:CS:51:PRO:HG2	16:CS:54:ARG:HB2	1.97	0.46
23:Cj:149:TYR:CZ	23:Cj:160:PRO:HG3	2.49	0.46
28:DB:747:SER:HA	28:DB:754:VAL:HB	1.95	0.46
31:DE:491:GLN:HB3	31:DE:495:ARG:HH21	1.81	0.46
32:DF:215:LEU:HD23	32:DF:215:LEU:H	1.80	0.46
35:DI:292:TYR:CE1	35:DI:294:ASN:HB2	2.50	0.46
51:F3:354:ASP:OD1	51:F3:358:ALA:N	2.47	0.46
51:F3:644:MET:HG3	51:F3:648:VAL:HA	1.97	0.46
52:F5:481:CYS:O	52:F5:484:GLU:HG3	2.15	0.46
55:F9:329:LEU:HA	55:F9:332:ASN:HD21	1.78	0.46
64:Fd:24:HIS:HB3	64:Fd:32:ARG:CZ	2.46	0.46
66:Fg:310:ARG:HE	66:Fg:310:ARG:H	1.61	0.46
66:Fg:365:ARG:NH1	66:Fg:483:ALA:O	2.48	0.46
68:Fi:311:ARG:HD2	68:Fi:314:MET:HE2	1.97	0.46
69:IA:700:ARG:HB2	69:IA:705:LEU:HD23	1.97	0.46
1:CA:119:A:H4'	12:CO:352:ASN:HB2	1.98	0.46
1:CA:449:G:H2'	1:CA:450:A:C8	2.51	0.46
1:CA:504:U:O2	44:DV:58:ALA:HB1	2.15	0.46
21:Cg:77:MET:HE2	21:Cg:412:PHE:HA	1.98	0.46
21:Cg:439:ARG:HB2	21:Cg:470:GLN:HE22	1.80	0.46
28:DB:280:PHE:CZ	28:DB:282:GLY:HA2	2.50	0.46
28:DB:350:GLU:OE2	31:DE:557:TYR:OH	2.16	0.46
29:DC:30:THR:HB	29:DC:31:PRO:HD3	1.97	0.46
29:DC:71:TRP:HB2	29:DC:540:LEU:HD11	1.97	0.46
29:DC:1110:HIS:N	29:DC:1125:SER:OG	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DF:367:PRO:HB3	36:DJ:110:LEU:HA	1.96	0.46
39:DO:193:LEU:HD13	39:DO:234:LEU:HD23	1.96	0.46
41:DR:16:ASN:ND2	43:DU:53:LEU:O	2.42	0.46
42:DT:69:ASP:N	42:DT:69:ASP:OD1	2.48	0.46
42:DT:197:VAL:HG12	42:DT:204:LYS:HG2	1.97	0.46
50:F2:107:PRO:HB3	50:F2:185:GLU:HG2	1.98	0.46
51:F3:297:PHE:HB2	51:F3:314:THR:HG23	1.98	0.46
58:FP:328:ASP:OD1	58:FP:328:ASP:N	2.49	0.46
66:Fg:228:VAL:HG12	66:Fg:229:ASN:HD22	1.80	0.46
8:CJ:423:LEU:HD11	8:CJ:429:CYS:SG	2.56	0.46
18:Ca:370:GLU:HB2	50:F2:588:THR:HG21	1.97	0.46
19:Cb:57:MET:HG3	50:F2:380:LYS:HB2	1.97	0.46
20:Cd:91:TRP:HB3	30:DD:270:TRP:CE2	2.50	0.46
29:DC:86:THR:HB	29:DC:959:VAL:HG21	1.96	0.46
29:DC:470:SER:OG	37:DK:285:GLU:OE2	2.34	0.46
31:DE:144:PRO:HD2	31:DE:147:MET:HB2	1.98	0.46
31:DE:703:GLN:OE1	34:DH:232:ARG:NH2	2.47	0.46
33:DG:164:LEU:HD23	33:DG:202:LEU:HD11	1.97	0.46
37:DK:280:PHE:HE2	42:DT:102:TRP:HB2	1.79	0.46
52:F5:247:ARG:NH1	61:FZ:126:CYS:SG	2.89	0.46
52:F5:614:MET:O	52:F5:617:ARG:HG2	2.15	0.46
54:F7:570:ASN:ND2	54:F7:614:ASP:OD1	2.49	0.46
55:F9:272:MET:HA	55:F9:272:MET:HE2	1.98	0.46
56:FM:108:ILE:HG21	56:FM:165:MET:HE3	1.97	0.46
56:FN:274:LEU:HD21	56:FN:284:PHE:HE2	1.80	0.46
59:FW:50:LEU:HD21	59:FW:218:HIS:CE1	2.50	0.46
60:FX:132:LEU:HD11	60:FX:168:HIS:CD2	2.50	0.46
66:Fg:51:GLN:NE2	69:IA:230:SER:O	2.48	0.46
69:IA:348:ARG:NH2	88:IA:1000:GDP:O2'	2.49	0.46
70:IB:634:LYS:HB2	70:IB:639:GLU:HB3	1.98	0.46
14:CQ:210:LEU:O	14:CQ:214:ILE:HG12	2.15	0.46
28:DB:138:TRP:CD2	28:DB:225:PRO:HB3	2.51	0.46
33:DG:173:MET:HE2	33:DG:210:VAL:HG22	1.97	0.46
37:DK:97:ASP:N	37:DK:97:ASP:OD1	2.48	0.46
43:DU:99:GLN:HG2	43:DU:127:LEU:HD21	1.98	0.46
49:Da:25:ARG:O	49:Da:28:ARG:HG2	2.16	0.46
52:F5:309:LEU:HD22	52:F5:582:ALA:HB2	1.98	0.46
54:F7:518:SER:HA	54:F7:521:LYS:HE2	1.98	0.46
56:FM:264:LEU:HD21	56:FM:294:LEU:HB3	1.97	0.46
56:FN:48:ARG:HA	56:FN:51:ASP:OD2	2.16	0.46
65:Ff:215:ASP:HA	65:Ff:538:GLY:HA3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:IA:589:ILE:HG22	69:IA:591:PHE:HD1	1.80	0.46
12:CO:144:ARG:HD3	20:Cd:144:ASN:HB2	1.98	0.46
15:CR:148:LEU:HB2	15:CR:149:PRO:HD3	1.97	0.46
24:Ck:279:PHE:HE1	24:Ck:307:MET:HE1	1.80	0.46
31:DE:311:VAL:O	31:DE:315:HIS:HB3	2.16	0.46
38:DL:122:TRP:NE1	38:DL:216:GLU:OE1	2.48	0.46
40:DP:46:LEU:HD11	57:FO:188:SER:HB2	1.97	0.46
45:DW:111:LYS:HB3	53:F6:598:TYR:HD1	1.80	0.46
65:Ff:617:TRP:CE2	65:Ff:652:LEU:HB2	2.51	0.46
65:Ff:781:TRP:NE1	65:Ff:791:GLY:H	2.14	0.46
70:IB:177:VAL:HG13	70:IB:181:ASP:HB3	1.97	0.46
1:CA:565:A:OP2	66:Fg:310:ARG:NH1	2.48	0.46
3:CC:74:THR:HG23	34:DH:440:VAL:HG12	1.97	0.46
7:CI:126:TRP:CD1	7:CI:148:LEU:HD13	2.51	0.46
18:Ca:279:PRO:HB2	18:Ca:379:MET:HE2	1.97	0.46
18:Ca:359:ARG:NH2	50:F2:599:GLU:OE1	2.48	0.46
20:Cd:157:ARG:HA	20:Cd:160:ILE:HG12	1.98	0.46
24:Ck:82:THR:OG1	24:Ck:88:ASP:OD2	2.25	0.46
28:DB:227:THR:O	28:DB:228:THR:OG1	2.27	0.46
29:DC:155:VAL:HA	29:DC:158:TYR:CD1	2.51	0.46
30:DD:300:GLN:OE1	30:DD:395:GLU:HB3	2.15	0.46
33:DG:46:TRP:CE2	33:DG:93:ARG:HG3	2.50	0.46
33:DG:240:HIS:CG	33:DG:241:PRO:HD2	2.51	0.46
34:DH:119:LEU:HD11	34:DH:127:LEU:HD12	1.98	0.46
38:DL:34:ILE:HD11	70:IB:771:LEU:HD21	1.98	0.46
40:DP:119:LEU:HD23	40:DP:131:ALA:HB1	1.98	0.46
42:DT:133:ASP:HA	42:DT:158:HIS:HB2	1.98	0.46
44:DV:149:ASP:OD1	44:DV:149:ASP:N	2.48	0.46
50:F2:209:LEU:HA	50:F2:212:VAL:HG12	1.97	0.46
51:F3:162:PRO:HD2	51:F3:171:LEU:HD22	1.98	0.46
54:F7:141:ALA:O	54:F7:645:ARG:NH1	2.48	0.46
54:F7:549:ASN:N	54:F7:549:ASN:OD1	2.47	0.46
56:FM:292:ARG:CZ	56:FM:321:LEU:HD22	2.46	0.46
57:FO:50:VAL:O	57:FO:54:GLN:HG2	2.16	0.46
65:Ff:250:PHE:HA	65:Ff:262:GLN:HB2	1.97	0.46
68:Fi:288:GLN:HG2	68:Fi:290:SER:H	1.80	0.46
68:Fi:386:LEU:HD12	68:Fi:392:PRO:HD2	1.98	0.46
68:Fi:474:PRO:HB3	68:Fi:506:PHE:CZ	2.51	0.46
70:IB:635:LYS:HE3	70:IB:637:PRO:HD2	1.97	0.46
8:CJ:256:HIS:NE2	36:DJ:32:TYR:O	2.38	0.46
8:CJ:793:HIS:ND1	8:CJ:794:GLU:HG2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CR:69:HIS:CE1	15:CR:72:PRO:HA	2.51	0.46
19:Cb:63:HIS:NE2	38:DL:168:SER:O	2.30	0.46
19:Cb:106:ALA:HA	19:Cb:110:MET:HB2	1.98	0.46
21:Cg:319:ASP:OD2	28:DB:1138:HIS:NE2	2.40	0.46
28:DB:154:ARG:HG3	31:DE:216:LEU:HG	1.97	0.46
28:DB:189:VAL:O	28:DB:194:GLN:NE2	2.49	0.46
28:DB:358:ASN:OD1	28:DB:361:ARG:NH2	2.49	0.46
29:DC:148:LEU:O	29:DC:152:ARG:HG2	2.16	0.46
31:DE:463:LEU:HG	31:DE:467:MET:HE3	1.98	0.46
31:DE:581:THR:H	31:DE:585:ARG:HB2	1.81	0.46
34:DH:288:HIS:ND1	34:DH:293:GLN:OE1	2.45	0.46
35:DI:18:HIS:CD2	35:DI:65:MET:HE3	2.51	0.46
36:DJ:53:GLN:HE22	36:DJ:232:ARG:NH2	2.14	0.46
37:DK:123:GLU:HG2	37:DK:127:HIS:CE1	2.51	0.46
52:F5:633:LEU:O	52:F5:637:GLU:HG2	2.15	0.46
54:F7:387:HIS:CE1	54:F7:421:LEU:HB2	2.51	0.46
55:F9:275:GLU:HG2	69:IA:478:ARG:HH21	1.81	0.46
55:F9:379:SER:O	55:F9:380:ASP:C	2.58	0.46
56:FM:253:PRO:HD2	56:FM:302:MET:HE2	1.98	0.46
57:FO:298:TRP:CH2	67:Fh:298:LEU:HB3	2.51	0.46
61:FZ:66:ALA:HA	61:FZ:69:ASN:ND2	2.31	0.46
66:Fg:417:ASN:HB3	66:Fg:486:VAL:HG22	1.98	0.46
67:Fh:122:ARG:HG2	67:Fh:134:LYS:HG2	1.97	0.46
70:IB:633:ASP:OD1	70:IB:634:LYS:NZ	2.49	0.46
1:CA:162:U:H4'	40:DP:18:TYR:CD1	2.51	0.46
20:Cd:128:GLU:OE1	39:DO:190:TYR:OH	2.31	0.46
20:Cd:174:PRO:HD3	53:F6:394:GLN:HG2	1.97	0.46
29:DC:598:ASP:HB3	29:DC:601:GLU:HG3	1.98	0.46
31:DE:311:VAL:HA	31:DE:324:LEU:HD21	1.98	0.46
32:DF:523:LEU:HD11	32:DF:585:TYR:HE1	1.81	0.46
50:F2:579:HIS:CD2	50:F2:590:ARG:HD2	2.51	0.46
51:F3:887:ALA:H	51:F3:892:ARG:HH21	1.62	0.46
54:F7:229:GLU:OE1	54:F7:229:GLU:N	2.47	0.46
56:FM:72:THR:O	56:FM:107:GLN:NE2	2.49	0.46
57:FO:246:ASP:OD1	57:FO:246:ASP:N	2.49	0.46
65:Ff:625:PRO:HD2	65:Ff:731:HIS:HA	1.98	0.46
66:Fg:45:LYS:NZ	66:Fg:160:ASP:OD2	2.43	0.46
8:CJ:758:TRP:CG	8:CJ:759:PRO:HA	2.51	0.45
11:CN:70:LYS:HE2	28:DB:1107:THR:HG23	1.98	0.45
12:CO:101:GLY:HA2	12:CO:105:ASN:HB2	1.98	0.45
13:CP:156:GLU:HG3	30:DD:637:ARG:CZ	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CQ:67:LEU:HG	30:DD:708:TRP:HH2	1.81	0.45
16:CS:124:SER:HB3	32:DF:76:GLU:HB2	1.98	0.45
24:Ck:218:ILE:HG23	24:Ck:239:LEU:HD12	1.98	0.45
28:DB:337:TYR:O	31:DE:38:GLN:NE2	2.49	0.45
28:DB:763:GLU:O	28:DB:767:GLU:HG2	2.16	0.45
29:DC:688:LYS:HG2	29:DC:691:GLN:HE21	1.80	0.45
31:DE:652:GLU:HG3	31:DE:655:ARG:HH21	1.82	0.45
33:DG:563:PHE:HD1	33:DG:623:MET:HG2	1.80	0.45
52:F5:108:MET:HE1	52:F5:119:THR:HB	1.98	0.45
53:F6:217:LEU:HD21	53:F6:250:ASN:HB3	1.98	0.45
65:Ff:602:ASP:OD1	65:Ff:602:ASP:N	2.49	0.45
69:IA:568:ILE:HG23	69:IA:588:VAL:HA	1.98	0.45
1:CA:60:A:N3	1:CA:154:G:H2'	2.31	0.45
4:CE:158:ASP:HB2	67:Fh:59:ASN:HB3	1.98	0.45
5:CF:87:GLN:HA	64:Fd:30:ARG:HE	1.81	0.45
7:CI:241:ARG:HH12	8:CJ:60:LEU:HD13	1.80	0.45
7:CI:245:ARG:HH12	33:DG:50:LEU:HB3	1.80	0.45
9:CK:252:ASN:HA	53:F6:570:ARG:HH12	1.80	0.45
12:CO:123:ASN:OD1	12:CO:123:ASN:N	2.46	0.45
24:Ck:682:ASN:HA	24:Ck:686:LYS:HD2	1.98	0.45
28:DB:1035:ARG:HD2	34:DH:450:ASN:ND2	2.31	0.45
30:DD:763:TYR:OH	60:FX:11:PHE:O	2.24	0.45
45:DW:55:TRP:HA	45:DW:55:TRP:CE3	2.52	0.45
45:DW:155:ARG:HD3	45:DW:161:TYR:CE2	2.52	0.45
51:F3:379:CYS:C	51:F3:381:ASP:H	2.24	0.45
53:F6:300:LEU:O	53:F6:303:GLU:HG3	2.16	0.45
57:FO:150:GLN:OE1	57:FO:150:GLN:N	2.47	0.45
59:FW:87:ASP:CG	59:FW:93:ARG:HH22	2.24	0.45
70:IB:358:ASN:HD22	70:IB:361:ARG:HH21	1.64	0.45
1:CA:443:U:O2'	11:CN:20:ARG:NH2	2.49	0.45
10:CL:42:PHE:CE1	10:CL:49:TRP:HB2	2.51	0.45
18:Ca:232:GLN:OE1	61:FZ:47:ASN:ND2	2.49	0.45
20:Cd:41:LYS:HE2	20:Cd:45:LEU:HD21	1.99	0.45
21:Cg:61:PRO:HG2	21:Cg:79:CYS:SG	2.56	0.45
25:Cm:103:LEU:O	25:Cm:107:MET:HG2	2.17	0.45
29:DC:487:ALA:HB2	29:DC:524:GLU:HG2	1.98	0.45
29:DC:1120:PRO:HD2	29:DC:1123:SER:HB2	1.99	0.45
30:DD:347:GLU:OE2	41:DR:25:TYR:N	2.47	0.45
34:DH:89:VAL:HA	34:DH:92:ASP:OD2	2.16	0.45
50:F2:746:LEU:HD23	50:F2:750:ARG:HH21	1.79	0.45
51:F3:168:ASP:OD1	51:F3:172:ARG:NE	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:FM:129:ARG:HH21	56:FM:130:ARG:HH12	1.64	0.45
65:Ff:317:GLN:HB3	65:Ff:322:GLU:HB3	1.98	0.45
1:CA:292:U:H2'	1:CA:293:A:C8	2.52	0.45
5:CF:52:ARG:HD2	5:CF:57:THR:O	2.16	0.45
8:CJ:140:ARG:HB3	8:CJ:218:TYR:CE1	2.51	0.45
15:CR:123:LYS:HG3	15:CR:128:ASN:ND2	2.32	0.45
18:Ca:450:ASN:ND2	30:DD:693:ASP:H	2.14	0.45
22:Ci:125:HIS:CD2	34:DH:9:THR:HG1	2.32	0.45
24:Ck:754:GLU:HG2	28:DB:1086:HIS:HB2	1.98	0.45
31:DE:62:GLU:HA	31:DE:65:ILE:HG12	1.97	0.45
33:DG:445:LEU:HD22	33:DG:531:ASP:HB2	1.98	0.45
35:DI:196:PHE:HE2	35:DI:198:ASP:HB3	1.81	0.45
36:DJ:294:MET:HE3	36:DJ:297:HIS:HB3	1.99	0.45
50:F2:559:MET:HE3	50:F2:567:PRO:HG3	1.99	0.45
52:F5:72:GLU:O	52:F5:76:ARG:HG2	2.16	0.45
52:F5:108:MET:HA	52:F5:111:VAL:HG12	1.99	0.45
66:Fg:348:SER:HA	66:Fg:351:ILE:HD11	1.98	0.45
70:IB:514:PHE:HB3	70:IB:544:LEU:HD23	1.99	0.45
1:CA:517:U:H4'	47:DY:145:ARG:HD3	1.97	0.45
8:CJ:44:PHE:HB3	38:DL:283:ILE:O	2.17	0.45
8:CJ:702:ASN:OD1	28:DB:1129:GLN:NE2	2.38	0.45
8:CJ:709:GLU:OE2	28:DB:1132:ARG:N	2.42	0.45
14:CQ:193:ARG:HG2	54:F7:91:LYS:HD2	1.98	0.45
18:Ca:466:GLU:OE2	18:Ca:533:ARG:NH2	2.42	0.45
21:Cg:140:ASN:HB2	44:DV:178:THR:HG22	1.99	0.45
28:DB:258:THR:HG22	34:DH:459:PRO:HB3	1.99	0.45
28:DB:627:HIS:HD2	28:DB:631:LEU:HD21	1.82	0.45
29:DC:305:ARG:NH2	29:DC:352:GLU:HA	2.32	0.45
29:DC:581:GLU:HB2	29:DC:623:LYS:HE3	1.98	0.45
29:DC:1034:LEU:HD23	37:DK:107:ILE:HD11	1.97	0.45
35:DI:236:LEU:HG	35:DI:240:MET:HE2	1.98	0.45
40:DP:115:LEU:HD21	40:DP:135:LEU:HD12	1.98	0.45
51:F3:692:LEU:HB3	51:F3:714:TYR:HE2	1.81	0.45
52:F5:337:THR:OG1	52:F5:338:GLY:N	2.50	0.45
65:Ff:520:ASN:HB2	65:Ff:708:HIS:HA	1.99	0.45
66:Fg:14:GLN:HE21	66:Fg:14:GLN:HB3	1.54	0.45
69:IA:516:LYS:HG2	69:IA:547:GLU:HB2	1.97	0.45
8:CJ:230:PHE:O	8:CJ:239:ARG:NH2	2.49	0.45
8:CJ:432:HIS:HB3	8:CJ:817:PRO:HG3	1.98	0.45
8:CJ:615:VAL:HA	8:CJ:655:ARG:HA	1.99	0.45
8:CJ:781:HIS:HD2	8:CJ:782:SER:H	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CP:52:LYS:HE2	13:CP:52:LYS:HB2	1.84	0.45
29:DC:57:GLU:HG2	29:DC:58:VAL:H	1.81	0.45
30:DD:561:ASP:O	30:DD:565:GLN:HG2	2.16	0.45
32:DF:238:THR:O	32:DF:242:VAL:HG23	2.17	0.45
35:DI:186:ILE:HG12	35:DI:197:VAL:HG22	1.98	0.45
36:DJ:114:GLU:OE1	36:DJ:117:ARG:NH2	2.50	0.45
45:DW:83:THR:HG21	45:DW:163:GLU:HG2	1.98	0.45
51:F3:418:ASP:N	51:F3:418:ASP:OD1	2.49	0.45
61:FZ:93:LEU:O	61:FZ:97:LEU:HG	2.17	0.45
66:Fg:65:ASN:HA	66:Fg:92:LYS:HB2	1.98	0.45
69:IA:157:HIS:CD2	69:IA:159:LEU:HB2	2.51	0.45
1:CA:96:U:OP1	14:CQ:73:ARG:NH2	2.50	0.45
6:CH:50:ARG:NH2	6:CH:124:ASP:OD1	2.49	0.45
11:CN:23:HIS:CE1	32:DF:155:ALA:HB1	2.50	0.45
13:CP:111:SER:HB2	13:CP:114:PRO:HD2	1.98	0.45
20:Cd:110:ASP:HB3	35:DI:280:SER:HB3	1.98	0.45
29:DC:973:PRO:HA	29:DC:976:VAL:HG22	1.98	0.45
33:DG:102:MET:HG3	33:DG:127:LEU:HD23	1.99	0.45
33:DG:326:THR:HG23	33:DG:329:LEU:H	1.81	0.45
34:DH:155:LEU:O	34:DH:159:GLU:HG2	2.17	0.45
39:DO:123:LEU:HD12	39:DO:123:LEU:HA	1.86	0.45
39:DO:172:ALA:HB2	54:F7:564:LEU:HB3	1.99	0.45
47:DY:66:GLN:O	47:DY:69:HIS:ND1	2.36	0.45
50:F2:332:LEU:HD11	50:F2:362:LEU:HD23	1.99	0.45
51:F3:881:LEU:HD11	51:F3:895:ALA:HB2	1.98	0.45
52:F5:93:TRP:NE1	52:F5:101:LYS:HZ2	2.15	0.45
52:F5:235:LEU:HD21	52:F5:614:MET:HG3	1.99	0.45
52:F5:723:ARG:HH22	52:F5:730:LEU:HD13	1.81	0.45
54:F7:378:ASP:N	54:F7:378:ASP:OD1	2.49	0.45
55:F9:300:ARG:HD2	69:IA:339:ASP:HB2	1.99	0.45
56:FM:11:GLY:HA2	56:FM:37:GLN:O	2.17	0.45
56:FM:320:GLU:O	56:FM:324:ARG:HG2	2.16	0.45
65:Ff:553:THR:HG23	65:Ff:562:VAL:HG22	1.98	0.45
69:IA:261:HIS:HB3	69:IA:264:PHE:HD2	1.81	0.45
1:CA:270:U:OP1	49:Da:10:ILE:N	2.50	0.45
1:CA:477:U:H2'	1:CA:478:A:C8	2.52	0.45
4:CE:303:TYR:CE1	50:F2:607:PRO:HG2	2.52	0.45
4:CE:334:ARG:NH2	50:F2:564:ASP:OD1	2.37	0.45
8:CJ:436:ARG:HH21	24:Ck:671:PRO:HB3	1.82	0.45
8:CJ:446:PHE:CZ	8:CJ:474:PRO:HG3	2.52	0.45
13:CP:154:LYS:NZ	30:DD:663:ASP:OD1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CS:70:TYR:C	16:CS:72:TRP:H	2.25	0.45
18:Ca:388:THR:OG1	18:Ca:389:GLU:N	2.50	0.45
18:Ca:577:PRO:HB3	58:FP:127:ARG:HG2	1.99	0.45
21:Cg:139:THR:HG21	21:Cg:144:GLY:H	1.81	0.45
28:DB:336:VAL:HG11	28:DB:356:ILE:HG12	1.98	0.45
32:DF:29:ARG:HB3	32:DF:34:PRO:HA	1.98	0.45
33:DG:359:ARG:HE	33:DG:370:ARG:HH12	1.64	0.45
34:DH:147:CYS:O	34:DH:322:ARG:NH1	2.39	0.45
35:DI:317:HIS:HB2	39:DO:240:PRO:HG3	1.98	0.45
36:DJ:205:LYS:O	36:DJ:209:ARG:HG2	2.17	0.45
37:DK:321:ARG:NH2	55:F9:263:GLN:OE1	2.50	0.45
51:F3:745:LYS:HB2	51:F3:752:TRP:CD1	2.52	0.45
52:F5:585:LEU:HD13	52:F5:588:ILE:HD11	1.98	0.45
53:F6:344:LEU:HD21	53:F6:386:GLN:HA	1.99	0.45
53:F6:562:ARG:NH1	53:F6:564:ASP:OD1	2.50	0.45
56:FM:129:ARG:HH21	56:FM:130:ARG:NH1	2.15	0.45
56:FM:207:LEU:HD12	56:FM:242:LEU:HB2	1.99	0.45
57:FO:250:LEU:HD23	57:FO:250:LEU:H	1.82	0.45
58:FP:326:THR:HB	58:FP:329:HIS:HB3	1.98	0.45
65:Ff:444:THR:HG23	65:Ff:447:GLU:H	1.81	0.45
65:Ff:533:PRO:HB3	65:Ff:672:ILE:HG13	1.98	0.45
68:Fi:318:ARG:O	68:Fi:322:ILE:HG12	2.17	0.45
69:IA:316:GLN:HE21	69:IA:318:ARG:HB2	1.81	0.45
69:IA:659:ARG:HH22	69:IA:726:ARG:H	1.65	0.45
1:CA:439:U:H1'	22:Ci:156:VAL:HG12	1.98	0.45
6:CH:271:GLU:HG3	6:CH:273:ILE:HG12	1.99	0.45
7:CI:86:PHE:HB3	21:Cg:476:GLN:HE22	1.81	0.45
7:CI:297:ALA:HB1	7:CI:299:VAL:HG23	1.99	0.45
8:CJ:69:GLN:HA	8:CJ:82:HIS:CE1	2.51	0.45
8:CJ:105:ASN:OD1	8:CJ:105:ASN:N	2.50	0.45
13:CP:107:ARG:NH2	20:Cd:55:GLU:OE1	2.50	0.45
13:CP:126:PRO:HG2	18:Ca:432:ARG:HB3	1.98	0.45
18:Ca:80:ASP:HB2	52:F5:741:TRP:CD1	2.52	0.45
19:Cb:105:VAL:O	19:Cb:110:MET:N	2.48	0.45
19:Cb:117:TRP:NE1	53:F6:198:PRO:O	2.44	0.45
21:Cg:430:LEU:HD11	47:DY:57:ARG:HG2	1.98	0.45
29:DC:240:VAL:HG23	29:DC:248:ARG:HE	1.82	0.45
29:DC:626:ALA:O	29:DC:628:ASN:N	2.46	0.45
30:DD:357:TRP:CZ2	41:DR:258:CYS:HB3	2.52	0.45
30:DD:394:LYS:HE2	30:DD:456:SER:HB2	1.99	0.45
30:DD:463:GLU:HG3	30:DD:466:ARG:HH21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DD:558:TRP:CE2	41:DR:200:PRO:HG3	2.52	0.45
30:DD:687:HIS:CE1	30:DD:689:LEU:HB2	2.52	0.45
30:DD:797:PHE:O	43:DU:218:ARG:NH2	2.49	0.45
31:DE:704:LEU:HD22	37:DK:116:ARG:HH22	1.82	0.45
32:DF:269:GLU:HG2	32:DF:312:TRP:CH2	2.52	0.45
32:DF:359:ARG:NH2	36:DJ:80:GLU:HB3	2.32	0.45
33:DG:530:PHE:CE2	33:DG:596:VAL:HG13	2.52	0.45
34:DH:161:GLY:HA3	34:DH:217:CYS:O	2.17	0.45
34:DH:172:PHE:CG	34:DH:210:LEU:HD22	2.52	0.45
40:DP:97:TRP:CH2	40:DP:110:PRO:HB3	2.52	0.45
51:F3:712:THR:HG22	51:F3:755:LEU:HD11	1.99	0.45
56:FN:63:ARG:HG2	56:FN:65:HIS:CD2	2.51	0.45
57:FO:56:LEU:HD21	66:Fg:320:PRO:HB2	1.99	0.45
65:Ff:411:HIS:O	65:Ff:414:VAL:HG12	2.17	0.45
66:Fg:135:VAL:HG23	66:Fg:413:VAL:HG13	1.98	0.45
69:IA:516:LYS:NZ	69:IA:555:ASP:OD1	2.47	0.45
1:CA:150:A:OP1	14:CQ:40:ARG:NH1	2.50	0.45
1:CA:561:U:H4'	69:IA:47:GLN:O	2.17	0.45
8:CJ:733:TYR:HE1	8:CJ:738:LEU:HD13	1.82	0.45
12:CO:128:ARG:NH1	20:Cd:136:GLU:OE1	2.50	0.45
24:Ck:150:VAL:O	24:Ck:251:ASN:ND2	2.50	0.45
24:Ck:213:MET:HE3	24:Ck:213:MET:HB3	1.82	0.45
24:Ck:325:LEU:HA	24:Ck:632:MET:HE2	1.98	0.45
29:DC:587:ASN:N	29:DC:609:VAL:HG11	2.32	0.45
29:DC:1134:HIS:HE1	34:DH:2:LEU:HB3	1.81	0.45
34:DH:55:ARG:HG3	34:DH:143:CYS:HA	1.98	0.45
34:DH:413:ASP:OD1	34:DH:413:ASP:N	2.41	0.45
35:DI:160:PHE:CD2	35:DI:161:MET:HG3	2.52	0.45
36:DJ:317:PHE:HB3	42:DT:242:MET:HE2	1.99	0.45
50:F2:432:VAL:O	50:F2:436:VAL:HG23	2.17	0.45
54:F7:418:ASP:OD1	54:F7:418:ASP:N	2.49	0.45
54:F7:487:GLU:OE1	54:F7:522:ARG:NH1	2.50	0.45
55:F9:585:ASP:O	55:F9:587:GLY:N	2.45	0.45
58:FP:288:ILE:O	58:FP:292:ILE:HG13	2.16	0.45
68:Fi:236:LEU:HB3	68:Fi:262:PRO:HG2	1.98	0.45
69:IA:208:ILE:HG22	69:IA:216:LYS:HB3	1.99	0.45
69:IA:288:VAL:H	69:IA:325:GLN:NE2	2.15	0.45
70:IB:383:MET:N	70:IB:383:MET:SD	2.90	0.45
1:CA:99:G:H2'	1:CA:99:G:N3	2.32	0.44
4:CE:256:LEU:O	4:CE:259:THR:OG1	2.35	0.44
13:CP:85:ASP:OD2	18:Ca:484:LYS:NZ	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CS:118:ARG:HH21	32:DF:83:ILE:HG13	1.82	0.44
26:Cn:207:LEU:HD23	68:Fi:334:TYR:HB3	1.99	0.44
28:DB:495:LEU:HB3	28:DB:589:ASP:HB3	1.98	0.44
28:DB:673:GLY:O	28:DB:674:ARG:NH1	2.49	0.44
29:DC:112:TYR:HB3	29:DC:960:VAL:HG13	1.98	0.44
32:DF:55:ARG:HB2	32:DF:59:GLY:HA3	1.98	0.44
32:DF:471:ASP:N	32:DF:471:ASP:OD1	2.49	0.44
33:DG:134:PRO:HB2	33:DG:167:LEU:HD11	1.99	0.44
33:DG:230:ASN:O	33:DG:234:GLU:HG2	2.16	0.44
36:DJ:223:MET:HA	36:DJ:226:VAL:HG12	1.97	0.44
42:DT:225:ASP:HB3	42:DT:228:LEU:HB2	1.99	0.44
44:DV:153:LEU:HB3	44:DV:157:LEU:HD13	1.98	0.44
52:F5:346:TYR:HE1	52:F5:381:TRP:HB2	1.83	0.44
55:F9:303:LEU:HD12	55:F9:324:LEU:HD22	1.99	0.44
56:FM:20:VAL:HG23	56:FM:21:PRO:HD3	1.99	0.44
58:FP:237:LEU:HG	58:FP:239:GLY:N	2.31	0.44
66:Fg:436:ASP:O	66:Fg:440:SER:HB3	2.17	0.44
1:CA:466:G:H2'	1:CA:467:A:C8	2.52	0.44
8:CJ:12:TRP:HH2	34:DH:16:MET:HG2	1.82	0.44
14:CQ:144:LEU:HB3	14:CQ:166:GLU:HB3	2.00	0.44
18:Ca:430:PRO:HA	18:Ca:433:GLN:HG2	1.98	0.44
21:Cg:410:ARG:HA	21:Cg:441:LEU:HD11	1.99	0.44
22:Ci:60:SER:OG	22:Ci:71:TYR:O	2.34	0.44
23:Cj:99:ASN:HD21	23:Cj:167:ASP:HA	1.81	0.44
24:Ck:731:ARG:NH1	24:Ck:785:PRO:HG2	2.33	0.44
29:DC:690:LYS:O	29:DC:693:GLU:HG3	2.17	0.44
31:DE:72:ARG:HE	31:DE:194:HIS:HB2	1.82	0.44
32:DF:275:MET:O	32:DF:279:ILE:HG12	2.17	0.44
33:DG:101:THR:HA	33:DG:104:VAL:HG12	1.97	0.44
33:DG:594:ARG:HA	33:DG:597:VAL:HB	1.99	0.44
35:DI:171:GLY:O	35:DI:175:GLN:HG2	2.17	0.44
36:DJ:335:ILE:H	36:DJ:335:ILE:HG13	1.45	0.44
37:DK:45:TYR:HB2	37:DK:164:GLU:OE2	2.17	0.44
39:DO:76:SER:O	39:DO:79:THR:OG1	2.25	0.44
44:DV:56:ARG:HD3	44:DV:89:TRP:CG	2.52	0.44
50:F2:960:GLY:HA2	55:F9:145:TYR:CE2	2.53	0.44
51:F3:84:LEU:H	57:FO:76:GLN:HE22	1.64	0.44
62:Fb:129:ASP:O	62:Fb:133:LYS:HG2	2.17	0.44
69:IA:700:ARG:HD2	75:UG:4:ALA:H	1.82	0.44
1:CA:529:A:N6	7:CI:419:ASP:OD2	2.50	0.44
4:CE:113:GLU:H	4:CE:116:GLN:HE21	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CJ:46:ASP:HB3	38:DL:282:TRP:CD2	2.51	0.44
8:CJ:393:GLU:OE2	8:CJ:395:ARG:NH2	2.47	0.44
12:CO:74:TRP:CZ2	50:F2:191:LYS:HG2	2.52	0.44
12:CO:91:PRO:HA	12:CO:94:ARG:HG2	1.98	0.44
22:CI:20:PRO:HA	22:CI:23:LEU:HD12	1.98	0.44
28:DB:209:GLN:HG3	31:DE:447:ARG:HB3	1.99	0.44
28:DB:315:GLN:O	28:DB:319:ARG:HG2	2.17	0.44
29:DC:238:PRO:HB2	29:DC:240:VAL:HG12	1.98	0.44
29:DC:663:GLY:HA3	29:DC:760:LEU:HG	2.00	0.44
29:DC:673:VAL:H	29:DC:748:TRP:N	2.16	0.44
42:DT:82:HIS:CD2	42:DT:128:PRO:HB3	2.52	0.44
43:DU:196:MET:HE2	43:DU:196:MET:HB2	1.85	0.44
50:F2:854:GLU:O	55:F9:165:ARG:NH2	2.49	0.44
50:F2:897:SER:H	50:F2:939:LYS:NZ	2.15	0.44
55:F9:507:LYS:HD3	67:Fh:284:ASN:ND2	2.32	0.44
57:FO:95:GLY:HA3	57:FO:287:SER:O	2.18	0.44
59:FW:176:GLN:NE2	59:FW:183:GLU:OE1	2.50	0.44
60:FX:40:TRP:O	60:FX:44:MET:HG2	2.17	0.44
60:FX:40:TRP:CD1	60:FX:72:PRO:HG2	2.51	0.44
66:Fg:136:ILE:HG12	66:Fg:146:ALA:HB1	1.99	0.44
68:Fi:324:ALA:HB1	68:Fi:514:VAL:HB	2.00	0.44
70:IB:490:ASP:HA	70:IB:493:ARG:HG2	2.00	0.44
5:CF:86:HIS:CD2	5:CF:88:ASP:H	2.34	0.44
8:CJ:231:GLU:HG2	8:CJ:244:THR:HG21	1.99	0.44
8:CJ:285:ARG:NE	34:DH:303:GLU:OE1	2.42	0.44
9:CK:311:THR:HG23	17:CU:43:PRO:HG3	1.99	0.44
13:CP:54:ARG:O	13:CP:59:ARG:NH2	2.50	0.44
18:Ca:532:PHE:O	18:Ca:536:ARG:HG3	2.16	0.44
22:CI:82:GLN:HA	22:CI:87:TYR:CD1	2.53	0.44
24:Ck:310:ASP:HA	28:DB:891:GLN:HG3	2.00	0.44
28:DB:206:LEU:O	28:DB:210:ALA:HB2	2.17	0.44
29:DC:229:THR:OG1	29:DC:231:THR:O	2.35	0.44
30:DD:597:LEU:HD23	30:DD:600:LEU:HD12	1.98	0.44
32:DF:447:TYR:HE2	32:DF:490:ASN:HB2	1.81	0.44
36:DJ:316:TYR:CZ	42:DT:212:PHE:HB3	2.52	0.44
37:DK:237:PRO:HD2	37:DK:240:SER:HB3	2.00	0.44
40:DP:94:VAL:HG22	40:DP:134:LEU:HD11	2.00	0.44
51:F3:759:SER:HB3	51:F3:788:LEU:HD21	1.99	0.44
51:F3:779:ALA:HA	51:F3:828:LEU:HD13	1.98	0.44
52:F5:329:THR:HG23	52:F5:505:TYR:CG	2.52	0.44
54:F7:17:LYS:O	54:F7:20:GLU:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Fh:223:MET:HE3	67:Fh:227:TYR:CE2	2.51	0.44
69:IA:423:GLU:O	69:IA:426:GLN:NE2	2.51	0.44
8:CJ:740:LYS:HE3	8:CJ:740:LYS:HB3	1.79	0.44
14:CQ:198:LEU:HG	54:F7:99:PRO:HG3	2.00	0.44
16:CS:98:PHE:HE2	32:DF:73:HIS:HB2	1.82	0.44
23:Cj:127:ASP:HB2	23:Cj:207:LYS:HD3	1.99	0.44
28:DB:508:ARG:HG3	28:DB:509:LEU:H	1.81	0.44
28:DB:1076:ASN:HB3	32:DF:223:ARG:HB2	1.99	0.44
29:DC:1095:LEU:HD11	37:DK:18:LEU:HD21	1.98	0.44
30:DD:220:VAL:HG12	30:DD:301:VAL:HB	1.98	0.44
32:DF:499:THR:HG22	32:DF:580:ASP:HB3	1.99	0.44
34:DH:427:LEU:HD23	38:DL:57:ALA:HA	2.00	0.44
42:DT:98:PRO:HB2	42:DT:99:HIS:CD2	2.53	0.44
42:DT:110:TYR:O	42:DT:114:LEU:HG	2.16	0.44
52:F5:383:LYS:HE3	52:F5:383:LYS:HB3	1.76	0.44
53:F6:124:ARG:HD3	53:F6:155:ALA:HB3	1.99	0.44
53:F6:375:LEU:HD23	53:F6:378:ILE:HD11	1.99	0.44
56:FN:116:ASP:OD1	56:FN:116:ASP:N	2.41	0.44
57:FO:131:ASP:OD1	57:FO:131:ASP:N	2.50	0.44
65:Ff:249:MET:HE3	65:Ff:321:HIS:CE1	2.52	0.44
66:Fg:488:TRP:HE1	66:Fg:492:MET:HE3	1.81	0.44
67:Fh:195:ARG:HA	67:Fh:195:ARG:HD2	1.85	0.44
68:Fi:562:ASN:HD21	68:Fi:565:GLU:HB3	1.81	0.44
70:IB:384:ASP:OD1	70:IB:384:ASP:N	2.50	0.44
1:CA:64:G:N7	57:FO:316:ARG:HD2	2.33	0.44
1:CA:178:A:H5'	41:DR:250:ARG:NH2	2.32	0.44
3:CC:30:TYR:CZ	34:DH:420:THR:HB	2.53	0.44
4:CE:261:ASN:OD1	4:CE:261:ASN:N	2.50	0.44
7:CI:170:GLN:HA	7:CI:173:VAL:HG12	2.00	0.44
8:CJ:249:LEU:HD13	8:CJ:260:LEU:HG	1.99	0.44
13:CP:138:PRO:HB3	59:FW:135:LEU:O	2.18	0.44
22:Ci:87:TYR:O	22:Ci:91:LYS:HB3	2.18	0.44
30:DD:250:LYS:O	30:DD:287:ARG:NE	2.44	0.44
31:DE:145:PRO:HB2	34:DH:535:VAL:HG23	1.98	0.44
31:DE:327:ASN:HB3	31:DE:328:PRO:HD3	1.98	0.44
33:DG:315:LEU:HD13	33:DG:318:ILE:HD11	2.00	0.44
37:DK:303:TYR:HB3	42:DT:177:MET:HE1	1.99	0.44
50:F2:205:THR:OG1	50:F2:206:GLU:N	2.50	0.44
51:F3:694:GLU:HA	51:F3:697:VAL:HG12	1.99	0.44
52:F5:226:GLU:OE1	61:FZ:15:PHE:HB2	2.18	0.44
58:FP:38:ALA:HB1	58:FP:303:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:FX:34:ASN:ND2	60:FX:37:ALA:HB2	2.33	0.44
65:Ff:300:ILE:O	65:Ff:304:VAL:HG23	2.18	0.44
66:Fg:469:SER:HB2	66:Fg:472:ASP:HB2	2.00	0.44
68:Fi:85:ASP:O	68:Fi:382:ARG:NH2	2.50	0.44
69:IA:397:VAL:HB	69:IA:433:PRO:HA	1.99	0.44
70:IB:192:ASP:OD2	70:IB:196:ARG:NH2	2.45	0.44
1:CA:178:A:N6	20:Cd:12:ILE:O	2.51	0.44
1:CA:512:G:N2	46:DX:160:LYS:O	2.50	0.44
5:CF:22:LEU:HD21	5:CF:65:ILE:HD13	2.00	0.44
7:CI:393:MET:HE1	7:CI:418:VAL:HG23	1.98	0.44
8:CJ:773:GLU:HB3	44:DV:100:LYS:HG2	1.99	0.44
11:CN:48:ILE:HD13	28:DB:1100:LEU:HD21	1.98	0.44
11:CN:86:TYR:HA	11:CN:89:LEU:HD13	2.00	0.44
29:DC:622:TYR:HE2	29:DC:766:VAL:HG23	1.83	0.44
32:DF:460:ARG:HD2	32:DF:468:MET:HE3	1.99	0.44
34:DH:140:ILE:HG13	34:DH:144:ASP:OD1	2.18	0.44
34:DH:405:ARG:NH2	36:DJ:48:PHE:HB3	2.33	0.44
34:DH:562:THR:HG23	34:DH:563:HIS:HD2	1.83	0.44
35:DI:351:LEU:O	35:DI:381:TYR:OH	2.25	0.44
36:DJ:95:THR:O	36:DJ:127:HIS:NE2	2.43	0.44
46:DX:84:PHE:O	46:DX:88:ASP:HB2	2.17	0.44
47:DY:118:ARG:HA	47:DY:159:TYR:CZ	2.53	0.44
51:F3:287:ALA:HB3	51:F3:337:LEU:HD13	1.99	0.44
54:F7:132:LEU:HD21	54:F7:137:LEU:HD13	2.00	0.44
65:Ff:322:GLU:HA	65:Ff:325:VAL:HG12	2.00	0.44
69:IA:71:ASN:ND2	69:IA:74:THR:OG1	2.51	0.44
69:IA:512:VAL:HG13	69:IA:544:LYS:HG3	2.00	0.44
4:CE:31:ALA:HB2	30:DD:91:TYR:CZ	2.53	0.44
8:CJ:806:GLU:OE2	11:CN:151:ARG:NH1	2.44	0.44
10:CL:48:VAL:HG21	66:Fg:313:PHE:CD2	2.53	0.44
20:Cd:186:LEU:HB3	20:Cd:195:GLU:HB2	2.00	0.44
24:Ck:113:ASN:HB3	28:DB:558:ASN:OD1	2.18	0.44
24:Ck:728:GLN:HG3	24:Ck:784:TRP:CE2	2.53	0.44
28:DB:148:GLU:O	28:DB:151:THR:HG22	2.18	0.44
29:DC:882:ASP:OD1	29:DC:882:ASP:N	2.50	0.44
34:DH:526:ASN:OD1	34:DH:529:TYR:HB2	2.18	0.44
54:F7:224:CYS:SG	54:F7:226:LYS:HE2	2.57	0.44
54:F7:275:THR:O	54:F7:279:VAL:HG23	2.18	0.44
54:F7:352:GLU:OE2	54:F7:382:SER:OG	2.23	0.44
54:F7:502:GLN:HG2	54:F7:617:ILE:HD12	1.99	0.44
60:FX:207:LEU:HD11	60:FX:211:HIS:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Ff:487:HIS:HE1	65:Ff:530:ARG:HB3	1.83	0.44
65:Ff:510:MET:HB3	65:Ff:568:GLU:HG2	1.99	0.44
66:Fg:506:GLU:O	66:Fg:542:CYS:HA	2.17	0.44
69:IA:655:PHE:CE1	69:IA:733:GLN:HB3	2.52	0.44
1:CA:108:A:OP1	14:CQ:154:SER:OG	2.30	0.44
4:CE:116:GLN:HB3	4:CE:117:TRP:H	1.62	0.44
4:CE:341:ARG:HD2	4:CE:341:ARG:HA	1.81	0.44
6:CH:235:LYS:HE3	30:DD:744:ARG:HD3	2.00	0.44
8:CJ:709:GLU:HA	28:DB:1132:ARG:HH21	1.82	0.44
11:CN:25:VAL:O	11:CN:29:ARG:HG2	2.18	0.44
15:CR:212:TRP:O	15:CR:215:THR:OG1	2.34	0.44
19:Cb:125:MET:SD	19:Cb:146:VAL:HA	2.58	0.44
28:DB:1021:ASN:ND2	33:DG:29:ASP:O	2.51	0.44
31:DE:34:THR:HA	31:DE:38:GLN:HG3	2.00	0.44
34:DH:260:GLU:O	34:DH:264:ILE:HG22	2.18	0.44
36:DJ:252:GLU:HA	36:DJ:255:LYS:HD3	1.99	0.44
38:DL:121:ILE:HD11	38:DL:153:ALA:HB2	2.00	0.44
39:DO:72:GLU:O	39:DO:75:LEU:HG	2.18	0.44
56:FM:315:GLU:CD	56:FM:315:GLU:H	2.26	0.44
59:FW:55:MET:HG3	59:FW:62:ILE:HD13	2.00	0.44
61:FZ:104:ILE:HG23	61:FZ:109:ILE:HD11	1.99	0.44
65:Ff:785:ALA:HB2	65:Ff:800:HIS:HE1	1.83	0.44
66:Fg:231:ASN:HB3	66:Fg:516:MET:SD	2.58	0.44
66:Fg:318:ARG:O	66:Fg:323:GLY:N	2.51	0.44
67:Fh:115:ILE:HG21	67:Fh:141:ALA:HB2	1.99	0.44
69:IA:527:MET:HE2	69:IA:527:MET:HA	2.00	0.44
4:CE:216:ARG:CZ	54:F7:674:PRO:HD2	2.48	0.43
9:CK:222:ALA:HB3	9:CK:228:LYS:HZ1	1.83	0.43
13:CP:142:LYS:NZ	30:DD:649:GLN:OE1	2.40	0.43
14:CQ:216:GLU:HG3	68:Fi:519:TYR:HD1	1.83	0.43
27:Cp:66:HIS:CD2	27:Cp:68:LEU:HB2	2.53	0.43
29:DC:688:LYS:O	29:DC:691:GLN:HG3	2.18	0.43
33:DG:476:GLN:HE22	33:DG:560:GLU:H	1.64	0.43
50:F2:312:GLU:HB3	50:F2:354:HIS:CE1	2.53	0.43
50:F2:707:ASP:OD1	50:F2:707:ASP:N	2.51	0.43
55:F9:311:ARG:NE	55:F9:320:VAL:HB	2.33	0.43
55:F9:351:LYS:HD3	67:Fh:224:ASP:HA	2.00	0.43
56:FN:190:MET:HB3	56:FN:270:LEU:HB2	1.99	0.43
59:FW:44:GLU:OE1	59:FW:154:ARG:NH2	2.41	0.43
62:Fb:87:PHE:HA	62:Fb:90:HIS:CE1	2.52	0.43
64:Fd:66:HIS:HD2	64:Fd:67:MET:HG3	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:IB:178:LEU:HD23	70:IB:178:LEU:H	1.83	0.43
3:CC:47:ILE:HG23	70:IB:758:PRO:HD2	2.00	0.43
5:CF:11:LYS:HD2	5:CF:52:ARG:HG2	2.00	0.43
6:CH:56:LEU:HD13	20:Cd:119:HIS:HB3	2.00	0.43
7:CI:149:ASP:OD1	7:CI:150:ALA:N	2.50	0.43
7:CI:161:PHE:HB2	7:CI:164:LEU:HD21	1.99	0.43
8:CJ:633:CYS:HB3	8:CJ:660:ALA:HA	2.00	0.43
13:CP:84:GLN:HE22	18:Ca:477:ASP:HB3	1.82	0.43
16:CS:98:PHE:CE2	32:DF:82:ILE:HD11	2.52	0.43
18:Ca:337:ARG:HD3	30:DD:66:TRP:CE2	2.53	0.43
21:Cg:318:ILE:O	46:DX:123:ASN:ND2	2.51	0.43
24:Ck:156:LEU:HD21	24:Ck:244:ARG:HB2	1.99	0.43
24:Ck:312:VAL:HB	28:DB:893:ILE:HG12	1.99	0.43
24:Ck:753:TYR:HE2	24:Ck:762:PHE:HB2	1.81	0.43
28:DB:72:TRP:CE2	28:DB:207:LYS:HD2	2.54	0.43
29:DC:863:LEU:HA	29:DC:866:GLU:HG2	2.00	0.43
31:DE:634:ARG:NH1	31:DE:672:PHE:HB2	2.33	0.43
34:DH:221:HIS:O	34:DH:225:ILE:HG13	2.18	0.43
39:DO:232:ASN:HD21	54:F7:522:ARG:HD2	1.83	0.43
50:F2:283:MET:HB3	50:F2:295:VAL:HG13	1.99	0.43
50:F2:292:TYR:N	50:F2:293:PRO:HD2	2.33	0.43
50:F2:959:PHE:CG	55:F9:175:GLU:HB2	2.53	0.43
54:F7:371:GLN:HB2	54:F7:389:LEU:HD21	2.00	0.43
66:Fg:413:VAL:HG11	66:Fg:499:HIS:CE1	2.53	0.43
67:Fh:212:MET:HA	67:Fh:215:VAL:HG12	1.99	0.43
69:IA:654:THR:HB	69:IA:734:TYR:CZ	2.53	0.43
6:CH:182:ALA:HB1	6:CH:194:PHE:CE1	2.54	0.43
8:CJ:138:PRO:O	8:CJ:218:TYR:OH	2.36	0.43
8:CJ:564:CYS:HB3	8:CJ:603:CYS:SG	2.58	0.43
11:CN:106:GLU:O	11:CN:115:TYR:N	2.49	0.43
12:CO:323:GLY:HA3	12:CO:345:TYR:CE1	2.53	0.43
18:Ca:347:ARG:HG3	30:DD:82:ASN:HD22	1.82	0.43
19:Cb:188:ALA:O	19:Cb:192:LYS:HG2	2.18	0.43
27:Cp:165:TYR:HA	27:Cp:168:ILE:HG12	1.99	0.43
28:DB:160:LEU:HA	29:DC:648:LEU:HD22	1.99	0.43
28:DB:496:ASP:HA	28:DB:499:LYS:HG2	2.01	0.43
30:DD:173:GLN:H	30:DD:176:HIS:CD2	2.36	0.43
30:DD:428:ASP:OD1	30:DD:428:ASP:N	2.51	0.43
32:DF:103:VAL:HG11	32:DF:140:HIS:HB3	1.99	0.43
32:DF:465:LYS:HE3	32:DF:470:LYS:HG3	2.01	0.43
35:DI:100:LEU:HD13	35:DI:156:GLY:HA2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:DP:17:PRO:HB2	40:DP:19:TRP:CD1	2.53	0.43
51:F3:380:LYS:HB3	51:F3:380:LYS:HE2	1.84	0.43
51:F3:734:ALA:O	51:F3:759:SER:OG	2.32	0.43
52:F5:75:ARG:HA	52:F5:75:ARG:HD2	1.69	0.43
52:F5:477:ARG:O	52:F5:480:ARG:HG2	2.18	0.43
53:F6:273:HIS:HA	53:F6:276:MET:HE2	2.00	0.43
54:F7:204:ILE:HG21	68:Fi:507:GLU:HG2	2.00	0.43
54:F7:325:PRO:HA	54:F7:328:VAL:HG22	2.00	0.43
56:FM:27:GLY:HA2	56:FM:60:CYS:SG	2.59	0.43
60:FX:148:LEU:HD11	60:FX:173:ALA:HA	1.99	0.43
65:Ff:203:LEU:HD23	65:Ff:438:ARG:HG2	2.00	0.43
69:IA:240:VAL:HG23	69:IA:267:MET:HE2	2.01	0.43
70:IB:386:SER:HB3	70:IB:504:PRO:HB2	1.99	0.43
1:CA:33:A:H2'	1:CA:34:U:C6	2.54	0.43
7:CI:240:ASN:ND2	7:CI:242:ASP:OD1	2.51	0.43
8:CJ:284:ARG:HH11	24:Ck:108:GLN:HE21	1.66	0.43
22:CI:39:ARG:NH2	24:Ck:773:ASP:OD1	2.50	0.43
24:Ck:787:VAL:HG23	44:DV:109:ILE:HB	2.01	0.43
28:DB:652:ARG:HD3	28:DB:655:LEU:HD12	2.00	0.43
28:DB:999:TYR:CE1	52:F5:160:LYS:HD2	2.54	0.43
29:DC:885:LEU:HB3	29:DC:889:ARG:NH1	2.33	0.43
31:DE:594:LEU:HD21	31:DE:636:TYR:CE1	2.54	0.43
32:DF:321:LEU:HD13	32:DF:336:ILE:HB	1.99	0.43
34:DH:162:GLU:OE1	34:DH:221:HIS:NE2	2.47	0.43
35:DI:83:GLN:HE21	35:DI:175:GLN:HE21	1.64	0.43
35:DI:347:PRO:HG2	35:DI:350:TYR:O	2.18	0.43
39:DO:136:ASP:O	39:DO:140:ARG:HG3	2.18	0.43
44:DV:177:MET:HB3	44:DV:183:LEU:HD13	2.00	0.43
50:F2:817:THR:O	50:F2:821:GLN:HG3	2.18	0.43
53:F6:434:LEU:HA	53:F6:437:ILE:HG12	2.01	0.43
54:F7:497:SER:HB3	54:F7:498:PRO:HD3	1.99	0.43
56:FM:322:ARG:NH1	56:FN:280:GLU:OE2	2.51	0.43
57:FO:135:ASN:ND2	57:FO:167:HIS:HB2	2.31	0.43
58:FP:201:ARG:NE	60:FX:45:GLU:OE2	2.52	0.43
64:Fd:48:ALA:HB2	64:Fd:69:PRO:HB2	2.00	0.43
65:Ff:617:TRP:CE3	65:Ff:652:LEU:HD22	2.53	0.43
70:IB:668:MET:HE2	70:IB:668:MET:HB3	1.84	0.43
4:CE:329:ARG:NH2	50:F2:564:ASP:OD1	2.51	0.43
7:CI:90:GLU:N	7:CI:90:GLU:OE1	2.51	0.43
7:CI:372:ILE:HG21	7:CI:391:LEU:HD22	1.99	0.43
16:CS:71:PHE:HB3	28:DB:1130:PHE:HZ	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Ca:111:GLU:O	18:Ca:114:LYS:HG2	2.18	0.43
18:Ca:316:GLU:OE1	56:FM:7:SER:OG	2.31	0.43
18:Ca:331:ILE:HG13	18:Ca:500:PHE:HZ	1.83	0.43
22:Ci:62:SER:HB3	22:Ci:65:PHE:HD2	1.83	0.43
24:Ck:178:ASP:HB3	24:Ck:181:ASP:HB2	2.00	0.43
28:DB:344:ASP:HA	34:DH:552:ARG:HB3	2.00	0.43
28:DB:999:TYR:CD1	52:F5:155:LEU:HD23	2.54	0.43
28:DB:1023:ARG:HD2	28:DB:1043:THR:O	2.19	0.43
34:DH:156:LEU:O	34:DH:164:ARG:NH2	2.52	0.43
34:DH:318:GLU:HG3	34:DH:371:LEU:HD22	2.00	0.43
37:DK:24:ARG:NH2	37:DK:175:HIS:O	2.51	0.43
49:Da:17:HIS:CD2	49:Da:18:LYS:HG3	2.53	0.43
53:F6:233:LEU:HD22	53:F6:269:PRO:HG3	2.00	0.43
54:F7:329:GLU:O	54:F7:333:LEU:HG	2.18	0.43
55:F9:479:ARG:O	69:IA:546:THR:N	2.32	0.43
56:FM:248:ASN:HD21	69:IA:188:TYR:HB3	1.82	0.43
57:FO:13:LEU:HD13	57:FO:46:HIS:HD2	1.83	0.43
65:Ff:318:TYR:OH	65:Ff:580:HIS:ND1	2.51	0.43
65:Ff:386:TRP:HB3	65:Ff:392:HIS:HE1	1.84	0.43
65:Ff:663:GLY:O	65:Ff:667:LEU:HG	2.18	0.43
66:Fg:185:MET:HB2	66:Fg:353:LEU:HB2	2.00	0.43
66:Fg:226:GLU:HB2	66:Fg:442:ASN:HB3	1.99	0.43
1:CA:31:U:H2'	1:CA:32:A:H8	1.82	0.43
6:CH:254:ILE:HD12	6:CH:279:MET:SD	2.59	0.43
8:CJ:776:GLN:HE21	46:DX:131:ILE:HB	1.84	0.43
13:CP:106:LYS:NZ	43:DU:208:TYR:O	2.50	0.43
20:Cd:188:ASP:HB2	20:Cd:194:VAL:HG21	2.00	0.43
21:Cg:114:GLU:CD	21:Cg:114:GLU:H	2.26	0.43
21:Cg:443:LYS:HD3	21:Cg:465:TRP:CZ3	2.54	0.43
29:DC:56:ALA:HA	37:DK:267:ARG:HH11	1.83	0.43
33:DG:232:LEU:HD13	33:DG:252:VAL:HG13	1.99	0.43
34:DH:532:ARG:HA	34:DH:532:ARG:HD3	1.79	0.43
35:DI:103:ASP:HB2	35:DI:152:LEU:HD13	2.00	0.43
35:DI:243:LEU:HD21	35:DI:375:ILE:HD11	2.00	0.43
36:DJ:232:ARG:HA	36:DJ:232:ARG:HD3	1.82	0.43
38:DL:235:PRO:HB2	38:DL:238:GLN:HB3	2.00	0.43
39:DO:109:VAL:O	39:DO:113:LEU:HG	2.18	0.43
53:F6:202:LEU:O	53:F6:206:ILE:HG12	2.17	0.43
55:F9:377:GLN:HA	55:F9:380:ASP:OD2	2.19	0.43
56:FN:102:ASN:HA	56:FN:130:ARG:HE	1.84	0.43
65:Ff:618:CYS:HB2	65:Ff:666:TRP:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Fg:423:PHE:HE1	66:Fg:477:VAL:HG11	1.83	0.43
68:Fi:132:VAL:HG12	68:Fi:190:SER:HB2	2.01	0.43
68:Fi:301:GLN:HE22	70:IB:411:MET:HA	1.83	0.43
69:IA:420:VAL:HG22	69:IA:439:LEU:HD12	2.00	0.43
69:IA:729:ASP:OD1	69:IA:730:ILE:N	2.52	0.43
1:CA:451:U:H2'	1:CA:452:A:C8	2.53	0.43
3:CC:33:LEU:O	34:DH:439:ALA:HA	2.19	0.43
14:CQ:63:MET:HE1	14:CQ:70:ARG:HB2	2.01	0.43
14:CQ:193:ARG:CZ	54:F7:113:LEU:HD23	2.49	0.43
18:Ca:402:VAL:O	18:Ca:406:MET:HG3	2.18	0.43
19:Cb:137:VAL:HG23	19:Cb:138:ASP:H	1.83	0.43
21:Cg:138:LEU:HD23	44:DV:183:LEU:HD23	2.01	0.43
23:Cj:115:ARG:HD3	23:Cj:129:TYR:CE1	2.53	0.43
24:Ck:776:LYS:HE3	24:Ck:776:LYS:HB2	1.81	0.43
25:Cm:115:CYS:HB2	25:Cm:118:GLU:HB2	2.01	0.43
27:Cp:44:GLN:HB2	59:FW:147:VAL:HG22	1.99	0.43
29:DC:570:HIS:ND1	29:DC:803:ALA:O	2.41	0.43
33:DG:259:LEU:HD23	33:DG:280:ASP:HA	1.99	0.43
35:DI:290:PHE:HB2	35:DI:301:ILE:HB	2.00	0.43
36:DJ:87:PRO:HB3	36:DJ:92:LEU:HD23	1.99	0.43
36:DJ:313:ARG:NH2	42:DT:28:GLU:OE1	2.52	0.43
36:DJ:347:LYS:NZ	36:DJ:356:TYR:H	2.16	0.43
51:F3:51:ARG:HD2	51:F3:51:ARG:HA	1.89	0.43
53:F6:245:PRO:HB2	53:F6:260:THR:HG22	2.01	0.43
56:FN:46:ALA:HB2	56:FN:64:ILE:HG21	2.01	0.43
57:FO:94:HIS:CD2	57:FO:144:PRO:HD2	2.54	0.43
58:FP:133:PHE:O	58:FP:137:HIS:CB	2.63	0.43
59:FW:211:ILE:HD12	59:FW:211:ILE:HA	1.91	0.43
65:Ff:200:CYS:HB2	65:Ff:203:LEU:HD13	2.00	0.43
66:Fg:198:GLU:H	66:Fg:198:GLU:CD	2.26	0.43
66:Fg:215:ALA:O	66:Fg:219:SER:OG	2.31	0.43
1:CA:49:U:OP2	20:Cd:13:ARG:HD3	2.19	0.43
5:CF:32:ASN:HB3	5:CF:75:GLU:HB3	2.01	0.43
8:CJ:234:GLU:HA	8:CJ:329:ARG:HH21	1.84	0.43
9:CK:230:GLY:O	65:Ff:710:GLN:NE2	2.52	0.43
15:CR:143:TYR:CZ	15:CR:146:ASP:HB2	2.54	0.43
15:CR:210:TYR:HE2	19:Cb:185:GLY:HA3	1.84	0.43
18:Ca:497:TRP:CD1	30:DD:106:ALA:HB1	2.54	0.43
28:DB:600:ARG:NE	28:DB:608:LEU:O	2.52	0.43
28:DB:1092:PHE:HB3	28:DB:1095:GLU:HB2	2.01	0.43
29:DC:1164:TRP:CE3	34:DH:374:GLU:HG3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DD:277:ASP:HB3	30:DD:280:LEU:HD13	2.01	0.43
31:DE:459:ASP:N	31:DE:459:ASP:OD1	2.52	0.43
31:DE:670:ASP:OD2	31:DE:714:PHE:N	2.52	0.43
49:Da:37:HIS:CE1	54:F7:112:ALA:HB2	2.54	0.43
50:F2:764:ASP:OD1	50:F2:764:ASP:N	2.52	0.43
51:F3:345:ASP:HB2	51:F3:348:LYS:HE2	1.99	0.43
53:F6:245:PRO:HD2	53:F6:259:GLY:O	2.18	0.43
54:F7:336:TRP:CH2	54:F7:346:ARG:HD3	2.54	0.43
54:F7:394:ARG:HB2	54:F7:431:LEU:HD12	2.01	0.43
55:F9:541:PHE:CE1	69:IA:504:ARG:HB2	2.54	0.43
56:FM:254:PRO:O	56:FM:306:ASP:N	2.50	0.43
65:Ff:300:ILE:HD12	65:Ff:329:ILE:HD13	2.01	0.43
70:IB:363:GLN:HA	70:IB:366:THR:HG22	2.01	0.43
1:CA:101:A:OP2	14:CQ:193:ARG:HD3	2.18	0.43
1:CA:599:A:OP2	68:Fi:312:LYS:NZ	2.45	0.43
7:CI:202:LEU:HD22	38:DL:191:LEU:HD12	2.01	0.43
7:CI:344:LEU:HD12	7:CI:351:MET:HG2	2.01	0.43
8:CJ:408:GLN:O	24:Ck:656:ARG:HD3	2.19	0.43
9:CK:295:VAL:HG13	17:CU:54:ILE:HD11	2.00	0.43
9:CK:300:ASN:ND2	9:CK:301:GLU:OE2	2.52	0.43
10:CL:39:TYR:CE1	10:CL:50:MET:HB3	2.53	0.43
12:CO:352:ASN:O	12:CO:356:GLN:HG3	2.19	0.43
14:CQ:151:ARG:HD2	43:DU:49:TYR:CE2	2.53	0.43
19:Cb:88:SER:OG	19:Cb:90:GLU:OE1	2.37	0.43
24:Ck:834:MET:HA	24:Ck:838:LEU:HB2	2.01	0.43
28:DB:1015:ASP:CG	33:DG:38:ARG:HH22	2.25	0.43
29:DC:439:ALA:HB2	29:DC:497:PRO:O	2.19	0.43
30:DD:423:LYS:HE2	30:DD:469:GLY:HA2	2.01	0.43
30:DD:542:HIS:HA	30:DD:545:ASP:OD2	2.19	0.43
32:DF:229:PRO:HG2	32:DF:234:TYR:CE2	2.54	0.43
36:DJ:276:LEU:HD22	36:DJ:284:LEU:HG	2.01	0.43
37:DK:12:ALA:O	37:DK:16:ARG:HG2	2.18	0.43
54:F7:287:ARG:HB2	54:F7:290:MET:HG3	2.01	0.43
54:F7:440:ALA:O	54:F7:444:GLN:HG2	2.18	0.43
56:FM:21:PRO:HB2	56:FM:146:CYS:SG	2.59	0.43
61:FZ:136:MET:HA	61:FZ:139:TRP:CD1	2.54	0.43
62:Fb:97:GLU:HA	62:Fb:100:VAL:HG12	2.00	0.43
63:Fc:68:ASN:OD1	63:Fc:68:ASN:N	2.51	0.43
64:Fd:58:TRP:CH2	64:Fd:72:ILE:HD12	2.54	0.43
65:Ff:607:TRP:HA	65:Ff:607:TRP:CE3	2.54	0.43
68:Fi:131:GLU:OE1	68:Fi:131:GLU:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:562:U:OP1	10:CL:52:ARG:NH2	2.52	0.43
4:CE:121:THR:HG21	67:Fh:74:VAL:HG21	2.01	0.43
6:CH:126:PRO:HB2	6:CH:158:ARG:HH22	1.83	0.43
7:CI:276:ASP:CG	7:CI:279:ARG:HH21	2.27	0.43
12:CO:70:HIS:N	50:F2:163:ARG:HD3	2.34	0.43
14:CQ:248:MET:HA	68:Fi:36:VAL:HG13	2.00	0.43
24:Ck:395:MET:HG3	24:Ck:564:LEU:HD11	2.00	0.43
28:DB:517:GLU:OE1	28:DB:517:GLU:N	2.52	0.43
28:DB:1047:TRP:CD1	36:DJ:41:PRO:HG3	2.53	0.43
29:DC:99:LYS:HE2	29:DC:99:LYS:HB3	1.76	0.43
29:DC:456:ALA:HA	29:DC:460:SER:HB3	2.00	0.43
29:DC:635:MET:HG3	29:DC:762:LYS:HD3	2.00	0.43
32:DF:125:TYR:CD2	32:DF:179:TYR:HB2	2.54	0.43
33:DG:450:MET:HA	33:DG:453:ASP:OD2	2.19	0.43
38:DL:190:ARG:HG2	38:DL:231:TRP:CD2	2.54	0.43
41:DR:84:LEU:HD13	41:DR:179:HIS:HB2	2.00	0.43
42:DT:82:HIS:CG	42:DT:128:PRO:HB3	2.54	0.43
45:DW:111:LYS:HB3	53:F6:598:TYR:CD1	2.54	0.43
50:F2:782:VAL:O	50:F2:786:ARG:HG3	2.19	0.43
55:F9:337:ALA:O	55:F9:340:GLU:HG2	2.19	0.43
1:CA:105:G:H5'	12:CO:421:TRP:CD1	2.54	0.42
1:CA:253:U:H2'	1:CA:254:A:H8	1.84	0.42
1:CA:435:G:H5''	32:DF:14:GLY:HA3	2.01	0.42
1:CA:561:U:OP1	69:IA:60:ARG:NH2	2.50	0.42
13:CP:86:ARG:HD3	27:Cp:32:PRO:HG2	2.01	0.42
18:Ca:221:THR:HG23	48:DZ:79:ALA:HB2	2.01	0.42
18:Ca:241:LEU:HB3	61:FZ:49:ARG:NH1	2.33	0.42
18:Ca:247:PHE:CD2	50:F2:815:VAL:HG21	2.54	0.42
24:Ck:392:PHE:O	24:Ck:395:MET:HG2	2.19	0.42
28:DB:255:LEU:HA	28:DB:411:MET:HE1	2.00	0.42
29:DC:41:ASN:O	29:DC:44:PRO:HD2	2.19	0.42
30:DD:334:ASN:HD22	30:DD:337:LEU:HG	1.84	0.42
30:DD:405:LYS:HG2	30:DD:412:CYS:SG	2.59	0.42
31:DE:174:VAL:HG11	31:DE:550:ALA:HB2	1.99	0.42
31:DE:545:ARG:HG2	31:DE:548:ARG:HH12	1.84	0.42
32:DF:119:HIS:CD2	32:DF:121:LEU:H	2.37	0.42
33:DG:490:ARG:O	33:DG:494:THR:HG22	2.19	0.42
34:DH:478:GLY:HA2	38:DL:39:THR:HA	2.01	0.42
40:DP:124:ARG:HB2	40:DP:125:PRO:HD2	2.01	0.42
52:F5:120:THR:HG22	52:F5:123:GLN:HG3	2.01	0.42
52:F5:601:GLU:O	52:F5:604:ARG:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:F7:305:MET:HE2	54:F7:305:MET:HB3	1.82	0.42
65:Ff:194:ARG:NH2	65:Ff:353:ASP:OD1	2.52	0.42
65:Ff:688:GLU:O	65:Ff:691:ARG:NH2	2.34	0.42
69:IA:409:VAL:HG12	69:IA:414:TYR:HB2	2.01	0.42
69:IA:529:SER:HB2	69:IA:598:LEU:HD11	2.01	0.42
70:IB:461:ILE:HD11	70:IB:484:HIS:HB2	2.01	0.42
4:CE:154:PHE:H	4:CE:159:HIS:HB2	1.84	0.42
5:CF:14:GLN:HB2	5:CF:17:PHE:CD2	2.54	0.42
5:CF:144:MET:HG3	19:Cb:101:LYS:HD2	2.01	0.42
7:CI:279:ARG:HH11	7:CI:285:ASP:HA	1.84	0.42
8:CJ:44:PHE:CZ	38:DL:289:ARG:HG2	2.54	0.42
11:CN:161:LEU:HD23	22:Ci:71:TYR:HB3	2.01	0.42
18:Ca:401:ASP:O	18:Ca:405:ARG:HD3	2.20	0.42
27:Cp:55:ASN:OD1	27:Cp:55:ASN:N	2.52	0.42
28:DB:853:GLU:HA	28:DB:856:THR:HG22	2.00	0.42
29:DC:279:GLU:HG2	29:DC:280:VAL:H	1.84	0.42
29:DC:288:VAL:O	29:DC:291:VAL:HG12	2.20	0.42
29:DC:659:LEU:HD22	29:DC:662:ARG:HD3	2.01	0.42
30:DD:518:PHE:CZ	30:DD:602:VAL:HG11	2.54	0.42
31:DE:688:THR:O	31:DE:691:THR:OG1	2.37	0.42
31:DE:718:SER:HA	31:DE:733:TYR:CZ	2.54	0.42
32:DF:347:ARG:C	32:DF:351:HIS:HD1	2.26	0.42
32:DF:499:THR:O	34:DH:245:TYR:OH	2.31	0.42
38:DL:180:LYS:O	38:DL:184:GLU:HG2	2.19	0.42
44:DV:114:VAL:HB	44:DV:118:GLN:HB2	2.02	0.42
46:DX:83:ARG:HB3	47:DY:120:TYR:CE1	2.54	0.42
46:DX:102:MET:HG2	46:DX:124:ILE:HD11	2.01	0.42
47:DY:52:GLN:OE1	47:DY:52:GLN:N	2.52	0.42
51:F3:792:LYS:HE2	51:F3:794:ASN:HD22	1.84	0.42
52:F5:663:ARG:HG3	52:F5:666:ARG:NH2	2.34	0.42
56:FM:56:ASP:O	59:FW:184:PRO:HB3	2.20	0.42
57:FO:8:ASP:OD1	57:FO:8:ASP:N	2.50	0.42
66:Fg:157:VAL:O	66:Fg:161:LEU:HG	2.19	0.42
1:CA:115:A:H5''	41:DR:11:ARG:HH12	1.85	0.42
1:CA:441:G:C2	1:CA:483:A:H5'	2.54	0.42
3:CC:35:PHE:HB2	3:CC:74:THR:C	2.43	0.42
6:CH:38:LEU:HD23	20:Cd:116:LYS:HG3	2.01	0.42
7:CI:8:ARG:HB2	33:DG:498:TYR:HB3	2.02	0.42
8:CJ:154:THR:HG23	8:CJ:203:ARG:HG2	2.01	0.42
8:CJ:488:SER:H	8:CJ:491:ALA:HB3	1.84	0.42
19:Cb:120:LYS:HB3	19:Cb:121:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Cd:81:ASN:HA	20:Cd:84:LYS:HG2	2.00	0.42
21:Cg:373:VAL:HG21	44:DV:51:ASN:HB3	2.00	0.42
26:Cn:175:ARG:HA	26:Cn:178:LYS:HG2	2.02	0.42
28:DB:158:ARG:HH11	31:DE:212:LEU:HG	1.85	0.42
28:DB:1020:ASP:OD1	28:DB:1020:ASP:N	2.51	0.42
28:DB:1149:MET:O	28:DB:1163:LYS:HG2	2.20	0.42
29:DC:402:VAL:HA	29:DC:405:ILE:HG22	2.00	0.42
30:DD:561:ASP:OD1	30:DD:561:ASP:N	2.52	0.42
31:DE:656:ARG:HD2	31:DE:738:ALA:O	2.20	0.42
32:DF:228:VAL:HG22	32:DF:261:LEU:HD22	2.02	0.42
33:DG:616:ARG:HD3	33:DG:627:TRP:NE1	2.33	0.42
34:DH:328:ALA:HB2	34:DH:346:GLU:HB2	2.01	0.42
37:DK:166:ALA:HB1	37:DK:170:MET:HB2	2.01	0.42
39:DO:81:LEU:HD22	39:DO:85:LYS:HD3	2.00	0.42
41:DR:238:ARG:NH1	41:DR:241:GLN:OE1	2.52	0.42
45:DW:156:THR:HG1	45:DW:157:ASN:N	2.16	0.42
50:F2:485:ASN:HB3	50:F2:534:TYR:CD2	2.54	0.42
50:F2:638:GLU:OE2	60:FX:87:ARG:NH2	2.50	0.42
51:F3:831:ARG:O	51:F3:834:GLU:HG3	2.20	0.42
52:F5:564:ILE:HG12	52:F5:567:ARG:HH21	1.84	0.42
52:F5:753:ASN:OD1	52:F5:753:ASN:N	2.51	0.42
53:F6:140:ILE:HD12	53:F6:145:GLU:HB3	2.01	0.42
60:FX:164:HIS:CD2	60:FX:165:THR:HG23	2.54	0.42
62:Fb:57:ARG:O	62:Fb:61:GLU:HG2	2.20	0.42
68:Fi:559:ASP:OD1	68:Fi:559:ASP:N	2.48	0.42
8:CJ:249:LEU:O	8:CJ:398:PHE:HA	2.20	0.42
20:Cd:64:GLN:HB3	30:DD:685:VAL:HG23	2.01	0.42
21:Cg:374:GLU:HG3	21:Cg:375:THR:HG23	2.00	0.42
21:Cg:392:LYS:HG2	44:DV:169:LEU:HD21	2.01	0.42
23:Cj:149:TYR:CE1	23:Cj:189:PRO:HB3	2.54	0.42
27:Cp:129:TYR:O	27:Cp:132:GLN:HG2	2.19	0.42
28:DB:137:VAL:HG22	31:DE:548:ARG:HD3	2.00	0.42
28:DB:843:ASN:HB3	28:DB:846:GLU:HB3	2.02	0.42
28:DB:995:VAL:O	28:DB:998:LYS:HG2	2.19	0.42
29:DC:399:SER:HB3	29:DC:402:VAL:HG23	2.01	0.42
29:DC:1157:ALA:O	29:DC:1161:LYS:HG2	2.19	0.42
31:DE:47:TYR:O	31:DE:51:ARG:HG2	2.19	0.42
33:DG:452:TRP:CE2	33:DG:539:LEU:HD22	2.53	0.42
35:DI:222:ASP:OD2	35:DI:235:SER:OG	2.35	0.42
35:DI:304:ALA:HB2	35:DI:345:LEU:HD11	2.01	0.42
36:DJ:53:GLN:HE22	36:DJ:232:ARG:HH22	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DK:172:LEU:HD13	37:DK:180:GLU:HB3	2.01	0.42
42:DT:34:PRO:HA	42:DT:37:TYR:HD1	1.84	0.42
43:DU:133:HIS:CD2	43:DU:161:ILE:HB	2.53	0.42
50:F2:826:ARG:HH11	50:F2:838:TYR:HH	1.63	0.42
52:F5:589:ILE:O	52:F5:593:LYS:HB2	2.20	0.42
55:F9:538:THR:O	69:IA:496:ARG:NH2	2.53	0.42
61:FZ:80:GLU:O	61:FZ:84:GLU:HG3	2.19	0.42
64:Fd:25:ILE:HG21	64:Fd:35:MET:HE2	2.00	0.42
66:Fg:379:LEU:HD13	66:Fg:385:MET:HE1	2.01	0.42
67:Fh:183:SER:HA	67:Fh:189:ALA:HB3	2.00	0.42
69:IA:362:LEU:O	69:IA:365:GLU:HG2	2.19	0.42
1:CA:234:C:P	69:IA:130:ARG:HH12	2.42	0.42
1:CA:452:A:N6	1:CA:473:U:O4	2.53	0.42
4:CE:49:PRO:O	50:F2:786:ARG:NH1	2.53	0.42
4:CE:232:ILE:HA	4:CE:250:ALA:O	2.20	0.42
7:CI:333:ILE:HD13	21:Cg:446:PHE:HE1	1.84	0.42
10:CL:15:ARG:HA	10:CL:15:ARG:HD3	1.80	0.42
14:CQ:78:TYR:OH	30:DD:719:ARG:O	2.25	0.42
24:Ck:130:MET:HB2	24:Ck:275:TRP:HE1	1.85	0.42
28:DB:539:GLN:HG3	28:DB:585:MET:HA	2.01	0.42
29:DC:163:ASN:OD1	29:DC:163:ASN:N	2.53	0.42
29:DC:291:VAL:HG11	29:DC:378:THR:HG21	2.00	0.42
29:DC:655:GLU:O	29:DC:658:GLU:HG3	2.19	0.42
29:DC:1104:MET:HB2	34:DH:55:ARG:HD3	2.01	0.42
32:DF:247:LEU:HD21	32:DF:286:ARG:HG2	2.00	0.42
32:DF:254:PHE:CG	32:DF:274:LEU:HD11	2.55	0.42
32:DF:320:ALA:O	32:DF:324:LEU:HG	2.20	0.42
34:DH:51:ARG:HA	34:DH:51:ARG:HD3	1.89	0.42
34:DH:66:ARG:HA	34:DH:69:VAL:HG12	2.02	0.42
35:DI:28:HIS:ND1	35:DI:170:TYR:OH	2.50	0.42
35:DI:163:MET:HA	35:DI:163:MET:HE3	2.00	0.42
44:DV:49:ASP:OD1	44:DV:50:ALA:N	2.52	0.42
50:F2:106:PRO:HA	50:F2:107:PRO:HD3	1.94	0.42
51:F3:84:LEU:H	57:FO:76:GLN:NE2	2.17	0.42
51:F3:84:LEU:HD22	66:Fg:260:THR:HG21	2.01	0.42
51:F3:799:ASP:O	51:F3:803:LEU:HG	2.19	0.42
53:F6:396:LEU:HA	53:F6:399:THR:HG22	2.01	0.42
61:FZ:52:ILE:HA	61:FZ:56:ILE:HD12	2.01	0.42
66:Fg:488:TRP:NE1	66:Fg:492:MET:HE3	2.34	0.42
67:Fh:69:GLU:HB2	70:IB:753:TYR:CE1	2.55	0.42
1:CA:31:U:O2'	1:CA:142:U:OP1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:322:A:O2'	49:Da:34:GLN:OE1	2.37	0.42
1:CA:509:U:O2'	16:CS:75:MET:HA	2.19	0.42
4:CE:349:TRP:HD1	60:FX:194:TRP:CZ3	2.37	0.42
8:CJ:154:THR:HG21	8:CJ:202:ASP:HA	2.01	0.42
11:CN:35:SER:OG	11:CN:86:TYR:OH	2.23	0.42
13:CP:174:THR:HG22	18:Ca:545:TRP:CZ2	2.55	0.42
14:CQ:20:GLN:O	14:CQ:24:LEU:HG	2.19	0.42
18:Ca:160:GLU:OE1	18:Ca:223:ASN:ND2	2.53	0.42
21:Cg:339:LEU:HD22	21:Cg:353:PHE:HE2	1.83	0.42
21:Cg:440:LYS:HE2	21:Cg:462:GLU:OE2	2.19	0.42
21:Cg:463:LEU:HD13	47:DY:56:ARG:HG2	2.01	0.42
24:Ck:271:GLY:O	24:Ck:274:VAL:HG22	2.19	0.42
28:DB:285:MET:HE3	28:DB:512:MET:HB2	2.01	0.42
28:DB:840:ASN:ND2	28:DB:846:GLU:OE1	2.52	0.42
32:DF:416:VAL:HA	32:DF:417:ARG:HH21	1.83	0.42
43:DU:28:PHE:O	43:DU:32:THR:OG1	2.31	0.42
47:DY:130:LYS:HE2	47:DY:130:LYS:HB3	1.83	0.42
50:F2:812:GLY:O	50:F2:816:ARG:HG3	2.19	0.42
53:F6:215:ARG:HA	53:F6:215:ARG:HD2	1.89	0.42
54:F7:173:GLN:O	54:F7:177:ILE:HG13	2.20	0.42
54:F7:240:GLU:HA	54:F7:243:LYS:HG2	2.02	0.42
55:F9:193:ASN:O	55:F9:197:ILE:HG12	2.19	0.42
57:FO:139:ILE:O	57:FO:143:ILE:HG23	2.19	0.42
65:Ff:246:ASP:OD1	65:Ff:246:ASP:N	2.46	0.42
66:Fg:11:PHE:CE2	66:Fg:507:ILE:HD11	2.55	0.42
4:CE:153:LYS:HG2	4:CE:158:ASP:HA	2.01	0.42
8:CJ:46:ASP:HB2	38:DL:104:ARG:HH12	1.84	0.42
8:CJ:698:HIS:CD2	8:CJ:699:LEU:HG	2.54	0.42
14:CQ:234:ASN:HD21	57:FO:5:VAL:HG13	1.84	0.42
15:CR:146:ASP:O	15:CR:149:PRO:HD2	2.19	0.42
18:Ca:157:LYS:NZ	61:FZ:52:ILE:O	2.31	0.42
21:Cg:191:SER:O	24:Ck:837:TRP:NE1	2.46	0.42
22:Ci:81:GLY:H	22:Ci:84:LEU:HD21	1.83	0.42
22:Ci:166:PRO:HB3	42:DT:244:PHE:CE1	2.55	0.42
24:Ck:656:ARG:NH1	34:DH:306:ASP:OD1	2.52	0.42
27:Cp:144:PRO:HG2	40:DP:30:LYS:HG2	2.01	0.42
29:DC:828:ARG:NH1	29:DC:828:ARG:HA	2.35	0.42
31:DE:405:ILE:HA	31:DE:408:LEU:HB3	2.01	0.42
31:DE:489:ARG:O	31:DE:493:ILE:HG12	2.18	0.42
32:DF:325:LEU:HD13	32:DF:325:LEU:HA	1.86	0.42
33:DG:44:ARG:HD2	33:DG:44:ARG:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DG:166:GLU:HA	33:DG:207:ARG:HH12	1.84	0.42
35:DI:240:MET:HE1	35:DI:290:PHE:CG	2.55	0.42
37:DK:21:SER:OG	37:DK:231:SER:O	2.31	0.42
37:DK:156:LEU:HD13	37:DK:158:PHE:CZ	2.54	0.42
45:DW:157:ASN:N	45:DW:157:ASN:OD1	2.52	0.42
48:DZ:88:PHE:HB3	52:F5:688:LEU:O	2.20	0.42
51:F3:644:MET:O	51:F3:647:SER:OG	2.30	0.42
52:F5:188:ARG:HG2	61:FZ:19:ASN:HA	2.02	0.42
55:F9:533:ASP:OD2	55:F9:540:TYR:OH	2.30	0.42
62:Fb:98:ARG:O	62:Fb:101:LYS:HG3	2.20	0.42
64:Fd:26:ARG:HB2	64:Fd:29:ASN:HA	2.02	0.42
65:Ff:184:TYR:OH	65:Ff:456:LEU:O	2.24	0.42
65:Ff:249:MET:SD	65:Ff:261:ARG:NH2	2.80	0.42
68:Fi:446:LEU:HD13	68:Fi:446:LEU:HA	1.94	0.42
69:IA:222:TYR:HE2	69:IA:353:VAL:HG11	1.84	0.42
1:CA:318:A:H4'	1:CA:319:U:H5'	2.00	0.42
1:CA:467:A:H5'	33:DG:56:ARG:NH2	2.35	0.42
3:CC:56:TYR:HA	3:CC:73:SER:HB2	2.00	0.42
7:CI:299:VAL:HG22	7:CI:402:LEU:HA	2.01	0.42
8:CJ:411:GLU:O	8:CJ:415:ARG:HG2	2.19	0.42
8:CJ:778:TRP:HE1	44:DV:96:ARG:HB3	1.85	0.42
8:CJ:795:LYS:HG3	11:CN:156:LEU:HD22	2.01	0.42
9:CK:293:ARG:HG2	53:F6:590:TRP:CE2	2.55	0.42
10:CL:18:LEU:HD11	55:F9:481:PHE:HZ	1.84	0.42
18:Ca:574:VAL:HG11	58:FP:119:LYS:HB3	2.02	0.42
21:Cg:365:ASP:OD2	44:DV:24:VAL:N	2.53	0.42
24:Ck:358:LYS:HA	28:DB:927:THR:HA	2.00	0.42
25:Cm:107:MET:HE1	45:DW:105:LEU:HD13	2.01	0.42
28:DB:508:ARG:HH11	33:DG:26:ASN:HA	1.83	0.42
29:DC:664:PHE:CD1	29:DC:792:PHE:HB2	2.55	0.42
30:DD:92:MET:HA	30:DD:785:MET:SD	2.60	0.42
30:DD:113:TYR:O	30:DD:116:GLN:HG2	2.20	0.42
32:DF:51:TRP:CD2	32:DF:150:ARG:HG3	2.54	0.42
34:DH:62:PHE:CG	34:DH:139:ARG:HG3	2.55	0.42
40:DP:98:HIS:CE1	40:DP:102:HIS:HD2	2.38	0.42
42:DT:194:GLY:O	42:DT:207:THR:OG1	2.28	0.42
47:DY:148:ARG:HD3	47:DY:148:ARG:HA	1.85	0.42
51:F3:359:VAL:HG11	51:F3:365:LEU:HD22	2.01	0.42
51:F3:626:HIS:HA	51:F3:659:ARG:HH22	1.85	0.42
53:F6:430:TRP:CD2	53:F6:453:LEU:HD13	2.55	0.42
54:F7:411:ARG:HB3	54:F7:412:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:FM:17:ASN:OD1	56:FM:18:MET:N	2.53	0.42
56:FM:255:THR:HG22	56:FM:305:ARG:HD2	2.00	0.42
60:FX:148:LEU:HD13	60:FX:181:MET:HG2	2.02	0.42
68:Fi:514:VAL:HG13	68:Fi:516:HIS:CE1	2.55	0.42
69:IA:314:ASP:OD1	69:IA:314:ASP:N	2.53	0.42
70:IB:593:PRO:O	70:IB:600:LYS:NZ	2.42	0.42
3:CC:8:HIS:CE1	31:DE:578:GLN:HB3	2.55	0.42
5:CF:48:TYR:HD1	15:CR:170:LEU:HA	1.85	0.42
7:CI:379:MET:HE3	7:CI:379:MET:HB2	1.96	0.42
8:CJ:800:LEU:HB2	8:CJ:803:ILE:HD12	2.02	0.42
28:DB:883:PRO:HD3	28:DB:931:VAL:HG12	2.02	0.42
31:DE:455:ARG:HH21	31:DE:498:GLN:HA	1.84	0.42
33:DG:590:ARG:H	33:DG:590:ARG:HG3	1.70	0.42
41:DR:46:PRO:HA	41:DR:49:GLU:HG2	2.01	0.42
47:DY:139:ASP:OD1	47:DY:140:SER:N	2.50	0.42
49:Da:24:MET:HE2	49:Da:43:PHE:HE2	1.84	0.42
50:F2:954:GLY:HA2	55:F9:126:ARG:NH1	2.35	0.42
51:F3:895:ALA:HA	51:F3:898:VAL:HG22	2.02	0.42
52:F5:446:LEU:O	52:F5:450:MET:HG3	2.19	0.42
53:F6:280:GLU:OE1	53:F6:280:GLU:N	2.52	0.42
56:FM:70:THR:HA	56:FM:73:LYS:HG2	2.02	0.42
57:FO:24:SER:HA	57:FO:57:TRP:NE1	2.35	0.42
57:FO:111:HIS:CE1	57:FO:143:ILE:HD11	2.55	0.42
57:FO:134:HIS:HB3	57:FO:159:MET:SD	2.60	0.42
66:Fg:330:GLU:OE1	67:Fh:307:ARG:NH2	2.53	0.42
68:Fi:249:ARG:O	68:Fi:252:ARG:NH1	2.50	0.42
69:IA:515:CYS:O	69:IA:546:THR:HA	2.20	0.42
69:IA:647:THR:HG22	69:IA:710:GLU:HA	2.02	0.42
1:CA:233:C:H5	70:IB:677:LYS:HD3	1.84	0.42
5:CF:41:ASN:HD21	5:CF:63:ARG:HH11	1.68	0.42
7:CI:158:ALA:HA	7:CI:164:LEU:HD11	2.01	0.42
8:CJ:796:ASP:HB3	22:CI:87:TYR:OH	2.20	0.42
13:CP:177:GLU:OE1	13:CP:177:GLU:N	2.53	0.42
15:CR:138:ARG:HH21	17:CU:44:MET:HB3	1.85	0.42
18:Ca:544:LYS:HE2	18:Ca:544:LYS:HB2	1.92	0.42
19:Cb:41:VAL:HG21	19:Cb:48:PRO:HB3	2.02	0.42
21:Cg:35:GLY:HA3	21:Cg:431:TRP:NE1	2.35	0.42
22:CI:145:ASN:HB3	42:DT:17:HIS:CE1	2.54	0.42
23:Cj:82:VAL:O	23:Cj:86:VAL:HG23	2.20	0.42
24:Ck:373:ARG:HH22	28:DB:637:THR:HG21	1.84	0.42
24:Ck:414:MET:SD	24:Ck:544:ARG:NH2	2.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DB:493:ARG:HH22	33:DG:32:GLY:HA3	1.85	0.42
28:DB:686:GLN:HA	28:DB:689:LEU:HB2	2.02	0.42
28:DB:1043:THR:HB	28:DB:1048:ILE:HD11	2.02	0.42
29:DC:119:THR:HB	29:DC:132:SER:HB2	2.02	0.42
29:DC:542:ARG:HA	29:DC:545:ASP:OD2	2.20	0.42
34:DH:532:ARG:HA	34:DH:535:VAL:HG12	2.01	0.42
39:DO:127:LEU:H	39:DO:127:LEU:HG	1.52	0.42
42:DT:56:GLN:H	42:DT:56:GLN:CD	2.28	0.42
47:DY:29:PRO:HA	47:DY:33:ALA:HB3	2.01	0.42
51:F3:152:THR:H	51:F3:170:ARG:HH12	1.67	0.42
51:F3:464:LEU:O	51:F3:468:GLN:HG2	2.20	0.42
52:F5:121:GLU:HA	52:F5:124:ARG:HD2	2.01	0.42
65:Ff:583:GLY:HA3	65:Ff:677:PHE:HD1	1.85	0.42
67:Fh:138:LEU:HB3	67:Fh:175:CYS:HB2	2.01	0.42
68:Fi:338:ASP:HB3	68:Fi:341:GLU:HG2	2.02	0.42
1:CA:45:G:N2	1:CA:47:U:OP1	2.53	0.41
5:CF:93:LEU:HD13	15:CR:168:ILE:HG23	2.02	0.41
7:CI:17:ARG:HH11	33:DG:387:ARG:HH22	1.68	0.41
8:CJ:137:PHE:CD2	44:DV:129:ILE:HG22	2.55	0.41
8:CJ:554:THR:HG23	8:CJ:557:GLU:H	1.85	0.41
11:CN:149:GLU:HG2	11:CN:153:ASN:HD21	1.85	0.41
11:CN:164:SER:HB3	24:Ck:749:ASP:H	1.85	0.41
14:CQ:143:ASP:OD1	14:CQ:168:ASN:N	2.49	0.41
14:CQ:200:LEU:HD13	54:F7:137:LEU:HA	2.02	0.41
21:Cg:102:PRO:HG2	21:Cg:105:HIS:HB2	2.02	0.41
23:Cj:87:VAL:HG23	40:DP:176:PRO:HB2	2.01	0.41
28:DB:882:ARG:HH22	28:DB:927:THR:HG21	1.85	0.41
28:DB:1050:ILE:HG23	36:DJ:43:SER:HB3	2.02	0.41
29:DC:280:VAL:HG12	29:DC:282:GLY:H	1.85	0.41
29:DC:434:THR:HG23	29:DC:443:ARG:HG3	2.02	0.41
30:DD:592:TRP:CD1	30:DD:592:TRP:H	2.37	0.41
32:DF:222:TYR:CE1	32:DF:229:PRO:HG3	2.53	0.41
33:DG:530:PHE:CZ	33:DG:597:VAL:HA	2.54	0.41
34:DH:523:ARG:HH21	34:DH:524:HIS:CE1	2.32	0.41
38:DL:282:TRP:CD1	38:DL:283:ILE:HG13	2.55	0.41
45:DW:115:ASN:HD22	45:DW:120:ASN:ND2	2.18	0.41
51:F3:500:GLN:CD	51:F3:500:GLN:H	2.27	0.41
52:F5:197:LYS:HG3	52:F5:622:ILE:HD12	2.02	0.41
55:F9:59:VAL:HG22	55:F9:134:ILE:HD11	2.02	0.41
55:F9:325:LYS:HE2	55:F9:325:LYS:HB3	1.89	0.41
56:FN:37:GLN:HB2	56:FN:75:CYS:SG	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:FX:66:LEU:O	60:FX:70:VAL:HG23	2.20	0.41
64:Fd:76:HIS:HE1	64:Fd:78:GLN:HB2	1.85	0.41
65:Ff:290:LEU:HD23	65:Ff:292:ARG:HH21	1.84	0.41
66:Fg:33:CYS:SG	66:Fg:34:LEU:N	2.92	0.41
66:Fg:185:MET:HG2	66:Fg:240:VAL:HG12	2.02	0.41
66:Fg:232:ILE:HG13	66:Fg:236:GLN:HB3	2.01	0.41
67:Fh:273:PRO:HB2	67:Fh:274:LYS:H	1.61	0.41
1:CA:76:A:P	23:Cj:10:ARG:HH21	2.43	0.41
4:CE:158:ASP:OD2	67:Fh:58:ARG:N	2.52	0.41
4:CE:161:GLN:HE22	67:Fh:56:PHE:HA	1.85	0.41
8:CJ:434:ILE:HA	24:Ck:674:LEU:O	2.20	0.41
8:CJ:752:TYR:CD1	22:Ci:23:LEU:HD22	2.55	0.41
14:CQ:151:ARG:N	43:DU:49:TYR:O	2.52	0.41
24:Ck:344:LEU:HB3	24:Ck:587:VAL:HG11	2.01	0.41
31:DE:406:ASP:HA	31:DE:409:TRP:NE1	2.35	0.41
34:DH:503:THR:HG23	34:DH:505:TYR:H	1.85	0.41
38:DL:190:ARG:HG2	38:DL:231:TRP:CE2	2.55	0.41
52:F5:145:ARG:O	52:F5:149:GLU:HG2	2.19	0.41
52:F5:398:PRO:HD2	52:F5:562:ARG:NH1	2.35	0.41
55:F9:371:ARG:O	55:F9:375:GLN:HG3	2.20	0.41
55:F9:449:VAL:HG11	67:Fh:191:ARG:NH1	2.36	0.41
56:FM:82:LEU:HD12	56:FM:88:SER:HA	2.02	0.41
60:FX:146:GLU:OE1	60:FX:146:GLU:N	2.52	0.41
65:Ff:192:GLU:CD	65:Ff:192:GLU:H	2.28	0.41
67:Fh:74:VAL:HG12	70:IB:747:THR:HA	2.02	0.41
67:Fh:76:HIS:NE2	70:IB:745:PRO:HB3	2.34	0.41
69:IA:485:LEU:HD23	69:IA:485:LEU:HA	1.91	0.41
69:IA:528:LYS:O	69:IA:532:GLU:HG2	2.20	0.41
4:CE:395:THR:OG1	4:CE:396:LEU:N	2.52	0.41
11:CN:125:GLY:HA3	36:DJ:22:MET:HE2	2.03	0.41
12:CO:400:ARG:HG2	12:CO:406:PHE:HE2	1.84	0.41
15:CR:173:ARG:HG3	17:CU:41:ARG:NH1	2.35	0.41
27:Cp:60:LEU:O	27:Cp:71:THR:OG1	2.36	0.41
28:DB:675:ALA:HB3	31:DE:475:LEU:HD23	2.01	0.41
29:DC:265:PHE:O	29:DC:269:VAL:HG23	2.21	0.41
30:DD:181:MET:HE2	30:DD:218:VAL:HG21	2.02	0.41
30:DD:399:ILE:HD13	30:DD:399:ILE:HA	1.94	0.41
32:DF:504:SER:OG	32:DF:516:ARG:NE	2.36	0.41
34:DH:279:GLU:HA	34:DH:282:ASN:ND2	2.36	0.41
34:DH:497:MET:O	37:DK:301:ARG:NH2	2.53	0.41
35:DI:126:LEU:HD22	35:DI:149:PHE:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DI:278:LEU:HD11	35:DI:314:GLN:HG3	2.01	0.41
39:DO:231:SER:HB3	54:F7:518:SER:OG	2.20	0.41
41:DR:15:TYR:OH	43:DU:59:ASP:OD2	2.32	0.41
43:DU:179:THR:OG1	43:DU:180:VAL:N	2.53	0.41
47:DY:107:HIS:O	47:DY:111:ARG:HG2	2.19	0.41
50:F2:368:PRO:HB2	55:F9:91:ALA:HB3	2.01	0.41
50:F2:598:MET:HB3	50:F2:603:ILE:HB	2.01	0.41
50:F2:820:ASP:OD1	50:F2:839:ARG:NH2	2.29	0.41
51:F3:146:THR:HA	51:F3:149:MET:HE2	2.01	0.41
52:F5:685:GLN:N	52:F5:686:PRO:HD3	2.35	0.41
52:F5:703:TRP:CE2	63:Fc:113:PHE:HB3	2.55	0.41
52:F5:732:PRO:HA	52:F5:733:PRO:HD3	1.93	0.41
53:F6:215:ARG:NH1	53:F6:217:LEU:O	2.54	0.41
54:F7:269:VAL:HG21	54:F7:301:LEU:HB2	2.03	0.41
54:F7:442:PHE:CE2	54:F7:478:ARG:HD2	2.55	0.41
60:FX:152:ARG:NE	60:FX:181:MET:HE1	2.35	0.41
65:Ff:608:ARG:O	65:Ff:658:GLN:HA	2.20	0.41
65:Ff:642:ASP:OD2	87:Ff:901:FDA:N6A	2.54	0.41
66:Fg:298:ASP:HB3	66:Fg:315:ARG:HG3	2.02	0.41
1:CA:17:G:O2'	30:DD:82:ASN:N	2.45	0.41
1:CA:184:A:H2	27:Cp:90:ARG:HG3	1.84	0.41
1:CA:448:U:H2'	1:CA:449:G:C8	2.54	0.41
6:CH:235:LYS:NZ	30:DD:703:GLY:O	2.53	0.41
7:CI:86:PHE:HA	9:CK:36:GLN:HE21	1.85	0.41
13:CP:81:PRO:HG2	58:FP:19:LYS:HG3	2.02	0.41
14:CQ:206:THR:HG21	54:F7:61:HIS:CE1	2.47	0.41
14:CQ:216:GLU:HG3	68:Fi:519:TYR:CD1	2.55	0.41
16:CS:104:GLN:O	16:CS:140:MET:HG2	2.20	0.41
20:Cd:48:ASN:HA	20:Cd:51:GLU:HG2	2.03	0.41
21:Cg:77:MET:HG3	21:Cg:415:PHE:HB2	2.02	0.41
22:Ci:119:LEU:HG	34:DH:399:PHE:HD2	1.85	0.41
24:Ck:283:GLU:OE2	28:DB:886:SER:HA	2.21	0.41
24:Ck:557:ARG:O	24:Ck:561:SER:OG	2.36	0.41
28:DB:155:ALA:HA	28:DB:158:ARG:HE	1.85	0.41
28:DB:158:ARG:NH1	31:DE:212:LEU:HG	2.35	0.41
28:DB:302:LEU:HD23	31:DE:489:ARG:HG3	2.02	0.41
28:DB:446:LYS:HG2	37:DK:127:HIS:CD2	2.55	0.41
31:DE:404:PRO:HD2	31:DE:407:MET:SD	2.61	0.41
41:DR:75:HIS:CD2	51:F3:432:GLN:HB2	2.55	0.41
44:DV:109:ILE:HG21	44:DV:114:VAL:HG13	2.01	0.41
45:DW:57:PRO:HB2	47:DY:111:ARG:HH22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:F3:274:ASP:H	51:F3:279:SER:HB3	1.84	0.41
52:F5:576:SER:HB2	52:F5:579:ALA:HB3	2.03	0.41
54:F7:587:SER:HB3	54:F7:590:VAL:HG23	2.02	0.41
56:FM:116:ASP:OD1	56:FM:116:ASP:N	2.41	0.41
56:FM:243:GLN:HG3	56:FM:247:ARG:HD3	2.02	0.41
59:FW:49:PRO:HA	59:FW:52:VAL:HG12	2.03	0.41
66:Fg:488:TRP:CD1	66:Fg:492:MET:HE3	2.55	0.41
69:IA:261:HIS:O	69:IA:268:ARG:NH1	2.38	0.41
69:IA:658:CYS:SG	69:IA:688:ARG:HB3	2.61	0.41
7:CI:213:LEU:HD23	7:CI:213:LEU:HA	1.93	0.41
7:CI:334:THR:HG21	8:CJ:209:GLN:HG2	2.02	0.41
11:CN:47:ALA:HB2	22:CI:88:ILE:HG21	2.03	0.41
16:CS:89:TYR:CD2	32:DF:93:PRO:HG2	2.55	0.41
18:Ca:93:PRO:HG2	18:Ca:96:ALA:HB2	2.01	0.41
20:Cd:63:ARG:HG3	20:Cd:64:GLN:N	2.35	0.41
20:Cd:158:GLU:OE1	20:Cd:158:GLU:N	2.46	0.41
20:Cd:185:PHE:CE1	20:Cd:196:VAL:HG23	2.56	0.41
21:Cg:174:LEU:HD22	21:Cg:207:PHE:CZ	2.56	0.41
24:Ck:268:LEU:O	24:Ck:273:SER:HB2	2.20	0.41
28:DB:309:SER:HB3	52:F5:217:ARG:CZ	2.50	0.41
29:DC:894:HIS:H	29:DC:894:HIS:CD2	2.38	0.41
30:DD:262:GLU:HA	43:DU:21:ALA:HB1	2.02	0.41
31:DE:656:ARG:HB3	31:DE:740:PRO:HD3	2.03	0.41
31:DE:659:ARG:HG2	31:DE:737:MET:HB3	2.01	0.41
34:DH:245:TYR:CD2	34:DH:268:LEU:HD21	2.55	0.41
34:DH:405:ARG:HH12	34:DH:413:ASP:CG	2.27	0.41
34:DH:429:ASP:N	34:DH:429:ASP:OD1	2.46	0.41
35:DI:78:LEU:HD13	35:DI:229:SER:HA	2.02	0.41
37:DK:323:THR:HG23	67:Fh:99:SER:HB2	2.01	0.41
41:DR:144:LEU:HD11	41:DR:154:LEU:HD13	2.02	0.41
50:F2:330:ASN:HD22	50:F2:334:GLU:HG2	1.85	0.41
53:F6:31:SER:HB3	53:F6:60:LEU:HG	2.03	0.41
56:FN:63:ARG:HG2	56:FN:65:HIS:HD2	1.86	0.41
65:Ff:403:MET:O	65:Ff:585:ARG:NH1	2.44	0.41
65:Ff:440:ASP:OD1	65:Ff:440:ASP:N	2.52	0.41
65:Ff:705:ALA:HB1	65:Ff:731:HIS:ND1	2.36	0.41
66:Fg:24:GLU:O	66:Fg:27:ARG:NH1	2.53	0.41
67:Fh:167:THR:O	67:Fh:170:GLN:HG3	2.20	0.41
1:CA:184:A:C2	27:Cp:90:ARG:HG3	2.55	0.41
5:CF:123:ARG:NH2	12:CO:139:LEU:O	2.53	0.41
8:CJ:44:PHE:HA	38:DL:283:ILE:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CO:107:LEU:HD13	12:CO:111:GLN:HB3	2.03	0.41
18:Ca:439:GLU:OE2	27:Cp:38:ARG:HB2	2.20	0.41
21:Cg:435:SER:O	21:Cg:440:LYS:HE3	2.21	0.41
28:DB:122:HIS:CD2	28:DB:690:ARG:HB2	2.55	0.41
28:DB:122:HIS:HD2	28:DB:690:ARG:HB2	1.85	0.41
28:DB:347:ALA:HB1	28:DB:351:GLN:HB3	2.01	0.41
28:DB:489:ALA:O	28:DB:493:ARG:HG2	2.20	0.41
29:DC:667:VAL:HG21	29:DC:768:LEU:HD11	2.03	0.41
34:DH:119:LEU:O	34:DH:120:HIS:ND1	2.54	0.41
37:DK:40:VAL:HG22	37:DK:51:VAL:HG22	2.02	0.41
40:DP:20:MET:HE3	40:DP:29:TRP:HB2	2.03	0.41
40:DP:165:ASP:OD1	40:DP:166:CYS:N	2.53	0.41
47:DY:22:ILE:HD13	47:DY:96:ARG:HD3	2.03	0.41
50:F2:630:ALA:HB2	50:F2:710:PRO:HD3	2.02	0.41
50:F2:662:ARG:NH2	50:F2:664:ASP:OD1	2.51	0.41
51:F3:73:PRO:HB2	51:F3:76:GLU:HG2	2.03	0.41
51:F3:765:GLU:O	51:F3:768:ARG:HG2	2.21	0.41
52:F5:128:PHE:CD2	52:F5:148:TYR:HB2	2.56	0.41
52:F5:245:ARG:O	52:F5:249:VAL:HG23	2.19	0.41
53:F6:156:ALA:O	53:F6:159:GLU:HG3	2.21	0.41
53:F6:430:TRP:CD1	53:F6:470:TYR:HA	2.55	0.41
54:F7:326:GLU:CD	54:F7:326:GLU:H	2.29	0.41
56:FM:150:GLN:H	56:FM:150:GLN:HG2	1.70	0.41
56:FM:225:LEU:HD13	56:FM:225:LEU:HA	1.89	0.41
59:FW:39:GLY:HA3	59:FW:70:LEU:HG	2.02	0.41
61:FZ:16:SER:O	61:FZ:23:GLU:HG3	2.21	0.41
64:Fd:106:PRO:HA	64:Fd:109:VAL:HG12	2.02	0.41
65:Ff:408:ARG:HD2	65:Ff:694:PHE:HB3	2.03	0.41
67:Fh:121:SER:O	67:Fh:125:VAL:HG23	2.20	0.41
69:IA:189:ASP:OD1	69:IA:189:ASP:N	2.53	0.41
69:IA:377:CYS:SG	69:IA:408:LEU:HD21	2.61	0.41
70:IB:513:PRO:O	70:IB:526:LYS:NZ	2.36	0.41
70:IB:584:TYR:HB2	70:IB:656:ARG:HH22	1.85	0.41
1:CA:59:U:H5''	1:CA:167:A:C8	2.55	0.41
3:CC:9:TYR:HB2	28:DB:240:ARG:NH2	2.35	0.41
4:CE:102:GLU:O	55:F9:76:ASN:ND2	2.52	0.41
4:CE:299:ASN:HB2	6:CH:247:HIS:CD2	2.55	0.41
8:CJ:776:GLN:NE2	46:DX:131:ILE:HB	2.36	0.41
17:CU:36:SER:H	17:CU:39:TYR:HB3	1.86	0.41
18:Ca:251:LYS:HB2	50:F2:809:SER:HB3	2.03	0.41
19:Cb:133:LYS:HZ2	19:Cb:139:HIS:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Ck:384:LEU:HD13	24:Ck:408:VAL:HG23	2.01	0.41
24:Ck:407:GLU:HB3	24:Ck:548:ILE:HD11	2.02	0.41
28:DB:442:LEU:HD22	28:DB:467:ASN:HD22	1.85	0.41
29:DC:642:ALA:CA	29:DC:647:SER:HB2	2.50	0.41
29:DC:699:VAL:HB	29:DC:702:LEU:HD22	2.02	0.41
29:DC:1111:GLU:O	34:DH:45:HIS:ND1	2.45	0.41
31:DE:78:ASP:HA	31:DE:81:ASP:OD2	2.21	0.41
31:DE:704:LEU:HD23	31:DE:707:ARG:HH11	1.84	0.41
36:DJ:208:GLY:HA3	36:DJ:240:ILE:HG22	2.02	0.41
40:DP:17:PRO:HG2	40:DP:20:MET:SD	2.60	0.41
40:DP:54:LEU:HD13	40:DP:58:TYR:HB3	2.02	0.41
45:DW:108:VAL:HA	47:DY:93:THR:HG21	2.01	0.41
50:F2:40:ASP:OD1	50:F2:43:ARG:NH2	2.53	0.41
51:F3:613:LYS:O	51:F3:616:GLU:HG2	2.21	0.41
52:F5:324:VAL:HG12	52:F5:565:THR:HG22	2.01	0.41
52:F5:609:GLN:HG2	61:FZ:78:GLY:HA3	2.02	0.41
52:F5:723:ARG:HG3	52:F5:728:LEU:HB2	2.02	0.41
56:FM:302:MET:HE1	67:Fh:177:ARG:HH12	1.85	0.41
61:FZ:59:LYS:HG3	61:FZ:63:ASN:HD21	1.86	0.41
61:FZ:75:PHE:CE1	61:FZ:80:GLU:HG3	2.55	0.41
63:Fc:109:VAL:HA	63:Fc:112:VAL:HG22	2.01	0.41
65:Ff:482:ALA:HB3	65:Ff:718:TRP:CE2	2.56	0.41
68:Fi:234:LYS:O	68:Fi:264:ASP:HA	2.19	0.41
69:IA:202:ARG:HH12	69:IA:205:VAL:HG12	1.86	0.41
4:CE:375:ARG:HH12	35:DI:373:LEU:HA	1.86	0.41
8:CJ:220:VAL:O	8:CJ:224:ARG:HG2	2.20	0.41
9:CK:231:ASP:N	65:Ff:520:ASN:HD21	2.19	0.41
13:CP:30:ARG:HA	13:CP:114:PRO:HG2	2.02	0.41
16:CS:105:VAL:HA	16:CS:139:GLU:HA	2.02	0.41
19:Cb:115:ILE:HG13	19:Cb:118:VAL:HG12	2.03	0.41
21:Cg:296:HIS:HE1	21:Cg:297:PHE:CZ	2.39	0.41
28:DB:268:ASP:HA	28:DB:271:ILE:HG12	2.02	0.41
28:DB:568:ARG:NH2	28:DB:853:GLU:OE2	2.49	0.41
29:DC:152:ARG:NH2	29:DC:171:GLU:OE2	2.54	0.41
29:DC:862:PRO:HG2	29:DC:865:CYS:HB2	2.02	0.41
32:DF:198:HIS:CD2	32:DF:199:GLU:HG2	2.50	0.41
32:DF:466:ASP:N	32:DF:466:ASP:OD1	2.45	0.41
36:DJ:139:LEU:H	36:DJ:139:LEU:HD12	1.86	0.41
38:DL:132:ASN:O	38:DL:138:SER:OG	2.20	0.41
39:DO:228:LYS:NZ	51:F3:923:PRO:O	2.54	0.41
51:F3:130:VAL:HG11	51:F3:187:VAL:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:F3:714:TYR:CE1	51:F3:720:ILE:HD12	2.55	0.41
53:F6:184:ASP:HA	53:F6:187:VAL:HG22	2.02	0.41
54:F7:186:HIS:O	54:F7:190:GLN:HG2	2.21	0.41
55:F9:265:GLN:HG2	69:IA:489:GLN:HB2	2.03	0.41
55:F9:545:ALA:HB3	55:F9:547:HIS:CE1	2.56	0.41
58:FP:34:LEU:HD12	58:FP:311:ALA:HB2	2.02	0.41
60:FX:47:TRP:CH2	60:FX:51:ARG:HD2	2.56	0.41
65:Ff:502:LEU:HD21	65:Ff:549:LEU:HD23	2.02	0.41
68:Fi:263:ILE:HB	68:Fi:293:ARG:HG3	2.03	0.41
68:Fi:444:THR:O	68:Fi:548:SER:OG	2.29	0.41
68:Fi:566:PRO:HB3	68:Fi:569:LYS:HD2	2.02	0.41
69:IA:307:VAL:HG23	69:IA:341:GLN:HG3	2.01	0.41
69:IA:706:VAL:HG21	69:IA:709:VAL:HG13	2.02	0.41
1:CA:45:G:C8	27:Cp:68:LEU:HG	2.56	0.41
1:CA:435:G:N1	32:DF:27:ARG:HB2	2.35	0.41
1:CA:503:A:N7	44:DV:55:GLY:HA3	2.36	0.41
4:CE:99:LEU:HD11	55:F9:79:LYS:HB3	2.02	0.41
4:CE:160:ARG:CZ	67:Fh:67:ASN:HD22	2.34	0.41
4:CE:337:ASP:OD1	50:F2:600:ARG:NH2	2.54	0.41
6:CH:126:PRO:HB2	6:CH:158:ARG:HH12	1.85	0.41
8:CJ:10:TYR:OH	34:DH:471:GLU:OE1	2.37	0.41
8:CJ:96:PRO:HB3	28:DB:501:PHE:CG	2.56	0.41
8:CJ:718:PRO:HA	8:CJ:719:PRO:HD3	1.97	0.41
9:CK:232:ARG:HH21	65:Ff:727:PRO:HB2	1.85	0.41
13:CP:123:LEU:O	20:Cd:61:TYR:OH	2.39	0.41
13:CP:136:PRO:HG2	59:FW:137:PRO:HG2	2.03	0.41
13:CP:136:PRO:HG3	23:Cj:230:VAL:HG22	2.03	0.41
14:CQ:165:LEU:O	30:DD:261:ARG:HD3	2.21	0.41
18:Ca:421:TYR:N	18:Ca:480:LEU:O	2.48	0.41
21:Cg:7:LYS:H	21:Cg:7:LYS:HD2	1.86	0.41
24:Ck:658:ILE:HD12	24:Ck:658:ILE:HA	1.96	0.41
24:Ck:810:ILE:HD13	24:Ck:810:ILE:HA	1.98	0.41
27:Cp:37:GLN:OE1	27:Cp:38:ARG:N	2.54	0.41
28:DB:93:LYS:HB3	31:DE:449:TYR:CD1	2.56	0.41
29:DC:161:LEU:HD22	37:DK:294:SER:HB2	2.02	0.41
29:DC:298:ILE:HG21	29:DC:363:ILE:HG22	2.03	0.41
29:DC:757:ARG:HD2	29:DC:934:ARG:HB3	2.03	0.41
31:DE:246:ILE:HD11	31:DE:420:VAL:HA	2.02	0.41
31:DE:298:LYS:HB2	31:DE:336:ILE:HG23	2.02	0.41
32:DF:472:ARG:N	32:DF:473:PRO:HD2	2.36	0.41
32:DF:536:GLU:N	32:DF:536:GLU:OE1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DG:104:VAL:HA	33:DG:107:THR:HG22	2.01	0.41
33:DG:156:TRP:NE1	33:DG:160:ARG:HE	2.19	0.41
33:DG:530:PHE:HD1	33:DG:579:PHE:HE2	1.68	0.41
34:DH:101:GLY:HA2	34:DH:133:CYS:SG	2.61	0.41
34:DH:151:LEU:HD12	34:DH:154:LYS:HD2	2.03	0.41
34:DH:253:SER:HB2	34:DH:287:GLY:CA	2.51	0.41
36:DJ:113:ASP:HB3	36:DJ:116:THR:CG2	2.51	0.41
43:DU:45:ASP:HB3	51:F3:538:ALA:HA	2.03	0.41
46:DX:47:GLN:NE2	46:DX:51:GLU:OE2	2.45	0.41
50:F2:807:GLN:HG2	50:F2:831:THR:HG22	2.03	0.41
51:F3:444:LEU:HD23	51:F3:453:ALA:HB1	2.03	0.41
51:F3:543:LEU:HB2	51:F3:581:ALA:HB2	2.03	0.41
51:F3:638:GLN:HG2	51:F3:698:VAL:HG21	2.03	0.41
51:F3:744:LEU:HD21	51:F3:751:ALA:HB3	2.02	0.41
52:F5:85:ALA:HA	52:F5:88:MET:HG3	2.02	0.41
52:F5:699:PRO:HD2	63:Fc:82:ASN:ND2	2.36	0.41
53:F6:113:ALA:HB3	53:F6:118:HIS:ND1	2.36	0.41
54:F7:154:PHE:CD2	54:F7:161:LEU:HD21	2.56	0.41
54:F7:189:PHE:O	54:F7:193:VAL:HG13	2.21	0.41
54:F7:482:LEU:HD23	54:F7:482:LEU:HA	1.89	0.41
55:F9:95:ARG:NH1	55:F9:99:SER:OG	2.54	0.41
56:FM:55:VAL:HG12	59:FW:161:PRO:HG2	2.02	0.41
56:FM:110:VAL:HG22	56:FM:135:LEU:HB2	2.03	0.41
56:FN:13:VAL:HG12	56:FN:78:ILE:HD11	2.03	0.41
56:FN:292:ARG:HH12	56:FN:321:LEU:HD13	1.86	0.41
57:FO:51:LEU:HD23	57:FO:51:LEU:HA	1.92	0.41
58:FP:46:ARG:HG2	58:FP:91:HIS:C	2.46	0.41
58:FP:140:LEU:HB3	58:FP:267:ASP:HB3	2.02	0.41
60:FX:144:TYR:HB2	60:FX:176:ALA:HB2	2.02	0.41
64:Fd:58:TRP:HH2	64:Fd:72:ILE:HD12	1.86	0.41
65:Ff:391:VAL:HG21	65:Ff:414:VAL:HG23	2.03	0.41
65:Ff:420:ARG:NH1	70:IB:183:ASP:OD1	2.45	0.41
65:Ff:594:TYR:HB2	68:Fi:590:TYR:OH	2.21	0.41
67:Fh:139:LEU:HD11	67:Fh:195:ARG:HG3	2.03	0.41
67:Fh:170:GLN:HE21	67:Fh:170:GLN:HB2	1.65	0.41
68:Fi:398:ASP:O	68:Fi:402:GLN:HG3	2.21	0.41
69:IA:385:ASN:HB3	69:IA:519:THR:HG22	2.03	0.41
69:IA:700:ARG:HB3	75:UG:4:ALA:HB3	2.02	0.41
70:IB:589:CYS:SG	70:IB:590:TYR:N	2.94	0.41
1:CA:226:A:H2'	1:CA:227:U:C6	2.56	0.41
4:CE:28:ILE:HD12	30:DD:782:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CJ:74:TRP:CD2	8:CJ:75:TYR:HB2	2.56	0.41
8:CJ:413:GLU:O	8:CJ:416:MET:HG3	2.20	0.41
12:CO:264:ARG:HG2	12:CO:287:LEU:HD13	2.02	0.41
13:CP:145:LEU:HB3	30:DD:656:LEU:HB3	2.03	0.41
14:CQ:197:LYS:HE2	14:CQ:197:LYS:HB3	1.87	0.41
15:CR:229:HIS:ND1	19:Cb:172:GLY:HA3	2.36	0.41
24:Ck:145:LEU:HD13	24:Ck:145:LEU:HA	1.94	0.41
28:DB:443:LEU:HD11	28:DB:452:ARG:HD3	2.02	0.41
29:DC:301:LYS:HA	29:DC:301:LYS:HD3	1.87	0.41
29:DC:912:LEU:HD12	29:DC:912:LEU:H	1.86	0.41
30:DD:343:TRP:HD1	30:DD:344:ALA:C	2.29	0.41
33:DG:29:ASP:OD1	33:DG:29:ASP:N	2.54	0.41
34:DH:245:TYR:O	34:DH:249:MET:HG3	2.21	0.41
37:DK:285:GLU:HB3	37:DK:289:LYS:NZ	2.36	0.41
41:DR:194:LYS:HE3	41:DR:195:TYR:CZ	2.56	0.41
42:DT:52:ARG:HE	42:DT:52:ARG:HB3	1.60	0.41
45:DW:62:LEU:HA	47:DY:114:TRP:HH2	1.85	0.41
46:DX:107:LEU:HB3	46:DX:112:TYR:CE1	2.54	0.41
50:F2:99:GLY:HA3	50:F2:224:ILE:HG23	2.03	0.41
50:F2:411:LYS:HE2	50:F2:411:LYS:HB3	1.86	0.41
51:F3:549:ASN:ND2	51:F3:597:ASP:HB2	2.36	0.41
52:F5:125:ARG:HD3	52:F5:148:TYR:CD2	2.56	0.41
53:F6:49:HIS:CD2	53:F6:49:HIS:H	2.39	0.41
54:F7:129:MET:HA	54:F7:132:LEU:HB2	2.03	0.41
55:F9:354:MET:HE3	55:F9:354:MET:HB3	1.87	0.41
56:FN:15:MET:SD	56:FN:45:LYS:HB3	2.61	0.41
63:Fc:65:TYR:HD2	63:Fc:66:LEU:HG	1.86	0.41
66:Fg:213:LEU:HB3	66:Fg:272:VAL:HG11	2.03	0.41
66:Fg:503:GLU:OE2	66:Fg:505:HIS:NE2	2.45	0.41
68:Fi:96:LEU:HD13	68:Fi:209:SER:HB3	2.03	0.41
69:IA:157:HIS:CD2	69:IA:159:LEU:H	2.39	0.41
1:CA:514:A:N7	44:DV:67:ASN:HB3	2.36	0.40
7:CI:14:ARG:HA	7:CI:17:ARG:HE	1.86	0.40
7:CI:215:TRP:HD1	50:F2:56:GLN:HB3	1.86	0.40
7:CI:324:ARG:HG2	7:CI:325:GLU:N	2.35	0.40
8:CJ:381:SER:OG	8:CJ:384:GLU:HG2	2.21	0.40
8:CJ:568:GLU:O	8:CJ:571:GLN:HG3	2.21	0.40
12:CO:207:TYR:HB3	12:CO:226:VAL:HG21	2.03	0.40
14:CQ:223:ARG:NH2	54:F7:90:GLU:OE2	2.54	0.40
19:Cb:95:ARG:HA	19:Cb:98:LEU:HG	2.02	0.40
21:Cg:89:PHE:HZ	21:Cg:164:HIS:HB2	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Cj:123:GLU:OE2	41:DR:242:SER:OG	2.24	0.40
23:Cj:157:THR:OG1	30:DD:356:PRO:HB2	2.21	0.40
24:Ck:652:ARG:HD2	24:Ck:661:ILE:HD12	2.04	0.40
27:Cp:92:LEU:HD22	27:Cp:97:ILE:HD12	2.03	0.40
28:DB:173:ARG:HH22	29:DC:654:ARG:HE	1.68	0.40
28:DB:627:HIS:CD2	28:DB:631:LEU:HD11	2.56	0.40
28:DB:665:ARG:HH22	28:DB:841:ARG:HG3	1.86	0.40
28:DB:917:LEU:HB3	28:DB:930:GLU:HG2	2.03	0.40
30:DD:446:GLY:O	30:DD:490:LEU:HD21	2.21	0.40
31:DE:39:PHE:HD1	31:DE:39:PHE:HA	1.71	0.40
31:DE:659:ARG:HA	31:DE:659:ARG:HD2	1.91	0.40
33:DG:334:MET:HE3	33:DG:388:TYR:HB2	2.02	0.40
33:DG:483:THR:O	33:DG:487:VAL:HG22	2.21	0.40
38:DL:32:HIS:HD2	38:DL:34:ILE:HG22	1.86	0.40
39:DO:124:CYS:SG	39:DO:137:ASN:ND2	2.94	0.40
41:DR:81:PRO:HG3	41:DR:133:LEU:HD13	2.03	0.40
41:DR:143:PRO:HD3	41:DR:173:ASN:HD21	1.85	0.40
51:F3:114:GLU:HB2	51:F3:133:ARG:HH12	1.86	0.40
51:F3:157:GLU:O	51:F3:242:SER:HB3	2.21	0.40
51:F3:609:PRO:HD2	51:F3:612:LEU:HD13	2.03	0.40
51:F3:731:CYS:SG	51:F3:732:SER:N	2.95	0.40
53:F6:52:PRO:HA	53:F6:53:PRO:HD3	1.95	0.40
57:FO:52:PHE:HB2	57:FO:84:TYR:CE2	2.56	0.40
57:FO:147:ASN:HD21	57:FO:180:ARG:HD2	1.85	0.40
62:Fb:117:PHE:HA	62:Fb:120:ASP:OD2	2.20	0.40
66:Fg:17:HIS:CE1	66:Fg:107:THR:HG21	2.57	0.40
67:Fh:161:PRO:HB2	67:Fh:163:PRO:HD2	2.02	0.40
69:IA:418:ARG:CZ	69:IA:440:HIS:HB3	2.51	0.40
69:IA:539:ILE:HG21	69:IA:605:LEU:HD22	2.03	0.40
6:CH:221:PRO:HA	6:CH:279:MET:HB3	2.03	0.40
7:CI:36:GLU:H	7:CI:36:GLU:HG2	1.38	0.40
8:CJ:48:ILE:HB	38:DL:104:ARG:NH1	2.37	0.40
12:CO:268:LYS:HD2	12:CO:268:LYS:HA	1.89	0.40
18:Ca:102:TRP:CE2	18:Ca:159:LEU:HD13	2.56	0.40
18:Ca:315:VAL:HG21	56:FM:4:ILE:HD11	2.02	0.40
18:Ca:423:GLN:H	30:DD:675:ASN:ND2	2.19	0.40
21:Cg:73:ASP:O	21:Cg:76:SER:OG	2.35	0.40
24:Ck:580:ALA:HA	24:Ck:583:ARG:HB2	2.02	0.40
27:Cp:57:GLU:HG3	27:Cp:75:LYS:HB2	2.03	0.40
29:DC:307:LEU:O	29:DC:310:ARG:NH1	2.54	0.40
29:DC:1136:GLU:OE2	34:DH:2:LEU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DD:173:GLN:H	30:DD:176:HIS:HD2	1.70	0.40
30:DD:326:PRO:C	30:DD:385:ASN:HD21	2.29	0.40
32:DF:174:PHE:O	32:DF:178:ASN:ND2	2.54	0.40
33:DG:568:ALA:HA	33:DG:571:VAL:HG12	2.03	0.40
36:DJ:236:ARG:HG3	36:DJ:276:LEU:HD11	2.03	0.40
40:DP:110:PRO:HG2	40:DP:142:ASN:ND2	2.36	0.40
42:DT:11:ASP:OD1	42:DT:12:ARG:N	2.54	0.40
42:DT:233:HIS:CG	42:DT:238:PRO:HA	2.57	0.40
45:DW:126:ARG:O	45:DW:130:ARG:HD3	2.21	0.40
50:F2:846:PHE:CZ	50:F2:852:LYS:HG2	2.56	0.40
52:F5:664:GLU:H	52:F5:664:GLU:HG3	1.67	0.40
52:F5:738:GLU:OE1	52:F5:738:GLU:N	2.43	0.40
53:F6:225:ALA:HB2	53:F6:265:TRP:HB2	2.03	0.40
53:F6:542:ARG:N	53:F6:545:TYR:HB3	2.37	0.40
54:F7:331:MET:O	54:F7:334:GLU:HG2	2.21	0.40
57:FO:42:LEU:HA	57:FO:46:HIS:ND1	2.37	0.40
57:FO:147:ASN:ND2	57:FO:180:ARG:HH11	2.19	0.40
58:FP:287:GLY:HA3	58:FP:309:LEU:HD11	2.03	0.40
59:FW:204:TRP:CG	59:FW:235:ARG:HD3	2.55	0.40
65:Ff:386:TRP:HB3	65:Ff:392:HIS:CE1	2.57	0.40
65:Ff:649:ILE:HG12	65:Ff:683:CYS:HA	2.03	0.40
69:IA:324:GLN:HA	69:IA:327:ARG:HD2	2.02	0.40
1:CA:126:U:H5''	1:CA:127:G:C8	2.57	0.40
1:CA:304:U:H2'	1:CA:305:A:C8	2.56	0.40
4:CE:29:TYR:CE1	4:CE:33:MET:HG3	2.56	0.40
8:CJ:252:PHE:CE1	8:CJ:396:LYS:HE2	2.56	0.40
13:CP:87:HIS:HB2	18:Ca:441:ASN:ND2	2.35	0.40
14:CQ:150:CYS:HB3	14:CQ:160:TYR:CD1	2.56	0.40
14:CQ:190:PRO:HG3	54:F7:111:THR:HG21	2.03	0.40
21:Cg:238:ARG:HE	21:Cg:241:GLN:HE22	1.69	0.40
24:Ck:72:ASP:HB2	31:DE:655:ARG:HH22	1.86	0.40
24:Ck:133:TRP:NE1	24:Ck:317:VAL:O	2.45	0.40
24:Ck:381:ALA:O	24:Ck:385:HIS:ND1	2.34	0.40
24:Ck:602:LEU:HA	24:Ck:605:VAL:HG12	2.02	0.40
27:Cp:146:LEU:HD12	27:Cp:147:PRO:HD2	2.04	0.40
28:DB:82:GLY:HA2	31:DE:216:LEU:HD11	2.02	0.40
28:DB:1067:ILE:H	28:DB:1067:ILE:HG12	1.70	0.40
28:DB:1163:LYS:HE2	28:DB:1163:LYS:HB3	1.92	0.40
29:DC:29:TYR:OH	42:DT:42:PHE:HB3	2.20	0.40
33:DG:359:ARG:CZ	33:DG:370:ARG:HH22	2.33	0.40
33:DG:381:ASP:O	33:DG:384:VAL:HG12	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DI:307:ASN:ND2	35:DI:310:LEU:HD13	2.37	0.40
36:DJ:196:ASP:OD1	36:DJ:197:THR:N	2.54	0.40
40:DP:211:GLU:OE1	40:DP:211:GLU:N	2.55	0.40
50:F2:18:ALA:O	50:F2:22:VAL:HG23	2.22	0.40
50:F2:229:PHE:CG	50:F2:247:LEU:HD11	2.56	0.40
50:F2:438:SER:O	50:F2:442:ILE:HG13	2.21	0.40
51:F3:628:CYS:SG	51:F3:659:ARG:NE	2.94	0.40
52:F5:188:ARG:HH11	61:FZ:19:ASN:HB3	1.86	0.40
55:F9:211:GLN:NE2	61:FZ:25:TYR:OH	2.54	0.40
55:F9:295:THR:O	55:F9:298:GLU:HG3	2.22	0.40
56:FN:36:LEU:O	56:FN:62:MET:HA	2.21	0.40
56:FN:193:GLN:HG3	56:FN:266:ASP:HB3	2.02	0.40
57:FO:175:HIS:CG	57:FO:191:MET:HE2	2.56	0.40
63:Fc:132:GLN:N	63:Fc:136:ASP:OD2	2.42	0.40
63:Fc:141:ILE:HD13	63:Fc:141:ILE:HA	1.92	0.40
65:Ff:321:HIS:ND1	65:Ff:321:HIS:O	2.55	0.40
67:Fh:156:ASP:O	67:Fh:160:LEU:HG	2.21	0.40
67:Fh:163:PRO:HA	67:Fh:166:ASP:OD2	2.22	0.40
67:Fh:308:PRO:O	67:Fh:313:TRP:NE1	2.48	0.40
70:IB:544:LEU:O	70:IB:586:GLU:HA	2.21	0.40
1:CA:230:A:H62	1:CA:247:A:H2	1.69	0.40
1:CA:426:A:N6	34:DH:47:ILE:HD13	2.36	0.40
5:CF:108:ASN:O	5:CF:112:GLN:HG3	2.20	0.40
7:CI:95:PRO:HD3	33:DG:68:TYR:OH	2.22	0.40
7:CI:124:GLU:O	7:CI:128:ARG:HG3	2.22	0.40
8:CJ:112:ARG:HG2	28:DB:910:PHE:CE2	2.56	0.40
9:CK:182:TRP:HB3	20:CD:200:LEU:HD22	2.03	0.40
13:CP:148:TYR:OH	30:DD:663:ASP:OD2	2.38	0.40
15:CR:182:SER:HA	15:CR:185:PHE:HD2	1.86	0.40
15:CR:211:ASN:O	15:CR:215:THR:HG23	2.21	0.40
21:Cg:288:TRP:N	21:Cg:356:CYS:O	2.41	0.40
24:Ck:316:ASP:OD1	24:Ck:316:ASP:N	2.53	0.40
24:Ck:318:THR:HG22	24:Ck:319:GLY:H	1.86	0.40
24:Ck:414:MET:HE2	24:Ck:414:MET:HB3	1.94	0.40
28:DB:224:LEU:HD13	31:DE:636:TYR:CD2	2.57	0.40
28:DB:554:GLU:OE1	28:DB:863:TRP:NE1	2.37	0.40
28:DB:1022:TYR:HB3	33:DG:27:TRP:HE1	1.86	0.40
29:DC:97:ARG:HE	29:DC:97:ARG:HA	1.87	0.40
29:DC:975:ALA:HB1	29:DC:1059:LEU:HD21	2.02	0.40
29:DC:1014:SER:HB2	31:DE:617:ASP:OD1	2.22	0.40
30:DD:59:ASN:HB2	56:FM:55:VAL:HG21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DF:532:LEU:HD12	32:DF:532:LEU:HA	1.92	0.40
34:DH:334:GLU:N	34:DH:335:PRO:HD2	2.37	0.40
51:F3:557:ARG:HG2	51:F3:560:ARG:HH21	1.84	0.40
52:F5:653:TYR:OH	63:Fc:118:GLU:OE1	2.31	0.40
56:FM:190:MET:HB3	56:FM:270:LEU:HD13	2.02	0.40
57:FO:79:GLY:HA3	66:Fg:334:LEU:HD22	2.03	0.40
60:FX:28:LEU:HD21	60:FX:50:ALA:HA	2.03	0.40
61:FZ:120:LEU:HA	61:FZ:123:GLU:HG2	2.04	0.40
62:Fb:34:ARG:HH21	62:Fb:38:LYS:HE3	1.86	0.40
65:Ff:631:MET:HA	65:Ff:631:MET:HE3	2.03	0.40
66:Fg:103:LEU:O	66:Fg:107:THR:OG1	2.40	0.40
66:Fg:147:LEU:HD11	66:Fg:478:LEU:HD21	2.02	0.40
68:Fi:37:PRO:O	68:Fi:40:GLN:NE2	2.54	0.40
68:Fi:443:GLU:OE2	68:Fi:547:ARG:HB3	2.21	0.40
1:CA:410:U:O2'	1:CA:493:U:H5'	2.22	0.40
1:CA:501:A:C8	44:DV:63:ILE:HD11	2.57	0.40
7:CI:109:LEU:HD23	7:CI:109:LEU:HA	1.95	0.40
7:CI:317:TYR:CE1	7:CI:387:ALA:HB2	2.56	0.40
8:CJ:740:LYS:HD2	8:CJ:740:LYS:H	1.87	0.40
10:CL:18:LEU:HD23	69:IA:558:LEU:HG	2.03	0.40
12:CO:114:ARG:HA	12:CO:114:ARG:HD3	1.82	0.40
15:CR:143:TYR:CD2	15:CR:145:ALA:HB3	2.55	0.40
18:Ca:106:ASN:HD22	18:Ca:155:ARG:HD3	1.85	0.40
18:Ca:353:ILE:O	30:DD:771:TYR:OH	2.30	0.40
20:Cd:117:LYS:HD2	35:DI:282:ASP:HA	2.03	0.40
22:CI:121:ASP:HB3	22:CI:128:SER:HA	2.04	0.40
22:CI:130:PRO:HD3	32:DF:32:TRP:CD1	2.56	0.40
24:Ck:32:GLN:NE2	28:DB:285:MET:H	2.20	0.40
24:Ck:732:ARG:HD2	24:Ck:777:ALA:HB2	2.02	0.40
28:DB:514:ARG:HH21	28:DB:851:ILE:HG23	1.87	0.40
29:DC:708:TYR:CE1	37:DK:166:ALA:HA	2.56	0.40
31:DE:212:LEU:HD11	31:DE:405:ILE:HD13	2.03	0.40
32:DF:27:ARG:HH21	32:DF:29:ARG:CZ	2.35	0.40
33:DG:349:ASP:O	33:DG:353:VAL:HG22	2.22	0.40
33:DG:554:HIS:HB2	33:DG:559:VAL:HG21	2.02	0.40
34:DH:25:LYS:HD3	34:DH:415:HIS:CE1	2.57	0.40
41:DR:214:GLU:OE1	41:DR:217:ASN:ND2	2.54	0.40
41:DR:255:PRO:HA	41:DR:265:MET:SD	2.62	0.40
50:F2:398:ARG:O	50:F2:401:GLN:HG3	2.22	0.40
50:F2:569:ARG:NH2	50:F2:606:ARG:HH11	2.20	0.40
55:F9:165:ARG:O	55:F9:169:GLU:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:FO:317:ARG:HA	57:FO:320:ALA:O	2.22	0.40
58:FP:72:ASP:HB2	58:FP:289:LYS:HE2	2.03	0.40
61:FZ:59:LYS:HD2	61:FZ:59:LYS:HA	1.88	0.40
66:Fg:73:ILE:HG23	66:Fg:164:ARG:HG2	2.04	0.40
66:Fg:385:MET:HE2	66:Fg:385:MET:HB3	1.87	0.40
69:IA:150:PRO:O	69:IA:154:LEU:HG	2.22	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	
3	CC	72/74 (97%)	68 (94%)	4 (6%)	0	100	100
4	CE	369/435 (85%)	357 (97%)	12 (3%)	0	100	100
5	CF	153/160 (96%)	150 (98%)	3 (2%)	0	100	100
6	CH	213/282 (76%)	208 (98%)	5 (2%)	0	100	100
7	CI	417/443 (94%)	406 (97%)	11 (3%)	0	100	100
8	CJ	776/817 (95%)	748 (96%)	27 (4%)	1 (0%)	48	79
9	CK	173/326 (53%)	170 (98%)	3 (2%)	0	100	100
10	CL	81/87 (93%)	78 (96%)	3 (4%)	0	100	100
11	CN	155/166 (93%)	147 (95%)	8 (5%)	0	100	100
12	CO	358/429 (83%)	341 (95%)	17 (5%)	0	100	100
13	CP	178/188 (95%)	168 (94%)	10 (6%)	0	100	100
14	CQ	245/307 (80%)	239 (98%)	6 (2%)	0	100	100
15	CR	118/320 (37%)	110 (93%)	8 (7%)	0	100	100
16	CS	97/244 (40%)	88 (91%)	9 (9%)	0	100	100
17	CU	31/193 (16%)	30 (97%)	1 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	Ca	497/602 (83%)	486 (98%)	11 (2%)	0	100	100
19	Cb	145/325 (45%)	141 (97%)	4 (3%)	0	100	100
20	Cd	203/440 (46%)	199 (98%)	4 (2%)	0	100	100
21	Cg	485/498 (97%)	472 (97%)	13 (3%)	0	100	100
22	Ci	163/181 (90%)	157 (96%)	6 (4%)	0	100	100
23	Cj	224/257 (87%)	220 (98%)	4 (2%)	0	100	100
24	Ck	667/874 (76%)	650 (98%)	17 (2%)	0	100	100
25	Cm	29/215 (14%)	29 (100%)	0	0	100	100
26	Cn	47/250 (19%)	47 (100%)	0	0	100	100
27	Cp	166/187 (89%)	163 (98%)	3 (2%)	0	100	100
28	DB	1102/1181 (93%)	1061 (96%)	41 (4%)	0	100	100
29	DC	1093/1165 (94%)	1049 (96%)	44 (4%)	0	100	100
30	DD	760/812 (94%)	733 (96%)	27 (4%)	0	100	100
31	DE	620/747 (83%)	600 (97%)	20 (3%)	0	100	100
32	DF	592/666 (89%)	567 (96%)	25 (4%)	0	100	100
33	DG	549/631 (87%)	533 (97%)	16 (3%)	0	100	100
34	DH	566/581 (97%)	549 (97%)	17 (3%)	0	100	100
35	DI	388/407 (95%)	378 (97%)	10 (3%)	0	100	100
36	DJ	354/396 (89%)	341 (96%)	13 (4%)	0	100	100
37	DK	258/324 (80%)	247 (96%)	11 (4%)	0	100	100
38	DL	228/307 (74%)	226 (99%)	2 (1%)	0	100	100
39	DO	192/282 (68%)	188 (98%)	4 (2%)	0	100	100
40	DP	208/274 (76%)	201 (97%)	7 (3%)	0	100	100
41	DR	248/270 (92%)	239 (96%)	9 (4%)	0	100	100
42	DT	237/247 (96%)	232 (98%)	5 (2%)	0	100	100
43	DU	215/228 (94%)	209 (97%)	6 (3%)	0	100	100
44	DV	158/183 (86%)	149 (94%)	9 (6%)	0	100	100
45	DW	134/179 (75%)	132 (98%)	2 (2%)	0	100	100
46	DX	127/169 (75%)	117 (92%)	10 (8%)	0	100	100
47	DY	152/163 (93%)	144 (95%)	8 (5%)	0	100	100
48	DZ	26/94 (28%)	24 (92%)	2 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	Da	34/64 (53%)	33 (97%)	1 (3%)	0	100	100
50	F2	882/1024 (86%)	866 (98%)	16 (2%)	0	100	100
51	F3	907/966 (94%)	877 (97%)	30 (3%)	0	100	100
52	F5	614/754 (81%)	600 (98%)	14 (2%)	0	100	100
53	F6	514/676 (76%)	507 (99%)	7 (1%)	0	100	100
54	F7	646/679 (95%)	614 (95%)	32 (5%)	0	100	100
55	F9	536/607 (88%)	523 (98%)	13 (2%)	0	100	100
56	FM	325/370 (88%)	316 (97%)	9 (3%)	0	100	100
56	FN	318/370 (86%)	309 (97%)	9 (3%)	0	100	100
57	FO	324/334 (97%)	312 (96%)	12 (4%)	0	100	100
58	FP	346/349 (99%)	335 (97%)	11 (3%)	0	100	100
59	FW	234/263 (89%)	229 (98%)	5 (2%)	0	100	100
60	FX	218/239 (91%)	212 (97%)	6 (3%)	0	100	100
61	FZ	158/178 (89%)	153 (97%)	5 (3%)	0	100	100
62	Fb	123/151 (82%)	117 (95%)	6 (5%)	0	100	100
63	Fc	81/148 (55%)	79 (98%)	2 (2%)	0	100	100
64	Fd	91/143 (64%)	89 (98%)	2 (2%)	0	100	100
65	Ff	619/848 (73%)	587 (95%)	32 (5%)	0	100	100
66	Fg	514/550 (94%)	493 (96%)	21 (4%)	0	100	100
67	Fh	233/318 (73%)	226 (97%)	7 (3%)	0	100	100
68	Fi	465/629 (74%)	447 (96%)	18 (4%)	0	100	100
69	IA	700/787 (89%)	678 (97%)	22 (3%)	0	100	100
70	IB	487/803 (61%)	466 (96%)	19 (4%)	2 (0%)	30	61
73	UD	11/13 (85%)	11 (100%)	0	0	100	100
75	UG	13/15 (87%)	10 (77%)	3 (23%)	0	100	100
All	All	23662/28884 (82%)	22880 (97%)	779 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
70	IB	429	PRO
70	IB	783	PRO
8	CJ	540	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CC	73/73 (100%)	68 (93%)	5 (7%)	14	42
4	CE	314/372 (84%)	306 (98%)	8 (2%)	42	63
5	CF	139/144 (96%)	132 (95%)	7 (5%)	22	49
6	CH	192/246 (78%)	189 (98%)	3 (2%)	55	69
7	CI	354/371 (95%)	345 (98%)	9 (2%)	42	63
8	CJ	691/723 (96%)	668 (97%)	23 (3%)	33	58
9	CK	150/283 (53%)	145 (97%)	5 (3%)	33	58
10	CL	75/79 (95%)	73 (97%)	2 (3%)	39	61
11	CN	142/150 (95%)	142 (100%)	0	100	100
12	CO	316/377 (84%)	312 (99%)	4 (1%)	61	72
13	CP	160/168 (95%)	156 (98%)	4 (2%)	42	63
14	CQ	216/270 (80%)	211 (98%)	5 (2%)	44	64
15	CR	111/279 (40%)	105 (95%)	6 (5%)	20	47
16	CS	90/220 (41%)	89 (99%)	1 (1%)	65	74
17	CU	31/169 (18%)	29 (94%)	2 (6%)	15	43
18	Ca	440/543 (81%)	432 (98%)	8 (2%)	51	68
19	Cb	128/277 (46%)	123 (96%)	5 (4%)	28	54
20	Cd	186/381 (49%)	182 (98%)	4 (2%)	45	65
21	Cg	429/437 (98%)	420 (98%)	9 (2%)	47	65
22	Ci	144/160 (90%)	140 (97%)	4 (3%)	38	60
23	Cj	193/219 (88%)	188 (97%)	5 (3%)	40	62
24	Ck	583/746 (78%)	572 (98%)	11 (2%)	50	67
25	Cm	26/184 (14%)	25 (96%)	1 (4%)	29	55
26	Cn	43/210 (20%)	42 (98%)	1 (2%)	44	64
27	Cp	157/175 (90%)	157 (100%)	0	100	100
28	DB	972/1030 (94%)	941 (97%)	31 (3%)	34	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	DC	929/985 (94%)	905 (97%)	24 (3%)	40	62
30	DD	673/673 (100%)	663 (98%)	10 (2%)	57	70
31	DE	552/642 (86%)	537 (97%)	15 (3%)	39	61
32	DF	504/560 (90%)	497 (99%)	7 (1%)	59	71
33	DG	483/543 (89%)	471 (98%)	12 (2%)	42	63
34	DH	496/504 (98%)	480 (97%)	16 (3%)	34	58
35	DI	350/365 (96%)	343 (98%)	7 (2%)	48	66
36	DJ	312/347 (90%)	307 (98%)	5 (2%)	55	69
37	DK	218/261 (84%)	217 (100%)	1 (0%)	81	80
38	DL	199/263 (76%)	194 (98%)	5 (2%)	42	63
39	DO	163/229 (71%)	161 (99%)	2 (1%)	63	73
40	DP	189/239 (79%)	187 (99%)	2 (1%)	65	74
41	DR	221/235 (94%)	217 (98%)	4 (2%)	51	68
42	DT	220/228 (96%)	214 (97%)	6 (3%)	39	61
43	DU	179/201 (89%)	177 (99%)	2 (1%)	65	74
44	DV	145/165 (88%)	143 (99%)	2 (1%)	59	71
45	DW	126/163 (77%)	123 (98%)	3 (2%)	43	63
46	DX	114/149 (76%)	113 (99%)	1 (1%)	70	76
47	DY	137/146 (94%)	135 (98%)	2 (2%)	57	70
48	DZ	23/84 (27%)	23 (100%)	0	100	100
49	Da	32/59 (54%)	31 (97%)	1 (3%)	35	59
50	F2	752/867 (87%)	746 (99%)	6 (1%)	73	77
51	F3	767/809 (95%)	746 (97%)	21 (3%)	39	61
52	F5	533/642 (83%)	517 (97%)	16 (3%)	36	59
53	F6	462/590 (78%)	448 (97%)	14 (3%)	36	59
54	F7	553/577 (96%)	543 (98%)	10 (2%)	51	68
55	F9	449/503 (89%)	438 (98%)	11 (2%)	43	63
56	FM	258/292 (88%)	252 (98%)	6 (2%)	44	64
56	FN	252/292 (86%)	248 (98%)	4 (2%)	55	69
57	FO	285/290 (98%)	276 (97%)	9 (3%)	34	58
58	FP	270/286 (94%)	267 (99%)	3 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	FW	214/234 (92%)	214 (100%)	0	100	100
60	FX	178/195 (91%)	177 (99%)	1 (1%)	78	79
61	FZ	140/156 (90%)	132 (94%)	8 (6%)	18	46
62	Fb	113/135 (84%)	111 (98%)	2 (2%)	51	68
63	Fc	77/127 (61%)	74 (96%)	3 (4%)	28	54
64	Fd	77/119 (65%)	73 (95%)	4 (5%)	21	48
65	Ff	524/715 (73%)	514 (98%)	10 (2%)	50	67
66	Fg	446/469 (95%)	441 (99%)	5 (1%)	65	74
67	Fh	189/281 (67%)	182 (96%)	7 (4%)	30	56
68	Fi	413/536 (77%)	397 (96%)	16 (4%)	28	54
69	IA	590/661 (89%)	560 (95%)	30 (5%)	21	49
70	IB	393/675 (58%)	383 (98%)	10 (2%)	42	63
All	All	20555/24778 (83%)	20069 (98%)	486 (2%)	43	63

All (486) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CC	4	ILE
3	CC	10	LYS
3	CC	12	ILE
3	CC	23	ILE
3	CC	47	ILE
4	CE	28	ILE
4	CE	53	LEU
4	CE	59	LEU
4	CE	201	ILE
4	CE	232	ILE
4	CE	233	VAL
4	CE	256	LEU
4	CE	294	HIS
5	CF	6	PHE
5	CF	7	VAL
5	CF	46	ARG
5	CF	52	ARG
5	CF	61	TYR
5	CF	104	ILE
5	CF	105	ARG
6	CH	26	ARG

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Mol	Chain	Res	Type
6	CH	170	VAL
6	CH	236	MET
7	CI	36	GLU
7	CI	38	LEU
7	CI	67	LEU
7	CI	85	LEU
7	CI	99	VAL
7	CI	104	ASN
7	CI	163	GLU
7	CI	290	ILE
7	CI	399	LEU
8	CJ	71	VAL
8	CJ	105	ASN
8	CJ	229	VAL
8	CJ	323	LEU
8	CJ	341	CYS
8	CJ	445	VAL
8	CJ	454	THR
8	CJ	469	ASP
8	CJ	517	VAL
8	CJ	537	LEU
8	CJ	555	TRP
8	CJ	598	VAL
8	CJ	641	VAL
8	CJ	648	VAL
8	CJ	654	VAL
8	CJ	656	VAL
8	CJ	681	LEU
8	CJ	740	LYS
8	CJ	742	PHE
8	CJ	757	LEU
8	CJ	767	VAL
8	CJ	800	LEU
8	CJ	803	ILE
9	CK	193	VAL
9	CK	225	ARG
9	CK	228	LYS
9	CK	255	LEU
9	CK	300	ASN
10	CL	20	VAL
10	CL	38	LEU
12	CO	87	THR

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Mol	Chain	Res	Type
12	CO	146	LEU
12	CO	182	ASN
12	CO	396	LYS
13	CP	13	ILE
13	CP	47	VAL
13	CP	92	THR
13	CP	94	VAL
14	CQ	26	TYR
14	CQ	36	ASN
14	CQ	66	VAL
14	CQ	104	LEU
14	CQ	249	ILE
15	CR	64	VAL
15	CR	65	GLN
15	CR	68	TYR
15	CR	69	HIS
15	CR	176	ASN
15	CR	183	GLN
16	CS	53	LEU
17	CU	39	TYR
17	CU	66	HIS
18	Ca	63	GLN
18	Ca	192	GLN
18	Ca	208	VAL
18	Ca	305	HIS
18	Ca	388	THR
18	Ca	402	VAL
18	Ca	494	LYS
18	Ca	579	VAL
19	Cb	94	LEU
19	Cb	137	VAL
19	Cb	147	LEU
19	Cb	170	LEU
19	Cb	175	ILE
20	Cd	29	THR
20	Cd	32	LEU
20	Cd	190	ASP
20	Cd	201	LEU
21	Cg	7	LYS
21	Cg	43	ARG
21	Cg	107	ARG
21	Cg	114	GLU

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Mol	Chain	Res	Type
21	Cg	139	THR
21	Cg	172	VAL
21	Cg	262	GLN
21	Cg	269	LEU
21	Cg	296	HIS
22	Ci	15	VAL
22	Ci	84	LEU
22	Ci	136	HIS
22	Ci	149	LEU
23	Cj	50	VAL
23	Cj	59	VAL
23	Cj	130	VAL
23	Cj	167	ASP
23	Cj	209	TYR
24	Ck	146	LYS
24	Ck	161	GLU
24	Ck	175	LEU
24	Ck	239	LEU
24	Ck	274	VAL
24	Ck	318	THR
24	Ck	570	VAL
24	Ck	572	MET
24	Ck	746	LEU
24	Ck	787	VAL
24	Ck	831	VAL
25	Cm	101	MET
26	Cn	198	MET
28	DB	130	GLU
28	DB	151	THR
28	DB	329	VAL
28	DB	388	VAL
28	DB	556	VAL
28	DB	575	CYS
28	DB	670	HIS
28	DB	671	VAL
28	DB	679	VAL
28	DB	680	VAL
28	DB	689	LEU
28	DB	734	VAL
28	DB	741	THR
28	DB	756	THR
28	DB	773	THR

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Mol	Chain	Res	Type
28	DB	783	VAL
28	DB	792	ARG
28	DB	797	LEU
28	DB	834	ILE
28	DB	908	GLN
28	DB	912	ASN
28	DB	985	LYS
28	DB	987	GLU
28	DB	1013	ARG
28	DB	1034	ILE
28	DB	1036	MET
28	DB	1051	GLN
28	DB	1062	ILE
28	DB	1066	ASN
28	DB	1104	ASP
28	DB	1179	VAL
29	DC	47	ASP
29	DC	69	THR
29	DC	99	LYS
29	DC	158	TYR
29	DC	159	VAL
29	DC	207	GLU
29	DC	228	GLN
29	DC	231	THR
29	DC	240	VAL
29	DC	279	GLU
29	DC	286	GLN
29	DC	291	VAL
29	DC	434	THR
29	DC	449	VAL
29	DC	515	ILE
29	DC	648	LEU
29	DC	659	LEU
29	DC	702	LEU
29	DC	894	HIS
29	DC	961	THR
29	DC	968	THR
29	DC	1015	VAL
29	DC	1019	THR
29	DC	1096	GLU
30	DD	69	LEU
30	DD	86	ILE

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Mol	Chain	Res	Type
30	DD	209	THR
30	DD	381	ARG
30	DD	498	GLU
30	DD	504	ASN
30	DD	522	THR
30	DD	557	THR
30	DD	609	ASP
30	DD	801	GLU
31	DE	39	PHE
31	DE	50	GLU
31	DE	64	LEU
31	DE	76	THR
31	DE	219	ASN
31	DE	231	ILE
31	DE	261	THR
31	DE	295	TYR
31	DE	304	ASN
31	DE	405	ILE
31	DE	459	ASP
31	DE	568	SER
31	DE	580	VAL
31	DE	611	LEU
31	DE	654	VAL
32	DF	176	VAL
32	DF	325	LEU
32	DF	368	ILE
32	DF	432	ILE
32	DF	553	THR
32	DF	580	ASP
32	DF	592	HIS
33	DG	63	HIS
33	DG	98	ASP
33	DG	127	LEU
33	DG	175	GLU
33	DG	206	LEU
33	DG	220	THR
33	DG	229	HIS
33	DG	259	LEU
33	DG	379	VAL
33	DG	448	LEU
33	DG	559	VAL
33	DG	597	VAL

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Mol	Chain	Res	Type
34	DH	8	LYS
34	DH	54	GLU
34	DH	72	ARG
34	DH	119	LEU
34	DH	144	ASP
34	DH	216	THR
34	DH	259	VAL
34	DH	290	GLU
34	DH	307	ARG
34	DH	411	LEU
34	DH	445	ILE
34	DH	464	LEU
34	DH	466	VAL
34	DH	476	VAL
34	DH	477	ARG
34	DH	538	ARG
35	DI	24	VAL
35	DI	100	LEU
35	DI	145	LEU
35	DI	187	THR
35	DI	251	VAL
35	DI	279	VAL
35	DI	407	LEU
36	DJ	13	THR
36	DJ	111	VAL
36	DJ	144	CYS
36	DJ	185	LEU
36	DJ	335	ILE
37	DK	303	TYR
38	DL	61	VAL
38	DL	182	GLN
38	DL	190	ARG
38	DL	237	PHE
38	DL	286	THR
39	DO	127	LEU
39	DO	214	GLU
40	DP	111	THR
40	DP	185	ASP
41	DR	77	LEU
41	DR	118	VAL
41	DR	254	VAL
41	DR	268	HIS

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Mol	Chain	Res	Type
42	DT	52	ARG
42	DT	65	VAL
42	DT	69	ASP
42	DT	97	VAL
42	DT	112	LEU
42	DT	230	LYS
43	DU	42	THR
43	DU	46	THR
44	DV	156	VAL
44	DV	158	PHE
45	DW	83	THR
45	DW	102	MET
45	DW	148	THR
46	DX	141	ARG
47	DY	11	THR
47	DY	130	LYS
49	Da	34	GLN
50	F2	199	ASP
50	F2	574	CYS
50	F2	646	GLU
50	F2	746	LEU
50	F2	851	LEU
50	F2	861	VAL
51	F3	72	VAL
51	F3	82	VAL
51	F3	196	VAL
51	F3	270	LEU
51	F3	312	VAL
51	F3	418	ASP
51	F3	589	ASN
51	F3	592	LEU
51	F3	595	LEU
51	F3	620	ILE
51	F3	646	THR
51	F3	648	VAL
51	F3	654	GLN
51	F3	692	LEU
51	F3	720	ILE
51	F3	725	LEU
51	F3	752	TRP
51	F3	795	THR
51	F3	846	VAL

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Mol	Chain	Res	Type
51	F3	891	LEU
51	F3	940	VAL
52	F5	190	GLU
52	F5	248	GLN
52	F5	251	LEU
52	F5	262	GLU
52	F5	300	LEU
52	F5	315	GLN
52	F5	365	ASP
52	F5	379	VAL
52	F5	395	GLN
52	F5	404	LEU
52	F5	573	ARG
52	F5	586	ASN
52	F5	590	ARG
52	F5	599	ILE
52	F5	701	LEU
52	F5	753	ASN
53	F6	105	THR
53	F6	133	LEU
53	F6	184	ASP
53	F6	213	PHE
53	F6	229	LEU
53	F6	248	VAL
53	F6	257	LEU
53	F6	354	THR
53	F6	369	GLU
53	F6	397	GLU
53	F6	562	ARG
53	F6	565	THR
53	F6	568	VAL
53	F6	572	LEU
54	F7	25	GLU
54	F7	47	TRP
54	F7	150	LEU
54	F7	197	GLU
54	F7	211	VAL
54	F7	247	GLU
54	F7	472	THR
54	F7	549	ASN
54	F7	581	ARG
54	F7	589	VAL

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Mol	Chain	Res	Type
55	F9	83	LYS
55	F9	192	LEU
55	F9	195	MET
55	F9	223	GLU
55	F9	315	LYS
55	F9	320	VAL
55	F9	346	ASP
55	F9	372	GLU
55	F9	377	GLN
55	F9	498	GLU
55	F9	556	ILE
56	FM	20	VAL
56	FM	114	THR
56	FM	116	ASP
56	FM	176	VAL
56	FM	225	LEU
56	FM	248	ASN
56	FN	35	TYR
56	FN	71	MET
56	FN	84	ASP
56	FN	299	ASP
57	FO	119	LEU
57	FO	131	ASP
57	FO	138	LEU
57	FO	219	GLU
57	FO	244	ARG
57	FO	248	ARG
57	FO	322	ARG
57	FO	333	ARG
57	FO	334	ILE
58	FP	69	GLU
58	FP	258	LEU
58	FP	315	VAL
60	FX	29	GLN
61	FZ	70	VAL
61	FZ	88	GLN
61	FZ	93	LEU
61	FZ	96	LEU
61	FZ	100	LEU
61	FZ	104	ILE
61	FZ	116	ASP
61	FZ	142	LEU

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Mol	Chain	Res	Type
62	Fb	27	THR
62	Fb	107	MET
63	Fc	67	LEU
63	Fc	121	LEU
63	Fc	136	ASP
64	Fd	32	ARG
64	Fd	35	MET
64	Fd	60	ASP
64	Fd	77	VAL
65	Ff	224	LEU
65	Ff	244	VAL
65	Ff	248	ARG
65	Ff	289	LEU
65	Ff	338	TRP
65	Ff	499	LEU
65	Ff	584	LEU
65	Ff	609	HIS
65	Ff	692	ASP
65	Ff	764	TYR
66	Fg	14	GLN
66	Fg	33	CYS
66	Fg	310	ARG
66	Fg	421	THR
66	Fg	501	VAL
67	Fh	87	TYR
67	Fh	106	LEU
67	Fh	142	LEU
67	Fh	170	GLN
67	Fh	192	VAL
67	Fh	227	TYR
67	Fh	289	LEU
68	Fi	10	ASN
68	Fi	22	LEU
68	Fi	39	ILE
68	Fi	96	LEU
68	Fi	214	VAL
68	Fi	222	LEU
68	Fi	231	LEU
68	Fi	279	HIS
68	Fi	286	LEU
68	Fi	296	VAL
68	Fi	342	VAL

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Mol	Chain	Res	Type
68	Fi	350	VAL
68	Fi	364	LEU
68	Fi	418	VAL
68	Fi	464	ASP
68	Fi	567	THR
69	IA	100	GLU
69	IA	137	THR
69	IA	141	LYS
69	IA	152	LYS
69	IA	189	ASP
69	IA	196	LYS
69	IA	216	LYS
69	IA	275	ASN
69	IA	278	ILE
69	IA	279	VAL
69	IA	294	GLU
69	IA	351	ARG
69	IA	381	VAL
69	IA	384	THR
69	IA	389	THR
69	IA	390	THR
69	IA	396	ILE
69	IA	455	VAL
69	IA	545	VAL
69	IA	548	VAL
69	IA	568	ILE
69	IA	587	THR
69	IA	617	VAL
69	IA	626	VAL
69	IA	643	VAL
69	IA	688	ARG
69	IA	693	GLU
69	IA	703	LYS
69	IA	717	VAL
69	IA	764	GLU
70	IB	446	THR
70	IB	467	TYR
70	IB	475	VAL
70	IB	503	ARG
70	IB	510	ILE
70	IB	540	VAL
70	IB	542	ILE

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Mol	Chain	Res	Type
70	IB	556	VAL
70	IB	581	ARG
70	IB	724	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (491) such sidechains are listed below:

Mol	Chain	Res	Type
3	CC	8	HIS
3	CC	31	ASN
4	CE	116	GLN
4	CE	161	GLN
4	CE	218	ASN
4	CE	317	HIS
4	CE	361	ASN
5	CF	41	ASN
6	CH	29	HIS
6	CH	43	ASN
6	CH	54	GLN
6	CH	55	GLN
6	CH	165	GLN
6	CH	247	HIS
6	CH	267	HIS
7	CI	44	HIS
7	CI	104	ASN
7	CI	152	GLN
7	CI	208	HIS
7	CI	240	ASN
7	CI	318	HIS
8	CJ	20	GLN
8	CJ	69	GLN
8	CJ	82	HIS
8	CJ	116	GLN
8	CJ	134	GLN
8	CJ	209	GLN
8	CJ	274	GLN
8	CJ	301	ASN
8	CJ	321	ASN
8	CJ	339	ASN
8	CJ	421	HIS
8	CJ	432	HIS
8	CJ	438	ASN
8	CJ	441	HIS

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Mol	Chain	Res	Type
8	CJ	450	HIS
8	CJ	476	ASN
8	CJ	581	GLN
8	CJ	632	GLN
8	CJ	642	ASN
8	CJ	761	GLN
8	CJ	769	GLN
8	CJ	776	GLN
8	CJ	798	GLN
8	CJ	807	GLN
9	CK	218	ASN
9	CK	245	GLN
11	CN	42	HIS
11	CN	153	ASN
11	CN	162	GLN
12	CO	129	GLN
12	CO	149	GLN
12	CO	165	HIS
12	CO	197	GLN
12	CO	261	HIS
12	CO	288	GLN
12	CO	306	ASN
12	CO	325	ASN
13	CP	72	GLN
13	CP	87	HIS
13	CP	130	GLN
13	CP	152	ASN
14	CQ	20	GLN
14	CQ	33	ASN
14	CQ	36	ASN
14	CQ	49	ASN
14	CQ	57	HIS
14	CQ	122	GLN
14	CQ	158	HIS
14	CQ	199	ASN
14	CQ	234	ASN
15	CR	65	GLN
15	CR	151	ASN
15	CR	176	ASN
16	CS	62	HIS
16	CS	65	ASN
17	CU	66	HIS

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Mol	Chain	Res	Type
18	Ca	63	GLN
18	Ca	105	GLN
18	Ca	106	ASN
18	Ca	192	GLN
18	Ca	223	ASN
18	Ca	232	GLN
18	Ca	306	HIS
18	Ca	390	GLN
18	Ca	441	ASN
20	Cd	37	HIS
20	Cd	56	HIS
20	Cd	72	ASN
20	Cd	98	GLN
20	Cd	113	GLN
20	Cd	119	HIS
20	Cd	130	GLN
20	Cd	143	GLN
20	Cd	192	ASN
20	Cd	208	HIS
21	Cg	87	GLN
21	Cg	129	HIS
21	Cg	296	HIS
21	Cg	301	HIS
21	Cg	323	GLN
21	Cg	372	ASN
21	Cg	380	ASN
21	Cg	461	GLN
21	Cg	470	GLN
21	Cg	474	GLN
21	Cg	476	GLN
22	Ci	83	ASN
22	Ci	98	HIS
22	Ci	164	ASN
24	Ck	30	GLN
24	Ck	42	HIS
24	Ck	79	HIS
24	Ck	131	ASN
24	Ck	135	ASN
24	Ck	195	GLN
24	Ck	276	GLN
24	Ck	402	HIS
24	Ck	547	ASN

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Mol	Chain	Res	Type
24	Ck	550	GLN
24	Ck	584	ASN
24	Ck	611	ASN
24	Ck	619	GLN
24	Ck	644	HIS
24	Ck	669	ASN
24	Ck	684	GLN
24	Ck	695	GLN
24	Ck	701	HIS
24	Ck	704	ASN
24	Ck	715	GLN
27	Cp	66	HIS
27	Cp	154	GLN
28	DB	122	HIS
28	DB	141	HIS
28	DB	164	GLN
28	DB	194	GLN
28	DB	208	GLN
28	DB	239	GLN
28	DB	281	GLN
28	DB	300	GLN
28	DB	340	ASN
28	DB	467	ASN
28	DB	470	HIS
28	DB	486	HIS
28	DB	524	GLN
28	DB	539	GLN
28	DB	615	ASN
28	DB	627	HIS
28	DB	661	ASN
28	DB	733	HIS
28	DB	828	HIS
28	DB	860	GLN
28	DB	868	HIS
28	DB	891	GLN
28	DB	898	GLN
28	DB	908	GLN
28	DB	912	ASN
28	DB	981	HIS
28	DB	1029	HIS
28	DB	1051	GLN
28	DB	1101	GLN

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Mol	Chain	Res	Type
28	DB	1124	HIS
29	DC	81	HIS
29	DC	105	ASN
29	DC	205	GLN
29	DC	232	GLN
29	DC	263	GLN
29	DC	357	GLN
29	DC	384	HIS
29	DC	406	GLN
29	DC	424	GLN
29	DC	447	ASN
29	DC	500	ASN
29	DC	574	GLN
29	DC	610	ASN
29	DC	680	GLN
29	DC	761	ASN
29	DC	797	ASN
29	DC	821	GLN
29	DC	920	HIS
29	DC	1049	ASN
29	DC	1062	GLN
29	DC	1160	GLN
30	DD	59	ASN
30	DD	76	ASN
30	DD	79	GLN
30	DD	144	ASN
30	DD	156	GLN
30	DD	176	HIS
30	DD	273	HIS
30	DD	353	HIS
30	DD	385	ASN
30	DD	387	GLN
30	DD	507	GLN
30	DD	542	HIS
30	DD	607	GLN
30	DD	675	ASN
30	DD	679	ASN
30	DD	687	HIS
30	DD	733	GLN
31	DE	187	GLN
31	DE	202	HIS
31	DE	304	ASN

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Mol	Chain	Res	Type
31	DE	309	HIS
31	DE	319	ASN
31	DE	345	ASN
31	DE	414	ASN
31	DE	491	GLN
31	DE	567	HIS
31	DE	573	GLN
31	DE	685	HIS
32	DF	15	HIS
32	DF	41	ASN
32	DF	110	ASN
32	DF	119	HIS
32	DF	140	HIS
32	DF	187	ASN
32	DF	198	HIS
32	DF	272	HIS
32	DF	292	ASN
32	DF	399	HIS
32	DF	406	ASN
32	DF	572	HIS
33	DG	12	ASN
33	DG	191	GLN
33	DG	200	GLN
33	DG	332	GLN
33	DG	374	HIS
33	DG	393	ASN
33	DG	396	ASN
33	DG	476	GLN
34	DH	27	GLN
34	DH	58	HIS
34	DH	71	GLN
34	DH	82	GLN
34	DH	100	HIS
34	DH	105	GLN
34	DH	142	HIS
34	DH	255	GLN
34	DH	282	ASN
34	DH	450	ASN
34	DH	469	ASN
34	DH	498	ASN
34	DH	524	HIS
35	DI	18	HIS

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Mol	Chain	Res	Type
35	DI	101	ASN
35	DI	175	GLN
35	DI	193	ASN
35	DI	370	GLN
36	DJ	27	GLN
36	DJ	53	GLN
36	DJ	174	ASN
36	DJ	199	GLN
36	DJ	227	GLN
36	DJ	293	ASN
37	DK	144	HIS
37	DK	171	GLN
37	DK	278	GLN
37	DK	291	GLN
38	DL	32	HIS
38	DL	116	ASN
38	DL	144	HIS
39	DO	143	HIS
39	DO	206	GLN
40	DP	76	HIS
40	DP	98	HIS
40	DP	140	ASN
40	DP	142	ASN
40	DP	143	ASN
40	DP	194	GLN
41	DR	35	HIS
41	DR	62	HIS
41	DR	68	HIS
41	DR	173	ASN
42	DT	16	HIS
42	DT	23	GLN
42	DT	59	HIS
42	DT	72	HIS
42	DT	113	GLN
42	DT	215	GLN
42	DT	233	HIS
43	DU	19	GLN
43	DU	63	HIS
43	DU	99	GLN
43	DU	155	GLN
44	DV	35	GLN
44	DV	38	GLN

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Mol	Chain	Res	Type
44	DV	40	HIS
44	DV	145	ASN
45	DW	44	ASN
45	DW	66	HIS
45	DW	98	GLN
45	DW	115	ASN
45	DW	132	HIS
45	DW	139	ASN
45	DW	154	HIS
45	DW	160	GLN
45	DW	167	GLN
46	DX	130	GLN
47	DY	10	ASN
47	DY	41	GLN
47	DY	106	GLN
49	Da	17	HIS
49	Da	30	HIS
49	Da	34	GLN
50	F2	17	GLN
50	F2	219	GLN
50	F2	270	ASN
50	F2	307	ASN
50	F2	354	HIS
50	F2	427	HIS
50	F2	461	HIS
50	F2	530	GLN
50	F2	545	HIS
50	F2	579	HIS
50	F2	698	HIS
50	F2	743	GLN
50	F2	778	GLN
50	F2	830	GLN
50	F2	850	GLN
50	F2	958	ASN
51	F3	176	HIS
51	F3	206	GLN
51	F3	387	ASN
51	F3	405	ASN
51	F3	432	GLN
51	F3	650	GLN
51	F3	718	GLN
51	F3	747	HIS

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Mol	Chain	Res	Type
51	F3	770	ASN
51	F3	773	ASN
51	F3	794	ASN
51	F3	823	GLN
51	F3	960	HIS
52	F5	123	GLN
52	F5	158	HIS
52	F5	195	HIS
52	F5	234	HIS
52	F5	237	ASN
52	F5	248	GLN
52	F5	269	GLN
52	F5	315	GLN
52	F5	485	ASN
52	F5	608	GLN
52	F5	609	GLN
52	F5	624	ASN
52	F5	711	GLN
52	F5	716	HIS
53	F6	19	HIS
53	F6	49	HIS
53	F6	203	GLN
53	F6	278	HIS
53	F6	319	HIS
53	F6	330	HIS
53	F6	363	ASN
53	F6	547	GLN
53	F6	551	HIS
53	F6	587	GLN
54	F7	61	HIS
54	F7	71	HIS
54	F7	214	HIS
54	F7	252	ASN
54	F7	343	GLN
54	F7	387	HIS
54	F7	432	GLN
54	F7	450	ASN
54	F7	502	GLN
54	F7	542	ASN
54	F7	578	ASN
54	F7	612	GLN
54	F7	677	GLN

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Mol	Chain	Res	Type
55	F9	211	GLN
55	F9	217	GLN
55	F9	254	GLN
55	F9	302	GLN
55	F9	313	GLN
55	F9	332	ASN
55	F9	377	GLN
55	F9	464	GLN
55	F9	484	ASN
55	F9	525	ASN
55	F9	547	HIS
56	FM	25	ASN
56	FM	96	ASN
56	FM	102	ASN
56	FM	248	ASN
56	FN	9	ASN
56	FN	102	ASN
56	FN	170	HIS
56	FN	199	HIS
56	FN	312	HIS
57	FO	76	GLN
57	FO	94	HIS
57	FO	97	ASN
57	FO	111	HIS
57	FO	134	HIS
57	FO	135	ASN
57	FO	147	ASN
57	FO	247	GLN
57	FO	255	GLN
57	FO	265	ASN
57	FO	296	GLN
57	FO	303	HIS
58	FP	6	GLN
58	FP	129	HIS
58	FP	180	GLN
58	FP	293	HIS
58	FP	338	GLN
59	FW	157	GLN
59	FW	176	GLN
59	FW	218	HIS
60	FX	29	GLN
60	FX	68	GLN

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Mol	Chain	Res	Type
60	FX	168	HIS
60	FX	212	HIS
61	FZ	47	ASN
61	FZ	63	ASN
61	FZ	150	GLN
62	Fb	31	HIS
62	Fb	76	GLN
62	Fb	91	HIS
62	Fb	127	GLN
62	Fb	134	GLN
63	Fc	96	HIS
63	Fc	132	GLN
64	Fd	42	HIS
64	Fd	59	HIS
64	Fd	66	HIS
64	Fd	76	HIS
65	Ff	180	GLN
65	Ff	202	GLN
65	Ff	392	HIS
65	Ff	487	HIS
65	Ff	646	GLN
65	Ff	710	GLN
65	Ff	751	ASN
66	Fg	96	HIS
66	Fg	108	GLN
66	Fg	175	HIS
66	Fg	178	GLN
66	Fg	256	GLN
66	Fg	270	ASN
66	Fg	448	HIS
66	Fg	484	HIS
66	Fg	499	HIS
67	Fh	67	ASN
67	Fh	76	HIS
67	Fh	89	GLN
67	Fh	165	GLN
67	Fh	170	GLN
68	Fi	10	ASN
68	Fi	31	GLN
68	Fi	40	GLN
68	Fi	123	GLN
68	Fi	194	ASN

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Mol	Chain	Res	Type
68	Fi	205	HIS
68	Fi	215	GLN
68	Fi	272	GLN
68	Fi	288	GLN
68	Fi	301	GLN
68	Fi	326	GLN
68	Fi	380	GLN
68	Fi	405	HIS
68	Fi	482	GLN
68	Fi	485	GLN
68	Fi	562	ASN
68	Fi	594	GLN
69	IA	40	GLN
69	IA	53	GLN
69	IA	71	ASN
69	IA	85	ASN
69	IA	140	GLN
69	IA	157	HIS
69	IA	214	HIS
69	IA	227	ASN
69	IA	231	GLN
69	IA	261	HIS
69	IA	324	GLN
69	IA	325	GLN
69	IA	462	GLN
69	IA	509	GLN
69	IA	724	GLN
69	IA	733	GLN
70	IB	195	GLN
70	IB	358	ASN
70	IB	404	GLN
70	IB	406	HIS
70	IB	413	GLN
70	IB	448	GLN
70	IB	585	ASN
70	IB	605	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CA	494/621 (79%)	188 (38%)	5 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CB	2/3 (66%)	2 (100%)	0
All	All	496/624 (79%)	190 (38%)	5 (1%)

All (190) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CA	3	A
1	CA	5	U
1	CA	6	U
1	CA	7	A
1	CA	8	U
1	CA	10	G
1	CA	17	G
1	CA	18	U
1	CA	19	U
1	CA	20	A
1	CA	21	G
1	CA	22	U
1	CA	25	U
1	CA	26	C
1	CA	28	U
1	CA	29	A
1	CA	30	U
1	CA	38	U
1	CA	40	U
1	CA	42	A
1	CA	43	A
1	CA	44	U
1	CA	46	U
1	CA	52	C
1	CA	53	A
1	CA	56	U
1	CA	58	A
1	CA	59	U
1	CA	60	A
1	CA	61	A
1	CA	62	A
1	CA	63	G
1	CA	67	U
1	CA	69	U
1	CA	72	U
1	CA	73	U

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Mol	Chain	Res	Type
1	CA	74	G
1	CA	78	G
1	CA	79	A
1	CA	80	U
1	CA	82	U
1	CA	83	U
1	CA	84	U
1	CA	85	U
1	CA	87	U
1	CA	88	A
1	CA	90	A
1	CA	95	U
1	CA	98	A
1	CA	100	G
1	CA	102	A
1	CA	105	G
1	CA	106	U
1	CA	111	A
1	CA	115	A
1	CA	127	G
1	CA	135	U
1	CA	136	G
1	CA	138	U
1	CA	139	U
1	CA	146	U
1	CA	152	U
1	CA	155	A
1	CA	156	U
1	CA	157	G
1	CA	158	G
1	CA	159	G
1	CA	160	U
1	CA	161	G
1	CA	167	A
1	CA	170	U
1	CA	173	A
1	CA	178	A
1	CA	183	U
1	CA	184	A
1	CA	185	A
1	CA	205	A
1	CA	207	A

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Mol	Chain	Res	Type
1	CA	217	U
1	CA	221	C
1	CA	223	G
1	CA	224	A
1	CA	225	A
1	CA	226	A
1	CA	234	C
1	CA	236	G
1	CA	239	G
1	CA	240	U
1	CA	241	U
1	CA	242	G
1	CA	246	U
1	CA	247	A
1	CA	248	A
1	CA	249	U
1	CA	250	U
1	CA	251	U
1	CA	261	U
1	CA	262	A
1	CA	273	A
1	CA	287	A
1	CA	300	G
1	CA	315	A
1	CA	320	A
1	CA	321	A
1	CA	322	A
1	CA	323	U
1	CA	325	A
1	CA	327	U
1	CA	350	U
1	CA	351	A
1	CA	407	U
1	CA	408	C
1	CA	409	A
1	CA	410	U
1	CA	411	A
1	CA	412	U
1	CA	413	A
1	CA	414	A
1	CA	415	U
1	CA	416	U

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Mol	Chain	Res	Type
1	CA	417	A
1	CA	418	A
1	CA	421	G
1	CA	423	A
1	CA	429	U
1	CA	430	U
1	CA	433	U
1	CA	434	A
1	CA	435	G
1	CA	438	U
1	CA	441	G
1	CA	442	A
1	CA	443	U
1	CA	444	A
1	CA	445	C
1	CA	446	C
1	CA	447	A
1	CA	449	G
1	CA	455	G
1	CA	458	U
1	CA	459	A
1	CA	466	G
1	CA	468	A
1	CA	469	A
1	CA	472	G
1	CA	480	C
1	CA	481	A
1	CA	483	A
1	CA	484	A
1	CA	485	U
1	CA	486	C
1	CA	487	A
1	CA	491	U
1	CA	492	U
1	CA	493	U
1	CA	494	A
1	CA	495	U
1	CA	496	U
1	CA	498	U
1	CA	499	U
1	CA	502	U
1	CA	503	A

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Mol	Chain	Res	Type
1	CA	504	U
1	CA	505	U
1	CA	507	A
1	CA	512	G
1	CA	513	U
1	CA	518	G
1	CA	527	A
1	CA	528	U
1	CA	529	A
1	CA	532	A
1	CA	560	U
1	CA	563	U
1	CA	567	A
1	CA	568	A
1	CA	576	A
1	CA	581	G
1	CA	583	A
1	CA	584	G
1	CA	586	A
1	CA	587	A
1	CA	588	U
1	CA	590	A
1	CA	600	U
1	CA	601	A
1	CA	602	A
1	CA	604	A
2	CB	2	A
2	CB	3	U

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	CA	151	U
1	CA	169	A
1	CA	349	U
1	CA	465	U
1	CA	566	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 8 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
88	GDP	IA	1000	82	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
83	ATP	Cg	1000	82	32,33,33	0.31	0	48,52,52	0.30	0
85	PM8	Fc	201	63	26,31,31	0.22	0	30,38,38	0.46	0
84	PO4	IA	1001	82	4,4,4	0.98	0	6,6,6	0.49	0
84	PO4	FW	301	-	4,4,4	1.01	0	6,6,6	0.44	0
87	FDA	Ff	901	-	57,58,58	0.65	2 (3%)	78,89,89	0.55	2 (2%)

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
87	FDA	Ff	901	-	-	12/34/50/50	0/6/6/6
88	GDP	IA	1000	82	-	0/16/32/32	0/3/3/3
85	PM8	Fc	201	63	-	8/36/38/38	-
83	ATP	Cg	1000	82	-	2/22/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	IA	1000	GDP	C5-C4	3.15	1.47	1.38
87	Ff	901	FDA	C4X-N5	-2.88	1.30	1.35
87	Ff	901	FDA	C10-N1	-2.74	1.32	1.37
88	IA	1000	GDP	C6-N1	-2.44	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	IA	1000	GDP	C5-N7	-2.08	1.34	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	IA	1000	GDP	C5-C4-N3	-6.19	118.53	128.39
88	IA	1000	GDP	C2-N3-C4	5.06	121.01	112.30
88	IA	1000	GDP	N9-C4-N3	4.65	135.25	125.95
88	IA	1000	GDP	C6-C5-N7	3.15	136.01	130.29
88	IA	1000	GDP	C4-C5-N7	-2.52	106.68	110.67
87	Ff	901	FDA	N3-C2-N1	2.44	119.57	115.74
88	IA	1000	GDP	C3'-C2'-C1'	2.38	105.97	101.46
87	Ff	901	FDA	C9A-C5X-N5	2.20	122.05	119.37
88	IA	1000	GDP	O6-C6-C5	-2.13	120.91	126.53

There are no chirality outliers.

All (22) torsion outliers are listed below:

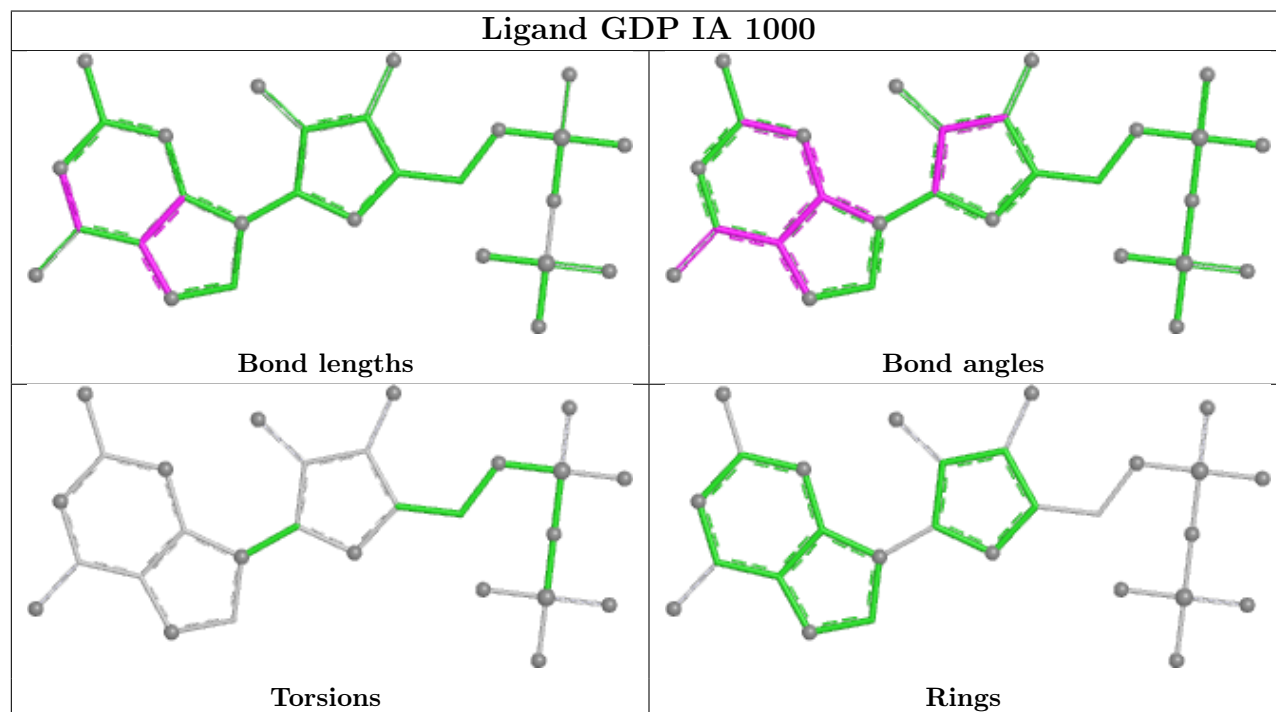
Mol	Chain	Res	Type	Atoms
83	Cg	1000	ATP	O4'-C4'-C5'-O5'
85	Fc	201	PM8	O1-C1-S1-C43
85	Fc	201	PM8	C2-C1-S1-C43
87	Ff	901	FDA	C5B-O5B-PA-O1A
87	Ff	901	FDA	C5B-O5B-PA-O2A
87	Ff	901	FDA	C5B-O5B-PA-O3P
87	Ff	901	FDA	O4B-C4B-C5B-O5B
87	Ff	901	FDA	N10-C1'-C2'-O2'
87	Ff	901	FDA	N10-C1'-C2'-C3'
87	Ff	901	FDA	C3B-C4B-C5B-O5B
83	Cg	1000	ATP	C3'-C4'-C5'-O5'
87	Ff	901	FDA	C2'-C3'-C4'-O4'
85	Fc	201	PM8	O33-C32-C34-O35
85	Fc	201	PM8	N41-C42-C43-S1
85	Fc	201	PM8	O33-C32-C34-N36
87	Ff	901	FDA	O3'-C3'-C4'-O4'
85	Fc	201	PM8	C42-C43-S1-C1
85	Fc	201	PM8	C43-C42-N41-C39
87	Ff	901	FDA	C2'-C3'-C4'-C5'
87	Ff	901	FDA	O3'-C3'-C4'-C5'
87	Ff	901	FDA	C4'-C5'-O5'-P
85	Fc	201	PM8	O40-C39-N41-C42

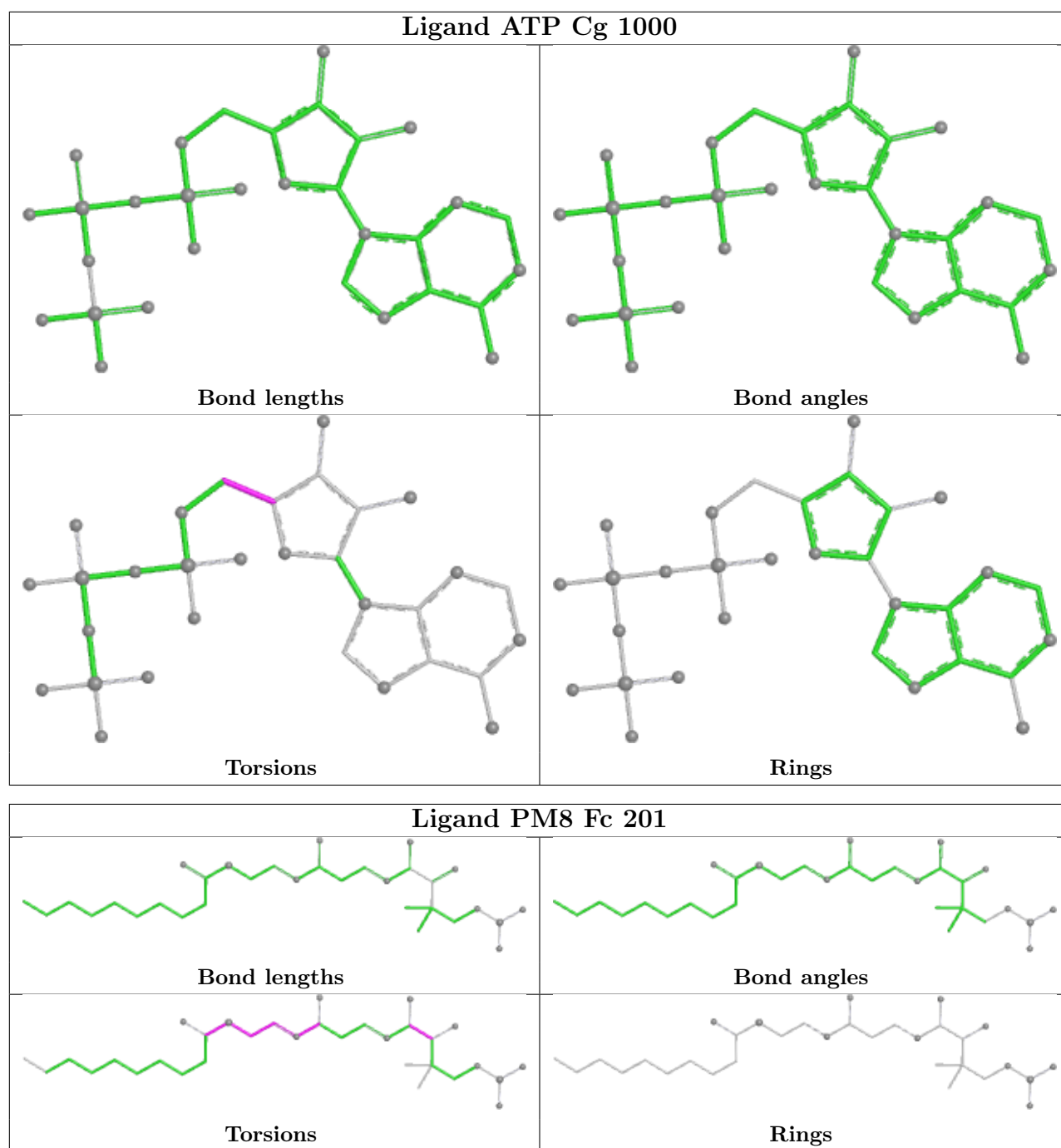
There are no ring outliers.

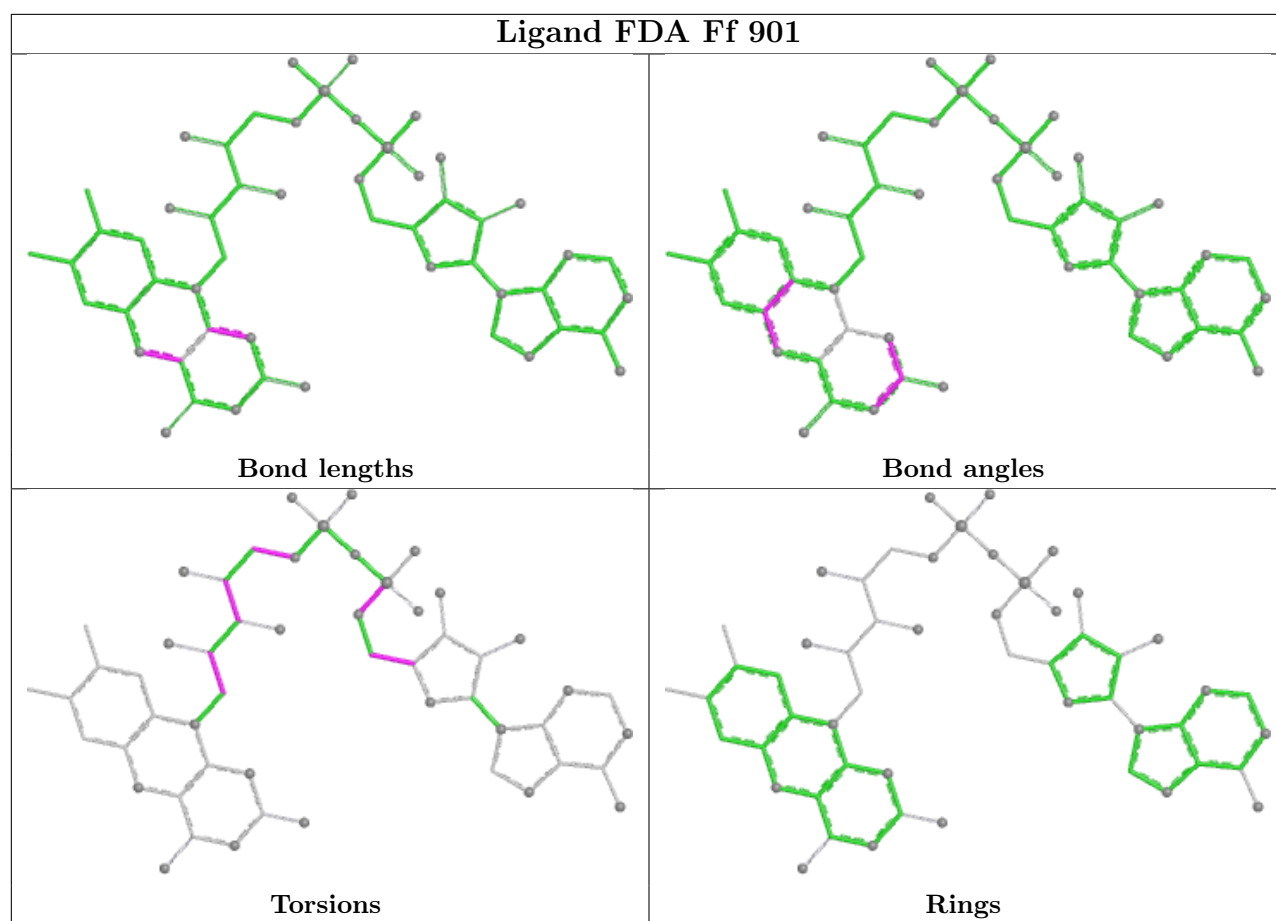
5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	IA	1000	GDP	1	0
85	Fc	201	PM8	1	0
84	IA	1001	PO4	1	0
84	FW	301	PO4	1	0
87	Ff	901	FDA	2	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

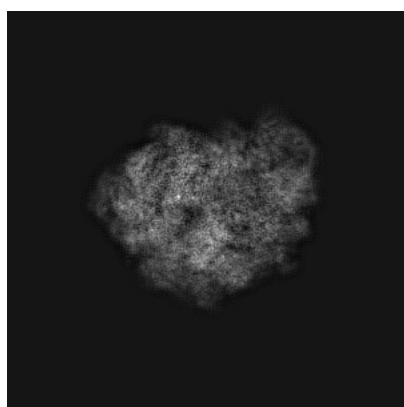
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13660. These allow visual inspection of the internal detail of the map and identification of artifacts.

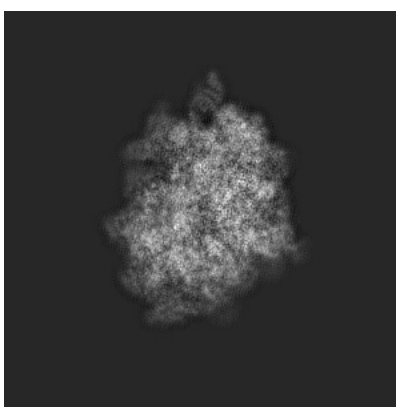
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

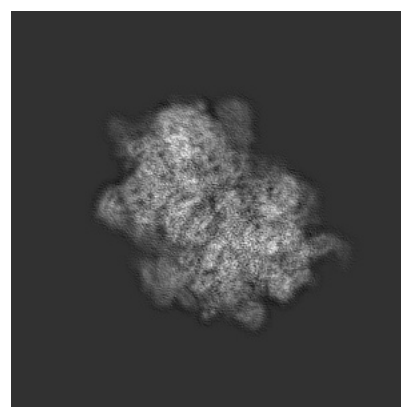
6.1.1 Primary map



X



Y

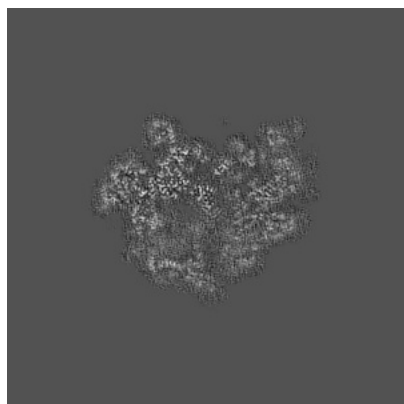


Z

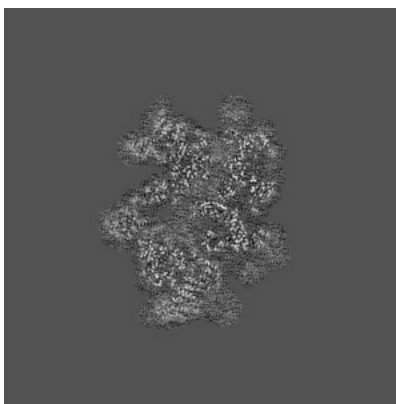
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

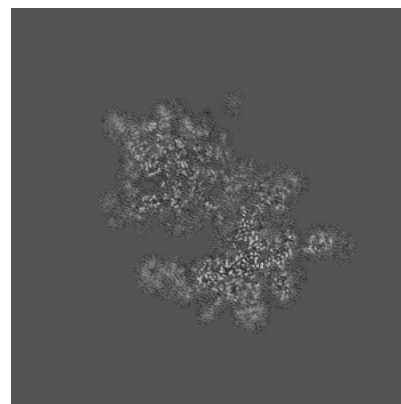
6.2.1 Primary map



X Index: 180



Y Index: 180

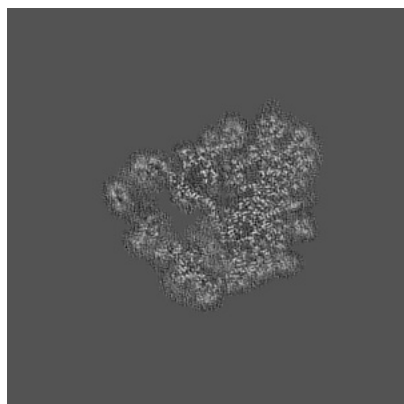


Z Index: 180

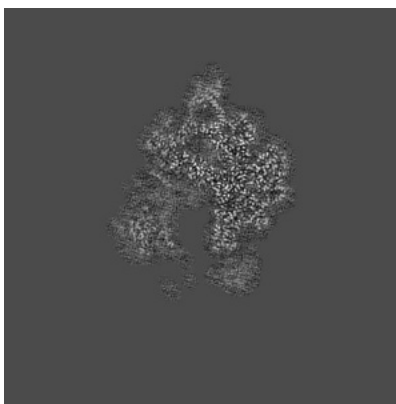
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

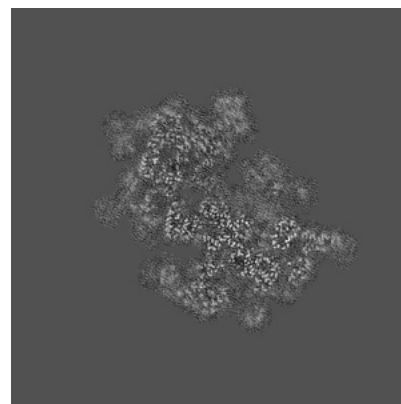
6.3.1 Primary map



X Index: 157



Y Index: 154

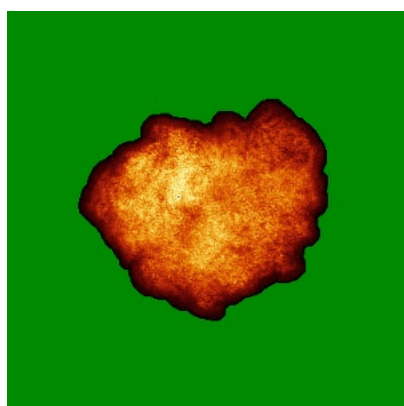


Z Index: 192

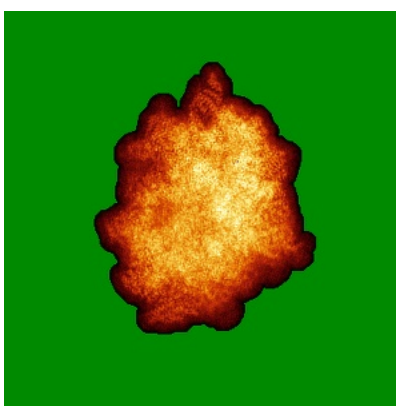
The images above show the largest variance slices of the map in three orthogonal directions.

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

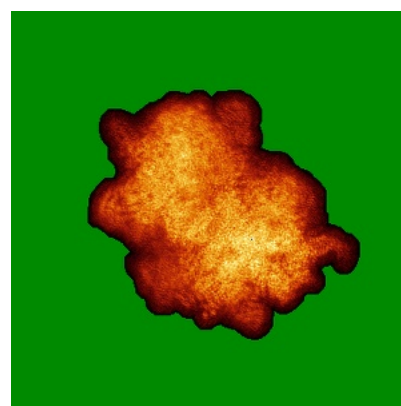
6.4.1 Primary map



X



Y

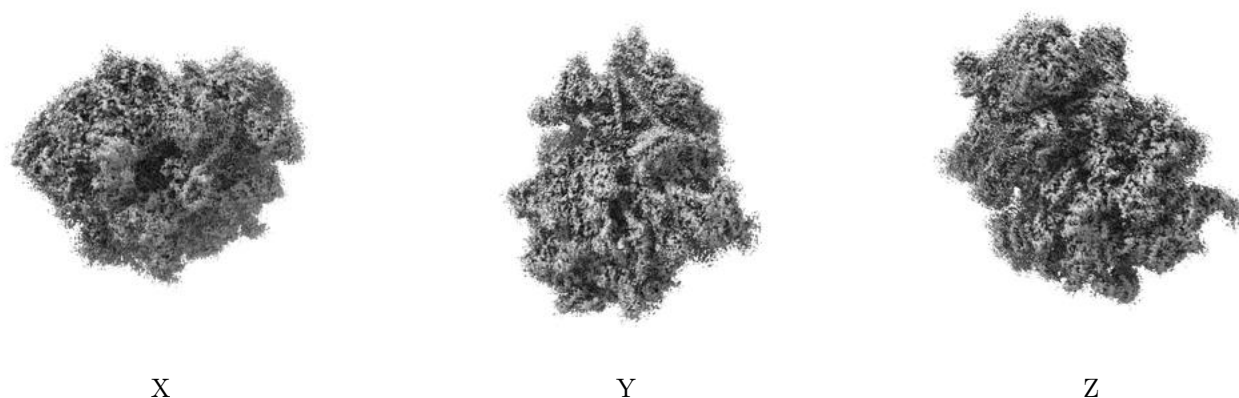


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

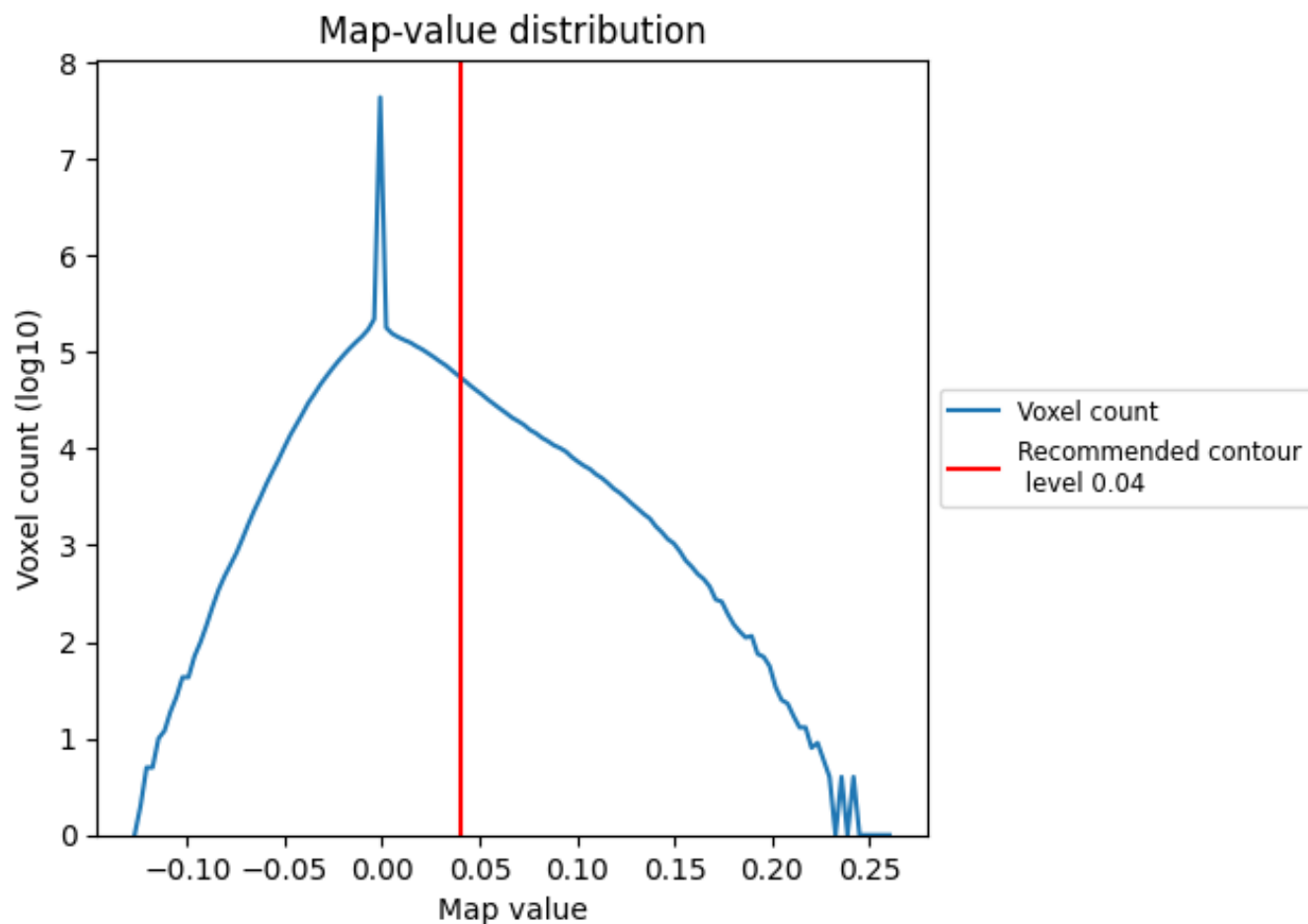
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

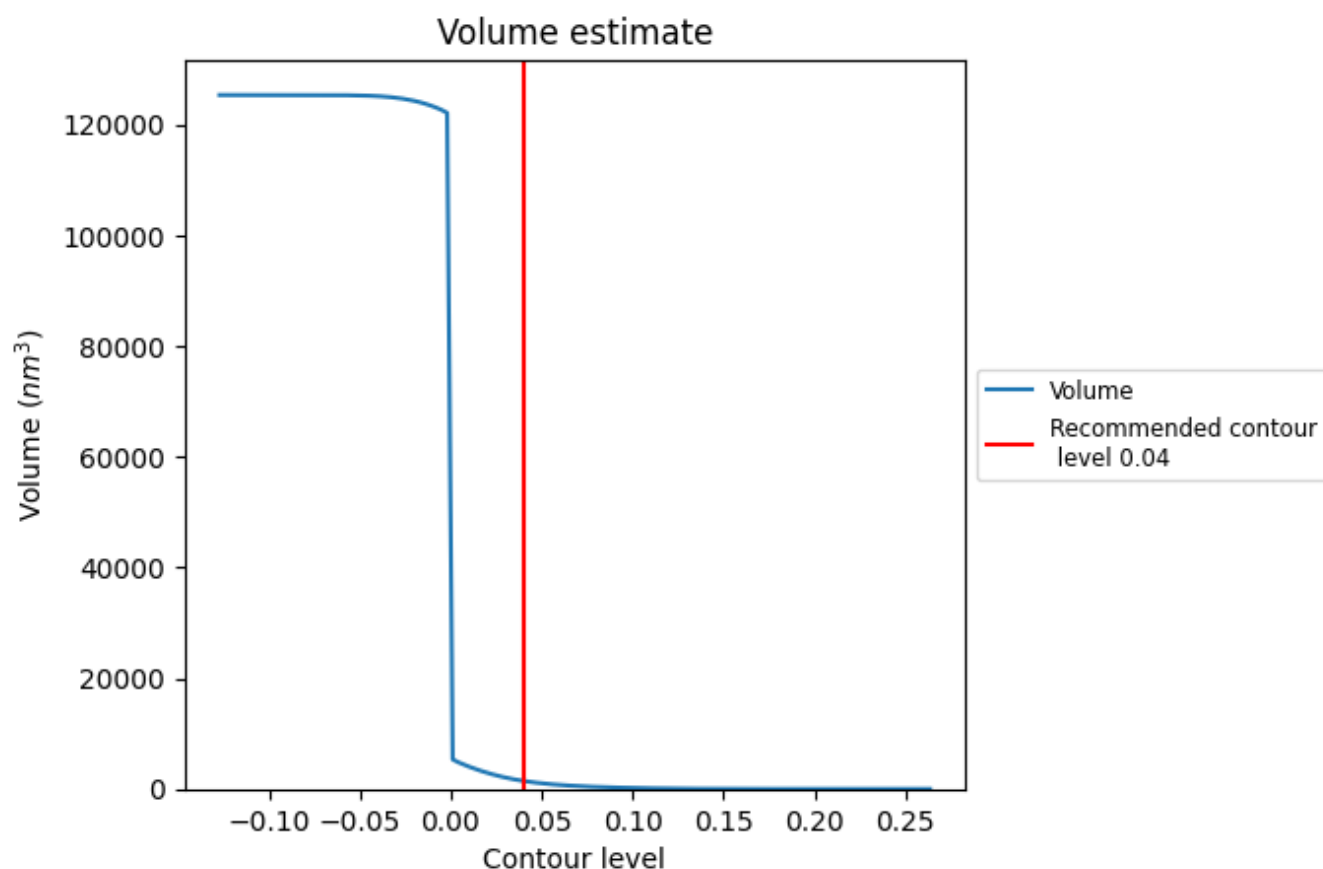
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

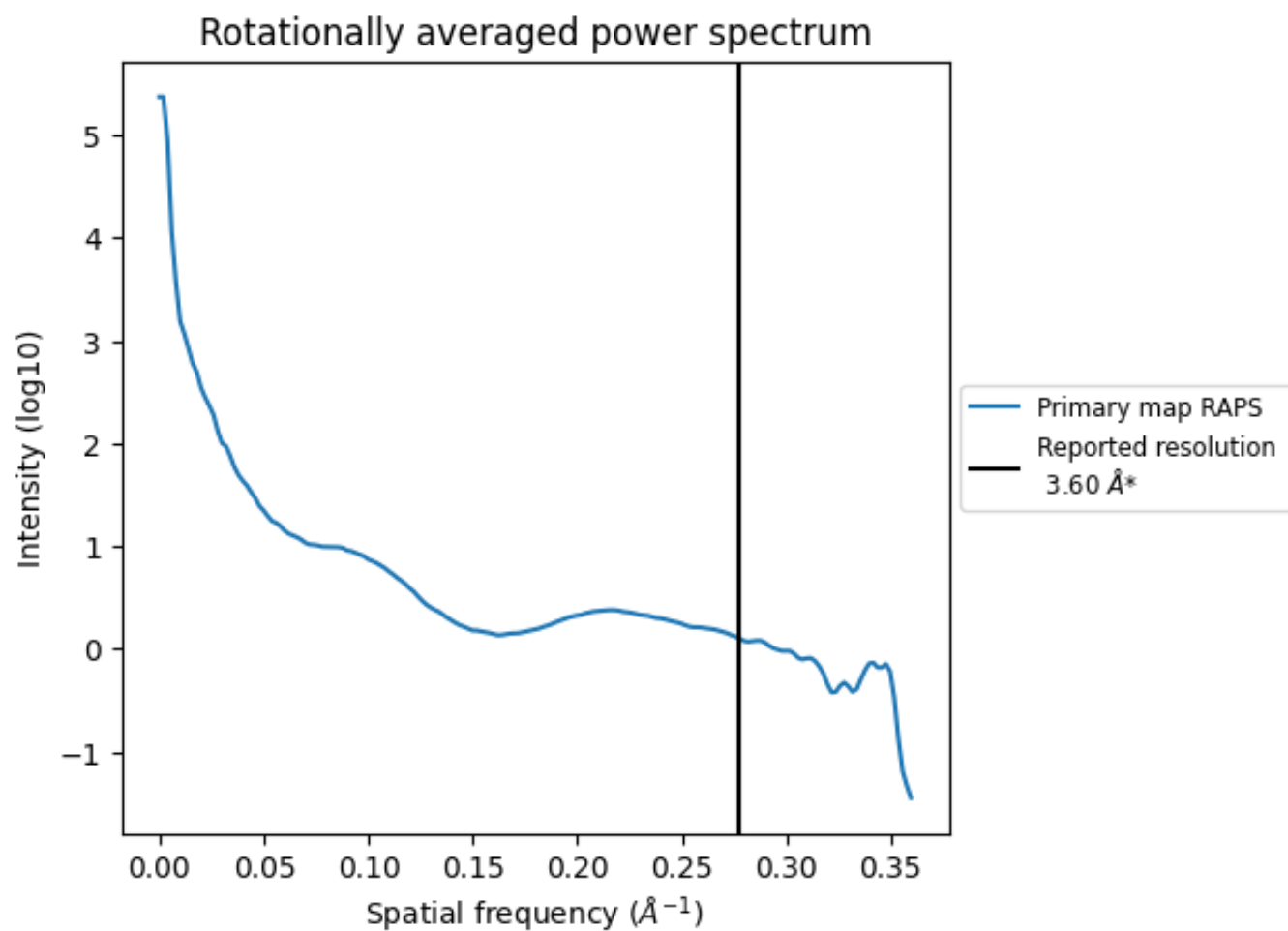
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1447 nm^3 ; this corresponds to an approximate mass of 1307 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

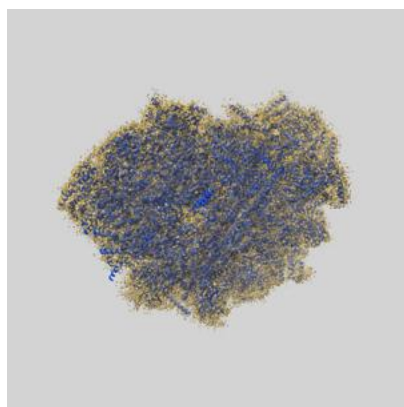
8 Fourier-Shell correlation

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

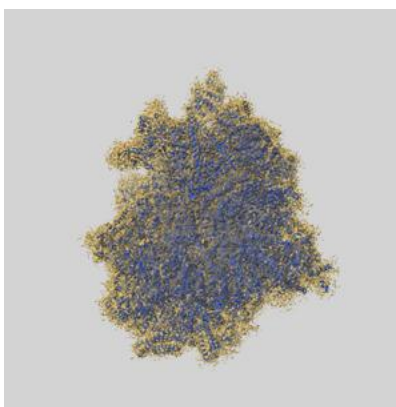
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13660 and PDB model 7PUA. Per-residue inclusion information can be found in section [3](#) on page [28](#).

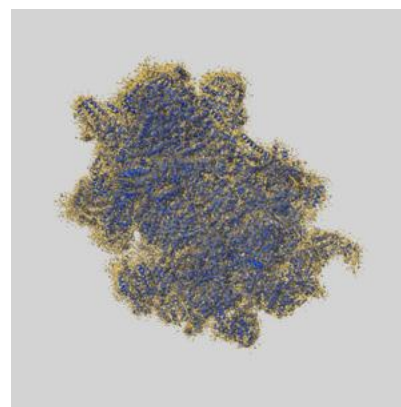
9.1 Map-model overlay [i](#)



X



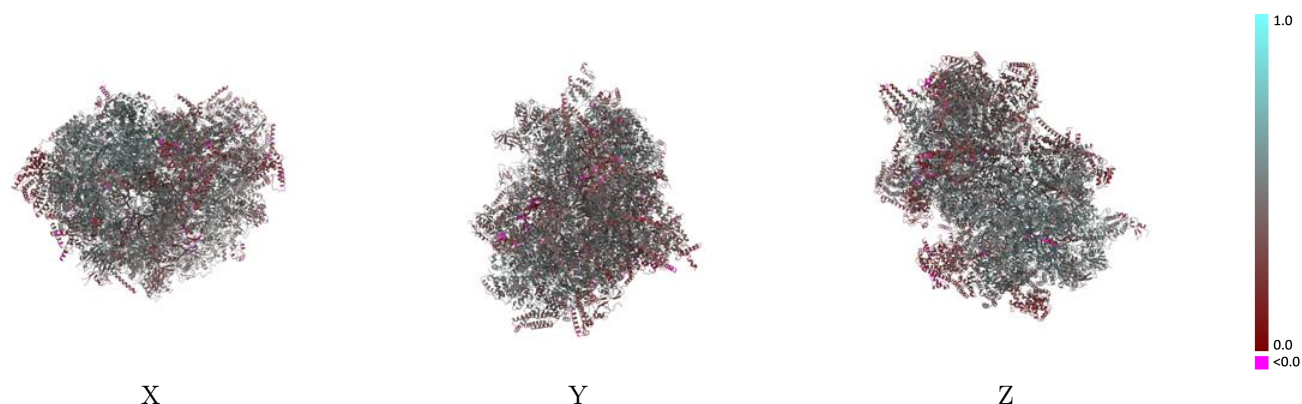
Y



Z

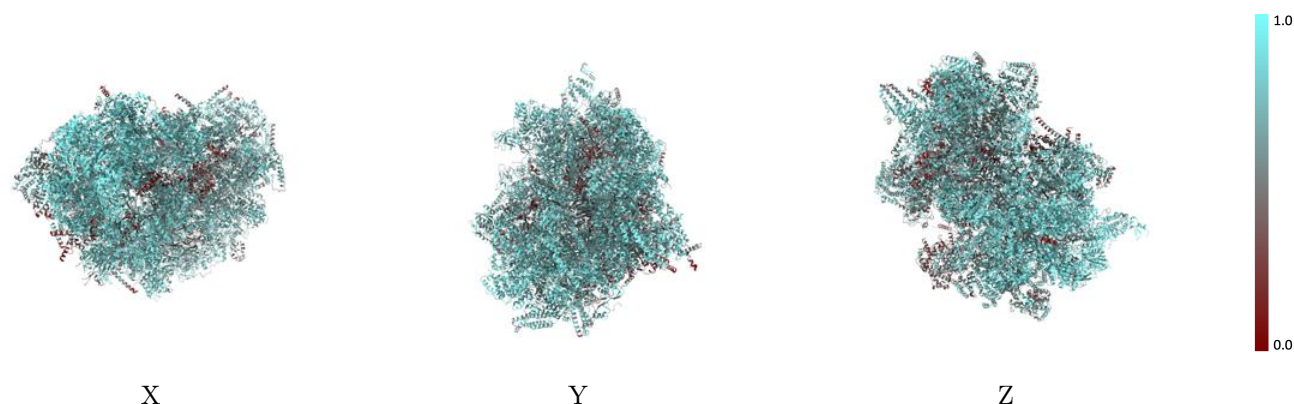
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



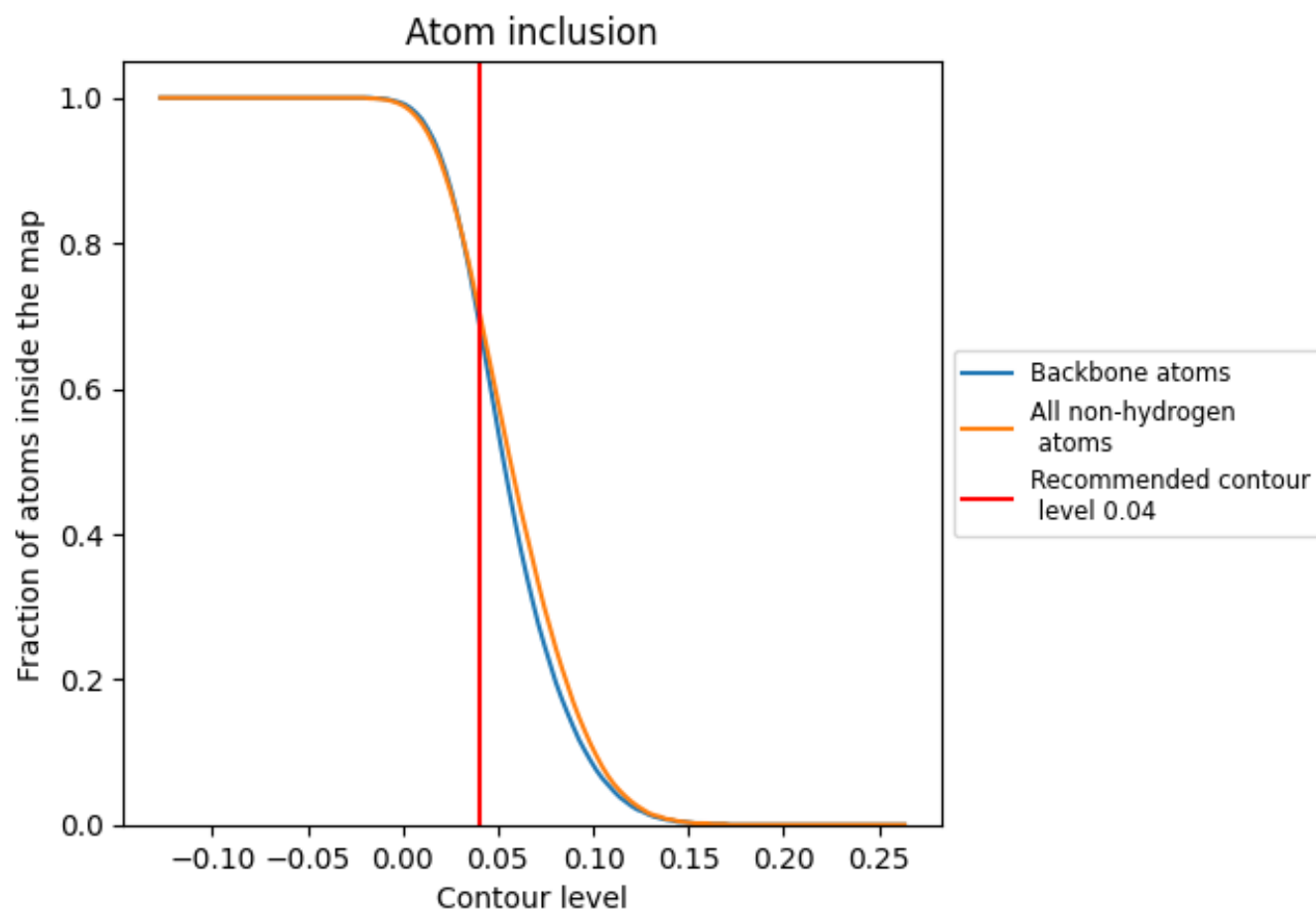
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 71% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7100	 0.4360
CA	 0.6750	 0.3930
CB	 0.7660	 0.5060
CC	 0.5800	 0.4770
CE	 0.7400	 0.4900
CF	 0.6810	 0.3790
CH	 0.7930	 0.5280
CI	 0.7290	 0.4640
CJ	 0.7620	 0.4680
CK	 0.7270	 0.4190
CL	 0.6900	 0.4860
CN	 0.7470	 0.4770
CO	 0.7800	 0.4940
CP	 0.8410	 0.5330
CQ	 0.8140	 0.5310
CR	 0.4710	 0.2810
CS	 0.6920	 0.4050
CU	 0.1400	 0.2270
Ca	 0.7750	 0.4990
Cb	 0.5580	 0.3210
Cd	 0.7460	 0.4670
Cg	 0.8240	 0.4850
Ci	 0.7470	 0.4780
Cj	 0.8650	 0.5050
Ck	 0.7320	 0.4280
Cm	 0.0530	 0.2130
Cn	 0.4860	 0.3440
Cp	 0.8160	 0.4790
DB	 0.7600	 0.4710
DC	 0.6870	 0.3600
DD	 0.8490	 0.5190
DE	 0.7060	 0.4070
DF	 0.7510	 0.4320
DG	 0.7460	 0.4180
DH	 0.6910	 0.4450



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Chain	Atom inclusion	Q-score
DI	 0.8250	 0.4890
DJ	 0.6850	 0.4120
DK	 0.6660	 0.4120
DL	 0.6510	 0.4720
DO	 0.7120	 0.3850
DP	 0.8560	 0.4490
DR	 0.8660	 0.5010
DT	 0.6990	 0.4590
DU	 0.7470	 0.4740
DV	 0.7800	 0.4910
DW	 0.7600	 0.4650
DX	 0.7890	 0.4570
DY	 0.7750	 0.4850
DZ	 0.6840	 0.4660
Da	 0.7880	 0.5410
F2	 0.8020	 0.4910
F3	 0.7150	 0.4020
F5	 0.5900	 0.3510
F6	 0.4590	 0.2390
F7	 0.7810	 0.4650
F9	 0.6810	 0.4310
FM	 0.7480	 0.4610
FN	 0.6640	 0.3450
FO	 0.8140	 0.4930
FP	 0.8140	 0.4800
FW	 0.8240	 0.4960
FX	 0.8310	 0.4700
FZ	 0.4680	 0.3690
Fb	 0.7530	 0.4010
Fc	 0.7080	 0.3510
Fd	 0.1810	 0.3420
Ff	 0.7490	 0.4420
Fg	 0.7710	 0.4280
Fh	 0.3060	 0.3430
Fi	 0.6850	 0.4200
IA	 0.7420	 0.4340
IB	 0.6230	 0.4120
U8	 0.3930	 0.4110
UC	 0.8440	 0.4780
UD	 0.7080	 0.3490
UF	 0.6110	 0.2410
UG	 0.8530	 0.3110

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Chain	Atom inclusion	Q-score
UI	 0.8000	 0.4160
UK	 0.0750	 0.0870
UM	 0.8000	 0.4530
UN	 0.7000	 0.3720
UP	 0.6000	 0.4030
UQ	 0.7000	 0.3670
Ua	 0.7400	 0.2550
Ug	 0.5460	 0.2760